

| Group | GO biological process complete                                     | Client Text Box Input<br>(fold Enrichment) | Client Text Box<br>Input (P-value) |
|-------|--|--|------------------------------------|
| i     | liquid clearance, open tracheal system (GO:0035002)                | 15.89                                      | 8.94E-06                           |
| i     | establishment of glial blood-brain barrier (GO:0060857)            | 13.91                                      | 1.65E-05                           |
| i     | establishment of blood-brain barrier (GO:0060856)                  | 12.36                                      | 2.84E-05                           |
| i     | transepithelial transport (GO:0070633)                             | 11.71                                      | 3.65E-05                           |
| i     | epithelial fluid transport (GO:0042045)                            | 11.71                                      | 3.65E-05                           |
| i     | fluid transport (GO:0042044)                                       | 10.59                                      | 5.84E-05                           |
| i     | septate junction assembly (GO:0019991)                             | 8.32                                       | 3.82E-07                           |
| i     | apical junction assembly (GO:0043297)                              | 7.9  | 5.63E-08                           |
| i     | cell-cell junction assembly (GO:0007043)                           | 7.52                                       | 2.97E-08                           |
| i     | regulation of tube size, open tracheal system (GO:0035151)         | 7.27                                       | 3.78E-06                           |
| i     | cell junction assembly (GO:0034329)                                | 7.11                                       | 5.52E-08                           |
| i     | regulation of tube size (GO:0035150)                               | 6.74                                       | 6.83E-06                           |
| i     | chorion-containing eggshell formation (GO:0007304)                 | 5.92                                       | 3.45E-09                           |
| i     | eggshell formation (GO:0030703)                                    | 5.82                                       | 4.40E-09                           |
| i     | cell-cell junction organization (GO:0045216)                       | 5.68                                       | 2.56E-07                           |
| i     | cell junction organization (GO:0034330)                            | 5.68                                       | 2.56E-07                           |
| i     | regulation of tube architecture, open tracheal system (GO:0035152) | 5.3  | 7.72E-06                           |
| i     | cellular component assembly involved in morphogenesis (GO:0010927) | 3.42                                       | 2.12E-04                           |
| i     | epithelial cell development (GO:0002064)                           | 3.21                                       | 3.89E-08                           |
| i     | ovarian follicle cell development (GO:0030707)                     | 3.09                                       | 6.09E-07                           |
| i     | columnar/cuboidal epithelial cell development (GO:0002066)         | 3.08                                       | 6.44E-07                           |
| i     | epithelial cell differentiation (GO:0030855)                       | 3.01                                       | 5.98E-08                           |
| i     | columnar/cuboidal epithelial cell differentiation (GO:0002065)     | 3  | 1.05E-06                           |
| i     | regulation of anatomical structure size (GO:0090066)               | 2.8  | 2.28E-04                           |
| i     | epithelium development (GO:0060429)                                | 2.21                                       | 2.82E-08                           |
| i     | tissue development (GO:0009888)                                    | 2.08                                       | 1.61E-07                           |
| i     | anatomical structure morphogenesis (GO:0009653)                    | 1.58                                       | 1.69E-04                           |
| i     | anatomical structure development (GO:0048856)                      | 1.48                                       | 1.15E-05                           |
| i     | multicellular organismal process (GO:0032501)                      | 1.42                                       | 2.14E-06                           |
| i     | developmental process (GO:0032502)                                 | 1.42                                       | 6.98E-05                           |
| i     | metabolic process (GO:0008152)                                     | 0.73                                       | 2.35E-04                           |
| i     | nitrogen compound metabolic process (GO:0006807)                   | 0.66                                       | 5.92E-05                           |
| i     | cellular metabolic process (GO:0044237)                            | 0.64                                       | 1.34E-05                           |
| i     | macromolecule metabolic process (GO:0043170)                       | 0.63                                       | 6.82E-05                           |
| i     | primary metabolic process (GO:0044238)                             | 0.63                                       | 5.33E-06                           |
| i     | cellular protein metabolic process (GO:0044267)                    | 0.48                                       | 1.51E-04                           |
| i     | organic cyclic compound metabolic process (GO:1901360)             | 0.46                                       | 6.64E-05                           |
| i     | cellular aromatic compound metabolic process (GO:0006725)          | 0.46                                       | 7.27E-05                           |
| i     | biosynthetic process (GO:0009058)                                  | 0.43                                       | 1.73E-04                           |
| i     | cellular macromolecule metabolic process (GO:0044260)              | 0.43                                       | 2.12E-08                           |
| i     | cellular nitrogen compound metabolic process (GO:0034641)          | 0.41                                       | 1.48E-06                           |
| i     | heterocycle metabolic process (GO:0046483)                         | 0.4  | 1.17E-05                           |
| i     | cellular biosynthetic process (GO:0044249)                         | 0.37                                       | 4.59E-05                           |
| i     | nucleobase-containing compound metabolic process (GO:0006139)      | 0.37                                       | 6.96E-06                           |
| i     | nucleic acid metabolic process (GO:0090304)                        | 0.27                                       | 4.39E-06                           |
| i     | RNA metabolic process (GO:0016070)                                 | 0.27                                       | 5.30E-05                           |
| i     | gene expression (GO:0010467)                                       | 0.21                                       | 4.18E-07                           |
| i     | cellular nitrogen compound biosynthetic process (GO:0044271)       | 0.15                                       | 4.96E-06                           |
| i     | chromosome organization (GO:0051276)                               | 0.14                                       | 2.10E-04                           |
| i     | macromolecule biosynthetic process (GO:0009059)                    | 0.09                                       | 1.52E-07                           |

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|----|---|-------|----------|
| i  | cellular macromolecule biosynthetic process (GO:0034645)                    | 0.05  | 2.32E-08 |
| ii | negative regulation of melanization defense response (GO:0035009)           | 51.33 | 1.32E-04 |
| ii | regulation of melanization defense response (GO:0035007)                    | 36.67 | 1.74E-06 |
| ii | regulation of defense response to fungus (GO:1900150)                       | 25.67 | 6.30E-06 |
| ii | positive regulation of antifungal peptide production (GO:0002804)           | 25.67 | 6.30E-06 |
| ii | regulation of antifungal peptide production (GO:0002788)                    | 25.67 | 6.30E-06 |
| ii | antibacterial humoral response (GO:0019731)                                 | 24.55 | 1.96E-11 |
| ii | positive regulation of biosynthetic process of antibacterial peptides activ | 21.39 | 1.26E-05 |
| ii | regulation of secondary metabolic process (GO:0043455)                      | 20.53 | 1.96E-06 |
| ii | defense response to Gram-positive bacterium (GO:0050830)                    | 19.01 | 4.85E-18 |
| ii | positive regulation of Toll signaling pathway (GO:0045752)                  | 18.67 | 1.51E-04 |
| ii | regulation of biosynthetic process of antibacterial peptides active agains  | 18.33 | 2.29E-05 |
| ii | positive regulation of antibacterial peptide production (GO:0002803)        | 15.4  | 7.69E-06 |
| ii | Toll signaling pathway (GO:0008063)   | 15.4  | 3.81E-08 |
| ii | positive regulation of antibacterial peptide biosynthetic process (GO:000   | 15.4  | 7.69E-06 |
| ii | positive regulation of defense response to bacterium (GO:1900426)           | 14.37 | 1.92E-06 |
| ii | regulation of Toll signaling pathway (GO:0008592)                           | 14    | 1.22E-05 |
| ii | phenol-containing compound biosynthetic process (GO:0046189)                | 14    | 1.22E-05 |
| ii | positive regulation of antimicrobial peptide biosynthetic process (GO:000   | 13.82 | 2.40E-06 |
| ii | positive regulation of antimicrobial peptide production (GO:0002225)        | 13.69 | 4.77E-07 |
| ii | melanin biosynthetic process (GO:0042438)                                   | 13.69 | 4.03E-04 |
| ii | positive regulation of humoral immune response (GO:0002922)                 | 13.69 | 4.77E-07 |
| ii | positive regulation of antimicrobial humoral response (GO:0002760)          | 13.69 | 4.77E-07 |
| ii | positive regulation of production of molecular mediator of immune resp      | 13.69 | 4.77E-07 |
| ii | positive regulation of immune effector process (GO:0002699)                 | 13.69 | 4.77E-07 |
| ii | regulation of antibacterial peptide biosynthetic process (GO:0002808)       | 13.39 | 1.51E-05 |
| ii | regulation of antibacterial peptide production (GO:0002786)                 | 13.39 | 1.51E-05 |
| ii | positive regulation of response to biotic stimulus (GO:0002833)             | 13.2  | 1.17E-07 |
| ii | antimicrobial humoral response (GO:0019730)                                 | 12.13 | 4.17E-10 |
| ii | response to fungus (GO:0009620)   | 11.78 | 1.22E-10 |
| ii | humoral immune response (GO:0006959)  | 11.48 | 1.71E-12 |
| ii | regulation of defense response to bacterium (GO:1900424)                    | 11.41 | 1.56E-06 |
| ii | positive regulation of multi-organism process (GO:0043902)                  | 9.24  | 1.62E-06 |
| ii | defense response to fungus (GO:0050832)                                     | 9.24  | 1.62E-06 |
| ii | regulation of antimicrobial peptide biosynthetic process (GO:0002805)       | 9.21  | 2.43E-05 |
| ii | response to bacterium (GO:0009617)  | 9.01  | 1.68E-24 |
| ii | positive regulation of response to external stimulus (GO:0032103)           | 8.88  | 2.16E-06 |
| ii | regulation of antimicrobial peptide production (GO:0002784)                 | 8.74  | 8.96E-06 |
| ii | regulation of production of molecular mediator of immune response (GC       | 8.56  | 1.03E-05 |
| ii | cuticle pigmentation (GO:0048067)   | 8.36  | 4.26E-05 |
| ii | secondary metabolite biosynthetic process (GO:0044550)                      | 8.11  | 1.77E-04 |
| ii | defense response to bacterium (GO:0042742)                                  | 7.78  | 5.39E-17 |
| ii | regulation of antimicrobial humoral response (GO:0002759)                   | 7.75  | 1.96E-05 |
| ii | regulation of humoral immune response (GO:0002920)                          | 7.6   | 2.22E-05 |
| ii | phenol-containing compound metabolic process (GO:0018958)                   | 7.55  | 2.20E-06 |
| ii | response to external biotic stimulus (GO:0043207)                           | 7.49  | 3.60E-26 |
| ii | response to other organism (GO:0051707)                                     | 7.49  | 3.60E-26 |
| ii | response to biotic stimulus (GO:0009607)                                    | 7.49  | 3.60E-26 |
| ii | immune response (GO:0006955)  | 7.41  | 1.91E-15 |
| ii | melanin metabolic process (GO:0006582)                                      | 7.33  | 2.81E-05 |
| ii | positive regulation of defense response (GO:0031349)                        | 7.15  | 1.11E-06 |
| ii | defense response to other organism (GO:0098542)                             | 7.13  | 4.05E-19 |

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| ii  | defense response (GO:0006952)  | 6.79   | 1.81E-23 |
| ii  | regulation of response to biotic stimulus (GO:0002831)               | 6.75   | 5.42E-06 |
| ii  | regulation of immune effector process (GO:0002697)                   | 6.73   | 4.89E-05 |
| ii  | organic hydroxy compound biosynthetic process (GO:1901617)           | 6.65   | 1.55E-04 |
| ii  | innate immune response (GO:0045087)                                  | 6.47   | 1.14E-07 |
| ii  | positive regulation of immune system process (GO:0002684)            | 6.42   | 2.88E-06 |
| ii  | positive regulation of immune response (GO:0050778)                  | 6.34   | 9.04E-06 |
| ii  | positive regulation of cellular amide metabolic process (GO:0034250) | 6.2    | 2.33E-04 |
| ii  | regulation of defense response (GO:0031347)                          | 6.04   | 3.39E-08 |
| ii  | secondary metabolic process (GO:0019748)                             | 5.9    | 1.60E-05 |
| ii  | developmental pigmentation (GO:0048066)                              | 5.82   | 6.77E-06 |
| ii  | defense response to Gram-negative bacterium (GO:0050829)             | 5.7    | 3.13E-06 |
| ii  | pigmentation (GO:0043473)  | 5.33   | 1.46E-05 |
| ii  | regulation of immune response (GO:0050776)                           | 5.17   | 5.80E-07 |
| ii  | immune system process (GO:0002376)                                   | 4.97   | 2.60E-12 |
| ii  | regulation of innate immune response (GO:0045088)                    | 4.86   | 1.68E-04 |
| ii  | organic hydroxy compound metabolic process (GO:1901615)              | 4.5    | 2.88E-05 |
| ii  | pigment metabolic process (GO:0042440)                               | 4.38   | 7.77E-05 |
| ii  | regulation of proteolysis (GO:0030162)                               | 4.21   | 2.21E-04 |
| ii  | regulation of immune system process (GO:0002682)                     | 4.18   | 7.83E-07 |
| ii  | regulation of response to external stimulus (GO:0032101)             | 3.95   | 3.56E-04 |
| ii  | regulation of multi-organism process (GO:0043900)                    | 3.89   | 3.99E-04 |
| ii  | regulation of response to stress (GO:0080134)                        | 3.73   | 3.63E-06 |
| ii  | response to external stimulus (GO:0009605)                           | 3.32   | 4.31E-16 |
| ii  | response to stress (GO:0006950)                                      | 2.76   | 1.45E-13 |
| ii  | drug metabolic process (GO:0017144)                                  | 2.57   | 3.47E-04 |
| ii  | proteolysis (GO:0006508)   | 2.47   | 3.38E-07 |
| ii  | multi-organism process (GO:0051704)                                  | 2.25   | 9.45E-10 |
| ii  | response to stimulus (GO:0050896)                                    | 1.64   | 1.36E-06 |
| ii  | cellular process (GO:0009987)  | 0.77   | 3.30E-04 |
| ii  | cellular metabolic process (GO:0044237)                              | 0.63   | 1.66E-04 |
| ii  | cellular component organization (GO:0016043)                         | 0.44   | 4.36E-06 |
| ii  | cellular component organization or biogenesis (GO:0071840)           | 0.42   | 4.56E-07 |
| ii  | cellular component biogenesis (GO:0044085)                           | 0.27   | 9.17E-05 |
| ii  | organelle organization (GO:0006996)                                  | 0.22   | 1.69E-07 |
| ii  | cellular protein metabolic process (GO:0044267)                      | 0.2    | 6.55E-08 |
| ii  | protein modification process (GO:0036211)                            | 0.2    | 1.70E-05 |
| ii  | cellular protein modification process (GO:0006464)                   | 0.2    | 1.70E-05 |
| ii  | macromolecule biosynthetic process (GO:0009059)                      | 0.19   | 2.50E-04 |
| ii  | macromolecule modification (GO:0043412)                              | 0.18   | 3.90E-06 |
| ii  | cellular macromolecule metabolic process (GO:0044260)                | 0.16   | 3.24E-14 |
| ii  | nucleic acid metabolic process (GO:0090304)                          | 0.14   | 1.37E-06 |
| ii  | gene expression (GO:0010467)   | 0.1    | 2.79E-07 |
| ii  | cellular macromolecule biosynthetic process (GO:0034645)             | 0.07   | 8.50E-06 |
| ii  | RNA metabolic process (GO:0016070)                                   | 0.06   | 1.64E-06 |
| ii  | RNA processing (GO:0006396)  | < 0.01 | 8.81E-05 |
| ii  | macromolecular complex subunit organization (GO:0043933)             | < 0.01 | 8.88E-05 |
| iii | response to light intensity (GO:0009642)                             | 7.31   | 9.07E-05 |
| iii | import across plasma membrane (GO:0098739)                           | 7.31   | 1.46E-03 |
| iii | rhodopsin mediated signaling pathway (GO:0016056)                    | 6.79   | 4.14E-06 |
| iii | deactivation of rhodopsin mediated signaling (GO:0016059)            | 6.45   | 1.15E-06 |
| iii | regulation of membrane potential in photoreceptor cell (GO:0016057)  | 6.4    | 9.62E-04 |

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| iii | phototransduction, visible light (GO:0007603)                             | 6.27 | 1.31E-07 |
| iii | regulation of rhodopsin mediated signaling pathway (GO:0022400)           | 6.09 | 1.88E-06 |
| iii | maintenance of synapse structure (GO:0099558)                             | 5.69 | 1.53E-03 |
| iii | maintenance of presynaptic active zone structure (GO:0048790)             | 5.69 | 1.53E-03 |
| iii | detection of visible light (GO:0009584)                                   | 5.55 | 2.47E-08 |
| iii | dopamine receptor signaling pathway (GO:0007212)                          | 5.32 | 9.56E-04 |
| iii | thermotaxis (GO:0043052)  | 5.28 | 2.67E-05 |
| iii | regulation of G-protein coupled receptor protein signaling pathway (GO:   | 5.15 | 5.06E-07 |
| iii | regulation of neurotransmitter secretion (GO:0046928)                     | 5.09 | 4.47E-06 |
| iii | regulation of neurotransmitter transport (GO:0051588)                     | 5.09 | 4.47E-06 |
| iii | regulation of regulated secretory pathway (GO:1903305)                    | 5.06 | 5.92E-04 |
| iii | mechanosensory behavior (GO:0007638)                                      | 5.06 | 5.92E-04 |
| iii | regulation of calcium ion-dependent exocytosis (GO:0017158)               | 5.06 | 5.92E-04 |
| iii | transmission of nerve impulse (GO:0019226)                                | 4.88 | 1.43E-03 |
| iii | multicellular organismal signaling (GO:0035637)                           | 4.88 | 1.43E-03 |
| iii | regulation of microtubule depolymerization (GO:0031114)                   | 4.88 | 1.43E-03 |
| iii | detection of light stimulus involved in sensory perception (GO:0050962)   | 4.88 | 1.43E-03 |
| iii | photoperiodism (GO:0009648)   | 4.88 | 1.43E-03 |
| iii | cellular response to light stimulus (GO:0071482)                          | 4.82 | 5.85E-09 |
| iii | adenylate cyclase-activating G-protein coupled receptor signaling pathw   | 4.7  | 8.70E-04 |
| iii | regulation of clathrin-dependent endocytosis (GO:2000369)                 | 4.7  | 8.70E-04 |
| iii | sensory perception of light stimulus (GO:0050953)                         | 4.6  | 5.99E-06 |
| iii | regulation of exocytosis (GO:0017157)                                     | 4.57 | 2.25E-05 |
| iii | entrainment of circadian clock (GO:0009649)                               | 4.39 | 1.97E-04 |
| iii | detection of chemical stimulus involved in sensory perception of smell (C | 4.28 | 1.12E-11 |
| iii | photoreceptor cell axon guidance (GO:0072499)                             | 4.22 | 4.49E-05 |
| iii | cAMP-mediated signaling (GO:0019933)                                      | 4.18 | 2.76E-04 |
| iii | phototransduction (GO:0007602)  | 4.14 | 1.21E-09 |
| iii | visual perception (GO:0007601)  | 4.13 | 1.68E-04 |
| iii | phospholipase C-activating G-protein coupled receptor signaling pathwa    | 4.11 | 1.74E-03 |
| iii | detection of light stimulus (GO:0009583)                                  | 4.04 | 3.90E-10 |
| iii | sensory perception of smell (GO:0007608)                                  | 4    | 9.18E-18 |
| iii | detection of chemical stimulus involved in sensory perception (GO:0050!   | 3.91 | 1.03E-13 |
| iii | R7 cell development (GO:0045467)  | 3.82 | 5.16E-04 |
| iii | cellular response to radiation (GO:0071478)                               | 3.79 | 8.73E-08 |
| iii | cellular response to environmental stimulus (GO:0104004)                  | 3.76 | 4.69E-09 |
| iii | cellular response to abiotic stimulus (GO:0071214)                        | 3.76 | 4.69E-09 |
| iii | detection of stimulus involved in sensory perception (GO:0050906)         | 3.68 | 1.11E-18 |
| iii | G-protein coupled receptor signaling pathway, coupled to cyclic nucleoti  | 3.66 | 9.28E-05 |
| iii | regulation of receptor-mediated endocytosis (GO:0048259)                  | 3.66 | 1.91E-03 |
| iii | sensory perception of sound (GO:0007605)                                  | 3.6  | 7.72E-08 |
| iii | adenylate cyclase-modulating G-protein coupled receptor signaling path    | 3.53 | 3.33E-04 |
| iii | regulation of synaptic plasticity (GO:0048167)                            | 3.51 | 9.10E-04 |
| iii | regulation of cytosolic calcium ion concentration (GO:0051480)            | 3.48 | 2.52E-03 |
| iii | response to mechanical stimulus (GO:0009612)                              | 3.48 | 2.22E-05 |
| iii | detection of abiotic stimulus (GO:0009582)                                | 3.41 | 4.26E-12 |
| iii | detection of external stimulus (GO:0009581)                               | 3.41 | 4.26E-12 |
| iii | rhabdomere development (GO:0042052)                                       | 3.39 | 4.72E-05 |
| iii | synaptic vesicle endocytosis (GO:0048488)                                 | 3.39 | 4.72E-05 |
| iii | energy taxis (GO:0009453)   | 3.35 | 1.97E-03 |
| iii | phototaxis (GO:0042331)   | 3.35 | 1.97E-03 |
| iii | neuromuscular synaptic transmission (GO:0007274)                          | 3.34 | 2.55E-06 |

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| iii | sensory perception of mechanical stimulus (GO:0050954)                        | 3.32 | 5.35E-08 |
| iii | epithelial cell migration, open tracheal system (GO:0007427)                  | 3.23 | 4.38E-04 |
| iii | G-protein coupled receptor signaling pathway (GO:0007186)                     | 3.2  | 3.17E-17 |
| iii | regulated exocytosis (GO:0045055)   | 3.2  | 2.03E-06 |
| iii | cyclic-nucleotide-mediated signaling (GO:0019935)                             | 3.2  | 7.19E-04 |
| iii | synaptic vesicle exocytosis (GO:0016079)                                      | 3.18 | 3.28E-06 |
| iii | calcium ion regulated exocytosis (GO:0017156)                                 | 3.18 | 3.28E-06 |
| iii | regulation of secretion (GO:0051046)  | 3.17 | 2.63E-08 |
| iii | clathrin-dependent endocytosis (GO:0072583)                                   | 3.16 | 9.92E-05 |
| iii | regulation of secretion by cell (GO:1903530)                                  | 3.15 | 6.86E-08 |
| iii | response to pheromone (GO:0019236)  | 3.13 | 1.95E-03 |
| iii | second-messenger-mediated signaling (GO:0019932)                              | 3.11 | 7.71E-05 |
| iii | sensory perception of chemical stimulus (GO:0007606)                          | 3.11 | 1.75E-21 |
| iii | associative learning (GO:0008306)   | 3.11 | 9.67E-07 |
| iii | modulation of chemical synaptic transmission (GO:0050804)                     | 3.1  | 3.77E-09 |
| iii | regulation of trans-synaptic signaling (GO:0099177)                           | 3.1  | 3.77E-09 |
| iii | synaptic vesicle recycling (GO:0036465)                                       | 3.09 | 1.25E-04 |
| iii | receptor-mediated endocytosis (GO:0006898)                                    | 3.07 | 5.98E-05 |
| iii | response to light stimulus (GO:0009416)                                       | 3.07 | 5.46E-12 |
| iii | synaptic signaling (GO:0099536)   | 3.06 | 3.19E-15 |
| iii | chemical synaptic transmission (GO:0007268)                                   | 3.04 | 6.29E-15 |
| iii | trans-synaptic signaling (GO:0099537)   | 3.04 | 6.29E-15 |
| iii | anterograde trans-synaptic signaling (GO:0098916)                             | 3.04 | 6.29E-15 |
| iii | heterophilic cell-cell adhesion via plasma membrane cell adhesion molecul     | 3.03 | 2.46E-03 |
| iii | regulation of heart contraction (GO:0008016)                                  | 3.03 | 2.46E-03 |
| iii | regulation of blood circulation (GO:1903522)                                  | 3.03 | 2.46E-03 |
| iii | protein oligomerization (GO:0051259)  | 3    | 5.40E-04 |
| iii | establishment of synaptic vesicle localization (GO:0097480)                   | 2.99 | 5.33E-09 |
| iii | synaptic vesicle transport (GO:0048489)                                       | 2.99 | 5.33E-09 |
| iii | vesicle-mediated transport in synapse (GO:0099003)                            | 2.99 | 5.33E-09 |
| iii | detection of stimulus (GO:0051606)  | 2.98 | 3.42E-20 |
| iii | synaptic vesicle cycle (GO:0099504)   | 2.98 | 8.45E-09 |
| iii | synaptic vesicle localization (GO:0097479)                                    | 2.98 | 3.98E-09 |
| iii | regulation of endocytosis (GO:0030100)  | 2.95 | 9.35E-05 |
| iii | olfactory learning (GO:0008355)   | 2.95 | 3.53E-05 |
| iii | neuropeptide signaling pathway (GO:0007218)                                   | 2.93 | 5.48E-05 |
| iii | detection of temperature stimulus involved in sensory perception of pain      | 2.93 | 6.73E-04 |
| iii | neurotransmitter secretion (GO:0007269)                                       | 2.93 | 5.14E-07 |
| iii | signal release from synapse (GO:0099643)                                      | 2.93 | 5.14E-07 |
| iii | learning (GO:0007612)   | 2.93 | 5.14E-07 |
| iii | presynaptic process involved in chemical synaptic transmission (GO:0099643)   | 2.91 | 3.81E-07 |
| iii | establishment of vesicle localization (GO:0051650)                            | 2.9  | 6.94E-09 |
| iii | olfactory behavior (GO:0042048)   | 2.9  | 3.04E-08 |
| iii | compound eye photoreceptor development (GO:0042051)                           | 2.89 | 1.28E-06 |
| iii | exocytosis (GO:0006887)   | 2.86 | 7.14E-07 |
| iii | neuron projection extension (GO:1990138)                                      | 2.84 | 1.77E-03 |
| iii | vesicle localization (GO:0051648)   | 2.84 | 1.17E-08 |
| iii | eye photoreceptor cell development (GO:0042462)                               | 2.83 | 1.79E-06 |
| iii | homophilic cell adhesion via plasma membrane adhesion molecules (GO:0042462)  | 2.8  | 2.88E-03 |
| iii | detection of temperature stimulus (GO:0016048)                                | 2.79 | 1.61E-03 |
| iii | detection of temperature stimulus involved in sensory perception (GO:0016048) | 2.79 | 1.61E-03 |
| iii | sensory perception of temperature stimulus (GO:0050951)                       | 2.79 | 1.61E-03 |

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| iii | synapse organization (GO:0050808)                                     | 2.77 | 6.79E-11 |
| iii | regulation of vesicle-mediated transport (GO:0060627)                 | 2.77 | 7.61E-08 |
| iii | detection of chemical stimulus (GO:0009593)                           | 2.75 | 3.48E-10 |
| iii | calcium ion transport (GO:0006816)                                    | 2.74 | 7.99E-04 |
| iii | sensory perception (GO:0007600)                                       | 2.73 | 5.44E-27 |
| iii | motor neuron axon guidance (GO:0008045)                               | 2.71 | 1.43E-04 |
| iii | regulation of neurotransmitter levels (GO:0001505)                    | 2.71 | 2.06E-08 |
| iii | signal release (GO:0023061)   | 2.71 | 1.78E-06 |
| iii | exocytic process (GO:0140029)   | 2.69 | 9.02E-04 |
| iii | nervous system process (GO:0050877)                                   | 2.68 | 3.59E-35 |
| iii | organelle membrane fusion (GO:0090174)                                | 2.68 | 2.76E-03 |
| iii | regulation of synaptic growth at neuromuscular junction (GO:0008582)  | 2.67 | 1.48E-06 |
| iii | regulation of neuromuscular junction development (GO:1904396)         | 2.67 | 1.09E-06 |
| iii | calcium ion homeostasis (GO:0055074)                                  | 2.66 | 1.97E-03 |
| iii | developmental cell growth (GO:0048588)                                | 2.65 | 3.54E-04 |
| iii | regulation of membrane potential (GO:0042391)                         | 2.64 | 7.01E-05 |
| iii | cell-cell adhesion via plasma-membrane adhesion molecules (GO:009874) | 2.64 | 2.63E-04 |
| iii | divalent inorganic cation homeostasis (GO:0072507)                    | 2.61 | 5.57E-04 |
| iii | cognition (GO:0050890)  | 2.61 | 2.37E-09 |
| iii | learning or memory (GO:0007611)                                       | 2.61 | 2.37E-09 |
| iii | cell-cell adhesion (GO:0098609)                                       | 2.6  | 1.58E-05 |
| iii | regulation of synapse assembly (GO:0051963)                           | 2.59 | 2.72E-06 |
| iii | memory (GO:0007613)   | 2.59 | 1.38E-06 |
| iii | regulation of synapse structure or activity (GO:0050803)              | 2.58 | 5.58E-09 |
| iii | photoreceptor cell development (GO:0042461)                           | 2.58 | 4.83E-06 |
| iii | behavioral response to ethanol (GO:0048149)                           | 2.57 | 8.77E-04 |
| iii | neurotransmitter transport (GO:0006836)                               | 2.57 | 3.91E-07 |
| iii | response to ethanol (GO:0045471)                                      | 2.57 | 1.35E-04 |
| iii | system process (GO:0003008)   | 2.56 | 1.50E-34 |
| iii | response to radiation (GO:0009314)                                    | 2.54 | 1.73E-09 |
| iii | neuromuscular junction development (GO:0007528)                       | 2.52 | 4.35E-05 |
| iii | regulation of synapse organization (GO:0050807)                       | 2.51 | 3.42E-07 |
| iii | synapse assembly (GO:0007416)   | 2.51 | 3.16E-04 |
| iii | chemosensory behavior (GO:0007635)                                    | 2.5  | 5.46E-08 |
| iii | developmental growth involved in morphogenesis (GO:0060560)           | 2.5  | 1.23E-04 |
| iii | adult behavior (GO:0030534)   | 2.5  | 4.09E-08 |
| iii | cellular divalent inorganic cation homeostasis (GO:0072503)           | 2.49 | 2.16E-03 |
| iii | regulation of circadian rhythm (GO:0042752)                           | 2.47 | 2.57E-04 |
| iii | regulation of transport (GO:0051049)                                  | 2.47 | 1.23E-11 |
| iii | cell adhesion (GO:0007155)  | 2.45 | 1.57E-07 |
| iii | photoreceptor cell fate commitment (GO:0046552)                       | 2.44 | 2.82E-03 |
| iii | divalent metal ion transport (GO:0070838)                             | 2.44 | 7.41E-04 |
| iii | long-term memory (GO:0007616)   | 2.44 | 3.96E-04 |
| iii | neuron recognition (GO:0008038)                                       | 2.44 | 1.95E-05 |
| iii | divalent inorganic cation transport (GO:0072511)                      | 2.44 | 7.41E-04 |
| iii | regulation of dendrite development (GO:0050773)                       | 2.44 | 2.00E-03 |
| iii | regulation of system process (GO:0044057)                             | 2.44 | 2.00E-03 |
| iii | cell growth (GO:0016049)  | 2.44 | 4.93E-05 |
| iii | biological adhesion (GO:0022610)                                      | 2.42 | 1.88E-07 |
| iii | cell recognition (GO:0008037)   | 2.39 | 2.80E-05 |
| iii | taxis (GO:0042330)  | 2.39 | 1.97E-13 |
| iii | adult locomotory behavior (GO:0008344)                                | 2.38 | 1.13E-04 |

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| iii | compound eye photoreceptor cell differentiation (GO:0001751)       | 2.34 | 1.47E-06 |
| iii | courtship behavior (GO:0007619)                                    | 2.31 | 2.92E-05 |
| iii | process utilizing autophagic mechanism (GO:0061919)                | 2.3  | 2.89E-04 |
| iii | autophagy (GO:0006914)   | 2.3  | 2.89E-04 |
| iii | eye-antennal disc development (GO:0035214)                         | 2.29 | 2.18E-03 |
| iii | eye photoreceptor cell differentiation (GO:0001754)                | 2.28 | 3.10E-06 |
| iii | axon guidance (GO:0007411)   | 2.27 | 5.37E-09 |
| iii | neuron projection guidance (GO:0097485)                            | 2.25 | 3.72E-09 |
| iii | mating behavior (GO:0007617)                                       | 2.24 | 3.32E-06 |
| iii | response to toxic substance (GO:0009636)                           | 2.21 | 1.84E-05 |
| iii | axonogenesis (GO:0007409)  | 2.21 | 5.80E-10 |
| iii | photoreceptor cell differentiation (GO:0046530)                    | 2.21 | 3.06E-06 |
| iii | secretion (GO:0046903)   | 2.21 | 8.49E-07 |
| iii | male courtship behavior (GO:0008049)                               | 2.2  | 2.66E-04 |
| iii | chemotaxis (GO:0006935)  | 2.2  | 7.31E-09 |
| iii | Ras protein signal transduction (GO:0007265)                       | 2.17 | 2.42E-03 |
| iii | response to temperature stimulus (GO:0009266)                      | 2.17 | 6.66E-06 |
| iii | secretion by cell (GO:0032940)                                     | 2.16 | 7.79E-06 |
| iii | reproductive behavior (GO:0019098)                                 | 2.16 | 6.06E-06 |
| iii | axon development (GO:0061564)                                      | 2.15 | 1.14E-09 |
| iii | compound eye morphogenesis (GO:0001745)                            | 2.15 | 2.50E-08 |
| iii | male mating behavior (GO:0060179)                                  | 2.15 | 3.56E-04 |
| iii | behavior (GO:0007610)  | 2.14 | 1.26E-17 |
| iii | regulation of localization (GO:0032879)                            | 2.13 | 1.14E-11 |
| iii | mating (GO:0007618)  | 2.1  | 1.26E-05 |
| iii | response to abiotic stimulus (GO:0009628)                          | 2.09 | 1.70E-12 |
| iii | sensory organ morphogenesis (GO:0090596)                           | 2.09 | 6.97E-08 |
| iii | eye morphogenesis (GO:0048592)                                     | 2.09 | 6.97E-08 |
| iii | cellular response to endogenous stimulus (GO:0071495)              | 2.07 | 1.20E-04 |
| iii | metal ion transport (GO:0030001)                                   | 2.06 | 4.48E-05 |
| iii | locomotory behavior (GO:0007626)                                   | 2.06 | 1.80E-05 |
| iii | positive regulation of transport (GO:0051050)                      | 2.05 | 1.31E-03 |
| iii | developmental growth (GO:0048589)                                  | 2.04 | 2.23E-05 |
| iii | cell-cell signaling (GO:0007267)                                   | 2.04 | 2.47E-12 |
| iii | growth (GO:0040007)  | 2.01 | 1.19E-05 |
| iii | response to chemical (GO:0042221)                                  | 2.01 | 2.37E-25 |
| iii | regulation of neuron projection development (GO:0010975)           | 2    | 1.93E-03 |
| iii | signaling (GO:0023052)   | 1.99 | 1.23E-33 |
| iii | response to endogenous stimulus (GO:0009719)                       | 1.97 | 1.15E-04 |
| iii | intracellular signal transduction (GO:0035556)                     | 1.97 | 1.20E-08 |
| iii | cell morphogenesis involved in neuron differentiation (GO:0048667) | 1.96 | 3.54E-10 |
| iii | establishment of organelle localization (GO:0051656)               | 1.96 | 1.36E-05 |
| iii | signal transduction (GO:0007165)                                   | 1.96 | 2.08E-23 |
| iii | regulation of cellular localization (GO:0060341)                   | 1.96 | 9.05E-04 |
| iii | compound eye development (GO:0048749)                              | 1.95 | 7.09E-08 |
| iii | locomotion (GO:0040011)  | 1.95 | 3.34E-13 |
| iii | response to alcohol (GO:0097305)                                   | 1.95 | 1.20E-03 |
| iii | regulation of developmental growth (GO:0048638)                    | 1.93 | 7.52E-06 |
| iii | neuron projection morphogenesis (GO:0048812)                       | 1.93 | 1.92E-11 |
| iii | cell projection morphogenesis (GO:0048858)                         | 1.93 | 2.02E-11 |
| iii | plasma membrane bounded cell projection morphogenesis (GO:0120039) | 1.93 | 2.02E-11 |
| iii | cell communication (GO:0007154)                                    | 1.93 | 3.81E-32 |

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| iii | cell morphogenesis involved in differentiation (GO:0000904)          | 1.93 | 1.91E-10 |
| iii | eye development (GO:0001654)   | 1.92 | 7.13E-08 |
| iii | neuron development (GO:0048666)                                      | 1.91 | 7.70E-14 |
| iii | neuron projection development (GO:0031175)                           | 1.9  | 2.92E-11 |
| iii | cell part morphogenesis (GO:0032990)                                 | 1.9  | 6.16E-11 |
| iii | response to organic substance (GO:0010033)                           | 1.88 | 5.97E-09 |
| iii | cell morphogenesis (GO:0000902)                                      | 1.87 | 3.28E-12 |
| iii | organelle localization (GO:0051640)                                  | 1.87 | 1.37E-05 |
| iii | neuron differentiation (GO:0030182)                                  | 1.87 | 1.07E-14 |
| iii | response to drug (GO:0042493)  | 1.86 | 1.36E-04 |
| iii | response to external stimulus (GO:0009605)                           | 1.85 | 1.16E-16 |
| iii | regulation of growth (GO:0040008)                                    | 1.85 | 2.54E-06 |
| iii | plasma membrane bounded cell projection organization (GO:0120036)    | 1.84 | 8.92E-13 |
| iii | regulation of nervous system development (GO:0051960)                | 1.84 | 3.32E-06 |
| iii | cell projection organization (GO:0030030)                            | 1.83 | 1.58E-12 |
| iii | cellular response to chemical stimulus (GO:0070887)                  | 1.82 | 1.40E-05 |
| iii | cellular response to organic substance (GO:0071310)                  | 1.81 | 2.13E-04 |
| iii | open tracheal system development (GO:0007424)                        | 1.81 | 1.22E-04 |
| iii | chemical homeostasis (GO:0048878)                                    | 1.79 | 3.66E-04 |
| iii | sensory organ development (GO:0007423)                               | 1.79 | 6.61E-08 |
| iii | import into cell (GO:0098657)  | 1.78 | 7.38E-06 |
| iii | imaginal disc-derived appendage development (GO:0048737)             | 1.78 | 7.71E-06 |
| iii | respiratory system development (GO:0060541)                          | 1.78 | 1.55E-04 |
| iii | regulation of cell communication (GO:0010646)                        | 1.77 | 1.02E-12 |
| iii | appendage development (GO:0048736)                                   | 1.77 | 8.67E-06 |
| iii | generation of neurons (GO:0048699)                                   | 1.77 | 1.69E-14 |
| iii | regulation of signaling (GO:0023051)                                 | 1.77 | 1.45E-12 |
| iii | negative regulation of multicellular organismal process (GO:0051241) | 1.77 | 8.18E-04 |
| iii | neurogenesis (GO:0022008)  | 1.76 | 9.10E-15 |
| iii | imaginal disc-derived wing morphogenesis (GO:0007476)                | 1.76 | 8.39E-05 |
| iii | appendage morphogenesis (GO:0035107)                                 | 1.76 | 1.90E-05 |
| iii | ameboidal-type cell migration (GO:0001667)                           | 1.76 | 1.55E-03 |
| iii | imaginal disc-derived appendage morphogenesis (GO:0035114)           | 1.75 | 1.82E-05 |
| iii | positive regulation of multicellular organismal process (GO:0051240) | 1.74 | 3.64E-04 |
| iii | wing disc morphogenesis (GO:0007472)                                 | 1.73 | 1.09E-04 |
| iii | nervous system development (GO:0007399)                              | 1.72 | 6.81E-16 |
| iii | negative regulation of signal transduction (GO:0009968)              | 1.72 | 1.40E-04 |
| iii | negative regulation of cell communication (GO:0010648)               | 1.72 | 8.90E-05 |
| iii | negative regulation of signaling (GO:0023057)                        | 1.72 | 8.90E-05 |
| iii | regulation of biological quality (GO:0065008)                        | 1.71 | 2.17E-16 |
| iii | regulation of multicellular organismal process (GO:0051239)          | 1.71 | 6.72E-10 |
| iii | post-embryonic appendage morphogenesis (GO:0035120)                  | 1.71 | 7.32E-05 |
| iii | response to oxygen-containing compound (GO:1901700)                  | 1.7  | 1.83E-04 |
| iii | regulation of cellular component biogenesis (GO:0044087)             | 1.69 | 2.35E-04 |
| iii | negative regulation of developmental process (GO:0051093)            | 1.69 | 1.64E-03 |
| iii | endocytosis (GO:0006897)   | 1.69 | 8.64E-05 |
| iii | regulation of multicellular organismal development (GO:2000026)      | 1.69 | 5.79E-07 |
| iii | vesicle-mediated transport (GO:0016192)                              | 1.69 | 7.15E-08 |
| iii | cation transport (GO:0006812)  | 1.68 | 2.81E-04 |
| iii | instar larval or pupal morphogenesis (GO:0048707)                    | 1.68 | 1.69E-06 |
| iii | post-embryonic animal morphogenesis (GO:0009886)                     | 1.68 | 1.25E-06 |
| iii | wing disc development (GO:0035220)                                   | 1.67 | 1.84E-05 |



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| iii | ion transport (GO:0006811)                                    | 1.67 | 3.40E-06 |
| iii | post-embryonic animal organ morphogenesis (GO:0048563)        | 1.67 | 2.87E-05 |
| iii | imaginal disc morphogenesis (GO:0007560)                      | 1.67 | 2.87E-05 |
| iii | metamorphosis (GO:0007552)                                    | 1.67 | 1.58E-06 |
| iii | cellular component morphogenesis (GO:0032989)                 | 1.66 | 2.77E-09 |
| iii | movement of cell or subcellular component (GO:0006928)        | 1.66 | 4.06E-08 |
| iii | negative regulation of response to stimulus (GO:0048585)      | 1.64 | 2.23E-04 |
| iii | epithelial tube morphogenesis (GO:0060562)                    | 1.64 | 9.59E-06 |
| iii | regulation of signal transduction (GO:0009966)                | 1.63 | 4.41E-08 |
| iii | response to stimulus (GO:0050896)                             | 1.62 | 2.00E-31 |
| iii | animal organ morphogenesis (GO:0009887)                       | 1.62 | 3.57E-08 |
| iii | instar larval or pupal development (GO:0002165)               | 1.61 | 1.32E-06 |
| iii | tissue morphogenesis (GO:0048729)                             | 1.61 | 1.34E-06 |
| iii | imaginal disc development (GO:0007444)                        | 1.6  | 4.51E-06 |
| iii | cell migration (GO:0016477)                                   | 1.6  | 1.40E-03 |
| iii | morphogenesis of an epithelium (GO:0002009)                   | 1.59 | 3.13E-06 |
| iii | regulation of anatomical structure morphogenesis (GO:0022603) | 1.58 | 2.84E-03 |
| iii | tube morphogenesis (GO:0035239)                               | 1.56 | 5.23E-05 |
| iii | regulation of cell development (GO:0060284)                   | 1.56 | 2.86E-03 |
| iii | regulation of response to stimulus (GO:0048583)               | 1.56 | 2.46E-08 |
| iii | tube development (GO:0035295)                                 | 1.56 | 1.12E-06 |
| iii | system development (GO:0048731)                               | 1.56 | 3.01E-16 |
| iii | regulation of developmental process (GO:0050793)              | 1.55 | 1.00E-06 |
| iii | cellular response to stimulus (GO:0051716)                    | 1.54 | 8.88E-14 |
| iii | homeostatic process (GO:0042592)                              | 1.54 | 3.11E-04 |
| iii | positive regulation of cell communication (GO:0010647)        | 1.52 | 2.07E-03 |
| iii | positive regulation of signaling (GO:0023056)                 | 1.52 | 2.07E-03 |
| iii | post-embryonic animal organ development (GO:0048569)          | 1.51 | 3.52E-04 |
| iii | anatomical structure morphogenesis (GO:0009653)               | 1.51 | 1.26E-12 |
| iii | cell motility (GO:0048870)                                    | 1.51 | 2.67E-03 |
| iii | post-embryonic development (GO:0009791)                       | 1.51 | 1.86E-05 |
| iii | cell surface receptor signaling pathway (GO:0007166)          | 1.51 | 4.98E-04 |
| iii | regulation of cell differentiation (GO:0045595)               | 1.49 | 2.43E-03 |
| iii | regulation of cellular component organization (GO:0051128)    | 1.47 | 1.83E-05 |
| iii | multicellular organismal process (GO:0032501)                 | 1.45 | 1.07E-26 |
| iii | animal organ development (GO:0048513)                         | 1.43 | 2.30E-07 |
| iii | intracellular transport (GO:0046907)                          | 1.42 | 3.68E-04 |
| iii | establishment of localization in cell (GO:0051649)            | 1.42 | 2.08E-04 |
| iii | multicellular organism development (GO:0007275)               | 1.41 | 2.66E-13 |
| iii | epithelium development (GO:0060429)                           | 1.4  | 2.19E-05 |
| iii | biological regulation (GO:0065007)                            | 1.4  | 1.17E-23 |
| iii | transport (GO:0006810)  | 1.39 | 7.71E-09 |
| iii | tissue development (GO:0009888)                               | 1.39 | 1.26E-05 |
| iii | cell differentiation (GO:0030154)                             | 1.38 | 3.21E-09 |
| iii | regulation of cellular process (GO:0050794)                   | 1.38 | 3.50E-17 |
| iii | regulation of biological process (GO:0050789)                 | 1.38 | 7.15E-19 |
| iii | localization (GO:0051179)                                     | 1.38 | 2.93E-10 |
| iii | cell development (GO:0048468)                                 | 1.37 | 7.34E-07 |
| iii | cellular developmental process (GO:0048869)                   | 1.37 | 9.41E-09 |
| iii | establishment of localization (GO:0051234)                    | 1.36 | 4.76E-08 |
| iii | cellular localization (GO:0051641)                            | 1.34 | 6.24E-04 |
| iii | anatomical structure development (GO:0048856)                 | 1.32 | 3.15E-10 |

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| iii | developmental process (GO:0032502)                               | 1.3  | 6.04E-10 |
| iii | positive regulation of biological process (GO:0048518)           | 1.27 | 3.90E-04 |
| iii | cellular component organization (GO:0016043)                     | 1.24 | 5.44E-06 |
| iii | negative regulation of biological process (GO:0048519)           | 1.24 | 2.42E-03 |
| iii | cellular component organization or biogenesis (GO:0071840)       | 1.18 | 3.18E-04 |
| iii | cellular process (GO:0009987)                                    | 1.12 | 3.26E-06 |
| iii | biological_process (GO:0008150)                                  | 1.04 | 1.33E-03 |
| iii | organonitrogen compound metabolic process (GO:1901564)           | 0.8  | 3.74E-05 |
| iii | cellular metabolic process (GO:0044237)                          | 0.78 | 1.05E-08 |
| iii | metabolic process (GO:0008152)                                   | 0.77 | 1.26E-11 |
| iii | cellular protein metabolic process (GO:0044267)                  | 0.74 | 1.26E-04 |
| iii | organic substance metabolic process (GO:0071704)                 | 0.73 | 1.46E-13 |
| iii | protein metabolic process (GO:0019538)                           | 0.73 | 2.81E-06 |
| iii | primary metabolic process (GO:0044238)                           | 0.7  | 3.03E-15 |
| iii | proteolysis (GO:0006508)   | 0.69 | 8.00E-04 |
| iii | nitrogen compound metabolic process (GO:0006807)                 | 0.69 | 8.41E-16 |
| iii | biosynthetic process (GO:0009058)                                | 0.64 | 5.32E-07 |
| iii | cellular biosynthetic process (GO:0044249)                       | 0.63 | 9.46E-07 |
| iii | organonitrogen compound biosynthetic process (GO:1901566)        | 0.63 | 1.69E-04 |
| iii | organic substance biosynthetic process (GO:1901576)              | 0.63 | 4.47E-07 |
| iii | macromolecule metabolic process (GO:0043170)                     | 0.63 | 3.27E-18 |
| iii | cell cycle (GO:0007049)  | 0.62 | 2.64E-04 |
| iii | cellular macromolecule metabolic process (GO:0044260)            | 0.6  | 5.31E-16 |
| iii | organic cyclic compound biosynthetic process (GO:1901362)        | 0.59 | 6.19E-04 |
| iii | mitotic cell cycle (GO:0000278)                                  | 0.58 | 9.57E-04 |
| iii | heterocycle biosynthetic process (GO:0018130)                    | 0.54 | 2.53E-04 |
| iii | cellular amide metabolic process (GO:0043603)                    | 0.53 | 3.15E-04 |
| iii | organic cyclic compound metabolic process (GO:1901360)           | 0.52 | 4.75E-15 |
| iii | peptide metabolic process (GO:0006518)                           | 0.51 | 2.85E-04 |
| iii | peptidyl-amino acid modification (GO:0018193)                    | 0.5  | 1.57E-03 |
| iii | aromatic compound biosynthetic process (GO:0019438)              | 0.49 | 3.97E-05 |
| iii | cellular aromatic compound metabolic process (GO:0006725)        | 0.49 | 4.30E-16 |
| iii | cellular nitrogen compound metabolic process (GO:0034641)        | 0.47 | 2.01E-20 |
| iii | regulation of cell cycle (GO:0051726)                            | 0.46 | 4.99E-05 |
| iii | nucleobase-containing compound biosynthetic process (GO:0034654) | 0.45 | 4.22E-05 |
| iii | heterocycle metabolic process (GO:0046483)                       | 0.45 | 1.51E-18 |
| iii | chromosome organization (GO:0051276)                             | 0.42 | 1.59E-07 |
| iii | regulation of mitotic cell cycle (GO:0007346)                    | 0.42 | 4.79E-04 |
| iii | nucleobase-containing compound metabolic process (GO:0006139)    | 0.41 | 5.89E-20 |
| iii | macromolecule biosynthetic process (GO:0009059)                  | 0.39 | 1.73E-12 |
| iii | nuclear chromosome segregation (GO:0098813)                      | 0.38 | 2.45E-03 |
| iii | mRNA metabolic process (GO:0016071)                              | 0.37 | 1.08E-05 |
| iii | chromatin organization (GO:0006325)                              | 0.35 | 2.38E-06 |
| iii | mRNA processing (GO:0006397)                                     | 0.35 | 4.90E-05 |
| iii | cellular nitrogen compound biosynthetic process (GO:0044271)     | 0.35 | 4.37E-13 |
| iii | RNA processing (GO:0006396)                                      | 0.35 | 2.29E-09 |
| iii | RNA metabolic process (GO:0016070)                               | 0.34 | 2.84E-15 |
| iii | cellular macromolecule biosynthetic process (GO:0034645)         | 0.34 | 3.48E-14 |
| iii | gene expression (GO:0010467)                                     | 0.33 | 3.84E-20 |
| iii | nucleic acid metabolic process (GO:0090304)                      | 0.3  | 8.28E-23 |
| iii | negative regulation of cell cycle (GO:0045786)                   | 0.28 | 3.60E-04 |
| iii | RNA splicing (GO:0008380)  | 0.26 | 8.09E-06 |

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| iii | histone modification (GO:0016570)  | 0.26   | 9.43E-05 |
| iii | covalent chromatin modification (GO:0016569)                               | 0.26   | 9.53E-05 |
| iii | ribonucleoprotein complex biogenesis (GO:0022613)                          | 0.26   | 1.81E-07 |
| iii | mRNA splicing, via spliceosome (GO:0000398)                                | 0.25   | 1.43E-05 |
| iii | RNA splicing, via transesterification reactions with bulged adenosine as r | 0.25   | 1.43E-05 |
| iii | RNA splicing, via transesterification reactions (GO:0000375)               | 0.25   | 9.99E-06 |
| iii | regulation of mitotic cell cycle phase transition (GO:1901990)             | 0.25   | 2.35E-04 |
| iii | tRNA metabolic process (GO:0006399)  | 0.25   | 1.15E-03 |
| iii | regulation of cell cycle phase transition (GO:1901987)                     | 0.24   | 1.66E-04 |
| iii | negative regulation of mitotic cell cycle (GO:0045930)                     | 0.24   | 5.68E-04 |
| iii | negative regulation of cell cycle process (GO:0010948)                     | 0.23   | 5.70E-04 |
| iii | DNA metabolic process (GO:0006259)   | 0.23   | 4.13E-08 |
| iii | ncRNA processing (GO:0034470)  | 0.22   | 9.01E-07 |
| iii | ncRNA metabolic process (GO:0034660)                                       | 0.22   | 2.07E-08 |
| iii | chromatin remodeling (GO:0006338)  | 0.22   | 2.01E-03 |
| iii | nucleic acid-templated transcription (GO:0097659)                          | 0.22   | 4.41E-06 |
| iii | transcription, DNA-templated (GO:0006351)                                  | 0.22   | 4.41E-06 |
| iii | macromolecule methylation (GO:0043414)                                     | 0.22   | 1.39E-03 |
| iii | RNA biosynthetic process (GO:0032774)                                      | 0.21   | 3.07E-06 |
| iii | peptidyl-lysine modification (GO:0018205)                                  | 0.21   | 1.40E-04 |
| iii | ribosome biogenesis (GO:0042254)   | 0.21   | 2.11E-06 |
| iii | methylation (GO:0032259)   | 0.2    | 6.82E-04 |
| iii | cellular response to DNA damage stimulus (GO:0006974)                      | 0.19   | 9.16E-10 |
| iii | DNA conformation change (GO:0071103)                                       | 0.18   | 2.31E-04 |
| iii | DNA replication (GO:0006260)   | 0.17   | 1.65E-03 |
| iii | rRNA processing (GO:0006364)   | 0.16   | 3.69E-05 |
| iii | rRNA metabolic process (GO:0016072)  | 0.15   | 1.76E-05 |
| iii | peptide biosynthetic process (GO:0043043)                                  | 0.15   | 1.09E-10 |
| iii | protein-DNA complex subunit organization (GO:0071824)                      | 0.14   | 3.65E-04 |
| iii | DNA packaging (GO:0006323)   | 0.14   | 3.74E-04 |
| iii | amide biosynthetic process (GO:0043604)                                    | 0.14   | 2.43E-11 |
| iii | cytoplasmic translation (GO:0002181)                                       | 0.14   | 1.71E-04 |
| iii | translation (GO:0006412)   | 0.12   | 3.39E-11 |
| iii | transcription from RNA polymerase II promoter (GO:0006366)                 | 0.12   | 2.56E-05 |
| iii | double-strand break repair (GO:0006302)                                    | 0.1    | 1.72E-03 |
| iii | DNA recombination (GO:0006310)   | 0.1    | 1.19E-03 |
| iii | DNA-templated transcription, initiation (GO:0006352)                       | 0.09   | 8.21E-04 |
| iii | mitotic DNA damage checkpoint (GO:0044773)                                 | 0.09   | 5.29E-04 |
| iii | mitotic DNA integrity checkpoint (GO:0044774)                              | 0.09   | 3.53E-04 |
| iii | regulation of G2/M transition of mitotic cell cycle (GO:0010389)           | 0.08   | 3.79E-04 |
| iii | regulation of cell cycle G2/M phase transition (GO:1902749)                | 0.08   | 2.42E-04 |
| iii | DNA damage checkpoint (GO:0000077)   | 0.08   | 1.60E-04 |
| iii | DNA integrity checkpoint (GO:0031570)                                      | 0.08   | 1.07E-04 |
| iii | mitotic cell cycle checkpoint (GO:0007093)                                 | 0.07   | 5.04E-05 |
| iii | negative regulation of mitotic cell cycle phase transition (GO:1901991)    | 0.07   | 3.51E-05 |
| iii | negative regulation of cell cycle phase transition (GO:1901988)            | 0.07   | 2.17E-05 |
| iii | cell cycle checkpoint (GO:0000075)   | 0.06   | 1.01E-05 |
| iii | DNA repair (GO:0006281)  | 0.04   | 3.64E-08 |
| iii | mitotic G2 DNA damage checkpoint (GO:0007095)                              | < 0.01 | 1.71E-04 |
| iii | mitotic G2/M transition checkpoint (GO:0044818)                            | < 0.01 | 1.12E-04 |
| iii | negative regulation of cell cycle G2/M phase transition (GO:1902750)       | < 0.01 | 7.30E-05 |
| iii | negative regulation of G2/M transition of mitotic cell cycle (GO:0010972)  | < 0.01 | 7.30E-05 |

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| iii | translational initiation (GO:0006413)                                       | < 0.01 | 2.14E-03 |
| iii | nucleosome organization (GO:0034728)  | < 0.01 | 3.94E-04 |
| iii | mitochondrial translation (GO:0032543)                                      | < 0.01 | 8.89E-06 |
| iii | mitochondrial gene expression (GO:0140053)                                  | < 0.01 | 2.52E-06 |
| iii | chromosome condensation (GO:0030261)  | < 0.01 | 2.14E-03 |
| iii | G2 DNA damage checkpoint (GO:0031572)                                       | < 0.01 | 1.71E-04 |
| iii | regulation of DNA metabolic process (GO:0051052)                            | < 0.01 | 1.50E-03 |
| iv  | glucan biosynthetic process (GO:0009250)                                    | 8.15   | 8.68E-04 |
| iv  | glycogen biosynthetic process (GO:0005978)                                  | 8.15   | 8.68E-04 |
| iv  | polysaccharide biosynthetic process (GO:0000271)                            | 5.65   | 2.86E-04 |
| iv  | cellular polysaccharide biosynthetic process (GO:0033692)                   | 5.65   | 2.86E-04 |
| iv  | mitochondrial electron transport, NADH to ubiquinone (GO:0006120)           | 5.51   | 2.02E-09 |
| iv  | regulation of muscle contraction (GO:0006937)                               | 5.44   | 7.50E-04 |
| iv  | flight (GO:0060361)   | 5.44   | 7.50E-04 |
| iv  | cellular carbohydrate biosynthetic process (GO:0034637)                     | 5.44   | 3.64E-05 |
| iv  | muscle contraction (GO:0006936)   | 5.44   | 3.64E-05 |
| iv  | hexose transmembrane transport (GO:0035428)                                 | 5.3    | 2.10E-05 |
| iv  | glucose transport (GO:0015758)  | 5.3    | 2.10E-05 |
| iv  | glucose import (GO:0046323)   | 5.3    | 2.10E-05 |
| iv  | monosaccharide transmembrane transport (GO:1905950)                         | 5.3    | 2.10E-05 |
| iv  | mitochondrial electron transport, ubiquinol to cytochrome c (GO:0006119)    | 5.1    | 2.40E-04 |
| iv  | hexose transport (GO:0008645)   | 5.05   | 3.06E-05 |
| iv  | monosaccharide transport (GO:0015749)                                       | 5.05   | 3.06E-05 |
| iv  | carbohydrate transmembrane transport (GO:0034219)                           | 5.05   | 3.06E-05 |
| iv  | muscle system process (GO:0003012)  | 5.02   | 3.98E-06 |
| iv  | ATP synthesis coupled proton transport (GO:0015986)                         | 4.95   | 2.28E-06 |
| iv  | energy coupled proton transport, down electrochemical gradient (GO:0005269) | 4.95   | 2.28E-06 |
| iv  | cell wall organization or biogenesis (GO:0071554)                           | 4.89   | 6.14E-04 |
| iv  | cell wall macromolecule metabolic process (GO:0044036)                      | 4.89   | 6.14E-04 |
| iv  | mitochondrial ATP synthesis coupled electron transport (GO:0042775)         | 4.89   | 2.45E-15 |
| iv  | ATP biosynthetic process (GO:0006754)                                       | 4.78   | 3.25E-06 |
| iv  | ATP synthesis coupled electron transport (GO:0042773)                       | 4.76   | 2.86E-15 |
| iv  | regulation of muscle system process (GO:0090257)                            | 4.66   | 1.56E-03 |
| iv  | oxidative phosphorylation (GO:0006119)                                      | 4.63   | 3.25E-15 |
| iv  | carbohydrate transport (GO:0008643)   | 4.57   | 3.50E-05 |
| iv  | electron transport chain (GO:0022900)                                       | 4.46   | 1.65E-15 |
| iv  | renal system process (GO:0003014)   | 4.45   | 1.52E-04 |
| iv  | respiratory electron transport chain (GO:0022904)                           | 4.42   | 6.95E-15 |
| iv  | ATP metabolic process (GO:0046034)  | 4.33   | 2.27E-21 |
| iv  | purine ribonucleoside triphosphate biosynthetic process (GO:0009206)        | 4.32   | 4.97E-06 |
| iv  | purine nucleoside triphosphate biosynthetic process (GO:0009145)            | 4.32   | 4.97E-06 |
| iv  | neuroblast development (GO:0014019)   | 4.32   | 1.20E-03 |
| iv  | ribonucleoside triphosphate biosynthetic process (GO:0009201)               | 4.19   | 6.77E-06 |
| iv  | purine ribonucleoside triphosphate metabolic process (GO:0009205)           | 4.18   | 6.04E-21 |
| iv  | myofibril assembly (GO:0030239)   | 4.17   | 4.01E-07 |
| iv  | ribonucleoside triphosphate metabolic process (GO:0009199)                  | 4.16   | 8.16E-21 |
| iv  | purine nucleoside triphosphate metabolic process (GO:0009144)               | 4.16   | 8.16E-21 |
| iv  | purine ribonucleoside monophosphate metabolic process (GO:0009167)          | 4.13   | 6.25E-21 |
| iv  | purine nucleoside monophosphate metabolic process (GO:0009126)              | 4.13   | 6.25E-21 |
| iv  | nucleoside triphosphate biosynthetic process (GO:0009142)                   | 4.08   | 9.12E-06 |
| iv  | stem cell development (GO:0048864)  | 4.08   | 1.63E-03 |
| iv  | midgut development (GO:0007494)   | 4.08   | 1.61E-05 |

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| iv | nucleoside triphosphate metabolic process (GO:0009141)                | 4.05 | 2.68E-20 |
| iv | ribonucleoside monophosphate metabolic process (GO:0009161)           | 4    | 2.71E-20 |
| iv | purine ribonucleoside monophosphate biosynthetic process (GO:0009166) | 3.97 | 6.91E-06 |
| iv | purine nucleoside monophosphate biosynthetic process (GO:0009127)     | 3.97 | 6.91E-06 |
| iv | nucleoside monophosphate metabolic process (GO:0009123)               | 3.93 | 6.39E-20 |
| iv | fatty acid elongation, polyunsaturated fatty acid (GO:0034626)        | 3.86 | 2.17E-03 |
| iv | fatty acid elongation, monounsaturated fatty acid (GO:0034625)        | 3.86 | 2.17E-03 |
| iv | fatty acid elongation, unsaturated fatty acid (GO:0019368)            | 3.86 | 2.17E-03 |
| iv | fatty acid elongation, saturated fatty acid (GO:0019367)              | 3.86 | 2.17E-03 |
| iv | cellular respiration (GO:0045333)                                     | 3.84 | 5.27E-16 |
| iv | generation of precursor metabolites and energy (GO:0006091)           | 3.76 | 4.64E-21 |
| iv | energy derivation by oxidation of organic compounds (GO:0015980)      | 3.74 | 1.29E-17 |
| iv | sarcomere organization (GO:0045214)                                   | 3.71 | 1.16E-04 |
| iv | striated muscle cell development (GO:0055002)                         | 3.67 | 2.98E-07 |
| iv | muscle cell development (GO:0055001)                                  | 3.61 | 3.86E-07 |
| iv | ribonucleoside monophosphate biosynthetic process (GO:0009156)        | 3.6  | 2.04E-05 |
| iv | purine ribonucleotide metabolic process (GO:0009150)                  | 3.49 | 2.99E-19 |
| iv | ribonucleotide metabolic process (GO:0009259)                         | 3.43 | 7.90E-19 |
| iv | purine nucleotide metabolic process (GO:0006163)                      | 3.43 | 7.90E-19 |
| iv | neuropeptide signaling pathway (GO:0007218)                           | 3.4  | 2.46E-06 |
| iv | carbohydrate biosynthetic process (GO:0016051)                        | 3.4  | 2.44E-05 |
| iv | ribose phosphate metabolic process (GO:0019693)                       | 3.38 | 9.26E-19 |
| iv | nucleoside monophosphate biosynthetic process (GO:0009124)            | 3.37 | 4.25E-05 |
| iv | tricarboxylic acid metabolic process (GO:0072350)                     | 3.34 | 7.42E-05 |
| iv | ADP metabolic process (GO:0046031)                                    | 3.32 | 1.88E-03 |
| iv | ribonucleoside diphosphate metabolic process (GO:0009185)             | 3.32 | 1.88E-03 |
| iv | purine ribonucleoside diphosphate metabolic process (GO:0009179)      | 3.32 | 1.88E-03 |
| iv | purine nucleoside diphosphate metabolic process (GO:0009135)          | 3.32 | 1.88E-03 |
| iv | purine-containing compound metabolic process (GO:0072521)             | 3.32 | 2.91E-20 |
| iv | fatty acid biosynthetic process (GO:0006633)                          | 3.26 | 5.48E-04 |
| iv | polysaccharide metabolic process (GO:0005976)                         | 3.26 | 1.34E-03 |
| iv | cellular polysaccharide metabolic process (GO:0044264)                | 3.26 | 1.34E-03 |
| iv | citrate metabolic process (GO:0006101)                                | 3.22 | 1.62E-04 |
| iv | aerobic respiration (GO:0009060)                                      | 3.15 | 2.52E-05 |
| iv | monocarboxylic acid biosynthetic process (GO:0072330)                 | 3.14 | 4.90E-04 |
| iv | tricarboxylic acid cycle (GO:0006099)                                 | 3.11 | 3.51E-04 |
| iv | nucleotide metabolic process (GO:0009117)                             | 3.07 | 8.70E-18 |
| iv | nucleoside phosphate metabolic process (GO:0006753)                   | 3.05 | 1.15E-17 |
| iv | drug catabolic process (GO:0042737)                                   | 2.97 | 1.13E-04 |
| iv | drug metabolic process (GO:0017144)                                   | 2.88 | 1.42E-21 |
| iv | striated muscle cell differentiation (GO:0051146)                     | 2.85 | 6.44E-07 |
| iv | potassium ion transport (GO:0006813)                                  | 2.84 | 1.11E-03 |
| iv | nucleobase-containing small molecule metabolic process (GO:0055086)   | 2.84 | 2.98E-19 |
| iv | muscle cell differentiation (GO:0042692)                              | 2.83 | 1.14E-07 |
| iv | carbohydrate catabolic process (GO:0016052)                           | 2.83 | 5.59E-04 |
| iv | actomyosin structure organization (GO:0031032)                        | 2.82 | 2.10E-05 |
| iv | purine ribonucleotide biosynthetic process (GO:0009152)               | 2.79 | 2.37E-05 |
| iv | nicotinamide nucleotide metabolic process (GO:0046496)                | 2.78 | 1.34E-03 |
| iv | pyridine nucleotide metabolic process (GO:0019362)                    | 2.78 | 1.34E-03 |
| iv | hexose metabolic process (GO:0019318)                                 | 2.78 | 9.49E-04 |
| iv | pyridine-containing compound metabolic process (GO:0072524)           | 2.77 | 1.10E-03 |
| iv | mesoderm development (GO:0007498)                                     | 2.77 | 2.03E-06 |

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| iv | purine nucleotide biosynthetic process (GO:0006164)                | 2.72 | 3.11E-05 |
| iv | purine-containing compound biosynthetic process (GO:0072522)       | 2.72 | 7.79E-06 |
| iv | monosaccharide metabolic process (GO:0005996)                      | 2.67 | 8.97E-04 |
| iv | ribonucleotide biosynthetic process (GO:0009260)                   | 2.65 | 4.19E-05 |
| iv | ribose phosphate biosynthetic process (GO:0046390)                 | 2.65 | 4.19E-05 |
| iv | hydrogen transport (GO:0006818)                                    | 2.64 | 2.39E-04 |
| iv | cellular carbohydrate metabolic process (GO:0044262)               | 2.6  | 1.94E-04 |
| iv | proton transport (GO:0015992)                                      | 2.56 | 4.49E-04 |
| iv | hydrogen ion transmembrane transport (GO:1902600)                  | 2.54 | 9.04E-04 |
| iv | oxidation-reduction process (GO:0055114)                           | 2.46 | 2.58E-23 |
| iv | organic acid biosynthetic process (GO:0016053)                     | 2.43 | 2.83E-04 |
| iv | carboxylic acid biosynthetic process (GO:0046394)                  | 2.43 | 2.83E-04 |
| iv | digestive system development (GO:0055123)                          | 2.35 | 1.22E-04 |
| iv | digestive tract development (GO:0048565)                           | 2.35 | 1.22E-04 |
| iv | carbohydrate metabolic process (GO:0005975)                        | 2.31 | 1.58E-08 |
| iv | carbohydrate derivative catabolic process (GO:1901136)             | 2.3  | 1.99E-03 |
| iv | regulation of membrane potential (GO:0042391)                      | 2.27 | 2.21E-03 |
| iv | nucleoside phosphate biosynthetic process (GO:1901293)             | 2.25 | 3.85E-04 |
| iv | nucleotide biosynthetic process (GO:0009165)                       | 2.25 | 3.85E-04 |
| iv | heart development (GO:0007507)                                     | 2.25 | 3.85E-04 |
| iv | circulatory system development (GO:0072359)                        | 2.25 | 3.85E-04 |
| iv | inorganic ion transmembrane transport (GO:0098660)                 | 2.22 | 3.47E-05 |
| iv | coenzyme metabolic process (GO:0006732)                            | 2.16 | 1.10E-04 |
| iv | small molecule metabolic process (GO:0044281)                      | 2.14 | 5.50E-21 |
| iv | inorganic cation transmembrane transport (GO:0098662)              | 2.14 | 3.58E-04 |
| iv | monovalent inorganic cation transport (GO:0015672)                 | 2.13 | 6.10E-05 |
| iv | organophosphate metabolic process (GO:0019637)                     | 2.13 | 4.80E-11 |
| iv | cation transmembrane transport (GO:0098655)                        | 2.12 | 2.30E-04 |
| iv | G-protein coupled receptor signaling pathway (GO:0007186)          | 2.07 | 1.41E-05 |
| iv | small molecule biosynthetic process (GO:0044283)                   | 2.07 | 1.87E-04 |
| iv | carbohydrate derivative metabolic process (GO:1901135)             | 2.04 | 4.11E-14 |
| iv | ion transmembrane transport (GO:0034220)                           | 2.02 | 1.60E-05 |
| iv | chitin-based cuticle development (GO:0040003)                      | 2    | 7.53E-05 |
| iv | monocarboxylic acid metabolic process (GO:0032787)                 | 1.97 | 8.55E-04 |
| iv | carboxylic acid metabolic process (GO:0019752)                     | 1.94 | 3.04E-07 |
| iv | transmembrane transport (GO:0055085)                               | 1.93 | 3.58E-10 |
| iv | cuticle development (GO:0042335)                                   | 1.92 | 1.27E-05 |
| iv | muscle structure development (GO:0061061)                          | 1.91 | 2.02E-05 |
| iv | cellular component assembly involved in morphogenesis (GO:0010927) | 1.91 | 1.38E-03 |
| iv | organic acid metabolic process (GO:0006082)                        | 1.88 | 8.60E-07 |
| iv | oxoacid metabolic process (GO:0043436)                             | 1.88 | 8.60E-07 |
| iv | locomotory behavior (GO:0007626)                                   | 1.85 | 5.56E-04 |
| iv | cation transport (GO:0006812)                                      | 1.82 | 4.59E-05 |
| iv | phosphorylation (GO:0016310)                                       | 1.78 | 1.65E-06 |
| iv | ion transport (GO:0006811)   | 1.78 | 3.78E-07 |
| iv | phosphorus metabolic process (GO:0006793)                          | 1.56 | 3.05E-07 |
| iv | phosphate-containing compound metabolic process (GO:0006796)       | 1.48 | 1.67E-05 |
| iv | cellular metabolic process (GO:0044237)                            | 0.85 | 2.65E-04 |
| iv | protein metabolic process (GO:0019538)                             | 0.79 | 4.10E-04 |
| iv | cellular aromatic compound metabolic process (GO:0006725)          | 0.77 | 1.47E-03 |
| iv | regulation of cellular metabolic process (GO:0031323)              | 0.77 | 3.80E-04 |
| iv | reproduction (GO:0000003)  | 0.77 | 1.35E-03 |

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| iv | regulation of primary metabolic process (GO:0080090)                             | 0.76 | 2.87E-04 |
| iv | positive regulation of biological process (GO:0048518)                           | 0.76 | 1.33E-03 |
| iv | heterocycle metabolic process (GO:0046483)                                       | 0.75 | 5.73E-04 |
| iv | multicellular organism reproduction (GO:0032504)                                 | 0.75 | 8.75E-04 |
| iv | regulation of metabolic process (GO:0019222)                                     | 0.75 | 4.80E-05 |
| iv | nucleobase-containing compound metabolic process (GO:0006139)                    | 0.75 | 5.85E-04 |
| iv | regulation of cellular biosynthetic process (GO:0031326)                         | 0.74 | 1.43E-03 |
| iv | regulation of biosynthetic process (GO:0009889)                                  | 0.74 | 1.23E-03 |
| iv | positive regulation of cellular process (GO:0048522)                             | 0.74 | 1.28E-03 |
| iv | regulation of cellular macromolecule biosynthetic process (GO:2000112)           | 0.73 | 1.33E-03 |
| iv | regulation of macromolecule biosynthetic process (GO:0010556)                    | 0.73 | 9.83E-04 |
| iv | cellular nitrogen compound metabolic process (GO:0034641)                        | 0.72 | 1.03E-05 |
| iv | reproductive process (GO:0022414)  | 0.72 | 3.72E-04 |
| iv | negative regulation of biological process (GO:0048519)                           | 0.71 | 1.65E-04 |
| iv | cellular component organization (GO:0016043)                                     | 0.7  | 6.54E-09 |
| iv | regulation of gene expression (GO:0010468)                                       | 0.7  | 6.86E-05 |
| iv | multi-organism reproductive process (GO:0044703)                                 | 0.69 | 2.04E-04 |
| iv | sexual reproduction (GO:0019953)   | 0.69 | 2.04E-04 |
| iv | multicellular organismal reproductive process (GO:0048609)                       | 0.69 | 1.95E-04 |
| iv | cellular component organization or biogenesis (GO:0071840)                       | 0.67 | 4.55E-11 |
| iv | regulation of nitrogen compound metabolic process (GO:0051171)                   | 0.67 | 7.22E-07 |
| iv | macromolecule metabolic process (GO:0043170)                                     | 0.67 | 2.61E-13 |
| iv | regulation of macromolecule metabolic process (GO:0060255)                       | 0.67 | 3.02E-07 |
| iv | developmental process involved in reproduction (GO:0003006)                      | 0.66 | 4.13E-04 |
| iv | cellular component biogenesis (GO:0044085)                                       | 0.66 | 3.61E-05 |
| iv | regulation of response to stimulus (GO:0048583)                                  | 0.65 | 1.42E-04 |
| iv | negative regulation of cellular process (GO:0048523)                             | 0.65 | 1.83E-05 |
| iv | negative regulation of macromolecule metabolic process (GO:0010605)              | 0.64 | 1.71E-03 |
| iv | regulation of cellular component organization (GO:0051128)                       | 0.61 | 9.89E-05 |
| iv | regulation of signal transduction (GO:0009966)                                   | 0.6  | 1.13E-04 |
| iv | cellular nitrogen compound biosynthetic process (GO:0044271)                     | 0.59 | 4.94E-05 |
| iv | oogenesis (GO:0048477)   | 0.56 | 5.54E-05 |
| iv | gamete generation (GO:0007276)   | 0.56 | 4.08E-07 |
| iv | cellular process involved in reproduction in multicellular organism (GO:0007276) | 0.56 | 8.81E-07 |
| iv | germ cell development (GO:0007281)   | 0.56 | 7.97E-06 |
| iv | female gamete generation (GO:0007292)  | 0.56 | 1.50E-05 |
| iv | cellular macromolecular complex assembly (GO:0034622)                            | 0.55 | 1.90E-03 |
| iv | macromolecular complex subunit organization (GO:0043933)                         | 0.53 | 1.08E-04 |
| iv | macromolecule localization (GO:0033036)  | 0.52 | 2.31E-06 |
| iv | organelle organization (GO:0006996)  | 0.52 | 1.67E-13 |
| iv | regulation of protein modification process (GO:0031399)                          | 0.5  | 1.65E-03 |
| iv | regulation of catalytic activity (GO:0050790)                                    | 0.5  | 1.65E-03 |
| iv | regulation of cellular protein metabolic process (GO:0032268)                    | 0.49 | 1.37E-05 |
| iv | macromolecule catabolic process (GO:0009057)                                     | 0.48 | 4.05E-05 |
| iv | protein modification process (GO:0036211)  | 0.48 | 1.51E-10 |
| iv | cellular protein modification process (GO:0006464)                               | 0.48 | 1.51E-10 |
| iv | regulation of protein metabolic process (GO:0051246)                             | 0.47 | 2.15E-06 |
| iv | macromolecule modification (GO:0043412)  | 0.46 | 6.36E-12 |
| iv | cellular localization (GO:0051641)   | 0.45 | 5.60E-10 |
| iv | cellular amide metabolic process (GO:0043603)                                    | 0.44 | 2.03E-05 |
| iv | vesicle-mediated transport (GO:0016192)  | 0.44 | 2.75E-07 |
| iv | protein localization (GO:0008104)  | 0.42 | 1.35E-07 |

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| iv | nitrogen compound transport (GO:0071705)                                | 0.42 | 8.75E-07 |
| iv | negative regulation of signal transduction (GO:0009968)                 | 0.41 | 3.88E-04 |
| iv | organelle localization (GO:0051640)                                     | 0.41 | 5.27E-04 |
| iv | spermatogenesis (GO:0007283)  | 0.41 | 3.95E-04 |
| iv | cellular protein metabolic process (GO:0044267)                         | 0.4  | 1.27E-20 |
| iv | cell division (GO:0051301)  | 0.39 | 4.09E-04 |
| iv | negative regulation of cellular protein metabolic process (GO:0032269)  | 0.39 | 1.88E-03 |
| iv | negative regulation of protein metabolic process (GO:0051248)           | 0.38 | 1.89E-03 |
| iv | establishment of localization in cell (GO:0051649)                      | 0.38 | 2.23E-10 |
| iv | response to extracellular stimulus (GO:0009991)                         | 0.38 | 1.95E-03 |
| iv | establishment of organelle localization (GO:0051656)                    | 0.38 | 7.76E-04 |
| iv | male gamete generation (GO:0048232)                                     | 0.38 | 3.87E-05 |
| iv | cellular protein localization (GO:0034613)                              | 0.36 | 2.46E-07 |
| iv | cellular macromolecule localization (GO:0070727)                        | 0.36 | 2.20E-08 |
| iv | cellular macromolecule metabolic process (GO:0044260)                   | 0.35 | 3.45E-41 |
| iv | cellular response to stress (GO:0033554)                                | 0.35 | 3.19E-10 |
| iv | microtubule-based process (GO:0007017)                                  | 0.35 | 3.35E-07 |
| iv | microtubule cytoskeleton organization (GO:0000226)                      | 0.35 | 1.60E-05 |
| iv | response to nutrient levels (GO:0031667)                                | 0.34 | 7.95E-04 |
| iv | endomembrane system organization (GO:0010256)                           | 0.32 | 1.91E-03 |
| iv | peptide metabolic process (GO:0006518)                                  | 0.32 | 2.23E-07 |
| iv | intracellular transport (GO:0046907)                                    | 0.31 | 6.83E-12 |
| iv | regulation of organelle organization (GO:0033043)                       | 0.31 | 2.97E-07 |
| iv | protein catabolic process (GO:0030163)                                  | 0.31 | 1.77E-06 |
| iv | detection of stimulus involved in sensory perception (GO:0050906)       | 0.3  | 1.03E-03 |
| iv | regulation of cell cycle (GO:0051726)                                   | 0.3  | 1.13E-07 |
| iv | regulation of gene expression, epigenetic (GO:0040029)                  | 0.29 | 1.85E-03 |
| iv | cell proliferation (GO:0008283)   | 0.28 | 3.87E-04 |
| iv | cell cycle (GO:0007049)   | 0.28 | 3.09E-13 |
| iv | macromolecule biosynthetic process (GO:0009059)                         | 0.28 | 2.08E-16 |
| iv | proteolysis involved in cellular protein catabolic process (GO:0051603) | 0.28 | 1.09E-06 |
| iv | cellular protein catabolic process (GO:0044257)                         | 0.27 | 1.10E-06 |
| iv | microtubule-based movement (GO:0007018)                                 | 0.27 | 6.83E-04 |
| iv | regulation of hydrolase activity (GO:0051336)                           | 0.27 | 2.02E-04 |
| iv | establishment of protein localization to organelle (GO:0072594)         | 0.27 | 6.95E-04 |
| iv | regulation of mitotic cell cycle (GO:0007346)                           | 0.27 | 9.42E-06 |
| iv | gene silencing (GO:0016458)   | 0.26 | 1.69E-03 |
| iv | cell cycle process (GO:0022402)   | 0.26 | 3.77E-12 |
| iv | protein localization to organelle (GO:0033365)                          | 0.25 | 3.76E-05 |
| iv | detection of chemical stimulus (GO:0009593)                             | 0.25 | 1.79E-04 |
| iv | cellular macromolecule biosynthetic process (GO:0034645)                | 0.24 | 1.21E-17 |
| iv | ubiquitin-dependent protein catabolic process (GO:0006511)              | 0.24 | 8.63E-07 |
| iv | modification-dependent protein catabolic process (GO:0019941)           | 0.24 | 8.63E-07 |
| iv | mitotic cell cycle (GO:0000278)   | 0.24 | 1.88E-10 |
| iv | proteasome-mediated ubiquitin-dependent protein catabolic process (G    | 0.24 | 1.27E-04 |
| iv | meiotic cell cycle (GO:0051321)   | 0.24 | 2.77E-05 |
| iv | modification-dependent macromolecule catabolic process (GO:0043632      | 0.24 | 4.31E-07 |
| iv | chromosome segregation (GO:0007059)                                     | 0.23 | 9.07E-05 |
| iv | peptide transport (GO:0015833)  | 0.23 | 1.46E-09 |
| iv | amide transport (GO:0042886)  | 0.23 | 1.52E-09 |
| iv | organelle fission (GO:0048285)  | 0.23 | 1.54E-07 |
| iv | establishment of protein localization (GO:0045184)                      | 0.23 | 5.16E-10 |



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|----|---|------|----------|
| iv | proteasomal protein catabolic process (GO:0010498)                      | 0.22 | 4.68E-05 |
| iv | cellular macromolecule catabolic process (GO:0044265)                   | 0.22 | 3.77E-10 |
| iv | gene expression (GO:0010467)  | 0.22 | 4.87E-26 |
| iv | meiotic nuclear division (GO:0140013)                                   | 0.22 | 3.20E-05 |
| iv | regulation of mitotic cell cycle phase transition (GO:1901990)          | 0.22 | 2.16E-04 |
| iv | cilium organization (GO:0044782)  | 0.22 | 1.48E-03 |
| iv | regulation of cell cycle phase transition (GO:1901987)                  | 0.22 | 2.24E-04 |
| iv | protein transport (GO:0015031)  | 0.21 | 6.07E-10 |
| iv | cell cycle checkpoint (GO:0000075)                                      | 0.21 | 1.04E-03 |
| iv | meiotic cell cycle process (GO:1903046)                                 | 0.21 | 1.68E-05 |
| iv | nuclear division (GO:0000280)   | 0.21 | 1.28E-07 |
| iv | tRNA metabolic process (GO:0006399)                                     | 0.21 | 1.09E-03 |
| iv | protein modification by small protein conjugation or removal (GO:00706) | 0.21 | 1.31E-07 |
| iv | mitotic cell cycle process (GO:1903047)                                 | 0.2  | 4.77E-09 |
| iv | negative regulation of mitotic cell cycle (GO:0045930)                  | 0.2  | 5.12E-04 |
| iv | chromatin organization (GO:0006325)                                     | 0.2  | 3.21E-09 |
| iv | negative regulation of cell cycle process (GO:0010948)                  | 0.2  | 5.16E-04 |
| iv | regulation of cell cycle process (GO:0010564)                           | 0.19 | 2.80E-06 |
| iv | regulation of chromosome organization (GO:0033044)                      | 0.18 | 1.84E-04 |
| iv | peptidyl-lysine modification (GO:0018205)                               | 0.18 | 1.84E-04 |
| iv | chromosome organization (GO:0051276)                                    | 0.17 | 3.50E-15 |
| iv | protein ubiquitination (GO:0016567)                                     | 0.16 | 2.16E-06 |
| iv | chromatin remodeling (GO:0006338)                                       | 0.16 | 1.20E-03 |
| iv | nucleic acid-templated transcription (GO:0097659)                       | 0.16 | 1.43E-06 |
| iv | transcription, DNA-templated (GO:0006351)                               | 0.16 | 1.43E-06 |
| iv | detection of chemical stimulus involved in sensory perception (GO:0050) | 0.16 | 1.22E-03 |
| iv | RNA biosynthetic process (GO:0032774)                                   | 0.16 | 9.84E-07 |
| iv | mitochondrial gene expression (GO:0140053)                              | 0.16 | 8.32E-04 |
| iv | nuclear chromosome segregation (GO:0098813)                             | 0.16 | 2.90E-05 |
| iv | negative regulation of cell cycle (GO:0045786)                          | 0.16 | 2.90E-05 |
| iv | amide biosynthetic process (GO:0043604)                                 | 0.16 | 5.86E-10 |
| iv | intracellular protein transport (GO:0006886)                            | 0.15 | 6.01E-10 |
| iv | protein modification by small protein conjugation (GO:0032446)          | 0.15 | 3.36E-07 |
| iv | RNA localization (GO:0006403)   | 0.15 | 9.32E-06 |
| iv | mitotic nuclear division (GO:0140014)                                   | 0.15 | 4.00E-04 |
| iv | histone modification (GO:0016570)                                       | 0.14 | 6.37E-06 |
| iv | covalent chromatin modification (GO:0016569)                            | 0.14 | 6.45E-06 |
| iv | ncRNA processing (GO:0034470)   | 0.14 | 1.14E-07 |
| iv | DNA metabolic process (GO:0006259)                                      | 0.14 | 1.23E-09 |
| iv | nucleobase-containing compound transport (GO:0015931)                   | 0.13 | 1.33E-04 |
| iv | ribonucleoprotein complex assembly (GO:0022618)                         | 0.12 | 4.09E-05 |
| iv | ribonucleoprotein complex subunit organization (GO:0071826)             | 0.11 | 2.05E-05 |
| iv | nucleic acid metabolic process (GO:0090304)                             | 0.11 | 1.37E-37 |
| iv | ncRNA metabolic process (GO:0034660)                                    | 0.11 | 7.72E-11 |
| iv | RNA metabolic process (GO:0016070)                                      | 0.11 | 2.00E-29 |
| iv | cellular response to DNA damage stimulus (GO:0006974)                   | 0.1  | 2.58E-11 |
| iv | DNA-templated transcription, initiation (GO:0006352)                    | 0.1  | 1.87E-03 |
| iv | mitotic sister chromatid segregation (GO:0000070)                       | 0.1  | 1.24E-03 |
| iv | protein acetylation (GO:0006473)  | 0.1  | 1.24E-03 |
| iv | RNA processing (GO:0006396)   | 0.1  | 1.13E-18 |
| iv | nucleic acid phosphodiester bond hydrolysis (GO:0090305)                | 0.09 | 8.77E-04 |
| iv | ribonucleoprotein complex biogenesis (GO:0022613)                       | 0.09 | 4.45E-11 |

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| iv | sister chromatid segregation (GO:0000819)                                  | 0.08   | 2.58E-04 |
| iv | translation (GO:0006412)   | 0.08   | 1.32E-11 |
| iv | peptide biosynthetic process (GO:0043043)                                  | 0.08   | 9.36E-12 |
| iv | cellularization (GO:0007349)   | 0.08   | 1.74E-04 |
| iv | protein-DNA complex subunit organization (GO:0071824)                      | 0.08   | 1.75E-04 |
| iv | DNA packaging (GO:0006323)   | 0.08   | 1.79E-04 |
| iv | macromolecule methylation (GO:0043414)                                     | 0.08   | 1.79E-04 |
| iv | ribosome biogenesis (GO:0042254)   | 0.08   | 1.77E-08 |
| iv | RNA transport (GO:0050658)   | 0.08   | 1.17E-04 |
| iv | nucleic acid transport (GO:0050657)  | 0.08   | 1.17E-04 |
| iv | establishment of RNA localization (GO:0051236)                             | 0.08   | 1.18E-04 |
| iv | cytoplasmic translation (GO:0002181)                                       | 0.08   | 7.90E-05 |
| iv | protein acylation (GO:0043543)   | 0.08   | 7.91E-05 |
| iv | endosomal transport (GO:0016197)   | 0.07   | 8.06E-05 |
| iv | methylation (GO:0032259)   | 0.07   | 8.06E-05 |
| iv | nuclear transport (GO:0051169)   | 0.07   | 5.73E-05 |
| iv | nucleocytoplasmic transport (GO:0006913)                                   | 0.07   | 5.73E-05 |
| iv | spindle organization (GO:0007051)  | 0.07   | 2.41E-05 |
| iv | DNA conformation change (GO:0071103)                                       | 0.07   | 2.41E-05 |
| iv | mRNA processing (GO:0006397)   | 0.06   | 1.52E-10 |
| iv | rRNA processing (GO:0006364)   | 0.06   | 3.29E-06 |
| iv | rRNA metabolic process (GO:0016072)  | 0.06   | 1.48E-06 |
| iv | mRNA metabolic process (GO:0016071)  | 0.05   | 1.06E-13 |
| iv | DNA repair (GO:0006281)  | 0.05   | 2.01E-07 |
| iv | mRNA splicing, via spliceosome (GO:0000398)                                | 0.04   | 2.37E-09 |
| iv | RNA splicing, via transesterification reactions with bulged adenosine as r | 0.04   | 2.37E-09 |
| iv | RNA splicing, via transesterification reactions (GO:0000375)               | 0.04   | 1.55E-09 |
| iv | RNA splicing (GO:0008380)  | 0.04   | 3.10E-10 |
| iv | protein polyubiquitination (GO:0000209)                                    | < 0.01 | 2.80E-04 |
| iv | Ras protein signal transduction (GO:0007265)                               | < 0.01 | 2.80E-04 |
| iv | protein-DNA complex assembly (GO:0065004)                                  | < 0.01 | 2.31E-03 |
| iv | protein export from nucleus (GO:0006611)                                   | < 0.01 | 1.49E-03 |
| iv | regulation of mitotic nuclear division (GO:0007088)                        | < 0.01 | 6.96E-04 |
| iv | positive regulation of chromosome organization (GO:2001252)                | < 0.01 | 2.27E-03 |
| iv | protein lipidation (GO:0006497)  | < 0.01 | 9.78E-04 |
| iv | RNA export from nucleus (GO:0006405)                                       | < 0.01 | 9.95E-04 |
| iv | mRNA catabolic process (GO:0006402)  | < 0.01 | 1.03E-03 |
| iv | RNA catabolic process (GO:0006401)   | < 0.01 | 2.02E-04 |
| iv | regulation of nuclear division (GO:0051783)                                | < 0.01 | 2.99E-04 |
| iv | DNA recombination (GO:0006310)   | < 0.01 | 2.86E-04 |
| iv | double-strand break repair (GO:0006302)                                    | < 0.01 | 4.29E-04 |
| iv | ribosomal large subunit biogenesis (GO:0042273)                            | < 0.01 | 1.54E-03 |
| iv | lipoprotein biosynthetic process (GO:0042158)                              | < 0.01 | 9.78E-04 |
| iv | lipoprotein metabolic process (GO:0042157)                                 | < 0.01 | 6.64E-04 |
| iv | nuclear export (GO:0051168)  | < 0.01 | 4.45E-04 |
| v  | spindle assembly involved in female meiosis (GO:0007056)                   | 3.48   | 2.03E-03 |
| v  | SMAD protein import into nucleus (GO:0007184)                              | 3.48   | 3.99E-03 |
| v  | regulation of DNA recombination (GO:0000018)                               | 3.48   | 1.31E-03 |
| v  | negative regulation of DNA recombination (GO:0045910)                      | 3.48   | 3.99E-03 |
| v  | nuclear pore organization (GO:0006999)                                     | 3.48   | 3.99E-03 |
| v  | nuclear-transcribed mRNA catabolic process, exonucleolytic (GO:000029)     | 3.48   | 6.00E-03 |
| v  | ncRNA transcription (GO:0098781)   | 3.48   | 1.77E-03 |

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|---|---|------|----------|
| v | snRNA metabolic process (GO:0016073)  | 3.38 | 1.31E-06 |
| v | snRNA processing (GO:0016180)   | 3.34 | 6.01E-05 |
| v | DNA replication initiation (GO:0006270)   | 3.33 | 9.00E-05 |
| v | establishment of chromosome localization (GO:0051303)                           | 3.33 | 9.00E-05 |
| v | DNA amplification (GO:0006277)  | 3.32 | 1.35E-04 |
| v | snRNA 3'-end processing (GO:0034472)  | 3.32 | 1.35E-04 |
| v | ribosomal large subunit assembly (GO:0000027)                                   | 3.31 | 2.03E-04 |
| v | eggshell chorion gene amplification (GO:0007307)                                | 3.31 | 3.06E-04 |
| v | metaphase plate congression (GO:0051310)  | 3.31 | 3.06E-04 |
| v | chromosome separation (GO:0051304)  | 3.31 | 3.06E-04 |
| v | negative regulation of chromosome segregation (GO:0051985)                      | 3.3  | 4.62E-04 |
| v | negative regulation of sister chromatid segregation (GO:0033046)                | 3.29 | 7.00E-04 |
| v | mitotic metaphase plate congression (GO:0007080)                                | 3.26 | 1.62E-03 |
| v | regulation of lamellipodium organization (GO:1902743)                           | 3.26 | 1.62E-03 |
| v | regulation of lamellipodium assembly (GO:0010591)                               | 3.26 | 1.62E-03 |
| v | negative regulation of metaphase/anaphase transition of cell cycle (GO:0000000) | 3.26 | 1.62E-03 |
| v | negative regulation of chromosome separation (GO:1905819)                       | 3.26 | 1.62E-03 |
| v | negative regulation of mitotic sister chromatid separation (GO:2000816)         | 3.25 | 2.48E-03 |
| v | negative regulation of mitotic sister chromatid segregation (GO:0033048)        | 3.25 | 2.48E-03 |
| v | negative regulation of mitotic metaphase/anaphase transition (GO:0045000)       | 3.25 | 2.48E-03 |
| v | ncRNA 3'-end processing (GO:0043628)  | 3.25 | 1.92E-05 |
| v | G1/S transition of mitotic cell cycle (GO:0000082)                              | 3.23 | 3.81E-03 |
| v | mitotic spindle assembly checkpoint (GO:0007094)                                | 3.23 | 3.81E-03 |
| v | cell cycle G1/S phase transition (GO:0044843)                                   | 3.23 | 3.81E-03 |
| v | mitotic spindle checkpoint (GO:0071174)   | 3.23 | 3.81E-03 |
| v | spindle assembly checkpoint (GO:0071173)  | 3.23 | 3.81E-03 |
| v | RNA surveillance (GO:0071025)   | 3.23 | 3.81E-03 |
| v | regulation of mitotic cell cycle, embryonic (GO:0009794)                        | 3.23 | 3.81E-03 |
| v | chromosome localization (GO:0050000)  | 3.22 | 3.92E-05 |
| v | DNA replication checkpoint (GO:0000076)   | 3.21 | 5.88E-03 |
| v | attachment of spindle microtubules to kinetochore (GO:0008608)                  | 3.21 | 5.88E-03 |
| v | nuclear RNA surveillance (GO:0071027)   | 3.21 | 5.88E-03 |
| v | spliceosomal snRNP assembly (GO:0000387)  | 3.13 | 6.32E-04 |
| v | nucleotide-excision repair (GO:0006289)   | 3.08 | 1.83E-04 |
| v | transcription initiation from RNA polymerase II promoter (GO:0006367)           | 3.06 | 1.10E-09 |
| v | maturation of LSU-rRNA (GO:0000470)   | 3.06 | 2.77E-04 |
| v | karyosome formation (GO:0030717)  | 3.05 | 3.07E-05 |
| v | negative regulation of chromosome organization (GO:2001251)                     | 3.03 | 6.16E-06 |
| v | ribosomal large subunit biogenesis (GO:0042273)                                 | 3.03 | 7.59E-09 |
| v | establishment or maintenance of neuroblast polarity (GO:0045196)                | 3.02 | 4.90E-03 |
| v | spindle checkpoint (GO:0031577)   | 3.02 | 4.90E-03 |
| v | DNA-dependent DNA replication (GO:0006261)                                      | 3.01 | 3.93E-10 |
| v | mitotic cell cycle checkpoint (GO:0007093)                                      | 3.01 | 1.52E-13 |
| v | cell cycle checkpoint (GO:0000075)  | 3    | 5.34E-15 |
| v | DNA integrity checkpoint (GO:0031570)   | 3    | 2.95E-12 |
| v | regulation of DNA metabolic process (GO:0051052)                                | 2.99 | 5.33E-08 |
| v | DNA damage checkpoint (GO:0000077)  | 2.98 | 5.81E-12 |
| v | mitotic DNA integrity checkpoint (GO:0044774)                                   | 2.98 | 4.47E-11 |
| v | regulation of transposition (GO:0010528)  | 2.98 | 8.85E-04 |
| v | RNA 3'-end processing (GO:0031123)  | 2.97 | 1.51E-08 |
| v | mitotic DNA damage checkpoint (GO:0044773)                                      | 2.97 | 9.79E-11 |
| v | mitotic G2/M transition checkpoint (GO:0044818)                                 | 2.97 | 5.25E-10 |

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| v | homologous recombination (GO:0035825)                                     | 2.97 | 2.82E-05 |
| v | DNA replication (GO:0006260)  | 2.97 | 1.83E-11 |
| v | cell cycle DNA replication (GO:0044786)                                   | 2.96 | 2.25E-04 |
| v | negative regulation of cell cycle phase transition (GO:1901988)           | 2.96 | 1.23E-13 |
| v | cytoplasmic translation (GO:0002181)                                      | 2.96 | 1.83E-13 |
| v | negative regulation of mitotic cell cycle phase transition (GO:1901991)   | 2.96 | 1.83E-13 |
| v | negative regulation of chromatin organization (GO:1905268)                | 2.96 | 1.31E-03 |
| v | negative regulation of transposition (GO:0010529)                         | 2.96 | 1.31E-03 |
| v | reciprocal meiotic recombination (GO:0007131)                             | 2.95 | 4.16E-05 |
| v | mitotic G2 DNA damage checkpoint (GO:0007095)                             | 2.95 | 1.65E-09 |
| v | G2 DNA damage checkpoint (GO:0031572)                                     | 2.95 | 1.65E-09 |
| v | pole plasm mRNA localization (GO:0019094)                                 | 2.94 | 1.11E-05 |
| v | negative regulation of cell cycle G2/M phase transition (GO:1902750)      | 2.94 | 4.73E-10 |
| v | negative regulation of G2/M transition of mitotic cell cycle (GO:0010972) | 2.94 | 4.73E-10 |
| v | pole plasm oskar mRNA localization (GO:0045451)                           | 2.94 | 6.13E-05 |
| v | chromosome condensation (GO:0030261)                                      | 2.93 | 5.66E-07 |
| v | regulation of cell cycle G2/M phase transition (GO:1902749)               | 2.93 | 3.72E-11 |
| v | mRNA cleavage (GO:0006379)  | 2.93 | 1.96E-03 |
| v | regulation of response to DNA damage stimulus (GO:2001020)                | 2.93 | 1.96E-03 |
| v | positive regulation of DNA metabolic process (GO:0051054)                 | 2.93 | 1.96E-03 |
| v | regulation of G2/M transition of mitotic cell cycle (GO:0010389)          | 2.92 | 8.23E-11 |
| v | RNA secondary structure unwinding (GO:0010501)                            | 2.92 | 9.05E-05 |
| v | sister chromatid segregation (GO:0000819)                                 | 2.91 | 5.77E-12 |
| v | proteasome assembly (GO:0043248)  | 2.9  | 2.92E-03 |
| v | negative regulation of nuclear division (GO:0051784)                      | 2.9  | 7.57E-04 |
| v | negative regulation of DNA metabolic process (GO:0051053)                 | 2.9  | 7.57E-04 |
| v | mitotic sister chromatid segregation (GO:0000070)                         | 2.89 | 2.42E-10 |
| v | negative regulation of mitotic cell cycle (GO:0045930)                    | 2.89 | 1.41E-14 |
| v | spindle assembly involved in meiosis (GO:0090306)                         | 2.87 | 1.14E-03 |
| v | DNA-templated transcription, initiation (GO:0006352)                      | 2.87 | 7.57E-10 |
| v | DNA biosynthetic process (GO:0071897)                                     | 2.87 | 1.41E-05 |
| v | pole plasm RNA localization (GO:0007316)                                  | 2.87 | 1.41E-05 |
| v | transcription from RNA polymerase III promoter (GO:0006383)               | 2.87 | 4.36E-03 |
| v | response to ionizing radiation (GO:0010212)                               | 2.87 | 8.15E-05 |
| v | germarium-derived oocyte fate determination (GO:0007294)                  | 2.86 | 2.92E-04 |
| v | tRNA aminoacylation (GO:0043039)  | 2.86 | 2.08E-05 |
| v | tRNA aminoacylation for protein translation (GO:0006418)                  | 2.86 | 2.08E-05 |
| v | positive regulation of chromatin silencing (GO:0031937)                   | 2.85 | 1.71E-03 |
| v | negative regulation of cell cycle process (GO:0010948)                    | 2.84 | 3.09E-14 |
| v | DNA recombination (GO:0006310)  | 2.84 | 3.47E-09 |
| v | pole cell development (GO:0007277)  | 2.84 | 4.33E-04 |
| v | intracellular mRNA localization (GO:0008298)                              | 2.83 | 1.92E-08 |
| v | negative regulation of cell cycle (GO:0045786)                            | 2.83 | 2.90E-17 |
| v | chromatin assembly or disassembly (GO:0006333)                            | 2.83 | 1.36E-05 |
| v | intracellular mRNA localization involved in anterior/posterior axis speci | 2.83 | 3.33E-06 |
| v | germarium-derived female germ-line cyst formation (GO:0030727)            | 2.82 | 2.57E-03 |
| v | nuclear chromosome segregation (GO:0098813)                               | 2.81 | 5.18E-17 |
| v | regulation of metaphase/anaphase transition of cell cycle (GO:1902099)    | 2.81 | 2.71E-04 |
| v | intracellular mRNA localization involved in pattern specification process | 2.8  | 1.97E-06 |
| v | regulation of cell cycle phase transition (GO:1901987)                    | 2.79 | 3.53E-16 |
| v | sister chromatid cohesion (GO:0007062)                                    | 2.78 | 4.04E-04 |
| v | RNA interference (GO:0016246)   | 2.78 | 4.04E-04 |

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| v | histone H3 acetylation (GO:0043966)                                  | 2.78 | 4.04E-04 |
| v | regulation of mitotic metaphase/anaphase transition (GO:0030071)     | 2.78 | 4.04E-04 |
| v | pole cell formation (GO:0007279)                                     | 2.78 | 3.86E-03 |
| v | regulation of cell cycle G1/S phase transition (GO:1902806)          | 2.78 | 9.53E-04 |
| v | amino acid activation (GO:0043038)                                   | 2.78 | 2.73E-05 |
| v | regulation of DNA replication (GO:0006275)                           | 2.78 | 9.53E-04 |
| v | regulation of G1/S transition of mitotic cell cycle (GO:2000045)     | 2.78 | 9.53E-04 |
| v | centriole assembly (GO:0098534)                                      | 2.78 | 9.53E-04 |
| v | rRNA metabolic process (GO:0016072)                                  | 2.78 | 1.90E-15 |
| v | histone acetylation (GO:0016573)                                     | 2.77 | 1.41E-08 |
| v | regulation of mitotic cell cycle phase transition (GO:1901990)       | 2.77 | 1.12E-15 |
| v | recombinational repair (GO:0000725)                                  | 2.77 | 1.58E-05 |
| v | double-strand break repair via homologous recombination (GO:0000724) | 2.77 | 1.58E-05 |
| v | germ-line cyst formation (GO:0048134)                                | 2.76 | 6.03E-04 |
| v | protein-DNA complex assembly (GO:0065004)                            | 2.76 | 6.68E-07 |
| v | nucleosome assembly (GO:0006334)                                     | 2.76 | 6.03E-04 |
| v | chromosome segregation (GO:0007059)                                  | 2.76 | 4.46E-18 |
| v | meiotic chromosome segregation (GO:0045132)                          | 2.76 | 1.21E-08 |
| v | transcription from RNA polymerase II promoter (GO:0006366)           | 2.76 | 2.82E-13 |
| v | centriole replication (GO:0007099)                                   | 2.76 | 1.41E-03 |
| v | histone H3-K4 methylation (GO:0051568)                               | 2.76 | 1.41E-03 |
| v | regulation of chromosome segregation (GO:0051983)                    | 2.75 | 2.33E-05 |
| v | internal protein amino acid acetylation (GO:0006475)                 | 2.75 | 1.78E-08 |
| v | peptidyl-lysine acetylation (GO:0018394)                             | 2.75 | 1.78E-08 |
| v | internal peptidyl-lysine acetylation (GO:0018393)                    | 2.75 | 1.78E-08 |
| v | regulation of meiotic cell cycle (GO:0051445)                        | 2.75 | 5.81E-03 |
| v | chromatin assembly (GO:0031497)                                      | 2.75 | 5.86E-05 |
| v | rRNA processing (GO:0006364)   | 2.74 | 2.66E-14 |
| v | germarium-derived oocyte differentiation (GO:0030706)                | 2.74 | 2.16E-04 |
| v | mitotic nuclear division (GO:0140014)                                | 2.73 | 7.94E-12 |
| v | DNA repair (GO:0006281)  | 2.73 | 1.69E-16 |
| v | gene silencing by RNA (GO:0031047)                                   | 2.73 | 5.63E-06 |
| v | mRNA 3'-end processing (GO:0031124)                                  | 2.72 | 3.19E-04 |
| v | histone lysine methylation (GO:0034968)                              | 2.72 | 5.07E-05 |
| v | regulation of sister chromatid segregation (GO:0033045)              | 2.72 | 5.07E-05 |
| v | ribosome biogenesis (GO:0042254)                                     | 2.71 | 2.88E-20 |
| v | protein import into nucleus (GO:0006606)                             | 2.7  | 1.24E-06 |
| v | nuclear import (GO:0051170)  | 2.7  | 1.24E-06 |
| v | pole plasm assembly (GO:0007315)                                     | 2.69 | 4.49E-06 |
| v | female germ-line cyst formation (GO:0048135)                         | 2.69 | 3.12E-03 |
| v | mitotic chromosome condensation (GO:0007076)                         | 2.69 | 3.12E-03 |
| v | peptidyl-lysine methylation (GO:0018022)                             | 2.69 | 2.84E-05 |
| v | ribonucleoprotein complex biogenesis (GO:0022613)                    | 2.69 | 4.18E-27 |
| v | regulation of chromosome separation (GO:1905818)                     | 2.68 | 1.84E-04 |
| v | protein acetylation (GO:0006473)                                     | 2.68 | 1.08E-08 |
| v | rRNA modification (GO:0000154)                                       | 2.68 | 1.24E-03 |
| v | RNA export from nucleus (GO:0006405)                                 | 2.68 | 4.14E-07 |
| v | regulation of mitotic cell cycle (GO:0007346)                        | 2.67 | 3.25E-23 |
| v | nuclear export (GO:0051168)  | 2.67 | 9.68E-08 |
| v | female meiosis chromosome segregation (GO:0016321)                   | 2.66 | 2.70E-04 |
| v | regulation of mitotic sister chromatid separation (GO:0010965)       | 2.66 | 2.70E-04 |
| v | ncRNA metabolic process (GO:0034660)                                 | 2.66 | 1.70E-27 |

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|---|--|------|----------|
| v | double-strand break repair (GO:0006302)                                    | 2.66 | 1.41E-07 |
| v | cellular response to DNA damage stimulus (GO:0006974)                      | 2.65 | 1.85E-28 |
| v | gene silencing (GO:0016458)  | 2.65 | 2.98E-12 |
| v | protein localization to nucleus (GO:0034504)                               | 2.65 | 8.78E-07 |
| v | RNA splicing, via transesterification reactions (GO:0000375)               | 2.65 | 5.25E-19 |
| v | positive regulation of chromatin organization (GO:1905269)                 | 2.65 | 2.48E-05 |
| v | peptidyl-lysine modification (GO:0018205)                                  | 2.65 | 2.82E-13 |
| v | histone methylation (GO:0016571)   | 2.64 | 1.41E-05 |
| v | regulation of embryonic pattern specification (GO:1902875)                 | 2.64 | 1.82E-03 |
| v | mitotic cell cycle phase transition (GO:0044772)                           | 2.64 | 1.03E-03 |
| v | mRNA splicing, via spliceosome (GO:0000398)                                | 2.64 | 1.12E-18 |
| v | RNA splicing, via transesterification reactions with bulged adenosine as r | 2.64 | 1.12E-18 |
| v | cell cycle phase transition (GO:0044770)                                   | 2.64 | 3.96E-04 |
| v | meiosis I (GO:0007127)   | 2.63 | 2.76E-08 |
| v | regulation of cell cycle process (GO:0010564)                              | 2.63 | 2.12E-19 |
| v | mRNA transport (GO:0051028)  | 2.63 | 3.60E-05 |
| v | DNA metabolic process (GO:0006259)   | 2.63 | 4.38E-26 |
| v | RNA phosphodiester bond hydrolysis (GO:0090501)                            | 2.63 | 8.09E-06 |
| v | cytoplasm organization (GO:0007028)  | 2.63 | 4.91E-06 |
| v | mitotic cell cycle process (GO:1903047)                                    | 2.62 | 2.41E-29 |
| v | ribosomal small subunit biogenesis (GO:0042274)                            | 2.62 | 4.37E-07 |
| v | female meiotic nuclear division (GO:0007143)                               | 2.62 | 1.73E-07 |
| v | covalent chromatin modification (GO:0016569)                               | 2.62 | 1.45E-15 |
| v | mitotic cell cycle (GO:0000278)  | 2.62 | 4.20E-39 |
| v | protein-DNA complex subunit organization (GO:0071824)                      | 2.62 | 8.73E-10 |
| v | histone modification (GO:0016570)  | 2.62 | 2.11E-15 |
| v | RNA splicing (GO:0008380)  | 2.61 | 8.54E-20 |
| v | positive regulation of chromosome organization (GO:2001252)                | 2.61 | 7.18E-06 |
| v | regulation of oocyte development (GO:0060281)                              | 2.61 | 2.68E-03 |
| v | regulation of transcription initiation from RNA polymerase II promoter (C  | 2.61 | 2.68E-03 |
| v | protein export from nucleus (GO:0006611)                                   | 2.61 | 2.70E-06 |
| v | mRNA polyadenylation (GO:0006378)  | 2.61 | 2.68E-03 |
| v | regulation of mitotic sister chromatid segregation (GO:0033047)            | 2.61 | 3.52E-04 |
| v | posttranscriptional gene silencing by RNA (GO:0035194)                     | 2.61 | 5.23E-05 |
| v | regulation of intracellular mRNA localization (GO:1904580)                 | 2.61 | 2.68E-03 |
| v | regulation of DNA-templated transcription, initiation (GO:2000142)         | 2.61 | 2.68E-03 |
| v | chromosome organization involved in meiotic cell cycle (GO:0070192)        | 2.61 | 2.68E-03 |
| v | regulation of pole plasm oskar mRNA localization (GO:0007317)              | 2.61 | 2.68E-03 |
| v | chromatin remodeling (GO:0006338)  | 2.61 | 1.27E-09 |
| v | mRNA processing (GO:0006397)   | 2.59 | 6.01E-22 |
| v | posttranscriptional gene silencing (GO:0016441)                            | 2.59 | 4.40E-05 |
| v | oocyte fate determination (GO:0030716)                                     | 2.59 | 5.18E-04 |
| v | nucleic acid-templated transcription (GO:0097659)                          | 2.58 | 1.33E-17 |
| v | transcription, DNA-templated (GO:0006351)                                  | 2.58 | 1.33E-17 |
| v | RNA biosynthetic process (GO:0032774)                                      | 2.58 | 7.28E-18 |
| v | chromosome organization (GO:0051276)                                       | 2.58 | 2.65E-44 |
| v | ribonucleoprotein complex localization (GO:0071166)                        | 2.58 | 1.53E-05 |
| v | nucleic acid metabolic process (GO:0090304)                                | 2.58 | 4.86E-97 |
| v | maturation of SSU-rRNA (GO:0030490)  | 2.58 | 2.48E-05 |
| v | regulation of protein stability (GO:0031647)                               | 2.58 | 2.48E-05 |
| v | positive regulation of plasma membrane bounded cell projection assembl     | 2.57 | 3.94E-03 |
| v | translation (GO:0006412)   | 2.57 | 4.29E-25 |

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|---|--|------|----------|
| v | positive regulation of cell cycle (GO:0045787)                             | 2.57 | 3.33E-06 |
| v | nuclear transport (GO:0051169)   | 2.56 | 2.55E-10 |
| v | nucleocytoplasmic transport (GO:0006913)                                   | 2.56 | 2.55E-10 |
| v | ribonucleoprotein complex export from nucleus (GO:0071426)                 | 2.56 | 2.24E-05 |
| v | RNA localization (GO:0006403)  | 2.56 | 1.96E-14 |
| v | ncRNA processing (GO:0034470)  | 2.56 | 1.86E-19 |
| v | RNA metabolic process (GO:0016070)   | 2.56 | 2.67E-71 |
| v | nuclear migration (GO:0007097)   | 2.55 | 1.24E-03 |
| v | oocyte microtubule cytoskeleton organization (GO:0016325)                  | 2.55 | 1.24E-03 |
| v | peptide biosynthetic process (GO:0043043)                                  | 2.55 | 5.20E-25 |
| v | mRNA metabolic process (GO:0016071)  | 2.55 | 3.79E-26 |
| v | regulation of chromatin silencing (GO:0031935)                             | 2.55 | 9.38E-05 |
| v | RNA processing (GO:0006396)  | 2.55 | 5.76E-42 |
| v | spindle assembly (GO:0051225)  | 2.55 | 1.59E-06 |
| v | RNA polyadenylation (GO:0043631)   | 2.54 | 3.32E-03 |
| v | mRNA-containing ribonucleoprotein complex export from nucleus (GO:0006406) | 2.54 | 4.06E-04 |
| v | mRNA export from nucleus (GO:0006406)                                      | 2.54 | 4.06E-04 |
| v | positive regulation of mitotic cell cycle (GO:0045931)                     | 2.54 | 4.06E-04 |
| v | maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S)  | 2.54 | 4.06E-04 |
| v | oocyte anterior/posterior axis specification (GO:0007314)                  | 2.54 | 5.38E-07 |
| v | ribonucleoprotein complex subunit organization (GO:0071826)                | 2.53 | 2.70E-12 |
| v | positive regulation of protein complex assembly (GO:0031334)               | 2.53 | 1.37E-04 |
| v | positive regulation of cell cycle phase transition (GO:1901989)            | 2.53 | 5.80E-03 |
| v | maternal determination of anterior/posterior axis, embryo (GO:0008358)     | 2.53 | 3.09E-07 |
| v | amide biosynthetic process (GO:0043604)                                    | 2.53 | 1.70E-25 |
| v | nuclear division (GO:0000280)  | 2.53 | 2.07E-22 |
| v | regulation of chromosome organization (GO:0033044)                         | 2.52 | 9.69E-12 |
| v | telomere maintenance (GO:0000723)  | 2.52 | 1.82E-03 |
| v | telomere organization (GO:0032200)   | 2.52 | 1.82E-03 |
| v | cell cycle (GO:0007049)  | 2.52 | 1.54E-51 |
| v | negative regulation of gene expression, epigenetic (GO:0045814)            | 2.51 | 1.12E-06 |
| v | ribonucleoprotein complex assembly (GO:0022618)                            | 2.51 | 2.44E-11 |
| v | microtubule organizing center organization (GO:0031023)                    | 2.51 | 6.41E-07 |
| v | regulation of DNA-templated transcription, elongation (GO:0032784)         | 2.51 | 4.89E-03 |
| v | regulation of gene silencing by RNA (GO:0060966)                           | 2.51 | 4.89E-03 |
| v | chromatin organization (GO:0006325)  | 2.5  | 4.33E-26 |
| v | chromatin silencing (GO:0006342)   | 2.5  | 1.63E-06 |
| v | meiotic cell cycle process (GO:1903046)                                    | 2.5  | 8.73E-16 |
| v | cell cycle process (GO:0022402)  | 2.5  | 2.26E-42 |
| v | meiotic nuclear division (GO:0140013)                                      | 2.5  | 6.45E-15 |
| v | regulation of cell cycle (GO:0051726)                                      | 2.49 | 1.96E-29 |
| v | gene expression (GO:0010467)   | 2.49 | 1.63E-86 |
| v | positive regulation of protein polymerization (GO:0032273)                 | 2.49 | 2.66E-03 |
| v | positive regulation of cell cycle process (GO:0090068)                     | 2.49 | 8.64E-04 |
| v | centrosome duplication (GO:0051298)  | 2.49 | 8.64E-04 |
| v | regulation of gene silencing (GO:0060968)                                  | 2.49 | 8.16E-07 |
| v | regulation of chromatin organization (GO:1902275)                          | 2.48 | 5.37E-08 |
| v | organelle fission (GO:0048285)   | 2.48 | 3.24E-22 |
| v | meiotic cell cycle (GO:0051321)  | 2.47 | 5.92E-16 |
| v | heterochromatin organization (GO:0070828)                                  | 2.47 | 4.89E-04 |
| v | centrosome cycle (GO:0007098)  | 2.47 | 3.38E-06 |
| v | nucleosome organization (GO:0034728)                                       | 2.46 | 5.80E-06 |

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|---|--|------|----------|
| v | ATP-dependent chromatin remodeling (GO:0043044)                                | 2.46 | 4.21E-04 |
| v | oocyte differentiation (GO:0009994)  | 2.45 | 3.18E-12 |
| v | establishment of RNA localization (GO:0051236)                                 | 2.45 | 1.14E-08 |
| v | oocyte axis specification (GO:0007309)   | 2.45 | 2.21E-09 |
| v | protein acylation (GO:0043543)   | 2.45 | 6.67E-09 |
| v | microtubule cytoskeleton organization involved in mitosis (GO:1902850)         | 2.45 | 1.04E-07 |
| v | nucleus localization (GO:0051647)  | 2.45 | 7.08E-04 |
| v | mitochondrial translation (GO:0032543)   | 2.44 | 8.57E-08 |
| v | RNA transport (GO:0050658)   | 2.44 | 1.64E-08 |
| v | nucleic acid transport (GO:0050657)  | 2.44 | 1.64E-08 |
| v | germarium-derived egg chamber formation (GO:0007293)                           | 2.44 | 6.16E-10 |
| v | protein methylation (GO:0006479)   | 2.44 | 7.02E-06 |
| v | protein alkylation (GO:0008213)  | 2.44 | 7.02E-06 |
| v | oocyte development (GO:0048599)  | 2.44 | 1.21E-10 |
| v | regulation of gene expression, epigenetic (GO:0040029)                         | 2.44 | 5.69E-11 |
| v | DNA conformation change (GO:0071103)   | 2.43 | 2.19E-09 |
| v | DNA packaging (GO:0006323)   | 2.42 | 3.35E-08 |
| v | oocyte construction (GO:0007308)   | 2.42 | 3.13E-09 |
| v | establishment of mitotic spindle localization (GO:0040001)                     | 2.41 | 5.69E-03 |
| v | regulation of organelle assembly (GO:1902115)                                  | 2.41 | 5.69E-03 |
| v | negative regulation of organelle organization (GO:0010639)                     | 2.41 | 1.34E-06 |
| v | mitotic spindle organization (GO:0007052)                                      | 2.4  | 4.73E-06 |
| v | maturation of 5.8S rRNA (GO:0000460)   | 2.4  | 3.26E-03 |
| v | cellular macromolecule biosynthetic process (GO:0034645)                       | 2.4  | 6.58E-55 |
| v | regulation of nuclear division (GO:0051783)                                    | 2.4  | 2.21E-06 |
| v | spindle localization (GO:0051653)  | 2.39 | 2.66E-03 |
| v | establishment of spindle localization (GO:0051293)                             | 2.39 | 2.66E-03 |
| v | regulation of actin filament length (GO:0030832)                               | 2.39 | 1.28E-04 |
| v | regulation of protein polymerization (GO:0032271)                              | 2.39 | 1.28E-04 |
| v | regulation of actin polymerization or depolymerization (GO:0008064)            | 2.39 | 1.28E-04 |
| v | regulation of mitotic nuclear division (GO:0007088)                            | 2.39 | 6.75E-06 |
| v | regulation of smoothed signaling pathway (GO:0008589)                          | 2.39 | 1.48E-03 |
| v | regulation of cellular protein localization (GO:1903827)                       | 2.38 | 6.11E-05 |
| v | establishment or maintenance of microtubule cytoskeleton polarity (GO:0007310) | 2.38 | 1.28E-03 |
| v | regulation of histone modification (GO:0031056)                                | 2.38 | 1.28E-03 |
| v | oocyte dorsal/ventral axis specification (GO:0007310)                          | 2.38 | 6.91E-04 |
| v | spindle organization (GO:0007051)  | 2.37 | 9.26E-09 |
| v | tRNA metabolic process (GO:0006399)  | 2.37 | 9.26E-09 |
| v | nuclear-transcribed mRNA catabolic process, deadenylation-dependent            | 2.36 | 4.72E-03 |
| v | cellular response to hypoxia (GO:0071456)                                      | 2.36 | 4.72E-03 |
| v | protein N-linked glycosylation (GO:0006487)                                    | 2.36 | 4.72E-03 |
| v | nuclear-transcribed mRNA catabolic process (GO:0000956)                        | 2.36 | 4.99E-05 |
| v | positive regulation of translation (GO:0045727)                                | 2.36 | 3.85E-03 |
| v | single fertilization (GO:0007338)  | 2.36 | 3.85E-03 |
| v | macromolecule biosynthetic process (GO:0009059)                                | 2.36 | 1.39E-53 |
| v | ovarian nurse cell to oocyte transport (GO:0007300)                            | 2.35 | 2.14E-03 |
| v | regulation of cell maturation (GO:1903429)                                     | 2.35 | 2.14E-03 |
| v | regulation of protein complex assembly (GO:0043254)                            | 2.35 | 4.89E-07 |
| v | ER to Golgi vesicle-mediated transport (GO:0006888)                            | 2.34 | 2.64E-04 |
| v | neural precursor cell proliferation (GO:0061351)                               | 2.34 | 1.25E-04 |
| v | neuroblast proliferation (GO:0007405)  | 2.34 | 1.25E-04 |
| v | stem cell proliferation (GO:0072089)   | 2.34 | 3.36E-05 |



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|---|---|------|----------|
| v | mitotic cell cycle, embryonic (GO:0045448)                                  | 2.32 | 5.58E-03 |
| v | mRNA catabolic process (GO:0006402)   | 2.32 | 2.77E-05 |
| v | ribosome assembly (GO:0042255)  | 2.32 | 1.79E-04 |
| v | regulation of filopodium assembly (GO:0051489)                              | 2.32 | 5.58E-03 |
| v | fertilization (GO:0009566)  | 2.32 | 3.08E-03 |
| v | regulation of mRNA splicing, via spliceosome (GO:0048024)                   | 2.32 | 3.55E-06 |
| v | positive regulation of Notch signaling pathway (GO:0045747)                 | 2.32 | 1.43E-03 |
| v | macromolecule methylation (GO:0043414)                                      | 2.32 | 2.20E-07 |
| v | mitochondrial gene expression (GO:0140053)                                  | 2.31 | 1.80E-07 |
| v | asymmetric cell division (GO:0008356)                                       | 2.31 | 1.80E-07 |
| v | nucleobase-containing compound transport (GO:0015931)                       | 2.3  | 1.59E-08 |
| v | protein modification by small protein removal (GO:0070646)                  | 2.3  | 6.80E-05 |
| v | establishment or maintenance of cytoskeleton polarity (GO:0030952)          | 2.3  | 5.38E-04 |
| v | regulation of actin filament polymerization (GO:0030833)                    | 2.3  | 5.38E-04 |
| v | regulation of actin filament-based process (GO:0032970)                     | 2.29 | 6.09E-06 |
| v | regulation of actin cytoskeleton organization (GO:0032956)                  | 2.29 | 6.09E-06 |
| v | positive regulation of supramolecular fiber organization (GO:1902905)       | 2.29 | 2.05E-03 |
| v | regulation of plasma membrane bounded cell projection assembly (GO:0030952) | 2.29 | 2.05E-03 |
| v | regulation of cell projection assembly (GO:0060491)                         | 2.29 | 2.05E-03 |
| v | negative regulation of neural precursor cell proliferation (GO:2000178)     | 2.28 | 4.43E-03 |
| v | negative regulation of neuroblast proliferation (GO:0007406)                | 2.28 | 4.43E-03 |
| v | male meiotic nuclear division (GO:0007140)                                  | 2.28 | 8.61E-06 |
| v | RNA catabolic process (GO:0006401)  | 2.28 | 8.61E-06 |
| v | morphogenesis of follicular epithelium (GO:0016333)                         | 2.27 | 4.44E-04 |
| v | methylation (GO:0032259)  | 2.27 | 1.97E-07 |
| v | cortical actin cytoskeleton organization (GO:0030866)                       | 2.27 | 1.39E-03 |
| v | positive regulation of cytoskeleton organization (GO:0051495)               | 2.27 | 1.39E-03 |
| v | peptide metabolic process (GO:0006518)                                      | 2.27 | 5.35E-23 |
| v | regulation of alternative mRNA splicing, via spliceosome (GO:0000381)       | 2.26 | 1.42E-05 |
| v | peptidyl-amino acid modification (GO:0018193)                               | 2.25 | 1.11E-16 |
| v | meiotic cytokinesis (GO:0033206)  | 2.24 | 1.09E-03 |
| v | regulation of RNA splicing (GO:0043484)                                     | 2.24 | 3.64E-06 |
| v | dorsal/ventral axis specification (GO:0009950)                              | 2.24 | 3.52E-05 |
| v | cellular nitrogen compound biosynthetic process (GO:0044271)                | 2.24 | 1.31E-42 |
| v | asymmetric neuroblast division (GO:0055059)                                 | 2.24 | 1.98E-03 |
| v | regulation of embryonic development (GO:0045995)                            | 2.24 | 7.73E-06 |
| v | adherens junction organization (GO:0034332)                                 | 2.24 | 1.98E-03 |
| v | regulation of mRNA metabolic process (GO:1903311)                           | 2.23 | 5.46E-07 |
| v | meiotic spindle organization (GO:0000212)                                   | 2.23 | 2.36E-03 |
| v | positive regulation of organelle organization (GO:0010638)                  | 2.23 | 6.69E-08 |
| v | regulation of actin filament organization (GO:0110053)                      | 2.23 | 1.57E-04 |
| v | male meiosis cytokinesis (GO:0007112)                                       | 2.22 | 4.19E-03 |
| v | RNA modification (GO:0009451)   | 2.22 | 1.09E-05 |
| v | stem cell population maintenance (GO:0019827)                               | 2.22 | 3.46E-06 |
| v | maintenance of cell number (GO:0098727)                                     | 2.22 | 3.46E-06 |
| v | cell maturation (GO:0048469)  | 2.22 | 4.74E-10 |
| v | neuroblast division (GO:0055057)  | 2.21 | 1.55E-03 |
| v | neuronal stem cell division (GO:0036445)                                    | 2.21 | 1.55E-03 |
| v | protein import (GO:0017038)   | 2.21 | 2.77E-06 |
| v | posttranscriptional regulation of gene expression (GO:0010608)              | 2.2  | 2.09E-10 |
| v | cellular response to stress (GO:0033554)                                    | 2.2  | 4.89E-34 |
| v | asymmetric stem cell division (GO:0098722)                                  | 2.2  | 1.46E-04 |

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|---|---|------|-----------|
| v | axis specification (GO:0009798)                                     | 2.19 | 6.27E-11  |
| v | nucleus organization (GO:0006997)                                   | 2.19 | 2.14E-05  |
| v | tRNA modification (GO:0006400)                                      | 2.19 | 2.19E-03  |
| v | cell proliferation (GO:0008283)                                     | 2.19 | 6.93E-10  |
| v | anterior/posterior axis specification (GO:0009948)                  | 2.18 | 6.64E-08  |
| v | regulation of mRNA processing (GO:0050684)                          | 2.18 | 9.50E-06  |
| v | nucleic acid phosphodiester bond hydrolysis (GO:0090305)            | 2.18 | 1.15E-05  |
| v | cellular amide metabolic process (GO:0043603)                       | 2.18 | 1.76E-22  |
| v | somatic stem cell division (GO:0048103)                             | 2.17 | 9.89E-04  |
| v | protein deubiquitination (GO:0016579)                               | 2.17 | 1.78E-03  |
| v | stem cell division (GO:0017145)                                     | 2.16 | 6.25E-06  |
| v | regulation of organelle organization (GO:0033043)                   | 2.16 | 2.96E-19  |
| v | cell division (GO:0051301)  | 2.15 | 4.16E-13  |
| v | germ-line stem cell population maintenance (GO:0030718)             | 2.15 | 8.97E-05  |
| v | regulation of translation (GO:0006417)                              | 2.15 | 3.65E-08  |
| v | anterior/posterior axis specification, embryo (GO:0008595)          | 2.14 | 3.69E-07  |
| v | tripartite regional subdivision (GO:0007351)                        | 2.14 | 3.69E-07  |
| v | embryonic axis specification (GO:0000578)                           | 2.14 | 2.49E-07  |
| v | MAPK cascade (GO:0000165)   | 2.14 | 5.63E-03  |
| v | positive regulation of catabolic process (GO:0009896)               | 2.14 | 5.82E-05  |
| v | positive regulation of cellular component biogenesis (GO:0044089)   | 2.14 | 1.19E-06  |
| v | nucleobase-containing compound metabolic process (GO:0006139)       | 2.14 | 3.61E-75  |
| v | regulation of cytoskeleton organization (GO:0051493)                | 2.14 | 1.97E-07  |
| v | female gamete generation (GO:0007292)                               | 2.12 | 2.17E-34  |
| v | germ-line stem cell division (GO:0042078)                           | 2.12 | 2.88E-03  |
| v | Golgi vesicle transport (GO:0048193)                                | 2.11 | 1.48E-06  |
| v | heterocycle metabolic process (GO:0046483)                          | 2.11 | 9.52E-77  |
| v | Golgi organization (GO:0007030)                                     | 2.11 | 7.41E-05  |
| v | cellular nitrogen compound metabolic process (GO:0034641)           | 2.1  | 3.93E-95  |
| v | negative regulation of cellular component organization (GO:0051129) | 2.1  | 7.13E-08  |
| v | regulation of cellular component size (GO:0032535)                  | 2.1  | 4.77E-08  |
| v | cellular response to starvation (GO:0009267)                        | 2.1  | 3.14E-06  |
| v | oogenesis (GO:0048477)  | 2.1  | 3.72E-30  |
| v | positive regulation of cellular catabolic process (GO:0031331)      | 2.1  | 2.95E-04  |
| v | cellular macromolecule metabolic process (GO:0044260)               | 2.1  | 7.84E-143 |
| v | nucleobase-containing compound biosynthetic process (GO:0034654)    | 2.09 | 8.47E-18  |
| v | encapsulation of foreign target (GO:0035010)                        | 2.09 | 6.14E-03  |
| v | cellular aromatic compound metabolic process (GO:0006725)           | 2.08 | 4.92E-76  |
| v | regulation of protein serine/threonine kinase activity (GO:0071900) | 2.07 | 2.08E-03  |
| v | regulation of supramolecular fiber organization (GO:1902903)        | 2.07 | 1.42E-04  |
| v | hemopoiesis (GO:0030097)  | 2.07 | 2.16E-04  |
| v | negative regulation of translation (GO:0017148)                     | 2.07 | 3.34E-04  |
| v | regulation of GTPase activity (GO:0043087)                          | 2.07 | 4.97E-05  |
| v | regulation of cellular component biogenesis (GO:0044087)            | 2.06 | 3.27E-13  |
| v | cellular response to nutrient levels (GO:0031669)                   | 2.06 | 5.36E-06  |
| v | regulation of protein catabolic process (GO:0042176)                | 2.06 | 2.59E-03  |
| v | anterior/posterior pattern specification (GO:0009952)               | 2.06 | 4.80E-08  |
| v | cellular response to extracellular stimulus (GO:0031668)            | 2.06 | 6.23E-06  |
| v | positive regulation of cell growth (GO:0030307)                     | 2.06 | 5.63E-03  |
| v | positive regulation of growth (GO:0045927)                          | 2.06 | 1.00E-06  |
| v | cellular response to organic cyclic compound (GO:0071407)           | 2.05 | 8.73E-04  |
| v | regulation of cellular response to stress (GO:0080135)              | 2.05 | 4.60E-05  |

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| v | tRNA processing (GO:0008033)   | 2.05 | 2.98E-04 |
| v | organic cyclic compound metabolic process (GO:1901360)                           | 2.04 | 1.77E-74 |
| v | regulation of cell size (GO:0008361)   | 2.04 | 5.46E-05 |
| v | protein localization to organelle (GO:0033365)                                   | 2.04 | 4.01E-09 |
| v | heterocycle biosynthetic process (GO:0018130)                                    | 2.04 | 2.87E-19 |
| v | cellular macromolecular complex assembly (GO:0034622)                            | 2.04 | 2.94E-16 |
| v | establishment of protein localization to organelle (GO:0072594)                  | 2.04 | 2.10E-07 |
| v | cytosolic transport (GO:0016482)   | 2.04 | 2.30E-03 |
| v | negative regulation of protein modification process (GO:0031400)                 | 2.03 | 1.42E-04 |
| v | protein transport (GO:0015031)   | 2.03 | 2.26E-16 |
| v | hematopoietic or lymphoid organ development (GO:0048534)                         | 2.02 | 1.16E-04 |
| v | immune system development (GO:0002520)   | 2.02 | 1.16E-04 |
| v | negative regulation of cellular amide metabolic process (GO:0034249)             | 2.02 | 4.74E-04 |
| v | microtubule cytoskeleton organization (GO:0000226)                               | 2.02 | 4.49E-13 |
| v | peptide transport (GO:0015833)   | 2.02 | 3.04E-16 |
| v | amide transport (GO:0042886)   | 2.01 | 3.72E-16 |
| v | positive regulation of cell projection organization (GO:0031346)                 | 2.01 | 1.67E-03 |
| v | negative regulation of protein phosphorylation (GO:0001933)                      | 2.01 | 1.67E-03 |
| v | macromolecular complex subunit organization (GO:0043933)                         | 2    | 1.19E-20 |
| v | response to ecdysone (GO:0035075)  | 2    | 4.99E-03 |
| v | response to sterol (GO:0036314)  | 2    | 4.99E-03 |
| v | regulation of protein localization (GO:0032880)                                  | 2    | 4.87E-05 |
| v | positive regulation of multicellular organism growth (GO:0040018)                | 2    | 3.65E-03 |
| v | negative regulation of phosphorylation (GO:0042326)                              | 2    | 1.88E-03 |
| v | positive regulation of cellular component organization (GO:0051130)              | 2    | 1.29E-10 |
| v | eggshell chorion assembly (GO:0007306)   | 1.99 | 2.66E-04 |
| v | cellular process involved in reproduction in multicellular organism (GO:0000000) | 1.99 | 1.15E-36 |
| v | intracellular protein transport (GO:0006886)                                     | 1.99 | 4.61E-13 |
| v | cellular macromolecule localization (GO:0070727)                                 | 1.99 | 3.05E-20 |
| v | aromatic compound biosynthetic process (GO:0019438)                              | 1.99 | 6.50E-18 |
| v | protein secretion (GO:0009306)   | 1.99 | 5.53E-03 |
| v | positive regulation of GTPase activity (GO:0043547)                              | 1.99 | 1.48E-03 |
| v | cellular response to external stimulus (GO:0071496)                              | 1.98 | 9.97E-06 |
| v | negative regulation of neurogenesis (GO:0050768)                                 | 1.98 | 8.87E-04 |
| v | establishment of protein localization (GO:0045184)                               | 1.98 | 7.28E-16 |
| v | Notch signaling pathway (GO:0007219)   | 1.98 | 4.39E-03 |
| v | cortical cytoskeleton organization (GO:0030865)                                  | 1.98 | 4.39E-03 |
| v | germ cell development (GO:0007281)   | 1.98 | 7.83E-30 |
| v | regulation of cellular localization (GO:0060341)                                 | 1.97 | 7.24E-06 |
| v | endomembrane system organization (GO:0010256)                                    | 1.97 | 1.34E-06 |
| v | regulation of kinase activity (GO:0043549)                                       | 1.97 | 1.71E-04 |
| v | positive regulation of developmental growth (GO:0048639)                         | 1.96 | 4.28E-05 |
| v | cellular biosynthetic process (GO:0044249)                                       | 1.96 | 1.79E-46 |
| v | regulation of organ growth (GO:0046620)  | 1.95 | 3.14E-03 |
| v | negative regulation of nervous system development (GO:0051961)                   | 1.95 | 3.06E-05 |
| v | lymph gland development (GO:0048542)   | 1.95 | 6.04E-03 |
| v | peptide secretion (GO:0002790)   | 1.95 | 6.04E-03 |
| v | macromolecular complex assembly (GO:0065003)                                     | 1.95 | 2.00E-15 |
| v | organelle organization (GO:0006996)  | 1.95 | 5.71E-63 |
| v | negative regulation of developmental growth (GO:0048640)                         | 1.94 | 6.73E-04 |
| v | regulation of protein kinase activity (GO:0045859)                               | 1.94 | 4.02E-04 |
| v | gamete generation (GO:0007276)   | 1.94 | 1.18E-35 |

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| v | developmental maturation (GO:0021700)  | 1.94 | 4.16E-08 |
| v | organic cyclic compound biosynthetic process (GO:1901362)                            | 1.93 | 1.58E-17 |
| v | cytoskeleton-dependent cytokinesis (GO:0061640)                                      | 1.92 | 1.34E-04 |
| v | regulation of cellular amide metabolic process (GO:0034248)                          | 1.92 | 1.59E-07 |
| v | cytokinesis (GO:0000910)   | 1.92 | 1.05E-04 |
| v | cellularization (GO:0007349)   | 1.91 | 2.00E-04 |
| v | regulation of reproductive process (GO:2000241)                                      | 1.91 | 8.12E-04 |
| v | mitotic cytokinesis (GO:0000281)   | 1.9  | 3.35E-03 |
| v | organic substance biosynthetic process (GO:1901576)                                  | 1.9  | 1.22E-43 |
| v | regulation of intracellular transport (GO:0032386)                                   | 1.9  | 2.67E-03 |
| v | regulation of transferase activity (GO:0051338)                                      | 1.9  | 1.27E-04 |
| v | blastoderm segmentation (GO:0007350)   | 1.89 | 5.10E-07 |
| v | establishment of cell polarity (GO:0030010)  | 1.89 | 5.13E-03 |
| v | establishment of organelle localization (GO:0051656)                                 | 1.89 | 8.11E-08 |
| v | regulation of catabolic process (GO:0009894)   | 1.89 | 2.54E-06 |
| v | biosynthetic process (GO:0009058)  | 1.88 | 1.29E-43 |
| v | developmental process involved in reproduction (GO:0003006)                          | 1.88 | 2.32E-28 |
| v | protein localization (GO:0008104)  | 1.88 | 4.93E-19 |
| v | regulation of multicellular organism growth (GO:0040014)                             | 1.88 | 2.10E-03 |
| v | cellular protein localization (GO:0034613)   | 1.88 | 6.33E-15 |
| v | negative regulation of phosphorus metabolic process (GO:0010563)                     | 1.87 | 1.35E-03 |
| v | negative regulation of phosphate metabolic process (GO:0045936)                      | 1.87 | 1.35E-03 |
| v | positive regulation of protein metabolic process (GO:0051247)                        | 1.87 | 4.60E-09 |
| v | cellular protein metabolic process (GO:0044267)                                      | 1.87 | 2.93E-52 |
| v | regulation of cellular component organization (GO:0051128)                           | 1.87 | 4.96E-24 |
| v | negative regulation of cell development (GO:0010721)                                 | 1.87 | 1.18E-03 |
| v | regulation of cell growth (GO:0001558)   | 1.86 | 2.82E-03 |
| v | regulation of cell shape (GO:0008360)  | 1.86 | 2.82E-03 |
| v | negative regulation of cell proliferation (GO:0008285)                               | 1.86 | 8.36E-04 |
| v | border follicle cell migration (GO:0007298)  | 1.86 | 1.13E-04 |
| v | positive regulation of cellular protein metabolic process (GO:0032270)               | 1.85 | 2.02E-08 |
| v | embryonic pattern specification (GO:0009880)   | 1.85 | 3.83E-07 |
| v | cellular component biogenesis (GO:0044085)   | 1.85 | 8.07E-35 |
| v | larval development (GO:0002164)  | 1.85 | 1.90E-05 |
| v | protein folding (GO:0006457)   | 1.84 | 1.51E-04 |
| v | negative regulation of cell differentiation (GO:0045596)                             | 1.84 | 1.22E-04 |
| v | regulation of developmental growth (GO:0048638)                                      | 1.84 | 4.67E-08 |
| v | positive regulation of protein modification process (GO:0031401)                     | 1.84 | 4.99E-06 |
| v | macromolecule localization (GO:0033036)  | 1.84 | 1.16E-21 |
| v | negative regulation of macromolecule biosynthetic process (GO:0010558)               | 1.84 | 2.76E-11 |
| v | negative regulation of cellular macromolecule biosynthetic process (GO:0010559)      | 1.84 | 2.76E-11 |
| v | regulation of synapse assembly (GO:0051963)  | 1.83 | 2.62E-04 |
| v | ovarian follicle cell migration (GO:0007297)   | 1.83 | 8.39E-05 |
| v | negative regulation of gene expression (GO:0010629)                                  | 1.83 | 1.60E-14 |
| v | nucleobase-containing compound catabolic process (GO:0034655)                        | 1.83 | 6.65E-05 |
| v | positive regulation of MAPK cascade (GO:0043410)                                     | 1.83 | 2.63E-03 |
| v | nitrogen compound transport (GO:0071705)   | 1.83 | 4.52E-15 |
| v | regulation of protein metabolic process (GO:0051246)                                 | 1.82 | 5.10E-17 |
| v | segmentation (GO:0035282)  | 1.82 | 2.31E-07 |
| v | proteasome-mediated ubiquitin-dependent protein catabolic process (GO:0010557)       | 1.82 | 7.93E-06 |
| v | negative regulation of nucleobase-containing compound metabolic process (GO:0010558) | 1.82 | 5.85E-10 |
| v | negative regulation of cellular biosynthetic process (GO:0031327)                    | 1.82 | 2.79E-11 |

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| v | negative regulation of biosynthetic process (GO:0009890)                    | 1.82 | 2.79E-11 |
| v | regulation of autophagy (GO:0010506)  | 1.82 | 1.63E-03 |
| v | regulation of gene expression (GO:0010468)                                  | 1.82 | 6.63E-40 |
| v | regulation of protein phosphorylation (GO:0001932)                          | 1.81 | 7.29E-07 |
| v | negative regulation of macromolecule metabolic process (GO:0010605)         | 1.81 | 1.87E-17 |
| v | regulation of small GTPase mediated signal transduction (GO:0051056)        | 1.81 | 1.87E-04 |
| v | regulation of growth (GO:0040008)   | 1.81 | 1.02E-09 |
| v | microtubule-based process (GO:0007017)                                      | 1.81 | 2.29E-12 |
| v | cellular localization (GO:0051641)  | 1.81 | 5.22E-25 |
| v | regulation of cellular protein metabolic process (GO:0032268)               | 1.81 | 2.53E-15 |
| v | organelle localization (GO:0051640)   | 1.81 | 5.43E-08 |
| v | regulation of synaptic growth at neuromuscular junction (GO:0008582)        | 1.81 | 7.07E-04 |
| v | negative regulation of cellular process (GO:0048523)                        | 1.81 | 3.21E-32 |
| v | regulation of macromolecule metabolic process (GO:0060255)                  | 1.81 | 9.91E-52 |
| v | protein localization to membrane (GO:0072657)                               | 1.8  | 3.09E-03 |
| v | regulation of protein modification process (GO:0031399)                     | 1.8  | 3.81E-09 |
| v | establishment of localization in cell (GO:0051649)                          | 1.8  | 7.98E-20 |
| v | regulation of cellular catabolic process (GO:0031329)                       | 1.8  | 5.10E-05 |
| v | positive regulation of molecular function (GO:0044093)                      | 1.8  | 1.57E-06 |
| v | vesicle organization (GO:0016050)   | 1.8  | 1.41E-03 |
| v | organonitrogen compound biosynthetic process (GO:1901566)                   | 1.8  | 2.65E-20 |
| v | protein targeting (GO:0006605)  | 1.8  | 1.22E-03 |
| v | ovarian follicle cell development (GO:0030707)                              | 1.79 | 2.19E-09 |
| v | negative regulation of metabolic process (GO:0009892)                       | 1.79 | 5.64E-18 |
| v | regulation of macromolecule biosynthetic process (GO:0010556)               | 1.79 | 1.96E-32 |
| v | cellular component organization or biogenesis (GO:0071840)                  | 1.79 | 1.61E-86 |
| v | regulation of neuromuscular junction development (GO:1904396)               | 1.79 | 6.10E-04 |
| v | columnar/cuboidal epithelial cell development (GO:0002066)                  | 1.79 | 2.30E-09 |
| v | regulation of Ras protein signal transduction (GO:0046578)                  | 1.78 | 3.74E-04 |
| v | regulation of cellular macromolecule biosynthetic process (GO:2000112)      | 1.78 | 1.56E-31 |
| v | response to starvation (GO:0042594)   | 1.78 | 1.83E-05 |
| v | epithelial cell development (GO:0002064)                                    | 1.78 | 4.66E-10 |
| v | intracellular transport (GO:0046907)  | 1.78 | 5.64E-17 |
| v | positive regulation of catalytic activity (GO:0043085)                      | 1.78 | 1.05E-05 |
| v | protein modification by small protein conjugation or removal (GO:00706)     | 1.78 | 5.39E-08 |
| v | negative regulation of biological process (GO:0048519)                      | 1.78 | 2.47E-35 |
| v | regulation of phosphorylation (GO:0042325)                                  | 1.78 | 7.37E-07 |
| v | negative regulation of multicellular organismal process (GO:0051241)        | 1.78 | 8.01E-06 |
| v | negative regulation of nitrogen compound metabolic process (GO:00511)       | 1.77 | 1.74E-13 |
| v | macromolecule modification (GO:0043412)                                     | 1.77 | 4.61E-30 |
| v | cytoskeleton organization (GO:0007010)                                      | 1.77 | 4.20E-14 |
| v | regulation of nucleobase-containing compound metabolic process (GO:0007010) | 1.77 | 9.22E-31 |
| v | negative regulation of RNA biosynthetic process (GO:1902679)                | 1.77 | 4.38E-08 |
| v | negative regulation of transcription, DNA-templated (GO:0045892)            | 1.77 | 4.38E-08 |
| v | negative regulation of nucleic acid-templated transcription (GO:1903507)    | 1.77 | 4.38E-08 |
| v | negative regulation of cellular metabolic process (GO:0031324)              | 1.77 | 2.73E-14 |
| v | positive regulation of macromolecule metabolic process (GO:0010604)         | 1.77 | 2.63E-17 |
| v | proteasomal protein catabolic process (GO:0010498)                          | 1.77 | 1.48E-05 |
| v | positive regulation of protein phosphorylation (GO:0001934)                 | 1.77 | 2.64E-04 |
| v | regulation of biosynthetic process (GO:0009889)                             | 1.77 | 5.21E-32 |
| v | negative regulation of developmental process (GO:0051093)                   | 1.77 | 4.29E-06 |
| v | dorsal/ventral pattern formation (GO:0009953)                               | 1.76 | 1.63E-04 |

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| v | negative regulation of RNA metabolic process (GO:0051253)                            | 1.76 | 2.50E-08 |
| v | regulation of cellular biosynthetic process (GO:0031326)                             | 1.76 | 1.25E-31 |
| v | regulation of nitrogen compound metabolic process (GO:0051171)                       | 1.76 | 7.43E-44 |
| v | macromolecule metabolic process (GO:0043170)   | 1.76 | 7.11E-99 |
| v | negative regulation of cellular protein metabolic process (GO:0032269)               | 1.76 | 1.11E-05 |
| v | establishment or maintenance of cell polarity (GO:0007163)                           | 1.76 | 5.28E-06 |
| v | positive regulation of nitrogen compound metabolic process (GO:0051171)              | 1.75 | 1.66E-16 |
| v | columnar/cuboidal epithelial cell differentiation (GO:0002065)                       | 1.75 | 6.50E-09 |
| v | negative regulation of protein metabolic process (GO:0051248)                        | 1.75 | 1.57E-05 |
| v | positive regulation of nucleobase-containing compound metabolic process (GO:0051248) | 1.75 | 1.89E-10 |
| v | positive regulation of macromolecule biosynthetic process (GO:0010557)               | 1.75 | 1.16E-10 |
| v | regulation of RNA metabolic process (GO:0051252)                                     | 1.75 | 1.12E-27 |
| v | protein modification process (GO:0036211)  | 1.74 | 5.94E-26 |
| v | cellular protein modification process (GO:0006464)                                   | 1.74 | 5.94E-26 |
| v | regulation of metabolic process (GO:0019222)   | 1.74 | 9.29E-51 |
| v | regulation of synapse organization (GO:0050807)                                      | 1.74 | 2.25E-04 |
| v | regulation of molecular function (GO:0065009)  | 1.74 | 2.22E-09 |
| v | positive regulation of metabolic process (GO:0009893)                                | 1.74 | 2.01E-17 |
| v | cellular component organization (GO:0016043)   | 1.73 | 3.74E-70 |
| v | regionalization (GO:0003002)   | 1.73 | 3.27E-11 |
| v | regulation of cell proliferation (GO:0042127)  | 1.73 | 5.75E-06 |
| v | regulation of primary metabolic process (GO:0080090)                                 | 1.73 | 1.70E-43 |
| v | response to organic cyclic compound (GO:0014070)                                     | 1.73 | 7.85E-04 |
| v | actin filament organization (GO:0007015)   | 1.72 | 1.82E-03 |
| v | multi-organism reproductive process (GO:0044703)                                     | 1.72 | 4.22E-27 |
| v | sexual reproduction (GO:0019953)   | 1.72 | 4.22E-27 |
| v | regulation of RNA biosynthetic process (GO:2001141)                                  | 1.72 | 1.07E-23 |
| v | regulation of transcription, DNA-templated (GO:0006355)                              | 1.72 | 1.07E-23 |
| v | regulation of nucleic acid-templated transcription (GO:1903506)                      | 1.72 | 1.07E-23 |
| v | reproductive process (GO:0022414)  | 1.72 | 1.20E-29 |
| v | embryo development (GO:0009790)  | 1.72 | 2.99E-12 |
| v | positive regulation of cellular metabolic process (GO:0031325)                       | 1.72 | 7.37E-16 |
| v | positive regulation of gene expression (GO:0010628)                                  | 1.72 | 2.65E-10 |
| v | regulation of plasma membrane bounded cell projection organization (GO:0031325)      | 1.71 | 4.43E-04 |
| v | positive regulation of RNA metabolic process (GO:0051254)                            | 1.71 | 3.71E-09 |
| v | regulation of catalytic activity (GO:0050790)  | 1.71 | 1.13E-07 |
| v | regulation of cellular metabolic process (GO:0031323)                                | 1.71 | 1.61E-42 |
| v | negative regulation of growth (GO:0045926)   | 1.71 | 2.04E-03 |
| v | positive regulation of hydrolase activity (GO:0051345)                               | 1.71 | 2.04E-03 |
| v | positive regulation of cellular biosynthetic process (GO:0031328)                    | 1.71 | 1.63E-10 |
| v | positive regulation of biosynthetic process (GO:0009891)                             | 1.71 | 1.63E-10 |
| v | multicellular organismal reproductive process (GO:0048609)                           | 1.7  | 7.42E-26 |
| v | negative regulation of intracellular signal transduction (GO:1902532)                | 1.7  | 5.12E-03 |
| v | regulation of cell projection organization (GO:0031344)                              | 1.7  | 6.06E-04 |
| v | positive regulation of phosphorylation (GO:0042327)                                  | 1.7  | 6.06E-04 |
| v | regulation of response to stress (GO:0080134)  | 1.7  | 3.46E-06 |
| v | response to extracellular stimulus (GO:0009991)                                      | 1.69 | 4.20E-05 |
| v | response to nutrient levels (GO:0031667)   | 1.69 | 5.16E-05 |
| v | heterocycle catabolic process (GO:0046700)   | 1.69 | 2.78E-04 |
| v | cellular nitrogen compound catabolic process (GO:0044270)                            | 1.69 | 3.40E-04 |
| v | epithelial cell differentiation (GO:0030855)   | 1.69 | 2.04E-09 |
| v | cellular macromolecule catabolic process (GO:0044265)                                | 1.69 | 3.08E-09 |

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| v | embryonic development via the syncytial blastoderm (GO:0001700)          | 1.69 | 1.04E-04  |
| v | positive regulation of nervous system development (GO:0051962)           | 1.69 | 2.84E-03  |
| v | cellular component assembly (GO:0022607)                                 | 1.69 | 5.67E-21  |
| v | positive regulation of cellular process (GO:0048522)                     | 1.69 | 7.40E-26  |
| v | regulation of anatomical structure size (GO:0090066)                     | 1.69 | 1.43E-05  |
| v | regulation of nervous system development (GO:0051960)                    | 1.69 | 2.15E-07  |
| v | regulation of MAPK cascade (GO:0043408)                                  | 1.68 | 1.05E-03  |
| v | cellular metabolic process (GO:0044237)                                  | 1.68 | 1.40E-104 |
| v | modification-dependent macromolecule catabolic process (GO:0043632)      | 1.68 | 1.40E-06  |
| v | embryo development ending in birth or egg hatching (GO:0009792)          | 1.68 | 9.38E-05  |
| v | pattern specification process (GO:0007389)                               | 1.68 | 7.75E-11  |
| v | regulation of cell differentiation (GO:0045595)                          | 1.68 | 6.09E-08  |
| v | small GTPase mediated signal transduction (GO:0007264)                   | 1.67 | 3.66E-03  |
| v | aromatic compound catabolic process (GO:0019439)                         | 1.67 | 3.99E-04  |
| v | dendrite development (GO:0016358)  | 1.67 | 4.53E-05  |
| v | regulation of cell development (GO:0060284)                              | 1.67 | 1.87E-06  |
| v | positive regulation of phosphorus metabolic process (GO:0010562)         | 1.67 | 5.63E-04  |
| v | positive regulation of phosphate metabolic process (GO:0045937)          | 1.67 | 5.63E-04  |
| v | eggshell formation (GO:0030703)  | 1.67 | 2.03E-03  |
| v | secretion by cell (GO:0032940)   | 1.67 | 2.23E-04  |
| v | chorion-containing eggshell formation (GO:0007304)                       | 1.67 | 1.91E-03  |
| v | positive regulation of biological process (GO:0048518)                   | 1.67 | 2.92E-28  |
| v | positive regulation of RNA biosynthetic process (GO:1902680)             | 1.66 | 5.55E-08  |
| v | positive regulation of transcription, DNA-templated (GO:0045893)         | 1.66 | 5.55E-08  |
| v | positive regulation of nucleic acid-templated transcription (GO:1903508) | 1.66 | 5.55E-08  |
| v | regulation of cell death (GO:0010941)                                    | 1.66 | 3.89E-06  |
| v | regulation of multi-organism process (GO:0043900)                        | 1.66 | 1.30E-03  |
| v | male gamete generation (GO:0048232)                                      | 1.66 | 9.22E-07  |
| v | regulation of apoptotic process (GO:0042981)                             | 1.66 | 6.81E-05  |
| v | organic cyclic compound catabolic process (GO:1901361)                   | 1.65 | 4.96E-04  |
| v | positive regulation of developmental process (GO:0051094)                | 1.65 | 2.82E-05  |
| v | regulation of phosphate metabolic process (GO:0019220)                   | 1.65 | 3.55E-06  |
| v | regulation of phosphorus metabolic process (GO:0051174)                  | 1.65 | 3.55E-06  |
| v | regulation of neurogenesis (GO:0050767)                                  | 1.65 | 3.95E-05  |
| v | response to stress (GO:0006950)  | 1.64 | 2.73E-23  |
| v | protein modification by small protein conjugation (GO:0032446)           | 1.64 | 4.57E-05  |
| v | ubiquitin-dependent protein catabolic process (GO:0006511)               | 1.64 | 6.05E-06  |
| v | modification-dependent protein catabolic process (GO:0019941)            | 1.64 | 6.05E-06  |
| v | regulation of programmed cell death (GO:0043067)                         | 1.64 | 2.56E-05  |
| v | dendrite morphogenesis (GO:0048813)                                      | 1.64 | 1.14E-04  |
| v | regulation of multicellular organismal development (GO:2000026)          | 1.64 | 2.39E-10  |
| v | regulation of transcription from RNA polymerase II promoter (GO:00063)   | 1.64 | 1.90E-11  |
| v | regulation of Notch signaling pathway (GO:0008593)                       | 1.63 | 3.83E-03  |
| v | epithelial cell migration (GO:0010631)                                   | 1.63 | 5.41E-04  |
| v | epithelium migration (GO:0090132)  | 1.63 | 5.41E-04  |
| v | nitrogen compound metabolic process (GO:0006807)                         | 1.63 | 9.79E-87  |
| v | protein phosphorylation (GO:0006468)                                     | 1.63 | 1.12E-05  |
| v | regulation of cell morphogenesis (GO:0022604)                            | 1.63 | 1.14E-03  |
| v | regulation of hydrolase activity (GO:0051336)                            | 1.62 | 3.31E-04  |
| v | regulation of developmental process (GO:0050793)                         | 1.62 | 1.95E-13  |
| v | positive regulation of multicellular organismal process (GO:0051240)     | 1.62 | 3.76E-05  |
| v | regulation of intracellular signal transduction (GO:1902531)             | 1.62 | 9.47E-07  |

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|---|---|------|----------|
| v | actin cytoskeleton organization (GO:0030036)                            | 1.62 | 9.38E-05 |
| v | cell migration (GO:0016477)   | 1.62 | 7.20E-06 |
| v | tissue migration (GO:0090130)   | 1.62 | 5.38E-04 |
| v | cell development (GO:0048468)   | 1.61 | 4.90E-27 |
| v | negative regulation of cell death (GO:0060548)                          | 1.61 | 3.82E-03 |
| v | endocytosis (GO:0006897)  | 1.61 | 2.35E-06 |
| v | ameboidal-type cell migration (GO:0001667)                              | 1.61 | 4.88E-04 |
| v | regulation of neuron differentiation (GO:0045664)                       | 1.61 | 8.75E-04 |
| v | vesicle-mediated transport (GO:0016192)                                 | 1.61 | 1.02E-10 |
| v | negative regulation of signal transduction (GO:0009968)                 | 1.6  | 1.60E-05 |
| v | primary metabolic process (GO:0044238)                                  | 1.6  | 1.20E-85 |
| v | localization of cell (GO:0051674)                                       | 1.6  | 2.92E-06 |
| v | lateral inhibition (GO:0046331)   | 1.6  | 2.53E-04 |
| v | positive regulation of intracellular signal transduction (GO:1902533)   | 1.59 | 1.04E-03 |
| v | cell-cell signaling involved in cell fate commitment (GO:0045168)       | 1.59 | 2.64E-04 |
| v | proteolysis involved in cellular protein catabolic process (GO:0051603) | 1.59 | 1.34E-05 |
| v | photoreceptor cell differentiation (GO:0046530)                         | 1.59 | 1.14E-03 |
| v | negative regulation of response to stimulus (GO:0048585)                | 1.58 | 5.25E-06 |
| v | import into cell (GO:0098657)   | 1.58 | 3.93E-06 |
| v | cellular protein catabolic process (GO:0044257)                         | 1.58 | 1.39E-05 |
| v | organelle assembly (GO:0070925)   | 1.58 | 2.87E-06 |
| v | actin filament-based process (GO:0030029)                               | 1.58 | 1.36E-04 |
| v | cellular amino acid metabolic process (GO:0006520)                      | 1.58 | 2.36E-03 |
| v | spermatogenesis (GO:0007283)  | 1.57 | 6.15E-05 |
| v | compound eye development (GO:0048749)                                   | 1.57 | 5.01E-06 |
| v | organic substance transport (GO:0071702)                                | 1.57 | 2.78E-10 |
| v | anatomical structure formation involved in morphogenesis (GO:0048646)   | 1.57 | 1.05E-08 |
| v | eye development (GO:0001654)  | 1.57 | 2.60E-06 |
| v | protein ubiquitination (GO:0016567)                                     | 1.57 | 6.07E-04 |
| v | regulation of response to stimulus (GO:0048583)                         | 1.57 | 2.19E-14 |
| v | supramolecular fiber organization (GO:0097435)                          | 1.57 | 1.48E-03 |
| v | regulation of synapse structure or activity (GO:0050803)                | 1.56 | 1.79E-03 |
| v | regulation of defense response (GO:0031347)                             | 1.56 | 4.45E-03 |
| v | eye photoreceptor cell differentiation (GO:0001754)                     | 1.56 | 2.67E-03 |
| v | regulation of immune system process (GO:0002682)                        | 1.56 | 3.14E-04 |
| v | cell motility (GO:0048870)  | 1.56 | 1.39E-05 |
| v | cell death (GO:0008219)   | 1.56 | 3.65E-04 |
| v | compound eye morphogenesis (GO:0001745)                                 | 1.55 | 1.04E-04 |
| v | positive regulation of response to stimulus (GO:0048584)                | 1.55 | 1.03E-06 |
| v | multi-organism process (GO:0051704)                                     | 1.55 | 2.96E-22 |
| v | cell fate determination (GO:0001709)                                    | 1.55 | 3.72E-03 |
| v | positive regulation of signal transduction (GO:0009967)                 | 1.55 | 2.55E-05 |
| v | regulation of multicellular organismal process (GO:0051239)             | 1.55 | 6.91E-11 |
| v | phagocytosis (GO:0006909)   | 1.54 | 4.23E-04 |
| v | membrane organization (GO:0061024)                                      | 1.54 | 1.08E-03 |
| v | sensory organ morphogenesis (GO:0090596)                                | 1.54 | 1.09E-04 |
| v | eye morphogenesis (GO:0048592)  | 1.54 | 1.09E-04 |
| v | cell fate commitment (GO:0045165)                                       | 1.54 | 2.80E-07 |
| v | organic substance metabolic process (GO:0071704)                        | 1.54 | 1.03E-79 |
| v | compound eye photoreceptor cell differentiation (GO:0001751)            | 1.53 | 5.02E-03 |
| v | cell differentiation (GO:0030154)                                       | 1.53 | 1.16E-27 |
| v | negative regulation of cell communication (GO:0010648)                  | 1.53 | 6.26E-05 |



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|---|---|------|-----------|
| v | negative regulation of signaling (GO:0023057)                                     | 1.53 | 6.26E-05  |
| v | protein metabolic process (GO:0019538)  | 1.53 | 1.15E-29  |
| v | secretion (GO:0046903)  | 1.53 | 1.55E-03  |
| v | cellular developmental process (GO:0048869)                                       | 1.53 | 8.86E-28  |
| v | macromolecule catabolic process (GO:0009057)                                      | 1.52 | 5.83E-07  |
| v | regulation of signal transduction (GO:0009966)                                    | 1.52 | 6.25E-10  |
| v | regulation of biological process (GO:0050789)                                     | 1.52 | 3.24E-60  |
| v | protein catabolic process (GO:0030163)  | 1.52 | 5.17E-05  |
| v | regulation of cellular process (GO:0050794)                                       | 1.52 | 4.54E-53  |
| v | animal organ development (GO:0048513)   | 1.51 | 1.58E-16  |
| v | generation of neurons (GO:0048699)  | 1.51 | 1.37E-12  |
| v | programmed cell death (GO:0012501)  | 1.51 | 1.34E-03  |
| v | regulation of localization (GO:0032879)   | 1.51 | 8.32E-06  |
| v | positive regulation of cell communication (GO:0010647)                            | 1.51 | 4.39E-05  |
| v | positive regulation of signaling (GO:0023056)                                     | 1.51 | 4.39E-05  |
| v | cellular response to stimulus (GO:0051716)  | 1.51 | 2.67E-21  |
| v | neuron differentiation (GO:0030182)   | 1.5  | 2.52E-10  |
| v | regulation of anatomical structure morphogenesis (GO:0022603)                     | 1.5  | 4.11E-04  |
| v | sensory organ development (GO:0007423)  | 1.5  | 1.87E-06  |
| v | epithelium development (GO:0060429)   | 1.5  | 1.47E-12  |
| v | enzyme linked receptor protein signaling pathway (GO:0007167)                     | 1.5  | 4.25E-03  |
| v | reproduction (GO:0000003)   | 1.49 | 4.50E-18  |
| v | neuron projection development (GO:0031175)  | 1.48 | 4.00E-07  |
| v | protein complex subunit organization (GO:0071822)                                 | 1.48 | 4.30E-04  |
| v | neurogenesis (GO:0022008)   | 1.48 | 6.90E-12  |
| v | neuron projection morphogenesis (GO:0048812)                                      | 1.48 | 9.65E-07  |
| v | neuron development (GO:0048666)   | 1.48 | 2.05E-08  |
| v | cell projection morphogenesis (GO:0048858)  | 1.47 | 9.87E-07  |
| v | plasma membrane bounded cell projection morphogenesis (GO:0120039)                | 1.47 | 9.87E-07  |
| v | nervous system development (GO:0007399)   | 1.47 | 1.57E-13  |
| v | cell part morphogenesis (GO:0032990)  | 1.47 | 9.60E-07  |
| v | cellular process (GO:0009987)   | 1.47 | 2.00E-136 |
| v | cell morphogenesis involved in neuron differentiation (GO:0048667)                | 1.47 | 1.36E-05  |
| v | post-embryonic animal organ development (GO:0048569)                              | 1.46 | 1.24E-05  |
| v | immune system process (GO:0002376)  | 1.46 | 3.89E-04  |
| v | cell morphogenesis (GO:0000902)   | 1.46 | 2.33E-07  |
| v | system development (GO:0048731)   | 1.46 | 3.00E-20  |
| v | cellular component morphogenesis (GO:0032989)                                     | 1.45 | 1.73E-08  |
| v | multicellular organism reproduction (GO:0032504)                                  | 1.45 | 1.34E-14  |
| v | muscle structure development (GO:0061061)   | 1.45 | 1.61E-03  |
| v | biological regulation (GO:0065007)  | 1.45 | 1.32E-53  |
| v | growth (GO:0040007)   | 1.45 | 4.35E-03  |
| v | metabolic process (GO:0008152)  | 1.45 | 9.60E-67  |
| v | positive regulation of transcription from RNA polymerase II promoter (GO:0009888) | 1.45 | 1.25E-03  |
| v | tissue development (GO:0009888)   | 1.44 | 2.73E-11  |
| v | cell morphogenesis involved in differentiation (GO:0000904)                       | 1.44 | 1.42E-05  |
| v | central nervous system development (GO:0007417)                                   | 1.43 | 1.94E-03  |
| v | anatomical structure morphogenesis (GO:0009653)                                   | 1.43 | 2.70E-16  |
| v | regulation of cell communication (GO:0010646)                                     | 1.43 | 2.61E-08  |
| v | regulation of signaling (GO:0023051)  | 1.43 | 2.66E-08  |
| v | post-embryonic development (GO:0009791)   | 1.42 | 1.04E-06  |
| v | intracellular signal transduction (GO:0035556)                                    | 1.42 | 3.27E-04  |

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|---|---|------|----------|
| v | cellular catabolic process (GO:0044248)                           | 1.42 | 5.22E-07 |
| v | imaginal disc development (GO:0007444)                            | 1.41 | 1.21E-05 |
| v | wing disc development (GO:0035220)                                | 1.41 | 3.28E-04 |
| v | morphogenesis of an epithelium (GO:0002009)                       | 1.41 | 1.01E-05 |
| v | imaginal disc-derived wing morphogenesis (GO:0007476)             | 1.4  | 3.30E-03 |
| v | anatomical structure development (GO:0048856)                     | 1.4  | 6.62E-26 |
| v | wing disc morphogenesis (GO:0007472)                              | 1.4  | 3.14E-03 |
| v | developmental process (GO:0032502)                                | 1.4  | 1.33E-27 |
| v | movement of cell or subcellular component (GO:0006928)            | 1.39 | 4.19E-06 |
| v | tissue morphogenesis (GO:0048729)                                 | 1.39 | 1.56E-05 |
| v | multicellular organism development (GO:0007275)                   | 1.39 | 4.90E-21 |
| v | animal organ morphogenesis (GO:0009887)                           | 1.39 | 1.24E-06 |
| v | chemotaxis (GO:0006935)   | 1.39 | 4.61E-03 |
| v | post-embryonic appendage morphogenesis (GO:0035120)               | 1.38 | 2.17E-03 |
| v | tube morphogenesis (GO:0035239)                                   | 1.38 | 1.31E-04 |
| v | post-embryonic animal organ morphogenesis (GO:0048563)            | 1.37 | 1.09E-03 |
| v | imaginal disc morphogenesis (GO:0007560)                          | 1.37 | 1.09E-03 |
| v | imaginal disc-derived appendage development (GO:0048737)          | 1.36 | 3.23E-03 |
| v | post-embryonic animal morphogenesis (GO:0009886)                  | 1.36 | 3.24E-04 |
| v | plasma membrane bounded cell projection organization (GO:0120036) | 1.36 | 1.35E-05 |
| v | imaginal disc-derived appendage morphogenesis (GO:0035114)        | 1.36 | 4.19E-03 |
| v | cell projection organization (GO:0030030)                         | 1.36 | 1.23E-05 |
| v | instar larval or pupal morphogenesis (GO:0048707)                 | 1.35 | 4.58E-04 |
| v | metamorphosis (GO:0007552)  | 1.35 | 3.16E-04 |
| v | locomotion (GO:0040011)   | 1.35 | 7.05E-05 |
| v | instar larval or pupal development (GO:0002165)                   | 1.35 | 1.06E-04 |
| v | appendage development (GO:0048736)                                | 1.35 | 4.09E-03 |
| v | cell surface receptor signaling pathway (GO:0007166)              | 1.35 | 1.04E-03 |
| v | appendage morphogenesis (GO:0035107)                              | 1.34 | 5.17E-03 |
| v | tube development (GO:0035295)                                     | 1.34 | 2.89E-05 |
| v | response to abiotic stimulus (GO:0009628)                         | 1.34 | 1.03E-03 |
| v | epithelial tube morphogenesis (GO:0060562)                        | 1.34 | 8.56E-04 |
| v | organonitrogen compound metabolic process (GO:1901564)            | 1.33 | 3.87E-18 |
| v | organic substance catabolic process (GO:1901575)                  | 1.32 | 7.91E-05 |
| v | organonitrogen compound catabolic process (GO:1901565)            | 1.32 | 1.90E-03 |
| v | localization (GO:0051179)   | 1.31 | 1.89E-12 |
| v | cell-cell signaling (GO:0007267)                                  | 1.31 | 2.10E-03 |
| v | catabolic process (GO:0009056)                                    | 1.28 | 2.09E-04 |
| v | response to stimulus (GO:0050896)                                 | 1.26 | 4.16E-12 |
| v | establishment of localization (GO:0051234)                        | 1.26 | 8.02E-08 |
| v | regulation of biological quality (GO:0065008)                     | 1.26 | 1.99E-05 |
| v | cell communication (GO:0007154)                                   | 1.26 | 1.73E-06 |
| v | response to external stimulus (GO:0009605)                        | 1.24 | 8.30E-04 |
| v | transport (GO:0006810)  | 1.22 | 5.44E-06 |
| v | signaling (GO:0023052)  | 1.2  | 2.76E-04 |
| v | signal transduction (GO:0007165)                                  | 1.19 | 3.94E-03 |
| v | multicellular organismal process (GO:0032501)                     | 1.18 | 2.22E-09 |
| v | biological_process (GO:0008150)                                   | 1.07 | 1.79E-17 |
| v | carbohydrate derivative metabolic process (GO:1901135)            | 0.77 | 5.22E-03 |
| v | oxidation-reduction process (GO:0055114)                          | 0.71 | 3.13E-04 |
| v | cuticle development (GO:0042335)                                  | 0.62 | 1.90E-03 |
| v | nucleotide metabolic process (GO:0009117)                         | 0.61 | 1.49E-03 |

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|---|---|------|----------|
| v | nucleoside phosphate metabolic process (GO:0006753)                 | 0.6  | 1.21E-03 |
| v | nervous system process (GO:0050877)                                 | 0.58 | 2.05E-08 |
| v | transmembrane transport (GO:0055085)                                | 0.58 | 3.69E-07 |
| v | system process (GO:0003008)   | 0.54 | 4.62E-11 |
| v | ion transport (GO:0006811)  | 0.52 | 1.77E-08 |
| v | metal ion transport (GO:0030001)                                    | 0.46 | 2.05E-04 |
| v | ion transmembrane transport (GO:0034220)                            | 0.46 | 2.32E-05 |
| v | cation transport (GO:0006812)                                       | 0.44 | 4.56E-07 |
| v | energy derivation by oxidation of organic compounds (GO:0015980)    | 0.44 | 1.40E-04 |
| v | purine-containing compound metabolic process (GO:0072521)           | 0.43 | 2.08E-06 |
| v | ribose phosphate metabolic process (GO:0019693)                     | 0.43 | 6.65E-06 |
| v | courtship behavior (GO:0007619)                                     | 0.42 | 7.08E-04 |
| v | male mating behavior (GO:0060179)                                   | 0.42 | 1.40E-03 |
| v | cellular respiration (GO:0045333)                                   | 0.41 | 2.57E-04 |
| v | male courtship behavior (GO:0008049)                                | 0.41 | 1.50E-03 |
| v | chitin-based cuticle development (GO:0040003)                       | 0.39 | 5.11E-06 |
| v | ribonucleotide metabolic process (GO:0009259)                       | 0.39 | 1.36E-06 |
| v | purine nucleotide metabolic process (GO:0006163)                    | 0.39 | 1.36E-06 |
| v | generation of precursor metabolites and energy (GO:0006091)         | 0.38 | 2.75E-06 |
| v | reproductive behavior (GO:0019098)                                  | 0.38 | 1.05E-05 |
| v | cation transmembrane transport (GO:0098655)                         | 0.37 | 8.33E-05 |
| v | drug metabolic process (GO:0017144)                                 | 0.37 | 2.67E-11 |
| v | inorganic ion transmembrane transport (GO:0098660)                  | 0.37 | 3.11E-05 |
| v | purine ribonucleotide metabolic process (GO:0009150)                | 0.36 | 4.22E-07 |
| v | inorganic cation transmembrane transport (GO:0098662)               | 0.34 | 6.37E-05 |
| v | nucleoside monophosphate metabolic process (GO:0009123)             | 0.34 | 3.31E-06 |
| v | detection of stimulus (GO:0051606)                                  | 0.33 | 3.18E-10 |
| v | sensory perception (GO:0007600)                                     | 0.32 | 3.72E-17 |
| v | mating behavior (GO:0007617)  | 0.32 | 1.19E-06 |
| v | mating (GO:0007618)   | 0.31 | 2.27E-07 |
| v | G-protein coupled receptor signaling pathway (GO:0007186)           | 0.31 | 4.45E-08 |
| v | nucleoside triphosphate metabolic process (GO:0009141)              | 0.29 | 4.04E-07 |
| v | ribonucleoside monophosphate metabolic process (GO:0009161)         | 0.28 | 2.01E-07 |
| v | detection of stimulus involved in sensory perception (GO:0050906)   | 0.26 | 6.38E-08 |
| v | respiratory electron transport chain (GO:0022904)                   | 0.26 | 5.72E-05 |
| v | electron transport chain (GO:0022900)                               | 0.25 | 2.72E-05 |
| v | purine nucleoside triphosphate metabolic process (GO:0009144)       | 0.25 | 8.33E-08 |
| v | aminoglycan metabolic process (GO:0006022)                          | 0.25 | 8.33E-08 |
| v | purine ribonucleoside monophosphate metabolic process (GO:0009167)  | 0.25 | 5.80E-08 |
| v | purine nucleoside monophosphate metabolic process (GO:0009126)      | 0.25 | 5.80E-08 |
| v | neuropeptide signaling pathway (GO:0007218)                         | 0.23 | 8.13E-04 |
| v | purine ribonucleoside triphosphate metabolic process (GO:0009205)   | 0.23 | 3.51E-08 |
| v | ribonucleoside triphosphate metabolic process (GO:0009199)          | 0.23 | 2.41E-08 |
| v | amino sugar metabolic process (GO:0006040)                          | 0.2  | 5.52E-08 |
| v | female mating behavior (GO:0060180)                                 | 0.17 | 2.83E-03 |
| v | potassium ion transport (GO:0006813)                                | 0.16 | 1.89E-03 |
| v | glucosamine-containing compound metabolic process (GO:1901071)      | 0.16 | 4.45E-09 |
| v | ATP metabolic process (GO:0046034)                                  | 0.14 | 3.85E-10 |
| v | monovalent inorganic cation transport (GO:0015672)                  | 0.14 | 7.55E-11 |
| v | sensory perception of taste (GO:0050909)                            | 0.14 | 5.44E-06 |
| v | mitochondrial ATP synthesis coupled electron transport (GO:0042775) | 0.13 | 3.69E-06 |
| v | sodium ion transport (GO:0006814)                                   | 0.13 | 1.63E-04 |

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|----|---|--------|----------|
| v  | ATP synthesis coupled electron transport (GO:0042773)                     | 0.12   | 1.64E-06 |
| v  | oxidative phosphorylation (GO:0006119)                                    | 0.12   | 7.25E-07 |
| v  | cyclic nucleotide metabolic process (GO:0009187)                          | 0.11   | 4.97E-03 |
| v  | sensory perception of smell (GO:0007608)                                  | 0.11   | 5.93E-10 |
| v  | proton transport (GO:0015992)   | 0.1    | 8.22E-06 |
| v  | hydrogen transport (GO:0006818)   | 0.1    | 8.35E-06 |
| v  | regulation of female receptivity (GO:0045924)                             | 0.1    | 3.40E-03 |
| v  | sensory perception of chemical stimulus (GO:0007606)                      | 0.1    | 7.55E-21 |
| v  | ATP hydrolysis coupled proton transport (GO:0015991)                      | 0.09   | 1.37E-03 |
| v  | ATP hydrolysis coupled transmembrane transport (GO:0090662)               | 0.09   | 1.37E-03 |
| v  | ATP hydrolysis coupled cation transmembrane transport (GO:0099132)        | 0.09   | 1.37E-03 |
| v  | ATP hydrolysis coupled ion transmembrane transport (GO:0099131)           | 0.09   | 1.37E-03 |
| v  | energy coupled proton transmembrane transport, against electrochemic      | 0.09   | 1.47E-03 |
| v  | response to carbon dioxide (GO:0010037)                                   | 0.08   | 5.78E-04 |
| v  | chitin metabolic process (GO:0006030)                                     | 0.08   | 8.60E-11 |
| v  | sensory perception of bitter taste (GO:0050913)                           | 0.08   | 3.69E-04 |
| v  | hydrogen ion transmembrane transport (GO:1902600)                         | 0.06   | 4.46E-06 |
| v  | detection of chemical stimulus (GO:0009593)                               | 0.02   | 4.44E-17 |
| v  | ATP biosynthetic process (GO:0006754)                                     | < 0.01 | 1.16E-03 |
| v  | ATP synthesis coupled proton transport (GO:0015986)                       | < 0.01 | 1.15E-03 |
| v  | energy coupled proton transport, down electrochemical gradient (GO:00     | < 0.01 | 1.15E-03 |
| v  | sperm competition (GO:0046692)  | < 0.01 | 4.97E-03 |
| v  | mitochondrial electron transport, NADH to ubiquinone (GO:0006120)         | < 0.01 | 1.90E-04 |
| v  | detection of chemical stimulus involved in sensory perception of taste (C | < 0.01 | 4.65E-03 |
| v  | detection of chemical stimulus involved in sensory perception of smell (C | < 0.01 | 4.38E-08 |
| v  | detection of chemical stimulus involved in sensory perception (GO:0050    | < 0.01 | 1.61E-11 |
| vi | mitochondrial respiratory chain complex I assembly (GO:0032981)           | 10.9   | 3.32E-04 |
| vi | mitochondrial respiratory chain complex I biogenesis (GO:0097031)         | 10.9   | 3.32E-04 |
| vi | NADH dehydrogenase complex assembly (GO:0010257)                          | 10.9   | 3.32E-04 |
| vi | positive regulation of mitochondrion organization (GO:0010822)            | 9.91   | 4.66E-04 |
| vi | mitochondrial respiratory chain complex IV assembly (GO:0033617)          | 9.91   | 4.66E-04 |
| vi | mitochondrial respiratory chain complex IV biogenesis (GO:0097034)        | 8.18   | 2.84E-04 |
| vi | mitochondrial RNA metabolic process (GO:0000959)                          | 7.27   | 4.75E-04 |
| vi | mitochondrion disassembly (GO:0061726)                                    | 6.94   | 2.02E-04 |
| vi | autophagy of mitochondrion (GO:0000422)                                   | 6.94   | 2.02E-04 |
| vi | vacuolar acidification (GO:0007035)                                       | 6.88   | 6.02E-04 |
| vi | intracellular pH reduction (GO:0051452)                                   | 6.64   | 2.54E-04 |
| vi | pH reduction (GO:0045851)   | 6.64   | 2.54E-04 |
| vi | retrograde vesicle-mediated transport, Golgi to ER (GO:0006890)           | 6.54   | 7.54E-04 |
| vi | ATP hydrolysis coupled proton transport (GO:0015991)                      | 6.48   | 5.43E-06 |
| vi | ATP hydrolysis coupled transmembrane transport (GO:0090662)               | 6.48   | 5.43E-06 |
| vi | ATP hydrolysis coupled cation transmembrane transport (GO:0099132)        | 6.48   | 5.43E-06 |
| vi | ATP hydrolysis coupled ion transmembrane transport (GO:0099131)           | 6.48   | 5.43E-06 |
| vi | energy coupled proton transmembrane transport, against electrochemic      | 6.31   | 6.73E-06 |
| vi | protein targeting to membrane (GO:0006612)                                | 6.23   | 9.34E-04 |
| vi | mitochondrial respiratory chain complex assembly (GO:0033108)             | 6.13   | 5.63E-05 |
| vi | mitochondrial gene expression (GO:0140053)                                | 5.87   | 2.54E-12 |
| vi | autophagosome assembly (GO:0000045)                                       | 5.65   | 5.77E-04 |
| vi | mitochondrial translation (GO:0032543)                                    | 5.57   | 2.38E-10 |
| vi | organelle disassembly (GO:1903008)  | 5.45   | 6.94E-04 |
| vi | autophagosome organization (GO:1905037)                                   | 5.26   | 8.29E-04 |
| vi | RNA methylation (GO:0001510)  | 5.16   | 1.73E-04 |

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| vi | vacuole organization (GO:0007033)  | 5.13 | 1.56E-05 |
| vi | regulation of intracellular pH (GO:0051453)                              | 4.47 | 9.04E-04 |
| vi | macroautophagy (GO:0016236)  | 4.36 | 1.26E-04 |
| vi | regulation of pH (GO:0006885)  | 4.36 | 1.04E-03 |
| vi | regulation of cellular pH (GO:0030641)                                   | 4.36 | 1.04E-03 |
| vi | monovalent inorganic cation homeostasis (GO:0055067)                     | 4.36 | 1.04E-03 |
| vi | cellular monovalent inorganic cation homeostasis (GO:0030004)            | 4.36 | 1.04E-03 |
| vi | hydrogen ion transmembrane transport (GO:1902600)                        | 4.29 | 7.20E-05 |
| vi | establishment of protein localization to membrane (GO:0090150)           | 4.27 | 5.91E-04 |
| vi | process utilizing autophagic mechanism (GO:0061919)                      | 4.16 | 3.38E-06 |
| vi | autophagy (GO:0006914)   | 4.16 | 3.38E-06 |
| vi | proton transport (GO:0015992)  | 3.9  | 1.58E-04 |
| vi | mitochondrion organization (GO:0007005)                                  | 3.89 | 4.28E-10 |
| vi | hydrogen transport (GO:0006818)  | 3.85 | 1.78E-04 |
| vi | protein ubiquitination involved in ubiquitin-dependent protein catabolic | 3.83 | 1.01E-04 |
| vi | protein targeting (GO:0006605)   | 3.44 | 8.90E-05 |
| vi | cellular cation homeostasis (GO:0030003)                                 | 3.31 | 4.80E-05 |
| vi | cellular ion homeostasis (GO:0006873)                                    | 3.11 | 9.40E-05 |
| vi | cation homeostasis (GO:0055080)  | 3.11 | 3.71E-05 |
| vi | ion homeostasis (GO:0050801)   | 3.07 | 2.80E-05 |
| vi | inorganic ion homeostasis (GO:0098771)                                   | 3.02 | 5.32E-05 |
| vi | cation transmembrane transport (GO:0098655)                              | 3    | 9.25E-05 |
| vi | cellular chemical homeostasis (GO:0055082)                               | 2.94 | 1.75E-04 |
| vi | cellular response to nutrient levels (GO:0031669)                        | 2.89 | 4.84E-04 |
| vi | inorganic cation transmembrane transport (GO:0098662)                    | 2.86 | 3.59E-04 |
| vi | cellular response to extracellular stimulus (GO:0031668)                 | 2.84 | 5.71E-04 |
| vi | methylation (GO:0032259)   | 2.8  | 9.86E-04 |
| vi | Golgi vesicle transport (GO:0048193)                                     | 2.8  | 6.71E-04 |
| vi | cellular response to external stimulus (GO:0071496)                      | 2.7  | 9.17E-04 |
| vi | cellular protein complex assembly (GO:0043623)                           | 2.7  | 4.64E-05 |
| vi | regulation of cellular catabolic process (GO:0031329)                    | 2.63 | 3.90E-04 |
| vi | cellular homeostasis (GO:0019725)  | 2.63 | 1.58E-05 |
| vi | regulation of catabolic process (GO:0009894)                             | 2.6  | 2.26E-04 |
| vi | inorganic ion transmembrane transport (GO:0098660)                       | 2.59 | 6.62E-04 |
| vi | response to nutrient levels (GO:0031667)                                 | 2.51 | 2.38E-04 |
| vi | response to extracellular stimulus (GO:0009991)                          | 2.49 | 2.57E-04 |
| vi | protein complex biogenesis (GO:0070271)                                  | 2.46 | 6.98E-05 |
| vi | protein complex assembly (GO:0006461)                                    | 2.42 | 1.19E-04 |
| vi | response to starvation (GO:0042594)                                      | 2.38 | 1.01E-03 |
| vi | translation (GO:0006412)   | 2.36 | 2.46E-05 |
| vi | intracellular protein transport (GO:0006886)                             | 2.35 | 1.43E-05 |
| vi | peptide biosynthetic process (GO:0043043)                                | 2.33 | 3.01E-05 |
| vi | protein complex subunit organization (GO:0071822)                        | 2.32 | 7.87E-05 |
| vi | chemical homeostasis (GO:0048878)  | 2.26 | 9.41E-04 |
| vi | programmed cell death (GO:0012501)                                       | 2.26 | 9.41E-04 |
| vi | establishment of protein localization (GO:0045184)                       | 2.25 | 4.42E-06 |
| vi | amide transport (GO:0042886)   | 2.25 | 6.12E-06 |
| vi | protein transport (GO:0015031)   | 2.23 | 9.23E-06 |
| vi | cellular protein localization (GO:0034613)                               | 2.23 | 1.65E-06 |
| vi | amide biosynthetic process (GO:0043604)                                  | 2.22 | 7.93E-05 |
| vi | cell death (GO:0008219)  | 2.21 | 1.09E-03 |
| vi | peptide transport (GO:0015833)   | 2.21 | 1.66E-05 |

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| vi | regulation of programmed cell death (GO:0043067)                                 | 2.15 | 1.03E-03 |
| vi | intracellular transport (GO:0046907)   | 2.1  | 1.78E-07 |
| vi | vesicle-mediated transport (GO:0016192)  | 2.09 | 6.16E-07 |
| vi | cellular macromolecule localization (GO:0070727)                                 | 2.07 | 6.15E-06 |
| vi | nitrogen compound transport (GO:0071705)   | 2.06 | 6.55E-06 |
| vi | negative regulation of signal transduction (GO:0009968)                          | 2.05 | 9.53E-04 |
| vi | peptide metabolic process (GO:0006518)   | 2.04 | 1.36E-04 |
| vi | establishment of localization in cell (GO:0051649)                               | 2.04 | 1.73E-07 |
| vi | protein localization (GO:0008104)  | 2.03 | 3.46E-06 |
| vi | homeostatic process (GO:0042592)   | 2.01 | 1.07E-04 |
| vi | macromolecule localization (GO:0033036)  | 2.01 | 3.23E-07 |
| vi | organonitrogen compound biosynthetic process (GO:1901566)                        | 2    | 2.74E-07 |
| vi | regulation of catalytic activity (GO:0050790)                                    | 1.98 | 1.10E-03 |
| vi | cellular localization (GO:0051641)   | 1.97 | 4.10E-08 |
| vi | cellular catabolic process (GO:0044248)  | 1.9  | 3.26E-06 |
| vi | cellular amide metabolic process (GO:0043603)                                    | 1.9  | 4.37E-04 |
| vi | epithelial tube morphogenesis (GO:0060562)                                       | 1.88 | 3.30E-04 |
| vi | organic substance transport (GO:0071702)   | 1.87 | 3.07E-05 |
| vi | cellular nitrogen compound biosynthetic process (GO:0044271)                     | 1.81 | 2.32E-05 |
| vi | instar larval or pupal morphogenesis (GO:0048707)                                | 1.81 | 6.52E-04 |
| vi | tube morphogenesis (GO:0035239)  | 1.8  | 5.26E-04 |
| vi | post-embryonic animal morphogenesis (GO:0009886)                                 | 1.8  | 5.37E-04 |
| vi | macromolecule catabolic process (GO:0009057)                                     | 1.8  | 8.57E-04 |
| vi | regulation of cellular protein metabolic process (GO:0032268)                    | 1.79 | 3.76E-04 |
| vi | regulation of signal transduction (GO:0009966)                                   | 1.79 | 4.24E-05 |
| vi | metamorphosis (GO:0007552)   | 1.76 | 8.98E-04 |
| vi | catabolic process (GO:0009056)   | 1.75 | 2.04E-05 |
| vi | regulation of signaling (GO:0023051)   | 1.75 | 2.04E-05 |
| vi | developmental process involved in reproduction (GO:0003006)                      | 1.75 | 1.42E-05 |
| vi | instar larval or pupal development (GO:0002165)                                  | 1.74 | 4.68E-04 |
| vi | regulation of response to stimulus (GO:0048583)                                  | 1.74 | 1.15E-05 |
| vi | post-embryonic development (GO:0009791)  | 1.73 | 2.22E-04 |
| vi | regulation of cell communication (GO:0010646)                                    | 1.73 | 4.08E-05 |
| vi | germ cell development (GO:0007281)   | 1.72 | 9.94E-05 |
| vi | transport (GO:0006810)   | 1.71 | 7.64E-10 |
| vi | positive regulation of metabolic process (GO:0009893)                            | 1.71 | 1.92E-04 |
| vi | regulation of protein metabolic process (GO:0051246)                             | 1.7  | 8.78E-04 |
| vi | morphogenesis of an epithelium (GO:0002009)                                      | 1.7  | 9.66E-04 |
| vi | cellular macromolecule biosynthetic process (GO:0034645)                         | 1.69 | 1.57E-04 |
| vi | tissue morphogenesis (GO:0048729)  | 1.69 | 8.09E-04 |
| vi | establishment of localization (GO:0051234)                                       | 1.69 | 1.71E-09 |
| vi | cellular process involved in reproduction in multicellular organism (GO:0000000) | 1.68 | 4.48E-05 |
| vi | positive regulation of cellular metabolic process (GO:0031325)                   | 1.67 | 5.39E-04 |
| vi | oogenesis (GO:0048477)   | 1.67 | 7.66E-04 |
| vi | macromolecule biosynthetic process (GO:0009059)                                  | 1.67 | 1.91E-04 |
| vi | localization (GO:0051179)  | 1.66 | 5.23E-11 |
| vi | positive regulation of macromolecule metabolic process (GO:0010604)              | 1.66 | 8.92E-04 |
| vi | positive regulation of biological process (GO:0048518)                           | 1.65 | 1.32E-06 |
| vi | female gamete generation (GO:0007292)  | 1.64 | 6.93E-04 |
| vi | gamete generation (GO:0007276)   | 1.64 | 7.78E-05 |
| vi | cellular protein metabolic process (GO:0044267)                                  | 1.64 | 2.82E-07 |
| vi | cellular biosynthetic process (GO:0044249)                                       | 1.63 | 8.83E-06 |

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| vi | biosynthetic process (GO:0009058)                          | 1.63 | 4.42E-06 |
| vi | macromolecule modification (GO:0043412)                    | 1.63 | 2.54E-05 |
| vi | positive regulation of cellular process (GO:0048522)       | 1.62 | 1.46E-05 |
| vi | regulation of biological quality (GO:0065008)              | 1.62 | 1.06E-05 |
| vi | organic substance biosynthetic process (GO:1901576)        | 1.59 | 1.72E-05 |
| vi | epithelium development (GO:0060429)                        | 1.56 | 3.18E-04 |
| vi | protein modification process (GO:0036211)                  | 1.53 | 5.71E-04 |
| vi | cellular protein modification process (GO:0006464)         | 1.53 | 5.71E-04 |
| vi | tissue development (GO:0009888)                            | 1.53 | 5.09E-04 |
| vi | organelle organization (GO:0006996)                        | 1.52 | 1.30E-05 |
| vi | cellular macromolecule metabolic process (GO:0044260)      | 1.46 | 4.71E-07 |
| vi | protein metabolic process (GO:0019538)                     | 1.45 | 1.08E-05 |
| vi | reproductive process (GO:0022414)                          | 1.45 | 9.27E-04 |
| vi | cellular metabolic process (GO:0044237)                    | 1.44 | 1.99E-10 |
| vi | cell development (GO:0048468)                              | 1.43 | 5.29E-04 |
| vi | organonitrogen compound metabolic process (GO:1901564)     | 1.42 | 1.22E-06 |
| vi | cellular component organization (GO:0016043)               | 1.42 | 3.34E-06 |
| vi | regulation of cellular metabolic process (GO:0031323)      | 1.4  | 3.52E-04 |
| vi | system development (GO:0048731)                            | 1.39 | 3.27E-04 |
| vi | cellular component organization or biogenesis (GO:0071840) | 1.39 | 6.72E-06 |
| vi | cellular developmental process (GO:0048869)                | 1.37 | 3.79E-04 |
| vi | regulation of metabolic process (GO:0019222)               | 1.37 | 4.56E-04 |
| vi | cellular nitrogen compound metabolic process (GO:0034641)  | 1.36 | 9.79E-04 |
| vi | primary metabolic process (GO:0044238)                     | 1.34 | 3.86E-07 |
| vi | anatomical structure development (GO:0048856)              | 1.34 | 5.25E-05 |
| vi | metabolic process (GO:0008152)                             | 1.34 | 5.15E-09 |
| vi | cellular process (GO:0009987)                              | 1.34 | 6.25E-15 |
| vi | nitrogen compound metabolic process (GO:0006807)           | 1.33 | 1.73E-06 |
| vi | biological regulation (GO:0065007)                         | 1.33 | 3.57E-07 |
| vi | developmental process (GO:0032502)                         | 1.33 | 4.08E-05 |
| vi | multicellular organism development (GO:0007275)            | 1.33 | 3.59E-04 |
| vi | organic substance metabolic process (GO:0071704)           | 1.32 | 2.43E-07 |
| vi | macromolecule metabolic process (GO:0043170)               | 1.31 | 7.20E-05 |
| vi | regulation of biological process (GO:0050789)              | 1.3  | 2.27E-05 |
| vi | regulation of cellular process (GO:0050794)                | 1.26 | 4.65E-04 |
| vi | biological_process (GO:0008150)                            | 1.08 | 1.98E-05 |