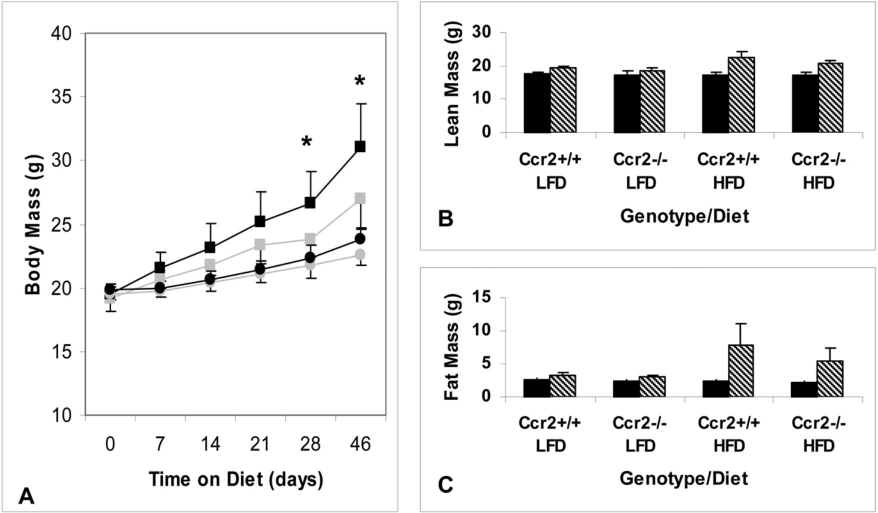

Body Mass (g)
40
35
30
25
20
15
10
*
*
0
7
14
21
28
46
Time on Diet (days)
A
Lean Mass (g)
30
20
10
0
Ccr2+/+ LFD
Ccr2-/- LFD
Ccr2+/+ HFD
Ccr2-/- HFD
Genotype/Diet
B
Fat Mass (g)
15
10
5
0
Ccr2+/+ LFD
Ccr2-/- LFD
Ccr2+/+ HFD
Ccr2-/- HFD
Genotype/Diet
C

**Supplemental Data Table 1. Classes of genes downregulated in adipose tissue from Ccr2 obese mice** An algorithm that identifies predefined functional classes (based on the Gene Ontology (GO) Group gene classification scheme - http://geneontology.org) of co-regulated genes found seventy-one classes of functionally related genes that were significantly down-regulated ($p < 0.001$ corrected for multiple testing) (29) in epididymal adipose tissue of obese *Ccr2-/-* mice when compared to adipose tissue from weight matched *Ccr2+/+* mice. Classes in bold are significantly up-regulated; Underlined classes are metabolism related.

**Supplemental Data Table 2. Classes of genes upregulated in adipose tissue from Ccr2 obese mice** An algorithm that identifies predefined functional classes (based on the Gene Ontology (GO) Group gene classification scheme - http://geneontology.org) of co-regulated genes found fifty-two classes of functionally related genes that were significantly up-regulated ($p < 0.001$ corrected for multiple testing) (29) in epididymal adipose tissue of obese *Ccr2-/-* mice when compared to adipose tissue from weight matched *Ccr2+/+* mice. Classes in bold are significantly up-regulated; Underlined classes are immune/inflammation related.

**Supplemental Data Table 3. Circulating Concentrations of Hormones and Cytokines.** Lean (n = 5) and obese *Ccr2*-/- (n = 10) and *Ccr2*+/+ (n = 15) mice with body mass > 40g were studied. After an eight hour fast, plasma samples were obtained and assayed for a panel of inflammatory biomarkers. * $p < 0.05$ compared to mice of the same genotype on low fat chow, § $p < 0.05$ compared to adiposity matched *Ccr2*+/+ mice. Values are mean ± S.D.

**Supplemental Figure 1. Effects of *Ccr2* genotype on growth and body composition.** A. Eight week old C57BL/6J *Ccr2-/-* and *Ccr2+/+* mice were fed either a high fat (HFD; 60% of calories from fat) or low fat (LFD; 10% of calories from fat) diet for six weeks. Weekly body mass was measured. The body masses of *Ccr2-/-* (gray circles) and *Ccr2+/+* (black circles) mice were not significantly different on a low fat diet. However, the *Ccr2-/-* weighed significantly less than *Ccr2+/+* mice fed a high fat diet; a difference apparent after eating a HFD for four weeks. B. Lean and C. fat mass was determined prior (solid black bars) and at the conclusion (stripped bars) of the six week feeding study. In mice fed a high fat diet lean mass increased modestly whereas there was a greater than 100% increase in fat mass. *Ccr2*-deficiency attenuated gains in both lean and body mass. Values are mean ± S.D. * p-value < 0.05 for body mass difference between *Ccr2-/-* and *Ccr2+/+* fed a high fat diet at indicated time points.

## Supplemental Table 1
## Classes of genes downregulated in adipose tissue from *Ccr2* obese mice

| | Class Name | Class ID | Class size | Effective Class Size | Raw Score | p-value | Corrected p-value |
|---|---|---|---|---|---|---|---|
| 1 | double-stranded DNA binding | GO:0003690 | 203 | 98 | 1.05549412 | 0 | 0 |
| 2 | MHC class II receptor activity | GO:0045012 | 19 | 8 | 2.29261505 | 0 | 0 |
| 3 | positive regulation of protein metabolism | GO:0051247 | 95 | 59 | 1.02396173 | 0 | 0 |
| 4 | transmembrane receptor protein tyrosine kinase docking protein activity | GO:0005069 | 157 | 68 | 1.09745802 | 0 | 0 |
| 5 | positive regulation of lymphocyte activation | GO:0051251 | 98 | 49 | 1.16547788 | 0 | 0 |
| 6 | antigen presentation, exogenous antigen via MHC class II | GO:0042591 | 25 | 10 | 2.18500688 | 0 | 0 |
| 7 | chromosome segregation | GO:0007059 | 112 | 43 | 1.07873507 | 0 | 0 |
| 8 | B-cell activation | GO:0042113 | 112 | 60 | 1.09468558 | 0 | 0 |
| 9 | cell projection organization and biogenesis | GO:0030030 | 97 | 40 | 1.26598752 | 0 | 0 |
| 10 | cytokine binding | GO:0019955 | 164 | 100 | 0.95663938 | 0 | 0 |
| 11 | regulation of lymphocyte differentiation | GO:0045619 | 57 | 28 | 1.23611286 | 0 | 0 |
| 12 | T-cell differentiation | GO:0030217 | 82 | 38 | 1.17047494 | 0 | 0 |
| 13 | lymphocyte differentiation | GO:0030098 | 143 | 74 | 1.06957288 | 0 | 0 |
| 14 | antigen presentation, exogenous antigen | GO:0019884 | 37 | 16 | 1.83830671 | 0 | 0 |
| 15 | positive regulation of cell activation | GO:0050867 | 99 | 50 | 1.16310071 | 0 | 0 |
| 16 | non-membrane spanning protein tyrosine kinase activity | GO:0004715 | 46 | 19 | 1.37448732 | 0 | 0 |
| 17 | SH3/SH2 adaptor protein activity | GO:0005070 | 154 | 66 | 1.09222083 | 0 | 0 |
| 18 | regulation of lymphocyte activation | GO:0051249 | 128 | 69 | 1.11055088 | 0 | 0 |
| 19 | DNA recombination | GO:0006310 | 190 | 87 | 0.95693144 | 0 | 0 |
| 20 | positive regulation of organismal physiological process | GO:0051240 | 162 | 89 | 1.04078907 | 0 | 0 |
| 21 | antimicrobial humoral response (sensu Vertebrata) | GO:0019735 | 168 | 88 | 1.05015095 | 0 | 0 |
| 22 | transmembrane receptor protein tyrosine kinase signaling protein activity | GO:0005066 | 181 | 79 | 1.04724864 | 0 | 0 |
| 23 | hematopoietin/interferon-class (D200-domain) cytokine receptor activity | GO:0004896 | 166 | 90 | 0.96483961 | 0 | 0 |
| 24 | regulation of cytokine biosynthesis | GO:0042035 | 69 | 46 | 1.05131343 | 0 | 0 |
| 25 | regulation of cell activation | GO:0050865 | 130 | 71 | 1.10288414 | 0 | 0 |
| 26 | regulation of T-cell differentiation | GO:0045580 | 49 | 23 | 1.36494579 | 0 | 0 |
| 27 | antimicrobial humoral response | GO:0019730 | 171 | 91 | 1.04652841 | 0 | 0 |
| 28 | positive regulation of immune response | GO:0050778 | 147 | 79 | 1.1155588 | 0 | 0 |
| 29 | T-cell activation | GO:0042110 | 175 | 92 | 0.98726983 | 0 | 0 |
| 30 | lysosomal membrane | GO:0005765 | 40 | 18 | 1.36709551 | 0 | 0 |
| 31 | positive regulation of T-cell activation | GO:0050870 | 71 | 34 | 1.17436874 | 0 | 0 |
| 32 | humoral defense mechanism (sensu Protostomia) | GO:0016065 | 38 | 16 | 1.43478824 | 0 | 0 |
| 33 | DNA-dependent DNA replication | GO:0006261 | 188 | 84 | 0.9893001 | 0 | 0 |
| 34 | regulation of T-cell activation | GO:0050863 | 86 | 45 | 1.11871479 | 0 | 0 |
| 35 | macrophage activation | GO:0042116 | 17 | 11 | 1.61443838 | 0 | 0 |
| 36 | lamellipodium | GO:0030027 | 148 | 54 | 1.10218009 | 0 | 0 |
| 37 | cytokine production | GO:0001816 | 95 | 62 | 1.02887506 | 0 | 0 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| **38** | **lamellipodium biogenesis** | **GO:0030032** | **43** | **19** | **1.30535144** | **0** | **0** |
| **39** | **cytokine metabolism** | **GO:0042107** | **78** | **52** | **1.02884514** | **0** | **0** |
| **40** | **antigen processing, exogenous antigen via MHC class II** | **GO:0019886** | **25** | **12** | **1.97446991** | **0** | **0** |
| **41** | **peptidyl-amino acid modification** | **GO:0018193** | **183** | **82** | **0.94758368** | **0** | **0** |
| **42** | **immunological synapse** | **GO:0001772** | **56** | **29** | **1.16544032** | **0.00001** | **0.000475** |
| **43** | **regulation of gene expression, epigenetic** | **GO:0040029** | **234** | **97** | **0.9192906** | **0.00001** | **0.00046395** |
| **44** | **cellular defense response (sensu Vertebrata)** | **GO:0016066** | **83** | **50** | **1.03419756** | **0.00001** | **0.00045341** |
| **45** | **immune cell migration** | **GO:0050900** | **93** | **47** | **1.0482441** | **0.00001** | **0.00044333** |
| **46** | **detection of pest, pathogen or parasite** | **GO:0009596** | **17** | **10** | **1.80468208** | **0.00001** | **0.0004337** |
| **47** | **antigen presentation** | **GO:0019882** | **80** | **40** | **1.05240133** | **0.00001** | **0.00042447** |
| **48** | **endosome transport** | **GO:0016197** | **150** | **61** | **1.00583493** | **0.00001** | **0.00041563** |
| **49** | **phagocytosis** | **GO:0006909** | **77** | **38** | **1.08789932** | **0.00001** | **0.00040714** |
| **50** | **peptidyl-tyrosine modification** | **GO:0018212** | **135** | **59** | **0.97402995** | **0.00001** | **0.000399** |
| **51** | **late endosome** | **GO:0005770** | **53** | **24** | **1.19906805** | **0.00001** | **0.00039118** |
| **52** | **endosome organization and biogenesis** | **GO:0007032** | **171** | **69** | **0.96882659** | **0.00001** | **0.00038365** |
| **53** | **MHC protein complex** | **GO:0042611** | **18** | **8** | **1.87643538** | **0.00001** | **0.00037642** |
| **54** | **spliceosome complex** | **GO:0005681** | **163** | **69** | **0.9417044** | **0.00002** | **0.00073889** |
| **55** | **myeloid blood cell differentiation** | **GO:0030099** | **138** | **83** | **0.9190809** | **0.00002** | **0.00072545** |
| **56** | **casein kinase activity** | **GO:0004680** | **248** | **94** | **0.89626184** | **0.00002** | **0.0007125** |
| **57** | **nuclear chromosome** | **GO:0000228** | **194** | **89** | **0.90000464** | **0.00002** | **0.0007** |
| **58** | **lymphocyte proliferation** | **GO:0046651** | **116** | **66** | **0.96211562** | **0.00002** | **0.00068793** |
| **59** | **regulation of I-kappaB kinase/NF-kappaB cascade** | **GO:0043122** | **171** | **83** | **0.90961293** | **0.00002** | **0.00067627** |
| **60** | **peptidyl-tyrosine phosphorylation** | **GO:0018108** | **133** | **57** | **0.98310712** | **0.00002** | **0.000665** |
| **61** | **regulation of DNA metabolism** | **GO:0051052** | **86** | **38** | **1.0508178** | **0.00003** | **0.00098115** |
| **62** | **pore complex** | **GO:0046930** | **121** | **45** | **1.02202032** | **0.00003** | **0.00096532** |
| **63** | **G1/S transition of mitotic cell cycle** | **GO:0000082** | **193** | **78** | **0.92318731** | **0.00003** | **0.00095** |
| **64** | **actin polymerization and/or depolymerization** | **GO:0008154** | **104** | **39** | **1.109908** | **0.00003** | **0.00093516** |
| **65** | **positive regulation of cytokine biosynthesis** | **GO:0042108** | **49** | **33** | **1.07726365** | **0.00003** | **0.00092077** |
| **66** | **immune cell chemotaxis** | **GO:0030595** | **82** | **40** | **1.04705729** | **0.00003** | **0.00090682** |
| **67** | **positive regulation of lymphocyte differentiation** | **GO:0045621** | **44** | **19** | **1.28893539** | **0.00003** | **0.00089328** |
| **68** | **cell-mediated immune response** | **GO:0042087** | **64** | **41** | **1.02655264** | **0.00003** | **0.00088015** |
| **69** | **positive regulation of protein biosynthesis** | **GO:0045727** | **57** | **39** | **1.10367317** | **0.00003** | **0.00086739** |
| **70** | **monocyte differentiation** | **GO:0030224** | **67** | **40** | **1.03796467** | **0.00003** | **0.000855** |
| **71** | **phagocytosis, engulfment** | **GO:0006911** | **34** | **15** | **1.34546127** | **0.00003** | **0.00084296** |
| 72 | regulation of cytokine production | GO:0001817 | 74 | 49 | 1.0125992 | 0.00004 | 0.00110833 |
| 73 | positive regulation of signal transduction | GO:0009967 | 207 | 96 | 0.88213432 | 0.00004 | 0.00109315 |
| 74 | specific RNA polymerase II transcription factor activity | GO:0003704 | 133 | 64 | 0.95515861 | 0.00004 | 0.00107838 |
| 75 | protein tyrosine phosphatase activity | GO:0004725 | 182 | 79 | 0.89909531 | 0.00004 | 0.001064 |
| 76 | pre-mRNA splicing factor activity | GO:0008248 | 190 | 75 | 0.91905977 | 0.00004 | 0.00105 |
| 77 | spindle | GO:0005819 | 220 | 92 | 0.89111112 | 0.00004 | 0.00103636 |
| 78 | cell cycle regulator | GO:0003750 | 95 | 39 | 1.04777334 | 0.00004 | 0.00102308 |
| 79 | regulation of cell shape | GO:0008360 | 122 | 51 | 0.98753437 | 0.00005 | 0.00126266 |
| 80 | positive regulation of T-cell differentiation | GO:0045582 | 42 | 18 | 1.25632571 | 0.00005 | 0.00124688 |
| 81 | protein kinase CK2 activity | GO:0004682 | 223 | 86 | 0.89490032 | 0.00005 | 0.00123148 |
| 82 | regulation of lymphocyte proliferation | GO:0050670 | 67 | 37 | 1.07543516 | 0.00005 | 0.00121646 |
| 83 | bone remodeling | GO:0046849 | 193 | 95 | 0.87179918 | 0.00005 | 0.00120181 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 84 | positive regulation of cytokine production | GO:0001819 | 51 | 35 | 1.05852176 | 0.00006 | 0.001425 |
| 85 | cell cycle checkpoint | GO:0000075 | 115 | 53 | 0.99322542 | 0.00006 | 0.00140824 |
| 86 | interleukin receptor activity | GO:0004907 | 91 | 54 | 0.98751176 | 0.00007 | 0.00162384 |
| 87 | antigen processing | GO:0030333 | 77 | 41 | 1.00169401 | 0.00007 | 0.00160517 |
| 88 | mast cell activation | GO:0045576 | 21 | 10 | 1.56936768 | 0.00007 | 0.00158693 |
| 89 | Rac protein signal transduction | GO:0016601 | 45 | 17 | 1.29201605 | 0.00007 | 0.0015691 |
| 90 | regulation of myeloid blood cell differentiation | GO:0045637 | 62 | 35 | 1.04911429 | 0.00007 | 0.00155167 |
| 91 | tubulin binding | GO:0015631 | 159 | 54 | 0.97860425 | 0.00007 | 0.00153462 |
| 92 | UDP-glycosyltransferase activity | GO:0008194 | 206 | 90 | 0.88146116 | 0.00008 | 0.00173478 |
| 93 | interleukin-6 biosynthesis | GO:0042226 | 19 | 11 | 1.4590123 | 0.00008 | 0.00171613 |
| 94 | positive regulation of biosynthesis | GO:0009891 | 78 | 49 | 0.99327609 | 0.00008 | 0.00169787 |
| 95 | regulation of B-cell activation | GO:0050864 | 56 | 29 | 1.08775802 | 0.00008 | 0.00168 |
| 96 | Golgi vesicle | GO:0005798 | 70 | 29 | 1.09193594 | 0.00008 | 0.0016625 |
| 97 | sphingolipid metabolism | GO:0006665 | 114 | 56 | 0.94005233 | 0.00009 | 0.00185103 |
| 98 | interleukin binding | GO:0019965 | 95 | 57 | 0.94392268 | 0.00009 | 0.00183214 |
| 99 | lectin | GO:0005530 | 61 | 36 | 1.05591521 | 0.00009 | 0.00181364 |
| 100 | negative regulation of organismal physiological process | GO:0051241 | 52 | 35 | 1.03990482 | 0.00009 | 0.0017955 |
| 101 | positive regulation of interleukin-6 biosynthesis | GO:0045410 | 14 | 9 | 1.53330663 | 0.00009 | 0.00177772 |
| 102 | DNA modification | GO:0006304 | 137 | 59 | 0.94866033 | 0.00009 | 0.00176029 |
| 103 | receptor complex | GO:0043235 | 175 | 83 | 0.88364934 | 0.00009 | 0.0017432 |
| 104 | viral nucleocapsid | GO:0019013 | 98 | 37 | 1.03953872 | 0.0001 | 0.00191827 |
| 105 | positive regulation of tumor necrosis factor-alpha biosynthesis | GO:0042535 | 14 | 11 | 1.45098056 | 0.0001 | 0.0019 |
| 106 | B-cell proliferation | GO:0042100 | 42 | 21 | 1.19462533 | 0.0001 | 0.00188208 |
| 107 | JNK cascade | GO:0007254 | 203 | 84 | 0.87493689 | 0.0001 | 0.00186449 |
| 108 | ruffles | GO:0001726 | 39 | 16 | 1.27560986 | 0.00011 | 0.00203194 |
| 109 | detection of biotic stimulus | GO:0009595 | 27 | 18 | 1.23164653 | 0.00011 | 0.0020133 |
| 110 | DNA methylation | GO:0006306 | 121 | 50 | 0.96422818 | 0.00012 | 0.00217636 |
| 111 | RNA helicase activity | GO:0003724 | 76 | 35 | 1.0293853 | 0.00012 | 0.00215676 |
| 112 | glycerophospholipid metabolism | GO:0006650 | 125 | 47 | 0.97013005 | 0.00013 | 0.00231563 |
| 113 | B-cell differentiation | GO:0030183 | 54 | 29 | 1.0803313 | 0.00013 | 0.00229513 |
| 114 | T-helper 1 type immune response | GO:0042088 | 55 | 37 | 1.02401473 | 0.00014 | 0.00245 |
| 115 | actin filament polymerization | GO:0030041 | 67 | 26 | 1.11415307 | 0.00014 | 0.0024287 |
| 116 | actin filament-based movement | GO:0030048 | 74 | 33 | 1.05555644 | 0.00014 | 0.00240776 |
| 117 | N-linked glycosylation | GO:0006487 | 84 | 46 | 0.9636041 | 0.00015 | 0.00255769 |
| 118 | double-stranded RNA binding | GO:0003725 | 93 | 38 | 1.0142502 | 0.00015 | 0.00253602 |
| 119 | positive regulation of I-kappaB kinase/NF-kappaB cascade | GO:0043123 | 165 | 80 | 0.89866646 | 0.00015 | 0.00251471 |
| 120 | receptor signaling protein serine/threonine kinase activity | GO:0004702 | 141 | 56 | 0.93847379 | 0.00016 | 0.00266 |
| 121 | profilin binding | GO:0005522 | 31 | 9 | 1.4882412 | 0.00018 | 0.00296777 |
| 122 | positive regulation of B-cell activation | GO:0050871 | 38 | 19 | 1.19224641 | 0.00018 | 0.00294344 |
| 123 | osteoclast differentiation | GO:0030316 | 46 | 26 | 1.10252999 | 0.0002 | 0.0032439 |
| 124 | cyclic nucleotide-dependent protein kinase activity | GO:0004690 | 207 | 82 | 0.86258077 | 0.00022 | 0.00353952 |
| 125 | spliceosome assembly | GO:0000245 | 107 | 30 | 1.04123464 | 0.00022 | 0.0035112 |
| 126 | regulation of osteoclast differentiation | GO:0045670 | 40 | 23 | 1.13647309 | 0.00022 | 0.00348333 |
| 127 | receptor mediated endocytosis | GO:0006898 | 115 | 47 | 0.957723 | 0.00022 | 0.00345591 |
| 128 | Rac GTPase activator activity | GO:0030675 | 23 | 8 | 1.52267842 | 0.00022 | 0.00342891 |
| 129 | prenylated protein tyrosine phosphatase activity | GO:0004727 | 94 | 37 | 1.01036771 | 0.00022 | 0.00340233 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 130 | meiosis | GO:0007126 | 204 | 94 | 0.85043364 | 0.00023 | 0.00352962 |
| 131 | replication fork | GO:0005657 | 46 | 21 | 1.14984459 | 0.00024 | 0.00365496 |
| 132 | DNA-dependent ATPase activity | GO:0008094 | 73 | 34 | 1.04620761 | 0.00026 | 0.00392955 |
| 133 | neutrophil chemotaxis | GO:0030593 | 45 | 19 | 1.17929265 | 0.00026 | 0.0039 |
| 134 | kinetochore | GO:0000776 | 63 | 25 | 1.09998182 | 0.00027 | 0.00401978 |
| 135 | T-cell selection | GO:0045058 | 28 | 14 | 1.27454569 | 0.00028 | 0.00413778 |
| 136 | tumor suppressor | GO:0008181 | 92 | 39 | 0.99543252 | 0.00028 | 0.00410735 |
| 137 | sphingoid metabolism | GO:0046519 | 64 | 32 | 1.02459057 | 0.00031 | 0.00451423 |
| 138 | mRNA splice site selection | GO:0006376 | 79 | 19 | 1.16705703 | 0.00031 | 0.00448152 |
| 139 | SH3 domain binding | GO:0017124 | 66 | 23 | 1.12378698 | 0.00032 | 0.00459281 |
| 140 | cAMP-dependent protein kinase activity | GO:0004691 | 201 | 81 | 0.86161049 | 0.00032 | 0.00456 |
| 141 | negative regulation of cell activation | GO:0050866 | 29 | 20 | 1.14212388 | 0.00032 | 0.00452766 |
| 142 | epidermal growth factor receptor signaling pathway | GO:0007173 | 69 | 31 | 1.04062891 | 0.00033 | 0.00463627 |
| 143 | protein polymerization | GO:0051258 | 109 | 45 | 0.95565165 | 0.00033 | 0.00460385 |
| 144 | thymic T-cell selection | GO:0045061 | 25 | 12 | 1.32668303 | 0.00034 | 0.00471042 |
| 145 | chromosome, pericentric region | GO:0000775 | 111 | 47 | 0.94200371 | 0.00037 | 0.00509069 |
| 146 | virion | GO:0019012 | 141 | 59 | 0.90433175 | 0.00039 | 0.00532911 |
| 147 | actin filament organization | GO:0007015 | 149 | 68 | 0.88237133 | 0.00042 | 0.0057 |
| 148 | mannosidase activity | GO:0015923 | 21 | 11 | 1.34642991 | 0.00047 | 0.00633547 |
| 149 | replisome | GO:0030894 | 43 | 19 | 1.14962074 | 0.0005 | 0.00669463 |
| 150 | viral capsid | GO:0019028 | 123 | 50 | 0.9165313 | 0.00052 | 0.006916 |
| 151 | interleukin-12 biosynthesis | GO:0042090 | 17 | 12 | 1.31243171 | 0.00053 | 0.00700232 |
| 152 | ossification | GO:0001503 | 175 | 85 | 0.84260435 | 0.00056 | 0.00735 |
| 153 | activation of JNK | GO:0007257 | 56 | 23 | 1.09139181 | 0.00059 | 0.00769314 |
| 154 | regulation of B-cell proliferation | GO:0030888 | 32 | 14 | 1.22888965 | 0.00059 | 0.00764318 |
| 155 | activation of NF-kappaB-inducing kinase | GO:0007250 | 25 | 14 | 1.234123 | 0.00059 | 0.00759387 |
| 156 | interleukin-1, Type I, activating binding | GO:0019967 | 18 | 11 | 1.3435299 | 0.0006 | 0.00767308 |
| 157 | nucleocytoplasmic transporter activity | GO:0005487 | 38 | 12 | 1.28639037 | 0.00064 | 0.00813248 |
| 158 | trans-Golgi network transport vesicle | GO:0030140 | 56 | 21 | 1.09825939 | 0.00064 | 0.00808101 |
| 159 | hydrolase activity, hydrolyzing O-glycosyl compounds | GO:0004553 | 189 | 96 | 0.83075024 | 0.00067 | 0.0084066 |
| 160 | T-cell proliferation | GO:0042098 | 80 | 47 | 0.92325489 | 0.00067 | 0.00835406 |
| 161 | heterogeneous nuclear ribonucleoprotein complex | GO:0030530 | 50 | 16 | 1.18331583 | 0.00068 | 0.00842609 |
| 162 | acetylgalactosaminyltransferase activity | GO:0008376 | 46 | 20 | 1.10709061 | 0.0007 | 0.00862037 |
| 163 | negative regulation of lymphocyte activation | GO:0051250 | 28 | 19 | 1.13331307 | 0.0007 | 0.00856748 |
| 164 | regulation of monocyte differentiation | GO:0045655 | 46 | 28 | 1.02078387 | 0.00071 | 0.00863689 |
| 165 | growth factor binding | GO:0019838 | 154 | 68 | 0.87029183 | 0.00072 | 0.00870545 |
| 166 | cell adhesion molecule binding | GO:0050839 | 37 | 13 | 1.26103661 | 0.00073 | 0.00877319 |
| 167 | lymph gland development | GO:0007515 | 47 | 24 | 1.05100365 | 0.00074 | 0.00884012 |
| 168 | negative regulation of immune response | GO:0050777 | 36 | 26 | 1.03747662 | 0.00075 | 0.00890625 |
| 169 | barbed-end actin filament capping | GO:0051016 | 28 | 10 | 1.35051557 | 0.0008 | 0.00944379 |
| 170 | intracellular transporter activity | GO:0005478 | 96 | 34 | 0.97924504 | 0.00082 | 0.00962294 |
| 171 | DNA replication initiation | GO:0006270 | 54 | 22 | 1.07555988 | 0.00084 | 0.0098 |
| 172 | nuclear matrix | GO:0016363 | 45 | 17 | 1.15318823 | 0.00085 | 0.00985901 |
| 173 | regulation of cell organization and biogenesis | GO:0051128 | 87 | 33 | 0.98019335 | 0.00087 | 0.01003266 |
| 174 | negative regulation of lymphocyte proliferation | GO:0050672 | 22 | 14 | 1.19692088 | 0.00088 | 0.01008966 |
| 175 | olfactory receptor activity | GO:0004984 | 124 | 92 | 0.82164583 | 0.00089 | 0.010146 |

Supplemental Table 1

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|---|---|---|---|---|---|---|---|---|
| | 176 | heavy metal ion transport | GO:0006823 | 23 | 11 | 1.29656386 | 0.00091 | 0.01031506 |
| | 177 | hindbrain development | GO:0030902 | 29 | 9 | 1.34449994 | 0.00097 | 0.01093305 |
| | 178 | diacylglycerol binding | GO:0019992 | 107 | 47 | 0.91287364 | 0.00101 | 0.01131994 |
| | 179 | condensed chromosome | GO:0000793 | 103 | 47 | 0.91353759 | 0.00101 | 0.0112567 |
| | 180 | synaptic vesicle transport | GO:0048489 | 121 | 47 | 0.91848436 | 0.00101 | 0.01119417 |
| | 181 | phospholipid transporter activity | GO:0005548 | 68 | 24 | 1.02924348 | 0.00109 | 0.01201409 |
| | 182 | clathrin coat of trans-Golgi network vesicle | GO:0030130 | 40 | 15 | 1.17373873 | 0.00111 | 0.01216731 |
| | 183 | neurotransmitter secretion | GO:0007269 | 196 | 76 | 0.84733494 | 0.00114 | 0.01242787 |
| | 184 | synaptic vesicle | GO:0008021 | 167 | 81 | 0.83331516 | 0.00117 | 0.0126856 |
| | 185 | mesoderm development | GO:0007498 | 131 | 60 | 0.87808588 | 0.0012 | 0.01294054 |
| | 186 | positive regulation of transcription from Pol II promoter | GO:0045944 | 215 | 89 | 0.82441413 | 0.0013 | 0.01394355 |
| | 187 | transmembrane receptor protein serine/threonine kinase | GO:0007178 | 199 | 89 | 0.82941818 | 0.0013 | 0.01386898 |
| | 188 | regulation of translation | GO:0006445 | 237 | 90 | 0.82230971 | 0.00132 | 0.01400745 |
| | 189 | positive regulation of lymphocyte proliferation | GO:0050671 | 46 | 24 | 1.02252823 | 0.00133 | 0.01403889 |
| | 190 | vesicle membrane | GO:0012506 | 118 | 50 | 0.89628864 | 0.00133 | 0.013965 |
| | 191 | Rho GTPase activator activity | GO:0005100 | 46 | 18 | 1.09905925 | 0.0014 | 0.01462304 |
| | 192 | ceramide metabolism | GO:0006672 | 58 | 29 | 0.99147037 | 0.0014 | 0.01454688 |
| | 193 | regulation of adenylate cyclase activity | GO:0045761 | 122 | 59 | 0.87127722 | 0.00141 | 0.01457487 |
| | 194 | bacterial binding | GO:0008367 | 9 | 8 | 1.37877281 | 0.00146 | 0.01501392 |
| | 195 | heterochromatin | GO:0000792 | 83 | 22 | 1.03824934 | 0.0015 | 0.01534615 |
| | 196 | sterol transporter activity | GO:0015248 | 23 | 11 | 1.25508603 | 0.00156 | 0.01587857 |
| | 197 | positive regulation of interleukin-12 biosynthesis | GO:0045084 | 16 | 11 | 1.26355265 | 0.00156 | 0.01579797 |
| | 198 | proteoglycan | GO:0005203 | 26 | 8 | 1.37248701 | 0.00157 | 0.01581894 |
| | 199 | antigen presentation, peptide antigen | GO:0048002 | 34 | 15 | 1.14964039 | 0.00158 | 0.0158397 |
| | 200 | B-cell homeostasis | GO:0001782 | 24 | 9 | 1.31133696 | 0.00164 | 0.016359 |
| ! | | transport vesicle | GO:0030133 | 64 | 27 | 1.00429628 | 0.00166 | 0.01647612 |
| ! | | histone acetyltransferase activity | GO:0004402 | 28 | 12 | 1.21707952 | 0.00169 | 0.01669084 |
| ! | | F-actin capping activity | GO:0003782 | 33 | 11 | 1.25071244 | 0.00169 | 0.01660862 |
| ! | | polypeptide N-acetylgalactosaminyltransferase activity | GO:0004653 | 27 | 12 | 1.21678118 | 0.00169 | 0.01652721 |
| ! | | di-, tri-valent inorganic cation transporter activity | GO:0015082 | 80 | 35 | 0.94780209 | 0.00172 | 0.01673854 |
| ! | | spindle pole | GO:0000922 | 148 | 64 | 0.85505003 | 0.00177 | 0.0171415 |
| ! | | pathogenesis | GO:0009405 | 184 | 81 | 0.822599 | 0.00179 | 0.01725145 |
| ! | | external side of plasma membrane | GO:0009897 | 146 | 82 | 0.82196848 | 0.0018 | 0.01726442 |
| ! | | cytokine and chemokine mediated signaling pathway | GO:0019221 | 73 | 42 | 0.91526202 | 0.00197 | 0.01880455 |
| ! | | neuronal cell projection | GO:0043005 | 127 | 59 | 0.86489946 | 0.00197 | 0.018715 |
| ! | | negative regulation of osteoclast differentiation | GO:0045671 | 31 | 18 | 1.08361488 | 0.002 | 0.01890995 |
| ! | | clathrin binding | GO:0030276 | 31 | 11 | 1.23642224 | 0.002 | 0.01882075 |
| ! | | phosphoinositide 3-kinase complex | GO:0005942 | 28 | 12 | 1.20498201 | 0.00203 | 0.01901338 |
| ! | | heart development | GO:0007507 | 205 | 89 | 0.81080407 | 0.00208 | 0.01939065 |
| ! | | endocytic vesicle | GO:0030139 | 73 | 30 | 0.96081507 | 0.00208 | 0.01930047 |
| ! | | synaptic vesicle membrane | GO:0030672 | 52 | 21 | 1.04074454 | 0.00209 | 0.01930347 |
| ! | | ATP-dependent RNA helicase activity | GO:0004004 | 52 | 24 | 0.99863653 | 0.0021 | 0.01930645 |
| ! | | negative regulation of cell differentiation | GO:0045596 | 96 | 51 | 0.88707658 | 0.00211 | 0.0193094 |
| ! | | phospholipid binding | GO:0005543 | 205 | 85 | 0.81518649 | 0.00218 | 0.0198589 |
| ! | | clathrin coat | GO:0030118 | 94 | 40 | 0.91852043 | 0.0022 | 0.01995 |
| ! | | hydrogen:potassium-exchanging ATPase activity | GO:0008900 | 15 | 8 | 1.33439394 | 0.00226 | 0.02040136 |

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|---|---|---|---|---|---|---|---|
| ! | positive regulation of cytosolic calcium ion concentration | GO:0007204 | 119 | 71 | 0.83710074 | 0.00247 | 0.02219662 |
| ! | activation of MAPK | GO:0000187 | 156 | 78 | 0.82471567 | 0.0025 | 0.02236547 |
| ! | lipid transporter activity | GO:0005319 | 190 | 84 | 0.81279689 | 0.00251 | 0.02235469 |
| ! | DNA helicase activity | GO:0003678 | 68 | 28 | 0.97240573 | 0.00253 | 0.02243267 |
| ! | autophosphorylation | GO:0046777 | 50 | 20 | 1.04188548 | 0.0026 | 0.02295133 |
| ! | nuclear chromatin | GO:0000790 | 78 | 20 | 1.04610349 | 0.0026 | 0.02285022 |
| ! | nuclear heterochromatin | GO:0005720 | 67 | 16 | 1.09069372 | 0.00267 | 0.0233625 |
| ! | prostaglandin receptor activity | GO:0004955 | 16 | 8 | 1.32335719 | 0.00271 | 0.02360895 |
| ! | exonuclease activity | GO:0004527 | 114 | 54 | 0.86142757 | 0.00277 | 0.02402674 |
| ! | telomerase-dependent telomere maintenance | GO:0007004 | 43 | 18 | 1.05785364 | 0.00279 | 0.02409545 |
| ! | positive regulation of cell differentiation | GO:0045597 | 120 | 53 | 0.86399543 | 0.00293 | 0.02519547 |
| ! | regulation of actin filament length | GO:0030832 | 66 | 27 | 0.97006987 | 0.00301 | 0.02577232 |
| ! | rRNA processing | GO:0006364 | 116 | 62 | 0.84394538 | 0.00305 | 0.02600321 |
| ! | cytokinesis | GO:0007104 | 166 | 68 | 0.83522725 | 0.00306 | 0.02597745 |
| ! | acetylglucosaminyltransferase activity | GO:0008375 | 61 | 28 | 0.95980047 | 0.00311 | 0.02629004 |
| ! | Ras protein signal transduction | GO:0007265 | 135 | 66 | 0.83540685 | 0.00321 | 0.02702089 |
| ! | positive regulation of endocytosis | GO:0045807 | 38 | 19 | 1.04615569 | 0.00322 | 0.02699118 |
| ! | guanylate kinase activity | GO:0004385 | 50 | 17 | 1.06723448 | 0.00323 | 0.02696172 |
| ! | regulation of bone remodeling | GO:0046850 | 56 | 29 | 0.95578057 | 0.00324 | 0.0269325 |
| ! | proteoglycan metabolism | GO:0006029 | 51 | 29 | 0.9551009 | 0.00324 | 0.02682075 |
| ! | transforming growth factor beta receptor signaling pathway | GO:0007179 | 174 | 79 | 0.81944777 | 0.00325 | 0.02679236 |
| ! | positive regulation of T-cell proliferation | GO:0042102 | 29 | 16 | 1.08216716 | 0.00331 | 0.02717469 |
| ! | chaperone cofactor dependent protein folding | GO:0051085 | 40 | 16 | 1.07956319 | 0.00331 | 0.02706332 |
| ! | chromatin | GO:0005717 | 76 | 22 | 0.99986136 | 0.00335 | 0.02727857 |
| ! | post-Golgi transport | GO:0006892 | 92 | 35 | 0.91054354 | 0.00347 | 0.02814085 |
| ! | phosphoinositide metabolism | GO:0030384 | 83 | 34 | 0.92530756 | 0.00349 | 0.02818846 |
| ! | RNA polymerase III transcription factor activity | GO:0003709 | 58 | 34 | 0.92548442 | 0.00349 | 0.0280748 |
| ! | translational initiation | GO:0006413 | 166 | 61 | 0.84759678 | 0.0035 | 0.02804217 |
| ! | positive regulation of transcription factor activity | GO:0051091 | 19 | 8 | 1.2877512 | 0.00358 | 0.0285684 |
| ! | cell maturation | GO:0048469 | 104 | 47 | 0.87806906 | 0.00364 | 0.02893147 |
| ! | regulation of T-cell proliferation | GO:0042129 | 39 | 23 | 0.99672694 | 0.00377 | 0.02984583 |
| ! | icosanoid receptor activity | GO:0004953 | 17 | 9 | 1.24234057 | 0.00379 | 0.02988557 |
| ! | mitotic sister chromatid segregation | GO:0000070 | 23 | 9 | 1.23669492 | 0.00379 | 0.02976791 |
| ! | microtubule binding | GO:0008017 | 132 | 43 | 0.88711157 | 0.00382 | 0.02988588 |
| ! | site of polarized growth | GO:0030427 | 36 | 18 | 1.0388715 | 0.00389 | 0.03031465 |
| ! | mitotic checkpoint | GO:0007093 | 33 | 16 | 1.06927774 | 0.0039 | 0.03027432 |
| ! | phosphoinositide 3-kinase activity | GO:0035004 | 26 | 12 | 1.14382457 | 0.00412 | 0.03185814 |
| ! | Rho protein signal transduction | GO:0007266 | 124 | 56 | 0.84325225 | 0.00418 | 0.0321973 |
| ! | microtubule | GO:0005874 | 131 | 62 | 0.8387244 | 0.00422 | 0.03238038 |
| ! | superoxide metabolism | GO:0006801 | 36 | 21 | 1.00214557 | 0.00429 | 0.03279138 |
| ! | isotype switching | GO:0045190 | 16 | 11 | 1.16676743 | 0.00437 | 0.03327538 |
| ! | oligosaccharide metabolism | GO:0009311 | 28 | 13 | 1.1232548 | 0.0044 | 0.03337643 |
| ! | mRNA transport | GO:0051028 | 79 | 28 | 0.9420028 | 0.00448 | 0.03385455 |
| ! | glycosphingolipid metabolism | GO:0006687 | 39 | 19 | 1.02129855 | 0.00455 | 0.03425377 |
| ! | growth cone | GO:0030426 | 33 | 16 | 1.0626897 | 0.00457 | 0.034275 |
| ! | response to pathogen | GO:0042828 | 62 | 44 | 0.87046394 | 0.00466 | 0.0348191 |

Supplemental Table 1

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|---|---|---|---|---|---|---|---|
| ! | actin filament binding | GO:0051015 | 38 | 18 | 1.03420408 | 0.00468 | 0.03483806 |
| ! | Wnt receptor signaling pathway | GO:0016055 | 236 | 98 | 0.78224627 | 0.00473 | 0.03507937 |
| ! | regulation of mitosis | GO:0007088 | 81 | 37 | 0.89882185 | 0.00481 | 0.03554056 |
| ! | heparan sulfate proteoglycan metabolism | GO:0030201 | 27 | 11 | 1.16036734 | 0.00489 | 0.03599834 |
| ! | interstitial collagenase activity | GO:0004232 | 21 | 13 | 1.11315219 | 0.00496 | 0.03637941 |
| ! | galactosyltransferase activity | GO:0008378 | 72 | 29 | 0.93679587 | 0.00497 | 0.03631923 |
| ! | synaptosome | GO:0019717 | 111 | 40 | 0.88030541 | 0.00504 | 0.03669635 |
| ! | N-glycan processing | GO:0006491 | 18 | 9 | 1.21246076 | 0.00514 | 0.03728836 |
| ! | uridine nucleotide receptor activity | GO:0015065 | 13 | 9 | 1.2145666 | 0.00514 | 0.03715326 |
| ! | female gamete generation | GO:0007292 | 137 | 54 | 0.84193311 | 0.00523 | 0.03766733 |
| ! | membrane lipid biosynthesis | GO:0046467 | 167 | 77 | 0.80404872 | 0.00524 | 0.0376036 |
| ! | transforming growth factor beta receptor activity | GO:0005024 | 50 | 19 | 1.01261758 | 0.00527 | 0.03768333 |
| ! | negative regulation of adenylate cyclase activity | GO:0007194 | 37 | 19 | 1.01728729 | 0.00527 | 0.03754875 |
| ! | hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in cyclic amidines | GO:0016814 | 42 | 23 | 0.97210735 | 0.00536 | 0.03805409 |
| ! | kinase inhibitor activity | GO:0019210 | 96 | 42 | 0.870978 | 0.00539 | 0.03813138 |
| ! | regulation of transcription from Pol III promoter | GO:0006359 | 60 | 35 | 0.89851038 | 0.00558 | 0.03933604 |
| ! | regulation of translational initiation | GO:0006446 | 98 | 35 | 0.89424812 | 0.00558 | 0.03919754 |
| ! | alpha DNA polymerase activity | GO:0003889 | 26 | 13 | 1.10102032 | 0.00558 | 0.03906 |
| ! | mitotic anaphase | GO:0000090 | 39 | 15 | 1.06123721 | 0.00564 | 0.03934196 |
| ! | negative regulation of enzyme activity | GO:0043086 | 137 | 58 | 0.83092754 | 0.00569 | 0.03955244 |
| ! | chromatin remodeling | GO:0006338 | 132 | 58 | 0.83300708 | 0.00569 | 0.0394151 |
| ! | stromelysin 3 activity | GO:0004249 | 17 | 9 | 1.20444592 | 0.0057 | 0.03934775 |
| ! | histone acetyltransferase complex | GO:0000123 | 17 | 9 | 1.19621293 | 0.0057 | 0.03921207 |
| ! | transmembrane receptor protein kinase activity | GO:0019199 | 242 | 96 | 0.78786344 | 0.00571 | 0.03914588 |
| ! | delta DNA polymerase activity | GO:0003891 | 28 | 14 | 1.08495823 | 0.00575 | 0.0392851 |
| ! | carboxypeptidase activity | GO:0004180 | 124 | 57 | 0.83974594 | 0.00578 | 0.03935529 |
| ! | regulation of endocytosis | GO:0030100 | 91 | 44 | 0.86015643 | 0.00594 | 0.04030714 |
| ! | negative regulation of monocyte differentiation | GO:0045656 | 34 | 21 | 0.98116799 | 0.00602 | 0.04071153 |
| ! | O-linked glycosylation | GO:0006493 | 66 | 25 | 0.95058819 | 0.00606 | 0.04084358 |
| ! | N-acetyltransferase activity | GO:0008080 | 100 | 47 | 0.85176341 | 0.00613 | 0.04117626 |
| ! | extrachromosomal DNA | GO:0046821 | 33 | 13 | 1.09621031 | 0.00616 | 0.04123893 |
| ! | sister chromatid segregation | GO:0000819 | 30 | 11 | 1.1420818 | 0.00618 | 0.04123445 |
| ! | interleukin-1 receptor binding | GO:0005149 | 57 | 37 | 0.88555019 | 0.00618 | 0.041097 |
| ! | phosphatidylinositol 3-kinase activity | GO:0016303 | 24 | 11 | 1.14420393 | 0.00618 | 0.04096047 |
| ! | response to virus | GO:0009615 | 68 | 46 | 0.85400933 | 0.00628 | 0.04148543 |
| ! | posttranslational protein folding | GO:0051084 | 47 | 18 | 1.0157914 | 0.0063 | 0.0414802 |
| ! | heparan sulfate proteoglycan biosynthesis | GO:0015012 | 22 | 9 | 1.19516012 | 0.00634 | 0.04160625 |
| ! | interleukin-2 biosynthesis | GO:0042094 | 24 | 14 | 1.06953996 | 0.00649 | 0.04245098 |
| ! | telomere maintenance | GO:0000723 | 62 | 27 | 0.92983406 | 0.00657 | 0.04283382 |
| ! | rRNA metabolism | GO:0016072 | 123 | 66 | 0.81079908 | 0.00667 | 0.04334414 |
| ! | regulation of G-protein coupled receptor protein signaling | GO:0008277 | 85 | 38 | 0.88350499 | 0.00669 | 0.04333295 |
| ! | microfilament motor activity | GO:0000146 | 40 | 17 | 1.02586451 | 0.00674 | 0.04351553 |
| ! | collagenase activity | GO:0008133 | 29 | 17 | 1.02131981 | 0.00674 | 0.04337516 |
| ! | platelet activating factor receptor activity | GO:0004992 | 18 | 10 | 1.14686763 | 0.00682 | 0.04374887 |
| ! | regulation of S phase of mitotic cell cycle | GO:0007090 | 21 | 11 | 1.13233472 | 0.00689 | 0.04405625 |

Supplemental Table 1

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|---|---|---|---|---|---|---|---|
| ! | basic amino acid transporter activity | GO:0015174 | 18 | 9 | 1.17770865 | 0.00696 | 0.04436166 |
| ! | chromatin binding | GO:0003682 | 171 | 71 | 0.80602124 | 0.00701 | 0.04453806 |
| ! | phosphoric diester hydrolase activity | GO:0008081 | 146 | 64 | 0.81080908 | 0.00704 | 0.04458667 |
| ! | transmembrane receptor protein tyrosine phosphatase | GO:0007185 | 51 | 21 | 0.9705718 | 0.00704 | 0.04444557 |
| ! | lipoprotein biosynthesis | GO:0042158 | 113 | 53 | 0.83262047 | 0.00736 | 0.04631924 |
| ! | regulation of ossification | GO:0030278 | 50 | 26 | 0.93828077 | 0.00741 | 0.04648726 |
| ! | glycolipid metabolism | GO:0006664 | 51 | 26 | 0.93796015 | 0.00741 | 0.04634154 |
| ! | regulation of GTPase activity | GO:0043087 | 66 | 26 | 0.92943826 | 0.00741 | 0.04619672 |
| ! | mRNA-nucleus export | GO:0006406 | 70 | 26 | 0.92940369 | 0.00741 | 0.0460528 |
| ! | protein processing | GO:0016485 | 80 | 45 | 0.8542438 | 0.00743 | 0.0460337 |
| ! | F-actin capping protein complex | GO:0008290 | 25 | 10 | 1.14262318 | 0.0075 | 0.04632353 |
| ! | cell soma | GO:0043025 | 21 | 9 | 1.16968845 | 0.00768 | 0.04728889 |
| ! | sterol transport | GO:0015918 | 13 | 9 | 1.17268031 | 0.00768 | 0.04714338 |
| ! | coated membrane | GO:0048475 | 111 | 49 | 0.84671977 | 0.00779 | 0.04767193 |
| ! | negative regulation of myeloid blood cell differentiation | GO:0045638 | 36 | 23 | 0.94876748 | 0.00799 | 0.04874633 |
| ! | dendrite morphogenesis | GO:0016358 | 47 | 23 | 0.9582146 | 0.00799 | 0.04859771 |
| ! | cell development | GO:0048468 | 152 | 68 | 0.80049414 | 0.00823 | 0.04990532 |
| ! | amine transport | GO:0015837 | 150 | 68 | 0.80702935 | 0.00823 | 0.04975409 |
| ! | DNA damage response, signal transduction | GO:0042770 | 78 | 40 | 0.86268932 | 0.00828 | 0.04990514 |
| ! | mitotic spindle organization and biogenesis | GO:0007052 | 71 | 32 | 0.89131248 | 0.00848 | 0.05095663 |
| ! | negative regulation of bone remodeling | GO:0046851 | 16 | 9 | 1.16081588 | 0.0086 | 0.05152252 |
| ! | establishment of mitotic spindle localization | GO:0040001 | 22 | 8 | 1.20099079 | 0.00865 | 0.05166692 |
| ! | protein amino acid acetylation | GO:0006473 | 47 | 20 | 0.97760909 | 0.0087 | 0.05181045 |
| ! | rhythmic behavior | GO:0007622 | 45 | 20 | 0.97155536 | 0.0087 | 0.05165625 |
| ! | phosphoinositide phospholipase C activity | GO:0004435 | 46 | 20 | 0.97808785 | 0.0087 | 0.05150297 |
| ! | interleukin-1 receptor activity | GO:0004908 | 23 | 15 | 1.03031041 | 0.00871 | 0.05140962 |
| ! | metallocarboxypeptidase activity | GO:0004181 | 98 | 42 | 0.85521167 | 0.00879 | 0.05172876 |
| ! | nucleotide kinase activity | GO:0019201 | 68 | 26 | 0.92502631 | 0.00908 | 0.05327824 |
| ! | B-cell mediated immunity | GO:0019724 | 23 | 10 | 1.1247837 | 0.00925 | 0.05411657 |
| ! | DNA-methyltransferase activity | GO:0009008 | 23 | 10 | 1.12199412 | 0.00925 | 0.05395833 |
| ! | dipeptidyl-peptidase and tripeptidyl-peptidase activity | GO:0016806 | 21 | 10 | 1.1257419 | 0.00925 | 0.05380102 |
| ! | pyrimidine nucleoside metabolism | GO:0006213 | 24 | 9 | 1.14950413 | 0.00958 | 0.05555843 |
| ! | proteoglycan biosynthesis | GO:0030166 | 35 | 21 | 0.94972711 | 0.00959 | 0.05545522 |
| ! | leukocyte cell adhesion | GO:0007159 | 25 | 11 | 1.09819041 | 0.00975 | 0.05621749 |
| ! | chromosome, telomeric region | GO:0000781 | 37 | 16 | 1.01348991 | 0.00976 | 0.05611297 |
| ! | embryonic development (sensu Mammalia) | GO:0001701 | 134 | 64 | 0.80913441 | 0.00987 | 0.05658233 |
| ! | protein kinase inhibitor activity | GO:0004860 | 88 | 37 | 0.86289807 | 0.00987 | 0.0564202 |
| ! | lipid kinase activity | GO:0001727 | 60 | 27 | 0.91344868 | 0.00995 | 0.056715 |
| ! | drug transporter activity | GO:0015238 | 44 | 20 | 0.96193919 | 0.01003 | 0.05700812 |
| ! | heterotrimeric G-protein GTPase activity | GO:0003927 | 109 | 45 | 0.84906004 | 0.01005 | 0.05695952 |
| ! | amino acid transport | GO:0006865 | 124 | 58 | 0.81393807 | 0.01011 | 0.05713725 |
| ! | zeta DNA polymerase activity | GO:0003894 | 23 | 12 | 1.07176542 | 0.01012 | 0.0570322 |
| ! | phosphatidylinositol-4,5-bisphosphate hydrolysis | GO:0007203 | 19 | 8 | 1.17934124 | 0.01053 | 0.05917563 |
| ! | positive regulation of growth | GO:0045927 | 79 | 36 | 0.8609501 | 0.01101 | 0.0616993 |
| ! | protease activator activity | GO:0016504 | 35 | 16 | 1.00392772 | 0.01105 | 0.06175 |
| ! | integral to endoplasmic reticulum membrane | GO:0030176 | 59 | 29 | 0.89829527 | 0.01109 | 0.06180042 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ! | general RNA polymerase II transcription factor activity | GO:0016251 | 94 | 51 | 0.82320567 | 0.01111 | 0.06173942 |
| ! | gamma-tubulin ring complex | GO:0008274 | 26 | 11 | 1.0897491 | 0.01114 | 0.06173417 |
| ! | MHC protein binding | GO:0042287 | 36 | 19 | 0.96377287 | 0.01128 | 0.06233684 |
| ! | apoptotic protease activator activity | GO:0016505 | 21 | 12 | 1.0636947 | 0.01132 | 0.06238508 |
| ! | inositol or phosphatidylinositol phosphatase activity | GO:0004437 | 51 | 24 | 0.91948725 | 0.01143 | 0.06281777 |
| ! | aging | GO:0007568 | 61 | 24 | 0.92194767 | 0.01143 | 0.06264519 |
| ! | dihydropyridine-sensitive calcium channel activity | GO:0015270 | 27 | 8 | 1.17153636 | 0.01158 | 0.06329342 |
| ! | caspase activator activity | GO:0008656 | 18 | 10 | 1.10048918 | 0.01164 | 0.06344754 |
| ! | meiotic recombination | GO:0007131 | 45 | 22 | 0.92948986 | 0.01178 | 0.06403569 |
| ! | kidney development | GO:0001822 | 68 | 31 | 0.88015624 | 0.01184 | 0.06418696 |
| ! | carboxypeptidase A activity | GO:0004182 | 91 | 41 | 0.84289133 | 0.01229 | 0.06644593 |
| ! | spindle organization and biogenesis | GO:0007051 | 84 | 37 | 0.85041077 | 0.0124 | 0.06685946 |
| ! | amine transporter activity | GO:0005275 | 177 | 84 | 0.77417185 | 0.01241 | 0.06673302 |
| ! | mitochondrial transport | GO:0006839 | 71 | 25 | 0.9164821 | 0.01247 | 0.0668754 |
| ! | immune cell homeostasis | GO:0001776 | 30 | 13 | 1.02940429 | 0.01253 | 0.06701702 |
| ! | amino acid transporter activity | GO:0015171 | 143 | 67 | 0.79195672 | 0.01257 | 0.0670512 |
| ! | extrinsic to plasma membrane | GO:0019897 | 208 | 95 | 0.76431941 | 0.01257 | 0.0668724 |
| ! | clathrin vesicle coat | GO:0030125 | 84 | 38 | 0.85024535 | 0.01265 | 0.06711902 |
| ! | lipoprotein binding | GO:0008034 | 52 | 26 | 0.90857858 | 0.01279 | 0.06768183 |
| ! | tissue homeostasis | GO:0001894 | 41 | 19 | 0.95192987 | 0.01299 | 0.06855833 |
| ! | ATP-binding cassette (ABC) transporter activity | GO:0004009 | 107 | 49 | 0.82220166 | 0.013 | 0.06843008 |
| ! | pancreatic ribonuclease activity | GO:0004522 | 26 | 15 | 1.00035885 | 0.0131 | 0.068775 |
| ! | lipid transport | GO:0006869 | 187 | 91 | 0.76786544 | 0.0132 | 0.06911811 |
| ! | urogenital system development | GO:0001655 | 85 | 40 | 0.84012808 | 0.01325 | 0.0691983 |
| ! | transmembrane receptor protein tyrosine phosphatase activity | GO:0005001 | 44 | 18 | 0.96812765 | 0.01326 | 0.06906971 |
| ! | sphingolipid biosynthesis | GO:0030148 | 40 | 20 | 0.94340651 | 0.01353 | 0.07029258 |
| ! | nuclear export | GO:0051168 | 137 | 52 | 0.81780067 | 0.01366 | 0.07078364 |
| ! | cytokinesis | GO:0016288 | 91 | 36 | 0.85923861 | 0.01375 | 0.07106541 |
| ! | phospholipase C activity | GO:0004629 | 54 | 24 | 0.91855217 | 0.01375 | 0.07088178 |
| ! | regulation of interleukin-2 biosynthesis | GO:0045076 | 19 | 11 | 1.06950687 | 0.01381 | 0.0710076 |
| ! | T-helper 2 type immune response | GO:0042092 | 13 | 9 | 1.11231096 | 0.01386 | 0.07108149 |
| ! | calcium ion sensing | GO:0005513 | 41 | 13 | 1.02475664 | 0.0139 | 0.07110385 |
| ! | regulation of DNA recombination | GO:0000018 | 30 | 13 | 1.02192027 | 0.0139 | 0.07092199 |
| ! | regulation of DNA replication | GO:0006275 | 25 | 13 | 1.02122757 | 0.0139 | 0.07074107 |
| ! | positive regulation of B-cell proliferation | GO:0030890 | 19 | 8 | 1.1490266 | 0.01412 | 0.07167786 |
| ! | integrin complex | GO:0008305 | 68 | 34 | 0.86050644 | 0.01414 | 0.07159721 |
| ! | JAK-STAT cascade | GO:0007259 | 97 | 46 | 0.82486565 | 0.01415 | 0.07146646 |
| ! | RNA catabolism | GO:0006401 | 128 | 63 | 0.7990878 | 0.01416 | 0.07133636 |
| ! | DNA-directed DNA polymerase activity | GO:0003887 | 69 | 31 | 0.87496411 | 0.0145 | 0.07286524 |
| ! | cell adhesion receptor activity | GO:0004895 | 68 | 28 | 0.88506494 | 0.01531 | 0.07674234 |
| ! | caspase regulator activity | GO:0043028 | 27 | 14 | 1.00719552 | 0.01541 | 0.07705 |
| ! | gamma DNA-directed DNA polymerase activity | GO:0003895 | 32 | 14 | 1.0061247 | 0.01541 | 0.07685738 |
| ! | heterogeneous nuclear ribonucleoprotein | GO:0008436 | 33 | 11 | 1.06265169 | 0.01544 | 0.07681496 |
| ! | NLS-bearing substrate-nucleus import | GO:0006607 | 25 | 11 | 1.06158479 | 0.01544 | 0.07662388 |
| ! | positive regulation of myeloid blood cell differentiation | GO:0045639 | 19 | 9 | 1.10578673 | 0.01546 | 0.07653275 |
| ! | GTPase binding | GO:0051020 | 44 | 23 | 0.91638038 | 0.01553 | 0.07668899 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ! | lipoprotein metabolism | GO:0042157 | 134 | 68 | 0.78320092 | 0.01553 | 0.07649963 |
| ! | SH2 domain binding | GO:0042169 | 20 | 8 | 1.13934416 | 0.01563 | 0.07680259 |
| ! | UDP-galactosyltransferase activity | GO:0035250 | 55 | 20 | 0.9363022 | 0.01586 | 0.07774128 |
| ! | response to metal ion | GO:0010038 | 32 | 12 | 1.03730227 | 0.01594 | 0.07794191 |
| ! | aminophospholipid transporter activity | GO:0015247 | 33 | 12 | 1.03192612 | 0.01594 | 0.07775134 |
| ! | pericentriolar material | GO:0000242 | 41 | 16 | 0.9707224 | 0.01627 | 0.07916744 |
| ! | copper ion transport | GO:0006825 | 23 | 10 | 1.07184027 | 0.01642 | 0.07970292 |
| ! | calcium ion transporter activity | GO:0015085 | 26 | 10 | 1.0760789 | 0.01642 | 0.07950947 |
| ! | phospholipid transport | GO:0015914 | 25 | 10 | 1.07515234 | 0.01642 | 0.07931695 |
| ! | double-strand break repair | GO:0006302 | 43 | 24 | 0.90432624 | 0.01645 | 0.07926993 |
| ! | damaged DNA binding | GO:0003684 | 94 | 45 | 0.82342585 | 0.01652 | 0.07941542 |
| ! | synaptic vesicle endocytosis | GO:0008099 | 36 | 15 | 0.98524723 | 0.01695 | 0.08128666 |
| ! | regulator of G-protein signaling activity | GO:0016299 | 19 | 8 | 1.13167649 | 0.01707 | 0.08166583 |
| ! | translation initiation factor activity | GO:0003743 | 184 | 75 | 0.77387732 | 0.01711 | 0.08166136 |
| ! | purine ribonucleoside monophosphate metabolism | GO:0009167 | 24 | 14 | 0.99479369 | 0.01717 | 0.08175215 |
| ! | cytoskeletal adaptor activity | GO:0008093 | 36 | 14 | 0.99059756 | 0.01717 | 0.0815575 |
| ! | metanephros development | GO:0001656 | 61 | 27 | 0.88888458 | 0.01722 | 0.08160071 |
| ! | single-stranded DNA binding | GO:0003697 | 109 | 43 | 0.82650011 | 0.01727 | 0.08164372 |
| ! | transition metal ion transporter activity | GO:0046915 | 54 | 25 | 0.89649136 | 0.0174 | 0.08206383 |
| ! | unlocalized protein complex | GO:0005941 | 224 | 84 | 0.76534965 | 0.01767 | 0.08314068 |
| ! | presynaptic membrane | GO:0042734 | 50 | 12 | 1.02300332 | 0.01802 | 0.084588 |
| ! | response to pathogenic bacteria | GO:0009618 | 41 | 30 | 0.86285049 | 0.01824 | 0.08541972 |
| ! | positive regulation of interleukin-2 biosynthesis | GO:0045086 | 18 | 10 | 1.06192897 | 0.0183 | 0.0855 |
| ! | RNA-directed DNA polymerase activity | GO:0003964 | 32 | 16 | 0.96236297 | 0.01846 | 0.08604603 |
| ! | ureteric bud development | GO:0001657 | 43 | 16 | 0.96261781 | 0.01846 | 0.08584545 |
| ! | centrosome | GO:0005813 | 127 | 56 | 0.79157895 | 0.01857 | 0.08615616 |
| ! | maintenance of fidelity during DNA-dependent DNA replication | GO:0045005 | 39 | 20 | 0.92110579 | 0.01858 | 0.08600255 |
| ! | protein lipidation | GO:0006497 | 109 | 51 | 0.80530667 | 0.01858 | 0.08580347 |
| ! | antibacterial humoral response | GO:0019731 | 10 | 8 | 1.11963597 | 0.01872 | 0.08625035 |
| ! | origin recognition complex | GO:0000808 | 54 | 32 | 0.85675019 | 0.01904 | 0.08752258 |
| ! | calcium channel activity | GO:0005262 | 143 | 71 | 0.77104923 | 0.01929 | 0.08846793 |
| ! | early endosome | GO:0005769 | 87 | 41 | 0.82413048 | 0.01958 | 0.08959197 |
| ! | hyperosmotic response | GO:0006972 | 22 | 14 | 0.98251515 | 0.01965 | 0.08970652 |
| ! | receptor signaling protein tyrosine kinase activity | GO:0004716 | 34 | 13 | 0.9884834 | 0.02001 | 0.09114144 |
| ! | vascular endothelial growth factor receptor activity | GO:0005021 | 33 | 10 | 1.05481515 | 0.02014 | 0.0915246 |
| ! | alkaline phosphatase activity | GO:0004035 | 16 | 9 | 1.07478872 | 0.02014 | 0.09131659 |
| ! | regulation of B-cell differentiation | GO:0045577 | 17 | 9 | 1.07300101 | 0.02014 | 0.09110952 |
| ! | cyclin-dependent protein kinase holoenzyme complex | GO:0000307 | 19 | 9 | 1.07627192 | 0.02014 | 0.09090339 |
| ! | SAP kinase activity | GO:0016909 | 30 | 9 | 1.06939777 | 0.02014 | 0.09069819 |
| ! | platelet activation | GO:0030168 | 42 | 25 | 0.88514442 | 0.0204 | 0.09166216 |
| ! | protein amino acid prenylation | GO:0018346 | 40 | 18 | 0.9346659 | 0.02054 | 0.09208382 |
| ! | negative regulation of T-cell activation | GO:0050868 | 15 | 11 | 1.0291033 | 0.02117 | 0.0946954 |
| ! | protein-membrane targeting | GO:0006612 | 123 | 49 | 0.80298743 | 0.02118 | 0.09452819 |
| ! | fibroblast growth factor receptor binding | GO:0005104 | 46 | 26 | 0.87106005 | 0.02148 | 0.09565312 |
| ! | response to inorganic substance | GO:0010035 | 35 | 15 | 0.96657182 | 0.02164 | 0.096151 |
| ! | protein-nucleus import, docking | GO:0000059 | 39 | 15 | 0.96596918 | 0.02164 | 0.09593733 |

Supplemental Table 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ! | lung development | GO:0030324 | 88 | 39 | 0.82549768 | 0.02177 | 0.09629967 |
| ! | protein secretion | GO:0009306 | 97 | 48 | 0.80114719 | 0.02181 | 0.09626316 |
| ! | amino sugar metabolism | GO:0006040 | 53 | 21 | 0.90030666 | 0.02185 | 0.09622682 |
| ! | chloroplast | GO:0009507 | 16 | 8 | 1.10059 | 0.02208 | 0.09702555 |
| ! | tumor antigen | GO:0008222 | 22 | 9 | 1.06367558 | 0.0223 | 0.09777692 |
| ! | respiratory tube development | GO:0030323 | 93 | 42 | 0.81625714 | 0.02293 | 0.10031875 |
| ! | interleukin-1 binding | GO:0019966 | 26 | 17 | 0.93249097 | 0.02306 | 0.10066674 |
| ! | collagen catabolism | GO:0030574 | 49 | 32 | 0.84103094 | 0.02317 | 0.10092609 |
| ! | sialyltransferase activity | GO:0008373 | 40 | 19 | 0.91332559 | 0.02331 | 0.10131471 |
| ! | protein phosphatase binding | GO:0019903 | 22 | 11 | 1.02022552 | 0.02332 | 0.10113783 |
| ! | odontogenesis (sensu Vertebrata) | GO:0042475 | 47 | 18 | 0.92704519 | 0.02339 | 0.10122137 |
| ! | regulation of secretion | GO:0051046 | 78 | 38 | 0.82667426 | 0.02357 | 0.10177955 |
| ! | negative regulation of cytokine biosynthesis | GO:0042036 | 10 | 8 | 1.09369661 | 0.02378 | 0.10246458 |
| ! | meiosis I | GO:0007127 | 55 | 29 | 0.85855123 | 0.02388 | 0.10267371 |
| ! | muscle motor activity | GO:0003776 | 64 | 29 | 0.85390234 | 0.02388 | 0.1024529 |
| ! | N-acyltransferase activity | GO:0016410 | 122 | 57 | 0.78912371 | 0.02393 | 0.1024471 |
| ! | neurotransmitter transport | GO:0006836 | 133 | 57 | 0.79039068 | 0.02393 | 0.10222773 |
| ! | meiotic prophase I | GO:0007128 | 50 | 27 | 0.86912304 | 0.024 | 0.10230769 |
| ! | basolateral plasma membrane | GO:0016323 | 128 | 56 | 0.78112699 | 0.02421 | 0.10298284 |
| ! | epsilon DNA polymerase activity | GO:0003893 | 33 | 16 | 0.94685802 | 0.02429 | 0.1031033 |
| ! | dosage compensation | GO:0007549 | 36 | 12 | 0.99261786 | 0.02453 | 0.10390096 |
| ! | DNA unwinding | GO:0006268 | 20 | 10 | 1.03215206 | 0.02456 | 0.10380763 |
| ! | purinergic nucleotide receptor activity, G-protein coupled | GO:0045028 | 101 | 73 | 0.76932687 | 0.02462 | 0.10384123 |
| ! | glycerophospholipid biosynthesis | GO:0046474 | 77 | 31 | 0.84928452 | 0.02514 | 0.10581076 |
| ! | nuclear origin of replication recognition complex | GO:0005664 | 50 | 31 | 0.84494369 | 0.02514 | 0.105588 |
| ! | regulation of neurogenesis | GO:0050767 | 160 | 70 | 0.76315361 | 0.02545 | 0.10666544 |
| ! | apical part of cell | GO:0045177 | 47 | 22 | 0.88832917 | 0.0262 | 0.10957862 |
| ! | protein prenyltransferase activity | GO:0008318 | 50 | 24 | 0.87737892 | 0.02653 | 0.11072667 |
| ! | cytoskeletal regulator activity | GO:0008580 | 26 | 9 | 1.04499087 | 0.02653 | 0.11049551 |
| ! | rhythmic process | GO:0048511 | 162 | 80 | 0.75255629 | 0.02686 | 0.11163688 |
| ! | bone resorption | GO:0045453 | 37 | 19 | 0.90155302 | 0.027 | 0.11198545 |
| ! | transcriptional repressor complex | GO:0017053 | 27 | 10 | 1.01790914 | 0.02707 | 0.11204284 |
| ! | phosphotransferase activity, phosphate group as acceptor | GO:0016776 | 95 | 43 | 0.80048718 | 0.02715 | 0.1121413 |
| ! | kappa DNA polymerase activity | GO:0016450 | 23 | 12 | 0.98774503 | 0.02722 | 0.11219814 |
| ! | ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism | GO:0015662 | 171 | 79 | 0.75600895 | 0.02751 | 0.11315969 |
| ! | embryonic development (sensu Vertebrata) | GO:0043009 | 160 | 79 | 0.75879972 | 0.02751 | 0.11292685 |
| ! | alpha-sialidase activity | GO:0016997 | 29 | 15 | 0.94182606 | 0.02784 | 0.11404682 |
| ! | nuclear inner membrane | GO:0005637 | 35 | 15 | 0.94610916 | 0.02784 | 0.11381311 |
| ! | cyclin-dependent protein kinase activity | GO:0004693 | 29 | 15 | 0.94646634 | 0.02784 | 0.11358037 |
| ! | SRP-dependent cotranslational protein-membrane targeting | GO:0006614 | 33 | 14 | 0.95246256 | 0.02794 | 0.11375571 |
| ! | transcription from Pol III promoter | GO:0006383 | 103 | 53 | 0.78754611 | 0.02801 | 0.11380845 |
| ! | ubiquitin conjugating enzyme activity | GO:0004840 | 212 | 90 | 0.74527002 | 0.02803 | 0.11365823 |
| ! | Golgi membrane | GO:0000139 | 167 | 78 | 0.75103309 | 0.02805 | 0.11350862 |
| ! | steroid hormone receptor signaling pathway | GO:0030518 | 71 | 25 | 0.86045315 | 0.02828 | 0.11420769 |
| ! | hydrogen-translocating V-type ATPase complex | GO:0016471 | 28 | 11 | 1.0058273 | 0.02832 | 0.11413818 |

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|---|---|---|---|---|---|---|---|
| ! | RNA-nucleus export | GO:0006405 | 95 | 38 | 0.81531928 | 0.02885 | 0.11603982 |
| ! | bone mineralization | GO:0030282 | 42 | 23 | 0.86983065 | 0.02903 | 0.11652887 |
| ! | odontogenesis | GO:0042476 | 55 | 23 | 0.87783981 | 0.02903 | 0.11629488 |
| ! | negative regulation of DNA metabolism | GO:0051053 | 13 | 9 | 1.03052919 | 0.02909 | 0.1163017 |
| ! | filopodium | GO:0030175 | 29 | 9 | 1.03174969 | 0.02909 | 0.1160691 |
| ! | Golgi to endosome transport | GO:0006895 | 26 | 9 | 1.03494966 | 0.02909 | 0.11583743 |
| ! | plasma membrane organization and biogenesis | GO:0007009 | 47 | 21 | 0.8866025 | 0.02917 | 0.1159246 |
| ! | microtubule organizing center | GO:0005815 | 141 | 67 | 0.76320762 | 0.02925 | 0.11601143 |
| ! | traversing start control point of mitotic cell cycle | GO:0007089 | 14 | 10 | 1.01464787 | 0.0295 | 0.11677083 |
| ! | regulation of protein transport | GO:0051223 | 20 | 8 | 1.06532332 | 0.0302 | 0.11930495 |
| ! | RNA localization | GO:0006403 | 132 | 51 | 0.79036514 | 0.03062 | 0.1207251 |
| ! | Rho guanyl-nucleotide exchange factor activity | GO:0005089 | 43 | 16 | 0.9205563 | 0.03077 | 0.12107722 |
| ! | calmodulin regulated protein kinase activity | GO:0004683 | 60 | 28 | 0.84907969 | 0.03088 | 0.12127087 |
| ! | phosphatidylinositol binding | GO:0005545 | 44 | 15 | 0.93581583 | 0.03107 | 0.12177731 |
| ! | nucleobase, nucleoside, nucleotide kinase activity | GO:0019205 | 109 | 50 | 0.78902715 | 0.03115 | 0.12185147 |
| ! | macrophage elastase activity | GO:0004234 | 19 | 11 | 0.98963163 | 0.03122 | 0.1218863 |
| ! | glycosphingolipid biosynthesis | GO:0006688 | 24 | 11 | 0.98910326 | 0.03122 | 0.12164824 |
| ! | DNA-directed RNA polymerase II, holoenzyme | GO:0016591 | 106 | 57 | 0.77756128 | 0.0313 | 0.12172222 |
| ! | regulation of protein amino acid phosphorylation | GO:0001932 | 86 | 33 | 0.82746198 | 0.03177 | 0.12330963 |
| ! | regulation of synaptic plasticity | GO:0048167 | 74 | 33 | 0.82904602 | 0.03177 | 0.12307019 |
| ! | protein kinase activator activity | GO:0030295 | 23 | 9 | 1.02090884 | 0.03178 | 0.12287035 |
| ! | erythrocyte differentiation | GO:0030218 | 25 | 13 | 0.95423365 | 0.03178 | 0.12263269 |
| ! | cholesterol binding | GO:0015485 | 26 | 13 | 0.94905586 | 0.03178 | 0.12239595 |
| ! | no name yet | obsolete_cellular_component | 196 | 85 | 0.74294572 | 0.03183 | 0.12235231 |
| ! | voltage-gated potassium channel activity | GO:0005249 | 172 | 85 | 0.74235305 | 0.03183 | 0.12211702 |
| ! | signal complex formation | GO:0007172 | 32 | 10 | 1.0014727 | 0.0322 | 0.12329942 |
| ! | synapse organization and biogenesis | GO:0050808 | 178 | 84 | 0.74364716 | 0.03268 | 0.1248977 |
| ! | cilium | GO:0005929 | 46 | 25 | 0.85269847 | 0.03282 | 0.12519293 |
| ! | RNA editing | GO:0016547 | 15 | 8 | 1.05463699 | 0.03283 | 0.12499208 |
| ! | small nuclear ribonucleoprotein complex | GO:0030532 | 41 | 23 | 0.8671274 | 0.03376 | 0.128288 |
| ! | cartilage condensation | GO:0001502 | 42 | 23 | 0.86325334 | 0.03376 | 0.12804411 |
| ! | G-protein chemoattractant receptor activity | GO:0001637 | 52 | 35 | 0.81314465 | 0.03404 | 0.1288611 |
| ! | defense response to pathogen | GO:0042829 | 22 | 17 | 0.8998358 | 0.03418 | 0.12914602 |
| ! | nucleoside monophosphate metabolism | GO:0009123 | 45 | 21 | 0.87629162 | 0.03426 | 0.12920359 |
| ! | negative regulation of protein biosynthesis | GO:0017148 | 41 | 21 | 0.87579783 | 0.03426 | 0.12895981 |
| ! | actin modulating activity | GO:0003790 | 19 | 9 | 1.01178922 | 0.03475 | 0.13055791 |
| ! | regulation of synapse | GO:0007273 | 22 | 9 | 1.00875377 | 0.03475 | 0.1303125 |
| ! | porin activity | GO:0015288 | 56 | 26 | 0.84854799 | 0.03518 | 0.13167749 |
| ! | chromatin remodeling complex | GO:0016585 | 65 | 26 | 0.84904783 | 0.03518 | 0.1314309 |
| ! | hyaluronic acid binding | GO:0005540 | 39 | 16 | 0.91343905 | 0.0352 | 0.13125981 |
| ! | transcription initiation from Pol II promoter | GO:0006367 | 67 | 38 | 0.80033382 | 0.03523 | 0.13112659 |
| ! | inositol or phosphatidylinositol kinase activity | GO:0004428 | 82 | 38 | 0.80103844 | 0.03523 | 0.1308824 |
| ! | ribonucleoside monophosphate metabolism | GO:0009161 | 37 | 19 | 0.88761787 | 0.03558 | 0.13193699 |
| ! | mismatch repair | GO:0006298 | 37 | 19 | 0.88790514 | 0.03558 | 0.13169221 |
| ! | vesicle coat | GO:0030120 | 101 | 47 | 0.78846329 | 0.03632 | 0.13418222 |
| ! | icosanoid biosynthesis | GO:0046456 | 41 | 28 | 0.83217664 | 0.03681 | 0.13574113 |

Supplemental Table 1

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|---|---|---|---|---|---|---|---|
| ! | small protein conjugating enzyme activity | GO:0008639 | 221 | 93 | 0.73871494 | 0.03684 | 0.13560111 |
| ! | apoptosis regulator activity | GO:0016329 | 77 | 34 | 0.81312139 | 0.03693 | 0.13568204 |
| ! | purine ribonucleoside monophosphate biosynthesis | GO:0009168 | 20 | 12 | 0.95479579 | 0.03701 | 0.13572601 |
| ! | late endosome to vacuole transport | GO:0045324 | 29 | 11 | 0.96919819 | 0.03752 | 0.13734385 |
| ! | protein kinase binding | GO:0019901 | 163 | 67 | 0.75501897 | 0.0384 | 0.14030769 |
| ! | protein phosphorylated amino acid binding | GO:0045309 | 25 | 10 | 0.98234927 | 0.03866 | 0.14099945 |
| ! | death receptor binding | GO:0005123 | 17 | 10 | 0.97986502 | 0.03866 | 0.14074215 |
| ! | palmitoyltransferase activity | GO:0016409 | 22 | 10 | 0.98598307 | 0.03866 | 0.14048579 |
| ! | positive regulation of phagocytosis | GO:0050766 | 25 | 14 | 0.92080864 | 0.03891 | 0.14113718 |
| ! | N-methyltransferase activity | GO:0008170 | 112 | 51 | 0.77869963 | 0.03902 | 0.14127931 |
| ! | gene silencing | GO:0016458 | 47 | 23 | 0.85391559 | 0.0392 | 0.14167391 |
| ! | integrin-mediated signaling pathway | GO:0007229 | 169 | 76 | 0.74401985 | 0.03933 | 0.14188671 |
| ! | intracellular receptor-mediated signaling pathway | GO:0030522 | 75 | 27 | 0.83720603 | 0.03934 | 0.14166661 |
| ! | RNA polymerase II transcription factor activity, enhancer | GO:0003705 | 67 | 27 | 0.83707499 | 0.03934 | 0.14141135 |
| ! | insoluble fraction | GO:0005626 | 78 | 27 | 0.83283271 | 0.03934 | 0.14115701 |
| ! | apoptosis activator activity | GO:0016506 | 40 | 21 | 0.86592433 | 0.03943 | 0.14122594 |
| ! | negative regulation of cell adhesion | GO:0007162 | 36 | 21 | 0.86616204 | 0.03943 | 0.14097285 |
| ! | DNA catabolism | GO:0006308 | 23 | 13 | 0.93626569 | 0.03976 | 0.14189839 |
| ! | gastrulation | GO:0007369 | 106 | 45 | 0.78539857 | 0.04023 | 0.14331938 |
| ! | cell aging | GO:0007569 | 26 | 12 | 0.94656693 | 0.04124 | 0.14665561 |
| ! | calcium-transporting ATPase activity | GO:0005388 | 19 | 8 | 1.02210598 | 0.04125 | 0.14643016 |
| ! | response to bacteria | GO:0009617 | 110 | 87 | 0.73560284 | 0.04126 | 0.14620551 |
| ! | innate immune response | GO:0045087 | 41 | 24 | 0.8448579 | 0.04148 | 0.14672447 |
| ! | formation of primary germ layer | GO:0001704 | 61 | 26 | 0.83319403 | 0.04148 | 0.14646478 |
| ! | invasive growth | GO:0007125 | 60 | 26 | 0.83911059 | 0.04148 | 0.14620601 |
| ! | G-protein signaling, adenylate cyclase activating pathway | GO:0007189 | 127 | 63 | 0.75749426 | 0.04254 | 0.14967778 |
| ! | oogenesis | GO:0048477 | 45 | 15 | 0.90692075 | 0.04286 | 0.1505382 |
| ! | secretin-like receptor activity | GO:0001633 | 62 | 38 | 0.79637606 | 0.043 | 0.1507645 |
| ! | androgen receptor signaling pathway | GO:0030521 | 36 | 14 | 0.91452171 | 0.04347 | 0.152145 |
| ! | heavy metal binding | GO:0005505 | 43 | 17 | 0.88755272 | 0.04412 | 0.15414956 |
| ! | endoribonuclease activity, producing 3'-phosphomonoesters | GO:0016892 | 28 | 17 | 0.88592874 | 0.04412 | 0.15388007 |
| ! | sulfuric ester hydrolase activity | GO:0008484 | 29 | 13 | 0.92254345 | 0.0445 | 0.15493455 |
| ! | small monomeric GTPase activity | GO:0003925 | 70 | 30 | 0.81258822 | 0.04487 | 0.15595061 |
| ! | deaminase activity | GO:0019239 | 49 | 25 | 0.83569179 | 0.04498 | 0.15606104 |
| ! | lipid catabolism | GO:0016042 | 184 | 100 | 0.72394459 | 0.04507 | 0.15610182 |
| ! | negative regulation of signal transduction | GO:0009968 | 131 | 61 | 0.76004143 | 0.04515 | 0.15610789 |
| ! | negative regulation of transcription factor-nucleus import | GO:0042992 | 20 | 9 | 0.98289045 | 0.04521 | 0.1560449 |
| ! | cell wall organization and biogenesis | GO:0007047 | 18 | 9 | 0.98505811 | 0.04521 | 0.15577539 |
| ! | plastid | GO:0009536 | 18 | 9 | 0.98130144 | 0.04521 | 0.15550681 |
| ! | detection of bacteria | GO:0016045 | 15 | 11 | 0.95621039 | 0.04533 | 0.1556512 |
| ! | lambda DNA polymerase activity | GO:0016449 | 21 | 11 | 0.94942172 | 0.04533 | 0.15538376 |
| ! | spindle microtubule | GO:0005876 | 22 | 11 | 0.95182154 | 0.04533 | 0.15511724 |
| ! | phosphatase binding | GO:0019902 | 24 | 12 | 0.93740856 | 0.04552 | 0.15550068 |
| ! | positive regulation of peptidyl-tyrosine phosphorylation | GO:0050731 | 26 | 12 | 0.93085728 | 0.04552 | 0.15523487 |
| ! | iota DNA polymerase activity | GO:0016000 | 22 | 12 | 0.93331274 | 0.04552 | 0.15496997 |
| ! | deoxycytidyl transferase activity | GO:0017125 | 22 | 12 | 0.93789364 | 0.04552 | 0.15470596 |

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|---|---|---|---|---|---|---|---|
| ! | metalloexopeptidase activity | GO:0008235 | 147 | 70 | 0.74492679 | 0.04562 | 0.15478214 |
| ! | endoplasmic reticulum lumen | GO:0005788 | 43 | 18 | 0.87305902 | 0.04578 | 0.15506129 |
| ! | N-terminal protein myristoylation | GO:0006499 | 25 | 10 | 0.95845079 | 0.04582 | 0.15493373 |
| ! | response to osmotic stress | GO:0006970 | 51 | 27 | 0.82161267 | 0.04599 | 0.15524543 |
| ! | lipase activity | GO:0016298 | 146 | 83 | 0.73372912 | 0.04603 | 0.15511799 |
| ! | Golgi vesicle transport | GO:0048193 | 254 | 99 | 0.7256646 | 0.04615 | 0.15526012 |
| ! | phosphoinositide binding | GO:0035091 | 59 | 22 | 0.84929166 | 0.04672 | 0.15691313 |
| ! | calcium-dependent phospholipid binding | GO:0005544 | 72 | 29 | 0.81179382 | 0.04692 | 0.15732 |
| ! | chemokine binding | GO:0019956 | 53 | 36 | 0.7969894 | 0.04743 | 0.15876317 |
| ! | SNARE binding | GO:0000149 | 68 | 26 | 0.82154644 | 0.04876 | 0.16294171 |
| ! | gamma-tubulin complex | GO:0000930 | 30 | 14 | 0.90543468 | 0.04892 | 0.16320301 |
| ! | negative regulation of B-cell activation | GO:0050869 | 16 | 9 | 0.96857779 | 0.04916 | 0.16372988 |
| ! | immunoglobulin binding | GO:0019865 | 15 | 9 | 0.97574458 | 0.04916 | 0.163457 |
| ! | protein serine/threonine phosphatase activity | GO:0004722 | 119 | 50 | 0.7693271 | 0.04931 | 0.16368295 |
| ! | nucleic acid transport | GO:0050657 | 113 | 44 | 0.77822469 | 0.0501 | 0.16602907 |
| ! | G2/M transition of mitotic cell cycle | GO:0000086 | 91 | 44 | 0.77976662 | 0.0501 | 0.16575373 |
| ! | myoblast fusion | GO:0007520 | 18 | 10 | 0.94887999 | 0.05032 | 0.16620596 |
| ! | mitotic chromosome condensation | GO:0007076 | 21 | 10 | 0.95285843 | 0.05032 | 0.16593124 |
| ! | DNA topological change | GO:0006265 | 23 | 12 | 0.91933196 | 0.05035 | 0.16575619 |
| ! | regulation of peptidyl-tyrosine phosphorylation | GO:0050730 | 82 | 31 | 0.807816 | 0.05044 | 0.16577891 |
| ! | Notch signaling pathway | GO:0007219 | 59 | 28 | 0.81784888 | 0.05067 | 0.16626094 |
| ! | prenyltransferase activity | GO:0004659 | 61 | 28 | 0.81944416 | 0.05067 | 0.16598793 |
| ! | phospholipid biosynthesis | GO:0008654 | 128 | 57 | 0.75682563 | 0.05092 | 0.16653344 |
| ! | adenylate cyclase activation | GO:0007190 | 92 | 43 | 0.7784907 | 0.05132 | 0.16756694 |
| ! | protein complex disassembly | GO:0043241 | 16 | 8 | 0.99775013 | 0.05155 | 0.16804289 |
| ! | pigment cell differentiation | GO:0050931 | 19 | 8 | 0.98952557 | 0.05155 | 0.16776876 |
| ! | transmembrane receptor protein tyrosine kinase activity | GO:0004714 | 192 | 77 | 0.73240463 | 0.05156 | 0.16752801 |
| ! | transcription factor-nucleus import | GO:0042991 | 47 | 18 | 0.86865613 | 0.05176 | 0.16790439 |
| ! | detection of chemical substance | GO:0009593 | 55 | 21 | 0.84454724 | 0.0519 | 0.16808523 |
| ! | positive regulation of transport | GO:0051050 | 69 | 34 | 0.79175145 | 0.05256 | 0.16994684 |
| ! | syntaxin binding | GO:0019905 | 50 | 19 | 0.85400357 | 0.05279 | 0.17041432 |
| ! | icosanoid metabolism | GO:0006690 | 83 | 55 | 0.75730627 | 0.05322 | 0.17152488 |
| ! | endonuclease activity | GO:0004519 | 170 | 89 | 0.72354573 | 0.05348 | 0.17208484 |
| ! | transition metal ion transport | GO:0000041 | 92 | 48 | 0.76115173 | 0.05415 | 0.17396014 |
| ! | regulation of catabolism | GO:0009894 | 105 | 48 | 0.76767986 | 0.05415 | 0.17368047 |
| ! | copper ion transporter activity | GO:0005375 | 25 | 10 | 0.94704685 | 0.05474 | 0.17529101 |
| ! | C-C chemokine binding | GO:0019957 | 49 | 33 | 0.79935775 | 0.05506 | 0.17603317 |
| ! | respiratory gaseous exchange | GO:0007585 | 67 | 33 | 0.80001628 | 0.05506 | 0.17575152 |
| ! | regulation of mitotic cell cycle | GO:0007346 | 34 | 20 | 0.84322551 | 0.05509 | 0.17556637 |
| ! | apoptotic program | GO:0008632 | 176 | 87 | 0.72363691 | 0.05575 | 0.17738636 |
| ! | response to UV | GO:0009411 | 31 | 17 | 0.8622669 | 0.05589 | 0.17754865 |
| ! | microtubule motor activity | GO:0003777 | 150 | 62 | 0.74739102 | 0.05634 | 0.17869364 |
| ! | learning and/or memory | GO:0007611 | 139 | 62 | 0.74869522 | 0.05634 | 0.17841 |
| ! | voltage-gated potassium channel complex | GO:0008076 | 149 | 73 | 0.73720691 | 0.05657 | 0.17885444 |
| ! | kinase binding | GO:0019900 | 174 | 72 | 0.73605352 | 0.05672 | 0.17904494 |
| ! | zinc ion transporter activity | GO:0005385 | 12 | 9 | 0.95149504 | 0.05806 | 0.18298531 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ! | regulation of JNK cascade | GO:0046328 | 50 | 21 | 0.83641997 | 0.05926 | 0.18647271 |
| ! | cofactor catabolism | GO:0051187 | 17 | 11 | 0.92103941 | 0.05933 | 0.18639898 |
| ! | estrogen receptor signaling pathway | GO:0030520 | 31 | 11 | 0.92137359 | 0.05933 | 0.1861059 |
| ! | organelle lumen | GO:0043233 | 70 | 31 | 0.79267418 | 0.05942 | 0.1860956 |
| ! | transferase activity, transferring nitrogenous groups | GO:0016769 | 70 | 31 | 0.79531738 | 0.05942 | 0.18580392 |
| ! | glycosaminoglycan metabolism | GO:0030203 | 87 | 39 | 0.77451105 | 0.05955 | 0.18591901 |
| ! | DNA topoisomerase activity | GO:0003916 | 23 | 10 | 0.93225969 | 0.0597 | 0.18609609 |
| ! | rough endoplasmic reticulum | GO:0005791 | 30 | 10 | 0.93670058 | 0.0597 | 0.18580577 |
| ! | ribosome assembly | GO:0042255 | 22 | 10 | 0.9301359 | 0.0597 | 0.18551636 |
| ! | ureteric bud branching | GO:0001658 | 25 | 8 | 0.97009635 | 0.05988 | 0.18578631 |
| ! | rhodopsin mediated signaling | GO:0016056 | 18 | 8 | 0.97467075 | 0.05988 | 0.18549783 |
| ! | protein binding, bridging | GO:0030674 | 48 | 23 | 0.82422734 | 0.05993 | 0.18536488 |
| ! | perinuclear region | GO:0048471 | 57 | 23 | 0.82911419 | 0.05993 | 0.18507794 |
| ! | ATP-dependent DNA helicase activity | GO:0004003 | 33 | 15 | 0.87298751 | 0.05997 | 0.18491522 |
| ! | response to fungi | GO:0009620 | 26 | 15 | 0.87826497 | 0.05997 | 0.18462986 |
| ! | oogenesis (sensu Insecta) | GO:0009993 | 36 | 13 | 0.89474883 | 0.05998 | 0.18437612 |
| ! | DNA damage checkpoint | GO:0000077 | 52 | 25 | 0.81435256 | 0.0604 | 0.18538154 |
| ! | opioid receptor activity | GO:0004985 | 24 | 14 | 0.88790955 | 0.06068 | 0.18595484 |
| ! | synaptogenesis | GO:0007416 | 172 | 82 | 0.72616766 | 0.06072 | 0.18579202 |
| ! | nu DNA polymerase activity | GO:0016451 | 24 | 12 | 0.904299 | 0.0611 | 0.18666845 |
| ! | protein-lysine 6-oxidase activity | GO:0004720 | 23 | 12 | 0.90162405 | 0.0611 | 0.18638303 |
| ! | axon | GO:0030424 | 48 | 22 | 0.82142407 | 0.0614 | 0.18701221 |
| ! | establishment and/or maintenance of cell polarity | GO:0007163 | 77 | 30 | 0.79570683 | 0.06187 | 0.18815648 |
| ! | DNA damage response, signal transduction resulting in induction of apoptosis | GO:0008630 | 32 | 17 | 0.85184089 | 0.06221 | 0.18890251 |
| ! | mesoderm morphogenesis | GO:0048332 | 63 | 27 | 0.80839523 | 0.06253 | 0.18958564 |
| ! | CoA-ligase activity | GO:0016405 | 18 | 9 | 0.94654068 | 0.06269 | 0.18978232 |
| ! | heavy metal ion transporter activity | GO:0015076 | 18 | 9 | 0.94747484 | 0.06269 | 0.18949477 |
| ! | chloride transport | GO:0006821 | 136 | 67 | 0.73465259 | 0.0628 | 0.18954009 |
| ! | nerve maturation | GO:0042551 | 76 | 38 | 0.77471186 | 0.0629 | 0.18955514 |
| ! | nerve ensheathment | GO:0008366 | 72 | 37 | 0.77065584 | 0.06374 | 0.19179683 |
| ! | female sex differentiation | GO:0046660 | 53 | 24 | 0.81172706 | 0.06409 | 0.19255956 |
| ! | regulation of growth rate | GO:0040009 | 52 | 24 | 0.81438697 | 0.06409 | 0.19227 |
| ! | mRNA cleavage | GO:0006379 | 14 | 8 | 0.9607173 | 0.06458 | 0.1934491 |
| ! | Golgi trans face | GO:0005802 | 74 | 33 | 0.78750092 | 0.06481 | 0.193847 |
| ! | vacuole organization and biogenesis | GO:0007033 | 58 | 33 | 0.78299049 | 0.06481 | 0.19355681 |
| ! | sphingolipid catabolism | GO:0030149 | 22 | 11 | 0.91151553 | 0.06496 | 0.1937148 |
| ! | catecholamine biosynthesis | GO:0042423 | 18 | 10 | 0.92538615 | 0.06501 | 0.19357455 |
| ! | tumor necrosis factor receptor activity | GO:0005031 | 15 | 10 | 0.91924242 | 0.06501 | 0.19328607 |
| ! | ubiquitin-specific protease activity | GO:0004843 | 128 | 56 | 0.74619745 | 0.06514 | 0.19338438 |
| ! | secretory granule | GO:0030141 | 115 | 56 | 0.75044846 | 0.06514 | 0.19309703 |
| ! | Golgi stack | GO:0005795 | 43 | 18 | 0.84870955 | 0.06527 | 0.19319533 |
| ! | RNA polymerase II transcription mediator activity | GO:0016455 | 41 | 18 | 0.84899865 | 0.06527 | 0.19290911 |
| ! | nucleotide catabolism | GO:0009166 | 49 | 26 | 0.80623315 | 0.06532 | 0.1927713 |
| ! | calcium- and calmodulin-dependent protein kinase activity | GO:0004685 | 29 | 13 | 0.88295672 | 0.066 | 0.1944904 |
| ! | angiotensin receptor activity | GO:0001595 | 24 | 15 | 0.86581676 | 0.06665 | 0.19611615 |

Supplemental Table 1

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|---|---|---|---|---|---|---|---|
| ! | vesicle fusion | GO:0006906 | 27 | 14 | 0.87538119 | 0.06702 | 0.19691443 |
| ! | viral infectious cycle | GO:0019058 | 68 | 36 | 0.77379347 | 0.06712 | 0.19691824 |
| ! | endonuclease activity, active with either ribo- or deoxyribonucleic acids and producing 3'-phosphomonoesters | GO:0016894 | 35 | 21 | 0.82882567 | 0.06733 | 0.19724427 |
| ! | nucleoside monophosphate biosynthesis | GO:0009124 | 41 | 19 | 0.83855589 | 0.06771 | 0.19806664 |
| ! | apical plasma membrane | GO:0016324 | 107 | 54 | 0.74205784 | 0.06838 | 0.19973367 |
| ! | protein kinase C activation | GO:0007205 | 44 | 23 | 0.81119535 | 0.0684 | 0.1995 |
| ! | ATPase activity, coupled to transmembrane movement of ions | GO:0042625 | 198 | 92 | 0.71699662 | 0.06866 | 0.19996599 |
| ! | condensed nuclear chromosome | GO:0000794 | 51 | 28 | 0.79817365 | 0.06892 | 0.20043061 |
| ! | nuclear organization and biogenesis | GO:0006997 | 35 | 16 | 0.85672089 | 0.06918 | 0.20089389 |
| ! | defense/immunity protein activity | GO:0003793 | 61 | 35 | 0.7733304 | 0.0697 | 0.20210974 |
| ! | ribonucleoside monophosphate biosynthesis | GO:0009156 | 33 | 17 | 0.84677514 | 0.06991 | 0.20242446 |
| ! | ribonucleoprotein binding | GO:0043021 | 43 | 17 | 0.84250323 | 0.06991 | 0.20213109 |
| ! | regulation of protein-nucleus import | GO:0042306 | 37 | 17 | 0.84609099 | 0.06991 | 0.20183857 |
| ! | calcium channel regulator activity | GO:0005246 | 57 | 22 | 0.81174037 | 0.0703 | 0.20267124 |
| ! | MHC class I protein binding | GO:0042288 | 20 | 10 | 0.91815835 | 0.07064 | 0.20335758 |
| ! | DNA damage response, signal transduction by p53 class | GO:0030330 | 20 | 10 | 0.90947401 | 0.07064 | 0.20306455 |
| ! | structural constituent of cell wall | GO:0005199 | 120 | 53 | 0.74606914 | 0.07093 | 0.20360482 |
| ! | cyclin-dependent protein kinase regulator activity | GO:0016538 | 92 | 39 | 0.7686418 | 0.07207 | 0.20657996 |
| ! | histone binding | GO:0042393 | 26 | 13 | 0.87551771 | 0.07265 | 0.20794369 |
| ! | regulation of small GTPase mediated signal transduction | GO:0051056 | 28 | 13 | 0.87131311 | 0.07265 | 0.20764577 |
| ! | Rho GTPase binding | GO:0017048 | 25 | 13 | 0.87179321 | 0.07265 | 0.20734871 |
| ! | regulation of hormone secretion | GO:0046883 | 23 | 13 | 0.87292727 | 0.07265 | 0.2070525 |
| ! | protein-ER targeting | GO:0045047 | 112 | 45 | 0.76016239 | 0.07306 | 0.20792397 |
| ! | regulation of phosphorylation | GO:0042325 | 105 | 45 | 0.7518912 | 0.07306 | 0.20762778 |
| ! | metal ion transporter activity | GO:0046873 | 209 | 88 | 0.71532425 | 0.07308 | 0.20738919 |
| ! | nuclear body | GO:0016604 | 44 | 24 | 0.80309094 | 0.07318 | 0.20737798 |
| ! | ATP-binding cassette (ABC) transporter complex | GO:0043190 | 29 | 9 | 0.92863866 | 0.07354 | 0.20810255 |
| ! | positive regulation of inflammatory response | GO:0050729 | 19 | 9 | 0.92644218 | 0.07354 | 0.20780779 |
| ! | protein kinase A anchoring activity | GO:0005079 | 34 | 12 | 0.88712755 | 0.07378 | 0.20819109 |
| ! | lipid phosphatase activity | GO:0042577 | 33 | 14 | 0.85987593 | 0.07432 | 0.20941864 |
| ! | tube development | GO:0035295 | 200 | 86 | 0.7170183 | 0.07437 | 0.20926396 |
| ! | negative regulation of protein metabolism | GO:0051248 | 93 | 44 | 0.75373196 | 0.07451 | 0.20936261 |
| ! | positive regulation of neurogenesis | GO:0050769 | 64 | 26 | 0.79175672 | 0.07478 | 0.20982574 |
| ! | cotranslational protein-membrane targeting | GO:0006613 | 68 | 26 | 0.79143278 | 0.07478 | 0.20953104 |
| ! | protein amino acid alkylation | GO:0008213 | 102 | 38 | 0.76417965 | 0.07544 | 0.21108387 |
| ! | cell recognition | GO:0008037 | 73 | 33 | 0.77747391 | 0.0755 | 0.21095588 |
| ! | salivary gland morphogenesis | GO:0007435 | 29 | 11 | 0.89375866 | 0.07712 | 0.21518098 |
| ! | kinase activator activity | GO:0019209 | 25 | 11 | 0.89136721 | 0.07712 | 0.21488045 |
| ! | regulation of cell volume | GO:0006884 | 23 | 11 | 0.89035626 | 0.07712 | 0.21458075 |
| ! | magnesium-dependent protein serine/threonine phosphatase | GO:0004724 | 68 | 23 | 0.8100285 | 0.07821 | 0.21731052 |
| ! | positive regulation of growth rate | GO:0040010 | 49 | 23 | 0.80028575 | 0.07821 | 0.21700828 |
| ! | cell cycle arrest | GO:0007050 | 160 | 68 | 0.72359496 | 0.07916 | 0.21933917 |
| ! | calmodulin-dependent protein kinase I activity | GO:0004684 | 22 | 8 | 0.93549886 | 0.07962 | 0.22030777 |
| ! | sex differentiation | GO:0007548 | 184 | 82 | 0.71180768 | 0.07983 | 0.22058289 |
| ! | exocrine system development | GO:0035272 | 36 | 13 | 0.86689126 | 0.07987 | 0.22038817 |

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|---|---|---|---|---|---|---|---|
| ! | positive regulation of phosphorylation | GO:0042327 | 27 | 13 | 0.86555345 | 0.07987 | 0.22008377 |
| ! | calcium ion-dependent exocytosis | GO:0017156 | 64 | 25 | 0.79185107 | 0.08001 | 0.22016545 |
| ! | RAN protein binding | GO:0008536 | 28 | 12 | 0.87013432 | 0.08084 | 0.22214298 |
| ! | dipeptidase activity | GO:0016805 | 23 | 12 | 0.87627379 | 0.08084 | 0.22183741 |
| ! | mu DNA polymerase activity | GO:0016448 | 31 | 14 | 0.85348012 | 0.08162 | 0.22367019 |
| ! | arsenate reductase (thioredoxin) activity | GO:0030612 | 21 | 10 | 0.89346175 | 0.08324 | 0.22779671 |
| ! | aminoglycan metabolism | GO:0006022 | 88 | 40 | 0.75604979 | 0.08333 | 0.22773062 |
| ! | manganese ion binding | GO:0030145 | 146 | 65 | 0.72471998 | 0.08408 | 0.22946594 |
| ! | regulation of neurotransmitter secretion | GO:0046928 | 25 | 8 | 0.9245482 | 0.08519 | 0.23217766 |
| ! | double-strand break repair via homologous recombination | GO:0000724 | 14 | 8 | 0.91916636 | 0.08519 | 0.23186091 |
| ! | phosphatidylinositol metabolism | GO:0046488 | 47 | 19 | 0.81571391 | 0.08526 | 0.23173529 |
| ! | intramolecular transferase activity | GO:0016866 | 31 | 16 | 0.83895702 | 0.08532 | 0.23158286 |
| ! | transmembrane receptor protein tyrosine kinase adaptor | GO:0005068 | 18 | 9 | 0.90623958 | 0.08575 | 0.23243376 |
| ! | response to nutrients | GO:0007584 | 63 | 34 | 0.76569292 | 0.08625 | 0.23347185 |
| ! | protein amino acid ADP-ribosylation | GO:0006471 | 66 | 26 | 0.78970732 | 0.08634 | 0.23339878 |
| ! | cell wall | GO:0005618 | 118 | 53 | 0.73220576 | 0.08737 | 0.23586353 |
| ! | integrin binding | GO:0005178 | 93 | 45 | 0.7472477 | 0.08769 | 0.2364075 |
| ! | eta DNA polymerase activity | GO:0015999 | 25 | 13 | 0.85631616 | 0.08771 | 0.23614231 |
| ! | gliogenesis | GO:0042063 | 34 | 13 | 0.85800221 | 0.08771 | 0.23582406 |
| ! | substrate-bound cell migration | GO:0006929 | 27 | 13 | 0.85732649 | 0.08771 | 0.23550666 |
| ! | purine base metabolism | GO:0006144 | 26 | 13 | 0.85056938 | 0.08771 | 0.23519012 |
| ! | tryptase activity | GO:0030019 | 15 | 12 | 0.86152558 | 0.08803 | 0.23573134 |
| ! | hydrolase activity, acting on ether bonds | GO:0016801 | 19 | 12 | 0.8635563 | 0.08803 | 0.23541535 |
| ! | phototransduction, visible light | GO:0007603 | 15 | 10 | 0.8798826 | 0.09008 | 0.2405751 |
| ! | adult walking behavior | GO:0007628 | 27 | 10 | 0.88128703 | 0.09008 | 0.24025348 |
| ! | prostanoid biosynthesis | GO:0046457 | 21 | 14 | 0.84336525 | 0.09024 | 0.24035888 |
| ! | protein-hormone receptor activity | GO:0016500 | 31 | 15 | 0.83809681 | 0.09029 | 0.2401714 |
| ! | regulation of nucleocytoplasmic transport | GO:0046822 | 48 | 22 | 0.79513613 | 0.09046 | 0.2403032 |
| ! | nucleobase, nucleoside, nucleotide and nucleic acid | GO:0015932 | 53 | 20 | 0.80320364 | 0.09057 | 0.24027547 |
| ! | adult locomotory behavior | GO:0008344 | 46 | 20 | 0.80377564 | 0.09057 | 0.23995637 |
| ! | leukotriene metabolism | GO:0006691 | 32 | 20 | 0.80214482 | 0.09057 | 0.23963813 |
| ! | viral envelope | GO:0019031 | 22 | 11 | 0.87267985 | 0.09067 | 0.23958497 |
| ! | compartment specification | GO:0007386 | 24 | 8 | 0.91435369 | 0.0912 | 0.24066667 |
| ! | embryonic forelimb morphogenesis | GO:0035115 | 14 | 8 | 0.91731582 | 0.0912 | 0.24034875 |
| ! | mRNA modification | GO:0016556 | 13 | 8 | 0.91243978 | 0.0912 | 0.24003166 |
| ! | heterotrimeric G-protein complex | GO:0005834 | 101 | 43 | 0.75014203 | 0.09123 | 0.23979427 |
| ! | protein phosphatase type 2C activity | GO:0015071 | 78 | 28 | 0.77960194 | 0.09197 | 0.24142125 |
| ! | negative regulation of biosynthesis | GO:0009890 | 65 | 28 | 0.77462591 | 0.09197 | 0.24110401 |
| ! | viral life cycle | GO:0016032 | 97 | 50 | 0.73875869 | 0.09259 | 0.24241083 |
| ! | tRNA ligase activity | GO:0004812 | 166 | 89 | 0.70290924 | 0.0935 | 0.24447248 |
| ! | RAS small monomeric GTPase activity | GO:0003930 | 38 | 16 | 0.82252121 | 0.09424 | 0.24608482 |
| ! | glycolipid biosynthesis | GO:0009247 | 31 | 16 | 0.82822686 | 0.09424 | 0.24576314 |
| ! | mediator complex | GO:0000119 | 39 | 16 | 0.82808571 | 0.09424 | 0.2454423 |
| ! | external encapsulating structure | GO:0030312 | 131 | 59 | 0.72816132 | 0.09453 | 0.2458766 |
| ! | myogenesis | GO:0007519 | 133 | 59 | 0.72276628 | 0.09453 | 0.24555645 |
| ! | membrane organization and biogenesis | GO:0016044 | 99 | 49 | 0.7361517 | 0.09505 | 0.24658615 |

# Supplemental Table 1

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|---|---|---|---|---|---|---|---|
| ! | chromosome condensation | GO:0030261 | 48 | 24 | 0.78412662 | 0.09518 | 0.24660273 |
| ! | lysosome organization and biogenesis | GO:0007040 | 30 | 19 | 0.80447091 | 0.09531 | 0.24661926 |
| ! | leukotriene biosynthesis | GO:0019370 | 17 | 12 | 0.8564669 | 0.09552 | 0.24684249 |
| ! | two-component signal transduction system (phosphorelay) | GO:0000160 | 70 | 35 | 0.75739727 | 0.09722 | 0.25091061 |
| ! | oxysterol binding | GO:0008142 | 15 | 8 | 0.90484551 | 0.09736 | 0.25094729 |
| ! | intramolecular transferase activity, phosphotransferases | GO:0016868 | 20 | 10 | 0.87662652 | 0.09744 | 0.25082942 |
| ! | non-membrane spanning protein tyrosine phosphatase activity | GO:0004726 | 25 | 10 | 0.87912318 | 0.09744 | 0.25050619 |
| ! | chitin metabolism | GO:0006030 | 20 | 11 | 0.86127679 | 0.09823 | 0.25221216 |
| ! | poly(A) binding | GO:0008143 | 37 | 11 | 0.8605169 | 0.09823 | 0.25188798 |
| ! | lysosomal transport | GO:0007041 | 15 | 11 | 0.86702642 | 0.09823 | 0.25156463 |
| ! | synaptic vesicle endocytosis | GO:0048488 | 22 | 11 | 0.86343879 | 0.09823 | 0.25124212 |
| ! | protein phosphatase type 2B activity | GO:0030357 | 69 | 26 | 0.77597322 | 0.09835 | 0.25122695 |
| ! | regulation of myogenesis | GO:0016202 | 35 | 14 | 0.83816951 | 0.09864 | 0.25164552 |
| ! | amino acid-polyamine transporter activity | GO:0005279 | 99 | 47 | 0.73945601 | 0.0989 | 0.25198659 |
| ! | myosin phosphatase activity | GO:0017018 | 67 | 23 | 0.78626143 | 0.09936 | 0.25283571 |
| ! | DNA fragmentation during apoptosis | GO:0006309 | 16 | 9 | 0.88425768 | 0.0997 | 0.25337771 |
| ! | mannosyltransferase activity | GO:0000030 | 18 | 9 | 0.88451471 | 0.0997 | 0.25305534 |
| ! | cyclin-dependent protein kinase inhibitor activity | GO:0004861 | 17 | 9 | 0.88455455 | 0.0997 | 0.2527338 |
| ! | forelimb morphogenesis | GO:0035136 | 18 | 9 | 0.88538833 | 0.0997 | 0.25241307 |
| ! | nucleobase, nucleoside, nucleotide and nucleic acid transport | GO:0015931 | 134 | 55 | 0.72948601 | 0.10007 | 0.25302871 |
| ! | deoxyribonuclease activity | GO:0004536 | 52 | 29 | 0.77056948 | 0.10065 | 0.2541731 |
| ! | intracellular ligand-gated ion channel activity | GO:0005217 | 34 | 18 | 0.80078181 | 0.10148 | 0.25594513 |
| ! | calcium-dependent protein serine/threonine phosphatase | GO:0004723 | 70 | 25 | 0.77483271 | 0.10385 | 0.26159186 |
| ! | single-stranded RNA binding | GO:0003727 | 73 | 25 | 0.77412 | 0.10385 | 0.26126198 |
| ! | hormone secretion | GO:0046879 | 47 | 25 | 0.77906309 | 0.10385 | 0.26093293 |
| ! | somatostatin receptor activity | GO:0004994 | 35 | 25 | 0.77883432 | 0.10385 | 0.26060472 |
| ! | clathrin adaptor complex | GO:0030131 | 34 | 12 | 0.84855664 | 0.10413 | 0.26097908 |
| ! | defense response to bacteria | GO:0042742 | 78 | 65 | 0.72003702 | 0.10462 | 0.26187817 |
| ! | deoxyribonucleotide metabolism | GO:0009262 | 25 | 10 | 0.86183252 | 0.10537 | 0.263425 |
| ! | ubiquitin thiolesterase activity | GO:0004221 | 121 | 53 | 0.72694251 | 0.10544 | 0.26327009 |
| ! | nucleosome assembly | GO:0006334 | 117 | 64 | 0.71397086 | 0.1064 | 0.265335 |
| ! | detection of visible light | GO:0009584 | 16 | 11 | 0.8525591 | 0.10677 | 0.26592528 |
| ! | tumor necrosis factor binding | GO:0043120 | 16 | 11 | 0.85672543 | 0.10677 | 0.2655937 |
| ! | regulation of action potential | GO:0001508 | 89 | 44 | 0.73391277 | 0.10705 | 0.26595859 |
| ! | protein disulfide isomerase activity | GO:0003756 | 15 | 9 | 0.87736585 | 0.10741 | 0.26652108 |
| ! | endosome to lysosome transport | GO:0008333 | 13 | 9 | 0.87280751 | 0.10741 | 0.26619 |
| ! | microtubule cytoskeleton organization and biogenesis | GO:0000226 | 178 | 79 | 0.70176219 | 0.10783 | 0.26689932 |
| ! | protein prenylation | GO:0018342 | 49 | 24 | 0.77451107 | 0.10821 | 0.26750799 |
| ! | vacuolar transport | GO:0007034 | 25 | 14 | 0.82086616 | 0.10827 | 0.26732506 |
| ! | axis specification | GO:0009798 | 60 | 27 | 0.7697754 | 0.10903 | 0.26886879 |
| ! | ligase activity, forming phosphoric ester bonds | GO:0016886 | 187 | 99 | 0.70053927 | 0.10904 | 0.26856148 |
| ! | L-amino acid transporter activity | GO:0015179 | 70 | 36 | 0.74461134 | 0.1095 | 0.2693619 |
| ! | coreceptor activity | GO:0015026 | 55 | 31 | 0.75822863 | 0.10974 | 0.26961983 |
| ! | integral to Golgi membrane | GO:0030173 | 48 | 21 | 0.78175913 | 0.10992 | 0.26972989 |
| ! | regulation of transcription factor-nucleus import | GO:0042990 | 34 | 15 | 0.81626011 | 0.10992 | 0.26939853 |
| ! | ligand-dependent nuclear receptor transcription coactivator | GO:0030374 | 43 | 21 | 0.78815247 | 0.10992 | 0.26906798 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ! | carbon utilization | GO:0015976 | 17 | 8 | 0.88251207 | 0.11153 | 0.27267445 |
| ! | microtubule nucleation | GO:0007020 | 47 | 18 | 0.79100497 | 0.11272 | 0.27524651 |
| ! | memory | GO:0007613 | 44 | 18 | 0.79591992 | 0.11272 | 0.27491002 |
| ! | menstrual cycle | GO:0042698 | 44 | 18 | 0.79642102 | 0.11272 | 0.27457436 |
| ! | G1 phase of mitotic cell cycle | GO:0000080 | 43 | 23 | 0.77826605 | 0.11329 | 0.27562628 |
| ! | base-excision repair | GO:0006284 | 45 | 20 | 0.78893577 | 0.11345 | 0.27567935 |
| ! | acid-thiol ligase activity | GO:0016878 | 19 | 10 | 0.85708366 | 0.11361 | 0.2757323 |
| ! | ligand-regulated transcription factor activity | GO:0003706 | 23 | 10 | 0.85503753 | 0.11361 | 0.27539727 |
| ! | death receptor activity | GO:0005035 | 20 | 12 | 0.83313247 | 0.11363 | 0.27511147 |
| ! | membrane alanyl aminopeptidase activity | GO:0004179 | 13 | 9 | 0.86228117 | 0.11534 | 0.27891309 |
| ! | axon cargo transport | GO:0008088 | 35 | 9 | 0.86448948 | 0.11534 | 0.27857542 |
| ! | induction of programmed cell death by hormones | GO:0035081 | 12 | 9 | 0.86571834 | 0.11534 | 0.27823857 |
| ! | coated pit | GO:0005905 | 96 | 41 | 0.7406392 | 0.11568 | 0.27872174 |
| ! | response to extracellular stimulus | GO:0009991 | 74 | 41 | 0.73451253 | 0.11568 | 0.27838552 |
| ! | peptide hormone | GO:0005180 | 19 | 13 | 0.8222898 | 0.11592 | 0.27862699 |
| ! | negative regulation of protein catabolism | GO:0042177 | 31 | 13 | 0.82615444 | 0.11592 | 0.2782917 |
| ! | fibrillar collagen | GO:0005583 | 24 | 13 | 0.82056611 | 0.11592 | 0.27795721 |
| ! | vacuolar membrane | GO:0005774 | 31 | 14 | 0.81486307 | 0.11775 | 0.2820063 |
| ! | solute:sodium symporter activity | GO:0015370 | 98 | 46 | 0.72938654 | 0.11889 | 0.28439514 |
| ! | forebrain development | GO:0030900 | 35 | 17 | 0.79962762 | 0.1191 | 0.28455629 |
| ! | pseudouridylate synthase activity | GO:0004730 | 15 | 8 | 0.87329276 | 0.11912 | 0.28426364 |
| ! | imprinting | GO:0006349 | 25 | 8 | 0.87521021 | 0.11912 | 0.28392401 |
| ! | monocarboxylic acid transport | GO:0015718 | 78 | 39 | 0.73800392 | 0.11941 | 0.2842756 |
| ! | amino acid derivative biosynthesis | GO:0042398 | 52 | 33 | 0.74738514 | 0.11946 | 0.28405566 |
| ! | synaptic vesicle exocytosis | GO:0016079 | 69 | 28 | 0.75385317 | 0.12087 | 0.28706625 |
| ! | cytochrome P450 | GO:0005490 | 27 | 15 | 0.80722638 | 0.12093 | 0.28686724 |
| ! | peptide antigen binding | GO:0042605 | 35 | 15 | 0.80398255 | 0.12093 | 0.28652654 |
| ! | protein kinase A binding | GO:0051018 | 31 | 10 | 0.84550861 | 0.12236 | 0.28957082 |
| ! | negative regulation of coagulation | GO:0050819 | 36 | 24 | 0.7612357 | 0.12266 | 0.28993685 |
| ! | neutral amino acid transporter activity | GO:0015175 | 40 | 21 | 0.77988052 | 0.1232 | 0.29086864 |
| ! | protein C-terminus binding | GO:0008022 | 96 | 38 | 0.7354689 | 0.12334 | 0.29085496 |
| ! | histone acetylation | GO:0016573 | 23 | 12 | 0.82553174 | 0.12338 | 0.29060579 |
| ! | protein tyrosine/serine/threonine phosphatase activity | GO:0008138 | 88 | 45 | 0.72866325 | 0.12404 | 0.2918158 |
| ! | triacylglycerol lipase activity | GO:0004806 | 21 | 13 | 0.81725695 | 0.12594 | 0.29593675 |
| ! | acetyltransferase activity | GO:0016407 | 138 | 65 | 0.71004204 | 0.12882 | 0.30234812 |
| ! | voltage-gated calcium channel complex | GO:0005891 | 52 | 22 | 0.77004559 | 0.13037 | 0.3056265 |
| ! | negative regulation of protein kinase activity | GO:0006469 | 94 | 35 | 0.73768702 | 0.131 | 0.30674296 |
| ! | transaminase activity | GO:0008483 | 69 | 30 | 0.74213819 | 0.13122 | 0.30689789 |
| ! | response to cold | GO:0009409 | 20 | 10 | 0.83211618 | 0.13183 | 0.30796352 |
| ! | protein-nucleus import, translocation | GO:0000060 | 69 | 29 | 0.74616711 | 0.13192 | 0.30781333 |
| ! | sarcolemma | GO:0042383 | 32 | 15 | 0.79275362 | 0.13224 | 0.30819953 |
| ! | nucleoside diphosphate metabolism | GO:0009132 | 33 | 15 | 0.79819394 | 0.13224 | 0.30783991 |
| ! | negative regulation of blood coagulation | GO:0030195 | 22 | 15 | 0.79057233 | 0.13224 | 0.30748112 |
| ! | MAP kinase activity | GO:0004707 | 39 | 15 | 0.79964278 | 0.13224 | 0.30712317 |
| ! | G-protein signaling, adenylate cyclase inhibiting pathway | GO:0007193 | 79 | 51 | 0.71425481 | 0.13272 | 0.30787953 |
| ! | tropomyosin binding | GO:0005523 | 28 | 9 | 0.83981167 | 0.13282 | 0.30775366 |

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|---|---|---|---|---|---|---|---|
| ! | positive regulation of axonogenesis | GO:0050772 | 25 | 9 | 0.84550637 | 0.13282 | 0.30739664 |
| ! | peptide hormone processing | GO:0016486 | 26 | 12 | 0.81104174 | 0.13394 | 0.30962955 |
| ! | inorganic phosphate transporter activity | GO:0005315 | 20 | 12 | 0.81252393 | 0.13394 | 0.30927118 |
| ! | ovarian follicle development | GO:0001541 | 29 | 12 | 0.81925839 | 0.13394 | 0.30891364 |
| ! | MAP kinase kinase kinase activity | GO:0004709 | 30 | 12 | 0.82002941 | 0.13394 | 0.30855693 |
| ! | response to drug | GO:0042493 | 119 | 62 | 0.70592478 | 0.13427 | 0.30896038 |
| ! | nuclear localization sequence binding | GO:0008139 | 31 | 11 | 0.82923444 | 0.135 | 0.31028226 |
| ! | phosphate transport | GO:0006817 | 158 | 79 | 0.69291672 | 0.13507 | 0.3100859 |
| ! | peptide metabolism | GO:0006518 | 25 | 8 | 0.85534003 | 0.13598 | 0.31181621 |
| ! | calcium:sodium antiporter activity | GO:0005432 | 19 | 8 | 0.85615182 | 0.13598 | 0.31145821 |
| ! | regulation of circadian rhythm | GO:0042752 | 29 | 13 | 0.80980136 | 0.13774 | 0.31512764 |
| ! | polyamine metabolism | GO:0006595 | 28 | 13 | 0.80752498 | 0.13774 | 0.31476667 |
| ! | disassembly of cell structures during apoptosis | GO:0006921 | 26 | 18 | 0.77800952 | 0.13775 | 0.31442935 |
| ! | chitin binding | GO:0008061 | 27 | 18 | 0.77915059 | 0.13775 | 0.31407 |
| ! | osteoblast differentiation | GO:0001649 | 35 | 18 | 0.77291784 | 0.13775 | 0.31371147 |
| ! | neutral amino acid transport | GO:0015804 | 35 | 18 | 0.77593612 | 0.13775 | 0.31335376 |
| ! | phosphoinositide biosynthesis | GO:0046489 | 44 | 21 | 0.76974076 | 0.13797 | 0.31349675 |
| ! | hormone biosynthesis | GO:0042446 | 87 | 48 | 0.71166353 | 0.14065 | 0.3192227 |
| ! | regulation of coagulation | GO:0050818 | 39 | 27 | 0.74327174 | 0.14095 | 0.31954006 |
| ! | fibroblast growth factor receptor signaling pathway | GO:0008543 | 47 | 20 | 0.7667209 | 0.14154 | 0.32051339 |
| ! | specification of organ identity | GO:0010092 | 23 | 10 | 0.82320506 | 0.14171 | 0.32053452 |
| ! | intramolecular oxidoreductase activity, interconverting keto- | GO:0016862 | 16 | 10 | 0.82635268 | 0.14171 | 0.32017152 |
| ! | ether hydrolase activity | GO:0016803 | 12 | 9 | 0.83630695 | 0.14192 | 0.32028326 |
| ! | response to radiation | GO:0009314 | 170 | 98 | 0.6854351 | 0.14375 | 0.32404661 |
| ! | regulation of neuronal synaptic plasticity | GO:0048168 | 51 | 26 | 0.74965013 | 0.14442 | 0.3251895 |
| ! | ubiquitin activating enzyme activity | GO:0004839 | 24 | 8 | 0.84465717 | 0.14471 | 0.32547514 |
| ! | regulation of protein secretion | GO:0050708 | 28 | 15 | 0.78599315 | 0.14503 | 0.32582753 |
| ! | fucose metabolism | GO:0006004 | 23 | 11 | 0.81596932 | 0.14519 | 0.32582008 |
| ! | mRNA 3'-UTR binding | GO:0003730 | 34 | 11 | 0.81330335 | 0.14519 | 0.32545399 |
| ! | protein kinase C activity | GO:0004697 | 28 | 11 | 0.81548698 | 0.14519 | 0.32508872 |
| ! | phosphatidylinositol biosynthesis | GO:0006661 | 24 | 11 | 0.81369827 | 0.14519 | 0.32472427 |
| ! | apoptotic nuclear changes | GO:0030262 | 20 | 12 | 0.80980141 | 0.14531 | 0.32462872 |
| ! | cornified envelope | GO:0001533 | 25 | 12 | 0.8011358 | 0.14531 | 0.3242656 |
| ! | branching morphogenesis | GO:0001763 | 56 | 22 | 0.75533471 | 0.14604 | 0.3255305 |
| ! | hydrogen-transporting two-sector ATPase activity | GO:0003936 | 126 | 55 | 0.70754131 | 0.14704 | 0.32739375 |
| ! | smooth muscle contraction | GO:0006939 | 110 | 55 | 0.70377386 | 0.14704 | 0.32702876 |
| ! | germ cell development | GO:0007281 | 76 | 36 | 0.72954003 | 0.1481 | 0.32901949 |
| ! | myelination | GO:0042552 | 51 | 29 | 0.73673206 | 0.15094 | 0.33495584 |
| ! | carboxy-lyase activity | GO:0016831 | 64 | 29 | 0.73164606 | 0.15094 | 0.33458367 |
| ! | nucleoside metabolism | GO:0009116 | 56 | 29 | 0.7361867 | 0.15094 | 0.33421232 |
| ! | 3'-5' exonuclease activity | GO:0008408 | 66 | 35 | 0.72840712 | 0.15107 | 0.33412932 |
| ! | regulation of cyclin dependent protein kinase activity | GO:0000079 | 66 | 35 | 0.72759284 | 0.15107 | 0.3337593 |
| ! | regulation of cell adhesion | GO:0030155 | 105 | 54 | 0.71132492 | 0.15116 | 0.33358872 |
| ! | protein phosphatase type 1 activity | GO:0000163 | 70 | 25 | 0.74678601 | 0.15125 | 0.33341851 |
| ! | receptor antagonist activity | GO:0048019 | 11 | 9 | 0.82401186 | 0.15189 | 0.33445977 |
| ! | cation:cation antiporter activity | GO:0015491 | 39 | 18 | 0.76374637 | 0.15257 | 0.33558671 |

Supplemental Table 1

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|---|---|---|---|---|---|---|---|
| ! | regulation of cell migration | GO:0030334 | 130 | 67 | 0.69191882 | 0.15373 | 0.3377658 |
| ! | antigen receptor-mediated signaling pathway | GO:0050851 | 15 | 8 | 0.83741279 | 0.15388 | 0.33772343 |
| ! | oligosaccharide biosynthesis | GO:0009312 | 18 | 8 | 0.83509935 | 0.15388 | 0.33735231 |
| ! | L-fucose metabolism | GO:0042354 | 15 | 8 | 0.83639669 | 0.15388 | 0.336982 |
| ! | immunoglobulin secretion | GO:0048305 | 17 | 8 | 0.83472611 | 0.15388 | 0.3366125 |
| ! | neurexin binding | GO:0042043 | 31 | 21 | 0.75862844 | 0.15396 | 0.33641862 |
| ! | ligand-dependent nuclear receptor activity | GO:0004879 | 130 | 52 | 0.70564564 | 0.15463 | 0.33751296 |
| ! | organic anion transporter activity | GO:0008514 | 52 | 24 | 0.74845497 | 0.15522 | 0.33843049 |
| ! | BMP signaling pathway | GO:0030509 | 48 | 24 | 0.74937201 | 0.15522 | 0.33806103 |
| ! | macrophage differentiation | GO:0030225 | 18 | 11 | 0.8028071 | 0.156 | 0.33938931 |
| ! | intra-Golgi transport | GO:0006891 | 23 | 12 | 0.7991813 | 0.15737 | 0.3419969 |
| ! | regulation of protein catabolism | GO:0042176 | 70 | 33 | 0.72545708 | 0.15853 | 0.34414293 |
| ! | transcription factor TFIID complex | GO:0005669 | 25 | 17 | 0.76175761 | 0.15856 | 0.34383391 |
| ! | vasculogenesis | GO:0001570 | 38 | 17 | 0.76594749 | 0.15856 | 0.34346059 |
| ! | non-G-protein coupled 7TM receptor activity | GO:0004926 | 31 | 15 | 0.77934941 | 0.15925 | 0.34458107 |
| ! | type I hypersensitivity | GO:0016068 | 23 | 9 | 0.81881112 | 0.16223 | 0.35064881 |
| ! | DNA repair protein | GO:0003685 | 17 | 9 | 0.8197721 | 0.16223 | 0.35026932 |
| ! | negative regulation of JNK cascade | GO:0046329 | 19 | 9 | 0.81361542 | 0.16223 | 0.34989065 |
| ! | aldehyde dehydrogenase (NAD) activity | GO:0004029 | 22 | 13 | 0.7808985 | 0.16277 | 0.35067619 |
| ! | ribonucleoprotein | GO:0003733 | 41 | 13 | 0.78759471 | 0.16277 | 0.3502979 |
| ! | L-amino acid transport | GO:0015807 | 42 | 22 | 0.74408024 | 0.16294 | 0.35028588 |
| ! | solute:cation symporter activity | GO:0015294 | 122 | 62 | 0.69846667 | 0.16335 | 0.35078929 |
| ! | cation:chloride symporter activity | GO:0015377 | 21 | 8 | 0.8276435 | 0.16342 | 0.35056226 |
| ! | UDP-galactose beta-N-acetylglucosamine beta-1,3-galactosyltransferase activity | GO:0008499 | 26 | 8 | 0.82328128 | 0.16342 | 0.35018571 |
| ! | phosphotyrosine binding | GO:0001784 | 18 | 8 | 0.82606377 | 0.16342 | 0.34980998 |
| ! | sodium:potassium-exchanging ATPase activity | GO:0005391 | 25 | 10 | 0.80946104 | 0.16348 | 0.34956334 |
| ! | vesicle transport along actin filament | GO:0030050 | 17 | 10 | 0.8095854 | 0.16348 | 0.34918908 |
| ! | male meiosis | GO:0007140 | 34 | 16 | 0.76235016 | 0.16667 | 0.35562209 |
| ! | collagen fibril organization | GO:0030199 | 30 | 16 | 0.76088321 | 0.16667 | 0.35524215 |
| ! | negative regulation of catabolism | GO:0009895 | 32 | 14 | 0.77930303 | 0.16688 | 0.35531014 |
| ! | hemocyte differentiation (sensu Arthropoda) | GO:0042386 | 21 | 14 | 0.77307818 | 0.16688 | 0.35493134 |
| ! | NF-kappaB-nucleus import | GO:0042348 | 35 | 14 | 0.77314872 | 0.16688 | 0.35455335 |
| ! | regulation of bone mineralization | GO:0030500 | 15 | 11 | 0.79574059 | 0.16733 | 0.35513122 |
| ! | cortical actin cytoskeleton organization and biogenesis | GO:0030866 | 25 | 11 | 0.79721355 | 0.16733 | 0.35475383 |
| ! | microfibril | GO:0001527 | 73 | 37 | 0.71209467 | 0.16736 | 0.35444076 |
| ! | induction of apoptosis by intracellular signals | GO:0008629 | 76 | 37 | 0.71572244 | 0.16736 | 0.3540649 |
| ! | regulation of blood coagulation | GO:0030193 | 25 | 18 | 0.75873695 | 0.1682 | 0.35546504 |
| ! | regulation of inflammatory response | GO:0050727 | 35 | 18 | 0.75640431 | 0.1682 | 0.35508889 |
| ! | copper ion binding | GO:0005507 | 118 | 60 | 0.69269447 | 0.16912 | 0.3566537 |
| ! | actin filament | GO:0005884 | 62 | 30 | 0.73099634 | 0.16912 | 0.35627709 |
| ! | viral genome replication | GO:0019079 | 39 | 25 | 0.73159441 | 0.16945 | 0.35659573 |
| ! | CTD phosphatase activity | GO:0008420 | 69 | 25 | 0.74003279 | 0.16945 | 0.35621997 |
| ! | antiviral response protein activity | GO:0003800 | 19 | 12 | 0.78357726 | 0.17009 | 0.357189 |
| ! | bioactive lipid receptor activity | GO:0045125 | 20 | 12 | 0.78236925 | 0.17009 | 0.35681341 |
| ! | negative regulation of T-cell proliferation | GO:0042130 | 12 | 9 | 0.80544867 | 0.17336 | 0.36329118 |

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|---|---|---|---|---|---|---|---|
| ! | Rab GTPase activator activity | GO:0005097 | 20 | 9 | 0.80788693 | 0.17336 | 0.36290997 |
| ! | pronucleus | GO:0045120 | 16 | 8 | 0.81190178 | 0.17364 | 0.36311509 |
| ! | nuclear lamina | GO:0005652 | 16 | 8 | 0.81571918 | 0.17364 | 0.36273487 |
| ! | negative regulation of mitotic cell cycle | GO:0045930 | 15 | 8 | 0.81496073 | 0.17364 | 0.36235544 |
| ! | transcription initiation | GO:0006352 | 95 | 57 | 0.69254123 | 0.17382 | 0.36235204 |
| ! | neuromuscular junction development | GO:0007528 | 49 | 15 | 0.77061997 | 0.1741 | 0.36255689 |
| ! | receptor inhibitor activity | GO:0030547 | 13 | 10 | 0.79955771 | 0.17507 | 0.36419672 |
| ! | locomotory behavior | GO:0007626 | 150 | 73 | 0.68542187 | 0.17824 | 0.370405 |
| ! | membrane lipid catabolism | GO:0046466 | 39 | 19 | 0.74678306 | 0.17979 | 0.3732373 |
| ! | mesoderm cell differentiation | GO:0048333 | 24 | 11 | 0.78715662 | 0.18008 | 0.37345073 |
| ! | phorbol ester receptor activity | GO:0001565 | 34 | 14 | 0.76821985 | 0.18069 | 0.37432664 |
| ! | phosphatidylinositol phosphate kinase activity | GO:0016307 | 35 | 14 | 0.7640889 | 0.18069 | 0.37393833 |
| ! | glucosamine metabolism | GO:0006041 | 33 | 14 | 0.76408939 | 0.18069 | 0.37355083 |
| ! | antigen binding | GO:0003823 | 67 | 33 | 0.71314688 | 0.18101 | 0.373825 |
| ! | voltage-gated calcium channel activity | GO:0005245 | 72 | 33 | 0.7143252 | 0.18101 | 0.37343842 |
| ! | cyclic nucleotide binding | GO:0030551 | 48 | 16 | 0.75712515 | 0.18187 | 0.37482505 |
| ! | regulation of caspase activation | GO:0043026 | 28 | 16 | 0.75918909 | 0.18187 | 0.37443824 |
| ! | myosin | GO:0016459 | 111 | 52 | 0.69491178 | 0.18396 | 0.37835072 |
| ! | small molecule transport | GO:0006832 | 95 | 52 | 0.69194146 | 0.18396 | 0.37796107 |
| ! | phagocytosis, recognition | GO:0006910 | 13 | 8 | 0.80117481 | 0.18445 | 0.37857793 |
| ! | negative regulation of cyclin dependent protein kinase activity | GO:0045736 | 20 | 8 | 0.80778113 | 0.18445 | 0.37818885 |
| ! | anion channel activity | GO:0005253 | 98 | 50 | 0.6918749 | 0.18693 | 0.38288024 |
| ! | phospholipase activity | GO:0004620 | 119 | 66 | 0.69065007 | 0.18831 | 0.38531123 |
| ! | glycosaminoglycan biosynthesis | GO:0006024 | 45 | 21 | 0.74025849 | 0.18867 | 0.38565231 |
| ! | anaphylatoxin receptor activity | GO:0004942 | 23 | 15 | 0.76007849 | 0.18932 | 0.38658485 |
| ! | DNA-directed RNA polymerase activity | GO:0003899 | 85 | 39 | 0.70670277 | 0.18933 | 0.38620997 |
| ! | arsenate reductase activity | GO:0030611 | 27 | 13 | 0.76534848 | 0.19057 | 0.38834234 |
| ! | cellular nerve ensheathment | GO:0042553 | 52 | 30 | 0.71863169 | 0.19068 | 0.38817 |
| ! | prostaglandin metabolism | GO:0006693 | 45 | 30 | 0.71432381 | 0.19068 | 0.38777431 |
| ! | neuropeptide Y receptor activity | GO:0004983 | 95 | 65 | 0.6855947 | 0.19074 | 0.38750132 |
| ! | acid phosphatase activity | GO:0003993 | 33 | 17 | 0.74286487 | 0.19102 | 0.38767538 |
| ! | perception of pain | GO:0019233 | 31 | 17 | 0.75031462 | 0.19102 | 0.3872814 |
| ! | cytoskeletal anchoring | GO:0007016 | 47 | 17 | 0.74314465 | 0.19102 | 0.38688822 |
| ! | nucleotide-sugar metabolism | GO:0009225 | 46 | 17 | 0.74534167 | 0.19102 | 0.38649584 |
| ! | focal adhesion | GO:0005925 | 46 | 20 | 0.73838574 | 0.19221 | 0.38850957 |
| ! | protein phosphatase type 2A activity | GO:0000158 | 77 | 29 | 0.71936934 | 0.19309 | 0.38989327 |
| ! | calcium:cation antiporter activity | GO:0015368 | 23 | 11 | 0.77983215 | 0.19311 | 0.38953938 |
| ! | fucosyltransferase activity | GO:0008417 | 21 | 11 | 0.77554827 | 0.19311 | 0.38914591 |
| ! | low-density lipoprotein receptor activity | GO:0005041 | 25 | 11 | 0.7759857 | 0.19311 | 0.38875323 |
| ! | adult behavior | GO:0030534 | 50 | 24 | 0.72629309 | 0.19333 | 0.38880378 |
| ! | porphyrin metabolism | GO:0006778 | 46 | 24 | 0.7224828 | 0.19333 | 0.38841224 |
| ! | organic acid biosynthesis | GO:0016053 | 174 | 89 | 0.67284135 | 0.19336 | 0.38808169 |
| ! | Wnt receptor activity | GO:0042813 | 18 | 8 | 0.79368694 | 0.19571 | 0.39240347 |
| ! | regulation of BMP signaling pathway | GO:0030510 | 13 | 8 | 0.79164893 | 0.19571 | 0.39200949 |
| ! | receptor metabolism | GO:0043112 | 18 | 8 | 0.7911117 | 0.19571 | 0.3916163 |
| ! | membrane coat adaptor complex | GO:0030119 | 36 | 14 | 0.75345948 | 0.19578 | 0.39136383 |

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|---|---|---|---|---|---|---|---|
| ! | somatic muscle development | GO:0007525 | 40 | 9 | 0.78954025 | 0.19595 | 0.39131156 |
| ! | regulation of smooth muscle contraction | GO:0006940 | 30 | 12 | 0.76441076 | 0.19599 | 0.39100005 |
| ! | tubulin | GO:0045298 | 42 | 19 | 0.73875497 | 0.19724 | 0.3931007 |
| ! | C-X-C chemokine receptor activity | GO:0016494 | 27 | 19 | 0.73611168 | 0.19724 | 0.39270838 |
| ! | tyrosine phosphorylation of STAT protein | GO:0007260 | 45 | 22 | 0.72650023 | 0.19968 | 0.39717009 |
| ! | major (U2-dependent) spliceosome | GO:0005684 | 16 | 10 | 0.77763553 | 0.20009 | 0.39758919 |
| ! | sarcoplasmic reticulum | GO:0016529 | 19 | 10 | 0.77868385 | 0.20009 | 0.39719358 |
| ! | nucleobase metabolism | GO:0009112 | 38 | 18 | 0.73996199 | 0.20263 | 0.40183583 |
| ! | maintenance of protein localization | GO:0045185 | 39 | 18 | 0.73500761 | 0.20263 | 0.40143679 |
| ! | histone modification | GO:0016570 | 76 | 34 | 0.70400145 | 0.20395 | 0.40365104 |
| ! | nucleotide-excision repair | GO:0006289 | 58 | 26 | 0.71413467 | 0.20511 | 0.40554455 |
| ! | low-density lipoprotein binding | GO:0030169 | 27 | 13 | 0.75198175 | 0.20555 | 0.40601213 |
| ! | monovalent inorganic cation homeostasis | GO:0030004 | 81 | 33 | 0.70992898 | 0.20588 | 0.40626172 |
| ! | regulation of actin filament polymerization | GO:0030833 | 32 | 15 | 0.74944614 | 0.20592 | 0.40593913 |
| ! | regulation of axonogenesis | GO:0050770 | 81 | 32 | 0.70661107 | 0.2075 | 0.40865005 |
| ! | protein serine/threonine phosphatase complex | GO:0008287 | 97 | 32 | 0.71133015 | 0.2075 | 0.40824704 |
| ! | hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in cyclic amides | GO:0016812 | 16 | 8 | 0.78307353 | 0.20783 | 0.40849345 |
| ! | hexokinase activity | GO:0004396 | 14 | 9 | 0.77777805 | 0.20813 | 0.40868046 |
| ! | regulation of muscle contraction | GO:0006937 | 165 | 78 | 0.67802058 | 0.2084 | 0.40880826 |
| ! | keratinocyte differentiation | GO:0030216 | 31 | 17 | 0.73393393 | 0.20904 | 0.4096609 |
| ! | cortical cytoskeleton organization and biogenesis | GO:0030865 | 31 | 12 | 0.75531605 | 0.21027 | 0.41166698 |
| ! | actin filament bundle formation | GO:0051017 | 29 | 14 | 0.74884821 | 0.21126 | 0.41319971 |
| ! | posttranslational protein-membrane targeting | GO:0006620 | 50 | 20 | 0.72781302 | 0.21141 | 0.4130881 |
| ! | circadian rhythm | GO:0007623 | 101 | 53 | 0.69125163 | 0.21434 | 0.41840342 |
| ! | positive regulation of small GTPase mediated signal | GO:0051057 | 16 | 8 | 0.77434264 | 0.21956 | 0.42817419 |
| ! | spliceosomal snRNP biogenesis | GO:0000387 | 15 | 8 | 0.77177611 | 0.21956 | 0.42775605 |
| ! | aromatic compound biosynthesis | GO:0019438 | 29 | 11 | 0.75657907 | 0.22109 | 0.43031663 |
| ! | sheet-forming collagen | GO:0030935 | 25 | 11 | 0.75360984 | 0.22109 | 0.42989722 |
| ! | lysosphingolipid and lysophosphatidic acid receptor activity | GO:0001619 | 19 | 11 | 0.75648519 | 0.22109 | 0.42947863 |
| ! | amyloid precursor protein metabolism | GO:0042982 | 30 | 18 | 0.72136772 | 0.22116 | 0.42919669 |
| ! | pyrimidine ribonucleotide metabolism | GO:0009218 | 35 | 18 | 0.72852869 | 0.22116 | 0.42877959 |
| ! | nuclear hormone receptor binding | GO:0035257 | 60 | 28 | 0.70217797 | 0.2214 | 0.42882816 |
| ! | negative regulation of transforming growth factor beta receptor signaling pathway | GO:0030512 | 16 | 9 | 0.76162693 | 0.22156 | 0.42872182 |
| ! | aldehyde dehydrogenase [NAD(P)+] activity | GO:0004030 | 17 | 9 | 0.7687289 | 0.22156 | 0.4283064 |
| ! | caspase activation | GO:0006919 | 98 | 49 | 0.68270869 | 0.22158 | 0.4279304 |
| ! | aldehyde dehydrogenase activity | GO:0004028 | 25 | 15 | 0.73810012 | 0.22283 | 0.42992829 |
| ! | beta-catenin binding | GO:0008013 | 52 | 15 | 0.7335184 | 0.22283 | 0.4295129 |
| ! | DNA-directed RNA polymerase II, core complex | GO:0005665 | 26 | 15 | 0.73172172 | 0.22283 | 0.42909831 |
| ! | G-protein signaling, coupled to cGMP nucleotide second | GO:0007199 | 18 | 10 | 0.75095095 | 0.22893 | 0.44041982 |
| ! | biogenic amine biosynthesis | GO:0042401 | 43 | 26 | 0.7072538 | 0.22922 | 0.44055289 |
| ! | mRNA polyadenylylation | GO:0006378 | 47 | 21 | 0.71621597 | 0.22963 | 0.44091612 |
| ! | hydrolase activity, acting on carbon-nitrogen (but not peptide) | GO:0016810 | 168 | 96 | 0.66663034 | 0.23109 | 0.44329284 |
| ! | voltage-gated chloride channel activity | GO:0005247 | 45 | 20 | 0.71819465 | 0.23138 | 0.44342277 |
| ! | adenosine deaminase activity | GO:0004000 | 15 | 8 | 0.76959922 | 0.23205 | 0.44427999 |

Supplemental Table 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ! | establishment and/or maintenance of epithelial cell polarity | GO:0045197 | 19 | 8 | 0.76646382 | 0.23205 | 0.44385403 |
| ! | one-carbon compound metabolism | GO:0006730 | 68 | 33 | 0.6949297 | 0.23259 | 0.44446078 |
| ! | ligase activity, forming carbon-sulfur bonds | GO:0016877 | 28 | 16 | 0.7306064 | 0.23504 | 0.44871273 |
| ! | vitamin D receptor binding | GO:0042809 | 25 | 11 | 0.74173985 | 0.23601 | 0.4501338 |
| ! | ribonuclease activity | GO:0004540 | 160 | 90 | 0.66445684 | 0.2368 | 0.45120917 |
| ! | autophagy | GO:0006914 | 29 | 13 | 0.73813278 | 0.23719 | 0.45152104 |
| ! | acetylcholine receptor signaling, muscarinic pathway | GO:0007213 | 22 | 13 | 0.73707561 | 0.23719 | 0.45109061 |
| ! | hexosaminidase activity | GO:0015929 | 20 | 13 | 0.73978062 | 0.23719 | 0.450661 |
| ! | diacylglycerol kinase activity | GO:0004143 | 22 | 13 | 0.7327418 | 0.23719 | 0.45023221 |
| ! | ER-nuclear signaling pathway | GO:0006984 | 28 | 13 | 0.73698123 | 0.23719 | 0.44980423 |
| ! | inorganic anion transporter activity | GO:0015103 | 55 | 31 | 0.70099302 | 0.23809 | 0.45108219 |
| ! | embryonic eye morphogenesis | GO:0048048 | 53 | 30 | 0.69555695 | 0.24084 | 0.45585939 |
| ! | glutamine metabolism | GO:0006541 | 33 | 18 | 0.71868647 | 0.24126 | 0.45622152 |
| ! | frizzled signaling pathway | GO:0007222 | 41 | 18 | 0.71643923 | 0.24126 | 0.45578949 |
| ! | aminopeptidase activity | GO:0004177 | 83 | 40 | 0.69053012 | 0.2429 | 0.45845364 |
| ! | monocarboxylic acid transporter activity | GO:0008028 | 69 | 40 | 0.69155601 | 0.2429 | 0.45802032 |
| ! | regulation of membrane potential | GO:0042391 | 21 | 10 | 0.74981382 | 0.24313 | 0.4580211 |
| ! | intermediate filament cytoskeleton organization and | GO:0045104 | 26 | 10 | 0.74551986 | 0.24313 | 0.45758901 |
| ! | protein stabilization | GO:0050821 | 19 | 10 | 0.7449695 | 0.24313 | 0.45715773 |
| ! | polysaccharide catabolism | GO:0000272 | 18 | 10 | 0.75024495 | 0.24313 | 0.45672726 |
| ! | aminoglycan biosynthesis | GO:0006023 | 46 | 22 | 0.70824949 | 0.24328 | 0.45657912 |
| ! | membrane-associated guanylate kinase | GO:0004384 | 22 | 8 | 0.75134374 | 0.24462 | 0.4586625 |
| ! | muscle cell differentiation | GO:0042692 | 43 | 14 | 0.73035882 | 0.24597 | 0.4607607 |
| ! | pyrimidine nucleoside triphosphate metabolism | GO:0009147 | 29 | 17 | 0.71699127 | 0.24734 | 0.4628924 |
| ! | thyroid hormone receptor binding | GO:0046966 | 38 | 17 | 0.71945657 | 0.24734 | 0.46245858 |
| ! | glutamate receptor activity | GO:0008066 | 61 | 37 | 0.69045457 | 0.24826 | 0.4637441 |
| ! | protein heterodimerization activity | GO:0046982 | 178 | 80 | 0.662208 | 0.2493 | 0.46525117 |
| ! | dopamine receptor, adenylate cyclase activating pathway | GO:0007191 | 12 | 9 | 0.74861352 | 0.24945 | 0.46509603 |
| ! | histone methylation | GO:0016571 | 27 | 9 | 0.74994787 | 0.24945 | 0.46466176 |
| ! | sodium ion homeostasis | GO:0006883 | 19 | 9 | 0.74505675 | 0.24945 | 0.46422831 |
| ! | G-protein coupled photoreceptor activity | GO:0008020 | 49 | 27 | 0.69382836 | 0.25022 | 0.46522731 |
| ! | oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen | GO:0016706 | 42 | 21 | 0.71007611 | 0.25214 | 0.46836061 |
| ! | inactivation of MAPK | GO:0000188 | 59 | 21 | 0.70984077 | 0.25214 | 0.46792493 |
| ! | phospholipase C activation | GO:0007202 | 73 | 35 | 0.68558919 | 0.2525 | 0.46815753 |
| ! | anterior/posterior axis specification | GO:0009948 | 38 | 20 | 0.70165657 | 0.25286 | 0.46838969 |
| ! | C-X-C chemokine binding | GO:0019958 | 28 | 20 | 0.71088387 | 0.25286 | 0.46795519 |
| ! | signal recognition particle (sensu Eukaryota) | GO:0005786 | 35 | 13 | 0.7226572 | 0.25501 | 0.47149671 |
| ! | intermediate filament-based process | GO:0045103 | 35 | 13 | 0.72954727 | 0.25501 | 0.47106014 |
| ! | protein-nucleus export | GO:0006611 | 52 | 19 | 0.70632289 | 0.25786 | 0.47588409 |
| ! | C21-steroid hormone biosynthesis | GO:0006700 | 51 | 25 | 0.70067551 | 0.25791 | 0.47553646 |
| ! | O-acyltransferase activity | GO:0008374 | 43 | 25 | 0.69321997 | 0.25791 | 0.47509737 |
| ! | regulation of fatty acid metabolism | GO:0019217 | 19 | 10 | 0.73137119 | 0.25863 | 0.47598418 |
| ! | protein N-terminus binding | GO:0047485 | 24 | 12 | 0.72767866 | 0.25878 | 0.47582129 |
| ! | oligopeptide transport | GO:0006857 | 14 | 8 | 0.74267863 | 0.25884 | 0.47549337 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ! | RNA polymerase complex | GO:0030880 | 51 | 24 | 0.69187583 | 0.26156 | 0.48004802 |
| ! | calcium-mediated signaling | GO:0019722 | 63 | 32 | 0.68189845 | 0.262 | 0.4804136 |
| ! | regulation of body size | GO:0040014 | 38 | 18 | 0.70884053 | 0.26257 | 0.48101667 |
| ! | M phase specific microtubule process | GO:0000072 | 30 | 18 | 0.70935108 | 0.26257 | 0.48057537 |
| ! | metabotropic glutamate, GABA-B-like receptor activity | GO:0008067 | 24 | 18 | 0.7076687 | 0.26257 | 0.48013488 |
| ! | complement activity | GO:0003811 | 26 | 14 | 0.71881968 | 0.2641 | 0.48249038 |
| ! | locomotion | GO:0040011 | 21 | 9 | 0.73118126 | 0.26459 | 0.48294332 |
| ! | acrosome reaction | GO:0007340 | 16 | 9 | 0.73884736 | 0.26459 | 0.48250187 |
| ! | biogenic amine metabolism | GO:0006576 | 130 | 67 | 0.66319693 | 0.26556 | 0.48382849 |
| ! | vesicle docking during exocytosis | GO:0006904 | 80 | 31 | 0.69029334 | 0.2665 | 0.48509808 |
| ! | positive regulation of secretion | GO:0051047 | 14 | 11 | 0.73068315 | 0.26701 | 0.48558336 |
| ! | development of primary sexual characteristics | GO:0045137 | 89 | 44 | 0.6726922 | 0.26712 | 0.48534098 |
| ! | neuronal cell recognition | GO:0008038 | 42 | 23 | 0.69366171 | 0.26758 | 0.48573439 |
| ! | receptor regulator activity | GO:0030545 | 18 | 13 | 0.72077164 | 0.27244 | 0.49410709 |
| ! | tyrosine phosphorylation of Stat3 protein | GO:0042503 | 30 | 13 | 0.720309 | 0.27244 | 0.49365831 |
| ! | rhodopsin mediated phototransduction | GO:0009586 | 25 | 13 | 0.71350041 | 0.27244 | 0.49321034 |
| ! | N-acetylglucosamine metabolism | GO:0006044 | 31 | 13 | 0.7156285 | 0.27244 | 0.49276319 |
| ! | negative regulation of microtubule depolymerization | GO:0007026 | 20 | 8 | 0.73623222 | 0.27289 | 0.49313003 |
| ! | caspase activation via cytochrome c | GO:0008635 | 14 | 8 | 0.73559491 | 0.27289 | 0.49268376 |
| ! | GPI anchor biosynthesis | GO:0006506 | 20 | 10 | 0.72138749 | 0.27412 | 0.49445696 |
| ! | regulation of osteoblast differentiation | GO:0045667 | 19 | 10 | 0.72499641 | 0.27412 | 0.4940103 |
| ! | growth hormone-releasing hormone receptor activity | GO:0016520 | 23 | 16 | 0.70528938 | 0.2744 | 0.49406859 |
| ! | sulfur compound biosynthesis | GO:0044272 | 79 | 40 | 0.67268634 | 0.27484 | 0.49441461 |
| ! | translation elongation factor activity | GO:0003746 | 86 | 40 | 0.6773495 | 0.27484 | 0.49396919 |
| ! | nucleosome | GO:0005718 | 34 | 20 | 0.69441992 | 0.27485 | 0.49354253 |
| ! | lipoprotein receptor activity | GO:0030228 | 26 | 12 | 0.71192056 | 0.2764 | 0.4958795 |
| ! | energy coupled proton transport, against electrochemical | GO:0015988 | 29 | 12 | 0.71705357 | 0.2764 | 0.49543396 |
| ! | metalloendopeptidase activity | GO:0004222 | 184 | 100 | 0.65902357 | 0.27659 | 0.49532949 |
| ! | regulation of proteolysis and peptidolysis | GO:0030162 | 52 | 26 | 0.68753603 | 0.27956 | 0.50019928 |
| ! | beta-amyloid metabolism | GO:0050435 | 35 | 19 | 0.69961482 | 0.27966 | 0.49992984 |
| ! | host-pathogen interaction | GO:0030383 | 24 | 9 | 0.72639209 | 0.28048 | 0.50094682 |
| ! | pyrimidine nucleotide biosynthesis | GO:0006221 | 50 | 25 | 0.68414014 | 0.28329 | 0.50551301 |
| ! | vesicle targeting | GO:0006903 | 26 | 11 | 0.71159245 | 0.28346 | 0.50536434 |
| ! | cysteine protease inhibitor activity | GO:0004869 | 54 | 36 | 0.6742419 | 0.28379 | 0.50550094 |
| ! | endoribonuclease activity | GO:0004521 | 62 | 36 | 0.68043945 | 0.28379 | 0.50505 |
| ! | glutamate-gated ion channel activity | GO:0005234 | 37 | 18 | 0.70045946 | 0.28483 | 0.50644906 |
| ! | chloride transporter activity | GO:0015108 | 33 | 18 | 0.70107718 | 0.28483 | 0.50599809 |
| ! | FACIT collagen | GO:0005593 | 20 | 8 | 0.72414926 | 0.28708 | 0.50954146 |
| ! | drug transport | GO:0015893 | 28 | 17 | 0.69898713 | 0.28941 | 0.5132204 |
| ! | adrenoceptor activity | GO:0004935 | 27 | 17 | 0.69500023 | 0.28941 | 0.51276461 |
| ! | positive regulation of caspase activity | GO:0043280 | 99 | 50 | 0.66995275 | 0.2898 | 0.513 |
| ! | elastase activity | GO:0042708 | 49 | 34 | 0.67741657 | 0.29094 | 0.51456144 |
| ! | acid secretion | GO:0046717 | 21 | 13 | 0.70634438 | 0.29153 | 0.51514823 |
| ! | glutamate signaling pathway | GO:0007215 | 68 | 33 | 0.67974198 | 0.29166 | 0.51492186 |
| ! | scavenger receptor activity | GO:0005044 | 52 | 33 | 0.67789321 | 0.29166 | 0.51446658 |
| ! | pyrimidine nucleotide metabolism | GO:0006220 | 67 | 33 | 0.67536756 | 0.29166 | 0.5140121 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ! | vesicle docking | GO:0048278 | 81 | 32 | 0.67657214 | 0.29222 | 0.51454448 |
| ! | spermatid cell development | GO:0007286 | 123 | 49 | 0.66887821 | 0.29404 | 0.51729259 |
| ! | response to hormone stimulus | GO:0009725 | 32 | 16 | 0.70132435 | 0.29579 | 0.51991282 |
| ! | eye morphogenesis (sensu Vertebrata) | GO:0043010 | 54 | 31 | 0.67930102 | 0.29624 | 0.52024542 |
| ! | fatty acid biosynthesis | GO:0006633 | 154 | 78 | 0.65639539 | 0.29836 | 0.52350765 |
| ! | negative regulation of transport | GO:0051051 | 45 | 20 | 0.68931874 | 0.29866 | 0.52357355 |
| ! | protein amino acid methylation | GO:0006479 | 54 | 20 | 0.69122579 | 0.29866 | 0.52311387 |
| ! | neuropeptide receptor activity | GO:0008188 | 113 | 76 | 0.65883377 | 0.29983 | 0.5247025 |
| ! | peptide transport | GO:0015833 | 20 | 11 | 0.7085441 | 0.30041 | 0.52525675 |
| ! | transmembrane-ephrin receptor activity | GO:0005005 | 31 | 15 | 0.69170364 | 0.30051 | 0.5249715 |
| ! | glutamine family amino acid biosynthesis | GO:0009084 | 25 | 15 | 0.69507917 | 0.30051 | 0.5245122 |
| ! | specific transcriptional repressor activity | GO:0016566 | 27 | 15 | 0.7005061 | 0.30051 | 0.52405372 |
| ! | carbon-nitrogen ligase activity, with glutamine as amido-N- | GO:0016884 | 13 | 8 | 0.71558363 | 0.30198 | 0.52615729 |
| ! | photoreceptor activity | GO:0009881 | 50 | 28 | 0.67446939 | 0.3029 | 0.52729974 |
| ! | anion:cation symporter activity | GO:0015296 | 68 | 28 | 0.6764745 | 0.3029 | 0.52684002 |
| ! | auxiliary transport protein activity | GO:0015457 | 147 | 73 | 0.65367117 | 0.30541 | 0.53074299 |
| ! | catecholamine metabolism | GO:0006584 | 52 | 26 | 0.68099396 | 0.30715 | 0.53330222 |
| ! | hydrogen ion homeostasis | GO:0030641 | 65 | 26 | 0.67454403 | 0.30715 | 0.53283848 |
| ! | tubulin folding | GO:0007021 | 32 | 10 | 0.70767383 | 0.30724 | 0.53253154 |
| ! | dystrophin-associated glycoprotein complex | GO:0016010 | 26 | 10 | 0.7035427 | 0.30724 | 0.53206927 |
| ! | protein autoprocessing | GO:0016540 | 13 | 10 | 0.70332905 | 0.30724 | 0.53160781 |
| ! | channel regulator activity | GO:0016247 | 143 | 71 | 0.6606643 | 0.3076 | 0.5317695 |
| ! | negative regulation of angiogenesis | GO:0016525 | 30 | 18 | 0.69024866 | 0.30798 | 0.53196545 |
| ! | negative regulation of gene expression, epigenetic | GO:0045814 | 22 | 13 | 0.69912089 | 0.3111 | 0.53688971 |
| ! | adipocyte differentiation | GO:0045444 | 33 | 13 | 0.69519281 | 0.3111 | 0.53642567 |
| ! | biogenic amine catabolism | GO:0042402 | 22 | 13 | 0.69414643 | 0.3111 | 0.53596244 |
| ! | regulation of anti-apoptosis | GO:0045767 | 28 | 13 | 0.70005884 | 0.3111 | 0.5355 |
| ! | protein deubiquitination | GO:0016579 | 31 | 13 | 0.6989067 | 0.3111 | 0.53503836 |
| ! | glycine hydroxymethyltransferase activity | GO:0004372 | 21 | 9 | 0.71108607 | 0.31267 | 0.53727532 |
| ! | glial cell differentiation | GO:0010001 | 22 | 9 | 0.71132439 | 0.31267 | 0.53681295 |
| ! | establishment of cell polarity | GO:0030010 | 23 | 9 | 0.70662844 | 0.31267 | 0.53635138 |
| ! | oocyte axis determination (sensu Insecta) | GO:0048111 | 22 | 9 | 0.71086416 | 0.31267 | 0.53589059 |
| ! | C21-steroid hormone metabolism | GO:0008207 | 73 | 37 | 0.6708266 | 0.31336 | 0.53661219 |
| ! | amine receptor activity | GO:0008227 | 56 | 37 | 0.66478521 | 0.31336 | 0.53615197 |
| ! | ion channel clustering | GO:0045161 | 38 | 12 | 0.69190847 | 0.31343 | 0.53581221 |
| ! | carbohydrate kinase activity | GO:0019200 | 48 | 24 | 0.67952758 | 0.31479 | 0.53767641 |
| ! | germ cell migration | GO:0008354 | 42 | 24 | 0.67470799 | 0.31479 | 0.53721647 |
| ! | cell-substrate adherens junction | GO:0005924 | 50 | 22 | 0.681272 | 0.31655 | 0.53975833 |
| ! | anion exchanger activity | GO:0015380 | 21 | 11 | 0.69778858 | 0.3184 | 0.54244919 |
| ! | caspase activity | GO:0030693 | 20 | 11 | 0.69750919 | 0.3184 | 0.54198635 |
| ! | regulation of transforming growth factor beta receptor | GO:0017015 | 33 | 15 | 0.68523931 | 0.3211 | 0.54611637 |
| ! | retinoic acid metabolism | GO:0042573 | 24 | 15 | 0.68289954 | 0.3211 | 0.54565119 |
| ! | histone methyltransferase activity | GO:0042054 | 47 | 20 | 0.68098224 | 0.32395 | 0.55002574 |
| ! | histone deacetylase complex | GO:0000118 | 34 | 20 | 0.68048762 | 0.32395 | 0.54955804 |
| ! | frizzled-2 signaling pathway | GO:0007223 | 33 | 20 | 0.6743167 | 0.32395 | 0.54909112 |
| ! | axon guidance receptor activity | GO:0008046 | 51 | 20 | 0.68021694 | 0.32395 | 0.548625 |

Supplemental Table 1

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|---|---|---|---|---|---|---|---|
| ! | water-soluble vitamin biosynthesis | GO:0042364 | 19 | 10 | 0.6978412 | 0.32516 | 0.55020712 |
| ! | pancreatic elastase II activity | GO:0004281 | 13 | 10 | 0.70017256 | 0.32516 | 0.54974085 |
| ! | establishment of tissue polarity | GO:0007164 | 19 | 10 | 0.69268721 | 0.32516 | 0.54927536 |
| ! | nucleotide-sugar transporter activity | GO:0005338 | 25 | 10 | 0.6929085 | 0.32516 | 0.54881066 |
| ! | ionotropic glutamate receptor activity | GO:0004970 | 37 | 19 | 0.67414644 | 0.32812 | 0.55333846 |
| ! | adherens junction | GO:0005912 | 121 | 53 | 0.65760647 | 0.32819 | 0.55298906 |
| ! | post-embryonic development | GO:0009791 | 69 | 29 | 0.66966878 | 0.32899 | 0.55386924 |
| ! | blastoderm segmentation | GO:0007350 | 19 | 9 | 0.69829697 | 0.32937 | 0.55404144 |
| ! | membrane fusion | GO:0006944 | 102 | 50 | 0.65493728 | 0.33037 | 0.55525539 |
| ! | delayed rectifier potassium channel activity | GO:0005251 | 29 | 13 | 0.68233392 | 0.33174 | 0.55708864 |
| ! | metalloendopeptidase inhibitor activity | GO:0008191 | 26 | 13 | 0.68815441 | 0.33174 | 0.5566201 |
| ! | regulation of calcium ion-dependent exocytosis | GO:0017158 | 12 | 8 | 0.70093533 | 0.33294 | 0.55816412 |
| ! | cleavage of lamin | GO:0006922 | 9 | 8 | 0.69325164 | 0.33294 | 0.55769547 |
| ! | potassium channel regulator activity | GO:0015459 | 50 | 28 | 0.67080988 | 0.33296 | 0.55726107 |
| ! | cAMP-dependent protein kinase complex | GO:0005952 | 35 | 11 | 0.6900278 | 0.337 | 0.56354987 |
| ! | tubulin-tyrosine ligase activity | GO:0004835 | 22 | 11 | 0.68964461 | 0.337 | 0.56307789 |
| ! | establishment and/or maintenance of apical/basal cell polarity | GO:0035088 | 22 | 11 | 0.69140919 | 0.337 | 0.56260669 |
| ! | blood coagulation factor activity | GO:0003801 | 16 | 11 | 0.68893884 | 0.337 | 0.56213629 |
| ! | MAP kinase phosphatase activity | GO:0017017 | 21 | 11 | 0.6901806 | 0.337 | 0.56166667 |
| ! | transferase activity, transferring pentosyl groups | GO:0016763 | 46 | 25 | 0.6663406 | 0.33726 | 0.5616308 |
| ! | ephrin receptor activity | GO:0005003 | 34 | 16 | 0.67769344 | 0.33932 | 0.56458999 |
| ! | chloride channel activity | GO:0005254 | 86 | 45 | 0.65806523 | 0.34004 | 0.5653165 |
| ! | cytoskeleton-dependent intracellular transport | GO:0030705 | 194 | 89 | 0.64240003 | 0.3419 | 0.56793547 |
| ! | cell-matrix junction | GO:0030055 | 61 | 24 | 0.67035708 | 0.34235 | 0.56820986 |
| ! | oxidoreductase activity, acting on the CH-NH2 group of donors | GO:0016638 | 43 | 24 | 0.66967874 | 0.34235 | 0.56773753 |
| ! | sodium:potassium-exchanging ATPase complex | GO:0005890 | 25 | 10 | 0.68195771 | 0.34323 | 0.56872413 |
| ! | calcium-activated potassium channel activity | GO:0015269 | 22 | 10 | 0.68896583 | 0.34323 | 0.56825216 |
| ! | natural killer cell mediated cytotoxicity | GO:0042267 | 34 | 15 | 0.68062813 | 0.34352 | 0.5682607 |
| ! | cyclic-nucleotide phosphodiesterase activity | GO:0004112 | 58 | 22 | 0.66224063 | 0.34441 | 0.56926094 |
| ! | regulation of Wnt receptor signaling pathway | GO:0030111 | 49 | 22 | 0.66479064 | 0.34441 | 0.56878969 |
| ! | exonuclease activity, active with either ribo- or deoxyribonucleic acids and producing 5'-phosphomonoesters | GO:0016796 | 43 | 23 | 0.66607335 | 0.34541 | 0.56996935 |
| ! | maintenance of localization | GO:0051235 | 47 | 23 | 0.66579076 | 0.34541 | 0.56949831 |
| ! | cathepsin L activity | GO:0004217 | 20 | 14 | 0.67930302 | 0.34575 | 0.56958815 |
| ! | neurotransmitter uptake | GO:0001504 | 20 | 9 | 0.68605935 | 0.3469 | 0.57101114 |
| ! | nuclear membrane lumen | GO:0005641 | 17 | 9 | 0.68190082 | 0.3469 | 0.5705404 |
| ! | myosin binding | GO:0017022 | 22 | 8 | 0.6866766 | 0.349 | 0.57352142 |
| ! | defense response to pathogenic bacteria | GO:0042830 | 10 | 8 | 0.68629703 | 0.349 | 0.57304938 |
| ! | 3',5'-cyclic-nucleotide phosphodiesterase activity | GO:0004114 | 54 | 20 | 0.66660421 | 0.35019 | 0.57453047 |
| ! | immune cell mediated cytotoxicity | GO:0001909 | 42 | 20 | 0.66582021 | 0.35019 | 0.57405838 |
| ! | trypsin inhibitor activity | GO:0030304 | 23 | 13 | 0.67419449 | 0.35204 | 0.57661724 |
| ! | regulation of NF-kappaB-nucleus import | GO:0042345 | 29 | 13 | 0.67515952 | 0.35204 | 0.57614422 |
| ! | ribonucleoside metabolism | GO:0009119 | 24 | 13 | 0.68166317 | 0.35204 | 0.57567197 |
| ! | sarcoplasm | GO:0016528 | 25 | 13 | 0.6779509 | 0.35204 | 0.57520049 |
| ! | hemocyte development | GO:0007516 | 18 | 12 | 0.67341935 | 0.35315 | 0.57654194 |
| ! | gastrulation (sensu Mammalia) | GO:0010003 | 25 | 12 | 0.67315817 | 0.35315 | 0.57607052 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ! | synaptic vesicle docking during exocytosis | GO:0016081 | 29 | 12 | 0.67344609 | 0.35315 | 0.57559988 |
| ! | cGMP-mediated signaling | GO:0019934 | 21 | 12 | 0.67343881 | 0.35315 | 0.57513 |
| ! | outer membrane | GO:0019867 | 171 | 75 | 0.65183729 | 0.35549 | 0.57846864 |
| ! | adenosine receptor activity, G-protein coupled | GO:0001609 | 28 | 18 | 0.6713941 | 0.35617 | 0.57910281 |
| ! | sodium:dicarboxylate symporter activity | GO:0017153 | 32 | 11 | 0.67588234 | 0.35642 | 0.57903738 |
| ! | UDP-glucosyltransferase activity | GO:0035251 | 30 | 11 | 0.67710906 | 0.35642 | 0.57856623 |
| ! | ribonucleotide catabolism | GO:0009261 | 21 | 11 | 0.68056865 | 0.35642 | 0.57809585 |
| ! | response to temperature | GO:0009266 | 138 | 64 | 0.64521421 | 0.35931 | 0.58230987 |
| ! | dendrite | GO:0030425 | 53 | 29 | 0.66143096 | 0.36003 | 0.58300313 |
| ! | learning | GO:0007612 | 62 | 31 | 0.65840869 | 0.36083 | 0.5838247 |
| ! | ATP hydrolysis coupled proton transport | GO:0015991 | 25 | 10 | 0.6780546 | 0.36154 | 0.58449943 |
| ! | protein-lysine N-methyltransferase activity | GO:0016279 | 37 | 16 | 0.66987358 | 0.36328 | 0.58683692 |
| ! | protein phosphatase type 1 regulator activity | GO:0008599 | 36 | 16 | 0.66569673 | 0.36328 | 0.58636214 |
| ! | porphyrin biosynthesis | GO:0006779 | 34 | 16 | 0.6642637 | 0.36328 | 0.58588812 |
| ! | thyroid hormone generation | GO:0006590 | 21 | 9 | 0.6724352 | 0.36429 | 0.58704245 |
| ! | asymmetric protein localization | GO:0008105 | 24 | 9 | 0.67259874 | 0.36429 | 0.58656864 |
| ! | calcium ion homeostasis | GO:0006874 | 108 | 62 | 0.65143237 | 0.36432 | 0.58614387 |
| ! | 5'-nucleotidase activity | GO:0008253 | 17 | 8 | 0.67896147 | 0.3656 | 0.58772925 |
| ! | lysozyme activity | GO:0003796 | 12 | 8 | 0.68063293 | 0.3656 | 0.58725604 |
| ! | anchored to plasma membrane | GO:0046658 | 58 | 26 | 0.66183906 | 0.36579 | 0.58708854 |
| ! | alcohol dehydrogenase activity, zinc-dependent | GO:0004024 | 26 | 15 | 0.66669174 | 0.36583 | 0.58668075 |
| ! | Rho small monomeric GTPase activity | GO:0003931 | 34 | 15 | 0.67128056 | 0.36583 | 0.58620952 |
| ! | phenol metabolism | GO:0018958 | 53 | 27 | 0.6600712 | 0.36588 | 0.5858191 |
| ! | protein methyltransferase activity | GO:0008276 | 68 | 27 | 0.65958205 | 0.36588 | 0.58534932 |
| ! | antiporter activity | GO:0015297 | 116 | 58 | 0.64529593 | 0.36681 | 0.58636695 |
| ! | transcription from Pol I promoter | GO:0006360 | 24 | 14 | 0.66906304 | 0.36754 | 0.58706349 |
| ! | neurotransmitter:sodium symporter activity | GO:0005328 | 44 | 22 | 0.65528328 | 0.37274 | 0.59489304 |
| ! | negative regulation of Wnt receptor signaling pathway | GO:0030178 | 26 | 13 | 0.6638027 | 0.37333 | 0.59535839 |
| ! | FK506-sensitive peptidyl-prolyl cis-trans isomerase | GO:0030051 | 25 | 13 | 0.66904095 | 0.37333 | 0.59488287 |
| ! | wound healing | GO:0042060 | 84 | 47 | 0.65136871 | 0.37421 | 0.59580922 |
| ! | folic acid and derivative metabolism | GO:0006760 | 17 | 12 | 0.66546634 | 0.37456 | 0.59589091 |
| ! | exosome (RNase complex) | GO:0000178 | 18 | 11 | 0.67164944 | 0.37591 | 0.59756211 |
| ! | nucleoside kinase activity | GO:0019206 | 20 | 11 | 0.66669483 | 0.37591 | 0.59708635 |
| ! | steroid hormone receptor activity | GO:0003707 | 120 | 48 | 0.64882256 | 0.37773 | 0.59949988 |
| ! | endodeoxyribonuclease activity | GO:0004520 | 42 | 21 | 0.65308225 | 0.37832 | 0.59995898 |
| ! | negative regulation of growth | GO:0045926 | 88 | 45 | 0.6469909 | 0.38126 | 0.60414114 |
| ! | insulin-like growth factor receptor binding | GO:0005159 | 28 | 8 | 0.66741569 | 0.38235 | 0.6053875 |
| ! | estrogen receptor binding | GO:0030331 | 16 | 8 | 0.66372601 | 0.38235 | 0.60490741 |
| ! | fibroblast growth factor receptor activity | GO:0005007 | 20 | 8 | 0.66408684 | 0.38235 | 0.60442809 |
| ! | DNA-directed RNA polymerase I activity | GO:0003900 | 41 | 18 | 0.65491487 | 0.3825 | 0.60418646 |
| ! | tube morphogenesis | GO:0035239 | 85 | 38 | 0.65200829 | 0.38734 | 0.61134755 |
| ! | negative regulation of cell size | GO:0045792 | 75 | 38 | 0.64853421 | 0.38734 | 0.61086427 |
| ! | translational elongation | GO:0006414 | 76 | 36 | 0.6460358 | 0.38876 | 0.61261943 |
| ! | dicarboxylic acid transporter activity | GO:0005310 | 37 | 14 | 0.65711469 | 0.38999 | 0.61407265 |
| ! | insulin receptor binding | GO:0005158 | 25 | 14 | 0.66118401 | 0.38999 | 0.61358837 |
| ! | myoblast differentiation | GO:0045445 | 36 | 15 | 0.65749749 | 0.39009 | 0.61326206 |

Supplemental Table 1

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|---|---|---|---|---|---|---|---|
| ! | cell cortex | GO:0005938 | 71 | 34 | 0.65175557 | 0.391 | 0.61420866 |
| ! | epithelial cell differentiation | GO:0030855 | 64 | 31 | 0.64741269 | 0.39448 | 0.61918773 |
| ! | complement activation, classical pathway | GO:0006958 | 51 | 31 | 0.64853873 | 0.39448 | 0.61870094 |
| ! | 35S primary transcript processing | GO:0006365 | 22 | 13 | 0.65257006 | 0.39536 | 0.61959403 |
| ! | retinoic acid receptor activity | GO:0003708 | 20 | 11 | 0.65464016 | 0.3956 | 0.61948352 |
| ! | eye photoreceptor cell development | GO:0042462 | 28 | 11 | 0.66052943 | 0.3956 | 0.61899765 |
| ! | GPI anchor metabolism | GO:0006505 | 21 | 11 | 0.6570231 | 0.3956 | 0.61851254 |
| ! | tRNA binding | GO:0000049 | 21 | 12 | 0.65325263 | 0.3966 | 0.61959045 |
| ! | regulation of lipid metabolism | GO:0019216 | 50 | 27 | 0.64805105 | 0.39808 | 0.62141596 |
| ! | myo-inositol metabolism | GO:0006020 | 11 | 8 | 0.66175551 | 0.39908 | 0.62248991 |
| ! | galactose metabolism | GO:0006012 | 18 | 8 | 0.65511831 | 0.39908 | 0.62200359 |
| ! | hydrogen transport | GO:0006818 | 199 | 96 | 0.6419923 | 0.39957 | 0.62228115 |
| ! | amino acid derivative metabolism | GO:0006575 | 166 | 88 | 0.63509289 | 0.39983 | 0.62220035 |
| ! | oocyte axis determination | GO:0007309 | 24 | 10 | 0.65526014 | 0.40019 | 0.62227518 |
| ! | metabotropic glutamate receptor signaling pathway | GO:0007216 | 17 | 10 | 0.65870507 | 0.40019 | 0.62179054 |
| ! | thyroid hormone metabolism | GO:0042403 | 23 | 10 | 0.6592478 | 0.40019 | 0.62130665 |
| ! | methionine metabolism | GO:0006555 | 21 | 10 | 0.6534815 | 0.40019 | 0.62082352 |
| ! | reproductive behavior | GO:0019098 | 40 | 24 | 0.64813152 | 0.40167 | 0.62263531 |
| ! | regulation of pH | GO:0006885 | 54 | 22 | 0.64646257 | 0.40182 | 0.62238424 |
| ! | proton transport | GO:0015992 | 165 | 81 | 0.64221995 | 0.40329 | 0.62417653 |
| ! | vitamin A metabolism | GO:0006776 | 34 | 23 | 0.64589251 | 0.4049 | 0.62618256 |
| ! | aldehyde metabolism | GO:0006081 | 41 | 23 | 0.64486766 | 0.4049 | 0.62569752 |
| ! | PDZ domain binding | GO:0030165 | 54 | 23 | 0.64824782 | 0.4049 | 0.62521324 |
| ! | morphogenesis of an epithelium | GO:0002009 | 134 | 66 | 0.64051851 | 0.4067 | 0.62750696 |
| ! | peripheral nervous system development | GO:0007422 | 129 | 64 | 0.63986474 | 0.40988 | 0.63192473 |
| ! | structural constituent of muscle | GO:0008307 | 131 | 64 | 0.63955335 | 0.40988 | 0.63143676 |
| ! | transferase activity, transferring alkyl or aryl (other than | GO:0016765 | 136 | 68 | 0.63924349 | 0.4107 | 0.63221181 |
| ! | regulation of blood pressure | GO:0008217 | 104 | 63 | 0.63878301 | 0.41239 | 0.63432386 |
| ! | dopamine receptor activity | GO:0004952 | 23 | 14 | 0.64752746 | 0.41301 | 0.6347881 |
| ! | eye morphogenesis | GO:0001654 | 139 | 62 | 0.64149922 | 0.4138 | 0.6355127 |
| ! | 1-phosphatidylinositol-4-phosphate 5-kinase activity | GO:0016308 | 29 | 11 | 0.6488179 | 0.41594 | 0.63830792 |
| ! | ribonucleoside diphosphate metabolism | GO:0009185 | 21 | 11 | 0.64778376 | 0.41594 | 0.63781729 |
| ! | limb morphogenesis | GO:0035108 | 109 | 50 | 0.63288265 | 0.41686 | 0.6387371 |
| ! | kainate selective glutamate receptor activity | GO:0015277 | 14 | 8 | 0.64847946 | 0.41694 | 0.63836938 |
| ! | peptide YY receptor activity | GO:0001601 | 11 | 8 | 0.64365588 | 0.41694 | 0.63787983 |
| ! | viral replication | GO:0008166 | 12 | 8 | 0.64465808 | 0.41694 | 0.63739103 |
| ! | vitamin K biosynthesis | GO:0042371 | 22 | 8 | 0.64359371 | 0.41694 | 0.63690299 |
| ! | mesoderm cell fate commitment | GO:0001710 | 13 | 8 | 0.6513628 | 0.41694 | 0.63641568 |
| ! | purine nucleoside binding | GO:0001883 | 18 | 13 | 0.64248627 | 0.41696 | 0.63595963 |
| ! | RNA-dependent DNA replication | GO:0006278 | 29 | 13 | 0.65143514 | 0.41696 | 0.6354738 |
| ! | glucosyltransferase activity | GO:0046527 | 32 | 12 | 0.64346788 | 0.41887 | 0.63789744 |
| ! | male genitalia morphogenesis | GO:0030539 | 21 | 9 | 0.6461521 | 0.41898 | 0.63757826 |
| ! | nucleotide-sugar transport | GO:0015780 | 24 | 9 | 0.64942119 | 0.41898 | 0.6370923 |
| ! | chaperone binding | GO:0051087 | 24 | 10 | 0.64724157 | 0.42016 | 0.6384 |
| ! | apoptosis inhibitor activity | GO:0008189 | 106 | 46 | 0.64152211 | 0.42102 | 0.63921986 |
| ! | nucleosome | GO:0000786 | 83 | 48 | 0.63823228 | 0.42243 | 0.64087289 |

Supplemental Table 1

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|---|---|---|---|---|---|---|---|
| ! | G-protein coupled receptor activity, unknown ligand | GO:0016526 | 54 | 40 | 0.64050179 | 0.42277 | 0.64090133 |
| ! | cell fate determination | GO:0001709 | 71 | 35 | 0.63275285 | 0.42581 | 0.6450197 |
| ! | insulin receptor signaling pathway | GO:0008286 | 99 | 35 | 0.64048591 | 0.42581 | 0.64453031 |
| ! | glutamine family amino acid metabolism | GO:0009064 | 64 | 36 | 0.63951114 | 0.42677 | 0.64549367 |
| ! | intercellular junction assembly and/or maintenance | GO:0045216 | 64 | 34 | 0.63970875 | 0.42843 | 0.64751352 |
| ! | signal sequence binding | GO:0005048 | 76 | 30 | 0.63499025 | 0.43052 | 0.65017971 |
| ! | bile acid transport | GO:0015721 | 48 | 25 | 0.63705075 | 0.43066 | 0.64989917 |
| ! | cell killing | GO:0001906 | 44 | 22 | 0.63967295 | 0.43119 | 0.65020714 |
| ! | Golgi cis-face | GO:0005801 | 13 | 8 | 0.64018131 | 0.43536 | 0.6559994 |
| ! | smooth endoplasmic reticulum | GO:0005790 | 17 | 8 | 0.64130811 | 0.43536 | 0.6555043 |
| ! | phosphatase inhibitor activity | GO:0019212 | 41 | 21 | 0.63811314 | 0.43561 | 0.65538609 |
| ! | phospholipase inhibitor activity | GO:0004859 | 26 | 17 | 0.63243078 | 0.43663 | 0.65642566 |
| ! | adenylate cyclase activity | GO:0004016 | 21 | 11 | 0.63884652 | 0.43732 | 0.65696792 |
| ! | neuroblast proliferation | GO:0007405 | 24 | 11 | 0.6410553 | 0.43732 | 0.65647359 |
| ! | melatonin receptor activity | GO:0008502 | 19 | 14 | 0.63422559 | 0.43766 | 0.65649 |
| ! | hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amidines | GO:0016813 | 30 | 14 | 0.63766886 | 0.43766 | 0.65599677 |
| ! | pyrimidine ribonucleotide biosynthesis | GO:0009220 | 27 | 16 | 0.6382489 | 0.43801 | 0.65602849 |
| ! | sperm motility | GO:0030317 | 35 | 16 | 0.63311455 | 0.43801 | 0.65553635 |
| ! | intercellular junction assembly | GO:0007043 | 32 | 15 | 0.64102717 | 0.43933 | 0.657019 |
| ! | alpha2-adrenergic receptor activity | GO:0004938 | 18 | 10 | 0.63664771 | 0.44013 | 0.65772236 |
| ! | common-partner SMAD protein phosphorylation | GO:0007182 | 23 | 10 | 0.64038887 | 0.44013 | 0.65723005 |
| ! | metabolic compound salvage | GO:0043094 | 19 | 10 | 0.63316601 | 0.44013 | 0.65673848 |
| ! | eye photoreceptor cell differentiation | GO:0001754 | 34 | 13 | 0.63389688 | 0.44028 | 0.6564713 |
| ! | calpain activity | GO:0004198 | 23 | 13 | 0.63302752 | 0.44028 | 0.65598103 |
| ! | glycerol-3-phosphate metabolism | GO:0006072 | 16 | 8 | 0.62852856 | 0.45298 | 0.67439933 |
| ! | initiation of viral infection | GO:0019059 | 21 | 8 | 0.63065244 | 0.45298 | 0.67389642 |
| ! | protein amino acid sulfation | GO:0006477 | 18 | 9 | 0.63007277 | 0.45653 | 0.67867165 |
| ! | di-, tri-valent inorganic cation homeostasis | GO:0030005 | 174 | 94 | 0.62716635 | 0.45857 | 0.68119669 |
| ! | 3',5'-cAMP binding | GO:0030552 | 30 | 11 | 0.63197065 | 0.45942 | 0.68195156 |
| ! | homophilic cell adhesion | GO:0007156 | 179 | 98 | 0.63040261 | 0.45943 | 0.68145937 |
| ! | heterocycle metabolism | GO:0046483 | 168 | 98 | 0.63023728 | 0.45943 | 0.68095308 |
| ! | cell-substrate junction assembly | GO:0007044 | 21 | 10 | 0.63216479 | 0.46175 | 0.68388363 |
| ! | COPI-coated vesicle | GO:0030137 | 19 | 10 | 0.62376678 | 0.46175 | 0.6833763 |
| ! | cyclophilin | GO:0004600 | 27 | 14 | 0.62718477 | 0.46194 | 0.6831507 |
| ! | quinone cofactor biosynthesis | GO:0045426 | 31 | 14 | 0.62544371 | 0.46194 | 0.68264467 |
| ! | thiolester hydrolase activity | GO:0016790 | 177 | 87 | 0.63063923 | 0.4622 | 0.68252332 |
| ! | phototransduction | GO:0007602 | 89 | 56 | 0.62409512 | 0.46289 | 0.68303665 |
| ! | excretion | GO:0007588 | 110 | 55 | 0.62845333 | 0.46336 | 0.68322483 |
| ! | glycerol metabolism | GO:0006071 | 30 | 15 | 0.63126144 | 0.46412 | 0.68384003 |
| ! | receptor signaling complex scaffold activity | GO:0030159 | 40 | 18 | 0.62561393 | 0.46413 | 0.68335007 |
| ! | fat-soluble vitamin metabolism | GO:0006775 | 72 | 40 | 0.62371998 | 0.46433 | 0.68314038 |
| ! | hematopoietin/interferon-class (D200-domain) cytokine | GO:0005126 | 55 | 40 | 0.62698569 | 0.46433 | 0.68263696 |
| ! | RNA methyltransferase activity | GO:0008173 | 33 | 16 | 0.62943197 | 0.46447 | 0.68233995 |
| ! | amino acid derivative catabolism | GO:0042219 | 27 | 16 | 0.62960227 | 0.46447 | 0.68183786 |
| ! | glutamine family amino acid catabolism | GO:0009065 | 23 | 13 | 0.62875763 | 0.46452 | 0.68140985 |

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|---|---|---|---|---|---|---|---|
| ! | oxidoreductase activity, acting on the CH-NH group of donors, NAD or NADP as acceptor | GO:0016646 | 21 | 13 | 0.6254256 | 0.46452 | 0.68090918 |
| ! | exoribonuclease activity | GO:0004532 | 39 | 20 | 0.6309495 | 0.46456 | 0.68046784 |
| ! | protein kinase C binding | GO:0005080 | 50 | 20 | 0.62812201 | 0.46456 | 0.6799686 |
| ! | collagen | GO:0005581 | 89 | 46 | 0.62852717 | 0.46492 | 0.67999663 |
| ! | carbon-carbon lyase activity | GO:0016830 | 86 | 46 | 0.62821647 | 0.46492 | 0.67949846 |
| ! | basement membrane | GO:0005604 | 113 | 54 | 0.62362293 | 0.46563 | 0.68003796 |
| ! | cAMP metabolism | GO:0046058 | 36 | 21 | 0.63129488 | 0.46607 | 0.68018263 |
| ! | induction of apoptosis by extracellular signals | GO:0008624 | 82 | 48 | 0.62974026 | 0.4674 | 0.681625 |
| ! | indole and derivative metabolism | GO:0042430 | 13 | 8 | 0.62159348 | 0.47172 | 0.6874225 |
| ! | clathrin coat of endocytic vesicle | GO:0030128 | 19 | 8 | 0.61388646 | 0.47172 | 0.68692073 |
| ! | inorganic anion exchanger activity | GO:0005452 | 16 | 9 | 0.61511219 | 0.47651 | 0.69338982 |
| ! | snoRNA binding | GO:0030515 | 13 | 9 | 0.62125643 | 0.47651 | 0.69288444 |
| ! | negative regulation of neuron differentiation | GO:0045665 | 15 | 9 | 0.61420444 | 0.47651 | 0.69237979 |
| ! | regulation of tyrosine phosphorylation of Stat3 protein | GO:0042516 | 26 | 11 | 0.6178983 | 0.4813 | 0.69883079 |
| ! | nucleobase transporter activity | GO:0015205 | 31 | 11 | 0.61722532 | 0.4813 | 0.69832255 |
| ! | ATP/ADP exchange | GO:0006854 | 28 | 11 | 0.62085471 | 0.4813 | 0.69781504 |
| ! | sulfate transporter activity | GO:0015116 | 16 | 10 | 0.62135669 | 0.48308 | 0.69988715 |
| ! | lymphocyte antigen | GO:0005557 | 18 | 10 | 0.61536077 | 0.48308 | 0.69937925 |
| ! | pteridine and derivative biosynthesis | GO:0042559 | 26 | 10 | 0.61493883 | 0.48308 | 0.69887208 |
| ! | toxin activity | GO:0015070 | 18 | 12 | 0.61908622 | 0.48625 | 0.70294837 |
| ! | regulation of long-term neuronal synaptic plasticity | GO:0048169 | 29 | 14 | 0.61768999 | 0.48681 | 0.70324833 |
| ! | interleukin-8 binding | GO:0019959 | 19 | 14 | 0.61313408 | 0.48681 | 0.70273947 |
| ! | mitochondrial membrane organization and biogenesis | GO:0007006 | 27 | 13 | 0.6129294 | 0.48826 | 0.70432299 |
| ! | zymogen granule | GO:0042588 | 34 | 15 | 0.61570541 | 0.49014 | 0.70652406 |
| ! | glucuronosyltransferase activity | GO:0015020 | 31 | 15 | 0.61519655 | 0.49014 | 0.70601394 |
| ! | oxidoreductase activity, acting on sulfur group of donors, NAD or NADP as acceptor | GO:0016668 | 21 | 8 | 0.60386508 | 0.49086 | 0.70654091 |
| ! | internal side of plasma membrane | GO:0009898 | 16 | 8 | 0.6091222 | 0.49086 | 0.70603151 |
| ! | oxidoreductase activity, acting on the CH-NH2 group of donors, oxygen as acceptor | GO:0016641 | 37 | 22 | 0.61655965 | 0.49267 | 0.70812439 |
| ! | cell-cell adherens junction | GO:0005913 | 44 | 20 | 0.61892313 | 0.49395 | 0.70945302 |
| ! | AMP binding | GO:0016208 | 50 | 25 | 0.61333148 | 0.49636 | 0.71240158 |
| ! | fatty acid transport | GO:0015908 | 17 | 9 | 0.60364419 | 0.49718 | 0.71306549 |
| ! | GPI-anchored membrane-bound receptor | GO:0015025 | 14 | 9 | 0.61039052 | 0.49718 | 0.71255323 |
| ! | nucleotidase activity | GO:0008252 | 18 | 9 | 0.61099353 | 0.49718 | 0.71204171 |
| ! | N-methyl-D-aspartate selective glutamate receptor activity | GO:0004972 | 14 | 9 | 0.61168367 | 0.49718 | 0.71153092 |
| ! | proteasomal ubiquitin-dependent protein catabolism | GO:0043161 | 21 | 9 | 0.60708303 | 0.49718 | 0.71102086 |
| ! | organic anion transport | GO:0015711 | 41 | 26 | 0.61529664 | 0.49754 | 0.711026 |
| ! | striated muscle thin filament | GO:0005865 | 46 | 21 | 0.61395406 | 0.4976 | 0.71060272 |
| ! | regulation of exocytosis | GO:0017157 | 54 | 23 | 0.61335459 | 0.49855 | 0.71145011 |
| ! | male sex differentiation | GO:0046661 | 64 | 29 | 0.61658152 | 0.49943 | 0.71219646 |
| ! | serpin | GO:0004868 | 54 | 32 | 0.61659805 | 0.50096 | 0.713868 |
| ! | regulation of striated muscle contraction | GO:0006942 | 55 | 31 | 0.61928676 | 0.50237 | 0.71536627 |
| ! | oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor | GO:0016620 | 64 | 31 | 0.61575916 | 0.50237 | 0.71485603 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ! | regulation of nitric oxide biosynthesis | GO:0045428 | 22 | 10 | 0.61102192 | 0.50301 | 0.71525656 |
| ! | protein carrier activity | GO:0008320 | 26 | 10 | 0.60901891 | 0.50301 | 0.71474712 |
| ! | extracellular matrix structural constituent conferring tensile | GO:0030020 | 72 | 37 | 0.61842162 | 0.50587 | 0.7182994 |
| ! | hydro-lyase activity | GO:0016836 | 92 | 47 | 0.61997101 | 0.50676 | 0.71905135 |
| ! | embryonic limb morphogenesis | GO:0030326 | 94 | 46 | 0.61613372 | 0.50862 | 0.72117761 |
| ! | sulfotransferase activity | GO:0008146 | 55 | 41 | 0.61539664 | 0.50863 | 0.72067958 |
| ! | amino acid binding | GO:0016597 | 21 | 12 | 0.60303306 | 0.50889 | 0.72053623 |
| ! | electron carrier activity | GO:0009055 | 82 | 44 | 0.61820541 | 0.50977 | 0.72127032 |
| ! | response to pain | GO:0048265 | 14 | 8 | 0.60001404 | 0.50988 | 0.72091467 |
| ! | S-methyltransferase activity | GO:0008172 | 12 | 8 | 0.59510002 | 0.50988 | 0.72040411 |
| ! | prostaglandin-F synthase activity | GO:0047017 | 14 | 8 | 0.59796084 | 0.50988 | 0.71989427 |
| ! | intercellular canaliculus | GO:0046581 | 14 | 8 | 0.59648445 | 0.50988 | 0.71938515 |
| ! | cation-transporting ATPase activity | GO:0019829 | 91 | 42 | 0.61836035 | 0.51043 | 0.71965219 |
| ! | nitric-oxide synthase regulator activity | GO:0030235 | 39 | 14 | 0.60490996 | 0.51099 | 0.71993294 |
| ! | alpha-adrenergic receptor activity | GO:0004936 | 22 | 13 | 0.60280077 | 0.51222 | 0.7211566 |
| ! | regulation of heart contraction rate | GO:0008016 | 127 | 55 | 0.61388483 | 0.51245 | 0.72097161 |
| ! | complement activation | GO:0006956 | 91 | 57 | 0.61600388 | 0.51307 | 0.7213352 |
| ! | detection of light | GO:0009583 | 93 | 58 | 0.61337155 | 0.51506 | 0.72362303 |
| ! | cellular polysaccharide metabolism | GO:0044264 | 103 | 53 | 0.62224192 | 0.51532 | 0.72347882 |
| ! | inward rectifier potassium channel activity | GO:0005242 | 29 | 15 | 0.60291551 | 0.51582 | 0.72367152 |
| ! | photoreceptor cell differentiation | GO:0046530 | 40 | 16 | 0.60838251 | 0.51698 | 0.72478925 |
| ! | cellular morphogenesis during differentiation | GO:0000904 | 38 | 16 | 0.60860541 | 0.51698 | 0.72428027 |
| ! | thyroid hormone receptor activity | GO:0004887 | 19 | 9 | 0.59969405 | 0.51738 | 0.724332 |
| ! | neuron cell differentiation | GO:0030182 | 140 | 63 | 0.61547499 | 0.5178 | 0.72441164 |
| ! | cyclophilin-type peptidyl-prolyl cis-trans isomerase activity | GO:0042027 | 30 | 17 | 0.60696934 | 0.51942 | 0.72616882 |
| ! | perception of taste | GO:0050909 | 31 | 19 | 0.61091309 | 0.52118 | 0.72811912 |
| ! | microtubule-based movement | GO:0007018 | 177 | 79 | 0.62123732 | 0.52291 | 0.73002481 |
| ! | mating behavior | GO:0007617 | 34 | 22 | 0.60427916 | 0.52388 | 0.73086755 |
| ! | gamma-aminobutyric acid signaling pathway | GO:0007214 | 41 | 22 | 0.60896773 | 0.52388 | 0.73035681 |
| ! | coenzyme biosynthesis | GO:0009108 | 191 | 94 | 0.61992537 | 0.52396 | 0.72995824 |
| ! | associative learning | GO:0008306 | 14 | 10 | 0.60204055 | 0.52427 | 0.72988043 |
| ! | peptide transporter activity | GO:0015197 | 19 | 10 | 0.60030894 | 0.52427 | 0.72937144 |
| ! | glucosidase activity | GO:0015926 | 16 | 10 | 0.59510337 | 0.52427 | 0.72886317 |
| ! | ribonucleotide metabolism | GO:0009259 | 172 | 92 | 0.61428049 | 0.52624 | 0.73109248 |
| ! | steroid hormone receptor binding | GO:0035258 | 21 | 11 | 0.5946826 | 0.52663 | 0.73112516 |
| ! | ubiquinone biosynthesis | GO:0006744 | 18 | 11 | 0.59375168 | 0.52663 | 0.73061672 |
| ! | pyrimidine nucleotide sugar transporter activity | GO:0015165 | 17 | 8 | 0.58994429 | 0.52903 | 0.73343631 |
| ! | ionotropic glutamate receptor complex | GO:0008328 | 13 | 8 | 0.59043157 | 0.52903 | 0.73292698 |
| ! | nuclear positioning | GO:0040023 | 19 | 8 | 0.59048621 | 0.52903 | 0.73241836 |
| ! | dorsal/ventral pattern formation | GO:0009953 | 50 | 23 | 0.60604847 | 0.53156 | 0.73541068 |
| ! | morphogenesis of embryonic epithelium | GO:0016331 | 45 | 23 | 0.60701593 | 0.53156 | 0.73490104 |
| ! | organic acid:sodium symporter activity | GO:0005343 | 51 | 23 | 0.60360323 | 0.53156 | 0.73439211 |
| ! | glycine-inhibited chloride channel activity | GO:0004891 | 21 | 12 | 0.59672108 | 0.53253 | 0.73522308 |
| ! | tissue kallikrein activity | GO:0004293 | 38 | 29 | 0.60787479 | 0.5362 | 0.73977801 |
| ! | genitalia morphogenesis | GO:0035112 | 31 | 13 | 0.60235335 | 0.53626 | 0.73934948 |
| ! | cAMP-dependent protein kinase regulator activity | GO:0008603 | 35 | 13 | 0.59485097 | 0.53626 | 0.73883888 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ! | Golgi organization and biogenesis | GO:0007030 | 32 | 13 | 0.59581646 | 0.53626 | 0.73832899 |
| ! | dopamine receptor signaling pathway | GO:0007212 | 46 | 28 | 0.61096371 | 0.53724 | 0.73916814 |
| ! | lipid glycosylation | GO:0030259 | 17 | 9 | 0.59109165 | 0.53759 | 0.73913994 |
| ! | hydrogen-translocating V-type ATPase activity | GO:0000260 | 18 | 9 | 0.58497831 | 0.53759 | 0.73863089 |
| ! | clathrin-coated endocytic vesicle | GO:0045334 | 26 | 9 | 0.5913226 | 0.53759 | 0.73812254 |
| ! | dopamine metabolism | GO:0042417 | 21 | 9 | 0.59040342 | 0.53759 | 0.73761489 |
| ! | vitamin K metabolism | GO:0042373 | 23 | 9 | 0.58548677 | 0.53759 | 0.73710794 |
| ! | embryo implantation | GO:0007566 | 52 | 31 | 0.60687109 | 0.54008 | 0.74001346 |
| ! | transcriptional elongation regulator activity | GO:0003711 | 31 | 15 | 0.59555336 | 0.54092 | 0.74065573 |
| ! | RNA elongation | GO:0006354 | 28 | 15 | 0.59882932 | 0.54092 | 0.74014774 |
| ! | segmentation | GO:0035282 | 63 | 33 | 0.60407118 | 0.54307 | 0.74258029 |
| ! | polyol metabolism | GO:0019751 | 31 | 16 | 0.59513814 | 0.54394 | 0.74326048 |
| ! | SNAP receptor activity | GO:0005484 | 27 | 10 | 0.58563744 | 0.54524 | 0.7445269 |
| ! | positive regulation of cell migration | GO:0030335 | 21 | 10 | 0.58851893 | 0.54524 | 0.74401765 |
| ! | guanylate cyclase activity | GO:0004383 | 28 | 17 | 0.60239875 | 0.54631 | 0.74496818 |
| ! | oxidoreductase activity, acting on sulfur group of donors | GO:0016667 | 40 | 17 | 0.60170842 | 0.54631 | 0.74445932 |
| ! | mannose binding | GO:0005537 | 23 | 17 | 0.60252121 | 0.54631 | 0.74395116 |
| ! | protein threonine/tyrosine kinase activity | GO:0004712 | 26 | 11 | 0.58519858 | 0.54795 | 0.74567548 |
| ! | intercellular junction maintenance | GO:0045217 | 13 | 11 | 0.58535555 | 0.54795 | 0.74516718 |
| ! | Arp2/3 protein complex | GO:0005885 | 14 | 8 | 0.57773105 | 0.54849 | 0.74539343 |
| ! | tRNA processing | GO:0008033 | 70 | 38 | 0.60711333 | 0.54887 | 0.74540208 |
| ! | dicarboxylic acid transport | GO:0006835 | 44 | 18 | 0.60143508 | 0.54891 | 0.74494929 |
| ! | alcohol dehydrogenase activity | GO:0004022 | 30 | 19 | 0.59708807 | 0.55046 | 0.746545 |
| ! | phosphorus-oxygen lyase activity | GO:0016849 | 32 | 19 | 0.59670069 | 0.55046 | 0.74603784 |
| ! | ER to Golgi transport | GO:0006888 | 110 | 41 | 0.61010061 | 0.55068 | 0.74582933 |
| ! | nitric oxide metabolism | GO:0046209 | 50 | 20 | 0.5988492 | 0.55359 | 0.74926191 |
| ! | lipid binding | GO:0006630 | 26 | 12 | 0.59162873 | 0.55573 | 0.75164837 |
| ! | FAD binding | GO:0050660 | 31 | 12 | 0.59045232 | 0.55573 | 0.75113913 |
| ! | histone deacetylase activity | GO:0004407 | 16 | 12 | 0.58504292 | 0.55573 | 0.75063057 |
| ! | intramolecular oxidoreductase activity | GO:0016860 | 70 | 45 | 0.60610207 | 0.5573 | 0.75224188 |
| ! | protein phosphatase regulator activity | GO:0019888 | 111 | 48 | 0.60569735 | 0.55993 | 0.75528083 |
| ! | endoderm development | GO:0007492 | 34 | 13 | 0.58983858 | 0.56074 | 0.75586236 |
| ! | phosphatase regulator activity | GO:0019208 | 121 | 51 | 0.60310829 | 0.56138 | 0.75621411 |
| ! | nucleoside-diphosphate kinase activity | GO:0004550 | 22 | 14 | 0.5901096 | 0.56158 | 0.75597308 |
| ! | small nuclear ribonucleoprotein | GO:0003734 | 26 | 14 | 0.58708145 | 0.56158 | 0.75546332 |
| ! | mRNA catabolism | GO:0006402 | 55 | 25 | 0.60041093 | 0.56334 | 0.75732028 |
| ! | regulation of neuron differentiation | GO:0045664 | 57 | 25 | 0.59772593 | 0.56334 | 0.7568103 |
| ! | antigen presentation, endogenous antigen | GO:0019883 | 44 | 25 | 0.60065902 | 0.56334 | 0.75630101 |
| ! | small nucleolar ribonucleoprotein complex | GO:0005732 | 38 | 23 | 0.60198746 | 0.56345 | 0.75593998 |
| ! | vitamin biosynthesis | GO:0009110 | 47 | 23 | 0.59608337 | 0.56345 | 0.75543196 |
| ! | appendage morphogenesis | GO:0035107 | 114 | 53 | 0.60734675 | 0.56365 | 0.75519258 |
| ! | calcium-dependent cell-cell adhesion | GO:0016339 | 45 | 26 | 0.60166605 | 0.56457 | 0.75591755 |
| ! | insulin secretion | GO:0030073 | 31 | 15 | 0.58703264 | 0.56568 | 0.75689577 |
| ! | fructose metabolism | GO:0006000 | 33 | 15 | 0.59032119 | 0.56568 | 0.75638847 |
| ! | quinone cofactor metabolism | GO:0042375 | 32 | 15 | 0.59178954 | 0.56568 | 0.75588185 |
| ! | protein degradation tagging activity | GO:0000211 | 25 | 10 | 0.57560366 | 0.56633 | 0.75624388 |

Supplemental Table 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ! | ferric iron binding | GO:0008199 | 14 | 10 | 0.58203381 | 0.56633 | 0.75573803 |
| ! | cholesterol absorption | GO:0030299 | 19 | 10 | 0.58273114 | 0.56633 | 0.75523285 |
| ! | dopamine D2 receptor-like receptor activity | GO:0001591 | 15 | 8 | 0.56759292 | 0.56816 | 0.75716713 |
| ! | cofactor transporter activity | GO:0051184 | 32 | 16 | 0.59068979 | 0.57057 | 0.75987126 |
| ! | DNA-directed RNA polymerase III activity | GO:0003902 | 34 | 16 | 0.58660395 | 0.57057 | 0.75936434 |
| ! | response to light | GO:0009416 | 104 | 63 | 0.60941353 | 0.57137 | 0.7599221 |
| ! | DNA-directed RNA polymerase II activity | GO:0003901 | 33 | 17 | 0.58919922 | 0.57382 | 0.76267215 |
| ! | peptide hormone secretion | GO:0030072 | 33 | 17 | 0.59231987 | 0.57382 | 0.76216438 |
| ! | purine nucleotide biosynthesis | GO:0006164 | 140 | 77 | 0.60987843 | 0.57645 | 0.7651482 |
| ! | cAMP biosynthesis | GO:0006171 | 30 | 18 | 0.58958429 | 0.5777 | 0.76629754 |
| ! | regulation of JAK-STAT cascade | GO:0046425 | 27 | 12 | 0.57730945 | 0.57891 | 0.76739233 |
| ! | ATP:ADP antiporter activity | GO:0005471 | 29 | 12 | 0.57517833 | 0.57891 | 0.76688277 |
| ! | beta-amyloid binding | GO:0001540 | 15 | 9 | 0.5687067 | 0.57954 | 0.7672079 |
| ! | plasma membrane repair | GO:0001778 | 20 | 9 | 0.57251249 | 0.57954 | 0.76669914 |
| ! | hormone binding | GO:0042562 | 33 | 19 | 0.58847356 | 0.58033 | 0.76723549 |
| ! | N-formyl peptide receptor activity | GO:0004982 | 27 | 20 | 0.58457354 | 0.5836 | 0.77104768 |
| ! | mechanoreceptor differentiation | GO:0042490 | 36 | 13 | 0.57611897 | 0.58438 | 0.77156724 |
| ! | photoreceptor cell development | GO:0042461 | 30 | 13 | 0.57921467 | 0.58438 | 0.77105694 |
| ! | cation:amino acid symporter activity | GO:0005416 | 25 | 13 | 0.58098078 | 0.58438 | 0.77054732 |
| ! | purine ribonucleotide metabolism | GO:0009150 | 149 | 83 | 0.60677484 | 0.58597 | 0.77213352 |
| ! | purine nucleotide metabolism | GO:0006163 | 157 | 88 | 0.61136374 | 0.58636 | 0.77213743 |
| ! | embryonic pattern specification | GO:0009880 | 80 | 37 | 0.59885046 | 0.58691 | 0.77235188 |
| ! | activation of MAPKK | GO:0000186 | 21 | 8 | 0.55831658 | 0.58716 | 0.77217152 |
| ! | clathrin coat of coated pit | GO:0030132 | 15 | 8 | 0.55516306 | 0.58716 | 0.77166285 |
| ! | monocarboxylate porter activity | GO:0015355 | 11 | 8 | 0.55580109 | 0.58716 | 0.77115484 |
| ! | purine ribonucleotide catabolism | GO:0009154 | 12 | 8 | 0.55836177 | 0.58716 | 0.7706475 |
| ! | heme metabolism | GO:0042168 | 39 | 21 | 0.58858485 | 0.58891 | 0.77243619 |
| ! | lipid raft | GO:0045121 | 40 | 21 | 0.58692209 | 0.58891 | 0.77192868 |
| ! | neurotransmitter transporter activity | GO:0005326 | 77 | 38 | 0.6005889 | 0.58951 | 0.77220778 |
| ! | Golgi to plasma membrane transport | GO:0006893 | 23 | 11 | 0.57295711 | 0.59189 | 0.77481663 |
| ! | Z disc | GO:0030018 | 31 | 16 | 0.5787811 | 0.59771 | 0.78192226 |
| ! | oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, NAD or NADH as one donor, and incorporation of one atom of oxygen | GO:0016709 | 44 | 26 | 0.58832993 | 0.59831 | 0.78219427 |
| ! | dynactin complex | GO:0005869 | 21 | 9 | 0.55863034 | 0.5993 | 0.78297544 |
| ! | stem cell division | GO:0017145 | 19 | 9 | 0.56168239 | 0.5993 | 0.78246302 |
| ! | beta-adrenergic receptor activity | GO:0004939 | 16 | 9 | 0.56261707 | 0.5993 | 0.78195128 |
| ! | oxygen transport | GO:0015671 | 19 | 9 | 0.56285697 | 0.5993 | 0.7814402 |
| ! | mitochondrial outer membrane | GO:0005741 | 107 | 45 | 0.60162827 | 0.60186 | 0.78426564 |
| ! | centrosome cycle | GO:0007098 | 21 | 12 | 0.56637474 | 0.60193 | 0.78384488 |
| ! | aminoacyl-tRNA hydrolase reaction | GO:0006439 | 22 | 12 | 0.57270501 | 0.60193 | 0.78333356 |
| ! | ciliary or flagellar motility | GO:0001539 | 22 | 12 | 0.56603882 | 0.60193 | 0.78282291 |
| ! | G-protein-coupled receptor binding | GO:0001664 | 83 | 50 | 0.59288451 | 0.60435 | 0.78545814 |
| ! | regulation of carbohydrate metabolism | GO:0006109 | 24 | 8 | 0.54738089 | 0.60646 | 0.7876873 |
| ! | somatic stem cell division | GO:0048103 | 15 | 8 | 0.55314663 | 0.60646 | 0.78717482 |
| ! | ER-associated protein catabolism | GO:0030433 | 18 | 8 | 0.54551904 | 0.60646 | 0.786663 |

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|---|---|---|---|---|---|---|---|
| ! | iron ion transport | GO:0006826 | 52 | 28 | 0.58859406 | 0.6066 | 0.78633333 |
| ! | STAT protein nuclear translocation | GO:0007262 | 16 | 10 | 0.55761159 | 0.60874 | 0.788595 |
| ! | regulation of epithelial cell differentiation | GO:0030856 | 16 | 10 | 0.56267335 | 0.60874 | 0.78808326 |
| ! | sensory organ development | GO:0007423 | 62 | 32 | 0.5899064 | 0.61245 | 0.79237208 |
| ! | sulfate transport | GO:0008272 | 23 | 14 | 0.56451942 | 0.61276 | 0.79225936 |
| ! | neural plate morphogenesis | GO:0001839 | 27 | 14 | 0.56554911 | 0.61276 | 0.79174624 |
| ! | intestinal absorption | GO:0050892 | 21 | 11 | 0.56086352 | 0.61411 | 0.79297699 |
| ! | lipid modification | GO:0030258 | 22 | 11 | 0.55499621 | 0.61411 | 0.79246407 |
| ! | calcium activated cation channel activity | GO:0005227 | 17 | 11 | 0.553791 | 0.61411 | 0.79195181 |
| ! | tumor necrosis factor receptor binding | GO:0005164 | 32 | 20 | 0.58049112 | 0.61464 | 0.79212326 |
| ! | iron ion homeostasis | GO:0006879 | 41 | 21 | 0.57352542 | 0.61809 | 0.79605523 |
| ! | cyclase activity | GO:0009975 | 37 | 21 | 0.57984076 | 0.61809 | 0.79554165 |
| ! | eukaryotic translation initiation factor 3 complex | GO:0005852 | 20 | 9 | 0.55291507 | 0.61895 | 0.79613491 |
| ! | actin filament reorganization during cell cycle | GO:0030037 | 14 | 9 | 0.54838313 | 0.61895 | 0.79562194 |
| ! | solute:solute antiporter activity | GO:0015300 | 68 | 33 | 0.5892723 | 0.62022 | 0.79674108 |
| ! | 3'-5'-exoribonuclease activity | GO:0000175 | 29 | 16 | 0.56396978 | 0.62391 | 0.80096554 |
| ! | synaptonemal complex | GO:0000795 | 19 | 12 | 0.55442429 | 0.62518 | 0.80207981 |
| ! | embryonic heart tube development | GO:0035050 | 33 | 12 | 0.56300672 | 0.62518 | 0.80156433 |
| ! | tissue regeneration | GO:0042246 | 40 | 23 | 0.57450422 | 0.62654 | 0.8027921 |
| ! | extracellular ligand-gated ion channel activity | GO:0005230 | 122 | 68 | 0.59865594 | 0.62779 | 0.80387744 |
| ! | solute:hydrogen antiporter activity | GO:0015299 | 34 | 17 | 0.56761566 | 0.62864 | 0.80444952 |
| ! | carbohydrate phosphatase activity | GO:0019203 | 21 | 10 | 0.54684701 | 0.63026 | 0.80600558 |
| ! | cellular lipid catabolism | GO:0044242 | 64 | 40 | 0.58506578 | 0.6319 | 0.8075852 |
| ! | collagen | GO:0005202 | 55 | 26 | 0.58267261 | 0.63194 | 0.80711927 |
| ! | progesterone metabolism | GO:0042448 | 23 | 13 | 0.56259305 | 0.63209 | 0.80679434 |
| ! | aldo-keto reductase activity | GO:0004033 | 22 | 13 | 0.55411342 | 0.63209 | 0.80627848 |
| ! | inhibitory extracellular ligand-gated ion channel activity | GO:0005237 | 22 | 13 | 0.55859876 | 0.63209 | 0.80576329 |
| ! | striated muscle contraction | GO:0006941 | 150 | 73 | 0.60108197 | 0.63297 | 0.80636983 |
| ! | purine ribonucleotide biosynthesis | GO:0009152 | 133 | 73 | 0.59629976 | 0.63297 | 0.80585523 |
| ! | ear morphogenesis | GO:0042471 | 31 | 18 | 0.56873129 | 0.63467 | 0.80750424 |
| ! | hydrogen-exporting ATPase activity, phosphorylative | GO:0008553 | 82 | 41 | 0.58345102 | 0.63493 | 0.80732017 |
| ! | acylglycerol O-acyltransferase activity | GO:0016411 | 18 | 11 | 0.54388322 | 0.63657 | 0.8088899 |
| ! | alpha1-adrenergic receptor activity | GO:0004937 | 19 | 11 | 0.54642512 | 0.63657 | 0.80837502 |
| ! | isoprenoid binding | GO:0019840 | 19 | 14 | 0.5586405 | 0.63793 | 0.80958674 |
| ! | centriole | GO:0005814 | 15 | 9 | 0.53540513 | 0.63875 | 0.81011205 |
| ! | hemoglobin complex | GO:0005833 | 21 | 9 | 0.53411866 | 0.63875 | 0.80959736 |
| ! | deacetylase activity | GO:0019213 | 19 | 15 | 0.55622701 | 0.64316 | 0.81466933 |
| ! | protein phosphatase inhibitor activity | GO:0004864 | 39 | 20 | 0.56509134 | 0.64399 | 0.81520308 |
| ! | superoxide dismutase activity | GO:0004784 | 18 | 8 | 0.52752087 | 0.6456 | 0.81672289 |
| ! | chemosensory behavior | GO:0007635 | 16 | 8 | 0.53270128 | 0.6456 | 0.81620532 |
| ! | cell wall catabolism | GO:0016998 | 14 | 8 | 0.53090854 | 0.6456 | 0.81568841 |
| ! | GTPase inhibitor activity | GO:0005095 | 13 | 8 | 0.52958105 | 0.6456 | 0.81517215 |
| ! | negative regulation of axonogenesis | GO:0050771 | 17 | 8 | 0.52399615 | 0.6456 | 0.81465655 |
| ! | death receptor adaptor protein activity | GO:0005037 | 9 | 8 | 0.53091162 | 0.6456 | 0.81414159 |
| ! | pteridine and derivative metabolism | GO:0042558 | 28 | 12 | 0.54565886 | 0.64713 | 0.8155555 |
| ! | cytoplasmic vesicle membrane | GO:0030659 | 50 | 21 | 0.56851982 | 0.64854 | 0.81681648 |

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|---|---|---|---|---|---|---|---|
| ! | nitric oxide mediated signal transduction | GO:0007263 | 35 | 21 | 0.56394143 | 0.64854 | 0.81630114 |
| ! | protein oligomerization | GO:0051259 | 47 | 22 | 0.56992747 | 0.64945 | 0.81693112 |
| ! | response to heat | GO:0009408 | 110 | 49 | 0.58519862 | 0.64959 | 0.81659234 |
| ! | transition metal ion homeostasis | GO:0046916 | 66 | 32 | 0.58015094 | 0.64984 | 0.81639219 |
| ! | troponin complex | GO:0005861 | 36 | 16 | 0.56154748 | 0.64984 | 0.81587841 |
| ! | protein homodimerization activity | GO:0042803 | 196 | 93 | 0.59445548 | 0.65083 | 0.81660745 |
| ! | fatty-acid synthase activity | GO:0004312 | 24 | 10 | 0.53773839 | 0.65143 | 0.81684654 |
| ! | intermediate filament | GO:0005882 | 150 | 96 | 0.60111664 | 0.65524 | 0.82110791 |
| ! | inner ear morphogenesis | GO:0042472 | 29 | 17 | 0.56279777 | 0.65578 | 0.82126874 |
| ! | apoptotic mitochondrial changes | GO:0008637 | 29 | 13 | 0.54589732 | 0.65588 | 0.82087867 |
| ! | induction of apoptosis via death domain receptors | GO:0008625 | 21 | 13 | 0.54815802 | 0.65588 | 0.82036401 |
| ! | UTP biosynthesis | GO:0006228 | 18 | 13 | 0.55004328 | 0.65588 | 0.81985 |
| ! | intermediate filament cytoskeleton | GO:0045111 | 151 | 97 | 0.59620252 | 0.65595 | 0.81942408 |
| ! | Notch binding | GO:0005112 | 17 | 9 | 0.53100752 | 0.65793 | 0.8213832 |
| ! | regulation of Ras protein signal transduction | GO:0046578 | 15 | 9 | 0.52784583 | 0.65793 | 0.82086951 |
| ! | fat-soluble vitamin biosynthesis | GO:0042362 | 25 | 11 | 0.54098524 | 0.65794 | 0.82036894 |
| ! | sarcomere | GO:0030017 | 108 | 54 | 0.58908802 | 0.65946 | 0.82175059 |
| ! | chemokine receptor binding | GO:0042379 | 59 | 36 | 0.57572252 | 0.66264 | 0.82519775 |
| ! | anterior/posterior pattern formation | GO:0009952 | 117 | 58 | 0.58562275 | 0.66478 | 0.82734629 |
| ! | cortical actin cytoskeleton | GO:0030864 | 38 | 15 | 0.55036056 | 0.66801 | 0.83084785 |
| ! | carbonate dehydratase activity | GO:0004089 | 28 | 15 | 0.54558902 | 0.66801 | 0.83033019 |
| ! | benzodiazepine receptor activity | GO:0008503 | 24 | 12 | 0.53959604 | 0.67014 | 0.83245909 |
| ! | glutathione biosynthesis | GO:0006750 | 21 | 12 | 0.54335428 | 0.67014 | 0.83194107 |
| ! | RNA elongation from Pol II promoter | GO:0006368 | 18 | 10 | 0.52580589 | 0.67209 | 0.833843 |
| ! | phospholipid catabolism | GO:0009395 | 22 | 10 | 0.52965649 | 0.67209 | 0.83332477 |
| ! | glucose homeostasis | GO:0042593 | 41 | 20 | 0.55708114 | 0.67272 | 0.83358783 |
| ! | polysaccharide metabolism | GO:0005976 | 125 | 64 | 0.58536187 | 0.67293 | 0.83333045 |
| ! | aspartic-type endopeptidase activity | GO:0004190 | 48 | 28 | 0.56728701 | 0.67447 | 0.83471939 |
| ! | apocarotenoid metabolism | GO:0043288 | 17 | 9 | 0.52331281 | 0.67764 | 0.83812263 |
| ! | very-long-chain fatty acid metabolism | GO:0000038 | 21 | 9 | 0.52180721 | 0.67764 | 0.83760335 |
| ! | purine nucleoside metabolism | GO:0042278 | 19 | 11 | 0.5240717 | 0.67869 | 0.83838176 |
| ! | hormone-mediated signaling | GO:0009755 | 21 | 11 | 0.53326433 | 0.67869 | 0.83786296 |
| ! | water channel activity | GO:0015250 | 21 | 11 | 0.52585257 | 0.67869 | 0.83734481 |
| ! | protein phosphatase type 2A complex | GO:0000159 | 37 | 11 | 0.52900149 | 0.67869 | 0.83682729 |
| ! | heat shock protein activity | GO:0003773 | 105 | 43 | 0.57690218 | 0.67903 | 0.83672937 |
| ! | stress fiber | GO:0001725 | 26 | 13 | 0.53927679 | 0.67935 | 0.83660694 |
| ! | purine nucleoside diphosphate metabolism | GO:0009135 | 12 | 8 | 0.51328255 | 0.68256 | 0.84004146 |
| ! | protein amino acid deacetylation | GO:0006476 | 27 | 14 | 0.54125139 | 0.68635 | 0.84418511 |
| ! | acyl-CoA binding | GO:0000062 | 25 | 12 | 0.52651691 | 0.69236 | 0.8510525 |
| ! | feeding behavior | GO:0007631 | 51 | 33 | 0.57173896 | 0.69249 | 0.85068815 |
| ! | keratin filament | GO:0045095 | 18 | 15 | 0.53646938 | 0.6928 | 0.85054523 |
| ! | RAB small monomeric GTPase activity | GO:0003928 | 55 | 25 | 0.55728213 | 0.6936 | 0.85100369 |
| ! | ribonucleotide biosynthesis | GO:0009260 | 147 | 79 | 0.59065841 | 0.69426 | 0.85128992 |
| ! | GABA receptor activity | GO:0016917 | 63 | 34 | 0.56776158 | 0.69476 | 0.85137973 |
| ! | aspartate family amino acid catabolism | GO:0009068 | 15 | 9 | 0.51348719 | 0.69648 | 0.85296354 |
| ! | benzene and derivative metabolism | GO:0042537 | 13 | 8 | 0.49711839 | 0.70031 | 0.85712788 |

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|---|---|---|---|---|---|---|---|
| ! | positive regulation of lipid metabolism | GO:0045834 | 12 | 8 | 0.503091 | 0.70031 | 0.85660236 |
| ! | epidermal cell differentiation | GO:0009913 | 18 | 8 | 0.50341659 | 0.70031 | 0.85607748 |
| ! | response to oxidative stress | GO:0006979 | 161 | 86 | 0.58712866 | 0.70051 | 0.85579758 |
| ! | regulation of axon extension | GO:0030516 | 45 | 20 | 0.54514954 | 0.70081 | 0.85564012 |
| ! | anchoring collagen | GO:0030934 | 27 | 13 | 0.52803085 | 0.70226 | 0.85688606 |
| ! | phosphoenolpyruvate-dependent sugar phosphotransferase | GO:0009401 | 66 | 28 | 0.55989649 | 0.70701 | 0.86215461 |
| ! | monosaccharide binding | GO:0048029 | 41 | 28 | 0.55785016 | 0.70701 | 0.86162795 |
| ! | nerve-nerve synaptic transmission | GO:0007270 | 48 | 21 | 0.54715435 | 0.7076 | 0.86182051 |
| ! | pregnancy | GO:0007565 | 159 | 90 | 0.58869148 | 0.70773 | 0.86145293 |
| ! | development of primary male sexual characteristics | GO:0046546 | 30 | 17 | 0.54130029 | 0.7083 | 0.86162104 |
| ! | steroid catabolism | GO:0006706 | 23 | 17 | 0.53797363 | 0.7083 | 0.86109598 |
| ! | insulin-like growth factor binding | GO:0005520 | 46 | 22 | 0.54916824 | 0.70972 | 0.86229683 |
| ! | MHC class I receptor activity | GO:0030106 | 39 | 22 | 0.54780988 | 0.70972 | 0.861772 |
| ! | hydrolase activity, hydrolyzing N-glycosyl compounds | GO:0016799 | 26 | 14 | 0.52910206 | 0.71034 | 0.86200018 |
| ! | myofibril | GO:0030016 | 117 | 58 | 0.58273874 | 0.71183 | 0.86328319 |
| ! | histone deacetylation | GO:0016575 | 18 | 10 | 0.51019491 | 0.71257 | 0.86365562 |
| ! | oxygen transporter activity | GO:0005344 | 20 | 10 | 0.50746084 | 0.71257 | 0.86313124 |
| ! | rRNA binding | GO:0019843 | 27 | 12 | 0.51468258 | 0.71398 | 0.86431438 |
| ! | neuronal migration | GO:0001764 | 81 | 41 | 0.56672517 | 0.7147 | 0.86466131 |
| ! | purine nucleotide catabolism | GO:0006195 | 13 | 9 | 0.49709272 | 0.71484 | 0.86430655 |
| ! | biopolymer biosynthesis | GO:0043284 | 44 | 23 | 0.55278736 | 0.71674 | 0.86607892 |
| ! | nucleoside triphosphate biosynthesis | GO:0009142 | 116 | 62 | 0.57608515 | 0.71737 | 0.86631547 |
| ! | antigen processing, endogenous antigen via MHC class I | GO:0019885 | 44 | 24 | 0.5512642 | 0.71858 | 0.86725172 |
| ! | bile acid transporter activity | GO:0015125 | 35 | 24 | 0.55108646 | 0.71858 | 0.86672739 |
| ! | sulfur amino acid metabolism | GO:0000096 | 66 | 32 | 0.55860581 | 0.71966 | 0.86750556 |
| ! | amine binding | GO:0043176 | 58 | 32 | 0.55859683 | 0.71966 | 0.8669817 |
| ! | glycine-gated ion channel activity | GO:0016933 | 16 | 11 | 0.51026839 | 0.7215 | 0.86867381 |
| ! | nucleoside phosphate metabolism | GO:0006753 | 87 | 44 | 0.56583647 | 0.72247 | 0.86931704 |
| ! | solute:hydrogen symporter activity | GO:0015295 | 22 | 13 | 0.51594529 | 0.72483 | 0.87163101 |
| ! | somitogenesis | GO:0001756 | 27 | 16 | 0.53270955 | 0.72504 | 0.87135831 |
| ! | phosphotransferase activity, for other substituted phosphate | GO:0016780 | 29 | 10 | 0.4958119 | 0.73223 | 0.87946951 |
| ! | postsynaptic membrane | GO:0045211 | 131 | 70 | 0.57583345 | 0.73268 | 0.87948051 |
| ! | misfolded or incompletely synthesized protein catabolism | GO:0006515 | 20 | 9 | 0.48667434 | 0.73352 | 0.87995935 |
| ! | response to organic substance | GO:0010033 | 42 | 21 | 0.53916686 | 0.73509 | 0.88131283 |
| ! | arginine metabolism | GO:0006525 | 22 | 12 | 0.50401132 | 0.73512 | 0.88081946 |
| ! | voltage-gated sodium channel complex | GO:0001518 | 14 | 8 | 0.47955686 | 0.7355 | 0.8807458 |
| ! | protein homooligomerization | GO:0051260 | 40 | 18 | 0.52888237 | 0.74076 | 0.88651242 |
| ! | steroid binding | GO:0005496 | 141 | 76 | 0.58042516 | 0.74122 | 0.88653112 |
| ! | peptidyl-prolyl cis-trans isomerase activity | GO:0003755 | 51 | 29 | 0.54929284 | 0.74145 | 0.88627487 |
| ! | antigen presentation, endogenous peptide antigen | GO:0048004 | 24 | 11 | 0.5003525 | 0.74166 | 0.88599503 |
| ! | regulation of angiogenesis | GO:0045765 | 65 | 38 | 0.55671333 | 0.7417 | 0.88551257 |
| ! | carbon-oxygen lyase activity | GO:0016835 | 103 | 54 | 0.56354495 | 0.74716 | 0.89149773 |
| ! | basal lamina | GO:0005605 | 48 | 24 | 0.53737328 | 0.7472 | 0.89101255 |
| ! | cis-trans isomerase activity | GO:0016859 | 54 | 30 | 0.54755336 | 0.74722 | 0.89050412 |
| ! | GTP biosynthesis | GO:0006183 | 24 | 16 | 0.52065512 | 0.74925 | 0.8923903 |
| ! | calcium- and calmodulin-responsive adenylate cyclase activity | GO:0008294 | 17 | 9 | 0.47794555 | 0.75149 | 0.89452419 |

Supplemental Table 1

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ! | cytoskeletal regulatory protein binding | GO:0005519 | 27 | 10 | 0.48625037 | 0.75163 | 0.89415733 |
| ! | C-acyltransferase activity | GO:0016408 | 23 | 10 | 0.48612261 | 0.75163 | 0.89362446 |
| ! | extracellular matrix constituent, lubricant activity | GO:0030197 | 11 | 8 | 0.47204497 | 0.7528 | 0.89448243 |
| ! | negative regulation of immune cell mediated cytotoxicity | GO:0001911 | 21 | 8 | 0.47130286 | 0.7528 | 0.89395 |
| ! | nitrogen compound catabolism | GO:0044270 | 14 | 8 | 0.47079288 | 0.7528 | 0.8934182 |
| ! | dioxygenase activity | GO:0051213 | 56 | 32 | 0.55110458 | 0.75314 | 0.89329031 |
| ! | carbohydrate transporter activity | GO:0015144 | 167 | 83 | 0.57427248 | 0.75314 | 0.89275954 |
| ! | subtilase activity | GO:0004289 | 56 | 25 | 0.53962862 | 0.75415 | 0.89342592 |
| ! | protein phosphatase type 2A regulator activity | GO:0008601 | 35 | 12 | 0.50050047 | 0.75527 | 0.89422175 |
| ! | flagellum (sensu Eukaryota) | GO:0009434 | 24 | 12 | 0.49772128 | 0.75527 | 0.89369137 |
| ! | water transport | GO:0006833 | 26 | 14 | 0.50847359 | 0.75597 | 0.89398942 |
| ! | oxidoreduction coenzyme metabolism | GO:0006733 | 51 | 33 | 0.55329408 | 0.75934 | 0.89744271 |
| ! | oxidoreductase activity, acting on single donors with incorporation of molecular oxygen | GO:0016701 | 57 | 33 | 0.55023878 | 0.75934 | 0.89691137 |
| ! | serotonin receptor activity | GO:0004993 | 31 | 21 | 0.53184581 | 0.75998 | 0.89713615 |
| ! | regulation of vasoconstriction | GO:0019229 | 16 | 11 | 0.48760021 | 0.76134 | 0.89821011 |
| ! | mitochondrion organization and biogenesis | GO:0007005 | 74 | 34 | 0.54799265 | 0.76384 | 0.90062695 |
| ! | pyridine nucleotide metabolism | GO:0019362 | 33 | 22 | 0.53306529 | 0.76449 | 0.90086093 |
| ! | regulation of blood vessel size | GO:0050880 | 24 | 18 | 0.51776723 | 0.76587 | 0.90195434 |
| ! | aldehyde reductase activity | GO:0004032 | 23 | 13 | 0.49766408 | 0.76653 | 0.90219903 |
| ! | coenzyme and prosthetic group metabolism | GO:0006731 | 20 | 13 | 0.50271741 | 0.76653 | 0.90166707 |
| ! | neuropeptide hormone activity | GO:0005184 | 37 | 28 | 0.54005247 | 0.76809 | 0.90296968 |
| ! | cyclic nucleotide biosynthesis | GO:0009190 | 44 | 28 | 0.53470663 | 0.76809 | 0.9024379 |
| ! | hydrogen-transporting ATPase activity, rotational mechanism | GO:0046961 | 72 | 36 | 0.54683834 | 0.76882 | 0.90276392 |
| ! | NAD+ ADP-ribosyltransferase activity | GO:0003950 | 14 | 8 | 0.46061267 | 0.76904 | 0.90249106 |
| ! | regulation of interferon-gamma biosynthesis | GO:0045072 | 10 | 8 | 0.46107485 | 0.76904 | 0.90196049 |
| ! | DNA-directed RNA polymerase III complex | GO:0005666 | 17 | 8 | 0.45939641 | 0.76904 | 0.90143055 |
| ! | antioxidant activity | GO:0016209 | 126 | 66 | 0.56573809 | 0.76918 | 0.90106524 |
| ! | interferon-gamma biosynthesis | GO:0042095 | 12 | 10 | 0.47837831 | 0.7692 | 0.90055986 |
| ! | negative regulation of cell migration | GO:0030336 | 18 | 9 | 0.46800088 | 0.77036 | 0.90138897 |
| ! | embryonic epithelial tube formation | GO:0001838 | 29 | 16 | 0.50993446 | 0.77193 | 0.90269657 |
| ! | neurotransmitter biosynthesis | GO:0042136 | 20 | 16 | 0.50591365 | 0.77193 | 0.90216775 |
| ! | pancreatic elastase activity | GO:0008132 | 30 | 23 | 0.52809632 | 0.77231 | 0.9020834 |
| ! | transferase activity, transferring sulfur-containing groups | GO:0016782 | 67 | 48 | 0.56266504 | 0.77272 | 0.90203417 |
| ! | ATP metabolism | GO:0046034 | 95 | 49 | 0.55917347 | 0.77338 | 0.90227667 |
| ! | peroxidase reaction | GO:0006804 | 43 | 24 | 0.52422384 | 0.77439 | 0.90292697 |
| ! | striated muscle thick filament | GO:0005863 | 19 | 12 | 0.48683861 | 0.77538 | 0.90355321 |
| ! | desmosome | GO:0030057 | 26 | 12 | 0.49219095 | 0.77538 | 0.90302574 |
| ! | nicotinic acetylcholine-gated receptor-channel complex | GO:0005892 | 23 | 14 | 0.49762692 | 0.77631 | 0.90358136 |
| ! | nucleoside triphosphate metabolism | GO:0009141 | 128 | 70 | 0.57197167 | 0.77734 | 0.90425265 |
| ! | excitatory extracellular ligand-gated ion channel activity | GO:0005231 | 88 | 51 | 0.55804729 | 0.77875 | 0.90536495 |
| ! | fatty acid binding | GO:0005504 | 51 | 25 | 0.52873811 | 0.78229 | 0.90895082 |
| ! | oxidoreductase activity, acting on peroxide as acceptor | GO:0016684 | 94 | 52 | 0.56286911 | 0.78261 | 0.90879334 |
| ! | long-chain-fatty-acid-CoA ligase activity | GO:0004467 | 11 | 8 | 0.45175381 | 0.78524 | 0.91131693 |
| ! | acrosome | GO:0001669 | 26 | 15 | 0.50014893 | 0.78583 | 0.91147142 |
| ! | oxidoreductase activity, acting on the aldehyde or oxo group of | GO:0016903 | 77 | 41 | 0.54360992 | 0.78607 | 0.91122002 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ! | aryl sulfotransferase activity | GO:0004062 | 10 | 9 | 0.45812798 | 0.78708 | 0.91186098 |
| ! | sodium:amino acid symporter activity | GO:0005283 | 18 | 9 | 0.45574886 | 0.78708 | 0.91133175 |
| ! | oxidoreductase activity, acting on the CH-CH group of donors, oxygen as acceptor | GO:0016634 | 19 | 9 | 0.45844329 | 0.78708 | 0.91080313 |
| ! | oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, reduced iron-sulfur protein as one donor, and incorporation of one atom of | GO:0016713 | 16 | 9 | 0.46399831 | 0.78708 | 0.91027513 |
| ! | water transporter activity | GO:0005372 | 19 | 10 | 0.47404193 | 0.78717 | 0.90985177 |
| ! | drug binding | GO:0008144 | 40 | 22 | 0.51424628 | 0.78869 | 0.9110808 |
| ! | cytolysis | GO:0019835 | 43 | 33 | 0.54050355 | 0.79069 | 0.91286259 |
| ! | ATP biosynthesis | GO:0006754 | 85 | 43 | 0.54556931 | 0.79078 | 0.91243846 |
| ! | response to reactive oxygen species | GO:0000302 | 30 | 16 | 0.49853638 | 0.79297 | 0.9144365 |
| ! | fluid transport | GO:0042044 | 30 | 16 | 0.49597437 | 0.79297 | 0.91390823 |
| ! | arachidonic acid metabolism | GO:0019369 | 22 | 19 | 0.51130231 | 0.79375 | 0.91427901 |
| ! | trans-1,2-dihydrobenzene-1,2-diol dehydrogenase activity | GO:0047115 | 20 | 12 | 0.48148069 | 0.79461 | 0.91474146 |
| ! | sugar transporter activity | GO:0051119 | 164 | 80 | 0.56839554 | 0.79568 | 0.91544498 |
| ! | cofactor transport | GO:0051181 | 29 | 14 | 0.49135578 | 0.7965 | 0.91586023 |
| ! | polyisoprenoid metabolism | GO:0016096 | 21 | 11 | 0.46497034 | 0.79927 | 0.91851593 |
| ! | collagen binding | GO:0005518 | 43 | 24 | 0.51963494 | 0.80068 | 0.91960656 |
| ! | cholesterol metabolism | GO:0008203 | 158 | 85 | 0.56744186 | 0.80089 | 0.9193185 |
| ! | oxidoreductase activity, acting on NADH or NADPH | GO:0016651 | 177 | 85 | 0.56826019 | 0.80089 | 0.91878985 |
| ! | pepsin A activity | GO:0004194 | 16 | 8 | 0.43857214 | 0.80142 | 0.91886948 |
| ! | cortical cytoskeleton | GO:0030863 | 40 | 17 | 0.49532162 | 0.80212 | 0.91914383 |
| ! | cytoplasmic dynein complex | GO:0005868 | 28 | 13 | 0.47967819 | 0.80541 | 0.92238401 |
| ! | glutathione metabolism | GO:0006749 | 44 | 25 | 0.51902486 | 0.80724 | 0.9239494 |
| ! | aspartate family amino acid metabolism | GO:0009066 | 46 | 25 | 0.52200241 | 0.80724 | 0.92341961 |
| ! | channel inhibitor activity | GO:0016248 | 31 | 21 | 0.50634097 | 0.80797 | 0.92372501 |
| ! | group transfer coenzyme metabolism | GO:0006752 | 123 | 65 | 0.55434241 | 0.80873 | 0.92406435 |
| ! | sterol metabolism | GO:0016125 | 174 | 95 | 0.57133482 | 0.81589 | 0.93171182 |
| ! | phosphotransferase activity, nitrogenous group as acceptor | GO:0016775 | 32 | 19 | 0.49477498 | 0.81623 | 0.93156685 |
| ! | retinol dehydrogenase activity | GO:0004745 | 17 | 11 | 0.45780997 | 0.8163 | 0.93111407 |
| ! | fatty-acid ligase activity | GO:0015645 | 17 | 11 | 0.45602559 | 0.8163 | 0.930582 |
| ! | purine transporter activity | GO:0005345 | 21 | 8 | 0.43311372 | 0.81669 | 0.93049489 |
| ! | omega peptidase activity | GO:0008242 | 12 | 8 | 0.43434724 | 0.81669 | 0.92996378 |
| ! | muscle fiber | GO:0030484 | 139 | 70 | 0.55591457 | 0.81813 | 0.93107208 |
| ! | GABA-A receptor activity | GO:0004890 | 58 | 33 | 0.53249885 | 0.81914 | 0.93169002 |
| ! | aldehyde-lyase activity | GO:0016832 | 15 | 10 | 0.44544108 | 0.82036 | 0.93254598 |
| ! | folic acid binding | GO:0005542 | 17 | 10 | 0.45137894 | 0.82036 | 0.93201492 |
| ! | tight junction | GO:0005923 | 107 | 55 | 0.54724347 | 0.82141 | 0.93267669 |
| ! | protein-mitochondrial targeting | GO:0006626 | 56 | 23 | 0.50821496 | 0.82221 | 0.93305401 |
| ! | determination of bilateral symmetry | GO:0009855 | 29 | 17 | 0.49056544 | 0.82315 | 0.93358968 |
| ! | monosaccharide transporter activity | GO:0015145 | 32 | 17 | 0.48994527 | 0.82315 | 0.93305923 |
| ! | mechanosensory behavior | GO:0007638 | 21 | 13 | 0.46915739 | 0.8241 | 0.93360562 |
| ! | urea cycle intermediate metabolism | GO:0000051 | 23 | 13 | 0.47076209 | 0.8241 | 0.93307577 |
| ! | transferase activity, transferring amino-acyl groups | GO:0016755 | 30 | 13 | 0.47002556 | 0.8241 | 0.93254651 |
| ! | glycogen metabolism | GO:0005977 | 74 | 35 | 0.5325484 | 0.82475 | 0.93275298 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ! | disulfide oxidoreductase activity | GO:0015036 | 72 | 35 | 0.52448125 | 0.82475 | 0.9322245 |
| ! | carbohydrate transport | GO:0008643 | 172 | 74 | 0.56102011 | 0.82581 | 0.93289408 |
| ! | sugar porter activity | GO:0005351 | 158 | 76 | 0.55965248 | 0.82913 | 0.93611452 |
| ! | histogenesis and organogenesis | GO:0007397 | 141 | 77 | 0.55546075 | 0.83013 | 0.93671343 |
| ! | glucan metabolism | GO:0006073 | 75 | 36 | 0.52484291 | 0.83065 | 0.93677035 |
| ! | alcohol biosynthesis | GO:0046165 | 93 | 45 | 0.53421143 | 0.83091 | 0.93653415 |
| ! | acetylcholine receptor activity | GO:0015464 | 30 | 18 | 0.48479399 | 0.83172 | 0.93691779 |
| ! | response to hypoxia | GO:0001666 | 52 | 25 | 0.51203524 | 0.83215 | 0.93687317 |
| ! | carbon-sulfur lyase activity | GO:0016846 | 21 | 10 | 0.43497471 | 0.83577 | 0.94041802 |
| ! | cGMP biosynthesis | GO:0006182 | 14 | 10 | 0.43592686 | 0.83577 | 0.93988791 |
| ! | 3-beta-hydroxy-delta5-steroid dehydrogenase activity | GO:0003854 | 11 | 9 | 0.4259809 | 0.83604 | 0.93966186 |
| ! | mRNA catabolism, nonsense-mediated decay | GO:0000184 | 16 | 9 | 0.43317693 | 0.83604 | 0.93913277 |
| ! | amine biosynthesis | GO:0009309 | 143 | 81 | 0.55416252 | 0.8366 | 0.93923298 |
| ! | cyclic nucleotide metabolism | GO:0009187 | 64 | 39 | 0.52507711 | 0.83749 | 0.93970335 |
| ! | vitamin metabolism | GO:0006766 | 144 | 84 | 0.55884146 | 0.84154 | 0.94371686 |
| ! | nicotinic acetylcholine-activated cation-selective channel | GO:0004889 | 26 | 15 | 0.47346796 | 0.84357 | 0.94546188 |
| ! | voltage-gated sodium channel activity | GO:0005248 | 26 | 15 | 0.46921672 | 0.84357 | 0.94493102 |
| ! | endonuclease activity, active with either ribo- or deoxyribonucleic acids and producing 5'-phosphomonoesters | GO:0016893 | 38 | 23 | 0.50138008 | 0.8439 | 0.9447702 |
| ! | purine ribonucleoside triphosphate metabolism | GO:0009205 | 119 | 65 | 0.54969203 | 0.84531 | 0.94581798 |
| ! | regulated secretory pathway | GO:0045055 | 20 | 8 | 0.41421859 | 0.84625 | 0.94633899 |
| ! | water-soluble vitamin metabolism | GO:0006767 | 67 | 41 | 0.52679767 | 0.84723 | 0.94690412 |
| ! | gap junction | GO:0005921 | 67 | 34 | 0.51428387 | 0.84925 | 0.94863032 |
| ! | sulfur metabolism | GO:0006790 | 163 | 89 | 0.55855536 | 0.84931 | 0.94816645 |
| ! | L-glutamate transporter activity | GO:0005313 | 29 | 11 | 0.44450876 | 0.84989 | 0.94828331 |
| ! | estrogen metabolism | GO:0008210 | 18 | 11 | 0.44162285 | 0.84989 | 0.94775324 |
| ! | regulation of natural killer cell mediated cytotoxicity | GO:0042269 | 22 | 9 | 0.42086391 | 0.85073 | 0.94815997 |
| ! | neurotransmitter catabolism | GO:0042135 | 15 | 9 | 0.41744423 | 0.85073 | 0.94763057 |
| ! | fluid secretion | GO:0007589 | 23 | 16 | 0.47021359 | 0.85136 | 0.94780312 |
| ! | androgen metabolism | GO:0008209 | 34 | 21 | 0.48687597 | 0.85171 | 0.94766394 |
| ! | coenzyme binding | GO:0050662 | 64 | 30 | 0.50668575 | 0.85428 | 0.94999365 |
| ! | small-molecule carrier or transporter | GO:0005468 | 29 | 19 | 0.48370422 | 0.85614 | 0.95153164 |
| ! | arachidonic acid monooxygenase activity | GO:0008391 | 29 | 22 | 0.49267315 | 0.85632 | 0.95120178 |
| ! | ribonuclease P activity | GO:0004526 | 11 | 8 | 0.39621081 | 0.8593 | 0.9539808 |
| ! | imaginal disc development | GO:0007444 | 16 | 8 | 0.39675578 | 0.8593 | 0.95345022 |
| ! | deactivation of rhodopsin mediated signaling | GO:0016059 | 17 | 8 | 0.40190588 | 0.8593 | 0.95292023 |
| ! | ATP synthesis coupled proton transport | GO:0015986 | 74 | 37 | 0.51684237 | 0.86022 | 0.9534105 |
| ! | sulfur amino acid biosynthesis | GO:0000097 | 28 | 12 | 0.43737149 | 0.86247 | 0.95537349 |
| ! | response to unfolded protein | GO:0006986 | 128 | 58 | 0.53501375 | 0.86388 | 0.95640433 |
| ! | ribonucleoside triphosphate biosynthesis | GO:0009201 | 109 | 59 | 0.53881292 | 0.86721 | 0.95955849 |
| ! | segment specification | GO:0007379 | 24 | 14 | 0.44574267 | 0.86819 | 0.96011034 |
| ! | synaptic transmission, cholinergic | GO:0007271 | 27 | 16 | 0.45888641 | 0.86872 | 0.96016421 |
| ! | brush border | GO:0005903 | 25 | 18 | 0.47012581 | 0.86888 | 0.9598093 |
| ! | arachidonic acid epoxygenase activity | GO:0008392 | 20 | 18 | 0.46524121 | 0.86888 | 0.95927814 |
| ! | triacylglycerol metabolism | GO:0006641 | 29 | 18 | 0.47287803 | 0.86888 | 0.95874757 |
| ! | cell fate commitment | GO:0045165 | 112 | 60 | 0.537744 | 0.86897 | 0.95831683 |

Supplemental Table 1

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|---|---|---|---|---|---|---|---|
| ! | fibrinogen complex | GO:0005577 | 10 | 8 | 0.39114914 | 0.87194 | 0.96106094 |
| ! | energy reserve metabolism | GO:0006112 | 110 | 51 | 0.52921086 | 0.87403 | 0.96283261 |
| ! | heme binding | GO:0020037 | 46 | 35 | 0.51218974 | 0.87632 | 0.96482252 |
| ! | glutathione peroxidase activity | GO:0004602 | 18 | 12 | 0.426595 | 0.87672 | 0.9647305 |
| ! | oxidoreductase activity, acting on the CH-NH group of donors | GO:0016645 | 37 | 26 | 0.49022597 | 0.87795 | 0.96555141 |
| ! | clathrin adaptor | GO:0005906 | 14 | 9 | 0.39989052 | 0.87823 | 0.96532719 |
| ! | negative regulation of neurogenesis | GO:0050768 | 21 | 11 | 0.4158841 | 0.87835 | 0.96492745 |
| ! | sodium channel regulator activity | GO:0017080 | 28 | 17 | 0.46257502 | 0.87843 | 0.96448423 |
| ! | purine nucleoside triphosphate metabolism | GO:0009144 | 120 | 66 | 0.54146852 | 0.87907 | 0.96465602 |
| ! | ankyrin binding | GO:0030506 | 17 | 10 | 0.41353764 | 0.87974 | 0.96486053 |
| ! | proton-transporting two-sector ATPase complex | GO:0016469 | 72 | 36 | 0.50646486 | 0.88003 | 0.96464827 |
| ! | bile acid metabolism | GO:0008206 | 29 | 20 | 0.47367718 | 0.8827 | 0.96704366 |
| ! | vesicle transport | GO:0005480 | 36 | 18 | 0.45804068 | 0.88598 | 0.97010434 |
| ! | heme biosynthesis | GO:0006783 | 27 | 13 | 0.43453183 | 0.88696 | 0.97064465 |
| ! | fusion of sperm to egg plasma membrane | GO:0007342 | 24 | 13 | 0.42547233 | 0.88696 | 0.9701125 |
| ! | vasoconstriction | GO:0042310 | 18 | 13 | 0.42698215 | 0.88696 | 0.96958093 |
| ! | hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amides | GO:0016811 | 73 | 46 | 0.52012999 | 0.88743 | 0.96956344 |
| ! | acetylcholine binding | GO:0042166 | 31 | 19 | 0.46154371 | 0.89129 | 0.9732477 |
| ! | nicotinamide metabolism | GO:0006769 | 27 | 19 | 0.46417653 | 0.89129 | 0.97271529 |
| ! | phospholipase A2 activity | GO:0004623 | 43 | 29 | 0.49040254 | 0.89264 | 0.97365599 |
| ! | selenium binding | GO:0008430 | 28 | 15 | 0.44127558 | 0.89283 | 0.97333107 |
| ! | hexose transport | GO:0008645 | 74 | 34 | 0.50384895 | 0.89415 | 0.97423771 |
| ! | canalicular bile acid transport | GO:0015722 | 16 | 8 | 0.37458062 | 0.89582 | 0.97552451 |
| ! | cysteine metabolism | GO:0006534 | 11 | 8 | 0.36572911 | 0.89582 | 0.97499231 |
| ! | pigment metabolism | GO:0042440 | 53 | 30 | 0.49101805 | 0.89655 | 0.97525477 |
| ! | oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, reduced flavin or flavoprotein as one donor, and incorporation of one atom of | GO:0016712 | 69 | 51 | 0.51690075 | 0.89915 | 0.97755 |
| ! | structural constituent of epidermis | GO:0030280 | 23 | 16 | 0.43553625 | 0.89937 | 0.97725662 |
| ! | structural constituent of eye lens | GO:0005212 | 81 | 42 | 0.50413374 | 0.89963 | 0.977007 |
| ! | vitamin transporter activity | GO:0051183 | 31 | 13 | 0.42037694 | 0.90097 | 0.9779299 |
| ! | microvillus | GO:0005902 | 22 | 13 | 0.42365161 | 0.90097 | 0.97739812 |
| ! | negative regulation of phosphorylation | GO:0042326 | 20 | 9 | 0.37615099 | 0.90199 | 0.97797285 |
| ! | regulation of glucose import | GO:0046324 | 23 | 9 | 0.37714322 | 0.90199 | 0.97744163 |
| ! | calcium-dependent cytosolic phospholipase A2 activity | GO:0004627 | 12 | 9 | 0.37922653 | 0.90199 | 0.97691099 |
| ! | lactation | GO:0007595 | 49 | 31 | 0.48966153 | 0.90232 | 0.97673814 |
| ! | pancreatic elastase I activity | GO:0008125 | 15 | 12 | 0.40844035 | 0.90317 | 0.97712806 |
| ! | glycine-gated chloride channel activity | GO:0016934 | 14 | 10 | 0.39487241 | 0.90456 | 0.97810146 |
| ! | NADPH-hemoprotein reductase activity | GO:0003958 | 21 | 19 | 0.45417829 | 0.90605 | 0.97918188 |
| ! | negative regulation of translation | GO:0016478 | 23 | 8 | 0.35902228 | 0.90679 | 0.97945103 |
| ! | acetyl-CoA biosynthesis | GO:0006085 | 17 | 8 | 0.36320479 | 0.90679 | 0.97892102 |
| ! | acylglycerol metabolism | GO:0006639 | 38 | 22 | 0.45499597 | 0.9085 | 0.98023661 |
| ! | aromatic amino acid family metabolism | GO:0009072 | 40 | 25 | 0.47140094 | 0.91024 | 0.98158314 |
| ! | myosin II | GO:0016460 | 53 | 26 | 0.46968362 | 0.91271 | 0.98371499 |
| ! | response to toxin | GO:0009636 | 65 | 40 | 0.4974195 | 0.9129 | 0.9833885 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ! | hydrogen-transporting ATP synthase activity, rotational | GO:0046933 | 68 | 34 | 0.49237989 | 0.91301 | 0.98297623 |
| ! | palmitoyl-CoA hydrolase activity | GO:0016290 | 25 | 20 | 0.44620887 | 0.914 | 0.98351133 |
| ! | endoribonuclease activity, producing 5'-phosphomonoesters | GO:0016891 | 31 | 18 | 0.43613566 | 0.9148 | 0.98384151 |
| ! | cell fate specification | GO:0001708 | 17 | 12 | 0.39604335 | 0.91548 | 0.98404235 |
| ! | complement activation, alternative pathway | GO:0006957 | 18 | 12 | 0.39764075 | 0.91548 | 0.98351244 |
| ! | unspecific monooxygenase activity | GO:0050381 | 68 | 50 | 0.51104673 | 0.91899 | 0.98675191 |
| ! | neurotransmitter metabolism | GO:0042133 | 53 | 32 | 0.47728401 | 0.92044 | 0.98777719 |
| ! | L-phenylalanine metabolism | GO:0006558 | 15 | 9 | 0.35847355 | 0.92252 | 0.9894771 |
| ! | coumarin metabolism | GO:0009804 | 18 | 16 | 0.41912847 | 0.92489 | 0.99148606 |
| ! | NADP metabolism | GO:0006739 | 23 | 16 | 0.41662034 | 0.92489 | 0.99095357 |
| ! | protein-histidine kinase activity | GO:0004673 | 22 | 13 | 0.39584275 | 0.92492 | 0.99045378 |
| ! | protein-peroxisome targeting | GO:0006625 | 22 | 8 | 0.3412807 | 0.92578 | 0.99084286 |
| ! | retinoid metabolism | GO:0001523 | 15 | 11 | 0.37691735 | 0.92584 | 0.99037576 |
| ! | cGMP metabolism | GO:0046068 | 17 | 12 | 0.39115178 | 0.92637 | 0.99041166 |
| ! | eukaryotic 43S preinitiation complex | GO:0016282 | 105 | 39 | 0.48715745 | 0.92686 | 0.99040477 |
| ! | racemase and epimerase activity | GO:0016854 | 30 | 18 | 0.42665551 | 0.92729 | 0.99033381 |
| ! | glucose transporter activity | GO:0005355 | 28 | 15 | 0.41123208 | 0.93054 | 0.99327303 |
| ! | copper ion homeostasis | GO:0006878 | 27 | 9 | 0.34934385 | 0.93232 | 0.99464086 |
| ! | coenzyme A metabolism | GO:0015936 | 19 | 9 | 0.34998402 | 0.93232 | 0.99410925 |
| ! | melanocortin receptor activity | GO:0004977 | 9 | 9 | 0.35073168 | 0.93232 | 0.99357821 |
| ! | plasma membrane fusion | GO:0045026 | 25 | 14 | 0.40219744 | 0.93262 | 0.99336727 |
| ! | aspartate family amino acid biosynthesis | GO:0009067 | 22 | 13 | 0.39134652 | 0.93482 | 0.99517924 |
| ! | calcium-dependent secreted phospholipase A2 activity | GO:0004625 | 13 | 10 | 0.36175733 | 0.93491 | 0.99474424 |
| ! | glucose transport | GO:0015758 | 70 | 32 | 0.46782112 | 0.93549 | 0.99483078 |
| ! | fatty acid oxidation | GO:0019395 | 59 | 36 | 0.47461465 | 0.93552 | 0.99433266 |
| ! | smoothened signaling pathway | GO:0007224 | 22 | 12 | 0.38145192 | 0.93616 | 0.99448307 |
| ! | gluconeogenesis | GO:0006094 | 79 | 38 | 0.48293576 | 0.9384 | 0.99633209 |
| ! | gap-junction forming channel activity | GO:0005243 | 31 | 18 | 0.42282238 | 0.93863 | 0.9960462 |
| ! | nitrogen compound metabolism | GO:0006807 | 108 | 61 | 0.51165271 | 0.93956 | 0.99650303 |
| ! | integral to membrane of membrane fraction | GO:0000299 | 14 | 9 | 0.33773043 | 0.94055 | 0.99702298 |
| ! | organic acid catabolism | GO:0016054 | 10 | 9 | 0.33782841 | 0.94055 | 0.99649349 |
| ! | glycerolipid metabolism | GO:0046486 | 39 | 23 | 0.4370425 | 0.94064 | 0.99605987 |
| ! | vitamin transport | GO:0051180 | 30 | 15 | 0.39759974 | 0.94069 | 0.99558438 |
| ! | pheromone binding | GO:0005550 | 31 | 26 | 0.44871725 | 0.9408 | 0.99517285 |
| ! | carboxylesterase activity | GO:0004091 | 61 | 39 | 0.47799372 | 0.94225 | 0.99617846 |
| ! | isoprenoid biosynthesis | GO:0008299 | 32 | 14 | 0.38839127 | 0.94237 | 0.99577762 |
| ! | diacylglycerol metabolism | GO:0046339 | 15 | 8 | 0.31977369 | 0.94306 | 0.9959792 |
| ! | acute-phase response | GO:0006953 | 98 | 65 | 0.51203897 | 0.94578 | 0.99832333 |
| ! | protein translocase activity | GO:0015450 | 36 | 16 | 0.39636433 | 0.94578 | 0.9977954 |
| ! | acyl-CoA dehydrogenase activity | GO:0003995 | 27 | 15 | 0.39509797 | 0.9493 | 1.00097965 |
| ! | oxygen binding | GO:0019825 | 65 | 49 | 0.49267215 | 0.94978 | 1.00095674 |
| ! | glycerolipid biosynthesis | GO:0045017 | 15 | 8 | 0.30931697 | 0.95038 | 1.00106024 |
| ! | CoA hydrolase activity | GO:0016289 | 38 | 26 | 0.43912249 | 0.95189 | 1.00212166 |
| ! | oxidoreductase activity, acting on NADH or NADPH, NAD or NADP as acceptor | GO:0016652 | 35 | 26 | 0.44015871 | 0.95189 | 1.00159312 |
| ! | glycogen biosynthesis | GO:0005978 | 27 | 13 | 0.37181256 | 0.95196 | 1.00113875 |

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| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ! | long-chain fatty acid metabolism | GO:0001676 | 14 | 11 | 0.34827134 | 0.95196 | 1.00061128 |
| ! | aromatic amino acid family catabolism | GO:0009074 | 18 | 11 | 0.3482021 | 0.95196 | 1.00008436 |
| ! | iron ion binding | GO:0005506 | 120 | 59 | 0.49833498 | 0.95229 | 0.9999045 |
| ! | flagellum | GO:0019861 | 32 | 19 | 0.40998471 | 0.95261 | 0.99971433 |
| ! | organic cation transporter activity | GO:0015101 | 25 | 19 | 0.41352506 | 0.95261 | 0.99918872 |
| ! | amino acid biosynthesis | GO:0008652 | 96 | 51 | 0.48692796 | 0.95304 | 0.99911445 |
| ! | axoneme | GO:0005930 | 33 | 16 | 0.38916917 | 0.95442 | 1.00003566 |
| ! | L-glutamate transport | GO:0015813 | 25 | 9 | 0.32210635 | 0.95527 | 1.00040087 |
| ! | DNA N-glycosylase activity | GO:0019104 | 17 | 9 | 0.32197709 | 0.95527 | 0.999876 |
| ! | pigmentation | GO:0048066 | 58 | 34 | 0.4639695 | 0.9557 | 0.99980152 |
| ! | dynein ATPase activity | GO:0008567 | 13 | 8 | 0.29791454 | 0.95636 | 0.99996761 |
| ! | fructose transport | GO:0015755 | 15 | 8 | 0.29928563 | 0.95636 | 0.99944379 |
| ! | steroid hydroxylase activity | GO:0008395 | 51 | 40 | 0.46620071 | 0.95665 | 0.99922343 |
| ! | acyl-CoA thioesterase activity | GO:0016291 | 14 | 11 | 0.34079587 | 0.95933 | 1.00149835 |
| ! | regulation of immune cell mediated cytotoxicity | GO:0001910 | 25 | 11 | 0.34570595 | 0.95933 | 1.00097456 |
| ! | oxidoreductase activity, acting on the CH-CH group of donors, NAD or NADP as acceptor | GO:0016628 | 35 | 23 | 0.42177868 | 0.96034 | 1.0015046 |
| ! | cofactor binding | GO:0048037 | 88 | 42 | 0.47388785 | 0.96189 | 1.00259694 |
| ! | cytosolic large ribosomal subunit (sensu Eukaryota) | GO:0005842 | 87 | 37 | 0.45500714 | 0.96199 | 1.00217757 |
| ! | branched chain family amino acid metabolism | GO:0009081 | 16 | 8 | 0.28870365 | 0.96233 | 1.00200853 |
| ! | positive regulation of angiogenesis | GO:0045766 | 19 | 10 | 0.32361576 | 0.96448 | 1.00372332 |
| ! | tRNA-specific ribonuclease activity | GO:0004549 | 13 | 10 | 0.32250924 | 0.96448 | 1.0032 |
| ! | endothelial cell differentiation | GO:0045446 | 19 | 11 | 0.32739713 | 0.96509 | 1.00331139 |
| ! | dynein complex | GO:0030286 | 41 | 22 | 0.41211595 | 0.96526 | 1.00296547 |
| ! | tyrosine metabolism | GO:0006570 | 21 | 14 | 0.35586858 | 0.96561 | 1.00280685 |
| ! | secondary metabolism | GO:0019748 | 97 | 60 | 0.48423561 | 0.96709 | 1.00382131 |
| ! | inner mitochondrial membrane organization and biogenesis | GO:0007007 | 16 | 8 | 0.28357005 | 0.96771 | 1.00394251 |
| ! | oxidoreductase activity, acting on diphenols and related substances as donors | GO:0016679 | 15 | 8 | 0.27878334 | 0.96771 | 1.00342071 |
| ! | odorant binding | GO:0005549 | 38 | 32 | 0.44259404 | 0.96875 | 1.00397727 |
| ! | amine catabolism | GO:0009310 | 115 | 64 | 0.49219911 | 0.97048 | 1.00524798 |
| ! | muscle myosin | GO:0005859 | 46 | 24 | 0.4135424 | 0.97081 | 1.00506796 |
| ! | proteasome core complex (sensu Eukaryota) | GO:0005839 | 39 | 18 | 0.38004885 | 0.97126 | 1.00501229 |
| ! | carbon-nitrogen lyase activity | GO:0016840 | 11 | 9 | 0.29171005 | 0.97312 | 1.00641493 |
| ! | eukaryotic 48S initiation complex | GO:0016283 | 77 | 28 | 0.41557839 | 0.97393 | 1.00673075 |
| ! | serine family amino acid metabolism | GO:0009069 | 47 | 23 | 0.40403005 | 0.97441 | 1.00670531 |
| ! | cytochrome P450 activity | GO:0015034 | 13 | 10 | 0.30120348 | 0.97513 | 1.00692772 |
| ! | respiratory chain complex IV | GO:0045277 | 24 | 11 | 0.31124315 | 0.9757 | 1.00699509 |
| ! | response to pheromone | GO:0019236 | 28 | 24 | 0.40345379 | 0.97665 | 1.00745437 |
| ! | sterol biosynthesis | GO:0016126 | 65 | 36 | 0.43494159 | 0.97691 | 1.00720178 |
| ! | signalosome complex | GO:0008180 | 15 | 9 | 0.27859772 | 0.97771 | 1.00750591 |
| ! | organic cation transport | GO:0015695 | 21 | 16 | 0.34934325 | 0.97986 | 1.00920015 |
| ! | integral to peroxisomal membrane | GO:0005779 | 20 | 11 | 0.30249604 | 0.98039 | 1.009225 |
| ! | sodium channel activity | GO:0005272 | 38 | 26 | 0.39769767 | 0.98178 | 1.01013466 |
| ! | proteasome endopeptidase activity | GO:0004299 | 58 | 27 | 0.40031237 | 0.98268 | 1.01053948 |
| ! | vitamin binding | GO:0019842 | 58 | 36 | 0.42786203 | 0.9827 | 1.01003941 |

Supplemental Table 1

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|---|---|---|---|---|---|---|---|
| ! | pyruvate metabolism | GO:0006090 | 17 | 8 | 0.23854519 | 0.98479 | 1.01166635 |
| ! | hydrogen-translocating F-type ATPase complex | GO:0045255 | 33 | 18 | 0.35332348 | 0.98599 | 1.01237779 |
| ! | fatty acid beta-oxidation | GO:0006635 | 33 | 22 | 0.37204338 | 0.98628 | 1.01215463 |
| ! | cholesterol biosynthesis | GO:0006695 | 50 | 27 | 0.39350318 | 0.98673 | 1.01209581 |
| ! | aerobic respiration | GO:0009060 | 15 | 9 | 0.25582444 | 0.98785 | 1.01272392 |
| ! | amiloride-sensitive sodium channel activity | GO:0015280 | 11 | 10 | 0.26125201 | 0.98876 | 1.01313621 |
| ! | amino acid catabolism | GO:0009063 | 98 | 54 | 0.44725288 | 0.98888 | 1.01273901 |
| ! | cellular respiration | GO:0045333 | 33 | 18 | 0.34054527 | 0.98899 | 1.01233199 |
| ! | pigment biosynthesis | GO:0046148 | 41 | 22 | 0.36450788 | 0.98948 | 1.01231415 |
| ! | cytosolic ribosome (sensu Eukaryota) | GO:0005830 | 203 | 80 | 0.47633096 | 0.98953 | 1.01184641 |
| ! | peroxisome organization and biogenesis | GO:0007031 | 80 | 35 | 0.40661657 | 0.99021 | 1.01202303 |
| ! | isoprenoid metabolism | GO:0006720 | 65 | 35 | 0.41024226 | 0.99021 | 1.01150484 |
| ! | ATP-dependent proteolysis | GO:0006510 | 20 | 9 | 0.24618424 | 0.99039 | 1.01117096 |
| ! | serine family amino acid biosynthesis | GO:0009070 | 24 | 11 | 0.25829678 | 0.99193 | 1.01222524 |
| ! | fertilization | GO:0009566 | 93 | 53 | 0.4425119 | 0.99208 | 1.01186074 |
| ! | acetyl-CoA metabolism | GO:0006084 | 34 | 15 | 0.30278793 | 0.99269 | 1.01196553 |
| ! | sex determination | GO:0007530 | 39 | 21 | 0.3364425 | 0.99303 | 1.01179512 |
| ! | pheromone receptor activity | GO:0016503 | 31 | 30 | 0.38271696 | 0.9932 | 1.01145176 |
| ! | glutathione transferase activity | GO:0004364 | 36 | 23 | 0.34911539 | 0.99332 | 1.01105786 |
| ! | xenobiotic metabolism | GO:0006805 | 145 | 99 | 0.48283027 | 0.9945 | 1.01174273 |
| ! | fertilization (sensu Metazoa) | GO:0007338 | 90 | 52 | 0.42988153 | 0.99451 | 1.01123723 |
| ! | aromatic compound catabolism | GO:0019439 | 28 | 19 | 0.31976424 | 0.99462 | 1.01083388 |
| ! | oxidoreductase activity, acting on the CH-CH group of donors | GO:0016627 | 90 | 54 | 0.43016691 | 0.99497 | 1.01067472 |
| ! | oxidoreductase activity, acting on NADH or NADPH, quinone or similar compound as acceptor | GO:0016655 | 96 | 39 | 0.39747071 | 0.99499 | 1.01018069 |
| ! | L-serine metabolism | GO:0006563 | 22 | 10 | 0.21984306 | 0.99603 | 1.0107222 |
| ! | mitochondrial inner membrane presequence translocase | GO:0005744 | 15 | 10 | 0.22524985 | 0.99603 | 1.01020836 |
| ! | peroxisomal membrane | GO:0005778 | 49 | 23 | 0.33115317 | 0.99652 | 1.01019177 |
| ! | drug metabolism | GO:0017144 | 25 | 17 | 0.29610682 | 0.99679 | 1.00995229 |
| ! | oxidoreductase activity, acting on heme group of donors | GO:0016675 | 47 | 22 | 0.31852787 | 0.99697 | 1.0096219 |
| ! | mitochondrial translocation | GO:0006628 | 27 | 12 | 0.24413367 | 0.997 | 1.00914003 |
| ! | steroid dehydrogenase activity | GO:0016229 | 54 | 37 | 0.37794448 | 0.99722 | 1.00885086 |
| ! | large ribosomal subunit | GO:0015934 | 132 | 58 | 0.41924534 | 0.99791 | 1.00903723 |
| ! | mitochondrial large ribosomal subunit | GO:0005762 | 35 | 18 | 0.28190919 | 0.99825 | 1.00886968 |
| ! | tricarboxylic acid cycle intermediate metabolism | GO:0006100 | 48 | 20 | 0.28800117 | 0.9984 | 1.00851038 |
| ! | estradiol 17-beta-dehydrogenase activity | GO:0004303 | 17 | 12 | 0.223249 | 0.99849 | 1.00809087 |
| ! | sodium ion transporter activity | GO:0015081 | 98 | 42 | 0.38139153 | 0.99854 | 1.00763141 |
| ! | tricarboxylic acid cycle | GO:0006099 | 169 | 75 | 0.42165005 | 0.99941 | 1.00799947 |
| ! | 26S proteasome | GO:0005837 | 22 | 13 | 0.18285195 | 0.99983 | 1.00791352 |
| ! | NADPH regeneration | GO:0006740 | 18 | 12 | 0.14835931 | 0.99987 | 1.00744477 |
| ! | mitochondrial electron transport, NADH to ubiquinone | GO:0006120 | 64 | 25 | 0.26061889 | 0.99988 | 1.00694629 |
| ! | acyl-CoA metabolism | GO:0006637 | 40 | 25 | 0.26060149 | 0.99988 | 1.00643824 |
| ! | NADH dehydrogenase (ubiquinone) activity | GO:0008137 | 85 | 35 | 0.29208172 | 0.99995 | 1.00600113 |
| ! | oxidative phosphorylation | GO:0006119 | 154 | 73 | 0.37308996 | 0.99996 | 1.00550413 |
| ! | intramolecular oxidoreductase activity, transposing C=C bonds | GO:0016863 | 20 | 16 | 0.18793269 | 0.99996 | 1.00499758 |
| ! | proteasome complex (sensu Eukaryota) | GO:0000502 | 84 | 42 | 0.32233804 | 0.99996 | 1.00449154 |

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|---|---|---|---|---|---|---|---|
| ! | small ribosomal subunit | GO:0015935 | 120 | 49 | 0.33494047 | 0.99998 | 1.00400609 |
| ! | respiratory chain complex I | GO:0045271 | 21 | 10 | 0.1002483 | 0.99999 | 1.00351109 |
| ! | mitochondrial small ribosomal subunit | GO:0005763 | 30 | 16 | 0.16537742 | 0.99999 | 1.00300656 |
| ! | mitochondrial electron transport chain | GO:0005746 | 75 | 39 | 0.19891007 | 1 | 1.00251256 |
| ! | ATP synthesis coupled electron transport (sensu Eukaryota) | GO:0042775 | 73 | 32 | 0.23110298 | 1 | 1.00200904 |
| ! | NADH dehydrogenase activity | GO:0003954 | 95 | 39 | 0.27813404 | 1 | 1.00150602 |
| ! | peroxisome | GO:0005777 | 153 | 85 | 0.30197043 | 1 | 1.00100351 |
| ! | ATP synthesis coupled electron transport | GO:0042773 | 75 | 33 | 0.2342026 | 1 | 1.0005015 |
| ! | mitochondrial ribosome | GO:0005761 | 87 | 44 | 0.24836207 | 1 | 1 |

## Supplemental Table 2
## Classes of genes upregulated in adipose tissue from *Ccr2* obese mice

| | Class Name | Class ID | Class size | Effective Class Size | Raw Score | p-value | Corrected p-value |
|---|---|---|---|---|---|---|---|
| 1 | mitochondrial ribosome | GO:0005761 | 87 | 44 | 1.34262618 | 0 | 0 |
| 2 | tricarboxylic acid cycle | GO:0006099 | 169 | 75 | 1.19754073 | 0 | 0 |
| 3 | oxidative phosphorylation | GO:0006119 | 154 | 73 | 1.21927477 | 0 | 0 |
| 4 | ATP biosynthesis | GO:0006754 | 85 | 43 | 0.94826883 | 0 | 0 |
| 5 | hydrogen-translocating F-type ATPase complex | GO:0045255 | 33 | 18 | 1.23914127 | 0 | 0 |
| 6 | mitochondrial electron transport, NADH to ubiquinone | GO:0006120 | 64 | 25 | 1.65733148 | 0 | 0 |
| 7 | eukaryotic 48S initiation complex | GO:0016283 | 77 | 28 | 1.50793863 | 0 | 0 |
| 8 | cytosolic ribosome (sensu Eukaryota) | GO:0005830 | 203 | 80 | 1.42531183 | 0 | 0 |
| 9 | large ribosomal subunit | GO:0015934 | 132 | 58 | 1.37590684 | 0 | 0 |
| 10 | mitochondrial small ribosomal subunit | GO:0005763 | 30 | 16 | 1.36493917 | 0 | 0 |
| 11 | iron ion binding | GO:0005506 | 120 | 59 | 0.93166612 | 0 | 0 |
| 12 | NADH dehydrogenase (ubiquinone) activity | GO:0008137 | 85 | 35 | 1.50515848 | 0 | 0 |
| 13 | eukaryotic 43S preinitiation complex | GO:0016282 | 105 | 39 | 1.32427342 | 0 | 0 |
| 14 | ATP synthesis coupled electron transport | GO:0042773 | 75 | 33 | 1.47642191 | 0 | 0 |
| 15 | mitochondrial large ribosomal subunit | GO:0005762 | 35 | 18 | 1.32444346 | 0 | 0 |
| 16 | coenzyme biosynthesis | GO:0009108 | 191 | 94 | 0.86418198 | 0 | 0 |
| 17 | ER to Golgi transport | GO:0006888 | 110 | 41 | 0.97062029 | 0 | 0 |
| 18 | mitochondrial electron transport chain | GO:0005746 | 75 | 39 | 1.3323873 | 0 | 0 |
| 19 | oxidoreductase activity, acting on NADH or NADPH, quinone or similar compound as acceptor | GO:0016655 | 96 | 39 | 1.39871394 | 0 | 0 |
| 20 | ATP synthesis coupled electron transport (sensu Eukaryota) | GO:0042775 | 73 | 32 | 1.50948745 | 0 | 0 |
| 21 | metal ion transporter activity | GO:0046873 | 209 | 88 | 0.92360833 | 0 | 0 |
| 22 | glutathione transferase activity | GO:0004364 | 36 | 23 | 1.16980031 | 0 | 0 |
| 23 | glycerolipid metabolism | GO:0046486 | 39 | 23 | 1.13030733 | 0 | 0 |
| 24 | respiratory chain complex I | GO:0045271 | 21 | 10 | 1.61775185 | 0 | 0 |
| 25 | small ribosomal subunit | GO:0015935 | 120 | 49 | 1.43752147 | 0 | 0 |
| 26 | hydrogen-transporting ATP synthase activity, rotational mechanism | GO:0046933 | 68 | 34 | 1.04305195 | 0 | 0 |
| 27 | proteasome complex (sensu Eukaryota) | GO:0000502 | 84 | 42 | 0.96459838 | 0 | 0 |
| 28 | glycerolipid biosynthesis | GO:0045017 | 15 | 8 | 1.67944192 | 0 | 0 |
| 29 | regulation of translation | GO:0006445 | 237 | 90 | 0.82590218 | 0 | 0 |
| 30 | peroxisome organization and biogenesis | GO:0007031 | 80 | 35 | 1.11399644 | 0 | 0 |
| 31 | sodium ion transporter activity | GO:0015081 | 98 | 42 | 1.37018927 | 0 | 0 |
| 32 | cytosolic large ribosomal subunit (sensu Eukaryota) | GO:0005842 | 87 | 37 | 1.42575596 | 0 | 0 |
| 33 | oxidoreductase activity, acting on the CH-CH group of donors | GO:0016627 | 90 | 54 | 0.93205371 | 0 | 0 |
| 34 | oxidoreductase activity, acting on NADH or NADPH | GO:0016651 | 177 | 85 | 1.0544061 | 0 | 0 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| **35** | **NADH dehydrogenase activity** | **GO:0003954** | **95** | **39** | **1.53516888** | **0** | **0** |
| **36** | **ATP synthesis coupled proton transport** | **GO:0015986** | **74** | **37** | **1.01458485** | **0** | **0** |
| **37** | **peroxisomal membrane** | **GO:0005778** | **49** | **23** | **1.1856295** | **0** | **0** |
| **38** | **group transfer coenzyme metabolism** | **GO:0006752** | **123** | **65** | **0.92410863** | **0** | **0** |
| **39** | **peroxisome** | **GO:0005777** | **153** | **85** | **1.03545881** | **0** | **0** |
| **40** | **acylglycerol metabolism** | **GO:0006639** | **38** | **22** | **1.13465239** | **0.00001** | **0.00049875** |
| **41** | **nucleoside phosphate metabolism** | **GO:0006753** | **87** | **44** | **0.92822459** | **0.00001** | **0.00048659** |
| **42** | **ATPase activity, coupled to transmembrane movement of ions** | **GO:0042625** | **198** | **92** | **0.77522484** | **0.00001** | **0.000475** |
| **43** | **oxidoreductase activity, acting on heme group of donors** | **GO:0016675** | **47** | **22** | **1.18995793** | **0.00001** | **0.00046395** |
| **44** | **acyl-CoA dehydrogenase activity** | **GO:0003995** | **27** | **15** | **1.30896781** | **0.00001** | **0.00045341** |
| **45** | **diacylglycerol metabolism** | **GO:0046339** | **15** | **8** | **1.64002681** | **0.00001** | **0.00044333** |
| **46** | **hydrogen-transporting ATPase activity, rotational mechanism** | **GO:0046961** | **72** | **36** | **0.98714862** | **0.00001** | **0.0004337** |
| **47** | **proton-transporting two-sector ATPase complex** | **GO:0016469** | **72** | **36** | **1.01844497** | **0.00001** | **0.00042447** |
| **48** | **translational initiation** | **GO:0006413** | **166** | **61** | **0.86398619** | **0.00001** | **0.00041563** |
| **49** | **cation-transporting ATPase activity** | **GO:0019829** | **91** | **42** | **0.93671966** | **0.00002** | **0.00081429** |
| **50** | **Golgi vesicle transport** | **GO:0048193** | **254** | **99** | **0.77088801** | **0.00002** | **0.000798** |
| **51** | **mitochondrial translocation** | **GO:0006628** | **27** | **12** | **1.31541006** | **0.00002** | **0.00078235** |
| **52** | **pigment biosynthesis** | **GO:0046148** | **41** | **22** | **1.11572488** | **0.00002** | **0.00076731** |
| 53 | antioxidant activity | GO:0016209 | 126 | 66 | 0.83218629 | 0.00003 | 0.00112925 |
| 54 | protein kinase binding | GO:0019901 | 163 | 67 | 0.81661987 | 0.00003 | 0.00110833 |
| 55 | protein-mitochondrial targeting | GO:0006626 | 56 | 23 | 1.01302756 | 0.00004 | 0.00145091 |
| 56 | cofactor binding | GO:0048037 | 88 | 42 | 0.91882299 | 0.00004 | 0.001425 |
| 57 | kinase binding | GO:0019900 | 174 | 72 | 0.81059205 | 0.00004 | 0.0014 |
| 58 | ATP metabolism | GO:0046034 | 95 | 49 | 0.89476118 | 0.00004 | 0.00137586 |
| 59 | ribonucleotide metabolism | GO:0009259 | 172 | 92 | 0.76247159 | 0.00004 | 0.00135254 |
| 60 | ribonucleotide biosynthesis | GO:0009260 | 147 | 79 | 0.79526687 | 0.00004 | 0.00133 |
| 61 | sulfur metabolism | GO:0006790 | 163 | 89 | 0.77022681 | 0.00005 | 0.00163525 |
| 62 | nucleoside triphosphate biosynthesis | GO:0009142 | 116 | 62 | 0.82323909 | 0.00005 | 0.00160887 |
| 63 | proteasome endopeptidase activity | GO:0004299 | 58 | 27 | 0.98953789 | 0.00005 | 0.00158333 |
| 64 | ribonucleoside triphosphate biosynthesis | GO:0009201 | 109 | 59 | 0.84052502 | 0.00005 | 0.00155859 |
| 65 | disulfide oxidoreductase activity | GO:0015036 | 72 | 35 | 0.93456461 | 0.00005 | 0.00153462 |
| 66 | hydrogen-transporting two-sector ATPase activity | GO:0003936 | 126 | 55 | 0.83904366 | 0.00005 | 0.00151136 |
| 67 | purine nucleoside triphosphate metabolism | GO:0009144 | 120 | 66 | 0.82513005 | 0.00005 | 0.00148881 |
| 68 | nucleoside triphosphate metabolism | GO:0009141 | 128 | 70 | 0.80210241 | 0.00006 | 0.00176029 |
| 69 | acetyl-CoA metabolism | GO:0006084 | 34 | 15 | 1.19688223 | 0.00006 | 0.00173478 |
| 70 | protein translocase activity | GO:0015450 | 36 | 16 | 1.18734338 | 0.00007 | 0.001995 |
| 71 | respiratory chain complex IV | GO:0045277 | 24 | 11 | 1.32968583 | 0.00007 | 0.0019669 |
| 72 | electron carrier activity | GO:0009055 | 82 | 44 | 0.87165799 | 0.00007 | 0.00193958 |
| 73 | carboxy-lyase activity | GO:0016831 | 64 | 29 | 0.9777997 | 0.00007 | 0.00191301 |
| 74 | protein kinase C binding | GO:0005080 | 50 | 20 | 1.07994731 | 0.00007 | 0.00188716 |
| 75 | hydrogen transport | GO:0006818 | 199 | 96 | 0.75577238 | 0.00007 | 0.001862 |
| 76 | purine ribonucleotide biosynthesis | GO:0009152 | 133 | 73 | 0.79536641 | 0.00008 | 0.0021 |

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|---|---|---|---|---|---|---|---|
| 77 | carbohydrate transport | GO:0008643 | 172 | 74 | 0.78959908 | 0.00008 | 0.00207273 |
| 78 | purine nucleotide biosynthesis | GO:0006164 | 140 | 77 | 0.7871533 | 0.00009 | 0.00230192 |
| 79 | purine ribonucleoside triphosphate metabolism | GO:0009205 | 119 | 65 | 0.81013406 | 0.0001 | 0.00252532 |
| 80 | isoprenoid metabolism | GO:0006720 | 65 | 35 | 0.91058023 | 0.0001 | 0.00249375 |
| 81 | hydrogen-exporting ATPase activity, phosphorylative mechanism | GO:0008553 | 82 | 41 | 0.87655345 | 0.00011 | 0.00270926 |
| 82 | mitochondrion organization and biogenesis | GO:0007005 | 74 | 34 | 0.9080615 | 0.00011 | 0.00267622 |
| 83 | pigment metabolism | GO:0042440 | 53 | 30 | 0.92444453 | 0.00012 | 0.00288434 |
| 84 | purine nucleotide metabolism | GO:0006163 | 157 | 88 | 0.76030501 | 0.00013 | 0.0030875 |
| 85 | carbon-carbon lyase activity | GO:0016830 | 86 | 46 | 0.84501769 | 0.00014 | 0.00328588 |
| 86 | tricarboxylic acid cycle intermediate metabolism | GO:0006100 | 48 | 20 | 1.0559678 | 0.00015 | 0.00347965 |
| 87 | secondary metabolism | GO:0019748 | 97 | 60 | 0.80921035 | 0.00015 | 0.00343966 |
| 88 | heme biosynthesis | GO:0006783 | 27 | 13 | 1.18208894 | 0.00016 | 0.00362727 |
| 89 | sugar porter activity | GO:0005351 | 158 | 76 | 0.76670923 | 0.00016 | 0.00358652 |
| 90 | porphyrin biosynthesis | GO:0006779 | 34 | 16 | 1.10821869 | 0.00016 | 0.00354667 |
| 91 | sodium:amino acid symporter activity | GO:0005283 | 18 | 9 | 1.34116202 | 0.00017 | 0.00372692 |
| 92 | acylglycerol O-acyltransferase activity | GO:0016411 | 18 | 11 | 1.24734928 | 0.00017 | 0.00368641 |
| 93 | response to oxidative stress | GO:0006979 | 161 | 86 | 0.75975039 | 0.00018 | 0.00386129 |
| 94 | triacylglycerol metabolism | GO:0006641 | 29 | 18 | 1.08136023 | 0.00018 | 0.00382021 |
| 95 | copper ion homeostasis | GO:0006878 | 27 | 9 | 1.32669104 | 0.00019 | 0.00399 |
| 96 | purine ribonucleotide metabolism | GO:0009150 | 149 | 83 | 0.75370982 | 0.00021 | 0.00436406 |
| 97 | oxidoreductase activity, acting on sulfur group of donors | GO:0016667 | 40 | 17 | 1.06709749 | 0.00023 | 0.00473041 |
| 98 | insulin receptor signaling pathway | GO:0008286 | 99 | 35 | 0.87949378 | 0.00024 | 0.00488571 |
| 99 | oxidoreduction coenzyme metabolism | GO:0006733 | 51 | 33 | 0.90026801 | 0.00026 | 0.00523939 |
| 100 | carbon-oxygen lyase activity | GO:0016835 | 103 | 54 | 0.81091883 | 0.00027 | 0.0053865 |
| ! | ATP-binding cassette (ABC) transporter complex | GO:0043190 | 29 | 9 | 1.29520081 | 0.0003 | 0.00592574 |
| ! | amino acid biosynthesis | GO:0008652 | 96 | 51 | 0.81737852 | 0.00031 | 0.00606324 |
| ! | oxidoreductase activity, acting on the aldehyde or oxo group of donors | GO:0016903 | 77 | 41 | 0.84753055 | 0.00032 | 0.00619806 |
| ! | proton transport | GO:0015992 | 165 | 81 | 0.75549345 | 0.00033 | 0.00633029 |
| ! | myosin II | GO:0016460 | 53 | 26 | 0.93583774 | 0.00036 | 0.00684 |
| ! | muscle myosin | GO:0005859 | 46 | 24 | 0.94379685 | 0.00044 | 0.00828113 |
| ! | response to unfolded protein | GO:0006986 | 128 | 58 | 0.78499126 | 0.00048 | 0.00894953 |
| ! | mitochondrial inner membrane presequence translocase complex | GO:0005744 | 15 | 10 | 1.19535541 | 0.00049 | 0.00905139 |
| ! | water-soluble vitamin metabolism | GO:0006767 | 67 | 41 | 0.83218151 | 0.00051 | 0.0093344 |
| ! | proteasome core complex (sensu Eukaryota) | GO:0005839 | 39 | 18 | 1.01949517 | 0.00052 | 0.00943091 |
| ! | aminopeptidase activity | GO:0004177 | 83 | 40 | 0.83660329 | 0.00058 | 0.01042432 |
| ! | ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism | GO:0015662 | 171 | 79 | 0.74328687 | 0.0006 | 0.0106875 |
| ! | pigmentation | GO:0048066 | 58 | 34 | 0.86289216 | 0.00061 | 0.01076947 |
| ! | translation initiation factor activity | GO:0003743 | 184 | 75 | 0.74336673 | 0.00064 | 0.0112 |
| ! | serine family amino acid biosynthesis | GO:0009070 | 24 | 11 | 1.15560771 | 0.00064 | 0.01110261 |
| ! | outer membrane | GO:0019867 | 171 | 75 | 0.74405902 | 0.00064 | 0.0110069 |

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|---|---|---|---|---|---|---|---|
| ! | FAD binding | GO:0050660 | 31 | 12 | 1.11749075 | 0.0007 | 0.0119359 |
| ! | negative regulation of translation | GO:0016478 | 23 | 8 | 1.27900189 | 0.00071 | 0.01200381 |
| ! | 26S proteasome | GO:0005837 | 22 | 13 | 1.09582659 | 0.00071 | 0.01190294 |
| ! | L-glutamate transport | GO:0015813 | 25 | 9 | 1.24267413 | 0.00072 | 0.01197 |
| ! | NADP metabolism | GO:0006739 | 23 | 16 | 1.0217039 | 0.00074 | 0.01220083 |
| ! | selenium binding | GO:0008430 | 28 | 15 | 1.05539754 | 0.00079 | 0.01291844 |
| ! | pyruvate metabolism | GO:0006090 | 17 | 8 | 1.27105262 | 0.00082 | 0.0133 |
| ! | sugar transporter activity | GO:0051119 | 164 | 80 | 0.73732481 | 0.00084 | 0.01351452 |
| ! | NADPH regeneration | GO:0006740 | 18 | 12 | 1.10110946 | 0.00086 | 0.0137256 |
| ! | manganese ion binding | GO:0030145 | 146 | 65 | 0.7569133 | 0.00087 | 0.013775 |
| ! | carbohydrate transporter activity | GO:0015144 | 167 | 83 | 0.72785808 | 0.00088 | 0.01382362 |
| ! | myosin | GO:0016459 | 111 | 52 | 0.78494346 | 0.0009 | 0.01402734 |
| ! | serine family amino acid metabolism | GO:0009069 | 47 | 23 | 0.91532419 | 0.00093 | 0.01438256 |
| ! | external encapsulating structure | GO:0030312 | 131 | 59 | 0.76412654 | 0.00096 | 0.01473231 |
| ! | dynactin complex | GO:0005869 | 21 | 9 | 1.2044286 | 0.00098 | 0.01492443 |
| ! | coenzyme binding | GO:0050662 | 64 | 30 | 0.87576405 | 0.00104 | 0.01571818 |
| ! | integral to peroxisomal membrane | GO:0005779 | 20 | 11 | 1.12041671 | 0.00104 | 0.0156 |
| ! | basement membrane | GO:0005604 | 113 | 54 | 0.77748549 | 0.00117 | 0.01741903 |
| ! | organic acid:sodium symporter activity | GO:0005343 | 51 | 23 | 0.90898614 | 0.00123 | 0.01817667 |
| ! | cell-matrix junction | GO:0030055 | 61 | 24 | 0.90247499 | 0.00125 | 0.0183364 |
| ! | endothelial cell differentiation | GO:0045446 | 19 | 11 | 1.09816557 | 0.00127 | 0.0184938 |
| ! | gluconeogenesis | GO:0006094 | 79 | 38 | 0.82370181 | 0.00131 | 0.01893804 |
| ! | coenzyme A metabolism | GO:0015936 | 19 | 9 | 1.17575498 | 0.00131 | 0.0188018 |
| ! | vitamin metabolism | GO:0006766 | 144 | 84 | 0.71851109 | 0.00156 | 0.02223 |
| ! | beta-catenin binding | GO:0008013 | 52 | 15 | 1.00009792 | 0.0016 | 0.0226383 |
| ! | oxidoreductase activity, acting on diphenols and related substances as donors | GO:0016679 | 15 | 8 | 1.21728019 | 0.00162 | 0.02275986 |
| ! | rRNA binding | GO:0019843 | 27 | 12 | 1.06089037 | 0.00162 | 0.0226007 |
| ! | cation:amino acid symporter activity | GO:0005416 | 25 | 13 | 1.04140741 | 0.00162 | 0.02244375 |
| ! | ATP-dependent proteolysis | GO:0006510 | 20 | 9 | 1.15993861 | 0.00163 | 0.02242655 |
| ! | response to reactive oxygen species | GO:0000302 | 30 | 16 | 0.98294384 | 0.00165 | 0.02254623 |
| ! | amino acid catabolism | GO:0009063 | 98 | 54 | 0.76242757 | 0.00165 | 0.02239286 |
| ! | fatty acid binding | GO:0005504 | 51 | 25 | 0.87814861 | 0.00172 | 0.02318514 |
| ! | oxidoreductase activity, acting on peroxide as acceptor | GO:0016684 | 94 | 52 | 0.76974033 | 0.00174 | 0.02329732 |
| ! | cellular lipid catabolism | GO:0044242 | 64 | 40 | 0.80625718 | 0.00175 | 0.023275 |
| ! | xenobiotic metabolism | GO:0006805 | 145 | 99 | 0.70322628 | 0.00177 | 0.0233851 |
| ! | glial cell differentiation | GO:0010001 | 22 | 9 | 1.14912652 | 0.00185 | 0.02428125 |
| ! | Golgi membrane | GO:0000139 | 167 | 78 | 0.72238568 | 0.00196 | 0.02555686 |
| ! | mitochondrial outer membrane | GO:0005741 | 107 | 45 | 0.78112458 | 0.00198 | 0.02565 |
| ! | intramolecular oxidoreductase activity, transposing C=C bonds | GO:0016863 | 20 | 16 | 0.97169123 | 0.00201 | 0.02587065 |
| ! | amine biosynthesis | GO:0009309 | 143 | 81 | 0.72259672 | 0.00204 | 0.02608846 |
| ! | oxidoreductase activity, acting on sulfur group of donors, NAD or NADP as acceptor | GO:0016668 | 21 | 8 | 1.19120766 | 0.00207 | 0.0263035 |
| ! | acetyl-CoA biosynthesis | GO:0006085 | 17 | 8 | 1.19473407 | 0.00207 | 0.02613703 |

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|---|---|---|---|---|---|---|---|
| ! | microtubule-based movement | GO:0007018 | 177 | 79 | 0.71737898 | 0.00208 | 0.02609811 |
| ! | phosphoenolpyruvate-dependent sugar phosphotransferase system | GO:0009401 | 66 | 28 | 0.85555548 | 0.00209 | 0.02605969 |
| ! | L-serine metabolism | GO:0006563 | 22 | 10 | 1.10024133 | 0.00213 | 0.02639348 |
| ! | peroxidase reaction | GO:0006804 | 43 | 24 | 0.87978208 | 0.00218 | 0.0268463 |
| ! | fatty acid beta-oxidation | GO:0006635 | 33 | 22 | 0.903805 | 0.00223 | 0.02729356 |
| ! | cholesterol biosynthesis | GO:0006695 | 50 | 27 | 0.85365129 | 0.00225 | 0.02737043 |
| ! | hydro-lyase activity | GO:0016836 | 92 | 47 | 0.77526229 | 0.00234 | 0.02829273 |
| ! | heavy metal binding | GO:0005505 | 43 | 17 | 0.94558679 | 0.0024 | 0.02884337 |
| ! | zymogen granule | GO:0042588 | 34 | 15 | 0.97629005 | 0.00252 | 0.03010419 |
| ! | protein kinase A binding | GO:0051018 | 31 | 10 | 1.07731293 | 0.00276 | 0.032775 |
| ! | porphyrin metabolism | GO:0006778 | 46 | 24 | 0.87162032 | 0.00277 | 0.03269911 |
| ! | transferase activity, transferring alkyl or aryl (other than methyl) groups | GO:0016765 | 136 | 68 | 0.72674231 | 0.00278 | 0.03262412 |
| ! | glutathione peroxidase activity | GO:0004602 | 18 | 12 | 1.02232172 | 0.0028 | 0.03266667 |
| ! | RNA localization | GO:0006403 | 132 | 51 | 0.76086317 | 0.00299 | 0.03468052 |
| ! | phospholipid biosynthesis | GO:0008654 | 128 | 57 | 0.73357285 | 0.0032 | 0.03690173 |
| ! | heterocycle metabolism | GO:0046483 | 168 | 98 | 0.69206331 | 0.00325 | 0.03726293 |
| ! | negative regulation of transport | GO:0051051 | 45 | 20 | 0.89702258 | 0.00335 | 0.03819 |
| ! | glutathione metabolism | GO:0006749 | 44 | 25 | 0.85146693 | 0.00347 | 0.03933324 |
| ! | nitrogen compound metabolism | GO:0006807 | 108 | 61 | 0.7236575 | 0.00353 | 0.03978729 |
| ! | cytoplasmic vesicle membrane | GO:0030659 | 50 | 21 | 0.87797281 | 0.0037 | 0.0414691 |
| ! | heme metabolism | GO:0042168 | 39 | 21 | 0.88354975 | 0.0037 | 0.04123743 |
| ! | unlocalized protein complex | GO:0005941 | 224 | 84 | 0.7043791 | 0.00385 | 0.04267083 |
| ! | regulation of immune cell mediated cytotoxicity | GO:0001910 | 25 | 11 | 1.02465866 | 0.00387 | 0.04265552 |
| ! | embryonic epithelial tube formation | GO:0001838 | 29 | 16 | 0.93604164 | 0.0039 | 0.04275 |
| ! | nucleobase, nucleoside, nucleotide and nucleic acid transport | GO:0015931 | 134 | 55 | 0.73627935 | 0.00396 | 0.04317049 |
| ! | drug binding | GO:0008144 | 40 | 22 | 0.87005997 | 0.00405 | 0.04391168 |
| ! | cell-substrate adherens junction | GO:0005924 | 50 | 22 | 0.87059836 | 0.00405 | 0.04367432 |
| ! | cytoplasmic dynein complex | GO:0005868 | 28 | 13 | 0.98074115 | 0.00406 | 0.04354677 |
| ! | collagen | GO:0005581 | 89 | 46 | 0.75879781 | 0.00417 | 0.04448743 |
| ! | acyl-CoA metabolism | GO:0006637 | 40 | 25 | 0.84309389 | 0.00422 | 0.04478138 |
| ! | subtilase activity | GO:0004289 | 56 | 25 | 0.8472656 | 0.00422 | 0.04454444 |
| ! | inactivation of MAPK | GO:0000188 | 59 | 21 | 0.87214636 | 0.00444 | 0.04662 |
| ! | transition metal ion homeostasis | GO:0046916 | 66 | 32 | 0.80860815 | 0.00448 | 0.04679372 |
| ! | amine catabolism | GO:0009310 | 115 | 64 | 0.72264766 | 0.00454 | 0.04717344 |
| ! | hemoglobin complex | GO:0005833 | 21 | 9 | 1.0694889 | 0.0046 | 0.04754922 |
| ! | endonuclease activity | GO:0004519 | 170 | 89 | 0.68993743 | 0.00467 | 0.04802397 |
| ! | cytoskeleton-dependent intracellular transport | GO:0030705 | 194 | 89 | 0.68609447 | 0.00467 | 0.04777769 |
| ! | activation of MAPKK | GO:0000186 | 21 | 8 | 1.11625948 | 0.00475 | 0.04834821 |
| ! | inner mitochondrial membrane organization and biogenesis | GO:0007007 | 16 | 8 | 1.12101254 | 0.00475 | 0.04810279 |
| ! | DNA-directed RNA polymerase III complex | GO:0005666 | 17 | 8 | 1.11775107 | 0.00475 | 0.04785985 |
| ! | nicotinamide metabolism | GO:0006769 | 27 | 19 | 0.89087109 | 0.00482 | 0.04832111 |

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|---|---|---|---|---|---|---|---|
| ! | alcohol biosynthesis | GO:0046165 | 93 | 45 | 0.75526584 | 0.00482 | 0.0480795 |
| ! | tube development | GO:0035295 | 200 | 86 | 0.68964957 | 0.00496 | 0.04922985 |
| ! | asymmetric protein localization | GO:0008105 | 24 | 9 | 1.06104538 | 0.0051 | 0.05036881 |
| ! | L-glutamate transporter activity | GO:0005313 | 29 | 11 | 1.00458881 | 0.00522 | 0.0513 |
| ! | protein phosphatase type 2A complex | GO:0000159 | 37 | 11 | 0.99991919 | 0.00522 | 0.05104853 |
| ! | Rho protein signal transduction | GO:0007266 | 124 | 56 | 0.73180725 | 0.00526 | 0.05118878 |
| ! | nucleic acid transport | GO:0050657 | 113 | 44 | 0.75733023 | 0.00542 | 0.05248981 |
| ! | nitric-oxide synthase regulator activity | GO:0030235 | 39 | 14 | 0.94367231 | 0.00545 | 0.05252536 |
| ! | anion:cation symporter activity | GO:0015296 | 68 | 28 | 0.81783108 | 0.0055 | 0.0527524 |
| ! | cell cycle arrest | GO:0007050 | 160 | 68 | 0.71160713 | 0.00561 | 0.05355 |
| ! | regulation of exocytosis | GO:0017157 | 54 | 23 | 0.84045775 | 0.00564 | 0.05358 |
| ! | oxidoreductase activity, acting on the CH-CH group of donors, NAD or NADP as acceptor | GO:0016628 | 35 | 23 | 0.84361959 | 0.00564 | 0.05332607 |
| ! | sterol biosynthesis | GO:0016126 | 65 | 36 | 0.77932344 | 0.00567 | 0.05335684 |
| ! | apoptosis regulator activity | GO:0016329 | 77 | 34 | 0.78836211 | 0.00576 | 0.0539493 |
| ! | protein serine/threonine phosphatase complex | GO:0008287 | 97 | 32 | 0.79311062 | 0.00578 | 0.05388364 |
| ! | protein-peroxisome targeting | GO:0006625 | 22 | 8 | 1.09803454 | 0.00584 | 0.05418977 |
| ! | pyridine nucleotide metabolism | GO:0019362 | 33 | 22 | 0.85282547 | 0.00596 | 0.05504722 |
| ! | ubiquinone biosynthesis | GO:0006744 | 18 | 11 | 0.99515308 | 0.00598 | 0.05497742 |
| ! | C-acyltransferase activity | GO:0016408 | 23 | 10 | 1.01449536 | 0.00624 | 0.05710459 |
| ! | isoprenoid biosynthesis | GO:0008299 | 32 | 14 | 0.93510699 | 0.00626 | 0.05702603 |
| ! | aromatic compound catabolism | GO:0019439 | 28 | 19 | 0.86812764 | 0.00649 | 0.0588525 |
| ! | adherens junction | GO:0005912 | 121 | 53 | 0.73147848 | 0.00666 | 0.06012081 |
| ! | cell wall | GO:0005618 | 118 | 53 | 0.73133435 | 0.00666 | 0.05985 |
| ! | steroid hormone receptor activity | GO:0003707 | 120 | 48 | 0.74251035 | 0.00675 | 0.06038677 |
| ! | microvillus | GO:0005902 | 22 | 13 | 0.94786243 | 0.00691 | 0.06154219 |
| ! | tyrosine metabolism | GO:0006570 | 21 | 14 | 0.92741461 | 0.00697 | 0.06180067 |
| ! | synaptosome | GO:0019717 | 111 | 40 | 0.75300368 | 0.00713 | 0.0629396 |
| ! | integral to membrane of membrane fraction | GO:0000299 | 14 | 9 | 1.03148353 | 0.00718 | 0.06310176 |
| ! | centrosome | GO:0005813 | 127 | 56 | 0.72203139 | 0.00731 | 0.0639625 |
| ! | metalloendopeptidase activity | GO:0004222 | 184 | 100 | 0.67588609 | 0.00733 | 0.06385742 |
| ! | glycerophospholipid biosynthesis | GO:0046474 | 77 | 31 | 0.78814003 | 0.00753 | 0.06531457 |
| ! | membrane lipid catabolism | GO:0046466 | 39 | 19 | 0.85905134 | 0.00765 | 0.06606818 |
| ! | nucleotide-sugar transport | GO:0015780 | 24 | 9 | 1.02064387 | 0.00793 | 0.06819116 |
| ! | basal lamina | GO:0005605 | 48 | 24 | 0.82318981 | 0.00804 | 0.06884034 |
| ! | regulation of growth rate | GO:0040009 | 52 | 24 | 0.82101373 | 0.00804 | 0.06854615 |
| ! | nucleotide kinase activity | GO:0019201 | 68 | 26 | 0.80303575 | 0.00842 | 0.07148043 |
| ! | dynein complex | GO:0030286 | 41 | 22 | 0.83247439 | 0.00847 | 0.07160021 |
| ! | morphogenesis of embryonic epithelium | GO:0016331 | 45 | 23 | 0.81995443 | 0.00853 | 0.07180316 |
| ! | positive regulation of growth rate | GO:0040010 | 49 | 23 | 0.82252934 | 0.00853 | 0.07150147 |
| ! | apocarotenoid metabolism | GO:0043288 | 17 | 9 | 1.01078484 | 0.00876 | 0.07312218 |
| ! | carbon-sulfur lyase activity | GO:0016846 | 21 | 10 | 0.98635647 | 0.00891 | 0.07406438 |
| ! | phosphotransferase activity, for other substituted phosphate groups | GO:0016780 | 29 | 10 | 0.98097786 | 0.00891 | 0.07375705 |
| ! | steroid dehydrogenase activity | GO:0016229 | 54 | 37 | 0.75777911 | 0.00932 | 0.07683223 |

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|---|---|---|---|---|---|---|---|
| ! | quinone cofactor biosynthesis | GO:0045426 | 31 | 14 | 0.90785381 | 0.00933 | 0.07659815 |
| ! | phospholipase A2 activity | GO:0004623 | 43 | 29 | 0.78581522 | 0.00943 | 0.07710184 |
| ! | ligand-dependent nuclear receptor activity | GO:0004879 | 130 | 52 | 0.71468448 | 0.00945 | 0.07695 |
| ! | focal adhesion | GO:0005925 | 46 | 20 | 0.84376719 | 0.0095 | 0.07704268 |
| ! | estradiol 17-beta-dehydrogenase activity | GO:0004303 | 17 | 12 | 0.94051511 | 0.00954 | 0.07705385 |
| ! | collagen binding | GO:0005518 | 43 | 24 | 0.81532601 | 0.00959 | 0.07714536 |
| ! | dicarboxylic acid transport | GO:0006835 | 44 | 18 | 0.86587251 | 0.00968 | 0.07755663 |
| ! | antigen presentation, endogenous antigen | GO:0019883 | 44 | 25 | 0.80144365 | 0.00981 | 0.0782838 |
| ! | metalloexopeptidase activity | GO:0008235 | 147 | 70 | 0.68980044 | 0.00999 | 0.07940259 |
| ! | quinone cofactor metabolism | GO:0042375 | 32 | 15 | 0.88834655 | 0.01004 | 0.07948333 |
| ! | mitochondrial membrane organization and biogenesis | GO:0007006 | 27 | 13 | 0.91874749 | 0.01034 | 0.08153478 |
| ! | delayed rectifier potassium channel activity | GO:0005251 | 29 | 13 | 0.91825216 | 0.01034 | 0.08121378 |
| ! | regulation of translational initiation | GO:0006446 | 98 | 35 | 0.75789442 | 0.01038 | 0.08120824 |
| ! | oxidoreductase activity, acting on the CH-NH group of donors | GO:0016645 | 37 | 26 | 0.79598101 | 0.0104 | 0.08104687 |
| ! | collagen | GO:0005202 | 55 | 26 | 0.79595116 | 0.0104 | 0.08073152 |
| ! | response to heat | GO:0009408 | 110 | 49 | 0.7190622 | 0.01063 | 0.08219709 |
| ! | spermatid cell development | GO:0007286 | 123 | 49 | 0.7147118 | 0.01063 | 0.08187973 |
| ! | polyisoprenoid metabolism | GO:0016096 | 21 | 11 | 0.94911197 | 0.01122 | 0.08609192 |
| ! | plasma membrane repair | GO:0001778 | 20 | 9 | 0.99625908 | 0.01125 | 0.08599138 |
| ! | structural constituent of cell wall | GO:0005199 | 120 | 53 | 0.70760417 | 0.01218 | 0.09274466 |
| ! | lipid transporter activity | GO:0005319 | 190 | 84 | 0.67453197 | 0.01221 | 0.09261958 |
| ! | protein phosphatase type 1 activity | GO:0000163 | 70 | 25 | 0.79435872 | 0.01228 | 0.09279773 |
| ! | O-acyltransferase activity | GO:0008374 | 43 | 25 | 0.79684227 | 0.01228 | 0.09244755 |
| ! | transmembrane receptor protein kinase activity | GO:0019199 | 242 | 96 | 0.66600727 | 0.01231 | 0.092325 |
| ! | neural plate morphogenesis | GO:0001839 | 27 | 14 | 0.88653515 | 0.01231 | 0.09197921 |
| ! | heterotrimeric G-protein complex | GO:0005834 | 101 | 43 | 0.73303266 | 0.01245 | 0.09267817 |
| ! | solute:solute antiporter activity | GO:0015300 | 68 | 33 | 0.75486319 | 0.01268 | 0.09403941 |
| ! | striated muscle contraction | GO:0006941 | 150 | 73 | 0.6795069 | 0.01275 | 0.09420833 |
| ! | sphingolipid catabolism | GO:0030149 | 22 | 11 | 0.94063657 | 0.01275 | 0.0938607 |
| ! | positive regulation of cell migration | GO:0030335 | 21 | 10 | 0.95749878 | 0.01283 | 0.09410239 |
| ! | positive regulation of angiogenesis | GO:0045766 | 19 | 10 | 0.95345876 | 0.01283 | 0.09375769 |
| ! | glycerophospholipid metabolism | GO:0006650 | 125 | 47 | 0.71420586 | 0.0129 | 0.09392518 |
| ! | energy reserve metabolism | GO:0006112 | 110 | 51 | 0.70778334 | 0.01298 | 0.094164 |
| ! | peptide metabolism | GO:0006518 | 25 | 8 | 1.01298393 | 0.01335 | 0.09649728 |
| ! | gliogenesis | GO:0042063 | 34 | 13 | 0.89685622 | 0.01337 | 0.09629296 |
| ! | di-, tri-valent inorganic cation homeostasis | GO:0030005 | 174 | 94 | 0.66346035 | 0.0136 | 0.09759712 |
| ! | protein kinase A anchoring activity | GO:0005079 | 34 | 12 | 0.91306069 | 0.01383 | 0.09889194 |
| ! | small protein conjugating enzyme activity | GO:0008639 | 221 | 93 | 0.66349527 | 0.01383 | 0.09853875 |
| ! | tube morphogenesis | GO:0035239 | 85 | 38 | 0.73532753 | 0.01413 | 0.10031797 |
| ! | ATP-binding cassette (ABC) transporter activity | GO:0004009 | 107 | 49 | 0.70541561 | 0.01417 | 0.10024521 |
| ! | protein heterodimerization activity | GO:0046982 | 178 | 80 | 0.66897075 | 0.01427 | 0.10059594 |
| ! | protein degradation tagging activity | GO:0000211 | 25 | 10 | 0.94339519 | 0.01434 | 0.10073345 |
| ! | sodium:dicarboxylate symporter activity | GO:0017153 | 32 | 11 | 0.9287163 | 0.01447 | 0.10129 |
| ! | ubiquitin conjugating enzyme activity | GO:0004840 | 212 | 90 | 0.66345546 | 0.01477 | 0.1030285 |

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|---|---|---|---|---|---|---|---|
| ! | DNA damage checkpoint | GO:0000077 | 52 | 25 | 0.7855474 | 0.01481 | 0.10294756 |
| ! | myosin phosphatase activity | GO:0017018 | 67 | 23 | 0.79567527 | 0.01485 | 0.10286719 |
| ! | induction of apoptosis by intracellular signals | GO:0008629 | 76 | 37 | 0.73389153 | 0.01499 | 0.10347768 |
| ! | cellular respiration | GO:0045333 | 33 | 18 | 0.83544998 | 0.01527 | 0.10504707 |
| ! | nucleobase, nucleoside, nucleotide and nucleic acid transporter activity | GO:0015932 | 53 | 20 | 0.81020169 | 0.01543 | 0.10578299 |
| ! | ATP:ADP antiporter activity | GO:0005471 | 29 | 12 | 0.8975599 | 0.01565 | 0.1069238 |
| ! | sulfur amino acid biosynthesis | GO:0000097 | 28 | 12 | 0.89965231 | 0.01565 | 0.10655887 |
| ! | translational elongation | GO:0006414 | 76 | 36 | 0.73906953 | 0.01584 | 0.10748571 |
| ! | fatty acid oxidation | GO:0019395 | 59 | 36 | 0.74259588 | 0.01584 | 0.10712136 |
| ! | dystrophin-associated glycoprotein complex | GO:0016010 | 26 | 10 | 0.93777212 | 0.01613 | 0.10871402 |
| ! | branched chain family amino acid metabolism | GO:0009081 | 16 | 8 | 0.9967161 | 0.01616 | 0.10854949 |
| ! | cysteine metabolism | GO:0006534 | 11 | 8 | 0.99040941 | 0.01616 | 0.10818523 |
| ! | regulation of cell migration | GO:0030334 | 130 | 67 | 0.68420903 | 0.01625 | 0.10842391 |
| ! | germ cell migration | GO:0008354 | 42 | 24 | 0.78966038 | 0.01625 | 0.1080625 |
| ! | neurotransmitter:sodium symporter activity | GO:0005328 | 44 | 22 | 0.79533917 | 0.01637 | 0.10849884 |
| ! | lipid catabolism | GO:0016042 | 184 | 100 | 0.65131057 | 0.01672 | 0.11045166 |
| ! | nuclear export | GO:0051168 | 137 | 52 | 0.69546807 | 0.01684 | 0.11087723 |
| ! | somatic muscle development | GO:0007525 | 40 | 9 | 0.95797047 | 0.01704 | 0.111825 |
| ! | phosphatase regulator activity | GO:0019208 | 121 | 51 | 0.69909129 | 0.0172 | 0.11250492 |
| ! | tubulin | GO:0045298 | 42 | 19 | 0.8171014 | 0.01728 | 0.11265882 |
| ! | magnesium-dependent protein serine/threonine phosphatase activity | GO:0004724 | 68 | 23 | 0.78592185 | 0.0175 | 0.1137215 |
| ! | perinuclear region | GO:0048471 | 57 | 23 | 0.78118746 | 0.0175 | 0.11335227 |
| ! | apoptosis inhibitor activity | GO:0008189 | 106 | 46 | 0.70854228 | 0.01759 | 0.1135665 |
| ! | acetyltransferase activity | GO:0016407 | 138 | 65 | 0.67768401 | 0.01772 | 0.11403677 |
| ! | vesicle transport | GO:0005480 | 36 | 18 | 0.82501091 | 0.01775 | 0.11386254 |
| ! | racemase and epimerase activity | GO:0016854 | 30 | 18 | 0.81905969 | 0.01775 | 0.1134976 |
| ! | imaginal disc development | GO:0007444 | 16 | 8 | 0.98117568 | 0.01776 | 0.11319872 |
| ! | deactivation of rhodopsin mediated signaling | GO:0016059 | 17 | 8 | 0.98409061 | 0.01776 | 0.11283822 |
| ! | acid-thiol ligase activity | GO:0016878 | 19 | 10 | 0.9263776 | 0.018 | 0.114 |
| ! | spindle pole | GO:0000922 | 148 | 64 | 0.68287113 | 0.01812 | 0.11439684 |
| ! | lipid modification | GO:0030258 | 22 | 11 | 0.90768028 | 0.0185 | 0.11642744 |
| ! | antigen presentation, endogenous peptide antigen | GO:0048004 | 24 | 11 | 0.9045751 | 0.0185 | 0.11606132 |
| ! | membrane organization and biogenesis | GO:0016044 | 99 | 49 | 0.70352464 | 0.01872 | 0.11707335 |
| ! | sex determination | GO:0007530 | 39 | 21 | 0.79493842 | 0.01899 | 0.11839078 |
| ! | cortical cytoskeleton | GO:0030863 | 40 | 17 | 0.82638511 | 0.01923 | 0.11951355 |
| ! | guanylate kinase activity | GO:0004385 | 50 | 17 | 0.82415703 | 0.01923 | 0.11914239 |
| ! | muscle fiber | GO:0030484 | 139 | 70 | 0.67492674 | 0.01959 | 0.12099706 |
| ! | superoxide dismutase activity | GO:0004784 | 18 | 8 | 0.97853266 | 0.01963 | 0.12086991 |
| ! | embryonic heart tube development | GO:0035050 | 33 | 12 | 0.88092979 | 0.02012 | 0.12350585 |
| ! | pteridine and derivative biosynthesis | GO:0042559 | 26 | 10 | 0.9164995 | 0.02017 | 0.12343298 |
| ! | nucleotide-sugar transporter activity | GO:0005338 | 25 | 10 | 0.92231216 | 0.02017 | 0.1230555 |
| ! | solute:cation symporter activity | GO:0015294 | 122 | 62 | 0.67805964 | 0.02024 | 0.1231061 |
| ! | regulation of glucose import | GO:0046324 | 23 | 9 | 0.94080048 | 0.02026 | 0.12285319 |

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|---|---|---|---|---|---|---|---|
| ! | protein phosphatase regulator activity | GO:0019888 | 111 | 48 | 0.6987373 | 0.02037 | 0.12314591 |
| ! | glycogen metabolism | GO:0005977 | 74 | 35 | 0.7325603 | 0.02043 | 0.1231355 |
| ! | negative regulation of protein kinase activity | GO:0006469 | 94 | 35 | 0.72897457 | 0.02043 | 0.12276461 |
| ! | dicarboxylic acid transporter activity | GO:0005310 | 37 | 14 | 0.84864751 | 0.02046 | 0.12257568 |
| ! | protein homodimerization activity | GO:0042803 | 196 | 93 | 0.65069259 | 0.0206 | 0.12304491 |
| ! | sulfur amino acid metabolism | GO:0000096 | 66 | 32 | 0.73585528 | 0.02061 | 0.12273716 |
| ! | glucose transport | GO:0015758 | 70 | 32 | 0.74007876 | 0.02061 | 0.12237187 |
| ! | single-stranded RNA binding | GO:0003727 | 73 | 25 | 0.76523753 | 0.02138 | 0.12656706 |
| ! | CTD phosphatase activity | GO:0008420 | 69 | 25 | 0.76633584 | 0.02138 | 0.1261926 |
| ! | double-strand break repair via homologous recombination | GO:0000724 | 14 | 8 | 0.9657019 | 0.0214 | 0.12593805 |
| ! | membrane lipid biosynthesis | GO:0046467 | 167 | 77 | 0.65870565 | 0.0217 | 0.12732794 |
| ! | anchoring collagen | GO:0030934 | 27 | 13 | 0.86292465 | 0.02202 | 0.12882669 |
| ! | stress fiber | GO:0001725 | 26 | 13 | 0.86237123 | 0.02202 | 0.12845 |
| ! | cotranslational protein-membrane targeting | GO:0006613 | 68 | 26 | 0.76075859 | 0.02224 | 0.1293551 |
| ! | transcriptional repressor complex | GO:0017053 | 27 | 10 | 0.90682114 | 0.02226 | 0.12909506 |
| ! | protein amino acid alkylation | GO:0008213 | 102 | 38 | 0.71876795 | 0.02227 | 0.1287787 |
| ! | transmembrane receptor protein tyrosine kinase adaptor protein activity | GO:0005068 | 18 | 9 | 0.92581914 | 0.02233 | 0.12875246 |
| ! | CoA-ligase activity | GO:0016405 | 18 | 9 | 0.92400247 | 0.02233 | 0.12838141 |
| ! | L-phenylalanine metabolism | GO:0006558 | 15 | 9 | 0.93257588 | 0.02233 | 0.1280125 |
| ! | insulin-like growth factor binding | GO:0005520 | 46 | 22 | 0.77651083 | 0.02293 | 0.1310755 |
| ! | transcriptional elongation regulator activity | GO:0003711 | 31 | 15 | 0.83526673 | 0.0232 | 0.13224 |
| ! | intercellular junction assembly | GO:0007043 | 32 | 15 | 0.83448796 | 0.0232 | 0.13186325 |
| ! | carbohydrate kinase activity | GO:0019200 | 48 | 24 | 0.76363334 | 0.02328 | 0.13194205 |
| ! | carbon-nitrogen ligase activity, with glutamine as amido-N-donor | GO:0016884 | 13 | 8 | 0.95574132 | 0.0233 | 0.1316813 |
| ! | ATP/ADP exchange | GO:0006854 | 28 | 11 | 0.89393972 | 0.02349 | 0.13238008 |
| ! | apoptotic program | GO:0008632 | 176 | 87 | 0.65656858 | 0.02372 | 0.13329972 |
| ! | nucleobase, nucleoside, nucleotide kinase activity | GO:0019205 | 109 | 50 | 0.68678538 | 0.0238 | 0.1333736 |
| ! | membrane fusion | GO:0006944 | 102 | 50 | 0.69334582 | 0.0238 | 0.133 |
| ! | sulfur compound biosynthesis | GO:0044272 | 79 | 40 | 0.70615656 | 0.02435 | 0.13569344 |
| ! | Notch binding | GO:0005112 | 17 | 9 | 0.92244368 | 0.02467 | 0.13709373 |
| ! | structural constituent of muscle | GO:0008307 | 131 | 64 | 0.67564809 | 0.02468 | 0.13676833 |
| ! | polysaccharide metabolism | GO:0005976 | 125 | 64 | 0.66902373 | 0.02468 | 0.13638947 |
| ! | response to temperature | GO:0009266 | 138 | 64 | 0.67399756 | 0.02468 | 0.13601271 |
| ! | glucose homeostasis | GO:0042593 | 41 | 20 | 0.78590395 | 0.02471 | 0.13580289 |
| ! | signal recognition particle (sensu Eukaryota) | GO:0005786 | 35 | 13 | 0.85102001 | 0.02491 | 0.13652596 |
| ! | biopolymer biosynthesis | GO:0043284 | 44 | 23 | 0.76477581 | 0.02504 | 0.13686247 |
| ! | glucan metabolism | GO:0006073 | 75 | 36 | 0.72199848 | 0.02523 | 0.13752418 |
| ! | endodeoxyribonuclease activity | GO:0004520 | 42 | 21 | 0.7791052 | 0.02568 | 0.13959564 |
| ! | cellular morphogenesis during differentiation | GO:0000904 | 38 | 16 | 0.81760955 | 0.02597 | 0.14078845 |
| ! | ligase activity, forming phosphoric ester bonds | GO:0016886 | 187 | 99 | 0.64254504 | 0.02616 | 0.14143415 |
| ! | alcohol dehydrogenase activity, zinc-dependent | GO:0004024 | 26 | 15 | 0.81977622 | 0.02619 | 0.14121365 |
| ! | cyclic nucleotide-dependent protein kinase activity | GO:0004690 | 207 | 82 | 0.65508972 | 0.0265 | 0.1425 |

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|---|---|---|---|---|---|---|---|
| ! | microtubule binding | GO:0008017 | 132 | 43 | 0.69805839 | 0.02718 | 0.14576371 |
| ! | eukaryotic translation initiation factor 3 complex | GO:0005852 | 20 | 9 | 0.9124183 | 0.02721 | 0.14553338 |
| ! | aerobic respiration | GO:0009060 | 15 | 9 | 0.90655409 | 0.02721 | 0.14514425 |
| ! | ATP hydrolysis coupled proton transport | GO:0015991 | 25 | 10 | 0.88618035 | 0.02735 | 0.145502 |
| ! | tubulin folding | GO:0007021 | 32 | 10 | 0.89325624 | 0.02735 | 0.14511503 |
| ! | cAMP-dependent protein kinase activity | GO:0004691 | 201 | 81 | 0.65519461 | 0.02757 | 0.1458943 |
| ! | N-acetylglucosamine metabolism | GO:0006044 | 31 | 13 | 0.83872641 | 0.02772 | 0.1463 |
| ! | amino acid-polyamine transporter activity | GO:0005279 | 99 | 47 | 0.68986221 | 0.02774 | 0.14601926 |
| ! | neurotransmitter transporter activity | GO:0005326 | 77 | 38 | 0.70524589 | 0.02796 | 0.14679 |
| ! | pteridine and derivative metabolism | GO:0042558 | 28 | 12 | 0.85201784 | 0.02798 | 0.14650945 |
| ! | protein phosphatase type 2A regulator activity | GO:0008601 | 35 | 12 | 0.85153208 | 0.02798 | 0.14612592 |
| ! | intracellular transporter activity | GO:0005478 | 96 | 34 | 0.71697792 | 0.02823 | 0.14704661 |
| ! | copper ion binding | GO:0005507 | 118 | 60 | 0.6675183 | 0.02875 | 0.14936523 |
| ! | neuronal migration | GO:0001764 | 81 | 41 | 0.69778427 | 0.0289 | 0.14975455 |
| ! | extracellular matrix structural constituent conferring tensile strength | GO:0030020 | 72 | 37 | 0.70659342 | 0.02925 | 0.15117552 |
| ! | cis-trans isomerase activity | GO:0016859 | 54 | 30 | 0.73040042 | 0.02953 | 0.15222829 |
| ! | calcium-dependent protein serine/threonine phosphatase activity | GO:0004723 | 70 | 25 | 0.75017636 | 0.02954 | 0.15188737 |
| ! | casein kinase activity | GO:0004680 | 248 | 94 | 0.64514253 | 0.02972 | 0.15242005 |
| ! | signalosome complex | GO:0008180 | 15 | 9 | 0.9021635 | 0.02974 | 0.15213154 |
| ! | phosphate transport | GO:0006817 | 158 | 79 | 0.64754219 | 0.0299 | 0.15255882 |
| ! | dorsal/ventral pattern formation | GO:0009953 | 50 | 23 | 0.75507872 | 0.03004 | 0.15288214 |
| ! | receptor metabolism | GO:0043112 | 18 | 8 | 0.92577904 | 0.03009 | 0.15274695 |
| ! | protein methyltransferase activity | GO:0008276 | 68 | 27 | 0.74145068 | 0.03028 | 0.15332132 |
| ! | transmembrane receptor protein tyrosine kinase activity | GO:0004714 | 192 | 77 | 0.64747831 | 0.03059 | 0.15449886 |
| ! | microtubule organizing center | GO:0005815 | 141 | 67 | 0.65951419 | 0.03079 | 0.15511629 |
| ! | protein phosphatase type 2A activity | GO:0000158 | 77 | 29 | 0.73237252 | 0.03104 | 0.15598186 |
| ! | positive regulation of growth | GO:0045927 | 79 | 36 | 0.71041952 | 0.03105 | 0.15564008 |
| ! | L-amino acid transporter activity | GO:0015179 | 70 | 36 | 0.70946289 | 0.03105 | 0.15525 |
| ! | solute:hydrogen symporter activity | GO:0015295 | 22 | 13 | 0.83145016 | 0.03128 | 0.156009 |
| ! | lipoprotein receptor activity | GO:0030228 | 26 | 12 | 0.84557279 | 0.0315 | 0.15671446 |
| ! | acyl-CoA binding | GO:0000062 | 25 | 12 | 0.84074257 | 0.0315 | 0.15632463 |
| ! | steroid binding | GO:0005496 | 141 | 76 | 0.6509852 | 0.03166 | 0.15672878 |
| ! | antigen processing, endogenous antigen via MHC class I | GO:0019885 | 44 | 24 | 0.74737766 | 0.03265 | 0.16122958 |
| ! | organic acid biosynthesis | GO:0016053 | 174 | 89 | 0.63874419 | 0.03269 | 0.16102852 |
| ! | oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor | GO:0016620 | 64 | 31 | 0.72236601 | 0.03288 | 0.16156552 |
| ! | regulation of carbohydrate metabolism | GO:0006109 | 24 | 8 | 0.91416371 | 0.03294 | 0.16146265 |
| ! | filopodium | GO:0030175 | 29 | 9 | 0.89015469 | 0.03304 | 0.16155588 |
| ! | protein phosphatase type 2C activity | GO:0015071 | 78 | 28 | 0.72603623 | 0.03343 | 0.1630632 |
| ! | oxygen transporter activity | GO:0005344 | 20 | 10 | 0.86899215 | 0.03347 | 0.16286012 |
| ! | single-stranded DNA binding | GO:0003697 | 109 | 43 | 0.69365907 | 0.03417 | 0.16586168 |

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|---|---|---|---|---|---|---|---|
| ! | protein kinase CK2 activity | GO:0004682 | 223 | 86 | 0.64403592 | 0.03433 | 0.16623386 |
| ! | RNA-nucleus export | GO:0006405 | 95 | 38 | 0.70349155 | 0.03458 | 0.16703898 |
| ! | protein C-terminus binding | GO:0008022 | 96 | 38 | 0.69944812 | 0.03458 | 0.16663551 |
| ! | calcium ion-dependent exocytosis | GO:0017156 | 64 | 25 | 0.74247588 | 0.03481 | 0.16733964 |
| ! | aminophospholipid transporter activity | GO:0015247 | 33 | 12 | 0.83565083 | 0.03501 | 0.16789651 |
| ! | RAN protein binding | GO:0008536 | 28 | 12 | 0.83243625 | 0.03501 | 0.16749388 |
| ! | cholesterol metabolism | GO:0008203 | 158 | 85 | 0.64397669 | 0.03521 | 0.16804773 |
| ! | apoptotic mitochondrial changes | GO:0008637 | 29 | 13 | 0.82208266 | 0.03524 | 0.1677895 |
| ! | vesicle coat | GO:0030120 | 101 | 47 | 0.676344 | 0.0354 | 0.16815 |
| ! | female gamete generation | GO:0007292 | 137 | 54 | 0.67155202 | 0.03549 | 0.16817708 |
| ! | mRNA polyadenylylation | GO:0006378 | 47 | 21 | 0.75267741 | 0.03581 | 0.16929135 |
| ! | aromatic amino acid family catabolism | GO:0009074 | 18 | 11 | 0.85137584 | 0.03582 | 0.1689383 |
| ! | fertilization (sensu Metazoa) | GO:0007338 | 90 | 52 | 0.6672511 | 0.0369 | 0.17362146 |
| ! | male sex differentiation | GO:0046661 | 64 | 29 | 0.71503435 | 0.03692 | 0.17330682 |
| ! | hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amides | GO:0016811 | 73 | 46 | 0.68437331 | 0.03694 | 0.17299366 |
| ! | solute:sodium symporter activity | GO:0015370 | 98 | 46 | 0.6792066 | 0.03694 | 0.17258852 |
| ! | protein phosphatase type 2B activity | GO:0030357 | 69 | 26 | 0.72855793 | 0.03763 | 0.17540152 |
| ! | photoreceptor cell differentiation | GO:0046530 | 40 | 16 | 0.78343552 | 0.03856 | 0.17931748 |
| ! | 3'-5'-exoribonuclease activity | GO:0000175 | 29 | 16 | 0.78184618 | 0.03856 | 0.17890047 |
| ! | organic anion transporter activity | GO:0008514 | 52 | 24 | 0.74064514 | 0.03881 | 0.17964258 |
| ! | axon cargo transport | GO:0008088 | 35 | 9 | 0.8688973 | 0.03929 | 0.1814434 |
| ! | lipid binding | GO:0006630 | 26 | 12 | 0.82421549 | 0.03948 | 0.18189977 |
| ! | protein-histidine kinase activity | GO:0004673 | 22 | 13 | 0.81836853 | 0.03958 | 0.18194032 |
| ! | aromatic compound biosynthesis | GO:0019438 | 29 | 11 | 0.83855662 | 0.03968 | 0.18198069 |
| ! | poly(A) binding | GO:0008143 | 37 | 11 | 0.84552681 | 0.03968 | 0.1815633 |
| ! | negative regulation of enzyme activity | GO:0043086 | 137 | 58 | 0.66520661 | 0.03983 | 0.18183261 |
| ! | sterol metabolism | GO:0016125 | 174 | 95 | 0.62936459 | 0.04005 | 0.18241952 |
| ! | iron ion transport | GO:0006826 | 52 | 28 | 0.72134711 | 0.04024 | 0.18286743 |
| ! | monosaccharide binding | GO:0048029 | 41 | 28 | 0.72248148 | 0.04024 | 0.18245182 |
| ! | coated membrane | GO:0048475 | 111 | 49 | 0.66710037 | 0.0406 | 0.18366667 |
| ! | fatty-acid synthase activity | GO:0004312 | 24 | 10 | 0.84852095 | 0.04074 | 0.18388303 |
| ! | cell-substrate junction assembly | GO:0007044 | 21 | 10 | 0.85640945 | 0.04074 | 0.18346795 |
| ! | fatty acid biosynthesis | GO:0006633 | 154 | 78 | 0.6401569 | 0.04082 | 0.18341419 |
| ! | hexose transport | GO:0008645 | 74 | 34 | 0.7008911 | 0.04159 | 0.18645404 |
| ! | lipid raft | GO:0045121 | 40 | 21 | 0.74485871 | 0.04191 | 0.18746738 |
| ! | pyrimidine nucleotide sugar transporter activity | GO:0015165 | 17 | 8 | 0.88749293 | 0.04214 | 0.1880745 |
| ! | carbon utilization | GO:0015976 | 17 | 8 | 0.88942692 | 0.04214 | 0.18765469 |
| ! | heat shock protein activity | GO:0003773 | 105 | 43 | 0.67757831 | 0.04292 | 0.19070245 |
| ! | nucleobase transporter activity | GO:0015205 | 31 | 11 | 0.83714709 | 0.04364 | 0.19347067 |
| ! | GPI anchor metabolism | GO:0006505 | 21 | 11 | 0.83380449 | 0.04364 | 0.19304169 |
| ! | MHC class I receptor activity | GO:0030106 | 39 | 22 | 0.73884669 | 0.04372 | 0.1929677 |
| ! | immune cell mediated cytotoxicity | GO:0001909 | 42 | 20 | 0.75049553 | 0.04412 | 0.19430331 |
| ! | phospholipid catabolism | GO:0009395 | 22 | 10 | 0.84731757 | 0.04487 | 0.19717104 |
| ! | cell wall catabolism | GO:0016998 | 14 | 8 | 0.88349245 | 0.04538 | 0.19897385 |

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|---|---|---|---|---|---|---|---|
| ! | initiation of viral infection | GO:0019059 | 21 | 8 | 0.88118244 | 0.04538 | 0.1985375 |
| ! | amine binding | GO:0043176 | 58 | 32 | 0.69627568 | 0.04642 | 0.20264311 |
| ! | fertilization | GO:0009566 | 93 | 53 | 0.65846121 | 0.04672 | 0.20350742 |
| ! | negative regulation of phosphorylation | GO:0042326 | 20 | 9 | 0.85095965 | 0.04744 | 0.20619346 |
| ! | DNA N-glycosylase activity | GO:0019104 | 17 | 9 | 0.84863569 | 0.04744 | 0.20574522 |
| ! | glucosamine metabolism | GO:0006041 | 33 | 14 | 0.78965366 | 0.04773 | 0.2065539 |
| ! | lipid phosphatase activity | GO:0042577 | 33 | 14 | 0.78192719 | 0.04773 | 0.20610682 |
| ! | aldehyde metabolism | GO:0006081 | 41 | 23 | 0.73171453 | 0.04798 | 0.20673888 |
| ! | PDZ domain binding | GO:0030165 | 54 | 23 | 0.72487328 | 0.04798 | 0.20629332 |
| ! | aromatic amino acid family metabolism | GO:0009072 | 40 | 25 | 0.72338164 | 0.04833 | 0.20735129 |
| ! | insulin secretion | GO:0030073 | 31 | 15 | 0.77801178 | 0.04863 | 0.20819067 |
| ! | no name yet | obsolete_cellular_component | 196 | 85 | 0.62864749 | 0.04868 | 0.20795846 |
| ! | phosphatase binding | GO:0019902 | 24 | 12 | 0.79984257 | 0.04919 | 0.20968814 |
| ! | striated muscle thick filament | GO:0005863 | 19 | 12 | 0.8026788 | 0.04919 | 0.20924104 |
| ! | energy coupled proton transport, against electrochemical gradient | GO:0015988 | 29 | 12 | 0.80916239 | 0.04919 | 0.20879585 |
| ! | membrane-associated guanylate kinase | GO:0004384 | 22 | 8 | 0.87318865 | 0.04924 | 0.20856433 |
| ! | SNAP receptor activity | GO:0005484 | 27 | 10 | 0.83426423 | 0.04951 | 0.20926367 |
| ! | glycogen biosynthesis | GO:0005978 | 27 | 13 | 0.79110305 | 0.04969 | 0.20958044 |
| ! | cell cortex | GO:0005938 | 71 | 34 | 0.68626479 | 0.05079 | 0.21376804 |
| ! | one-carbon compound metabolism | GO:0006730 | 68 | 33 | 0.68862183 | 0.05221 | 0.219282 |
| ! | regulation of natural killer cell mediated cytotoxicity | GO:0042269 | 22 | 9 | 0.83849588 | 0.05225 | 0.21898897 |
| ! | protein amino acid ADP-ribosylation | GO:0006471 | 66 | 26 | 0.7051393 | 0.05265 | 0.22020283 |
| ! | regulation of neurotransmitter secretion | GO:0046928 | 25 | 8 | 0.86202889 | 0.05312 | 0.22170377 |
| ! | positive regulation of B-cell proliferation | GO:0030890 | 19 | 8 | 0.85941926 | 0.05312 | 0.22124092 |
| ! | fructose transport | GO:0015755 | 15 | 8 | 0.86098539 | 0.05312 | 0.22078 |
| ! | post-embryonic development | GO:0009791 | 69 | 29 | 0.70162936 | 0.05331 | 0.22110904 |
| ! | ceramide metabolism | GO:0006672 | 58 | 29 | 0.7036593 | 0.05331 | 0.22065031 |
| ! | protein-nucleus import, translocation | GO:0000060 | 69 | 29 | 0.69833693 | 0.05331 | 0.22019348 |
| ! | phorbol ester receptor activity | GO:0001565 | 34 | 14 | 0.77976894 | 0.0535 | 0.22052169 |
| ! | double-strand break repair | GO:0006302 | 43 | 24 | 0.72329516 | 0.05431 | 0.22339887 |
| ! | amino acid transporter activity | GO:0015171 | 143 | 67 | 0.64434225 | 0.05436 | 0.22314444 |
| ! | oogenesis | GO:0048477 | 45 | 15 | 0.76171155 | 0.05487 | 0.22477546 |
| ! | autophagy | GO:0006914 | 29 | 13 | 0.78302265 | 0.05545 | 0.22668596 |
| ! | eye photoreceptor cell differentiation | GO:0001754 | 34 | 13 | 0.78647307 | 0.05545 | 0.22622239 |
| ! | coenzyme and prosthetic group metabolism | GO:0006731 | 20 | 13 | 0.78111567 | 0.05545 | 0.22576071 |
| ! | transforming growth factor beta receptor activity | GO:0005024 | 50 | 19 | 0.74109831 | 0.05553 | 0.22562597 |
| ! | endonuclease activity, active with either ribo- or deoxyribonucleic acids and producing 3'-phosphomonoesters | GO:0016894 | 35 | 21 | 0.72978659 | 0.05616 | 0.22772195 |
| ! | germ cell development | GO:0007281 | 76 | 36 | 0.68131854 | 0.05635 | 0.2280289 |
| ! | microfilament motor activity | GO:0000146 | 40 | 17 | 0.75094288 | 0.05659 | 0.22853654 |
| ! | DNA-directed RNA polymerase III activity | GO:0003902 | 34 | 16 | 0.76111519 | 0.05659 | 0.22807485 |
| ! | aldehyde dehydrogenase [NAD(P)+] activity | GO:0004030 | 17 | 9 | 0.83096821 | 0.05705 | 0.22946522 |
| ! | mRNA 3'-UTR binding | GO:0003730 | 34 | 11 | 0.80417421 | 0.05766 | 0.23145211 |

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|---|---|---|---|---|---|---|---|
| ! | macrophage elastase activity | GO:0004234 | 19 | 11 | 0.79990481 | 0.05766 | 0.23098735 |
| ! | protein kinase C activity | GO:0004697 | 28 | 11 | 0.79992502 | 0.05766 | 0.23052445 |
| ! | retinoid metabolism | GO:0001523 | 15 | 11 | 0.80230637 | 0.05766 | 0.2300634 |
| ! | lamellipodium | GO:0030027 | 148 | 54 | 0.65540498 | 0.05845 | 0.23275 |
| ! | exoribonuclease activity | GO:0004532 | 39 | 20 | 0.72723218 | 0.05877 | 0.23355807 |
| ! | positive regulation of cell differentiation | GO:0045597 | 120 | 53 | 0.65662391 | 0.0591 | 0.23440258 |
| ! | protein oligomerization | GO:0051259 | 47 | 22 | 0.72243487 | 0.05953 | 0.23563958 |
| ! | regulation of nucleocytoplasmic transport | GO:0046822 | 48 | 22 | 0.71519216 | 0.05953 | 0.23517297 |
| ! | amino acid binding | GO:0016597 | 21 | 12 | 0.78357564 | 0.06014 | 0.23711324 |
| ! | complement activation, alternative pathway | GO:0006957 | 18 | 12 | 0.78099169 | 0.06014 | 0.23664556 |
| ! | signal sequence binding | GO:0005048 | 76 | 30 | 0.69411775 | 0.0605 | 0.2375935 |
| ! | regulation of lipid metabolism | GO:0019216 | 50 | 27 | 0.69893081 | 0.06078 | 0.23822417 |
| ! | microtubule nucleation | GO:0007020 | 47 | 18 | 0.73609644 | 0.06102 | 0.23869588 |
| ! | negative regulation of cell migration | GO:0030336 | 18 | 9 | 0.82189004 | 0.06163 | 0.24061027 |
| ! | neurotransmitter catabolism | GO:0042135 | 15 | 9 | 0.82732622 | 0.06163 | 0.24014033 |
| ! | oocyte axis determination (sensu Insecta) | GO:0048111 | 22 | 9 | 0.8232464 | 0.06163 | 0.23967222 |
| ! | photoreceptor cell development | GO:0042461 | 30 | 13 | 0.78073414 | 0.06166 | 0.23932237 |
| ! | Golgi trans face | GO:0005802 | 74 | 33 | 0.6793989 | 0.06253 | 0.24222786 |
| ! | mRNA splice site selection | GO:0006376 | 79 | 19 | 0.73109158 | 0.06404 | 0.24759651 |
| ! | exosome (RNase complex) | GO:0000178 | 18 | 11 | 0.79955287 | 0.06407 | 0.24723337 |
| ! | cytoskeletal anchoring | GO:0007016 | 47 | 17 | 0.73925468 | 0.06422 | 0.24733378 |
| ! | exonuclease activity, active with either ribo- or deoxyribonucleic acids and producing 5'-phosphomonoesters | GO:0016796 | 43 | 23 | 0.70598496 | 0.06449 | 0.24789509 |
| ! | maintenance of localization | GO:0051235 | 47 | 23 | 0.71382636 | 0.06449 | 0.24741837 |
| ! | protein kinase inhibitor activity | GO:0004860 | 88 | 37 | 0.67220409 | 0.0651 | 0.24927927 |
| ! | endosome organization and biogenesis | GO:0007032 | 171 | 69 | 0.63766814 | 0.06541 | 0.24998649 |
| ! | antiporter activity | GO:0015297 | 116 | 58 | 0.64689957 | 0.06551 | 0.24988996 |
| ! | amine transporter activity | GO:0005275 | 177 | 84 | 0.62376148 | 0.06638 | 0.25272538 |
| ! | JNK cascade | GO:0007254 | 203 | 84 | 0.62266657 | 0.06638 | 0.252244 |
| ! | plasma membrane fusion | GO:0045026 | 25 | 14 | 0.75507286 | 0.06665 | 0.2527885 |
| ! | calcium-mediated signaling | GO:0019722 | 63 | 32 | 0.67660508 | 0.06684 | 0.25302808 |
| ! | O-linked glycosylation | GO:0006493 | 66 | 25 | 0.69917476 | 0.06688 | 0.2527 |
| ! | mitochondrial transport | GO:0006839 | 71 | 25 | 0.70386464 | 0.06688 | 0.25222231 |
| ! | Notch signaling pathway | GO:0007219 | 59 | 28 | 0.69047871 | 0.06712 | 0.25264981 |
| ! | mRNA transport | GO:0051028 | 79 | 28 | 0.68703313 | 0.06712 | 0.25217401 |
| ! | structural constituent of eye lens | GO:0005212 | 81 | 42 | 0.65832258 | 0.06716 | 0.25185 |
| ! | cytokinesis | GO:0016288 | 91 | 36 | 0.67557757 | 0.06733 | 0.25201379 |
| ! | canalicular bile acid transport | GO:0015722 | 16 | 8 | 0.82949451 | 0.06755 | 0.25236376 |
| ! | transition metal ion transport | GO:0000041 | 92 | 48 | 0.64963361 | 0.06781 | 0.25286159 |
| ! | ribonucleoprotein | GO:0003733 | 41 | 13 | 0.76243955 | 0.06834 | 0.2543625 |
| ! | receptor signaling protein serine/threonine kinase activity | GO:0004702 | 141 | 56 | 0.64737448 | 0.06844 | 0.25426034 |
| ! | cell development | GO:0048468 | 152 | 68 | 0.63251221 | 0.06914 | 0.25638346 |
| ! | DNA-directed RNA polymerase I activity | GO:0003900 | 41 | 18 | 0.73281966 | 0.06941 | 0.25690714 |

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|---|---|---|---|---|---|---|---|
| ! | neutral amino acid transport | GO:0015804 | 35 | 18 | 0.72858246 | 0.06941 | 0.25643139 |
| ! | purine nucleoside metabolism | GO:0042278 | 19 | 11 | 0.78130822 | 0.07038 | 0.25953438 |
| ! | oocyte axis determination | GO:0007309 | 24 | 10 | 0.79584568 | 0.07076 | 0.26045424 |
| ! | transaminase activity | GO:0008483 | 69 | 30 | 0.67791221 | 0.07176 | 0.26364862 |
| ! | morphogenesis of an epithelium | GO:0002009 | 134 | 66 | 0.62845906 | 0.07197 | 0.2639341 |
| ! | type I hypersensitivity | GO:0016068 | 23 | 9 | 0.80901211 | 0.07245 | 0.26520688 |
| ! | misfolded or incompletely synthesized protein catabolism | GO:0006515 | 20 | 9 | 0.80685035 | 0.07245 | 0.26472115 |
| ! | SAP kinase activity | GO:0016909 | 30 | 9 | 0.80133455 | 0.07245 | 0.2642372 |
| ! | plastid | GO:0009536 | 18 | 9 | 0.80469123 | 0.07245 | 0.26375502 |
| ! | cytoskeletal regulator activity | GO:0008580 | 26 | 9 | 0.79988498 | 0.07245 | 0.26327459 |
| ! | flagellum | GO:0019861 | 32 | 19 | 0.71553443 | 0.07308 | 0.26508109 |
| ! | hormone binding | GO:0042562 | 33 | 19 | 0.7164075 | 0.07308 | 0.2646 |
| ! | nucleotide-excision repair | GO:0006289 | 58 | 26 | 0.69077305 | 0.07309 | 0.26415679 |
| ! | omega peptidase activity | GO:0008242 | 12 | 8 | 0.82517417 | 0.07311 | 0.26375127 |
| ! | tubulin binding | GO:0015631 | 159 | 54 | 0.6402891 | 0.07347 | 0.26457157 |
| ! | trans-1,2-dihydrobenzene-1,2-diol dehydrogenase activity | GO:0047115 | 20 | 12 | 0.76739473 | 0.07359 | 0.26452622 |
| ! | MAP kinase kinase kinase activity | GO:0004709 | 30 | 12 | 0.7634558 | 0.07359 | 0.26405045 |
| ! | microtubule cytoskeleton organization and biogenesis | GO:0000226 | 178 | 79 | 0.61917665 | 0.07366 | 0.26382711 |
| ! | cellular polysaccharide metabolism | GO:0044264 | 103 | 53 | 0.64210442 | 0.07383 | 0.2639621 |
| ! | small nuclear ribonucleoprotein | GO:0003734 | 26 | 14 | 0.74516485 | 0.07424 | 0.26495313 |
| ! | protein-ER targeting | GO:0045047 | 112 | 45 | 0.65424559 | 0.07488 | 0.26676 |
| ! | intramolecular oxidoreductase activity | GO:0016860 | 70 | 45 | 0.6489415 | 0.07488 | 0.26628449 |
| ! | deoxyribonuclease activity | GO:0004536 | 52 | 29 | 0.68182664 | 0.07501 | 0.26627215 |
| ! | peptidyl-prolyl cis-trans isomerase activity | GO:0003755 | 51 | 29 | 0.68387219 | 0.07501 | 0.2657992 |
| ! | fusion of sperm to egg plasma membrane | GO:0007342 | 24 | 13 | 0.76021073 | 0.07551 | 0.26709654 |
| ! | endoderm development | GO:0007492 | 34 | 13 | 0.75294197 | 0.07551 | 0.26662381 |
| ! | nitric oxide metabolism | GO:0046209 | 50 | 20 | 0.70974546 | 0.07679 | 0.2706644 |
| ! | protein threonine/tyrosine kinase activity | GO:0004712 | 26 | 11 | 0.77769889 | 0.0769 | 0.27057407 |
| ! | tRNA processing | GO:0008033 | 70 | 38 | 0.66302419 | 0.07702 | 0.27051919 |
| ! | regulation of nitric oxide biosynthesis | GO:0045428 | 22 | 10 | 0.78411196 | 0.07706 | 0.27018401 |
| ! | COPI-coated vesicle | GO:0030137 | 19 | 10 | 0.78787547 | 0.07706 | 0.26971 |
| ! | extrinsic to plasma membrane | GO:0019897 | 208 | 95 | 0.61306085 | 0.07712 | 0.26944729 |
| ! | glucose transporter activity | GO:0005355 | 28 | 15 | 0.73605306 | 0.07734 | 0.26974353 |
| ! | mRNA catabolism | GO:0006402 | 55 | 25 | 0.68856769 | 0.07797 | 0.27146623 |
| ! | bile acid transport | GO:0015721 | 48 | 25 | 0.69126157 | 0.07797 | 0.27099329 |
| ! | embryonic pattern specification | GO:0009880 | 80 | 37 | 0.66127563 | 0.0785 | 0.27236087 |
| ! | transmembrane receptor protein tyrosine phosphatase activity | GO:0005001 | 44 | 18 | 0.721107 | 0.07869 | 0.27254609 |
| ! | meiosis | GO:0007126 | 204 | 94 | 0.61102424 | 0.07871 | 0.27214289 |
| ! | cell killing | GO:0001906 | 44 | 22 | 0.70410257 | 0.079 | 0.27267301 |
| ! | locomotion | GO:0040011 | 21 | 9 | 0.79458741 | 0.0792 | 0.27289119 |
| ! | troponin complex | GO:0005861 | 36 | 16 | 0.724107 | 0.08075 | 0.27775216 |
| ! | thymic T-cell selection | GO:0045061 | 25 | 12 | 0.75459854 | 0.08093 | 0.27789217 |

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|---|---|---|---|---|---|---|---|
| ! | vesicle docking during exocytosis | GO:0006904 | 80 | 31 | 0.67451406 | 0.08101 | 0.27768892 |
| ! | lactation | GO:0007595 | 49 | 31 | 0.67305236 | 0.08101 | 0.27721261 |
| ! | vitamin binding | GO:0019842 | 58 | 36 | 0.66647836 | 0.0814 | 0.27807021 |
| ! | nucleotide-sugar metabolism | GO:0009225 | 46 | 17 | 0.71796193 | 0.08235 | 0.28083462 |
| ! | coated pit | GO:0005905 | 96 | 41 | 0.6540208 | 0.08266 | 0.28141075 |
| ! | RNA polymerase complex | GO:0030880 | 51 | 24 | 0.69287898 | 0.08317 | 0.28266465 |
| ! | alcohol dehydrogenase activity | GO:0004022 | 30 | 19 | 0.7082205 | 0.0832 | 0.28228571 |
| ! | small-molecule carrier or transporter | GO:0005468 | 29 | 19 | 0.71164771 | 0.0832 | 0.28180645 |
| ! | oogenesis (sensu Insecta) | GO:0009993 | 36 | 13 | 0.74578906 | 0.08321 | 0.28136263 |
| ! | oxidoreductase activity, acting on the CH-NH group of donors, NAD or NADP as acceptor | GO:0016646 | 21 | 13 | 0.74920244 | 0.08321 | 0.28088655 |
| ! | amino sugar metabolism | GO:0006040 | 53 | 21 | 0.70083874 | 0.08357 | 0.28162525 |
| ! | ribonuclease activity | GO:0004540 | 160 | 90 | 0.61502389 | 0.08383 | 0.28202504 |
| ! | nucleosome | GO:0000786 | 83 | 48 | 0.64658451 | 0.08416 | 0.28265859 |
| ! | transmembrane receptor protein serine/threonine kinase signaling pathway | GO:0007178 | 199 | 89 | 0.6094626 | 0.08435 | 0.28282059 |
| ! | G-protein signaling, coupled to cGMP nucleotide second messenger | GO:0007199 | 18 | 10 | 0.77204023 | 0.08463 | 0.28328331 |
| ! | oxidoreductase activity, acting on NADH or NADPH, NAD or NADP as acceptor | GO:0016652 | 35 | 26 | 0.68329407 | 0.085 | 0.28404523 |
| ! | spliceosome assembly | GO:0000245 | 107 | 30 | 0.6687077 | 0.08501 | 0.2836036 |
| ! | neurotransmitter transport | GO:0006836 | 133 | 57 | 0.63791187 | 0.08579 | 0.28572796 |
| ! | thiolester hydrolase activity | GO:0016790 | 177 | 87 | 0.61102094 | 0.08605 | 0.28611625 |
| ! | cortical actin cytoskeleton | GO:0030864 | 38 | 15 | 0.72689543 | 0.08635 | 0.28663602 |
| ! | glutamine family amino acid biosynthesis | GO:0009084 | 25 | 15 | 0.72777609 | 0.08635 | 0.28615988 |
| ! | natural killer cell mediated cytotoxicity | GO:0042267 | 34 | 15 | 0.73269671 | 0.08635 | 0.28568532 |
| ! | secretory granule | GO:0030141 | 115 | 56 | 0.63238213 | 0.08649 | 0.28567475 |
| ! | meiotic recombination | GO:0007131 | 45 | 22 | 0.68934074 | 0.09045 | 0.29826074 |
| ! | Golgi to plasma membrane transport | GO:0006893 | 23 | 11 | 0.75396749 | 0.09176 | 0.30208119 |
| ! | low-density lipoprotein receptor activity | GO:0005041 | 25 | 11 | 0.76027857 | 0.09176 | 0.30158353 |
| ! | heterotrimeric G-protein GTPase activity | GO:0003927 | 109 | 45 | 0.63952608 | 0.09187 | 0.30144844 |
| ! | GPI anchor biosynthesis | GO:0006506 | 20 | 10 | 0.76538212 | 0.09188 | 0.30098621 |
| ! | actin filament bundle formation | GO:0051017 | 29 | 14 | 0.73016439 | 0.092 | 0.30088525 |
| ! | muscle cell differentiation | GO:0042692 | 43 | 14 | 0.73130062 | 0.092 | 0.3003928 |
| ! | negative regulation of biosynthesis | GO:0009890 | 65 | 28 | 0.67493792 | 0.09261 | 0.30189044 |
| ! | solute:hydrogen antiporter activity | GO:0015299 | 34 | 17 | 0.70812422 | 0.09273 | 0.3017885 |
| ! | clathrin adaptor | GO:0005906 | 14 | 9 | 0.77479615 | 0.09304 | 0.30230423 |
| ! | oxygen transport | GO:0015671 | 19 | 9 | 0.77743072 | 0.09304 | 0.30181268 |
| ! | vesicle docking | GO:0048278 | 81 | 32 | 0.66460138 | 0.09344 | 0.30261818 |
| ! | nucleosome assembly | GO:0006334 | 117 | 64 | 0.62505086 | 0.09355 | 0.30248339 |
| ! | peptide antigen binding | GO:0042605 | 35 | 15 | 0.72144966 | 0.09554 | 0.30841796 |
| ! | nicotinic acetylcholine-activated cation-selective channel activity | GO:0004889 | 26 | 15 | 0.71814215 | 0.09554 | 0.30791971 |
| ! | gastrulation (sensu Mammalia) | GO:0010003 | 25 | 12 | 0.74192058 | 0.09848 | 0.31688323 |
| ! | regulation of cell shape | GO:0008360 | 122 | 51 | 0.63582072 | 0.09854 | 0.3165657 |

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|---|---|---|---|---|---|---|---|
| ! | UDP-galactose beta-N-acetylglucosamine beta-1,3-galactosyltransferase activity | GO:0008499 | 26 | 8 | 0.78883693 | 0.09883 | 0.3169869 |
| ! | rhodopsin mediated signaling | GO:0016056 | 18 | 8 | 0.78332116 | 0.09883 | 0.31647809 |
| ! | early endosome | GO:0005769 | 87 | 41 | 0.64367033 | 0.09914 | 0.31696202 |
| ! | copper ion transporter activity | GO:0005375 | 25 | 10 | 0.76025345 | 0.09967 | 0.31814664 |
| ! | integrin-mediated signaling pathway | GO:0007229 | 169 | 76 | 0.60981482 | 0.09972 | 0.31779776 |
| ! | protein serine/threonine phosphatase activity | GO:0004722 | 119 | 50 | 0.63298034 | 0.09982 | 0.31760909 |
| ! | 3'-5' exonuclease activity | GO:0008408 | 66 | 35 | 0.64844979 | 0.10004 | 0.31780223 |
| ! | ligase activity, forming carbon-sulfur bonds | GO:0016877 | 28 | 16 | 0.70540795 | 0.10041 | 0.31847051 |
| ! | DNA fragmentation during apoptosis | GO:0006309 | 16 | 9 | 0.76901614 | 0.10041 | 0.317965 |
| ! | oxidoreductase activity, acting on the CH-CH group of donors, oxygen as acceptor | GO:0016634 | 19 | 9 | 0.76197622 | 0.10041 | 0.31746109 |
| ! | positive regulation of T-cell differentiation | GO:0045582 | 42 | 18 | 0.70288164 | 0.10042 | 0.31699035 |
| ! | detection of bacteria | GO:0016045 | 15 | 11 | 0.74574874 | 0.1005 | 0.31674171 |
| ! | acyl-CoA thioesterase activity | GO:0016291 | 14 | 11 | 0.74416255 | 0.1005 | 0.31624211 |
| ! | caspase activity | GO:0030693 | 20 | 11 | 0.75037254 | 0.1005 | 0.31574409 |
| ! | ribonucleoside diphosphate metabolism | GO:0009185 | 21 | 11 | 0.74472096 | 0.1005 | 0.31524764 |
| ! | nucleoside kinase activity | GO:0019206 | 20 | 11 | 0.7487987 | 0.1005 | 0.31475275 |
| ! | regulation of NF-kappaB-nucleus import | GO:0042345 | 29 | 13 | 0.72675298 | 0.10125 | 0.31660462 |
| ! | ribonucleoside metabolism | GO:0009119 | 24 | 13 | 0.72519387 | 0.10125 | 0.31610915 |
| ! | cell adhesion molecule binding | GO:0050839 | 37 | 13 | 0.72396588 | 0.10125 | 0.31561523 |
| ! | ER-nuclear signaling pathway | GO:0006984 | 28 | 13 | 0.72384632 | 0.10125 | 0.31512285 |
| ! | protein-membrane targeting | GO:0006612 | 123 | 49 | 0.62979472 | 0.10148 | 0.31534673 |
| ! | DNA damage response, signal transduction | GO:0042770 | 78 | 40 | 0.64229667 | 0.10395 | 0.32251983 |
| ! | DNA-directed RNA polymerase II activity | GO:0003901 | 33 | 17 | 0.69785026 | 0.1042 | 0.32279348 |
| ! | peptide hormone secretion | GO:0030072 | 33 | 17 | 0.70182914 | 0.1042 | 0.32229302 |
| ! | myofibril | GO:0030016 | 117 | 58 | 0.6218208 | 0.10442 | 0.32247353 |
| ! | anterior/posterior pattern formation | GO:0009952 | 117 | 58 | 0.62816063 | 0.10442 | 0.32197512 |
| ! | voltage-gated potassium channel complex | GO:0008076 | 149 | 73 | 0.61568179 | 0.10477 | 0.32255579 |
| ! | nucleoside diphosphate metabolism | GO:0009132 | 33 | 15 | 0.70905407 | 0.10635 | 0.32691564 |
| ! | carbonate dehydratase activity | GO:0004089 | 28 | 15 | 0.71045474 | 0.10635 | 0.32641269 |
| ! | neuromuscular junction development | GO:0007528 | 49 | 15 | 0.71107 | 0.10635 | 0.32591129 |
| ! | DNA-directed RNA polymerase activity | GO:0003899 | 85 | 39 | 0.6448797 | 0.10664 | 0.32629877 |
| ! | chemosensory behavior | GO:0007635 | 16 | 8 | 0.77833119 | 0.10669 | 0.32595184 |
| ! | copper ion transport | GO:0006825 | 23 | 10 | 0.74326908 | 0.10795 | 0.32929702 |
| ! | apoptosis activator activity | GO:0016506 | 40 | 21 | 0.68422878 | 0.1082 | 0.32955573 |
| ! | transmembrane receptor protein tyrosine phosphatase signaling pathway | GO:0007185 | 51 | 21 | 0.67898691 | 0.1082 | 0.32905335 |
| ! | neutral amino acid transporter activity | GO:0015175 | 40 | 21 | 0.67747436 | 0.1082 | 0.32855251 |
| ! | carbon-nitrogen lyase activity | GO:0016840 | 11 | 9 | 0.75655016 | 0.10828 | 0.32829574 |
| ! | cAMP-dependent protein kinase complex | GO:0005952 | 35 | 11 | 0.73890961 | 0.10897 | 0.32988642 |
| ! | regulation of tyrosine phosphorylation of Stat3 protein | GO:0042516 | 26 | 11 | 0.73375571 | 0.10897 | 0.32938659 |
| ! | tubulin-tyrosine ligase activity | GO:0004835 | 22 | 11 | 0.74141378 | 0.10897 | 0.32888828 |
| ! | eye photoreceptor cell development | GO:0042462 | 28 | 11 | 0.74035154 | 0.10897 | 0.32839147 |
| ! | sphingoid metabolism | GO:0046519 | 64 | 32 | 0.65103042 | 0.10978 | 0.33033348 |

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|---|---|---|---|---|---|---|---|
| ! | excretion | GO:0007588 | 110 | 55 | 0.62159385 | 0.11037 | 0.33160866 |
| ! | regulation of heart contraction rate | GO:0008016 | 127 | 55 | 0.62034274 | 0.11037 | 0.33111 |
| ! | damaged DNA binding | GO:0003684 | 94 | 45 | 0.6285495 | 0.11133 | 0.33348851 |
| ! | protein polymerization | GO:0051258 | 109 | 45 | 0.63123356 | 0.11133 | 0.33298853 |
| ! | transferase activity, transferring nitrogenous groups | GO:0016769 | 70 | 31 | 0.65610117 | 0.11141 | 0.33272897 |
| ! | calcium ion sensing | GO:0005513 | 41 | 13 | 0.7200285 | 0.11147 | 0.33241054 |
| ! | rhodopsin mediated phototransduction | GO:0009586 | 25 | 13 | 0.71864819 | 0.11147 | 0.3319144 |
| ! | membrane coat adaptor complex | GO:0030119 | 36 | 14 | 0.71226978 | 0.11268 | 0.33501729 |
| ! | maintenance of protein localization | GO:0045185 | 39 | 18 | 0.68746068 | 0.11271 | 0.33460781 |
| ! | mRNA-nucleus export | GO:0006406 | 70 | 26 | 0.66415408 | 0.11381 | 0.3373714 |
| ! | appendage morphogenesis | GO:0035107 | 114 | 53 | 0.62757459 | 0.11449 | 0.33888361 |
| ! | negative regulation of immune cell mediated cytotoxicity | GO:0001911 | 21 | 8 | 0.7674236 | 0.11477 | 0.33920911 |
| ! | fibroblast growth factor receptor activity | GO:0005007 | 20 | 8 | 0.76510047 | 0.11477 | 0.33870732 |
| ! | phosphotransferase activity, phosphate group as acceptor | GO:0016776 | 95 | 43 | 0.63359255 | 0.11566 | 0.34082969 |
| ! | small molecule transport | GO:0006832 | 95 | 52 | 0.62075646 | 0.11616 | 0.34179823 |
| ! | phospholipase activity | GO:0004620 | 119 | 66 | 0.6148113 | 0.11633 | 0.34179433 |
| ! | drug metabolism | GO:0017144 | 25 | 17 | 0.68796844 | 0.11662 | 0.3421425 |
| ! | L-amino acid transport | GO:0015807 | 42 | 22 | 0.66934537 | 0.11685 | 0.34231388 |
| ! | lipase activity | GO:0016298 | 146 | 83 | 0.60251627 | 0.11729 | 0.34309905 |
| ! | meiosis I | GO:0007127 | 55 | 29 | 0.654973 | 0.11807 | 0.34487504 |
| ! | Rho small monomeric GTPase activity | GO:0003931 | 34 | 15 | 0.69867281 | 0.11857 | 0.34582917 |
| ! | protein phosphatase binding | GO:0019903 | 22 | 11 | 0.73204414 | 0.11866 | 0.34558642 |
| ! | folic acid and derivative metabolism | GO:0006760 | 17 | 12 | 0.72028201 | 0.11886 | 0.34566429 |
| ! | regulation of JAK-STAT cascade | GO:0046425 | 27 | 12 | 0.72134651 | 0.11886 | 0.34516114 |
| ! | cell aging | GO:0007569 | 26 | 12 | 0.72186447 | 0.11886 | 0.34465945 |
| ! | regulation of neuron differentiation | GO:0045664 | 57 | 25 | 0.65853139 | 0.11961 | 0.34633084 |
| ! | protein-nucleus export | GO:0006611 | 52 | 19 | 0.68143894 | 0.12054 | 0.34851783 |
| ! | intercellular junction assembly and/or maintenance | GO:0045216 | 64 | 34 | 0.64482635 | 0.12209 | 0.35248849 |
| ! | iron ion homeostasis | GO:0006879 | 41 | 21 | 0.67120025 | 0.12236 | 0.35275751 |
| ! | response to organic substance | GO:0010033 | 42 | 21 | 0.66966442 | 0.12236 | 0.35224848 |
| ! | adipocyte differentiation | GO:0045444 | 33 | 13 | 0.70609613 | 0.12291 | 0.35332197 |
| ! | polyamine metabolism | GO:0006595 | 28 | 13 | 0.71353488 | 0.12291 | 0.3528136 |
| ! | myosin binding | GO:0017022 | 22 | 8 | 0.75403103 | 0.12308 | 0.35279397 |
| ! | endosome transport | GO:0016197 | 150 | 61 | 0.61870016 | 0.1234 | 0.35320373 |
| ! | protein-lysine N-methyltransferase activity | GO:0016279 | 37 | 16 | 0.69410071 | 0.12369 | 0.35352658 |
| ! | polyol metabolism | GO:0019751 | 31 | 16 | 0.68656991 | 0.12369 | 0.35302082 |
| ! | sperm motility | GO:0030317 | 35 | 16 | 0.68914933 | 0.12369 | 0.3525165 |
| ! | nuclear hormone receptor binding | GO:0035257 | 60 | 28 | 0.64966806 | 0.12431 | 0.3537781 |
| ! | centriole | GO:0005814 | 15 | 9 | 0.74043913 | 0.12588 | 0.3577359 |
| ! | RNA elongation from Pol II promoter | GO:0006368 | 18 | 10 | 0.73162529 | 0.12671 | 0.35958243 |
| ! | regulation of membrane potential | GO:0042391 | 21 | 10 | 0.73307702 | 0.12671 | 0.35907166 |
| ! | cytochrome P450 activity | GO:0015034 | 13 | 10 | 0.72995635 | 0.12671 | 0.35856234 |
| ! | deoxyribonucleotide metabolism | GO:0009262 | 25 | 10 | 0.72814471 | 0.12671 | 0.35805446 |

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|---|---|---|---|---|---|---|---|
| ! | tissue regeneration | GO:0042246 | 40 | 23 | 0.65713964 | 0.12734 | 0.35932574 |
| ! | axis specification | GO:0009798 | 60 | 27 | 0.65319163 | 0.12793 | 0.36048072 |
| ! | synaptic vesicle transport | GO:0048489 | 121 | 47 | 0.62428018 | 0.1281 | 0.36045063 |
| ! | negative regulation of cell size | GO:0045792 | 75 | 38 | 0.63582961 | 0.12919 | 0.3630057 |
| ! | regulation of peptidyl-tyrosine phosphorylation | GO:0050730 | 82 | 31 | 0.64595988 | 0.1297 | 0.36392616 |
| ! | development of primary male sexual characteristics | GO:0046546 | 30 | 17 | 0.67694767 | 0.12982 | 0.36375126 |
| ! | ribonucleoprotein binding | GO:0043021 | 43 | 17 | 0.68026977 | 0.12982 | 0.36324109 |
| ! | endoribonuclease activity, producing 3'-phosphomonoesters | GO:0016892 | 28 | 17 | 0.68338036 | 0.12982 | 0.36273235 |
| ! | glutathione biosynthesis | GO:0006750 | 21 | 12 | 0.71394096 | 0.13036 | 0.36373175 |
| ! | dosage compensation | GO:0007549 | 36 | 12 | 0.71367375 | 0.13036 | 0.36322374 |
| ! | clathrin adaptor complex | GO:0030131 | 34 | 12 | 0.71223492 | 0.13036 | 0.36271715 |
| ! | antigen presentation, peptide antigen | GO:0048002 | 34 | 15 | 0.69167127 | 0.13098 | 0.36393468 |
| ! | sphingolipid metabolism | GO:0006665 | 114 | 56 | 0.61413681 | 0.133 | 0.36903338 |
| ! | vitamin transporter activity | GO:0051183 | 31 | 13 | 0.69815899 | 0.13504 | 0.37417333 |
| ! | beta-amyloid binding | GO:0001540 | 15 | 9 | 0.73272434 | 0.13605 | 0.37644903 |
| ! | host-pathogen interaction | GO:0030383 | 24 | 9 | 0.73174703 | 0.13605 | 0.37592763 |
| ! | negative regulation of neuron differentiation | GO:0045665 | 15 | 9 | 0.73284958 | 0.13605 | 0.37540768 |
| ! | regulation of Ras protein signal transduction | GO:0046578 | 15 | 9 | 0.72529063 | 0.13605 | 0.37488916 |
| ! | endoribonuclease activity | GO:0004521 | 62 | 36 | 0.63344595 | 0.1361 | 0.37450966 |
| ! | segment specification | GO:0007379 | 24 | 14 | 0.69459003 | 0.13661 | 0.37539525 |
| ! | RAB small monomeric GTPase activity | GO:0003928 | 55 | 25 | 0.65693393 | 0.13668 | 0.37507098 |
| ! | tRNA-specific ribonuclease activity | GO:0004549 | 13 | 10 | 0.71494402 | 0.13722 | 0.37603558 |
| ! | regulation of epithelial cell differentiation | GO:0030856 | 16 | 10 | 0.71740723 | 0.13722 | 0.37551975 |
| ! | Rho guanyl-nucleotide exchange factor activity | GO:0005089 | 43 | 16 | 0.68143833 | 0.13766 | 0.37620781 |
| ! | intramolecular transferase activity | GO:0016866 | 31 | 16 | 0.67745618 | 0.13766 | 0.37569316 |
| ! | nerve-nerve synaptic transmission | GO:0007270 | 48 | 21 | 0.65732425 | 0.13792 | 0.37588852 |
| ! | hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds | GO:0016810 | 168 | 96 | 0.59468895 | 0.13823 | 0.37621944 |
| ! | regulation of cell adhesion | GO:0030155 | 105 | 54 | 0.61589367 | 0.13935 | 0.37875102 |
| ! | sheet-forming collagen | GO:0030935 | 25 | 11 | 0.71266278 | 0.14011 | 0.38029857 |
| ! | protein homooligomerization | GO:0051260 | 40 | 18 | 0.6728979 | 0.14021 | 0.38005292 |
| ! | oligosaccharide biosynthesis | GO:0009312 | 18 | 8 | 0.73899371 | 0.14112 | 0.38200054 |
| ! | pepsin A activity | GO:0004194 | 16 | 8 | 0.7336368 | 0.14112 | 0.38148293 |
| ! | phospholipid transporter activity | GO:0005548 | 68 | 24 | 0.65648204 | 0.14222 | 0.38393627 |
| ! | aging | GO:0007568 | 61 | 24 | 0.64821078 | 0.14222 | 0.38341743 |
| ! | apoptotic nuclear changes | GO:0030262 | 20 | 12 | 0.7024225 | 0.14255 | 0.38378846 |
| ! | cGMP-mediated signaling | GO:0019934 | 21 | 12 | 0.69750065 | 0.14255 | 0.38327123 |
| ! | phosphoinositide metabolism | GO:0030384 | 83 | 34 | 0.63051044 | 0.14312 | 0.38428587 |
| ! | histone methyltransferase activity | GO:0042054 | 47 | 20 | 0.66285815 | 0.14318 | 0.38393024 |
| ! | cytokinesis | GO:0007104 | 166 | 68 | 0.600077 | 0.14385 | 0.38520906 |
| ! | growth factor binding | GO:0019838 | 154 | 68 | 0.60823532 | 0.14385 | 0.38469269 |
| ! | regulation of transforming growth factor beta receptor signaling pathway | GO:0017015 | 33 | 15 | 0.67887101 | 0.14409 | 0.38481867 |
| ! | acid phosphatase activity | GO:0003993 | 33 | 17 | 0.67089337 | 0.14421 | 0.38462426 |

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|---|---|---|---|---|---|---|---|
| ! | tRNA ligase activity | GO:0004812 | 166 | 89 | 0.59756951 | 0.14423 | 0.38416402 |
| ! | amino acid derivative metabolism | GO:0006575 | 166 | 88 | 0.594032 | 0.14499 | 0.3856734 |
| ! | protein kinase activator activity | GO:0030295 | 23 | 9 | 0.72222827 | 0.14647 | 0.38909141 |
| ! | cyclin-dependent protein kinase inhibitor activity | GO:0004861 | 17 | 9 | 0.72164298 | 0.14647 | 0.388574 |
| ! | positive regulation of caspase activity | GO:0043280 | 99 | 50 | 0.61687275 | 0.14843 | 0.3932508 |
| ! | metabolic compound salvage | GO:0043094 | 19 | 10 | 0.7114203 | 0.14873 | 0.39352301 |
| ! | T-cell selection | GO:0045058 | 28 | 14 | 0.67707049 | 0.14983 | 0.39590841 |
| ! | hydrolase activity, hydrolyzing N-glycosyl compounds | GO:0016799 | 26 | 14 | 0.67675458 | 0.14983 | 0.39538472 |
| ! | NF-kappaB-nucleus import | GO:0042348 | 35 | 14 | 0.68399753 | 0.14983 | 0.39486242 |
| ! | organelle lumen | GO:0043233 | 70 | 31 | 0.63255552 | 0.15075 | 0.39676286 |
| ! | positive regulation of lymphocyte differentiation | GO:0045621 | 44 | 19 | 0.66628476 | 0.15128 | 0.3976332 |
| ! | phosphotransferase activity, nitrogenous group as acceptor | GO:0016775 | 32 | 19 | 0.66583768 | 0.15128 | 0.39711 |
| ! | negative regulation of cyclin dependent protein kinase activity | GO:0045736 | 20 | 8 | 0.73124386 | 0.15153 | 0.39724356 |
| ! | microtubule | GO:0005874 | 131 | 62 | 0.60554813 | 0.15301 | 0.40059705 |
| ! | heterogeneous nuclear ribonucleoprotein complex | GO:0030530 | 50 | 16 | 0.67479897 | 0.15308 | 0.40025505 |
| ! | axoneme | GO:0005930 | 33 | 16 | 0.6676897 | 0.15308 | 0.39973115 |
| ! | microfibril | GO:0001527 | 73 | 37 | 0.61941671 | 0.15458 | 0.40312039 |
| ! | response to hypoxia | GO:0001666 | 52 | 25 | 0.64231579 | 0.15515 | 0.40407866 |
| ! | integral to Golgi membrane | GO:0030173 | 48 | 21 | 0.65222487 | 0.15525 | 0.40381193 |
| ! | muscle motor activity | GO:0003776 | 64 | 29 | 0.63543031 | 0.15808 | 0.4106375 |
| ! | myoblast differentiation | GO:0045445 | 36 | 15 | 0.67383766 | 0.15837 | 0.41085585 |
| ! | glycerol metabolism | GO:0006071 | 30 | 15 | 0.66983979 | 0.15837 | 0.41032227 |
| ! | monosaccharide transporter activity | GO:0015145 | 32 | 17 | 0.65815135 | 0.15994 | 0.41385253 |
| ! | two-component signal transduction system (phosphorelay) | GO:0000160 | 70 | 35 | 0.62496634 | 0.16014 | 0.41383329 |
| ! | signal complex formation | GO:0007172 | 32 | 10 | 0.70094036 | 0.16038 | 0.41391734 |
| ! | mechanosensory behavior | GO:0007638 | 21 | 13 | 0.67732347 | 0.1614 | 0.41601163 |
| ! | alpha-adrenergic receptor activity | GO:0004936 | 22 | 13 | 0.67785445 | 0.1614 | 0.41547484 |
| ! | tyrosine phosphorylation of Stat3 protein | GO:0042503 | 30 | 13 | 0.68276064 | 0.1614 | 0.41493943 |
| ! | low-density lipoprotein binding | GO:0030169 | 27 | 13 | 0.67706681 | 0.1614 | 0.41440541 |
| ! | purine transporter activity | GO:0005345 | 21 | 8 | 0.71792673 | 0.16193 | 0.41523181 |
| ! | insulin-like growth factor receptor binding | GO:0005159 | 28 | 8 | 0.71926052 | 0.16193 | 0.41469878 |
| ! | ER-associated protein catabolism | GO:0030433 | 18 | 8 | 0.71761275 | 0.16193 | 0.41416712 |
| ! | galactose metabolism | GO:0006012 | 18 | 8 | 0.71411011 | 0.16193 | 0.41363681 |
| ! | SH3 domain binding | GO:0017124 | 66 | 23 | 0.6466044 | 0.16344 | 0.4169601 |
| ! | 1-phosphatidylinositol-4-phosphate 5-kinase activity | GO:0016308 | 29 | 11 | 0.69093572 | 0.16425 | 0.41849138 |
| ! | antigen binding | GO:0003823 | 67 | 33 | 0.62682786 | 0.16562 | 0.42144375 |
| ! | actin filament-based movement | GO:0030048 | 74 | 33 | 0.61892089 | 0.16562 | 0.42090688 |
| ! | gap junction | GO:0005921 | 67 | 34 | 0.6215631 | 0.16601 | 0.42136126 |
| ! | sarcomere | GO:0030017 | 108 | 54 | 0.59985154 | 0.16781 | 0.42538875 |
| ! | RNA-directed DNA polymerase activity | GO:0003964 | 32 | 16 | 0.65967527 | 0.16784 | 0.42492487 |
| ! | kinase inhibitor activity | GO:0019210 | 96 | 42 | 0.61119799 | 0.16787 | 0.42446217 |
| ! | regulation of synapse | GO:0007273 | 22 | 9 | 0.69765555 | 0.16941 | 0.42781386 |

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|---|---|---|---|---|---|---|---|
| ! | hydrogen ion homeostasis | GO:0030641 | 65 | 26 | 0.63170169 | 0.17071 | 0.43055177 |
| ! | invasive growth | GO:0007125 | 60 | 26 | 0.63381386 | 0.17071 | 0.43000814 |
| ! | chromatin remodeling complex | GO:0016585 | 65 | 26 | 0.63333144 | 0.17071 | 0.42946589 |
| ! | nucleobase metabolism | GO:0009112 | 38 | 18 | 0.65020722 | 0.17268 | 0.43387481 |
| ! | carbohydrate phosphatase activity | GO:0019203 | 21 | 10 | 0.69036237 | 0.17275 | 0.43350472 |
| ! | chaperone binding | GO:0051087 | 24 | 10 | 0.68833861 | 0.17275 | 0.43296011 |
| ! | nuclear positioning | GO:0040023 | 19 | 8 | 0.7106668 | 0.17299 | 0.43301763 |
| ! | regulation of interferon-gamma biosynthesis | GO:0045072 | 10 | 8 | 0.70725035 | 0.17299 | 0.432475 |
| ! | clathrin coat | GO:0030118 | 94 | 40 | 0.60962471 | 0.173 | 0.4319587 |
| ! | antigen presentation | GO:0019882 | 80 | 40 | 0.61169964 | 0.173 | 0.43141875 |
| ! | fructose metabolism | GO:0006000 | 33 | 15 | 0.66444795 | 0.17329 | 0.43160243 |
| ! | plasma membrane organization and biogenesis | GO:0007009 | 47 | 21 | 0.64134112 | 0.17434 | 0.43367618 |
| ! | detection of chemical substance | GO:0009593 | 55 | 21 | 0.64220329 | 0.17434 | 0.43313611 |
| ! | monocarboxylic acid transport | GO:0015718 | 78 | 39 | 0.60989682 | 0.17457 | 0.4331681 |
| ! | cyclin-dependent protein kinase regulator activity | GO:0016538 | 92 | 39 | 0.61329745 | 0.17457 | 0.43263 |
| ! | steroid hormone receptor signaling pathway | GO:0030518 | 71 | 25 | 0.62984494 | 0.17526 | 0.43380112 |
| ! | mechanoreceptor differentiation | GO:0042490 | 36 | 13 | 0.66997089 | 0.17573 | 0.43442546 |
| ! | aspartate family amino acid biosynthesis | GO:0009067 | 22 | 13 | 0.67021661 | 0.17573 | 0.43388781 |
| ! | cAMP-dependent protein kinase regulator activity | GO:0008603 | 35 | 13 | 0.67441608 | 0.17573 | 0.43335148 |
| ! | clathrin vesicle coat | GO:0030125 | 84 | 38 | 0.61803259 | 0.17719 | 0.43641241 |
| ! | N-methyltransferase activity | GO:0008170 | 112 | 51 | 0.60311999 | 0.17745 | 0.43651387 |
| ! | vesicle membrane | GO:0012506 | 118 | 50 | 0.60371557 | 0.17751 | 0.43612371 |
| ! | limb morphogenesis | GO:0035108 | 109 | 50 | 0.60519555 | 0.17751 | 0.43558727 |
| ! | glycine-gated ion channel activity | GO:0016933 | 16 | 11 | 0.676516 | 0.1782 | 0.43674324 |
| ! | estrogen metabolism | GO:0008210 | 18 | 11 | 0.68189331 | 0.1782 | 0.43620736 |
| ! | 3',5'-cAMP binding | GO:0030552 | 30 | 11 | 0.67749326 | 0.1782 | 0.43567279 |
| ! | caspase activation | GO:0006919 | 98 | 49 | 0.60889699 | 0.17854 | 0.43596977 |
| ! | regulation of myogenesis | GO:0016202 | 35 | 14 | 0.66080095 | 0.17893 | 0.43638796 |
| ! | protein amino acid methylation | GO:0006479 | 54 | 20 | 0.64188637 | 0.17908 | 0.43622051 |
| ! | protein phosphatase inhibitor activity | GO:0004864 | 39 | 20 | 0.64066473 | 0.17908 | 0.43568854 |
| ! | axon guidance receptor activity | GO:0008046 | 51 | 20 | 0.64554749 | 0.17908 | 0.43515786 |
| ! | induction of apoptosis by extracellular signals | GO:0008624 | 82 | 48 | 0.60270973 | 0.18065 | 0.43843887 |
| ! | intra-Golgi transport | GO:0006891 | 23 | 12 | 0.67528228 | 0.18161 | 0.44023323 |
| ! | hydrolase activity, acting on ether bonds | GO:0016801 | 19 | 12 | 0.66916551 | 0.18161 | 0.43969897 |
| ! | tropomyosin binding | GO:0005523 | 28 | 9 | 0.69034453 | 0.18193 | 0.43993982 |
| ! | small nucleolar ribonucleoprotein complex | GO:0005732 | 38 | 23 | 0.62976052 | 0.1837 | 0.4436822 |
| ! | neuron cell differentiation | GO:0030182 | 140 | 63 | 0.59815486 | 0.18391 | 0.4436523 |
| ! | response to light | GO:0009416 | 104 | 63 | 0.59704772 | 0.18391 | 0.44311649 |
| ! | regulation of protein transport | GO:0051223 | 20 | 8 | 0.70076602 | 0.18425 | 0.44340018 |
| ! | dynein ATPase activity | GO:0008567 | 13 | 8 | 0.70456532 | 0.18425 | 0.44286596 |
| ! | Golgi cis-face | GO:0005801 | 13 | 8 | 0.69686792 | 0.18425 | 0.44233303 |
| ! | embryonic limb morphogenesis | GO:0030326 | 94 | 46 | 0.60268997 | 0.1851 | 0.44383954 |
| ! | rough endoplasmic reticulum | GO:0005791 | 30 | 10 | 0.68040847 | 0.18517 | 0.44347437 |
| ! | glycine-gated chloride channel activity | GO:0016934 | 14 | 10 | 0.6833093 | 0.18517 | 0.44294263 |
| ! | cytoskeletal regulatory protein binding | GO:0005519 | 27 | 10 | 0.68508131 | 0.18517 | 0.44241216 |

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|---|---|---|---|---|---|---|---|
| ! | interferon-gamma biosynthesis | GO:0042095 | 12 | 10 | 0.67915726 | 0.18517 | 0.44188295 |
| ! | acetylcholine binding | GO:0042166 | 31 | 19 | 0.64311093 | 0.18566 | 0.44252294 |
| ! | synaptic vesicle exocytosis | GO:0016079 | 69 | 28 | 0.61892427 | 0.18591 | 0.44259004 |
| ! | DNA recombination | GO:0006310 | 190 | 87 | 0.59022746 | 0.18804 | 0.44712729 |
| ! | Rho GTPase binding | GO:0017048 | 25 | 13 | 0.65784971 | 0.19016 | 0.45163 |
| ! | 35S primary transcript processing | GO:0006365 | 22 | 13 | 0.65715151 | 0.19016 | 0.45109298 |
| ! | phospholipid binding | GO:0005543 | 205 | 85 | 0.58812059 | 0.19041 | 0.45114958 |
| ! | voltage-gated potassium channel activity | GO:0005249 | 172 | 85 | 0.58145864 | 0.19041 | 0.45061441 |
| ! | myogenesis | GO:0007519 | 133 | 59 | 0.59674736 | 0.19113 | 0.45178241 |
| ! | regulation of protein amino acid phosphorylation | GO:0001932 | 86 | 33 | 0.61128291 | 0.19119 | 0.45138941 |
| ! | glutamine metabolism | GO:0006541 | 33 | 18 | 0.64438463 | 0.19145 | 0.45146897 |
| ! | Rho GTPase activator activity | GO:0005100 | 46 | 18 | 0.63986946 | 0.19145 | 0.45093595 |
| ! | sex differentiation | GO:0007548 | 184 | 82 | 0.5902535 | 0.19351 | 0.45525053 |
| ! | androgen metabolism | GO:0008209 | 34 | 21 | 0.62945646 | 0.19435 | 0.45668816 |
| ! | lipid glycosylation | GO:0030259 | 17 | 9 | 0.68019776 | 0.19461 | 0.45676112 |
| ! | negative regulation of transcription factor-nucleus import | GO:0042992 | 20 | 9 | 0.68183018 | 0.19461 | 0.45622438 |
| ! | nuclear membrane lumen | GO:0005641 | 17 | 9 | 0.67925894 | 0.19461 | 0.45568891 |
| ! | phospholipase inhibitor activity | GO:0004859 | 26 | 17 | 0.64462126 | 0.19545 | 0.45711928 |
| ! | forebrain development | GO:0030900 | 35 | 17 | 0.64730493 | 0.19545 | 0.45658402 |
| ! | benzene and derivative metabolism | GO:0042537 | 13 | 8 | 0.69199267 | 0.19615 | 0.45768333 |
| ! | regulated secretory pathway | GO:0045055 | 20 | 8 | 0.69237166 | 0.19615 | 0.45714866 |
| ! | metallocarboxypeptidase activity | GO:0004181 | 98 | 42 | 0.60496978 | 0.19626 | 0.4568713 |
| ! | death receptor activity | GO:0005035 | 20 | 12 | 0.65959208 | 0.19698 | 0.45801294 |
| ! | regulation of smooth muscle contraction | GO:0006940 | 30 | 12 | 0.66025797 | 0.19698 | 0.45747974 |
| ! | ion channel clustering | GO:0045161 | 38 | 12 | 0.65815669 | 0.19698 | 0.45694779 |
| ! | ciliary or flagellar motility | GO:0001539 | 22 | 12 | 0.65983584 | 0.19698 | 0.45641707 |
| ! | smoothened signaling pathway | GO:0007224 | 22 | 12 | 0.66494858 | 0.19698 | 0.45588759 |
| ! | regulation of muscle contraction | GO:0006937 | 165 | 78 | 0.58556477 | 0.19733 | 0.45616842 |
| ! | N-terminal protein myristoylation | GO:0006499 | 25 | 10 | 0.67468369 | 0.19836 | 0.45801875 |
| ! | alpha2-adrenergic receptor activity | GO:0004938 | 18 | 10 | 0.67060449 | 0.19836 | 0.45748925 |
| ! | tight junction | GO:0005923 | 107 | 55 | 0.592424 | 0.19883 | 0.45804371 |
| ! | protein tyrosine phosphatase activity | GO:0004725 | 182 | 79 | 0.58938921 | 0.19924 | 0.45845882 |
| ! | transforming growth factor beta receptor signaling pathway | GO:0007179 | 174 | 79 | 0.58423327 | 0.19924 | 0.45793065 |
| ! | exonuclease activity | GO:0004527 | 114 | 54 | 0.59497013 | 0.20044 | 0.46015857 |
| ! | neurotransmitter secretion | GO:0007269 | 196 | 76 | 0.58603066 | 0.20193 | 0.46304638 |
| ! | protein phosphatase type 1 regulator activity | GO:0008599 | 36 | 16 | 0.63967494 | 0.20298 | 0.46491975 |
| ! | pericentriolar material | GO:0000242 | 41 | 16 | 0.64630421 | 0.20298 | 0.46438658 |
| ! | organic cation transporter activity | GO:0015101 | 25 | 19 | 0.62904734 | 0.20555 | 0.46972766 |
| ! | integral to endoplasmic reticulum membrane | GO:0030176 | 59 | 29 | 0.60949914 | 0.20647 | 0.47129022 |
| ! | aldehyde dehydrogenase activity | GO:0004028 | 25 | 15 | 0.63904368 | 0.20672 | 0.4713216 |
| ! | RNA elongation | GO:0006354 | 28 | 15 | 0.64434212 | 0.20672 | 0.47078356 |
| ! | mitotic anaphase | GO:0000090 | 39 | 15 | 0.64157282 | 0.20672 | 0.47024675 |
| ! | MAP kinase activity | GO:0004707 | 39 | 15 | 0.64354784 | 0.20672 | 0.46971116 |

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|---|---|---|---|---|---|---|---|
| ! | vitamin transport | GO:0051180 | 30 | 15 | 0.63967702 | 0.20672 | 0.46917679 |
| ! | negative regulation of neurogenesis | GO:0050768 | 21 | 11 | 0.66324168 | 0.20799 | 0.47152278 |
| ! | heterogeneous nuclear ribonucleoprotein | GO:0008436 | 33 | 11 | 0.66200888 | 0.20799 | 0.47098757 |
| ! | purine nucleotide catabolism | GO:0006195 | 13 | 9 | 0.67204042 | 0.20811 | 0.470725 |
| ! | vitamin K metabolism | GO:0042373 | 23 | 9 | 0.67293483 | 0.20811 | 0.4701919 |
| ! | vitamin K biosynthesis | GO:0042371 | 22 | 8 | 0.68014608 | 0.20903 | 0.47173626 |
| ! | viral nucleocapsid | GO:0019013 | 98 | 37 | 0.60781605 | 0.20929 | 0.47178932 |
| ! | tyrosine phosphorylation of STAT protein | GO:0007260 | 45 | 22 | 0.62259593 | 0.20961 | 0.47197737 |
| ! | arachidonic acid monooxygenase activity | GO:0008391 | 29 | 22 | 0.62756945 | 0.20961 | 0.47144526 |
| ! | anion channel activity | GO:0005253 | 98 | 50 | 0.59266047 | 0.20965 | 0.47100422 |
| ! | viral capsid | GO:0019028 | 123 | 50 | 0.59276178 | 0.20965 | 0.47047441 |
| ! | protein lipidation | GO:0006497 | 109 | 51 | 0.59394625 | 0.21049 | 0.47182871 |
| ! | brush border | GO:0005903 | 25 | 18 | 0.6369245 | 0.21071 | 0.47179175 |
| ! | receptor signaling complex scaffold activity | GO:0030159 | 40 | 18 | 0.63218423 | 0.21071 | 0.47126284 |
| ! | acetylglucosaminyltransferase activity | GO:0008375 | 61 | 28 | 0.61765281 | 0.21095 | 0.47127128 |
| ! | inorganic phosphate transporter activity | GO:0005315 | 20 | 12 | 0.65246499 | 0.21246 | 0.47411376 |
| ! | cell fate determination | GO:0001709 | 71 | 35 | 0.60614559 | 0.21256 | 0.47380693 |
| ! | cholesterol absorption | GO:0030299 | 19 | 10 | 0.66180522 | 0.2133 | 0.47492578 |
| ! | SRP-dependent cotranslational protein-membrane targeting | GO:0006614 | 33 | 14 | 0.64218046 | 0.21348 | 0.47479666 |
| ! | androgen receptor signaling pathway | GO:0030521 | 36 | 14 | 0.64020379 | 0.21348 | 0.47426793 |
| ! | thyroid hormone receptor binding | GO:0046966 | 38 | 17 | 0.63409665 | 0.2145 | 0.47600389 |
| ! | amine transport | GO:0015837 | 150 | 68 | 0.58935052 | 0.21526 | 0.47715967 |
| ! | intracellular receptor-mediated signaling pathway | GO:0030522 | 75 | 27 | 0.61683909 | 0.21569 | 0.47758219 |
| ! | meiotic prophase I | GO:0007128 | 50 | 27 | 0.61095661 | 0.21569 | 0.47705272 |
| ! | CoA hydrolase activity | GO:0016289 | 38 | 26 | 0.61435242 | 0.21712 | 0.47968372 |
| ! | negative regulation of growth | GO:0045926 | 88 | 45 | 0.59425528 | 0.21894 | 0.48316958 |
| ! | cell recognition | GO:0008037 | 73 | 33 | 0.60533559 | 0.21915 | 0.48309862 |
| ! | nuclear chromatin | GO:0000790 | 78 | 20 | 0.62325244 | 0.22049 | 0.48551606 |
| ! | cell-cell adherens junction | GO:0005913 | 44 | 20 | 0.62113647 | 0.22049 | 0.48498076 |
| ! | AMP binding | GO:0016208 | 50 | 25 | 0.61615446 | 0.22064 | 0.48477621 |
| ! | coumarin metabolism | GO:0009804 | 18 | 16 | 0.63109122 | 0.22169 | 0.48654736 |
| ! | purine nucleoside diphosphate metabolism | GO:0009135 | 12 | 8 | 0.67084939 | 0.22211 | 0.48693346 |
| ! | glycine hydroxymethyltransferase activity | GO:0004372 | 21 | 9 | 0.66344186 | 0.22226 | 0.48672744 |
| ! | cell soma | GO:0043025 | 21 | 9 | 0.65741327 | 0.22226 | 0.48619375 |
| ! | proteasomal ubiquitin-dependent protein catabolism | GO:0043161 | 21 | 9 | 0.65926347 | 0.22226 | 0.48566123 |
| ! | protein amino acid sulfation | GO:0006477 | 18 | 9 | 0.65886267 | 0.22226 | 0.48512987 |
| ! | transferase activity, transferring amino-acyl groups | GO:0016755 | 30 | 13 | 0.6403785 | 0.22279 | 0.48575525 |
| ! | RNA-dependent DNA replication | GO:0006278 | 29 | 13 | 0.64404643 | 0.22279 | 0.48522495 |
| ! | FK506-sensitive peptidyl-prolyl cis-trans isomerase | GO:0030051 | 25 | 13 | 0.64126033 | 0.22279 | 0.4846958 |
| ! | nuclear localization sequence binding | GO:0008139 | 31 | 11 | 0.65460757 | 0.22389 | 0.48655833 |
| ! | water channel activity | GO:0015250 | 21 | 11 | 0.65554717 | 0.22389 | 0.48602889 |
| ! | dioxygenase activity | GO:0051213 | 56 | 32 | 0.60889073 | 0.22422 | 0.4862162 |
| ! | calcium ion homeostasis | GO:0006874 | 108 | 62 | 0.58854536 | 0.22452 | 0.48633811 |
| ! | regulation of transcription factor-nucleus import | GO:0042990 | 34 | 15 | 0.63420267 | 0.22595 | 0.48890483 |

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|---|---|---|---|---|---|---|---|
| ! | adenylate cyclase activation | GO:0007190 | 92 | 43 | 0.59390246 | 0.22692 | 0.49047172 |
| ! | bile acid transporter activity | GO:0015125 | 35 | 24 | 0.61642757 | 0.22751 | 0.49121477 |
| ! | specification of organ identity | GO:0010092 | 23 | 10 | 0.6551009 | 0.2279 | 0.49152486 |
| ! | calcium-activated potassium channel activity | GO:0015269 | 22 | 10 | 0.65304612 | 0.2279 | 0.49099406 |
| ! | spindle | GO:0005819 | 220 | 92 | 0.57831764 | 0.22868 | 0.49214304 |
| ! | protein N-terminus binding | GO:0047485 | 24 | 12 | 0.6443538 | 0.22921 | 0.4927521 |
| ! | small monomeric GTPase activity | GO:0003925 | 70 | 30 | 0.60745794 | 0.23042 | 0.49482013 |
| ! | acetylcholine receptor activity | GO:0015464 | 30 | 18 | 0.62188007 | 0.2318 | 0.49724839 |
| ! | cyclophilin | GO:0004600 | 27 | 14 | 0.63649059 | 0.23213 | 0.49742143 |
| ! | vacuolar transport | GO:0007034 | 25 | 14 | 0.6344433 | 0.23213 | 0.49688771 |
| ! | regulation of pH | GO:0006885 | 54 | 22 | 0.61082763 | 0.23284 | 0.49787331 |
| ! | regulation of Wnt receptor signaling pathway | GO:0030111 | 49 | 22 | 0.61343616 | 0.23284 | 0.49734026 |
| ! | axon | GO:0030424 | 48 | 22 | 0.61128837 | 0.23284 | 0.49680834 |
| ! | response to toxin | GO:0009636 | 65 | 40 | 0.59373896 | 0.23322 | 0.4970875 |
| ! | carboxypeptidase activity | GO:0004180 | 124 | 57 | 0.58409701 | 0.23426 | 0.49877129 |
| ! | prostaglandin-F synthase activity | GO:0047017 | 14 | 8 | 0.66507423 | 0.23573 | 0.50136604 |
| ! | aspartic-type endopeptidase activity | GO:0004190 | 48 | 28 | 0.60449372 | 0.23658 | 0.50263802 |
| ! | lipoprotein biosynthesis | GO:0042158 | 113 | 53 | 0.58603645 | 0.23943 | 0.50815197 |
| ! | cell cycle checkpoint | GO:0000075 | 115 | 53 | 0.59001593 | 0.23943 | 0.50761196 |
| ! | phosphatase inhibitor activity | GO:0019212 | 41 | 21 | 0.61065262 | 0.23969 | 0.50762373 |
| ! | nitric oxide mediated signal transduction | GO:0007263 | 35 | 21 | 0.61166368 | 0.23969 | 0.50708542 |
| ! | phosphoinositide biosynthesis | GO:0046489 | 44 | 21 | 0.61643874 | 0.23969 | 0.50654825 |
| ! | intestinal absorption | GO:0050892 | 21 | 11 | 0.64337873 | 0.24035 | 0.50740556 |
| ! | peptide transport | GO:0015833 | 20 | 11 | 0.64406687 | 0.24035 | 0.50686919 |
| ! | kinase activator activity | GO:0019209 | 25 | 11 | 0.64438883 | 0.24035 | 0.50633395 |
| ! | ribonucleotide catabolism | GO:0009261 | 21 | 11 | 0.64305728 | 0.24035 | 0.50579984 |
| ! | fibrillar collagen | GO:0005583 | 24 | 13 | 0.62952833 | 0.24126 | 0.50717987 |
| ! | fluid secretion | GO:0007589 | 23 | 16 | 0.62744015 | 0.2424 | 0.50904 |
| ! | cyclic nucleotide binding | GO:0030551 | 48 | 16 | 0.62110336 | 0.2424 | 0.50850473 |
| ! | fluid transport | GO:0042044 | 30 | 16 | 0.62334254 | 0.2424 | 0.50797059 |
| ! | post-Golgi transport | GO:0006892 | 92 | 35 | 0.5937972 | 0.24303 | 0.5087564 |
| ! | phospholipase C activation | GO:0007202 | 73 | 35 | 0.59459342 | 0.24303 | 0.50822311 |
| ! | glutamine family amino acid metabolism | GO:0009064 | 64 | 36 | 0.59321269 | 0.24421 | 0.51015597 |
| ! | peptide transporter activity | GO:0015197 | 19 | 10 | 0.64207426 | 0.24433 | 0.50987275 |
| ! | organic anion transport | GO:0015711 | 41 | 26 | 0.6038554 | 0.2445 | 0.50969436 |
| ! | unspecific monooxygenase activity | GO:0050381 | 68 | 50 | 0.59017401 | 0.24584 | 0.51195282 |
| ! | deaminase activity | GO:0019239 | 49 | 25 | 0.60142892 | 0.24649 | 0.51277117 |
| ! | hemocyte development | GO:0007516 | 18 | 12 | 0.63146463 | 0.24689 | 0.51306828 |
| ! | monovalent inorganic cation homeostasis | GO:0030004 | 81 | 33 | 0.5928946 | 0.24894 | 0.51679011 |
| ! | oxidoreductase activity, acting on single donors with incorporation of molecular oxygen | GO:0016701 | 57 | 33 | 0.59513799 | 0.24894 | 0.51625291 |
| ! | pyrimidine nucleotide metabolism | GO:0006220 | 67 | 33 | 0.59955187 | 0.24894 | 0.51571682 |
| ! | smooth endoplasmic reticulum | GO:0005790 | 17 | 8 | 0.6549094 | 0.24995 | 0.51727204 |
| ! | spliceosomal snRNP biogenesis | GO:0000387 | 15 | 8 | 0.65338745 | 0.24995 | 0.51673601 |
| ! | wound healing | GO:0042060 | 84 | 47 | 0.58316769 | 0.25138 | 0.51915435 |

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|---|---|---|---|---|---|---|---|
| ! | mu DNA polymerase activity | GO:0016448 | 31 | 14 | 0.62550727 | 0.25168 | 0.5192364 |
| ! | cofactor transport | GO:0051181 | 29 | 14 | 0.6228141 | 0.25168 | 0.5187 |
| ! | vesicle fusion | GO:0006906 | 27 | 14 | 0.62683568 | 0.25168 | 0.51816471 |
| ! | negative regulation of transforming growth factor beta receptor signaling pathway | GO:0030512 | 16 | 9 | 0.6468482 | 0.25191 | 0.51810356 |
| ! | mRNA catabolism, nonsense-mediated decay | GO:0000184 | 16 | 9 | 0.6410661 | 0.25191 | 0.51756998 |
| ! | auxiliary transport protein activity | GO:0015457 | 147 | 73 | 0.57637955 | 0.253 | 0.51927469 |
| ! | frizzled signaling pathway | GO:0007222 | 41 | 18 | 0.61421492 | 0.25324 | 0.51923309 |
| ! | transcription factor-nucleus import | GO:0042991 | 47 | 18 | 0.61202524 | 0.25324 | 0.5187 |
| ! | protein tyrosine/serine/threonine phosphatase activity | GO:0008138 | 88 | 45 | 0.58697512 | 0.25392 | 0.51955938 |
| ! | cyclophilin-type peptidyl-prolyl cis-trans isomerase activity | GO:0042027 | 30 | 17 | 0.6137389 | 0.25649 | 0.52428028 |
| ! | regulation of protein-nucleus import | GO:0042306 | 37 | 17 | 0.61322652 | 0.25649 | 0.52374365 |
| ! | DNA-directed DNA polymerase activity | GO:0003887 | 69 | 31 | 0.597307 | 0.25669 | 0.5236161 |
| ! | cofactor catabolism | GO:0051187 | 17 | 11 | 0.63749317 | 0.25714 | 0.52399826 |
| ! | alpha1-adrenergic receptor activity | GO:0004937 | 19 | 11 | 0.63745202 | 0.25714 | 0.52346357 |
| ! | DNA catabolism | GO:0006308 | 23 | 13 | 0.62092264 | 0.26003 | 0.52880719 |
| ! | progesterone metabolism | GO:0042448 | 23 | 13 | 0.62345063 | 0.26003 | 0.52826869 |
| ! | regulation of small GTPase mediated signal transduction | GO:0051056 | 28 | 13 | 0.62015286 | 0.26003 | 0.52773128 |
| ! | Golgi organization and biogenesis | GO:0007030 | 32 | 13 | 0.62168655 | 0.26003 | 0.52719497 |
| ! | water-soluble vitamin biosynthesis | GO:0042364 | 19 | 10 | 0.62878134 | 0.26126 | 0.52915096 |
| ! | ligand-regulated transcription factor activity | GO:0003706 | 23 | 10 | 0.63014999 | 0.26126 | 0.5286143 |
| ! | positive regulation of lipid metabolism | GO:0045834 | 12 | 8 | 0.64266255 | 0.26487 | 0.53537553 |
| ! | NAD+ ADP-ribosyltransferase activity | GO:0003950 | 14 | 8 | 0.64377902 | 0.26487 | 0.53483365 |
| ! | imprinting | GO:0006349 | 25 | 8 | 0.63809569 | 0.26487 | 0.53429287 |
| ! | cGMP metabolism | GO:0046068 | 17 | 12 | 0.62364801 | 0.2663 | 0.53663485 |
| ! | response to metal ion | GO:0010038 | 32 | 12 | 0.62769254 | 0.2663 | 0.53609334 |
| ! | protein-nucleus import, docking | GO:0000059 | 39 | 15 | 0.61768673 | 0.26642 | 0.53579425 |
| ! | DNA-directed RNA polymerase II, core complex | GO:0005665 | 26 | 15 | 0.61211337 | 0.26642 | 0.53525468 |
| ! | pancreatic ribonuclease activity | GO:0004522 | 26 | 15 | 0.61329281 | 0.26642 | 0.5347162 |
| ! | fat-soluble vitamin metabolism | GO:0006775 | 72 | 40 | 0.58185643 | 0.26672 | 0.5347803 |
| ! | translation elongation factor activity | GO:0003746 | 86 | 40 | 0.58836268 | 0.26672 | 0.53424337 |
| ! | response to drug | GO:0042493 | 119 | 62 | 0.57945528 | 0.26738 | 0.53502818 |
| ! | establishment of cell polarity | GO:0030010 | 23 | 9 | 0.63233422 | 0.26818 | 0.53609128 |
| ! | carboxylesterase activity | GO:0004091 | 61 | 39 | 0.58970673 | 0.26838 | 0.53595405 |
| ! | telomere maintenance | GO:0000723 | 62 | 27 | 0.59874679 | 0.27129 | 0.54122355 |
| ! | SNARE binding | GO:0000149 | 68 | 26 | 0.59949907 | 0.27133 | 0.54076259 |
| ! | nucleotide catabolism | GO:0009166 | 49 | 26 | 0.59049505 | 0.27133 | 0.5402229 |
| ! | nicotinic acetylcholine-gated receptor-channel complex | GO:0005892 | 23 | 14 | 0.61367047 | 0.27289 | 0.54278719 |
| ! | amino acid transport | GO:0006865 | 124 | 58 | 0.57757004 | 0.27296 | 0.54238566 |
| ! | detection of light | GO:0009583 | 93 | 58 | 0.57514609 | 0.27296 | 0.54184597 |
| ! | calcium activated cation channel activity | GO:0005227 | 17 | 11 | 0.62601211 | 0.27489 | 0.54513474 |
| ! | hormone secretion | GO:0046879 | 47 | 25 | 0.59539587 | 0.2753 | 0.54540566 |
| ! | response to radiation | GO:0009314 | 170 | 98 | 0.56188953 | 0.27534 | 0.54494375 |

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|---|---|---|---|---|---|---|---|
| ! | smooth muscle contraction | GO:0006939 | 110 | 55 | 0.5716601 | 0.27748 | 0.54863489 |
| ! | aldehyde-lyase activity | GO:0016832 | 15 | 10 | 0.62315586 | 0.27869 | 0.55048173 |
| ! | MHC class I protein binding | GO:0042288 | 20 | 10 | 0.62386196 | 0.27869 | 0.54993724 |
| ! | calcium- and calmodulin-dependent protein kinase activity | GO:0004685 | 29 | 13 | 0.6167811 | 0.27911 | 0.55022179 |
| ! | aldehyde reductase activity | GO:0004032 | 23 | 13 | 0.61797606 | 0.27911 | 0.54967863 |
| ! | inhibitory extracellular ligand-gated ion channel activity | GO:0005237 | 22 | 13 | 0.61678603 | 0.27911 | 0.54913654 |
| ! | mannose binding | GO:0005537 | 23 | 17 | 0.60085393 | 0.27925 | 0.54887069 |
| ! | chloroplast | GO:0009507 | 16 | 8 | 0.63097558 | 0.28017 | 0.55013696 |
| ! | heart development | GO:0007507 | 205 | 89 | 0.57109075 | 0.2838 | 0.55671681 |
| ! | histone methylation | GO:0016571 | 27 | 9 | 0.62490946 | 0.28431 | 0.5571694 |
| ! | actin modulating activity | GO:0003790 | 19 | 9 | 0.62679956 | 0.28431 | 0.55662262 |
| ! | cyclin-dependent protein kinase holoenzyme complex | GO:0000307 | 19 | 9 | 0.62805962 | 0.28431 | 0.55607691 |
| ! | hexokinase activity | GO:0004396 | 14 | 9 | 0.62084408 | 0.28431 | 0.55553227 |
| ! | glycine-inhibited chloride channel activity | GO:0004891 | 21 | 12 | 0.61131111 | 0.28597 | 0.55822911 |
| ! | viral life cycle | GO:0016032 | 97 | 50 | 0.57400643 | 0.28601 | 0.55776144 |
| ! | neurotransmitter metabolism | GO:0042133 | 53 | 32 | 0.58213425 | 0.28602 | 0.55723623 |
| ! | calcium channel regulator activity | GO:0005246 | 57 | 22 | 0.59483679 | 0.28602 | 0.55669259 |
| ! | oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, reduced flavin or flavoprotein as one donor, and incorporation of one atom of oxygen | GO:0016712 | 69 | 51 | 0.58003639 | 0.28768 | 0.55937778 |
| ! | non-G-protein coupled 7TM receptor activity | GO:0004926 | 31 | 15 | 0.60112115 | 0.28822 | 0.55988208 |
| ! | oxygen binding | GO:0019825 | 65 | 49 | 0.57965237 | 0.28893 | 0.56071532 |
| ! | actin filament | GO:0005884 | 62 | 30 | 0.58456967 | 0.29032 | 0.56286531 |
| ! | JAK-STAT cascade | GO:0007259 | 97 | 46 | 0.58021637 | 0.29153 | 0.56466248 |
| ! | neuroblast proliferation | GO:0007405 | 24 | 11 | 0.61781885 | 0.293 | 0.56695926 |
| ! | vitamin D receptor binding | GO:0042809 | 25 | 11 | 0.61832621 | 0.293 | 0.56640988 |
| ! | UDP-galactosyltransferase activity | GO:0035250 | 55 | 20 | 0.59631781 | 0.29349 | 0.56680789 |
| ! | gamma DNA-directed DNA polymerase activity | GO:0003895 | 32 | 14 | 0.60264881 | 0.29465 | 0.56849782 |
| ! | G1/S transition of mitotic cell cycle | GO:0000082 | 193 | 78 | 0.57022047 | 0.29568 | 0.56993391 |
| ! | clathrin coat of coated pit | GO:0030132 | 15 | 8 | 0.62762207 | 0.29643 | 0.57082804 |
| ! | calcium:sodium antiporter activity | GO:0005432 | 19 | 8 | 0.62692456 | 0.29643 | 0.57027758 |
| ! | FACIT collagen | GO:0005593 | 20 | 8 | 0.6234345 | 0.29643 | 0.56972818 |
| ! | histogenesis and organogenesis | GO:0007397 | 141 | 77 | 0.56897488 | 0.29701 | 0.5702935 |
| ! | development of primary sexual characteristics | GO:0045137 | 89 | 44 | 0.57460628 | 0.29919 | 0.57392697 |
| ! | regulation of endocytosis | GO:0030100 | 91 | 44 | 0.57255615 | 0.29919 | 0.57337565 |
| ! | erythrocyte differentiation | GO:0030218 | 25 | 13 | 0.60588526 | 0.29997 | 0.57431876 |
| ! | intermediate filament-based process | GO:0045103 | 35 | 13 | 0.605982 | 0.29997 | 0.57376812 |
| ! | endoribonuclease activity, producing 5'-phosphomonoesters | GO:0016891 | 31 | 18 | 0.59359174 | 0.3005 | 0.57423132 |
| ! | anchored to plasma membrane | GO:0046658 | 58 | 26 | 0.5830381 | 0.30142 | 0.57543818 |
| ! | very-long-chain fatty acid metabolism | GO:0000038 | 21 | 9 | 0.61313759 | 0.3018 | 0.57561281 |
| ! | profilin binding | GO:0005522 | 31 | 9 | 0.61885403 | 0.3018 | 0.57506304 |
| ! | nucleotidase activity | GO:0008252 | 18 | 9 | 0.61750388 | 0.3018 | 0.57451431 |

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|---|---|---|---|---|---|---|---|
| ! | calcium- and calmodulin-responsive adenylate cyclase activity | GO:0008294 | 17 | 9 | 0.61218121 | 0.3018 | 0.57396663 |
| ! | neurotransmitter uptake | GO:0001504 | 20 | 9 | 0.60974413 | 0.3018 | 0.57342 |
| ! | endosome to lysosome transport | GO:0008333 | 13 | 9 | 0.6098746 | 0.3018 | 0.57287441 |
| ! | melanocortin receptor activity | GO:0004977 | 9 | 9 | 0.61786104 | 0.3018 | 0.57232985 |
| ! | oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, reduced iron-sulfur protein as one donor, and incorporation of one atom of oxygen | GO:0016713 | 16 | 9 | 0.61267408 | 0.3018 | 0.57178632 |
| ! | aminoglycan metabolism | GO:0006022 | 88 | 40 | 0.57423231 | 0.30296 | 0.57343947 |
| ! | DNA damage response, signal transduction resulting in induction of apoptosis | GO:0008630 | 32 | 17 | 0.59135058 | 0.304 | 0.57486256 |
| ! | aspartate family amino acid metabolism | GO:0009066 | 46 | 25 | 0.58384647 | 0.30435 | 0.5749794 |
| ! | transition metal ion transporter activity | GO:0046915 | 54 | 25 | 0.5878003 | 0.30435 | 0.57443543 |
| ! | cyclic nucleotide metabolism | GO:0009187 | 64 | 39 | 0.57136897 | 0.30476 | 0.5746656 |
| ! | lung development | GO:0030324 | 88 | 39 | 0.57973552 | 0.30476 | 0.57412295 |
| ! | biogenic amine metabolism | GO:0006576 | 130 | 67 | 0.56754082 | 0.30556 | 0.57508698 |
| ! | postsynaptic membrane | GO:0045211 | 131 | 70 | 0.57040225 | 0.30666 | 0.57661329 |
| ! | lipoprotein metabolism | GO:0042157 | 134 | 68 | 0.56247397 | 0.3079 | 0.57839972 |
| ! | protein binding, bridging | GO:0030674 | 48 | 23 | 0.58500981 | 0.30812 | 0.57826849 |
| ! | phosphatidylinositol binding | GO:0005545 | 44 | 15 | 0.59354132 | 0.31084 | 0.582825 |
| ! | regulation of cyclin dependent protein kinase activity | GO:0000079 | 66 | 35 | 0.57315092 | 0.31106 | 0.58268986 |
| ! | UDP-glucosyltransferase activity | GO:0035251 | 30 | 11 | 0.60811892 | 0.31207 | 0.58403344 |
| ! | dopamine D2 receptor-like receptor activity | GO:0001591 | 15 | 8 | 0.61323865 | 0.31313 | 0.58546799 |
| ! | regulation of BMP signaling pathway | GO:0030510 | 13 | 8 | 0.61429243 | 0.31313 | 0.5849198 |
| ! | branching morphogenesis | GO:0001763 | 56 | 22 | 0.58935362 | 0.31361 | 0.58526843 |
| ! | water transporter activity | GO:0005372 | 19 | 10 | 0.60832941 | 0.31483 | 0.58699612 |
| ! | striated muscle thin filament | GO:0005865 | 46 | 21 | 0.58641101 | 0.31606 | 0.58873922 |
| ! | cyclase activity | GO:0009975 | 37 | 21 | 0.58640875 | 0.31606 | 0.58819002 |
| ! | regulation of adenylate cyclase activity | GO:0045761 | 122 | 59 | 0.56196299 | 0.31653 | 0.5885157 |
| ! | virion | GO:0019012 | 141 | 59 | 0.56395968 | 0.31653 | 0.58796774 |
| ! | positive regulation of transport | GO:0051050 | 69 | 34 | 0.57543019 | 0.31663 | 0.58760637 |
| ! | phosphatidylinositol phosphate kinase activity | GO:0016307 | 35 | 14 | 0.59863017 | 0.31716 | 0.58804294 |
| ! | vacuolar membrane | GO:0005774 | 31 | 14 | 0.59948628 | 0.31716 | 0.58749694 |
| ! | complement activity | GO:0003811 | 26 | 14 | 0.59547467 | 0.31716 | 0.58695195 |
| ! | thyroid hormone receptor activity | GO:0004887 | 19 | 9 | 0.60520417 | 0.32007 | 0.59178837 |
| ! | stem cell division | GO:0017145 | 19 | 9 | 0.6050404 | 0.32007 | 0.59124042 |
| ! | phototransduction | GO:0007602 | 89 | 56 | 0.56860387 | 0.32201 | 0.59427377 |
| ! | purine base metabolism | GO:0006144 | 26 | 13 | 0.59421056 | 0.32223 | 0.59413018 |
| ! | endocytic vesicle | GO:0030139 | 73 | 30 | 0.57922866 | 0.3237 | 0.59628947 |
| ! | negative regulation of adenylate cyclase activity | GO:0007194 | 37 | 19 | 0.58617015 | 0.32428 | 0.59680683 |
| ! | glucosyltransferase activity | GO:0046527 | 32 | 12 | 0.59915641 | 0.32633 | 0.60002613 |
| ! | ovarian follicle development | GO:0001541 | 29 | 12 | 0.5926922 | 0.32633 | 0.59947362 |
| ! | telomerase-dependent telomere maintenance | GO:0007004 | 43 | 18 | 0.58885699 | 0.32693 | 0.60002332 |
| ! | neuropeptide hormone activity | GO:0005184 | 37 | 28 | 0.57468344 | 0.32927 | 0.60376255 |

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|---|---|---|---|---|---|---|---|
| ! | cation:chloride symporter activity | GO:0015377 | 21 | 8 | 0.60798848 | 0.32975 | 0.60408747 |
| ! | compartment specification | GO:0007386 | 24 | 8 | 0.60597176 | 0.32975 | 0.60353326 |
| ! | excitatory extracellular ligand-gated ion channel activity | GO:0005231 | 88 | 51 | 0.56564635 | 0.33165 | 0.6064544 |
| ! | calcium:cation antiporter activity | GO:0015368 | 23 | 11 | 0.59389503 | 0.33224 | 0.60697692 |
| ! | fucosyltransferase activity | GO:0008417 | 21 | 11 | 0.5917779 | 0.33224 | 0.60642159 |
| ! | intramolecular transferase activity, phosphotransferases | GO:0016868 | 20 | 10 | 0.59258763 | 0.33352 | 0.60820146 |
| ! | DNA damage response, signal transduction by p53 class mediator | GO:0030330 | 20 | 10 | 0.59050626 | 0.33352 | 0.60764603 |
| ! | diacylglycerol binding | GO:0019992 | 107 | 47 | 0.56997801 | 0.33417 | 0.60827477 |
| ! | pore complex | GO:0046930 | 121 | 45 | 0.5668374 | 0.33447 | 0.60826586 |
| ! | regulation of phosphorylation | GO:0042325 | 105 | 45 | 0.56266483 | 0.33447 | 0.60771189 |
| ! | chloride channel activity | GO:0005254 | 86 | 45 | 0.56205848 | 0.33447 | 0.60715892 |
| ! | clathrin coat of trans-Golgi network vesicle | GO:0030130 | 40 | 15 | 0.58988344 | 0.33453 | 0.60671577 |
| ! | RNA methyltransferase activity | GO:0008173 | 33 | 16 | 0.58926156 | 0.33539 | 0.60772302 |
| ! | structural constituent of epidermis | GO:0030280 | 23 | 16 | 0.58790075 | 0.33539 | 0.60717155 |
| ! | Wnt receptor signaling pathway | GO:0016055 | 236 | 98 | 0.55450767 | 0.33554 | 0.60689238 |
| ! | inositol or phosphatidylinositol phosphatase activity | GO:0004437 | 51 | 24 | 0.57635758 | 0.33756 | 0.60999293 |
| ! | oxidoreductase activity, acting on the CH-NH2 group of donors | GO:0016638 | 43 | 24 | 0.57356701 | 0.33756 | 0.6094409 |
| ! | male genitalia morphogenesis | GO:0030539 | 21 | 9 | 0.59585154 | 0.33775 | 0.60923259 |
| ! | membrane alanyl aminopeptidase activity | GO:0004179 | 13 | 9 | 0.59711082 | 0.33775 | 0.60868225 |
| ! | positive regulation of myeloid blood cell differentiation | GO:0045639 | 19 | 9 | 0.59350184 | 0.33775 | 0.6081329 |
| ! | vitamin biosynthesis | GO:0009110 | 47 | 23 | 0.57869215 | 0.33867 | 0.60923954 |
| ! | neuronal cell recognition | GO:0008038 | 42 | 23 | 0.57346537 | 0.33867 | 0.60869068 |
| ! | endonuclease activity, active with either ribo- or deoxyribonucleic acids and producing 5'-phosphomonoesters | GO:0016893 | 38 | 23 | 0.57929959 | 0.33867 | 0.6081428 |
| ! | dopamine receptor activity | GO:0004952 | 23 | 14 | 0.58325378 | 0.34074 | 0.61130962 |
| ! | respiratory tube development | GO:0030323 | 93 | 42 | 0.56920206 | 0.34114 | 0.61147736 |
| ! | positive regulation of transcription from Pol II promoter | GO:0045944 | 215 | 89 | 0.5613554 | 0.34269 | 0.61370426 |
| ! | aminoglycan biosynthesis | GO:0006023 | 46 | 22 | 0.57173458 | 0.34334 | 0.61431686 |
| ! | regulation of JNK cascade | GO:0046328 | 50 | 21 | 0.57493617 | 0.3444 | 0.61566129 |
| ! | lipid transport | GO:0006869 | 187 | 91 | 0.55305188 | 0.3449 | 0.61600313 |
| ! | induction of apoptosis via death domain receptors | GO:0008625 | 21 | 13 | 0.58855442 | 0.34493 | 0.61550568 |
| ! | ribonuclease P activity | GO:0004526 | 11 | 8 | 0.59142078 | 0.34692 | 0.61850349 |
| ! | Wnt receptor activity | GO:0042813 | 18 | 8 | 0.59753787 | 0.34692 | 0.61795125 |
| ! | somatic stem cell division | GO:0048103 | 15 | 8 | 0.5909012 | 0.34692 | 0.6174 |
| ! | positive regulation of small GTPase mediated signal transduction | GO:0051057 | 16 | 8 | 0.5937644 | 0.34692 | 0.61684973 |
| ! | calmodulin-dependent protein kinase I activity | GO:0004684 | 22 | 8 | 0.59182451 | 0.34692 | 0.61630045 |
| ! | 3',5'-cyclic-nucleotide phosphodiesterase activity | GO:0004114 | 54 | 20 | 0.57525322 | 0.34868 | 0.61887598 |
| ! | base-excision repair | GO:0006284 | 45 | 20 | 0.57217447 | 0.34868 | 0.61832587 |
| ! | prenylated protein tyrosine phosphatase activity | GO:0004727 | 94 | 37 | 0.56943908 | 0.34894 | 0.61823739 |

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|---|---|---|---|---|---|---|---|
| ! | NADPH-hemoprotein reductase activity | GO:0003958 | 21 | 19 | 0.57664455 | 0.3513 | 0.62186646 |
| ! | activation of MAPK | GO:0000187 | 156 | 78 | 0.5582017 | 0.35131 | 0.62133285 |
| ! | steroid hormone receptor binding | GO:0035258 | 21 | 11 | 0.58852075 | 0.35352 | 0.62468769 |
| ! | macrophage differentiation | GO:0030225 | 18 | 11 | 0.58137878 | 0.35352 | 0.62413487 |
| ! | fat-soluble vitamin biosynthesis | GO:0042362 | 25 | 11 | 0.58671282 | 0.35352 | 0.62358302 |
| ! | palmitoyltransferase activity | GO:0016409 | 22 | 10 | 0.58293757 | 0.35357 | 0.62312027 |
| ! | vasculogenesis | GO:0001570 | 38 | 17 | 0.57877395 | 0.35453 | 0.62426068 |
| ! | mannosyltransferase activity | GO:0000030 | 18 | 9 | 0.58195016 | 0.35686 | 0.62780926 |
| ! | N-methyl-D-aspartate selective glutamate receptor activity | GO:0004972 | 14 | 9 | 0.58086256 | 0.35686 | 0.62725612 |
| ! | thyroid hormone generation | GO:0006590 | 21 | 9 | 0.585439 | 0.35686 | 0.62670396 |
| ! | inorganic anion transporter activity | GO:0015103 | 55 | 31 | 0.56452223 | 0.35807 | 0.62827586 |
| ! | channel regulator activity | GO:0016247 | 143 | 71 | 0.55450329 | 0.35845 | 0.62838994 |
| ! | RAS small monomeric GTPase activity | GO:0003930 | 38 | 16 | 0.5742687 | 0.36189 | 0.63386352 |
| ! | organic cation transport | GO:0015695 | 21 | 16 | 0.57712499 | 0.36189 | 0.6333075 |
| ! | protease activator activity | GO:0016504 | 35 | 16 | 0.57395885 | 0.36189 | 0.63275245 |
| ! | rRNA metabolism | GO:0016072 | 123 | 66 | 0.55394691 | 0.36235 | 0.63300197 |
| ! | cell adhesion receptor activity | GO:0004895 | 68 | 28 | 0.56680058 | 0.36342 | 0.63431575 |
| ! | calmodulin regulated protein kinase activity | GO:0004683 | 60 | 28 | 0.56685424 | 0.36342 | 0.63376128 |
| ! | eye morphogenesis | GO:0001654 | 139 | 62 | 0.5545379 | 0.36403 | 0.63427061 |
| ! | water transport | GO:0006833 | 26 | 14 | 0.57253044 | 0.36447 | 0.63448312 |
| ! | 5'-nucleotidase activity | GO:0008253 | 17 | 8 | 0.58928151 | 0.36477 | 0.63445174 |
| ! | glycerol-3-phosphate metabolism | GO:0006072 | 16 | 8 | 0.58865324 | 0.36477 | 0.63389909 |
| ! | epidermal cell differentiation | GO:0009913 | 18 | 8 | 0.58712826 | 0.36477 | 0.63334739 |
| ! | negative regulation of axonogenesis | GO:0050771 | 17 | 8 | 0.5881625 | 0.36477 | 0.63279665 |
| ! | regulator of G-protein signaling activity | GO:0016299 | 19 | 8 | 0.58818939 | 0.36477 | 0.63224687 |
| ! | establishment and/or maintenance of epithelial cell polarity | GO:0045197 | 19 | 8 | 0.58716439 | 0.36477 | 0.63169805 |
| ! | biogenic amine biosynthesis | GO:0042401 | 43 | 26 | 0.57063672 | 0.36543 | 0.63229215 |
| ! | vasoconstriction | GO:0042310 | 18 | 13 | 0.57424302 | 0.36689 | 0.63426824 |
| ! | receptor signaling protein tyrosine kinase activity | GO:0004716 | 34 | 13 | 0.5776673 | 0.36689 | 0.63371909 |
| ! | arsenate reductase activity | GO:0030611 | 27 | 13 | 0.57646408 | 0.36689 | 0.63317089 |
| ! | genitalia morphogenesis | GO:0035112 | 31 | 13 | 0.58010866 | 0.36689 | 0.63262364 |
| ! | cell fate commitment | GO:0045165 | 112 | 60 | 0.55776587 | 0.36817 | 0.63428251 |
| ! | chromatin remodeling | GO:0006338 | 132 | 58 | 0.56159633 | 0.36858 | 0.63444098 |
| ! | reproductive behavior | GO:0019098 | 40 | 24 | 0.56469984 | 0.36983 | 0.63604384 |
| ! | BMP signaling pathway | GO:0030509 | 48 | 24 | 0.5676016 | 0.36983 | 0.63549599 |
| ! | cortical cytoskeleton organization and biogenesis | GO:0030865 | 31 | 12 | 0.57759885 | 0.37018 | 0.63555 |
| ! | desmosome | GO:0030057 | 26 | 12 | 0.57892137 | 0.37018 | 0.63500353 |
| ! | regulation of T-cell differentiation | GO:0045580 | 49 | 23 | 0.56368051 | 0.37046 | 0.63493789 |
| ! | complement activation | GO:0006956 | 91 | 57 | 0.56051377 | 0.37196 | 0.63696155 |
| ! | transcription from Pol III promoter | GO:0006383 | 103 | 53 | 0.55371653 | 0.37228 | 0.63696278 |

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|---|---|---|---|---|---|---|---|
| ! | oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors | GO:0016706 | 42 | 21 | 0.56939156 | 0.37377 | 0.63896414 |
| ! | STAT protein nuclear translocation | GO:0007262 | 16 | 10 | 0.5760038 | 0.37428 | 0.63928818 |
| ! | non-membrane spanning protein tyrosine phosphatase activity | GO:0004726 | 25 | 10 | 0.57889278 | 0.37428 | 0.63874132 |
| ! | heparan sulfate proteoglycan metabolism | GO:0030201 | 27 | 11 | 0.5768875 | 0.37514 | 0.63966179 |
| ! | retinol dehydrogenase activity | GO:0004745 | 17 | 11 | 0.5776234 | 0.37514 | 0.63911554 |
| ! | stromelysin 3 activity | GO:0004249 | 17 | 9 | 0.57812908 | 0.37648 | 0.64085119 |
| ! | fibroblast growth factor receptor signaling pathway | GO:0008543 | 47 | 20 | 0.56356308 | 0.37709 | 0.64134233 |
| ! | gastrulation | GO:0007369 | 106 | 45 | 0.56061771 | 0.37755 | 0.64157773 |
| ! | general RNA polymerase II transcription factor activity | GO:0016251 | 94 | 51 | 0.5599262 | 0.3782 | 0.64213532 |
| ! | perception of taste | GO:0050909 | 31 | 19 | 0.56764969 | 0.38044 | 0.64538929 |
| ! | phosphatidylinositol metabolism | GO:0046488 | 47 | 19 | 0.56947934 | 0.38044 | 0.64484095 |
| ! | regulation of blood vessel size | GO:0050880 | 24 | 18 | 0.56993237 | 0.3806 | 0.64456452 |
| ! | arachidonic acid epoxygenase activity | GO:0008392 | 20 | 18 | 0.56904266 | 0.3806 | 0.64401781 |
| ! | Golgi stack | GO:0005795 | 43 | 18 | 0.56848311 | 0.3806 | 0.64347203 |
| ! | carboxypeptidase A activity | GO:0004182 | 91 | 41 | 0.56175028 | 0.38186 | 0.64505563 |
| ! | establishment of mitotic spindle localization | GO:0040001 | 22 | 8 | 0.57171308 | 0.38221 | 0.64510063 |
| ! | glycosaminoglycan metabolism | GO:0030203 | 87 | 39 | 0.56078553 | 0.38575 | 0.65052515 |
| ! | di-, tri-valent inorganic cation transporter activity | GO:0015082 | 80 | 35 | 0.56093943 | 0.38728 | 0.65255372 |
| ! | heme binding | GO:0020037 | 46 | 35 | 0.55438353 | 0.38728 | 0.65200304 |
| ! | regulation of B-cell proliferation | GO:0030888 | 32 | 14 | 0.56858018 | 0.38831 | 0.65318588 |
| ! | sulfate transport | GO:0008272 | 23 | 14 | 0.56356132 | 0.38831 | 0.65263559 |
| ! | gamma-tubulin complex | GO:0000930 | 30 | 14 | 0.5624698 | 0.38831 | 0.65208624 |
| ! | nuclear heterochromatin | GO:0005720 | 67 | 16 | 0.56954077 | 0.38888 | 0.6524942 |
| ! | viral infectious cycle | GO:0019058 | 68 | 36 | 0.55397318 | 0.38951 | 0.65300206 |
| ! | protein deubiquitination | GO:0016579 | 31 | 13 | 0.56767222 | 0.39088 | 0.65474861 |
| ! | glutamate signaling pathway | GO:0007215 | 68 | 33 | 0.56099254 | 0.39175 | 0.65565541 |
| ! | voltage-gated calcium channel activity | GO:0005245 | 72 | 33 | 0.55959391 | 0.39175 | 0.65510583 |
| ! | vacuole organization and biogenesis | GO:0007033 | 58 | 33 | 0.55694057 | 0.39175 | 0.65455716 |
| ! | segmentation | GO:0035282 | 63 | 33 | 0.56148419 | 0.39175 | 0.65400941 |
| ! | respiratory gaseous exchange | GO:0007585 | 67 | 33 | 0.5552451 | 0.39175 | 0.65346258 |
| ! | elastase activity | GO:0042708 | 49 | 34 | 0.56005737 | 0.39243 | 0.65405 |
| ! | sensory organ development | GO:0007423 | 62 | 32 | 0.55427705 | 0.39375 | 0.65570221 |
| ! | peptide hormone processing | GO:0016486 | 26 | 12 | 0.56294593 | 0.39379 | 0.65522189 |
| ! | ether hydrolase activity | GO:0016803 | 12 | 9 | 0.56370936 | 0.39554 | 0.65758525 |
| ! | beta-adrenergic receptor activity | GO:0004939 | 16 | 9 | 0.56231561 | 0.39554 | 0.65703772 |
| ! | positive regulation of interleukin-2 biosynthesis | GO:0045086 | 18 | 10 | 0.56460886 | 0.39562 | 0.65662388 |
| ! | folic acid binding | GO:0005542 | 17 | 10 | 0.56246095 | 0.39562 | 0.65607805 |
| ! | common-partner SMAD protein phosphorylation | GO:0007182 | 23 | 10 | 0.57066108 | 0.39562 | 0.65553314 |
| ! | establishment and/or maintenance of cell polarity | GO:0007163 | 77 | 30 | 0.55974813 | 0.39583 | 0.6553368 |
| ! | leukocyte cell adhesion | GO:0007159 | 25 | 11 | 0.57103915 | 0.39688 | 0.65653035 |
| ! | clathrin binding | GO:0030276 | 31 | 11 | 0.5686283 | 0.39688 | 0.65598641 |

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|---|---|---|---|---|---|---|---|
| ! | negative regulation of microtubule depolymerization | GO:0007026 | 20 | 8 | 0.56574468 | 0.40102 | 0.66228055 |
| ! | gene silencing | GO:0016458 | 47 | 23 | 0.56164331 | 0.40356 | 0.66592407 |
| ! | late endosome | GO:0005770 | 53 | 24 | 0.56013978 | 0.40369 | 0.66558806 |
| ! | synaptic vesicle membrane | GO:0030672 | 52 | 21 | 0.55448971 | 0.40475 | 0.66678468 |
| ! | heterochromatin | GO:0000792 | 83 | 22 | 0.5567421 | 0.4061 | 0.66845668 |
| ! | apical part of cell | GO:0045177 | 47 | 22 | 0.55815639 | 0.4061 | 0.66790561 |
| ! | UDP-glycosyltransferase activity | GO:0008194 | 206 | 90 | 0.54478007 | 0.40732 | 0.6693603 |
| ! | anterior/posterior axis specification | GO:0009948 | 38 | 20 | 0.55739013 | 0.40748 | 0.6690721 |
| ! | posttranslational protein-membrane targeting | GO:0006620 | 50 | 20 | 0.56078908 | 0.40748 | 0.66852188 |
| ! | positive regulation of signal transduction | GO:0009967 | 207 | 96 | 0.54438236 | 0.40844 | 0.66954626 |
| ! | ribonucleoside monophosphate biosynthesis | GO:0009156 | 33 | 17 | 0.55267724 | 0.40926 | 0.67033966 |
| ! | response to UV | GO:0009411 | 31 | 17 | 0.5558293 | 0.40926 | 0.66978975 |
| ! | adrenoceptor activity | GO:0004935 | 27 | 17 | 0.56131241 | 0.40926 | 0.66924074 |
| ! | cation:cation antiporter activity | GO:0015491 | 39 | 18 | 0.55860245 | 0.40941 | 0.66893771 |
| ! | menstrual cycle | GO:0042698 | 44 | 18 | 0.55404141 | 0.40941 | 0.6683903 |
| ! | detection of biotic stimulus | GO:0009595 | 27 | 18 | 0.56153979 | 0.40941 | 0.66784379 |
| ! | synaptic vesicle | GO:0008021 | 167 | 81 | 0.5466009 | 0.40949 | 0.66742855 |
| ! | positive regulation of B-cell activation | GO:0050871 | 38 | 19 | 0.55536706 | 0.41012 | 0.66790971 |
| ! | positive regulation of I-kappaB kinase/NF-kappaB cascade | GO:0043123 | 165 | 80 | 0.54298642 | 0.41058 | 0.66811346 |
| ! | transcription from Pol I promoter | GO:0006360 | 24 | 14 | 0.56166829 | 0.41368 | 0.67260929 |
| ! | insulin receptor binding | GO:0005158 | 25 | 14 | 0.5610971 | 0.41368 | 0.67206156 |
| ! | regulation of long-term neuronal synaptic plasticity | GO:0048169 | 29 | 14 | 0.56157197 | 0.41368 | 0.67151473 |
| ! | hemocyte differentiation (sensu Arthropoda) | GO:0042386 | 21 | 14 | 0.55369163 | 0.41368 | 0.67096878 |
| ! | 3-beta-hydroxy-delta5-steroid dehydrogenase activity | GO:0003854 | 11 | 9 | 0.56011557 | 0.41566 | 0.67363258 |
| ! | DNA repair protein | GO:0003685 | 17 | 9 | 0.55238147 | 0.41566 | 0.6730858 |
| ! | cofactor transporter activity | GO:0051184 | 32 | 16 | 0.55893294 | 0.41573 | 0.67265316 |
| ! | synaptic transmission, cholinergic | GO:0007271 | 27 | 16 | 0.55367968 | 0.41573 | 0.67210806 |
| ! | regulation of anti-apoptosis | GO:0045767 | 28 | 13 | 0.55992668 | 0.41605 | 0.67208077 |
| ! | substrate-bound cell migration | GO:0006929 | 27 | 13 | 0.55257801 | 0.41605 | 0.67153701 |
| ! | DNA topoisomerase activity | GO:0003916 | 23 | 10 | 0.56171766 | 0.41625 | 0.67131669 |
| ! | thyroid hormone metabolism | GO:0042403 | 23 | 10 | 0.56127004 | 0.41625 | 0.67077443 |
| ! | ribosome assembly | GO:0042255 | 22 | 10 | 0.55748121 | 0.41625 | 0.67023305 |
| ! | benzodiazepine receptor activity | GO:0008503 | 24 | 12 | 0.55935879 | 0.4172 | 0.67122097 |
| ! | aminoacyl-tRNA hydrolase reaction | GO:0006439 | 22 | 12 | 0.55730348 | 0.4172 | 0.6706801 |
| ! | fucose metabolism | GO:0006004 | 23 | 11 | 0.55339561 | 0.41928 | 0.67348116 |
| ! | adenylate cyclase activity | GO:0004016 | 21 | 11 | 0.5552287 | 0.41928 | 0.67293934 |
| ! | late endosome to vacuole transport | GO:0045324 | 29 | 11 | 0.55791923 | 0.41928 | 0.67239839 |
| ! | G-protein signaling, adenylate cyclase activating pathway | GO:0007189 | 127 | 63 | 0.54949957 | 0.42043 | 0.67370108 |
| ! | caspase activation via cytochrome c | GO:0008635 | 14 | 8 | 0.55745905 | 0.42095 | 0.67399298 |
| ! | basolateral plasma membrane | GO:0016323 | 128 | 56 | 0.54908199 | 0.42157 | 0.67444439 |
| ! | antigen processing | GO:0030333 | 77 | 41 | 0.54610991 | 0.4246 | 0.6787476 |
| ! | response to extracellular stimulus | GO:0009991 | 74 | 41 | 0.54811216 | 0.4246 | 0.67820416 |
| ! | cell projection organization and biogenesis | GO:0030030 | 97 | 40 | 0.55092208 | 0.42656 | 0.68078976 |

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|---|---|---|---|---|---|---|---|
| ! | monocarboxylic acid transporter activity | GO:0008028 | 69 | 40 | 0.54410716 | 0.42656 | 0.68024556 |
| ! | actin polymerization and/or depolymerization | GO:0008154 | 104 | 39 | 0.55178286 | 0.42976 | 0.68480128 |
| ! | regulation of secretion | GO:0051046 | 78 | 38 | 0.54622678 | 0.43022 | 0.68498715 |
| ! | spindle organization and biogenesis | GO:0007051 | 84 | 37 | 0.54525366 | 0.43085 | 0.68544318 |
| ! | chemokine receptor binding | GO:0042379 | 59 | 36 | 0.55216808 | 0.4311 | 0.68529442 |
| ! | cytolysis | GO:0019835 | 43 | 33 | 0.54735344 | 0.43147 | 0.6853365 |
| ! | histone modification | GO:0016570 | 76 | 34 | 0.55046527 | 0.43269 | 0.68672757 |
| ! | regulation of striated muscle contraction | GO:0006942 | 55 | 31 | 0.54473518 | 0.43328 | 0.68711733 |
| ! | epithelial cell differentiation | GO:0030855 | 64 | 31 | 0.54301965 | 0.43328 | 0.68657156 |
| ! | nucleoside metabolism | GO:0009116 | 56 | 29 | 0.54980816 | 0.4345 | 0.68795833 |
| ! | regulation of lymphocyte differentiation | GO:0045619 | 57 | 28 | 0.54605338 | 0.43533 | 0.68872589 |
| ! | photoreceptor activity | GO:0009881 | 50 | 28 | 0.54547551 | 0.43533 | 0.68818015 |
| ! | cyclic nucleotide biosynthesis | GO:0009190 | 44 | 28 | 0.5450227 | 0.43533 | 0.68763527 |
| ! | potassium channel regulator activity | GO:0015459 | 50 | 28 | 0.55050881 | 0.43533 | 0.68709126 |
| ! | glycosaminoglycan biosynthesis | GO:0006024 | 45 | 21 | 0.54664304 | 0.43636 | 0.68817249 |
| ! | cAMP metabolism | GO:0046058 | 36 | 21 | 0.55204798 | 0.43636 | 0.68762891 |
| ! | trans-Golgi network transport vesicle | GO:0030140 | 56 | 21 | 0.54394098 | 0.43636 | 0.68708619 |
| ! | calcium-dependent cytosolic phospholipase A2 activity | GO:0004627 | 12 | 9 | 0.54694039 | 0.43698 | 0.68751979 |
| ! | aspartate family amino acid catabolism | GO:0009068 | 15 | 9 | 0.54847657 | 0.43698 | 0.68697801 |
| ! | G-protein coupled photoreceptor activity | GO:0008020 | 49 | 27 | 0.5460391 | 0.4378 | 0.6877252 |
| ! | innate immune response | GO:0045087 | 41 | 24 | 0.54968778 | 0.43802 | 0.68752943 |
| ! | caspase activator activity | GO:0008656 | 18 | 10 | 0.54511724 | 0.43809 | 0.6870987 |
| ! | vascular endothelial growth factor receptor activity | GO:0005021 | 33 | 10 | 0.54515064 | 0.43809 | 0.68655896 |
| ! | voltage-gated calcium channel complex | GO:0005891 | 52 | 22 | 0.54935289 | 0.43833 | 0.68639588 |
| ! | cyclic-nucleotide phosphodiesterase activity | GO:0004112 | 58 | 22 | 0.54568308 | 0.43833 | 0.68585753 |
| ! | sodium channel regulator activity | GO:0017080 | 28 | 17 | 0.55136265 | 0.43854 | 0.68564835 |
| ! | drug transporter activity | GO:0015238 | 44 | 20 | 0.54281621 | 0.43859 | 0.68518955 |
| ! | cAMP biosynthesis | GO:0006171 | 30 | 18 | 0.54860765 | 0.43865 | 0.68474707 |
| ! | posttranslational protein folding | GO:0051084 | 47 | 18 | 0.55021119 | 0.43865 | 0.68421169 |
| ! | osteoblast differentiation | GO:0001649 | 35 | 18 | 0.54313618 | 0.43865 | 0.68367715 |
| ! | cathepsin L activity | GO:0004217 | 20 | 14 | 0.55081342 | 0.43977 | 0.6848877 |
| ! | protein amino acid deacetylation | GO:0006476 | 27 | 14 | 0.55063649 | 0.43977 | 0.68435347 |
| ! | estrogen receptor binding | GO:0030331 | 16 | 8 | 0.54683649 | 0.44044 | 0.68486189 |
| ! | nucleoside monophosphate biosynthesis | GO:0009124 | 41 | 19 | 0.5495727 | 0.44064 | 0.68463925 |
| ! | arachidonic acid metabolism | GO:0019369 | 22 | 19 | 0.54972014 | 0.44064 | 0.68410646 |
| ! | sialyltransferase activity | GO:0008373 | 40 | 19 | 0.55199981 | 0.44064 | 0.68357449 |
| ! | tRNA binding | GO:0000049 | 21 | 12 | 0.5440383 | 0.44064 | 0.68304336 |
| ! | presynaptic membrane | GO:0042734 | 50 | 12 | 0.54409269 | 0.44064 | 0.68251304 |
| ! | negative regulation of gene expression, epigenetic | GO:0045814 | 22 | 13 | 0.54997405 | 0.4415 | 0.68331458 |
| ! | glutamine family amino acid catabolism | GO:0009065 | 23 | 13 | 0.55012455 | 0.4415 | 0.68278488 |
| ! | negative regulation of Wnt receptor signaling pathway | GO:0030178 | 26 | 13 | 0.54688012 | 0.4415 | 0.682256 |
| ! | diacylglycerol kinase activity | GO:0004143 | 22 | 13 | 0.54531921 | 0.4415 | 0.68172794 |
| ! | GTP biosynthesis | GO:0006183 | 24 | 16 | 0.55096351 | 0.44348 | 0.68425568 |
| ! | ruffles | GO:0001726 | 39 | 16 | 0.54628466 | 0.44348 | 0.68372689 |
| ! | somitogenesis | GO:0001756 | 27 | 16 | 0.54352045 | 0.44348 | 0.68319892 |

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|---|---|---|---|---|---|---|---|
| ! | nuclear organization and biogenesis | GO:0006997 | 35 | 16 | 0.54668 | 0.44348 | 0.68267176 |
| ! | organic acid catabolism | GO:0016054 | 10 | 9 | 0.53680366 | 0.45794 | 0.70438728 |
| ! | heparan sulfate proteoglycan biosynthesis | GO:0015012 | 22 | 9 | 0.53352787 | 0.45794 | 0.70384461 |
| ! | calcium-dependent secreted phospholipase A2 activity | GO:0004625 | 13 | 10 | 0.53477422 | 0.46011 | 0.70663545 |
| ! | methionine metabolism | GO:0006555 | 21 | 10 | 0.54172451 | 0.46011 | 0.70609188 |
| ! | intermediate filament cytoskeleton organization and biogenesis | GO:0045104 | 26 | 10 | 0.54221595 | 0.46011 | 0.70554915 |
| ! | cGMP biosynthesis | GO:0006182 | 14 | 10 | 0.53856978 | 0.46011 | 0.70500726 |
| ! | fibrinogen complex | GO:0005577 | 10 | 8 | 0.53659293 | 0.46041 | 0.70492552 |
| ! | sarcolemma | GO:0042383 | 32 | 15 | 0.54032165 | 0.4639 | 0.70972431 |
| ! | response to inorganic substance | GO:0010035 | 35 | 15 | 0.54176701 | 0.4639 | 0.70918046 |
| ! | response to fungi | GO:0009620 | 26 | 15 | 0.53761148 | 0.4639 | 0.70863744 |
| ! | acrosome | GO:0001669 | 26 | 15 | 0.53577117 | 0.4639 | 0.70809526 |
| ! | retinoic acid metabolism | GO:0042573 | 24 | 15 | 0.53934475 | 0.4639 | 0.7075539 |
| ! | nucleocytoplasmic transporter activity | GO:0005487 | 38 | 12 | 0.53982285 | 0.4653 | 0.70914706 |
| ! | aldehyde dehydrogenase (NAD) activity | GO:0004029 | 22 | 13 | 0.53714153 | 0.46747 | 0.71191042 |
| ! | aldo-keto reductase activity | GO:0004033 | 22 | 13 | 0.54242117 | 0.46747 | 0.71136739 |
| ! | determination of bilateral symmetry | GO:0009855 | 29 | 17 | 0.53950525 | 0.46764 | 0.71108369 |
| ! | memory | GO:0007613 | 44 | 18 | 0.5333713 | 0.46891 | 0.71247178 |
| ! | protein kinase C activation | GO:0007205 | 44 | 23 | 0.54091918 | 0.47109 | 0.71523938 |
| ! | epsilon DNA polymerase activity | GO:0003893 | 33 | 16 | 0.5418836 | 0.47125 | 0.71493821 |
| ! | growth cone | GO:0030426 | 33 | 16 | 0.53355461 | 0.47125 | 0.71439495 |
| ! | collagen fibril organization | GO:0030199 | 30 | 16 | 0.53514143 | 0.47125 | 0.71385251 |
| ! | regulation of proteolysis and peptidolysis | GO:0030162 | 52 | 26 | 0.53348467 | 0.47159 | 0.71382553 |
| ! | mating behavior | GO:0007617 | 34 | 22 | 0.54258046 | 0.47203 | 0.71394985 |
| ! | gamma-aminobutyric acid signaling pathway | GO:0007214 | 41 | 22 | 0.5349098 | 0.47203 | 0.71340898 |
| ! | beta-amyloid metabolism | GO:0050435 | 35 | 19 | 0.53400146 | 0.47222 | 0.71315587 |
| ! | ionotropic glutamate receptor activity | GO:0004970 | 37 | 19 | 0.5424752 | 0.47222 | 0.71261641 |
| ! | feeding behavior | GO:0007631 | 51 | 33 | 0.53557594 | 0.47224 | 0.71210794 |
| ! | condensed nuclear chromosome | GO:0000794 | 51 | 28 | 0.53332716 | 0.47256 | 0.71205227 |
| ! | chromosome condensation | GO:0030261 | 48 | 24 | 0.54243054 | 0.47264 | 0.71163532 |
| ! | serpin | GO:0004868 | 54 | 32 | 0.54024461 | 0.47323 | 0.71198631 |
| ! | ubiquitin thiolesterase activity | GO:0004221 | 121 | 53 | 0.53494459 | 0.47327 | 0.71150991 |
| ! | integrin complex | GO:0008305 | 68 | 34 | 0.54200498 | 0.47349 | 0.71130463 |
| ! | regulation of angiogenesis | GO:0045765 | 65 | 38 | 0.54024603 | 0.47394 | 0.71144492 |
| ! | cell cycle regulator | GO:0003750 | 95 | 39 | 0.53476439 | 0.47428 | 0.71142 |
| ! | external side of plasma membrane | GO:0009897 | 146 | 82 | 0.54039567 | 0.47467 | 0.71147006 |
| ! | pre-mRNA splicing factor activity | GO:0008248 | 190 | 75 | 0.53960865 | 0.47492 | 0.71131036 |
| ! | phenol metabolism | GO:0018958 | 53 | 27 | 0.53427739 | 0.47506 | 0.71098627 |
| ! | insoluble fraction | GO:0005626 | 78 | 27 | 0.5417267 | 0.47506 | 0.7104533 |
| ! | rRNA processing | GO:0006364 | 116 | 62 | 0.53643791 | 0.47524 | 0.71019011 |
| ! | learning and/or memory | GO:0007611 | 139 | 62 | 0.53888592 | 0.47524 | 0.70965853 |
| ! | regulation of I-kappaB kinase/NF-kappaB cascade | GO:0043122 | 171 | 83 | 0.5352068 | 0.47533 | 0.70926204 |
| ! | cell maturation | GO:0048469 | 104 | 47 | 0.53843249 | 0.47553 | 0.70903016 |
| ! | actin filament organization | GO:0007015 | 149 | 68 | 0.53691843 | 0.47553 | 0.70850063 |

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|---|---|---|---|---|---|---|---|
| ! | ubiquitin-specific protease activity | GO:0004843 | 128 | 56 | 0.54088599 | 0.47564 | 0.70813567 |
| ! | RNA catabolism | GO:0006401 | 128 | 63 | 0.53423947 | 0.4775 | 0.71037472 |
| ! | acrosome reaction | GO:0007340 | 16 | 9 | 0.52876708 | 0.47937 | 0.7126253 |
| ! | internal side of plasma membrane | GO:0009898 | 16 | 8 | 0.53222502 | 0.48097 | 0.71447144 |
| ! | purine ribonucleotide catabolism | GO:0009154 | 12 | 8 | 0.53106182 | 0.48097 | 0.71393984 |
| ! | response to cold | GO:0009409 | 20 | 10 | 0.52450453 | 0.48332 | 0.71689472 |
| ! | ferric iron binding | GO:0008199 | 14 | 10 | 0.53033747 | 0.48332 | 0.71636211 |
| ! | polysaccharide catabolism | GO:0000272 | 18 | 10 | 0.53083643 | 0.48332 | 0.71583029 |
| ! | vesicle targeting | GO:0006903 | 26 | 11 | 0.52902706 | 0.48928 | 0.72411988 |
| ! | MAP kinase phosphatase activity | GO:0017017 | 21 | 11 | 0.52963805 | 0.48928 | 0.7235831 |
| ! | polypeptide N-acetylgalactosaminyltransferase activity | GO:0004653 | 27 | 12 | 0.52561388 | 0.49086 | 0.725382 |
| ! | flagellum (sensu Eukaryota) | GO:0009434 | 24 | 12 | 0.52451477 | 0.49086 | 0.72484508 |
| ! | regulation of actin filament polymerization | GO:0030833 | 32 | 15 | 0.53273089 | 0.49172 | 0.72557796 |
| ! | activation of NF-kappaB-inducing kinase | GO:0007250 | 25 | 14 | 0.52621469 | 0.49262 | 0.72636874 |
| ! | positive regulation of phosphorylation | GO:0042327 | 27 | 13 | 0.53000572 | 0.4937 | 0.72742356 |
| ! | sarcoplasm | GO:0016528 | 25 | 13 | 0.53217972 | 0.4937 | 0.72688672 |
| ! | amino acid derivative catabolism | GO:0042219 | 27 | 16 | 0.52614703 | 0.49946 | 0.734825 |
| ! | disassembly of cell structures during apoptosis | GO:0006921 | 26 | 18 | 0.52686494 | 0.49994 | 0.73498917 |
| ! | site of polarized growth | GO:0030427 | 36 | 18 | 0.52794016 | 0.49994 | 0.73444794 |
| ! | fatty acid transport | GO:0015908 | 17 | 9 | 0.52328529 | 0.50061 | 0.73489106 |
| ! | tumor antigen | GO:0008222 | 22 | 9 | 0.52226545 | 0.50061 | 0.7343507 |
| ! | ureteric bud branching | GO:0001658 | 25 | 8 | 0.51872854 | 0.50144 | 0.73502777 |
| ! | oxysterol binding | GO:0008142 | 15 | 8 | 0.51644825 | 0.50144 | 0.73448811 |
| ! | autophosphorylation | GO:0046777 | 50 | 20 | 0.52685795 | 0.50167 | 0.73428588 |
| ! | phosphoinositide binding | GO:0035091 | 59 | 22 | 0.52906427 | 0.50521 | 0.73892518 |
| ! | lymphocyte antigen | GO:0005557 | 18 | 10 | 0.52164311 | 0.50649 | 0.74025462 |
| ! | GTPase binding | GO:0051020 | 44 | 23 | 0.52689137 | 0.5071 | 0.74060359 |
| ! | catecholamine metabolism | GO:0006584 | 52 | 26 | 0.53060433 | 0.50923 | 0.74317034 |
| ! | C21-steroid hormone biosynthesis | GO:0006700 | 51 | 25 | 0.52793341 | 0.5095 | 0.74302083 |
| ! | viral genome replication | GO:0019079 | 39 | 25 | 0.52621119 | 0.5095 | 0.74247809 |
| ! | galactosyltransferase activity | GO:0008378 | 72 | 29 | 0.5240705 | 0.51154 | 0.74490679 |
| ! | transport vesicle | GO:0030133 | 64 | 27 | 0.53087583 | 0.512 | 0.74503282 |
| ! | regulation of cell organization and biogenesis | GO:0051128 | 87 | 33 | 0.52647235 | 0.51294 | 0.74585663 |
| ! | regulation of interleukin-2 biosynthesis | GO:0045076 | 19 | 11 | 0.51621256 | 0.51343 | 0.74602538 |
| ! | retinoic acid receptor activity | GO:0003708 | 20 | 11 | 0.52006601 | 0.51343 | 0.74548242 |
| ! | estrogen receptor signaling pathway | GO:0030520 | 31 | 11 | 0.52026205 | 0.51343 | 0.74494025 |
| ! | synaptic vesicle endocytosis | GO:0048488 | 22 | 11 | 0.51968052 | 0.51343 | 0.74439887 |
| ! | learning | GO:0007612 | 62 | 31 | 0.5242409 | 0.51547 | 0.74681383 |
| ! | embryo implantation | GO:0007566 | 52 | 31 | 0.53157423 | 0.51547 | 0.74627188 |
| ! | response to nutrients | GO:0007584 | 63 | 34 | 0.5314703 | 0.51697 | 0.74790076 |
| ! | T-cell differentiation | GO:0030217 | 82 | 38 | 0.52367958 | 0.51842 | 0.749455 |
| ! | C21-steroid hormone metabolism | GO:0008207 | 73 | 37 | 0.53137829 | 0.51859 | 0.74915789 |
| ! | regulation of mitosis | GO:0007088 | 81 | 37 | 0.52676991 | 0.51859 | 0.74861581 |
| ! | cytochrome P450 | GO:0005490 | 27 | 15 | 0.51579564 | 0.51974 | 0.74973341 |
| ! | regulation of circadian rhythm | GO:0042752 | 29 | 13 | 0.51675111 | 0.52021 | 0.74986918 |

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|---|---|---|---|---|---|---|---|
| ! | calpain activity | GO:0004198 | 23 | 13 | 0.51736294 | 0.52021 | 0.74932776 |
| ! | actin filament reorganization during cell cycle | GO:0030037 | 14 | 9 | 0.50825349 | 0.52312 | 0.75297576 |
| ! | negative regulation of protein metabolism | GO:0051248 | 93 | 44 | 0.53078118 | 0.5252 | 0.75542466 |
| ! | G2/M transition of mitotic cell cycle | GO:0000086 | 91 | 44 | 0.52778728 | 0.5252 | 0.7548804 |
| ! | G-protein-coupled receptor binding | GO:0001664 | 83 | 50 | 0.52755097 | 0.52655 | 0.75627592 |
| ! | steroid catabolism | GO:0006706 | 23 | 17 | 0.51652638 | 0.52727 | 0.75676522 |
| ! | inner ear morphogenesis | GO:0042472 | 29 | 17 | 0.51457723 | 0.52727 | 0.75622117 |
| ! | regulation of fatty acid metabolism | GO:0019217 | 19 | 10 | 0.51051996 | 0.52903 | 0.75820032 |
| ! | phospholipid transport | GO:0015914 | 25 | 10 | 0.51307719 | 0.52903 | 0.75765603 |
| ! | DNA-directed RNA polymerase II, holoenzyme | GO:0016591 | 106 | 57 | 0.53064153 | 0.52983 | 0.75825742 |
| ! | bile acid metabolism | GO:0008206 | 29 | 20 | 0.52010637 | 0.53393 | 0.76357731 |
| ! | lamellipodium biogenesis | GO:0030032 | 43 | 19 | 0.52243454 | 0.53482 | 0.76430222 |
| ! | superoxide metabolism | GO:0006801 | 36 | 21 | 0.51450556 | 0.53552 | 0.76475476 |
| ! | calcium channel activity | GO:0005262 | 143 | 71 | 0.53113854 | 0.53762 | 0.76720451 |
| ! | hormone-mediated signaling | GO:0009755 | 21 | 11 | 0.50706334 | 0.53764 | 0.76668463 |
| ! | long-chain fatty acid metabolism | GO:0001676 | 14 | 11 | 0.50612663 | 0.53764 | 0.766137 |
| ! | cortical actin cytoskeleton organization and biogenesis | GO:0030866 | 25 | 11 | 0.51407317 | 0.53764 | 0.76559015 |
| ! | lysosomal transport | GO:0007041 | 15 | 11 | 0.51128498 | 0.53764 | 0.76504408 |
| ! | chromatin | GO:0005717 | 76 | 22 | 0.51492772 | 0.53852 | 0.76575011 |
| ! | pathogenesis | GO:0009405 | 184 | 81 | 0.53120342 | 0.53969 | 0.7668672 |
| ! | peptidyl-amino acid modification | GO:0018193 | 183 | 82 | 0.52643916 | 0.54128 | 0.76857907 |
| ! | receptor complex | GO:0043235 | 175 | 83 | 0.53239451 | 0.54208 | 0.76916757 |
| ! | positive regulation of peptidyl-tyrosine phosphorylation | GO:0050731 | 26 | 12 | 0.51044191 | 0.54263 | 0.76940075 |
| ! | synaptic vesicle docking during exocytosis | GO:0016081 | 29 | 12 | 0.50467448 | 0.54263 | 0.7688543 |
| ! | ATP-dependent RNA helicase activity | GO:0004004 | 52 | 24 | 0.52160491 | 0.54307 | 0.76893162 |
| ! | phosphotyrosine binding | GO:0001784 | 18 | 8 | 0.49803073 | 0.54323 | 0.76861266 |
| ! | pregnancy | GO:0007565 | 159 | 90 | 0.5326464 | 0.5438 | 0.76887385 |
| ! | hydrogen-translocating V-type ATPase activity | GO:0000260 | 18 | 9 | 0.50358716 | 0.54488 | 0.76985524 |
| ! | transferase activity, transferring pentosyl groups | GO:0016763 | 46 | 25 | 0.5213655 | 0.54535 | 0.76997399 |
| ! | biogenic amine catabolism | GO:0042402 | 22 | 13 | 0.51277233 | 0.54632 | 0.77079802 |
| ! | triacylglycerol lipase activity | GO:0004806 | 21 | 13 | 0.51076739 | 0.54632 | 0.77025329 |
| ! | oligosaccharide metabolism | GO:0009311 | 28 | 13 | 0.5134282 | 0.54632 | 0.76970932 |
| ! | regulation of DNA replication | GO:0006275 | 25 | 13 | 0.50776048 | 0.54632 | 0.76916613 |
| ! | prenyltransferase activity | GO:0004659 | 61 | 28 | 0.52009088 | 0.54761 | 0.77043861 |
| ! | dopamine receptor signaling pathway | GO:0007212 | 46 | 28 | 0.52319451 | 0.54761 | 0.76989567 |
| ! | regulation of gene expression, epigenetic | GO:0040029 | 234 | 97 | 0.5289932 | 0.54953 | 0.77205095 |
| ! | calcium-dependent phospholipid binding | GO:0005544 | 72 | 29 | 0.52135046 | 0.5506 | 0.77300985 |
| ! | sodium:potassium-exchanging ATPase complex | GO:0005890 | 25 | 10 | 0.49944356 | 0.55248 | 0.7751038 |
| ! | associative learning | GO:0008306 | 14 | 10 | 0.50035768 | 0.55248 | 0.7745591 |
| ! | protein carrier activity | GO:0008320 | 26 | 10 | 0.4975431 | 0.55248 | 0.77401517 |
| ! | amino acid derivative biosynthesis | GO:0042398 | 52 | 33 | 0.51984685 | 0.55556 | 0.777784 |
| ! | regulation of synaptic plasticity | GO:0048167 | 74 | 33 | 0.5207575 | 0.55556 | 0.77723857 |
| ! | drug transport | GO:0015893 | 28 | 17 | 0.51398851 | 0.55812 | 0.78027288 |
| ! | GABA receptor activity | GO:0016917 | 63 | 34 | 0.51901342 | 0.55964 | 0.78185 |
| ! | adenosine receptor activity, G-protein coupled | GO:0001609 | 28 | 18 | 0.50517484 | 0.56226 | 0.7849606 |

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|---|---|---|---|---|---|---|---|
| ! | regulation of body size | GO:0040014 | 38 | 18 | 0.5056669 | 0.56226 | 0.78441168 |
| ! | intracellular ligand-gated ion channel activity | GO:0005217 | 34 | 18 | 0.51255628 | 0.56226 | 0.78386352 |
| ! | inositol or phosphatidylinositol kinase activity | GO:0004428 | 82 | 38 | 0.5198215 | 0.56347 | 0.78500185 |
| ! | phagocytosis, recognition | GO:0006910 | 13 | 8 | 0.49313729 | 0.56383 | 0.78495523 |
| ! | hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in cyclic amides | GO:0016812 | 16 | 8 | 0.49276934 | 0.56383 | 0.78440785 |
| ! | protein complex disassembly | GO:0043241 | 16 | 8 | 0.48650913 | 0.56383 | 0.78386122 |
| ! | tumor suppressor | GO:0008181 | 92 | 39 | 0.51850967 | 0.56395 | 0.78348207 |
| ! | ribonucleoside monophosphate metabolism | GO:0009161 | 37 | 19 | 0.50599662 | 0.56605 | 0.7858523 |
| ! | lysosome organization and biogenesis | GO:0007040 | 30 | 19 | 0.51022318 | 0.56605 | 0.78530581 |
| ! | dopamine metabolism | GO:0042417 | 21 | 9 | 0.49487445 | 0.56677 | 0.78575827 |
| ! | voltage-gated chloride channel activity | GO:0005247 | 45 | 20 | 0.51365971 | 0.56698 | 0.78550354 |
| ! | leukotriene metabolism | GO:0006691 | 32 | 20 | 0.51296122 | 0.56698 | 0.78495843 |
| ! | centrosome cycle | GO:0007098 | 21 | 12 | 0.49679443 | 0.56723 | 0.78475995 |
| ! | histone acetylation | GO:0016573 | 23 | 12 | 0.49850913 | 0.56723 | 0.78421611 |
| ! | nucleoside monophosphate metabolism | GO:0009123 | 45 | 21 | 0.50763352 | 0.56866 | 0.78564868 |
| ! | purine nucleoside binding | GO:0001883 | 18 | 13 | 0.50097879 | 0.5722 | 0.78999239 |
| ! | regulation of DNA recombination | GO:0000018 | 30 | 13 | 0.49546957 | 0.5722 | 0.78944606 |
| ! | acid secretion | GO:0046717 | 21 | 13 | 0.50342447 | 0.5722 | 0.78890048 |
| ! | oxidoreductase activity, acting on the CH-NH2 group of donors, oxygen as acceptor | GO:0016641 | 37 | 22 | 0.50641927 | 0.57264 | 0.78896188 |
| ! | hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amidines | GO:0016813 | 30 | 14 | 0.49515591 | 0.57444 | 0.79089565 |
| ! | histone deacetylation | GO:0016575 | 18 | 10 | 0.48580792 | 0.57486 | 0.79092807 |
| ! | sulfate transporter activity | GO:0015116 | 16 | 10 | 0.49119779 | 0.57486 | 0.79038298 |
| ! | myoblast fusion | GO:0007520 | 18 | 10 | 0.49300609 | 0.57486 | 0.78983864 |
| ! | calcium ion transporter activity | GO:0015085 | 26 | 10 | 0.49378726 | 0.57486 | 0.78929504 |
| ! | tumor necrosis factor receptor activity | GO:0005031 | 15 | 10 | 0.4878289 | 0.57486 | 0.7887522 |
| ! | regulation of catabolism | GO:0009894 | 105 | 48 | 0.52070848 | 0.57487 | 0.78822381 |
| ! | vitamin A metabolism | GO:0006776 | 34 | 23 | 0.50596083 | 0.57622 | 0.78953221 |
| ! | transmembrane-ephrin receptor activity | GO:0005005 | 31 | 15 | 0.50165253 | 0.57653 | 0.78941479 |
| ! | pyrimidine nucleotide biosynthesis | GO:0006221 | 50 | 25 | 0.50920506 | 0.5811 | 0.79512654 |
| ! | transcription initiation | GO:0006352 | 95 | 57 | 0.52268502 | 0.58423 | 0.79886145 |
| ! | peptidyl-tyrosine phosphorylation | GO:0018108 | 133 | 57 | 0.51691908 | 0.58423 | 0.79831428 |
| ! | porin activity | GO:0015288 | 56 | 26 | 0.51398032 | 0.58455 | 0.79820483 |
| ! | lipoprotein binding | GO:0008034 | 52 | 26 | 0.50548909 | 0.58455 | 0.79765886 |
| ! | pseudouridylate synthase activity | GO:0004730 | 15 | 8 | 0.48366108 | 0.58471 | 0.79733182 |
| ! | viral replication | GO:0008166 | 12 | 8 | 0.48212494 | 0.58471 | 0.79678719 |
| ! | immunoglobulin secretion | GO:0048305 | 17 | 8 | 0.48538071 | 0.58471 | 0.79624331 |
| ! | lysozyme activity | GO:0003796 | 12 | 8 | 0.48166551 | 0.58471 | 0.79570017 |
| ! | neuronal cell projection | GO:0043005 | 127 | 59 | 0.51927647 | 0.58558 | 0.7963409 |
| ! | peptidyl-tyrosine modification | GO:0018212 | 135 | 59 | 0.51909922 | 0.58558 | 0.79579843 |
| ! | sister chromatid segregation | GO:0000819 | 30 | 11 | 0.48602412 | 0.58601 | 0.79584067 |
| ! | gamma-tubulin ring complex | GO:0008274 | 26 | 11 | 0.48631613 | 0.58601 | 0.79529929 |

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|---|---|---|---|---|---|---|---|
| ! | establishment and/or maintenance of apical/basal cell polarity | GO:0035088 | 22 | 11 | 0.49458244 | 0.58601 | 0.79475863 |
| ! | sterol transporter activity | GO:0015248 | 23 | 11 | 0.4900795 | 0.58601 | 0.79421872 |
| ! | mesoderm development | GO:0007498 | 131 | 60 | 0.51697905 | 0.58756 | 0.79577882 |
| ! | regulation of actin filament length | GO:0030832 | 66 | 27 | 0.51358715 | 0.58799 | 0.79582093 |
| ! | Golgi to endosome transport | GO:0006895 | 26 | 9 | 0.48202718 | 0.58851 | 0.79598471 |
| ! | clathrin-coated endocytic vesicle | GO:0045334 | 26 | 9 | 0.48050039 | 0.58851 | 0.79544543 |
| ! | sodium ion homeostasis | GO:0006883 | 19 | 9 | 0.48026654 | 0.58851 | 0.79490687 |
| ! | microtubule motor activity | GO:0003777 | 150 | 62 | 0.5195428 | 0.58928 | 0.79540839 |
| ! | Golgi vesicle | GO:0005798 | 70 | 29 | 0.51163931 | 0.58946 | 0.79511339 |
| ! | phosphoric diester hydrolase activity | GO:0008081 | 146 | 64 | 0.52337433 | 0.59023 | 0.79561409 |
| ! | negative regulation of signal transduction | GO:0009968 | 131 | 61 | 0.5228317 | 0.59127 | 0.79647782 |
| ! | nu DNA polymerase activity | GO:0016451 | 24 | 12 | 0.48953063 | 0.59194 | 0.79684231 |
| ! | acute-phase response | GO:0006953 | 98 | 65 | 0.51705546 | 0.59226 | 0.79673547 |
| ! | endoplasmic reticulum lumen | GO:0005788 | 43 | 18 | 0.49765283 | 0.59363 | 0.79804033 |
| ! | Ras protein signal transduction | GO:0007265 | 135 | 66 | 0.51972616 | 0.59375 | 0.79766414 |
| ! | extracellular ligand-gated ion channel activity | GO:0005230 | 122 | 68 | 0.51835697 | 0.59464 | 0.79832221 |
| ! | complement activation, classical pathway | GO:0006958 | 51 | 31 | 0.5118495 | 0.59649 | 0.80026735 |
| ! | collagen catabolism | GO:0030574 | 49 | 32 | 0.50994349 | 0.59663 | 0.79991724 |
| ! | GABA-A receptor activity | GO:0004890 | 58 | 33 | 0.51070395 | 0.59754 | 0.80059926 |
| ! | mitotic chromosome condensation | GO:0007076 | 21 | 10 | 0.47866988 | 0.5982 | 0.80094564 |
| ! | exocrine system development | GO:0035272 | 36 | 13 | 0.49414674 | 0.59829 | 0.80052887 |
| ! | regulation of hormone secretion | GO:0046883 | 23 | 13 | 0.48720749 | 0.59829 | 0.79999233 |
| ! | bone resorption | GO:0045453 | 37 | 19 | 0.49819515 | 0.59838 | 0.79957676 |
| ! | phosphorus-oxygen lyase activity | GO:0016849 | 32 | 19 | 0.49929075 | 0.59838 | 0.79904157 |
| ! | chromatin binding | GO:0003682 | 171 | 71 | 0.51690996 | 0.59894 | 0.79925438 |
| ! | histone deacetylase complex | GO:0000118 | 34 | 20 | 0.50094467 | 0.59948 | 0.79944024 |
| ! | N-formyl peptide receptor activity | GO:0004982 | 27 | 20 | 0.50451681 | 0.59948 | 0.79890621 |
| ! | prostanoid biosynthesis | GO:0046457 | 21 | 14 | 0.48882355 | 0.6021 | 0.80186215 |
| ! | interleukin-8 binding | GO:0019959 | 19 | 14 | 0.49260708 | 0.6021 | 0.80132722 |
| ! | ligand-dependent nuclear receptor transcription coactivator activity | GO:0030374 | 43 | 21 | 0.50043238 | 0.60316 | 0.8022028 |
| ! | L-fucose metabolism | GO:0042354 | 15 | 8 | 0.47225577 | 0.60476 | 0.80379494 |
| ! | S-methyltransferase activity | GO:0008172 | 12 | 8 | 0.47472006 | 0.60476 | 0.80325979 |
| ! | Arp2/3 protein complex | GO:0005885 | 14 | 8 | 0.47146081 | 0.60476 | 0.80272535 |
| ! | clathrin coat of endocytic vesicle | GO:0030128 | 19 | 8 | 0.47213337 | 0.60476 | 0.80219162 |
| ! | voltage-gated sodium channel complex | GO:0001518 | 14 | 8 | 0.47434548 | 0.60476 | 0.8016586 |
| ! | oligopeptide transport | GO:0006857 | 14 | 8 | 0.47394439 | 0.60476 | 0.80112629 |
| ! | amine receptor activity | GO:0008227 | 56 | 37 | 0.50980824 | 0.60597 | 0.80219652 |
| ! | transcription initiation from Pol II promoter | GO:0006367 | 67 | 38 | 0.50928096 | 0.60702 | 0.80305365 |
| ! | regulation of G-protein coupled receptor protein signaling pathway | GO:0008277 | 85 | 38 | 0.50500157 | 0.60702 | 0.80252147 |
| ! | steroid hydroxylase activity | GO:0008395 | 51 | 40 | 0.51128618 | 0.6095 | 0.80526656 |
| ! | Rab GTPase activator activity | GO:0005097 | 20 | 9 | 0.47333822 | 0.61016 | 0.80560503 |
| ! | T-helper 2 type immune response | GO:0042092 | 13 | 9 | 0.47146783 | 0.61016 | 0.80507222 |

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|---|---|---|---|---|---|---|---|
| ! | mitotic sister chromatid segregation | GO:0000070 | 23 | 9 | 0.47425879 | 0.61016 | 0.80454012 |
| ! | tumor necrosis factor binding | GO:0043120 | 16 | 11 | 0.47836944 | 0.61079 | 0.80483887 |
| ! | lambda DNA polymerase activity | GO:0016449 | 21 | 11 | 0.48227126 | 0.61079 | 0.80430762 |
| ! | phosphatidylinositol biosynthesis | GO:0006661 | 24 | 11 | 0.48103567 | 0.61079 | 0.80377708 |
| ! | male meiosis | GO:0007140 | 34 | 16 | 0.49047012 | 0.61533 | 0.80921777 |
| ! | ephrin receptor activity | GO:0005003 | 34 | 16 | 0.48854618 | 0.61533 | 0.80868468 |
| ! | DNA topological change | GO:0006265 | 23 | 12 | 0.47618342 | 0.61719 | 0.81059516 |
| ! | transcription factor TFIID complex | GO:0005669 | 25 | 17 | 0.4938768 | 0.61733 | 0.81024563 |
| ! | actin filament polymerization | GO:0030041 | 67 | 26 | 0.49540705 | 0.62018 | 0.81345108 |
| ! | ear morphogenesis | GO:0042471 | 31 | 18 | 0.49315289 | 0.62408 | 0.81802865 |
| ! | pyrimidine ribonucleotide metabolism | GO:0009218 | 35 | 18 | 0.48905679 | 0.62408 | 0.81749153 |
| ! | RNA polymerase II transcription mediator activity | GO:0016455 | 41 | 18 | 0.49394685 | 0.62408 | 0.81695512 |
| ! | regulation of inflammatory response | GO:0050727 | 35 | 18 | 0.48608984 | 0.62408 | 0.81641941 |
| ! | eta DNA polymerase activity | GO:0015999 | 25 | 13 | 0.47668632 | 0.62475 | 0.81676032 |
| ! | acetylcholine receptor signaling, muscarinic pathway | GO:0007213 | 22 | 13 | 0.47914643 | 0.62475 | 0.81622544 |
| ! | ubiquitin activating enzyme activity | GO:0004839 | 24 | 8 | 0.46295705 | 0.62643 | 0.81788472 |
| ! | GTPase inhibitor activity | GO:0005095 | 13 | 8 | 0.46225249 | 0.62643 | 0.8173498 |
| ! | nuclear lamina | GO:0005652 | 16 | 8 | 0.46076456 | 0.62643 | 0.81681559 |
| ! | negative regulation of mitotic cell cycle | GO:0045930 | 15 | 8 | 0.46473169 | 0.62643 | 0.81628207 |
| ! | hyperosmotic response | GO:0006972 | 22 | 14 | 0.48552899 | 0.62898 | 0.81906991 |
| ! | melatonin receptor activity | GO:0008502 | 19 | 14 | 0.47613864 | 0.62898 | 0.81853562 |
| ! | MHC protein binding | GO:0042287 | 36 | 19 | 0.49278238 | 0.62949 | 0.81866529 |
| ! | protein amino acid acetylation | GO:0006473 | 47 | 20 | 0.49065329 | 0.6318 | 0.8211342 |
| ! | regulation of axon extension | GO:0030516 | 45 | 20 | 0.48899455 | 0.6318 | 0.82059961 |
| ! | prostaglandin metabolism | GO:0006693 | 45 | 30 | 0.50356212 | 0.63208 | 0.82042915 |
| ! | ATP-dependent DNA helicase activity | GO:0004003 | 33 | 15 | 0.48378727 | 0.63416 | 0.82259376 |
| ! | voltage-gated sodium channel activity | GO:0005248 | 26 | 15 | 0.47880687 | 0.63416 | 0.82205926 |
| ! | inward rectifier potassium channel activity | GO:0005242 | 29 | 15 | 0.4808616 | 0.63416 | 0.82152545 |
| ! | positive regulation of secretion | GO:0051047 | 14 | 11 | 0.46820857 | 0.63493 | 0.8219892 |
| ! | serotonin receptor activity | GO:0004993 | 31 | 21 | 0.49180801 | 0.63639 | 0.82334504 |
| ! | N-acyltransferase activity | GO:0016410 | 122 | 57 | 0.50631994 | 0.63669 | 0.82319932 |
| ! | apoptotic protease activator activity | GO:0016505 | 21 | 12 | 0.46719007 | 0.64328 | 0.83118109 |
| ! | growth hormone-releasing hormone receptor activity | GO:0016520 | 23 | 16 | 0.48009586 | 0.64341 | 0.83081097 |
| ! | establishment of tissue polarity | GO:0007164 | 19 | 10 | 0.45943631 | 0.64403 | 0.83107364 |
| ! | DNA unwinding | GO:0006268 | 20 | 10 | 0.46092709 | 0.64403 | 0.83053643 |
| ! | RNA helicase activity | GO:0003724 | 76 | 35 | 0.49606607 | 0.64413 | 0.83012878 |
| ! | ionotropic glutamate receptor complex | GO:0008328 | 13 | 8 | 0.44945605 | 0.64718 | 0.83352105 |
| ! | regulation of calcium ion-dependent exocytosis | GO:0017158 | 12 | 8 | 0.45510923 | 0.64718 | 0.83298329 |
| ! | cysteine protease inhibitor activity | GO:0004869 | 54 | 36 | 0.50349848 | 0.64751 | 0.8328707 |
| ! | nerve ensheathment | GO:0008366 | 72 | 37 | 0.49752772 | 0.64965 | 0.83508489 |
| ! | cholesterol binding | GO:0015485 | 26 | 13 | 0.47345111 | 0.65041 | 0.83552347 |
| ! | nerve maturation | GO:0042551 | 76 | 38 | 0.50091232 | 0.65042 | 0.83499865 |
| ! | inorganic anion exchanger activity | GO:0005452 | 16 | 9 | 0.44996405 | 0.65379 | 0.83878524 |
| ! | forelimb morphogenesis | GO:0035136 | 18 | 9 | 0.45430918 | 0.65379 | 0.83824618 |
| ! | regulation of B-cell differentiation | GO:0045577 | 17 | 9 | 0.4504115 | 0.65379 | 0.8377078 |

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|---|---|---|---|---|---|---|---|
| ! | caspase regulator activity | GO:0043028 | 27 | 14 | 0.47054786 | 0.65511 | 0.83886037 |
| ! | regulation of vasoconstriction | GO:0019229 | 16 | 11 | 0.46376317 | 0.6582 | 0.84227646 |
| ! | regulation of cell volume | GO:0006884 | 23 | 11 | 0.46551423 | 0.6582 | 0.84173654 |
| ! | positive regulation of endocytosis | GO:0045807 | 38 | 19 | 0.48126324 | 0.65966 | 0.84306323 |
| ! | syntaxin binding | GO:0019905 | 50 | 19 | 0.47721786 | 0.65966 | 0.8425235 |
| ! | response to osmotic stress | GO:0006970 | 51 | 27 | 0.49398505 | 0.66035 | 0.84286516 |
| ! | RNA polymerase II transcription factor activity, enhancer binding | GO:0003705 | 67 | 27 | 0.48884581 | 0.66035 | 0.84232625 |
| ! | anaphylatoxin receptor activity | GO:0004942 | 23 | 15 | 0.47114296 | 0.66201 | 0.84390412 |
| ! | regulation of protein secretion | GO:0050708 | 28 | 15 | 0.47454406 | 0.66201 | 0.84336523 |
| ! | nucleosome | GO:0005718 | 34 | 20 | 0.47923801 | 0.66322 | 0.84436752 |
| ! | dendrite | GO:0030425 | 53 | 29 | 0.49036179 | 0.66523 | 0.84638638 |
| ! | regulation of action potential | GO:0001508 | 89 | 44 | 0.49843858 | 0.66533 | 0.84597409 |
| ! | catecholamine biosynthesis | GO:0042423 | 18 | 10 | 0.45149291 | 0.66684 | 0.84735401 |
| ! | glucosidase activity | GO:0015926 | 16 | 10 | 0.45567474 | 0.66684 | 0.84681464 |
| ! | pancreatic elastase I activity | GO:0008125 | 15 | 12 | 0.46400697 | 0.66762 | 0.84726584 |
| ! | myo-inositol metabolism | GO:0006020 | 11 | 8 | 0.44053079 | 0.66763 | 0.84673989 |
| ! | pigment cell differentiation | GO:0050931 | 19 | 8 | 0.44416359 | 0.66763 | 0.84620194 |
| ! | DNA-dependent DNA replication | GO:0006261 | 188 | 84 | 0.51155732 | 0.66835 | 0.84657667 |
| ! | receptor mediated endocytosis | GO:0006898 | 115 | 47 | 0.49763351 | 0.67041 | 0.84864718 |
| ! | chromosome, telomeric region | GO:0000781 | 37 | 16 | 0.46685004 | 0.67134 | 0.84928554 |
| ! | humoral defense mechanism (sensu Protostomia) | GO:0016065 | 38 | 16 | 0.46893657 | 0.67134 | 0.84874734 |
| ! | hyaluronic acid binding | GO:0005540 | 39 | 16 | 0.46911447 | 0.67134 | 0.84820982 |
| ! | positive regulation of lymphocyte activation | GO:0051251 | 98 | 49 | 0.49731998 | 0.67511 | 0.8524332 |
| ! | guanylate cyclase activity | GO:0004383 | 28 | 17 | 0.47158442 | 0.67573 | 0.85267638 |
| ! | activation of JNK | GO:0007257 | 56 | 23 | 0.4796154 | 0.67804 | 0.85505044 |
| ! | regulation of protein catabolism | GO:0042176 | 70 | 33 | 0.49460828 | 0.67866 | 0.85529166 |
| ! | interleukin-2 biosynthesis | GO:0042094 | 24 | 14 | 0.460289 | 0.68078 | 0.85742178 |
| ! | F-actin capping activity | GO:0003782 | 33 | 11 | 0.45249457 | 0.68192 | 0.85831571 |
| ! | circadian rhythm | GO:0007623 | 101 | 53 | 0.50260545 | 0.68196 | 0.85782484 |
| ! | positive regulation of lymphocyte proliferation | GO:0050671 | 46 | 24 | 0.47945313 | 0.68282 | 0.85836541 |
| ! | response to pheromone | GO:0019236 | 28 | 24 | 0.48049626 | 0.68282 | 0.85782487 |
| ! | glucuronosyltransferase activity | GO:0015020 | 31 | 15 | 0.46314066 | 0.68871 | 0.86467996 |
| ! | negative regulation of blood coagulation | GO:0030195 | 22 | 15 | 0.46027011 | 0.68871 | 0.86413613 |
| ! | cyclin-dependent protein kinase activity | GO:0004693 | 29 | 15 | 0.46273733 | 0.68871 | 0.86359299 |
| ! | oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, NAD or NADH as one donor, and incorporation of one atom of oxygen | GO:0016709 | 44 | 26 | 0.48174512 | 0.68997 | 0.86462949 |
| ! | regulation of neuronal synaptic plasticity | GO:0048168 | 51 | 26 | 0.48457787 | 0.68997 | 0.86408672 |
| ! | protein phosphorylated amino acid binding | GO:0045309 | 25 | 10 | 0.43803399 | 0.69003 | 0.86361973 |
| ! | sarcoplasmic reticulum | GO:0016529 | 19 | 10 | 0.43833708 | 0.69003 | 0.86307828 |
| ! | sodium:potassium-exchanging ATPase activity | GO:0005391 | 25 | 10 | 0.44623111 | 0.69003 | 0.8625375 |
| ! | vesicle transport along actin filament | GO:0030050 | 17 | 10 | 0.4389469 | 0.69003 | 0.8619974 |
| ! | amiloride-sensitive sodium channel activity | GO:0015280 | 11 | 10 | 0.4426582 | 0.69003 | 0.86145798 |

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|---|---|---|---|---|---|---|
| ! | iota DNA polymerase activity | GO:0016000 | 22 | 12 | 0.44905917 | 0.69272 | 0.86427542 |
| ! | deoxycytidyl transferase activity | GO:0017125 | 22 | 12 | 0.44815565 | 0.69272 | 0.86373525 |
| ! | acetylgalactosaminyltransferase activity | GO:0008376 | 46 | 20 | 0.47385501 | 0.69395 | 0.86472845 |
| ! | sphingolipid biosynthesis | GO:0030148 | 40 | 20 | 0.46938425 | 0.69395 | 0.86418867 |
| ! | zinc ion transporter activity | GO:0005385 | 12 | 9 | 0.4361976 | 0.69627 | 0.8665369 |
| ! | mesoderm morphogenesis | GO:0048332 | 63 | 27 | 0.47693423 | 0.69628 | 0.8660091 |
| ! | chaperone cofactor dependent protein folding | GO:0051085 | 40 | 16 | 0.46610023 | 0.69914 | 0.86902449 |
| ! | urea cycle intermediate metabolism | GO:0000051 | 23 | 13 | 0.45550742 | 0.70127 | 0.8711293 |
| ! | interstitial collagenase activity | GO:0004232 | 21 | 13 | 0.45369555 | 0.70127 | 0.87058721 |
| ! | regulation of B-cell activation | GO:0050864 | 56 | 29 | 0.48150196 | 0.70179 | 0.87069095 |
| ! | positive regulation of phagocytosis | GO:0050766 | 25 | 14 | 0.45548907 | 0.70668 | 0.87621293 |
| ! | cytoskeletal adaptor activity | GO:0008093 | 36 | 14 | 0.45659653 | 0.70668 | 0.8756687 |
| ! | antigen receptor-mediated signaling pathway | GO:0050851 | 15 | 8 | 0.41946049 | 0.70673 | 0.87518706 |
| ! | embryonic forelimb morphogenesis | GO:0035115 | 14 | 8 | 0.42132858 | 0.70673 | 0.87464414 |
| ! | positive regulation of transcription factor activity | GO:0051091 | 19 | 8 | 0.42778379 | 0.70673 | 0.87410189 |
| ! | protein processing | GO:0016485 | 80 | 45 | 0.49424694 | 0.70937 | 0.87682351 |
| ! | regulation of osteoblast differentiation | GO:0045667 | 19 | 10 | 0.43596292 | 0.71232 | 0.87992471 |
| ! | amyloid precursor protein metabolism | GO:0042982 | 30 | 18 | 0.46062166 | 0.71235 | 0.87941723 |
| ! | mitotic spindle organization and biogenesis | GO:0007052 | 71 | 32 | 0.48164454 | 0.71272 | 0.87932987 |
| ! | keratin filament | GO:0045095 | 18 | 15 | 0.45137859 | 0.71453 | 0.88101814 |
| ! | kappa DNA polymerase activity | GO:0016450 | 23 | 12 | 0.4474702 | 0.71575 | 0.8819773 |
| ! | zeta DNA polymerase activity | GO:0003894 | 23 | 12 | 0.44229333 | 0.71575 | 0.88143287 |
| ! | chromosome, pericentric region | GO:0000775 | 111 | 47 | 0.48835396 | 0.71634 | 0.88161524 |
| ! | pyrimidine nucleoside metabolism | GO:0006213 | 24 | 9 | 0.42737695 | 0.71655 | 0.88132999 |
| ! | neuropeptide receptor activity | GO:0008188 | 113 | 76 | 0.49904552 | 0.71768 | 0.88217597 |
| ! | positive regulation of cell activation | GO:0050867 | 99 | 50 | 0.48819105 | 0.723 | 0.8881681 |
| ! | palmitoyl-CoA hydrolase activity | GO:0016290 | 25 | 20 | 0.46570381 | 0.72335 | 0.88805123 |
| ! | regulation of GTPase activity | GO:0043087 | 66 | 26 | 0.47220273 | 0.72398 | 0.88827804 |
| ! | pheromone binding | GO:0005550 | 31 | 26 | 0.4747894 | 0.72398 | 0.88773208 |
| ! | rhythmic process | GO:0048511 | 162 | 80 | 0.49527608 | 0.72401 | 0.88722356 |
| ! | positive regulation of T-cell activation | GO:0050870 | 71 | 34 | 0.47779772 | 0.72424 | 0.88696059 |
| ! | histone binding | GO:0042393 | 26 | 13 | 0.43882941 | 0.72575 | 0.88826457 |
| ! | negative regulation of protein catabolism | GO:0042177 | 31 | 13 | 0.44305672 | 0.72575 | 0.88771996 |
| ! | metalloendopeptidase inhibitor activity | GO:0008191 | 26 | 13 | 0.44456705 | 0.72575 | 0.88717601 |
| ! | regulation of caspase activation | GO:0043026 | 28 | 16 | 0.45271624 | 0.7258 | 0.88669382 |
| ! | dihydropyridine-sensitive calcium channel activity | GO:0015270 | 27 | 8 | 0.41423797 | 0.72604 | 0.88644419 |
| ! | negative regulation of cell differentiation | GO:0045596 | 96 | 51 | 0.49440605 | 0.72627 | 0.88618266 |
| ! | spindle microtubule | GO:0005876 | 22 | 11 | 0.43645397 | 0.72667 | 0.88612876 |
| ! | B-cell proliferation | GO:0042100 | 42 | 21 | 0.46148047 | 0.73022 | 0.88991381 |
| ! | negative regulation of protein biosynthesis | GO:0017148 | 41 | 21 | 0.46057767 | 0.73022 | 0.88937051 |
| ! | channel inhibitor activity | GO:0016248 | 31 | 21 | 0.46519445 | 0.73022 | 0.88882788 |
| ! | interleukin-1 binding | GO:0019966 | 26 | 17 | 0.44956815 | 0.73032 | 0.88840756 |
| ! | delta DNA polymerase activity | GO:0003891 | 28 | 14 | 0.44152965 | 0.73175 | 0.88960466 |
| ! | negative regulation of catabolism | GO:0009895 | 32 | 14 | 0.44634387 | 0.73175 | 0.88906288 |
| ! | B-cell mediated immunity | GO:0019724 | 23 | 10 | 0.42444003 | 0.73336 | 0.89047669 |

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|---|---|---|---|---|---|---|---|
| ! | antimicrobial humoral response (sensu Vertebrata) | GO:0019735 | 168 | 88 | 0.49590751 | 0.73474 | 0.89160967 |
| ! | dopamine receptor, adenylate cyclase activating pathway | GO:0007191 | 12 | 9 | 0.41499917 | 0.73686 | 0.89363872 |
| ! | histone deacetylase activity | GO:0004407 | 16 | 12 | 0.4288748 | 0.73872 | 0.89535018 |
| ! | specific transcriptional repressor activity | GO:0016566 | 27 | 15 | 0.4403662 | 0.73938 | 0.89560601 |
| ! | nuclear inner membrane | GO:0005637 | 35 | 15 | 0.44477562 | 0.73938 | 0.89506256 |
| ! | glutamate-gated ion channel activity | GO:0005234 | 37 | 18 | 0.4503578 | 0.74019 | 0.89549973 |
| ! | gap-junction forming channel activity | GO:0005243 | 31 | 18 | 0.45609252 | 0.74019 | 0.894957 |
| ! | hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in cyclic amidines | GO:0016814 | 42 | 23 | 0.4612568 | 0.74114 | 0.89556287 |
| ! | tissue homeostasis | GO:0001894 | 41 | 19 | 0.45248587 | 0.74614 | 0.9010589 |
| ! | regulation of axonogenesis | GO:0050770 | 81 | 32 | 0.46964869 | 0.74783 | 0.90255345 |
| ! | salivary gland morphogenesis | GO:0007435 | 29 | 11 | 0.42192866 | 0.74868 | 0.90303301 |
| ! | NLS-bearing substrate-nucleus import | GO:0006607 | 25 | 11 | 0.42262023 | 0.74868 | 0.90248737 |
| ! | frizzled-2 signaling pathway | GO:0007223 | 33 | 20 | 0.4479968 | 0.75183 | 0.90573723 |
| ! | cilium | GO:0005929 | 46 | 25 | 0.45726087 | 0.75208 | 0.90549161 |
| ! | metabotropic glutamate receptor signaling pathway | GO:0007216 | 17 | 10 | 0.41246151 | 0.7537 | 0.90689475 |
| ! | arsenate reductase (thioredoxin) activity | GO:0030612 | 21 | 10 | 0.41308375 | 0.7537 | 0.9063481 |
| ! | phototransduction, visible light | GO:0007603 | 15 | 10 | 0.41309625 | 0.7537 | 0.90580211 |
| ! | blastoderm segmentation | GO:0007350 | 19 | 9 | 0.40687203 | 0.75608 | 0.90811535 |
| ! | formation of primary germ layer | GO:0001704 | 61 | 26 | 0.46041229 | 0.7561 | 0.90759296 |
| ! | fibroblast growth factor receptor binding | GO:0005104 | 46 | 26 | 0.46304509 | 0.7561 | 0.9070472 |
| ! | keratinocyte differentiation | GO:0030216 | 31 | 17 | 0.43858632 | 0.75698 | 0.90755715 |
| ! | condensed chromosome | GO:0000793 | 103 | 47 | 0.48336219 | 0.75903 | 0.90946838 |
| ! | transferase activity, transferring sulfur-containing groups | GO:0016782 | 67 | 48 | 0.47765761 | 0.75963 | 0.90964097 |
| ! | arginine metabolism | GO:0006525 | 22 | 12 | 0.4253643 | 0.76071 | 0.91038779 |
| ! | purine ribonucleoside monophosphate biosynthesis | GO:0009168 | 20 | 12 | 0.42280517 | 0.76071 | 0.909842 |
| ! | dipeptidase activity | GO:0016805 | 23 | 12 | 0.42619938 | 0.76071 | 0.90929685 |
| ! | interleukin-1 receptor activity | GO:0004908 | 23 | 15 | 0.43088027 | 0.76265 | 0.91106991 |
| ! | regulation of neurogenesis | GO:0050767 | 160 | 70 | 0.48589337 | 0.76341 | 0.91143205 |
| ! | long-chain-fatty-acid-CoA ligase activity | GO:0004467 | 11 | 8 | 0.39557604 | 0.76435 | 0.91200852 |
| ! | extracellular matrix constituent, lubricant activity | GO:0030197 | 11 | 8 | 0.39779612 | 0.76435 | 0.91146339 |
| ! | locomotory behavior | GO:0007626 | 150 | 73 | 0.48979187 | 0.76771 | 0.91492321 |
| ! | lysosomal membrane | GO:0005765 | 40 | 18 | 0.44604313 | 0.7678 | 0.91448418 |
| ! | blood coagulation factor activity | GO:0003801 | 16 | 11 | 0.41307862 | 0.76963 | 0.91611686 |
| ! | cartilage condensation | GO:0001502 | 42 | 23 | 0.45514916 | 0.77159 | 0.91790224 |
| ! | barbed-end actin filament capping | GO:0051016 | 28 | 10 | 0.40100865 | 0.77365 | 0.91980438 |
| ! | pancreatic elastase II activity | GO:0004281 | 13 | 10 | 0.40882176 | 0.77365 | 0.91925655 |
| ! | female sex differentiation | GO:0046660 | 53 | 24 | 0.45487284 | 0.77486 | 0.92014625 |
| ! | protein prenylation | GO:0018342 | 49 | 24 | 0.4554068 | 0.77486 | 0.91959887 |
| ! | negative regulation of JNK cascade | GO:0046329 | 19 | 9 | 0.39817098 | 0.77526 | 0.91952658 |
| ! | positive regulation of inflammatory response | GO:0050729 | 19 | 9 | 0.39247422 | 0.77526 | 0.91898021 |
| ! | ureteric bud development | GO:0001657 | 43 | 16 | 0.42896261 | 0.77587 | 0.91915716 |
| ! | icosanoid metabolism | GO:0006690 | 83 | 55 | 0.47850537 | 0.77716 | 0.92013899 |

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|---|---|---|---|---|---|---|---|
| ! | phosphoinositide phospholipase C activity | GO:0004435 | 46 | 20 | 0.44596166 | 0.77821 | 0.92083568 |
| ! | isoprenoid binding | GO:0019840 | 19 | 14 | 0.42369255 | 0.77993 | 0.92232386 |
| ! | antiviral response protein activity | GO:0003800 | 19 | 12 | 0.41817374 | 0.78174 | 0.92391665 |
| ! | response to pain | GO:0048265 | 14 | 8 | 0.38635878 | 0.78228 | 0.92400746 |
| ! | mRNA cleavage | GO:0006379 | 14 | 8 | 0.38806302 | 0.78228 | 0.92346071 |
| ! | collagenase activity | GO:0008133 | 29 | 17 | 0.43330546 | 0.78234 | 0.92298539 |
| ! | DNA modification | GO:0006304 | 137 | 59 | 0.4774848 | 0.78411 | 0.92452686 |
| ! | deacetylase activity | GO:0019213 | 19 | 15 | 0.42642701 | 0.78564 | 0.9257837 |
| ! | protein-hormone receptor activity | GO:0016500 | 31 | 15 | 0.42581507 | 0.78564 | 0.92523719 |
| ! | sodium channel activity | GO:0005272 | 38 | 26 | 0.45030881 | 0.78586 | 0.92495027 |
| ! | chromosome segregation | GO:0007059 | 112 | 43 | 0.47165418 | 0.78601 | 0.92458134 |
| ! | anion exchanger activity | GO:0015380 | 21 | 11 | 0.40741607 | 0.78981 | 0.9285038 |
| ! | fatty-acid ligase activity | GO:0015645 | 17 | 11 | 0.40511592 | 0.78981 | 0.92795698 |
| ! | alpha DNA polymerase activity | GO:0003889 | 26 | 13 | 0.41311569 | 0.79298 | 0.93113308 |
| ! | adult walking behavior | GO:0007628 | 27 | 10 | 0.39385166 | 0.79389 | 0.93165326 |
| ! | protein autoprocessing | GO:0016540 | 13 | 10 | 0.39394849 | 0.79389 | 0.93110556 |
| ! | pancreatic elastase activity | GO:0008132 | 30 | 23 | 0.44534772 | 0.79921 | 0.93679433 |
| ! | dendrite morphogenesis | GO:0016358 | 47 | 23 | 0.44454021 | 0.79921 | 0.93624425 |
| ! | Z disc | GO:0030018 | 31 | 16 | 0.4271157 | 0.79966 | 0.93622165 |
| ! | hormone biosynthesis | GO:0042446 | 87 | 48 | 0.47554978 | 0.79999 | 0.93605868 |
| ! | protein-lysine 6-oxidase activity | GO:0004720 | 23 | 12 | 0.40390807 | 0.80242 | 0.93835164 |
| ! | phospholipase C activity | GO:0004629 | 54 | 24 | 0.43950244 | 0.80279 | 0.93823436 |
| ! | negative regulation of coagulation | GO:0050819 | 36 | 24 | 0.4472617 | 0.80279 | 0.93768504 |
| ! | chloride transport | GO:0006821 | 136 | 67 | 0.48495606 | 0.80301 | 0.93739318 |
| ! | regulation of DNA metabolism | GO:0051052 | 86 | 38 | 0.46474027 | 0.8038 | 0.93776667 |
| ! | double-stranded RNA binding | GO:0003725 | 93 | 38 | 0.46551706 | 0.8038 | 0.93721859 |
| ! | Rac protein signal transduction | GO:0016601 | 45 | 17 | 0.42105478 | 0.80594 | 0.93916489 |
| ! | DNA methylation | GO:0006306 | 121 | 50 | 0.47152328 | 0.80606 | 0.93875639 |
| ! | platelet activation | GO:0030168 | 42 | 25 | 0.44063657 | 0.80964 | 0.94237561 |
| ! | lysosphingolipid and lysophosphatidic acid receptor activity | GO:0001619 | 19 | 11 | 0.39980258 | 0.80997 | 0.94221 |
| ! | odorant binding | GO:0005549 | 38 | 32 | 0.45696378 | 0.81399 | 0.94633453 |
| ! | calcium-transporting ATPase activity | GO:0005388 | 19 | 8 | 0.37059981 | 0.81638 | 0.94856034 |
| ! | intercellular canaliculus | GO:0046581 | 14 | 8 | 0.36433276 | 0.81638 | 0.94800821 |
| ! | actin filament binding | GO:0051015 | 38 | 18 | 0.42591838 | 0.81705 | 0.94823429 |
| ! | chloride transporter activity | GO:0015108 | 33 | 18 | 0.42786861 | 0.81705 | 0.94768299 |
| ! | odontogenesis (sensu Vertebrata) | GO:0042475 | 47 | 18 | 0.42151173 | 0.81705 | 0.94713234 |
| ! | DNA replication initiation | GO:0006270 | 54 | 22 | 0.43736524 | 0.81813 | 0.94783354 |
| ! | pyrimidine ribonucleotide biosynthesis | GO:0009220 | 27 | 16 | 0.41262554 | 0.8221 | 0.95188015 |
| ! | nucleoside-diphosphate kinase activity | GO:0004550 | 22 | 14 | 0.40471699 | 0.82269 | 0.95201076 |
| ! | transmembrane receptor protein tyrosine kinase signaling protein activity | GO:0005066 | 181 | 79 | 0.48168434 | 0.8233 | 0.95216435 |
| ! | tumor necrosis factor receptor binding | GO:0005164 | 32 | 20 | 0.42575123 | 0.82768 | 0.95667532 |
| ! | regulation of mitotic cell cycle | GO:0007346 | 34 | 20 | 0.42253111 | 0.82768 | 0.95612137 |
| ! | hydrogen-translocating V-type ATPase complex | GO:0016471 | 28 | 11 | 0.38986187 | 0.82856 | 0.95658403 |

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|---|---|---|---|---|---|---|---|
| ! | detection of visible light | GO:0009584 | 16 | 11 | 0.38761384 | 0.82856 | 0.95603077 |
| ! | aryl sulfotransferase activity | GO:0004062 | 10 | 9 | 0.36290051 | 0.82879 | 0.95574338 |
| ! | GPI-anchored membrane-bound receptor | GO:0015025 | 14 | 9 | 0.36699885 | 0.82879 | 0.95519125 |
| ! | sterol transport | GO:0015918 | 13 | 9 | 0.3636541 | 0.82879 | 0.95463975 |
| ! | positive regulation of axonogenesis | GO:0050772 | 25 | 9 | 0.36748012 | 0.82879 | 0.95408889 |
| ! | pyrimidine nucleoside triphosphate metabolism | GO:0009147 | 29 | 17 | 0.4185815 | 0.82886 | 0.9536192 |
| ! | proteoglycan metabolism | GO:0006029 | 51 | 29 | 0.44584814 | 0.82907 | 0.95331104 |
| ! | nuclear body | GO:0016604 | 44 | 24 | 0.43427011 | 0.82929 | 0.95301472 |
| ! | N-linked glycosylation | GO:0006487 | 84 | 46 | 0.45889798 | 0.83102 | 0.95445302 |
| ! | pronucleus | GO:0045120 | 16 | 8 | 0.35782654 | 0.83217 | 0.95522391 |
| ! | indole and derivative metabolism | GO:0042430 | 13 | 8 | 0.35322077 | 0.83217 | 0.95467461 |
| ! | N-acetyltransferase activity | GO:0008080 | 100 | 47 | 0.46352883 | 0.83287 | 0.95492853 |
| ! | kinetochore | GO:0000776 | 63 | 25 | 0.43630267 | 0.83537 | 0.95724477 |
| ! | peripheral nervous system development | GO:0007422 | 129 | 64 | 0.46731627 | 0.83687 | 0.95841312 |
| ! | regulation of blood coagulation | GO:0030193 | 25 | 18 | 0.41672707 | 0.83975 | 0.96115964 |
| ! | cornified envelope | GO:0001533 | 25 | 12 | 0.38419606 | 0.84008 | 0.96098601 |
| ! | antimicrobial humoral response | GO:0019730 | 171 | 91 | 0.48189209 | 0.84141 | 0.96195585 |
| ! | mitotic checkpoint | GO:0007093 | 33 | 16 | 0.40857211 | 0.84324 | 0.96349588 |
| ! | mediator complex | GO:0000119 | 39 | 16 | 0.40346167 | 0.84324 | 0.96294436 |
| ! | mismatch repair | GO:0006298 | 37 | 19 | 0.41262831 | 0.84477 | 0.96413967 |
| ! | heavy metal ion transporter activity | GO:0015076 | 18 | 9 | 0.35392149 | 0.84534 | 0.96423859 |
| ! | basic amino acid transporter activity | GO:0015174 | 18 | 9 | 0.35350415 | 0.84534 | 0.9636876 |
| ! | viral envelope | GO:0019031 | 22 | 11 | 0.37456286 | 0.8466 | 0.96457282 |
| ! | ankyrin binding | GO:0030506 | 17 | 10 | 0.36362192 | 0.84726 | 0.9647738 |
| ! | protein stabilization | GO:0050821 | 19 | 10 | 0.36502213 | 0.84726 | 0.96422345 |
| ! | peptide YY receptor activity | GO:0001601 | 11 | 8 | 0.34549325 | 0.84736 | 0.96378746 |
| ! | mRNA modification | GO:0016556 | 13 | 8 | 0.35195623 | 0.84736 | 0.96323829 |
| ! | spliceosome complex | GO:0005681 | 163 | 69 | 0.47095768 | 0.84776 | 0.96314419 |
| ! | hydrolase activity, hydrolyzing O-glycosyl compounds | GO:0004553 | 189 | 96 | 0.48134518 | 0.848 | 0.96286853 |
| ! | perception of pain | GO:0019233 | 31 | 17 | 0.40099495 | 0.8497 | 0.96425 |
| ! | nuclear matrix | GO:0016363 | 45 | 17 | 0.40626551 | 0.8497 | 0.96370182 |
| ! | adult locomotory behavior | GO:0008344 | 46 | 20 | 0.41417955 | 0.85039 | 0.96393639 |
| ! | receptor regulator activity | GO:0030545 | 18 | 13 | 0.38210339 | 0.85226 | 0.9655075 |
| ! | myelination | GO:0042552 | 51 | 29 | 0.42942879 | 0.85523 | 0.96832228 |
| ! | response to pathogen | GO:0042828 | 62 | 44 | 0.451216 | 0.85587 | 0.96849725 |
| ! | histone acetyltransferase activity | GO:0004402 | 28 | 12 | 0.37361457 | 0.85753 | 0.9698256 |
| ! | toxin activity | GO:0015070 | 18 | 12 | 0.37456834 | 0.85753 | 0.96927612 |
| ! | integrin binding | GO:0005178 | 93 | 45 | 0.4568527 | 0.85845 | 0.96976656 |
| ! | proteoglycan biosynthesis | GO:0030166 | 35 | 21 | 0.41498825 | 0.85893 | 0.96975968 |
| ! | cellular nerve ensheathment | GO:0042553 | 52 | 30 | 0.4299103 | 0.86016 | 0.9705991 |
| ! | response to pathogenic bacteria | GO:0009618 | 41 | 30 | 0.42990403 | 0.86016 | 0.97005042 |
| ! | B-cell homeostasis | GO:0001782 | 24 | 9 | 0.34365749 | 0.86113 | 0.97059568 |
| ! | snoRNA binding | GO:0030515 | 13 | 9 | 0.35116307 | 0.86113 | 0.97004763 |
| ! | cell wall organization and biogenesis | GO:0007047 | 18 | 9 | 0.3456615 | 0.86113 | 0.9695002 |
| ! | coreceptor activity | GO:0015026 | 55 | 31 | 0.43605025 | 0.86483 | 0.97311667 |

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|---|---|---|---|---|---|---|---|
| ! | C-X-C chemokine receptor activity | GO:0016494 | 27 | 19 | 0.40076641 | 0.8657 | 0.97354651 |
| ! | trypsin inhibitor activity | GO:0030304 | 23 | 13 | 0.37760217 | 0.86925 | 0.97698803 |
| ! | regulation of coagulation | GO:0050818 | 39 | 27 | 0.41967838 | 0.87158 | 0.97905524 |
| ! | C-X-C chemokine binding | GO:0019958 | 28 | 20 | 0.39991683 | 0.87163 | 0.97856041 |
| ! | synaptonemal complex | GO:0000795 | 19 | 12 | 0.36860453 | 0.87384 | 0.98048976 |
| ! | bioactive lipid receptor activity | GO:0045125 | 20 | 12 | 0.36972772 | 0.87384 | 0.97993862 |
| ! | protein disulfide isomerase activity | GO:0003756 | 15 | 9 | 0.34030249 | 0.87558 | 0.98133826 |
| ! | phosphatidylinositol-4,5-bisphosphate hydrolysis | GO:0007203 | 19 | 8 | 0.33268647 | 0.87625 | 0.98153776 |
| ! | protein prenyltransferase activity | GO:0008318 | 50 | 24 | 0.4175844 | 0.8765 | 0.98126684 |
| ! | lymphocyte proliferation | GO:0046651 | 116 | 66 | 0.46485069 | 0.87804 | 0.9824396 |
| ! | death receptor binding | GO:0005123 | 17 | 10 | 0.34427394 | 0.87814 | 0.98200073 |
| ! | purine ribonucleoside monophosphate metabolism | GO:0009167 | 24 | 14 | 0.37800606 | 0.87827 | 0.98159588 |
| ! | opioid receptor activity | GO:0004985 | 24 | 14 | 0.37955119 | 0.87827 | 0.98104628 |
| ! | tissue kallikrein activity | GO:0004293 | 38 | 29 | 0.42025348 | 0.87847 | 0.98072057 |
| ! | DNA-dependent ATPase activity | GO:0008094 | 73 | 34 | 0.43104565 | 0.87867 | 0.98039522 |
| ! | negative regulation of angiogenesis | GO:0016525 | 30 | 18 | 0.396005 | 0.87873 | 0.97991411 |
| ! | intercellular junction maintenance | GO:0045217 | 13 | 11 | 0.35455333 | 0.87897 | 0.97963416 |
| ! | glycosphingolipid biosynthesis | GO:0006688 | 24 | 11 | 0.35727917 | 0.87897 | 0.97908719 |
| ! | mesoderm cell differentiation | GO:0048333 | 24 | 11 | 0.35682088 | 0.87897 | 0.97854082 |
| ! | glycolipid biosynthesis | GO:0009247 | 31 | 16 | 0.38283901 | 0.88084 | 0.98007574 |
| ! | hematopoietin/interferon-class (D200-domain) cytokine receptor activity | GO:0004896 | 166 | 90 | 0.47548158 | 0.88137 | 0.98011881 |
| ! | T-cell activation | GO:0042110 | 175 | 92 | 0.46718024 | 0.88433 | 0.98286259 |
| ! | synaptic vesicle endocytosis | GO:0008099 | 36 | 15 | 0.37947227 | 0.8845 | 0.98250418 |
| ! | UTP biosynthesis | GO:0006228 | 18 | 13 | 0.37092724 | 0.88536 | 0.98291219 |
| ! | immune cell homeostasis | GO:0001776 | 30 | 13 | 0.36505669 | 0.88536 | 0.98236552 |
| ! | hindbrain development | GO:0030902 | 29 | 9 | 0.3285452 | 0.88919 | 0.98606673 |
| ! | adenosine deaminase activity | GO:0004000 | 15 | 8 | 0.31481312 | 0.88926 | 0.9855965 |
| ! | nitrogen compound catabolism | GO:0044270 | 14 | 8 | 0.31911578 | 0.88926 | 0.98504925 |
| ! | prostaglandin receptor activity | GO:0004955 | 16 | 8 | 0.3185028 | 0.88926 | 0.98450261 |
| ! | maintenance of fidelity during DNA-dependent DNA replication | GO:0045005 | 39 | 20 | 0.39465699 | 0.89067 | 0.98551672 |
| ! | lipid kinase activity | GO:0001727 | 60 | 27 | 0.41076456 | 0.8926 | 0.98710477 |
| ! | heavy metal ion transport | GO:0006823 | 23 | 11 | 0.34315935 | 0.89352 | 0.98757474 |
| ! | icosanoid biosynthesis | GO:0046456 | 41 | 28 | 0.41470947 | 0.89627 | 0.9900657 |
| ! | response to hormone stimulus | GO:0009725 | 32 | 16 | 0.37646128 | 0.89669 | 0.98998149 |
| ! | embryonic development (sensu Vertebrata) | GO:0043009 | 160 | 79 | 0.46086884 | 0.89859 | 0.99153045 |
| ! | sulfotransferase activity | GO:0008146 | 55 | 41 | 0.43290663 | 0.89976 | 0.99227264 |
| ! | hexosaminidase activity | GO:0015929 | 20 | 13 | 0.35236476 | 0.90048 | 0.99251801 |
| ! | G-protein signaling, adenylate cyclase inhibiting pathway | GO:0007193 | 79 | 51 | 0.44646389 | 0.90174 | 0.99335798 |
| ! | death receptor adaptor protein activity | GO:0005037 | 9 | 8 | 0.30712677 | 0.9019 | 0.99298593 |
| ! | defense/immunity protein activity | GO:0003793 | 61 | 35 | 0.4205266 | 0.9019 | 0.99243822 |
| ! | phosphoinositide 3-kinase complex | GO:0005942 | 28 | 12 | 0.34517184 | 0.90308 | 0.99318886 |
| ! | F-actin capping protein complex | GO:0008290 | 25 | 10 | 0.32455264 | 0.90506 | 0.99481802 |

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|---|---|---|---|---|---|---|---|
| ! | traversing start control point of mitotic cell cycle | GO:0007089 | 14 | 10 | 0.32918004 | 0.90506 | 0.99427021 |
| ! | intramolecular oxidoreductase activity, interconverting keto- and enol-groups | GO:0016862 | 16 | 10 | 0.33063183 | 0.90506 | 0.993723 |
| ! | receptor inhibitor activity | GO:0030547 | 13 | 10 | 0.33035813 | 0.90506 | 0.9931764 |
| ! | positive regulation of neurogenesis | GO:0050769 | 64 | 26 | 0.40262326 | 0.90626 | 0.99394651 |
| ! | glutamate receptor activity | GO:0008066 | 61 | 37 | 0.42082493 | 0.90912 | 0.99653538 |
| ! | apical plasma membrane | GO:0016324 | 107 | 54 | 0.44418521 | 0.90916 | 0.99603196 |
| ! | M phase specific microtubule process | GO:0000072 | 30 | 18 | 0.37164767 | 0.91201 | 0.9986059 |
| ! | adult behavior | GO:0030534 | 50 | 24 | 0.39691351 | 0.91284 | 0.99896643 |
| ! | hydrogen:potassium-exchanging ATPase activity | GO:0008900 | 15 | 8 | 0.30144754 | 0.91357 | 0.99921719 |
| ! | cleavage of lamin | GO:0006922 | 9 | 8 | 0.29965759 | 0.91357 | 0.99866967 |
| ! | DNA helicase activity | GO:0003678 | 68 | 28 | 0.40386468 | 0.9147 | 0.99935734 |
| ! | scavenger receptor activity | GO:0005044 | 52 | 33 | 0.41237512 | 0.91493 | 0.99906149 |
| ! | protein secretion | GO:0009306 | 97 | 48 | 0.43738093 | 0.91672 | 1.00046849 |
| ! | embryonic eye morphogenesis | GO:0048048 | 53 | 30 | 0.40729117 | 0.92298 | 1.00674964 |
| ! | kainate selective glutamate receptor activity | GO:0015277 | 14 | 8 | 0.29096517 | 0.92411 | 1.00743139 |
| ! | SH2 domain binding | GO:0042169 | 20 | 8 | 0.28663272 | 0.92411 | 1.00688119 |
| ! | odontogenesis | GO:0042476 | 55 | 23 | 0.38936924 | 0.92464 | 1.00690873 |
| ! | negative regulation of B-cell activation | GO:0050869 | 16 | 9 | 0.29617369 | 0.92521 | 1.00697979 |
| ! | icosanoid receptor activity | GO:0004953 | 17 | 9 | 0.29729005 | 0.92521 | 1.00643073 |
| ! | induction of programmed cell death by hormones | GO:0035081 | 12 | 9 | 0.29679626 | 0.92521 | 1.00588226 |
| ! | protein amino acid prenylation | GO:0018346 | 40 | 18 | 0.3666119 | 0.92528 | 1.00541046 |
| ! | positive regulation of immune response | GO:0050778 | 147 | 79 | 0.45106197 | 0.92589 | 1.00552561 |
| ! | eye morphogenesis (sensu Vertebrata) | GO:0043010 | 54 | 31 | 0.40859246 | 0.92647 | 1.00560808 |
| ! | leukotriene biosynthesis | GO:0019370 | 17 | 12 | 0.33204563 | 0.92742 | 1.00609184 |
| ! | metanephros development | GO:0001656 | 61 | 27 | 0.39290303 | 0.92859 | 1.00681361 |
| ! | mannosidase activity | GO:0015923 | 21 | 11 | 0.31629534 | 0.92967 | 1.00743707 |
| ! | regulation of T-cell activation | GO:0050863 | 86 | 45 | 0.42525228 | 0.92972 | 1.0069443 |
| ! | secretin-like receptor activity | GO:0001633 | 62 | 38 | 0.41544792 | 0.92992 | 1.00661443 |
| ! | SH3/SH2 adaptor protein activity | GO:0005070 | 154 | 66 | 0.44749751 | 0.93173 | 1.00802676 |
| ! | synapse organization and biogenesis | GO:0050808 | 178 | 84 | 0.45316364 | 0.93272 | 1.00855089 |
| ! | regulation of lymphocyte activation | GO:0051249 | 128 | 69 | 0.43802936 | 0.93394 | 1.00932302 |
| ! | transmembrane receptor protein tyrosine kinase docking protein activity | GO:0005069 | 157 | 68 | 0.44740154 | 0.93411 | 1.00896018 |
| ! | monocarboxylate porter activity | GO:0015355 | 11 | 8 | 0.28256459 | 0.93431 | 1.00863011 |
| ! | negative regulation of DNA metabolism | GO:0051053 | 13 | 9 | 0.28844173 | 0.93513 | 1.00896936 |
| ! | G-protein coupled receptor activity, unknown ligand | GO:0016526 | 54 | 40 | 0.41557049 | 0.93528 | 1.00858573 |
| ! | neurotransmitter biosynthesis | GO:0042136 | 20 | 16 | 0.35057552 | 0.93687 | 1.00975454 |
| ! | calcium-dependent cell-cell adhesion | GO:0016339 | 45 | 26 | 0.38594163 | 0.93701 | 1.00936012 |
| ! | interleukin binding | GO:0019965 | 95 | 57 | 0.43410822 | 0.93702 | 1.00882617 |
| ! | nuclear chromosome | GO:0000228 | 194 | 89 | 0.45626494 | 0.93819 | 1.00954102 |
| ! | cell fate specification | GO:0001708 | 17 | 12 | 0.31553964 | 0.93832 | 1.0091366 |
| ! | positive regulation of tumor necrosis factor-alpha biosynthesis | GO:0042535 | 14 | 11 | 0.31091827 | 0.93989 | 1.01028047 |
| ! | epidermal growth factor receptor signaling pathway | GO:0007173 | 69 | 31 | 0.3963567 | 0.9403 | 1.0101769 |

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|---|---|---|---|---|---|---|---|
| ! | lectin | GO:0005530 | 61 | 36 | 0.40840399 | 0.94111 | 1.01050293 |
| ! | neurexin binding | GO:0042043 | 31 | 21 | 0.37017619 | 0.9423 | 1.01123642 |
| ! | non-membrane spanning protein tyrosine kinase activity | GO:0004715 | 46 | 19 | 0.35720609 | 0.9424 | 1.0108 |
| ! | glycosphingolipid metabolism | GO:0006687 | 39 | 19 | 0.35305316 | 0.9424 | 1.01025685 |
| ! | negative regulation of T-cell proliferation | GO:0042130 | 12 | 9 | 0.28101057 | 0.94428 | 1.01172857 |
| ! | regulation of blood pressure | GO:0008217 | 104 | 63 | 0.4320888 | 0.94481 | 1.01175306 |
| ! | somatostatin receptor activity | GO:0004994 | 35 | 25 | 0.37684555 | 0.94677 | 1.01330802 |
| ! | embryonic development (sensu Mammalia) | GO:0001701 | 134 | 64 | 0.43686392 | 0.94708 | 1.0130963 |
| ! | interleukin receptor activity | GO:0004907 | 91 | 54 | 0.42207322 | 0.94863 | 1.01421053 |
| ! | alpha-sialidase activity | GO:0016997 | 29 | 15 | 0.32551468 | 0.94898 | 1.0140413 |
| ! | interleukin-1, Type I, activating binding | GO:0019967 | 18 | 11 | 0.29659593 | 0.94953 | 1.01408584 |
| ! | mesoderm cell fate commitment | GO:0001710 | 13 | 8 | 0.26319283 | 0.95048 | 1.0145573 |
| ! | Rac GTPase activator activity | GO:0030675 | 23 | 8 | 0.25971296 | 0.95048 | 1.01401476 |
| ! | small nuclear ribonucleoprotein complex | GO:0030532 | 41 | 23 | 0.36604894 | 0.95076 | 1.01377135 |
| ! | G1 phase of mitotic cell cycle | GO:0000080 | 43 | 23 | 0.3712886 | 0.95076 | 1.01322981 |
| ! | T-cell proliferation | GO:0042098 | 80 | 47 | 0.41755929 | 0.95084 | 1.01277405 |
| ! | synaptogenesis | GO:0007416 | 172 | 82 | 0.44583716 | 0.9511 | 1.01251041 |
| ! | myeloid blood cell differentiation | GO:0030099 | 138 | 83 | 0.44745295 | 0.95128 | 1.01216192 |
| ! | neutrophil chemotaxis | GO:0030593 | 45 | 19 | 0.34566117 | 0.95278 | 1.01321754 |
| ! | kidney development | GO:0001822 | 68 | 31 | 0.3857753 | 0.9537 | 1.01365557 |
| ! | regulation of cell activation | GO:0050865 | 130 | 71 | 0.42942895 | 0.95566 | 1.01519792 |
| ! | sulfuric ester hydrolase activity | GO:0008484 | 29 | 13 | 0.31107377 | 0.95578 | 1.01478505 |
| ! | extrachromosomal DNA | GO:0046821 | 33 | 13 | 0.30994422 | 0.95578 | 1.01424527 |
| ! | positive regulation of biosynthesis | GO:0009891 | 78 | 49 | 0.4159251 | 0.95628 | 1.01423636 |
| ! | regulation of lymphocyte proliferation | GO:0050670 | 67 | 37 | 0.39301448 | 0.95654 | 1.01397306 |
| ! | tryptase activity | GO:0030019 | 15 | 12 | 0.29576243 | 0.95658 | 1.01347695 |
| ! | MHC protein complex | GO:0042611 | 18 | 8 | 0.25314518 | 0.95767 | 1.01409323 |
| ! | regulation of S phase of mitotic cell cycle | GO:0007090 | 21 | 11 | 0.28714867 | 0.95784 | 1.01373517 |
| ! | positive regulation of organismal physiological process | GO:0051240 | 162 | 89 | 0.44735871 | 0.95856 | 1.01395928 |
| ! | phagocytosis | GO:0006909 | 77 | 38 | 0.39296689 | 0.95865 | 1.01351709 |
| ! | lymphocyte differentiation | GO:0030098 | 143 | 74 | 0.43563086 | 0.95962 | 1.01400524 |
| ! | receptor antagonist activity | GO:0048019 | 11 | 9 | 0.25868954 | 0.96058 | 1.01448232 |
| ! | pheromone receptor activity | GO:0016503 | 31 | 30 | 0.37474879 | 0.96194 | 1.01538111 |
| ! | urogenital system development | GO:0001655 | 85 | 40 | 0.39735798 | 0.9626 | 1.01554045 |
| ! | regulation of transcription from Pol III promoter | GO:0006359 | 60 | 35 | 0.3900579 | 0.96333 | 1.01577344 |
| ! | bone remodeling | GO:0046849 | 193 | 95 | 0.44258329 | 0.96341 | 1.01532116 |
| ! | antigen presentation, exogenous antigen | GO:0019884 | 37 | 16 | 0.31562138 | 0.96456 | 1.01599641 |
| ! | homophilic cell adhesion | GO:0007156 | 179 | 98 | 0.43985997 | 0.96532 | 1.01626037 |
| ! | alkaline phosphatase activity | GO:0004035 | 16 | 9 | 0.25289452 | 0.96707 | 1.01756574 |
| ! | B-cell differentiation | GO:0030183 | 54 | 29 | 0.36314388 | 0.96777 | 1.0177655 |
| ! | mast cell activation | GO:0045576 | 21 | 10 | 0.26475737 | 0.96802 | 1.01749204 |
| ! | positive regulation of cytokine biosynthesis | GO:0042108 | 49 | 33 | 0.37524597 | 0.96865 | 1.01761809 |
| ! | positive regulation of protein metabolism | GO:0051247 | 95 | 59 | 0.41375623 | 0.96875 | 1.0171875 |
| ! | glycolipid metabolism | GO:0006664 | 51 | 26 | 0.35323607 | 0.96948 | 1.01741852 |

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|---|---|---|---|---|---|---|---|
| ! | negative regulation of monocyte differentiation | GO:0045656 | 34 | 21 | 0.33342004 | 0.96995 | 1.01737658 |
| ! | negative regulation of cell adhesion | GO:0007162 | 36 | 21 | 0.3346175 | 0.96995 | 1.01684196 |
| ! | isotype switching | GO:0045190 | 16 | 11 | 0.27185381 | 0.97165 | 1.01808915 |
| ! | response to bacteria | GO:0009617 | 110 | 87 | 0.42879939 | 0.97167 | 1.01757567 |
| ! | rhythmic behavior | GO:0007622 | 45 | 20 | 0.33154533 | 0.97265 | 1.01806755 |
| ! | positive regulation of cytokine production | GO:0001819 | 51 | 35 | 0.37402862 | 0.97284 | 1.01773246 |
| ! | regulation of myeloid blood cell differentiation | GO:0045637 | 62 | 35 | 0.37935816 | 0.97284 | 1.01719906 |
| ! | negative regulation of osteoclast differentiation | GO:0045671 | 31 | 18 | 0.31526335 | 0.97289 | 1.01671847 |
| ! | immunoglobulin binding | GO:0019865 | 15 | 9 | 0.24609063 | 0.97306 | 1.01636372 |
| ! | DNA-methyltransferase activity | GO:0009008 | 23 | 10 | 0.25526538 | 0.97376 | 1.01656264 |
| ! | neuropeptide Y receptor activity | GO:0004983 | 95 | 65 | 0.41736438 | 0.97541 | 1.01775259 |
| ! | replisome | GO:0030894 | 43 | 19 | 0.32160401 | 0.97558 | 1.01739786 |
| ! | T-helper 1 type immune response | GO:0042088 | 55 | 37 | 0.37987794 | 0.97569 | 1.01698096 |
| ! | interleukin-6 biosynthesis | GO:0042226 | 19 | 11 | 0.26324885 | 0.97691 | 1.01772086 |
| ! | positive regulation of interleukin-6 biosynthesis | GO:0045410 | 14 | 9 | 0.23803112 | 0.97744 | 1.01774154 |
| ! | histone acetyltransferase complex | GO:0000123 | 17 | 9 | 0.23268524 | 0.97744 | 1.01721064 |
| ! | intermediate filament cytoskeleton | GO:0045111 | 151 | 97 | 0.4297912 | 0.9776 | 1.01684672 |
| ! | negative regulation of cytokine biosynthesis | GO:0042036 | 10 | 8 | 0.21154245 | 0.97965 | 1.01844802 |
| ! | defense response to pathogenic bacteria | GO:0042830 | 10 | 8 | 0.2100222 | 0.97965 | 1.01791758 |
| ! | ossification | GO:0001503 | 175 | 85 | 0.42483929 | 0.98005 | 1.0178031 |
| ! | peptide hormone | GO:0005180 | 19 | 13 | 0.27439976 | 0.98059 | 1.01783405 |
| ! | phosphatidylinositol 3-kinase activity | GO:0016303 | 24 | 11 | 0.24772506 | 0.98147 | 1.01821771 |
| ! | N-glycan processing | GO:0006491 | 18 | 9 | 0.22533101 | 0.98182 | 1.0180514 |
| ! | specific RNA polymerase II transcription factor activity | GO:0003704 | 133 | 64 | 0.40312657 | 0.98214 | 1.01785418 |
| ! | phagocytosis, engulfment | GO:0006911 | 34 | 15 | 0.2798222 | 0.98231 | 1.01750179 |
| ! | cell-mediated immune response | GO:0042087 | 64 | 41 | 0.37316475 | 0.98254 | 1.01721188 |
| ! | lymph gland development | GO:0007515 | 47 | 24 | 0.32715916 | 0.9832 | 1.01736722 |
| ! | cellular defense response (sensu Vertebrata) | GO:0016066 | 83 | 50 | 0.38733054 | 0.98447 | 1.01815327 |
| ! | nuclear origin of replication recognition complex | GO:0005664 | 50 | 31 | 0.35065824 | 0.9851 | 1.01827694 |
| ! | chitin metabolism | GO:0006030 | 20 | 11 | 0.23991653 | 0.98517 | 1.01782193 |
| ! | regulation of bone mineralization | GO:0030500 | 15 | 11 | 0.24573563 | 0.98517 | 1.01729511 |
| ! | positive regulation of interleukin-12 biosynthesis | GO:0045084 | 16 | 11 | 0.2429176 | 0.98517 | 1.01676883 |
| ! | hematopoietin/interferon-class (D200-domain) cytokine receptor binding | GO:0005126 | 55 | 40 | 0.36748959 | 0.98559 | 1.01667634 |
| ! | bone mineralization | GO:0030282 | 42 | 23 | 0.32152205 | 0.98579 | 1.01635713 |
| ! | negative regulation of myeloid blood cell differentiation | GO:0045638 | 36 | 23 | 0.32251759 | 0.98579 | 1.01583215 |
| ! | intermediate filament | GO:0005882 | 150 | 96 | 0.42798135 | 0.98623 | 1.01576089 |
| ! | angiotensin receptor activity | GO:0001595 | 24 | 15 | 0.27364638 | 0.98644 | 1.01545294 |
| ! | replication fork | GO:0005657 | 46 | 21 | 0.30790852 | 0.98654 | 1.01503213 |
| ! | origin recognition complex | GO:0000808 | 54 | 32 | 0.34869492 | 0.98669 | 1.01466317 |
| ! | dipeptidyl-peptidase and tripeptidyl-peptidase activity | GO:0016806 | 21 | 10 | 0.22586068 | 0.98684 | 1.01429459 |
| ! | metabotropic glutamate, GABA-B-like receptor activity | GO:0008067 | 24 | 18 | 0.29241631 | 0.98749 | 1.01444004 |
| ! | cytokine binding | GO:0019955 | 164 | 100 | 0.41964524 | 0.98783 | 1.01426704 |
| ! | negative regulation of T-cell activation | GO:0050868 | 15 | 11 | 0.23167459 | 0.98835 | 1.01427894 |
| ! | macrophage activation | GO:0042116 | 17 | 11 | 0.23783974 | 0.98835 | 1.01375746 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ! | positive regulation of protein biosynthesis | GO:0045727 | 57 | 39 | 0.35823251 | 0.98989 | 1.01481529 |
| ! | C-C chemokine binding | GO:0019957 | 49 | 33 | 0.33820087 | 0.99099 | 1.01542119 |
| ! | phosphoinositide 3-kinase activity | GO:0035004 | 26 | 12 | 0.23474412 | 0.99149 | 1.01541199 |
| ! | response to virus | GO:0009615 | 68 | 46 | 0.36416213 | 0.99151 | 1.01491147 |
| ! | RNA polymerase III transcription factor activity | GO:0003709 | 58 | 34 | 0.33330016 | 0.9919 | 1.01479 |
| ! | detection of pest, pathogen or parasite | GO:0009596 | 17 | 10 | 0.20452621 | 0.99196 | 1.01433121 |
| ! | immune cell chemotaxis | GO:0030595 | 82 | 40 | 0.35034206 | 0.99314 | 1.01501757 |
| ! | regulation of ossification | GO:0030278 | 50 | 26 | 0.31413058 | 0.9932 | 1.01455914 |
| ! | G-protein chemoattractant receptor activity | GO:0001637 | 52 | 35 | 0.33520501 | 0.99322 | 1.01406034 |
| ! | chemokine binding | GO:0019956 | 53 | 36 | 0.33655418 | 0.99325 | 1.01357225 |
| ! | interleukin-12 biosynthesis | GO:0042090 | 17 | 12 | 0.2231892 | 0.9935 | 1.01330905 |
| ! | B-cell activation | GO:0042113 | 112 | 60 | 0.37803738 | 0.99441 | 1.01371893 |
| ! | monocyte differentiation | GO:0030224 | 67 | 40 | 0.34244406 | 0.9954 | 1.01420991 |
| ! | major (U2-dependent) spliceosome | GO:0005684 | 16 | 10 | 0.18667005 | 0.99581 | 1.01410972 |
| ! | double-stranded DNA binding | GO:0003690 | 203 | 98 | 0.4064151 | 0.99588 | 1.01366357 |
| ! | regulation of cytokine biosynthesis | GO:0042035 | 69 | 46 | 0.34473207 | 0.99643 | 1.0137062 |
| ! | cytokine metabolism | GO:0042107 | 78 | 52 | 0.35443235 | 0.99645 | 1.01320986 |
| ! | immunological synapse | GO:0001772 | 56 | 29 | 0.30088307 | 0.99672 | 1.01296811 |
| ! | regulation of monocyte differentiation | GO:0045655 | 46 | 28 | 0.30079419 | 0.99679 | 1.01252345 |
| ! | proteoglycan | GO:0005203 | 26 | 8 | 0.15134851 | 0.9968 | 1.01201832 |
| ! | RNA editing | GO:0016547 | 15 | 8 | 0.14678548 | 0.9968 | 1.01150356 |
| ! | osteoclast differentiation | GO:0030316 | 46 | 26 | 0.29462065 | 0.99692 | 1.01111103 |
| ! | regulation of cytokine production | GO:0001817 | 74 | 49 | 0.35130678 | 0.99706 | 1.01073918 |
| ! | chitin binding | GO:0008061 | 27 | 18 | 0.23957076 | 0.99729 | 1.01045889 |
| ! | regulation of osteoclast differentiation | GO:0045670 | 40 | 23 | 0.27568744 | 0.99737 | 1.01002698 |
| ! | positive regulation of T-cell proliferation | GO:0042102 | 29 | 16 | 0.22457831 | 0.99767 | 1.00981819 |
| ! | cytokine and chemokine mediated signaling pathway | GO:0019221 | 73 | 42 | 0.33193796 | 0.9977 | 1.00933646 |
| ! | regulation of bone remodeling | GO:0046850 | 56 | 29 | 0.29230477 | 0.9978 | 1.008926 |
| ! | platelet activating factor receptor activity | GO:0004992 | 18 | 10 | 0.16815426 | 0.99801 | 1.00862713 |
| ! | regulation of T-cell proliferation | GO:0042129 | 39 | 23 | 0.25971992 | 0.99821 | 1.00831846 |
| ! | defense response to pathogen | GO:0042829 | 22 | 17 | 0.21975373 | 0.99841 | 1.0080101 |
| ! | antibacterial humoral response | GO:0019731 | 10 | 8 | 0.13241821 | 0.99844 | 1.0075305 |
| ! | purinergic nucleotide receptor activity, G-protein coupled | GO:0045028 | 101 | 73 | 0.36520111 | 0.99876 | 1.00734388 |
| ! | negative regulation of bone remodeling | GO:0046851 | 16 | 9 | 0.12926697 | 0.99913 | 1.00720786 |
| ! | uridine nucleotide receptor activity | GO:0015065 | 13 | 9 | 0.12758832 | 0.99913 | 1.00669917 |
| ! | negative regulation of immune response | GO:0050777 | 36 | 26 | 0.26605432 | 0.99918 | 1.00624134 |
| ! | negative regulation of lymphocyte activation | GO:0051250 | 28 | 19 | 0.22123698 | 0.9992 | 1.00575378 |
| ! | negative regulation of lymphocyte proliferation | GO:0050672 | 22 | 14 | 0.18595589 | 0.99923 | 1.00527678 |
| ! | immune cell migration | GO:0050900 | 93 | 47 | 0.32145957 | 0.99934 | 1.0048807 |
| ! | defense response to bacteria | GO:0042742 | 78 | 65 | 0.34617335 | 0.99936 | 1.00439456 |
| ! | interleukin-1 receptor binding | GO:0005149 | 57 | 37 | 0.28753961 | 0.99937 | 1.00389887 |
| ! | cytokine production | GO:0001816 | 95 | 62 | 0.33584086 | 0.9995 | 1.00352416 |
| ! | negative regulation of cell activation | GO:0050866 | 29 | 20 | 0.21126681 | 0.99958 | 1.00309965 |

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|---|---|---|---|---|---|---|---|
| ! | antigen presentation, exogenous antigen via MHC class II | GO:0042591 | 25 | 10 | 0.12262919 | 0.99968 | 1.00269563 |
| | | | | | | | |
| ! | positive regulation of cytosolic calcium ion concentration | GO:0007204 | 119 | 71 | 0.34256878 | 0.9998 | 1.00231206 |
| ! | bacterial binding | GO:0008367 | 9 | 8 | 0.08147818 | 0.99985 | 1.00185874 |
| ! | MHC class II receptor activity | GO:0045012 | 19 | 8 | 0.07113127 | 0.99991 | 1.00141589 |
| | | | | | | | |
| ! | antigen processing, exogenous antigen via MHC class II | GO:0019886 | 25 | 12 | 0.10033533 | 0.99997 | 1.00097348 |
| ! | olfactory receptor activity | GO:0004984 | 124 | 92 | 0.31333913 | 0.99998 | 1.00048149 |
| ! | negative regulation of organismal physiological process | GO:0051241 | 52 | 35 | 0.23467031 | 0.99998 | 0.99998 |

| Genotype | Diet | % body fat | PAI-1 (ng/mL) | Resistin (ng/mL) | Leptin (ng/mL) | IL-6 (pg/mL) |
|---|---|---|---|---|---|---|
| Ccr2-/- | high fat | 45.4 ± 5.2 | 2 ± 2.0*§ | 4.9 ± 1.4* | 77.4 ± 33.8* | 12.2 ± 5.8* |
| Ccr2+/+ | high fat | 44 ± 2.8 | 4.7 ± 1.7* | 4 ± 1.2* | 74.9 ± 12.2* | 8.8 ± 4.0* |
| Ccr2-/- | low fat | 13.9 ± 0.9 | 0.62 ± 0.34§ | 1.6 ± 0.53 | 0.51 ± 0.14 | 5 ± 1.9 |
| Ccr2+/+ | low fat | 14.8 ± 1.5 | 2 ± 0.8 | 2 ± 0.87 | 0.97 ± 1.0 | 4.6 ± 0.84 |