**Supplemental Table 3**: GO enrichment in clustered H3K4me3 profiles

**Cluster1**

|  |  |  |  |
| --- | --- | --- | --- |
| Term | Count | Pop Hits | FDR |
| GO:0005515~protein binding | 744 | 8154 | 6.67E-27 |
| GO:0045202~synapse | 86 | 355 | 1.79E-23 |
| GO:0007399~nervous system development | 170 | 1088 | 3.5E-23 |
| GO:0044456~synapse part | 65 | 246 | 1.1E-19 |
| GO:0043005~neuron projection | 78 | 342 | 1.58E-19 |
| GO:0022008~neurogenesis | 103 | 601 | 2.61E-16 |
| GO:0048699~generation of neurons | 98 | 559 | 3.79E-16 |
| GO:0030182~neuron differentiation | 84 | 438 | 4.34E-16 |
| GO:0048666~neuron development | 70 | 339 | 7.99E-15 |
| GO:0007409~axonogenesis | 50 | 193 | 1.81E-14 |
| GO:0048667~cell morphogenesis involved in neuron differentiation | 52 | 209 | 2.82E-14 |
| GO:0031175~neuron projection development | 58 | 256 | 4.83E-14 |
| GO:0030030~cell projection organization | 72 | 368 | 5.23E-14 |
| GO:0048812~neuron projection morphogenesis | 51 | 213 | 2.82E-13 |
| GO:0000904~cell morphogenesis involved in differentiation | 54 | 244 | 1.37E-12 |
| GO:0042995~cell projection | 105 | 697 | 1.18E-12 |
| GO:0048858~cell projection morphogenesis | 53 | 245 | 6.24E-12 |
| GO:0048731~system development | 250 | 2330 | 7.08E-12 |
| GO:0048856~anatomical structure development | 266 | 2527 | 7.87E-12 |
| GO:0007275~multicellular organismal development | 293 | 2865 | 1.04E-11 |
| GO:0032990~cell part morphogenesis | 54 | 256 | 1.05E-11 |
| GO:0032502~developmental process | 314 | 3148 | 2.41E-11 |
| GO:0005488~binding | 962 | 12531 | 3.33E-11 |
| GO:0007268~synaptic transmission | 57 | 298 | 1.46E-10 |
| GO:0030424~axon | 39 | 159 | 1.82E-10 |
| GO:0048468~cell development | 93 | 644 | 5.17E-10 |
| GO:0000902~cell morphogenesis | 62 | 356 | 9.63E-10 |
| GO:0030425~dendrite | 38 | 163 | 1.68E-09 |
| GO:0045211~postsynaptic membrane | 34 | 135 | 2.14E-09 |
| GO:0044459~plasma membrane part | 229 | 2203 | 2.51E-09 |
| GO:0014069~postsynaptic density | 24 | 71 | 3.21E-09 |
| GO:0032989~cellular component morphogenesis | 65 | 397 | 4.57E-09 |
| GO:0019717~synaptosome | 26 | 85 | 5.47E-09 |
| GO:0019226~transmission of nerve impulse | 59 | 350 | 1.1E-08 |
| GO:0030054~cell junction | 76 | 518 | 1.67E-08 |
| GO:0005886~plasma membrane | 349 | 3777 | 2.47E-08 |
| GO:0051128~regulation of cellular component organization | 69 | 458 | 4.51E-08 |
| GO:0007267~cell-cell signaling | 83 | 600 | 5.66E-08 |
| GO:0050804~regulation of synaptic transmission | 32 | 136 | 6.23E-08 |
| GO:0044464~cell part | 1081 | 14826 | 6.18E-08 |
| GO:0005623~cell | 1081 | 14827 | 6.46E-08 |
| GO:0016020~membrane | 602 | 7266 | 7.06E-08 |
| GO:0022604~regulation of cell morphogenesis | 31 | 131 | 9.91E-08 |
| GO:0030154~cell differentiation | 175 | 1637 | 1E-07 |
| GO:0051969~regulation of transmission of nerve impulse | 33 | 147 | 1.17E-07 |
| GO:0007417~central nervous system development | 64 | 425 | 1.91E-07 |
| GO:0048869~cellular developmental process | 179 | 1706 | 2.58E-07 |
| GO:0043025~cell soma | 35 | 168 | 2.18E-07 |
| GO:0007411~axon guidance | 27 | 107 | 2.79E-07 |
| GO:0031644~regulation of neurological system process | 33 | 153 | 3.26E-07 |
| GO:0009653~anatomical structure morphogenesis | 135 | 1197 | 3.75E-07 |
| GO:0008092~cytoskeletal protein binding | 71 | 504 | 4.88E-07 |
| GO:0007611~learning or memory | 27 | 111 | 6.28E-07 |
| GO:0010975~regulation of neuron projection development | 21 | 70 | 6.92E-07 |
| GO:0007154~cell communication | 98 | 795 | 7.28E-07 |
| GO:0043687~post-translational protein modification | 132 | 1182 | 1E-06 |
| GO:0050789~regulation of biological process | 580 | 7106 | 1.08E-06 |
| GO:0006928~cell motion | 67 | 475 | 1.1E-06 |
| GO:0051239~regulation of multicellular organismal process | 110 | 937 | 1.29E-06 |
| GO:0009987~cellular process | 808 | 10541 | 1.37E-06 |
| GO:0065007~biological regulation | 604 | 7484 | 2.35E-06 |
| GO:0044057~regulation of system process | 49 | 309 | 2.66E-06 |
| GO:0006464~protein modification process | 153 | 1453 | 3.09E-06 |
| GO:0016301~kinase activity | 99 | 834 | 4.56E-06 |
| GO:0007420~brain development | 46 | 289 | 6.08E-06 |
| GO:0050794~regulation of cellular process | 555 | 6819 | 6.31E-06 |
| GO:0006468~protein amino acid phosphorylation | 83 | 667 | 6.33E-06 |
| GO:0022836~gated channel activity | 48 | 310 | 7.62E-06 |
| GO:0005856~cytoskeleton | 145 | 1381 | 6.98E-06 |
| GO:0043412~biopolymer modification | 157 | 1526 | 9.11E-06 |
| GO:0008066~glutamate receptor activity | 13 | 31 | 9E-06 |
| GO:0044433~cytoplasmic vesicle part | 34 | 187 | 1.03E-05 |
| GO:0006811~ion transport | 91 | 768 | 1.42E-05 |
| GO:0008021~synaptic vesicle | 20 | 76 | 1.16E-05 |
| GO:0044425~membrane part | 538 | 6578 | 1.2E-05 |
| GO:0016773~phosphotransferase activity, alcohol group as acceptor | 87 | 721 | 1.37E-05 |
| GO:0005737~cytoplasm | 590 | 7319 | 1.36E-05 |
| GO:0010769~regulation of cell morphogenesis involved in differentiation | 20 | 77 | 1.85E-05 |
| GO:0030659~cytoplasmic vesicle membrane | 28 | 139 | 1.53E-05 |
| GO:0004672~protein kinase activity | 76 | 606 | 1.75E-05 |
| GO:0050770~regulation of axonogenesis | 17 | 57 | 2.06E-05 |
| GO:0045664~regulation of neuron differentiation | 27 | 133 | 2.74E-05 |
| GO:0012506~vesicle membrane | 29 | 151 | 2.57E-05 |
| GO:0015075~ion transmembrane transporter activity | 86 | 725 | 3.23E-05 |
| GO:0005216~ion channel activity | 54 | 386 | 3.35E-05 |
| GO:0031344~regulation of cell projection organization | 21 | 89 | 4.72E-05 |
| GO:0006796~phosphate metabolic process | 107 | 973 | 4.81E-05 |
| GO:0006793~phosphorus metabolic process | 107 | 973 | 4.81E-05 |
| GO:0016043~cellular component organization | 231 | 2498 | 4.91E-05 |
| GO:0030426~growth cone | 16 | 54 | 4.01E-05 |
| GO:0005938~cell cortex | 28 | 146 | 4.12E-05 |
| GO:0031982~vesicle | 80 | 670 | 4.28E-05 |
| GO:0030001~metal ion transport | 61 | 465 | 5.42E-05 |
| GO:0050808~synapse organization | 17 | 61 | 5.53E-05 |
| GO:0048168~regulation of neuronal synaptic plasticity | 13 | 36 | 6.21E-05 |
| GO:0032553~ribonucleotide binding | 179 | 1836 | 5.64E-05 |
| GO:0032555~purine ribonucleotide binding | 179 | 1836 | 5.64E-05 |
| GO:0030427~site of polarized growth | 16 | 55 | 5.16E-05 |
| GO:0044430~cytoskeletal part | 104 | 952 | 7.15E-05 |
| GO:0032501~multicellular organismal process | 364 | 4280 | 9.45E-05 |
| GO:0022838~substrate specific channel activity | 54 | 398 | 8.37E-05 |
| GO:0012505~endomembrane system | 89 | 782 | 7.79E-05 |

**Cluster2**

|  |  |  |  |
| --- | --- | --- | --- |
| Term | Count | Pop Hits | FDR |
| GO:0044424~intracellular part | 552 | 10624 | 2.79E-12 |
| GO:0006139~nucleobase, nucleoside, nucleotide and nucleic acid metabolic process | 227 | 3409 | 3.59E-12 |
| GO:0005634~nucleus | 312 | 5077 | 6.96E-12 |
| GO:0005622~intracellular | 562 | 10995 | 4.49E-11 |
| GO:0034641~cellular nitrogen compound metabolic process | 235 | 3670 | 7.4E-11 |
| GO:0044260~cellular macromolecule metabolic process | 307 | 5214 | 9.26E-11 |
| GO:0006807~nitrogen compound metabolic process | 239 | 3778 | 1.63E-10 |
| GO:0043231~intracellular membrane-bounded organelle | 434 | 7982 | 8.27E-10 |
| GO:0043227~membrane-bounded organelle | 434 | 7989 | 9.66E-10 |
| GO:0044237~cellular metabolic process | 362 | 6636 | 6.43E-09 |
| GO:0044238~primary metabolic process | 374 | 6923 | 7.42E-09 |
| GO:0043170~macromolecule metabolic process | 321 | 5710 | 8.59E-09 |
| GO:0044464~cell part | 684 | 14826 | 4.05E-08 |
| GO:0005623~cell | 684 | 14827 | 4.19E-08 |
| GO:0043229~intracellular organelle | 467 | 8977 | 8.11E-08 |
| GO:0043226~organelle | 467 | 8989 | 1.03E-07 |
| GO:0010467~gene expression | 187 | 2999 | 4.31E-07 |
| GO:0034645~cellular macromolecule biosynthetic process | 177 | 2812 | 6.51E-07 |
| GO:0003676~nucleic acid binding | 204 | 3264 | 5.92E-07 |
| GO:0009987~cellular process | 510 | 10541 | 8.15E-07 |
| GO:0008152~metabolic process | 395 | 7647 | 8.45E-07 |
| GO:0009059~macromolecule biosynthetic process | 177 | 2832 | 1.11E-06 |
| GO:0060255~regulation of macromolecule metabolic process | 197 | 3259 | 1.73E-06 |
| GO:0080090~regulation of primary metabolic process | 196 | 3291 | 5.82E-06 |
| GO:0044249~cellular biosynthetic process | 203 | 3442 | 6.43E-06 |
| GO:0031323~regulation of cellular metabolic process | 204 | 3464 | 6.62E-06 |
| GO:0031981~nuclear lumen | 104 | 1450 | 7.12E-06 |
| GO:0010556~regulation of macromolecule biosynthetic process | 171 | 2830 | 2.08E-05 |
| GO:0009058~biosynthetic process | 205 | 3542 | 2.26E-05 |
| GO:0070013~intracellular organelle lumen | 120 | 1779 | 1.85E-05 |
| GO:0019222~regulation of metabolic process | 208 | 3621 | 3.05E-05 |
| GO:0010468~regulation of gene expression | 171 | 2856 | 3.75E-05 |
| GO:0043233~organelle lumen | 121 | 1820 | 3.38E-05 |
| GO:0031326~regulation of cellular biosynthetic process | 174 | 2947 | 6.92E-05 |
| GO:0009889~regulation of biosynthetic process | 174 | 2966 | 0.000106 |
| GO:0031974~membrane-enclosed lumen | 121 | 1856 | 8.71E-05 |
| GO:0044428~nuclear part | 119 | 1822 | 9.99E-05 |

**Cluster3**

|  |  |  |  |
| --- | --- | --- | --- |
| Term | Count | Pop Hits | FDR |
| GO:0005622~intracellular | 1172 | 10995 | 1.96E-48 |
| GO:0044424~intracellular part | 1133 | 10624 | 8.29E-43 |
| GO:0043227~membrane-bounded organelle | 908 | 7989 | 1.44E-35 |
| GO:0043231~intracellular membrane-bounded organelle | 907 | 7982 | 1.96E-35 |
| GO:0043226~organelle | 978 | 8989 | 5.83E-32 |
| GO:0043229~intracellular organelle | 977 | 8977 | 5.99E-32 |
| GO:0044464~cell part | 1351 | 14826 | 2.59E-23 |
| GO:0005623~cell | 1351 | 14827 | 2.8E-23 |
| GO:0044237~cellular metabolic process | 747 | 6636 | 1.09E-22 |
| GO:0008152~metabolic process | 826 | 7647 | 7.53E-21 |
| GO:0005737~cytoplasm | 793 | 7319 | 9.5E-20 |
| GO:0044238~primary metabolic process | 754 | 6923 | 2.72E-18 |
| GO:0044260~cellular macromolecule metabolic process | 595 | 5214 | 1.24E-16 |
| GO:0005634~nucleus | 578 | 5077 | 2.23E-16 |
| GO:0044422~organelle part | 501 | 4251 | 2.31E-16 |
| GO:0044446~intracellular organelle part | 498 | 4225 | 3.05E-16 |
| GO:0070013~intracellular organelle lumen | 252 | 1779 | 3.22E-15 |
| GO:0044444~cytoplasmic part | 555 | 4895 | 1.14E-14 |
| GO:0031974~membrane-enclosed lumen | 257 | 1856 | 1.47E-14 |
| GO:0043233~organelle lumen | 252 | 1820 | 3.11E-14 |
| GO:0044428~nuclear part | 249 | 1822 | 2.32E-13 |
| GO:0031981~nuclear lumen | 208 | 1450 | 4.94E-13 |
| GO:0043170~macromolecule metabolic process | 624 | 5710 | 6.94E-13 |
| GO:0006139~nucleobase, nucleoside, nucleotide and nucleic acid metabolic process | 409 | 3409 | 1.03E-12 |
| GO:0034641~cellular nitrogen compound metabolic process | 433 | 3670 | 1.8E-12 |
| GO:0009987~cellular process | 1021 | 10541 | 1.3E-11 |
| GO:0006807~nitrogen compound metabolic process | 439 | 3778 | 1.44E-11 |
| GO:0005488~binding | 1165 | 12531 | 5.43E-10 |
| GO:0016070~RNA metabolic process | 139 | 938 | 5.88E-09 |
| GO:0005730~nucleolus | 110 | 698 | 6.58E-09 |
| GO:0005829~cytosol | 177 | 1330 | 2.76E-08 |
| GO:0010467~gene expression | 346 | 2999 | 4.22E-08 |
| GO:0003824~catalytic activity | 547 | 5198 | 4.92E-08 |
| GO:0006396~RNA processing | 90 | 547 | 8.86E-08 |
| GO:0009058~biosynthetic process | 395 | 3542 | 1.3E-07 |
| GO:0034470~ncRNA processing | 43 | 187 | 1.47E-07 |
| GO:0044249~cellular biosynthetic process | 385 | 3442 | 1.62E-07 |
| GO:0034660~ncRNA metabolic process | 48 | 230 | 4.67E-07 |
| GO:0003723~RNA binding | 105 | 718 | 1.35E-06 |
| GO:0006281~DNA repair | 53 | 284 | 3.74E-06 |
| GO:0003676~nucleic acid binding | 357 | 3264 | 3.51E-06 |
| GO:0005739~mitochondrion | 142 | 1087 | 4.61E-06 |
| GO:0005654~nucleoplasm | 120 | 882 | 5.48E-06 |
| GO:0044431~Golgi apparatus part | 53 | 294 | 5.97E-06 |
| GO:0033554~cellular response to stress | 86 | 566 | 7.62E-06 |
| GO:0044248~cellular catabolic process | 136 | 1024 | 8.73E-06 |
| GO:0006974~response to DNA damage stimulus | 63 | 373 | 9.39E-06 |
| GO:0044265~cellular macromolecule catabolic process | 103 | 725 | 1.29E-05 |
| GO:0009059~macromolecule biosynthetic process | 315 | 2832 | 1.34E-05 |
| GO:0034645~cellular macromolecule biosynthetic process | 313 | 2812 | 1.42E-05 |
| GO:0006259~DNA metabolic process | 78 | 506 | 1.59E-05 |
| GO:0044267~cellular protein metabolic process | 267 | 2355 | 2.92E-05 |
| GO:0009057~macromolecule catabolic process | 107 | 781 | 4.29E-05 |
| GO:0043232~intracellular non-membrane-bounded organelle | 286 | 2596 | 3.57E-05 |
| GO:0043228~non-membrane-bounded organelle | 286 | 2596 | 3.57E-05 |
| GO:0009056~catabolic process | 156 | 1253 | 5.85E-05 |
| GO:0030529~ribonucleoprotein complex | 76 | 515 | 5.62E-05 |
| GO:0005515~protein binding | 782 | 8154 | 7.65E-05 |

**Cluster4**

|  |  |  |  |
| --- | --- | --- | --- |
| Term | Count | Pop Hits | FDR |
| GO:0005622~intracellular | 1694 | 10995 | 5.54E-62 |
| GO:0044424~intracellular part | 1645 | 10624 | 7.56E-58 |
| GO:0005737~cytoplasm | 1258 | 7319 | 5.67E-57 |
| GO:0044464~cell part | 1985 | 14826 | 1.74E-37 |
| GO:0005623~cell | 1985 | 14827 | 1.97E-37 |
| GO:0044444~cytoplasmic part | 862 | 4895 | 3.85E-34 |
| GO:0043227~membrane-bounded organelle | 1256 | 7989 | 6.28E-32 |
| GO:0043231~intracellular membrane-bounded organelle | 1253 | 7982 | 2.13E-31 |
| GO:0043229~intracellular organelle | 1370 | 8977 | 2.57E-30 |
| GO:0043226~organelle | 1370 | 8989 | 5.86E-30 |
| GO:0009987~cellular process | 1541 | 10541 | 5.44E-28 |
| GO:0044267~cellular protein metabolic process | 446 | 2355 | 2.7E-19 |
| GO:0051649~establishment of localization in cell | 195 | 852 | 4.11E-15 |
| GO:0046907~intracellular transport | 161 | 657 | 4.11E-15 |
| GO:0005829~cytosol | 269 | 1330 | 3.33E-15 |
| GO:0015031~protein transport | 178 | 762 | 8.22E-15 |
| GO:0051641~cellular localization | 206 | 928 | 8.22E-15 |
| GO:0005515~protein binding | 1213 | 8154 | 9.1E-15 |
| GO:0045184~establishment of protein localization | 178 | 769 | 2.26E-14 |
| GO:0044237~cellular metabolic process | 1011 | 6636 | 4.12E-14 |
| GO:0003824~catalytic activity | 823 | 5198 | 7.13E-14 |
| GO:0008104~protein localization | 195 | 882 | 1.03E-13 |
| GO:0016192~vesicle-mediated transport | 141 | 576 | 2.9E-13 |
| GO:0033036~macromolecule localization | 222 | 1076 | 2.53E-12 |
| GO:0005794~Golgi apparatus | 186 | 872 | 2.54E-12 |
| GO:0000166~nucleotide binding | 399 | 2245 | 6.03E-12 |
| GO:0043687~post-translational protein modification | 237 | 1182 | 8.17E-12 |
| GO:0005488~binding | 1718 | 12531 | 9.86E-12 |
| GO:0006464~protein modification process | 278 | 1453 | 1.67E-11 |
| GO:0019538~protein metabolic process | 478 | 2812 | 2.17E-11 |
| GO:0031090~organelle membrane | 218 | 1096 | 2.81E-11 |
| GO:0043412~biopolymer modification | 286 | 1526 | 8.58E-11 |
| GO:0006810~transport | 447 | 2629 | 1.64E-10 |
| GO:0051234~establishment of localization | 450 | 2656 | 2.37E-10 |
| GO:0051179~localization | 496 | 2993 | 4.96E-10 |
| GO:0005783~endoplasmic reticulum | 192 | 960 | 4.42E-10 |
| GO:0044257~cellular protein catabolic process | 134 | 603 | 2.19E-09 |
| GO:0017076~purine nucleotide binding | 338 | 1918 | 1.98E-09 |
| GO:0051603~proteolysis involved in cellular protein catabolic process | 133 | 600 | 3.1E-09 |
| GO:0032555~purine ribonucleotide binding | 325 | 1836 | 2.99E-09 |
| GO:0032553~ribonucleotide binding | 325 | 1836 | 2.99E-09 |
| GO:0008152~metabolic process | 1109 | 7647 | 3.37E-09 |
| GO:0030163~protein catabolic process | 136 | 622 | 4.98E-09 |
| GO:0070727~cellular macromolecule localization | 100 | 414 | 6.22E-09 |
| GO:0034613~cellular protein localization | 99 | 411 | 9.08E-09 |
| GO:0016740~transferase activity | 310 | 1751 | 8.65E-09 |
| GO:0006886~intracellular protein transport | 92 | 374 | 1.27E-08 |
| GO:0044260~cellular macromolecule metabolic process | 789 | 5214 | 1.53E-08 |
| GO:0016772~transferase activity, transferring phosphorus-containing groups | 189 | 964 | 1.77E-08 |
| GO:0044265~cellular macromolecule catabolic process | 150 | 725 | 3.3E-08 |
| GO:0016301~kinase activity | 167 | 834 | 4E-08 |
| GO:0044238~primary metabolic process | 1007 | 6923 | 6.78E-08 |
| GO:0019941~modification-dependent protein catabolic process | 124 | 574 | 7.27E-08 |
| GO:0043632~modification-dependent macromolecule catabolic process | 124 | 574 | 7.27E-08 |
| GO:0009057~macromolecule catabolic process | 157 | 781 | 1.09E-07 |
| GO:0044422~organelle part | 645 | 4251 | 8.83E-08 |
| GO:0006793~phosphorus metabolic process | 187 | 973 | 1.2E-07 |
| GO:0006796~phosphate metabolic process | 187 | 973 | 1.2E-07 |
| GO:0044446~intracellular organelle part | 641 | 4225 | 9.71E-08 |
| GO:0012505~endomembrane system | 154 | 782 | 1.54E-07 |
| GO:0016773~phosphotransferase activity, alcohol group as acceptor | 144 | 721 | 6.9E-07 |
| GO:0001882~nucleoside binding | 278 | 1612 | 1.13E-06 |
| GO:0001883~purine nucleoside binding | 276 | 1601 | 1.32E-06 |
| GO:0030554~adenyl nucleotide binding | 272 | 1577 | 1.57E-06 |
| GO:0044248~cellular catabolic process | 189 | 1024 | 2.25E-06 |
| GO:0005626~insoluble fraction | 158 | 839 | 2.06E-06 |
| GO:0031967~organelle envelope | 124 | 620 | 2.07E-06 |
| GO:0032559~adenyl ribonucleotide binding | 259 | 1497 | 2.63E-06 |
| GO:0031975~envelope | 124 | 622 | 2.49E-06 |
| GO:0005624~membrane fraction | 152 | 809 | 4.26E-06 |
| GO:0005524~ATP binding | 253 | 1477 | 8.67E-06 |
| GO:0016044~membrane organization | 84 | 381 | 1.27E-05 |
| GO:0042470~melanosome | 30 | 89 | 1.09E-05 |
| GO:0048770~pigment granule | 30 | 89 | 1.09E-05 |
| GO:0000267~cell fraction | 191 | 1083 | 1.15E-05 |
| GO:0016874~ligase activity | 85 | 390 | 1.56E-05 |
| GO:0006892~post-Golgi vesicle-mediated transport | 23 | 58 | 2.27E-05 |
| GO:0031301~integral to organelle membrane | 36 | 123 | 3.07E-05 |
| GO:0048193~Golgi vesicle transport | 38 | 131 | 3.84E-05 |
| GO:0009056~catabolic process | 216 | 1253 | 5.12E-05 |
| GO:0005739~mitochondrion | 188 | 1087 | 5.24E-05 |
| GO:0005634~nucleus | 730 | 5077 | 5.49E-05 |
| GO:0004674~protein serine/threonine kinase activity | 89 | 430 | 7.97E-05 |
| GO:0016310~phosphorylation | 147 | 800 | 9.14E-05 |
| GO:0043234~protein complex | 397 | 2588 | 9.16E-05 |

**Cluster5**

|  |  |  |  |
| --- | --- | --- | --- |
| Term | Count | Pop Hits | FDR |
| GO:0005622~intracellular | 1955 | 10995 | 2E-104 |
| GO:0044424~intracellular part | 1906 | 10624 | 5.9E-100 |
| GO:0043227~membrane-bounded organelle | 1556 | 7989 | 1.27E-88 |
| GO:0043231~intracellular membrane-bounded organelle | 1554 | 7982 | 3.49E-88 |
| GO:0043229~intracellular organelle | 1677 | 8977 | 2.58E-85 |
| GO:0043226~organelle | 1678 | 8989 | 4.29E-85 |
| GO:0044237~cellular metabolic process | 1319 | 6636 | 8.57E-70 |
| GO:0044260~cellular macromolecule metabolic process | 1072 | 5214 | 4.95E-56 |
| GO:0008152~metabolic process | 1412 | 7647 | 3.43E-53 |
| GO:0044446~intracellular organelle part | 890 | 4225 | 9.33E-49 |
| GO:0044422~organelle part | 894 | 4251 | 1.02E-48 |
| GO:0044238~primary metabolic process | 1294 | 6923 | 2.5E-47 |
| GO:0044444~cytoplasmic part | 985 | 4895 | 7.68E-46 |
| GO:0043170~macromolecule metabolic process | 1108 | 5710 | 5.5E-44 |
| GO:0005737~cytoplasm | 1331 | 7319 | 4.52E-43 |
| GO:0009987~cellular process | 1744 | 10541 | 1.74E-41 |
| GO:0010467~gene expression | 661 | 2999 | 1.11E-37 |
| GO:0006139~nucleobase, nucleoside, nucleotide and nucleic acid metabolic process | 728 | 3409 | 1.93E-37 |
| GO:0034641~cellular nitrogen compound metabolic process | 765 | 3670 | 6.73E-36 |
| GO:0005739~mitochondrion | 306 | 1087 | 2.81E-35 |
| GO:0006807~nitrogen compound metabolic process | 778 | 3778 | 1.1E-34 |
| GO:0005634~nucleus | 963 | 5077 | 2E-32 |
| GO:0044464~cell part | 2194 | 14826 | 4.36E-31 |
| GO:0005623~cell | 2194 | 14827 | 4.93E-31 |
| GO:0044249~cellular biosynthetic process | 710 | 3442 | 7.18E-31 |
| GO:0009058~biosynthetic process | 721 | 3542 | 1.58E-29 |
| GO:0070013~intracellular organelle lumen | 419 | 1779 | 1.64E-29 |
| GO:0034645~cellular macromolecule biosynthetic process | 601 | 2812 | 2.67E-29 |
| GO:0009059~macromolecule biosynthetic process | 602 | 2832 | 1.16E-28 |
| GO:0031974~membrane-enclosed lumen | 429 | 1856 | 2.17E-28 |
| GO:0043233~organelle lumen | 419 | 1820 | 2.94E-27 |
| GO:0006412~translation | 126 | 331 | 1.26E-25 |
| GO:0044429~mitochondrial part | 182 | 595 | 6.44E-25 |
| GO:0044428~nuclear part | 408 | 1822 | 6.68E-24 |
| GO:0015031~protein transport | 215 | 762 | 2.4E-23 |
| GO:0045184~establishment of protein localization | 216 | 769 | 3.47E-23 |
| GO:0044267~cellular protein metabolic process | 499 | 2355 | 1.81E-22 |
| GO:0032991~macromolecular complex | 622 | 3155 | 2.65E-22 |
| GO:0008104~protein localization | 233 | 882 | 3.23E-21 |
| GO:0030529~ribonucleoprotein complex | 157 | 515 | 3.1E-21 |
| GO:0016070~RNA metabolic process | 243 | 938 | 5.98E-21 |
| GO:0031090~organelle membrane | 264 | 1096 | 2.86E-19 |
| GO:0031967~organelle envelope | 173 | 620 | 5.85E-19 |
| GO:0031975~envelope | 173 | 622 | 8.37E-19 |
| GO:0046907~intracellular transport | 182 | 657 | 1.11E-18 |
| GO:0003676~nucleic acid binding | 633 | 3264 | 1.77E-18 |
| GO:0033036~macromolecule localization | 261 | 1076 | 2.28E-18 |
| GO:0031981~nuclear lumen | 319 | 1450 | 4.52E-17 |
| GO:0006396~RNA processing | 154 | 547 | 2.11E-16 |
| GO:0033279~ribosomal subunit | 58 | 128 | 5.97E-16 |
| GO:0034613~cellular protein localization | 124 | 411 | 2E-15 |
| GO:0070727~cellular macromolecule localization | 124 | 414 | 4.11E-15 |
| GO:0034660~ncRNA metabolic process | 83 | 230 | 6.11E-15 |
| GO:0005740~mitochondrial envelope | 123 | 419 | 5E-15 |
| GO:0003735~structural constituent of ribosome | 68 | 168 | 5.55E-15 |
| GO:0006886~intracellular protein transport | 114 | 374 | 1.83E-14 |
| GO:0031966~mitochondrial membrane | 116 | 394 | 3.49E-14 |
| GO:0005840~ribosome | 77 | 215 | 3.49E-14 |
| GO:0051649~establishment of localization in cell | 206 | 852 | 7.13E-14 |
| GO:0003824~catalytic activity | 909 | 5198 | 6.61E-14 |
| GO:0019538~protein metabolic process | 535 | 2812 | 1.85E-13 |
| GO:0044248~cellular catabolic process | 235 | 1024 | 3.34E-13 |
| GO:0031980~mitochondrial lumen | 78 | 227 | 2.96E-13 |
| GO:0005759~mitochondrial matrix | 78 | 227 | 2.96E-13 |
| GO:0051641~cellular localization | 217 | 928 | 5.13E-13 |
| GO:0008270~zinc ion binding | 452 | 2311 | 1.31E-12 |
| GO:0006414~translational elongation | 46 | 101 | 3.51E-12 |
| GO:0005743~mitochondrial inner membrane | 93 | 306 | 3.39E-12 |
| GO:0006091~generation of precursor metabolites and energy | 95 | 313 | 7.6E-12 |
| GO:0034470~ncRNA processing | 67 | 187 | 7.99E-12 |
| GO:0006399~tRNA metabolic process | 50 | 118 | 8.07E-12 |
| GO:0044455~mitochondrial membrane part | 51 | 125 | 1E-11 |
| GO:0048193~Golgi vesicle transport | 53 | 131 | 1.32E-11 |
| GO:0009057~macromolecule catabolic process | 185 | 781 | 1.6E-11 |
| GO:0010498~proteasomal protein catabolic process | 45 | 102 | 2.59E-11 |
| GO:0043161~proteasomal ubiquitin-dependent protein catabolic process | 45 | 102 | 2.59E-11 |
| GO:0046914~transition metal ion binding | 521 | 2785 | 2.91E-11 |
| GO:0044265~cellular macromolecule catabolic process | 173 | 725 | 5.14E-11 |
| GO:0019866~organelle inner membrane | 95 | 329 | 4.99E-11 |
| GO:0031145~anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process | 34 | 65 | 6.62E-11 |
| GO:0051436~negative regulation of ubiquitin-protein ligase activity during mitotic cell cycle | 34 | 65 | 6.62E-11 |
| GO:0015934~large ribosomal subunit | 34 | 67 | 9.21E-11 |
| GO:0003723~RNA binding | 171 | 718 | 1.09E-10 |
| GO:0005654~nucleoplasm | 197 | 882 | 1.24E-10 |
| GO:0005488~binding | 1907 | 12531 | 1.63E-10 |
| GO:0051352~negative regulation of ligase activity | 34 | 67 | 1.95E-10 |
| GO:0051444~negative regulation of ubiquitin-protein ligase activity | 34 | 67 | 1.95E-10 |
| GO:0009056~catabolic process | 264 | 1253 | 2.02E-10 |
| GO:0031397~negative regulation of protein ubiquitination | 36 | 74 | 2.04E-10 |
| GO:0006350~transcription | 404 | 2101 | 2.95E-10 |
| GO:0051437~positive regulation of ubiquitin-protein ligase activity during mitotic cell cycle | 34 | 68 | 3.26E-10 |
| GO:0022626~cytosolic ribosome | 37 | 81 | 4.55E-10 |
| GO:0051351~positive regulation of ligase activity | 35 | 73 | 6.85E-10 |
| GO:0031398~positive regulation of protein ubiquitination | 38 | 84 | 7.36E-10 |
| GO:0051443~positive regulation of ubiquitin-protein ligase activity | 34 | 70 | 8.82E-10 |
| GO:0006605~protein targeting | 69 | 215 | 1.11E-09 |
| GO:0044445~cytosolic part | 54 | 152 | 1.06E-09 |
| GO:0016071~mRNA metabolic process | 101 | 370 | 1.36E-09 |
| GO:0051439~regulation of ubiquitin-protein ligase activity during mitotic cell cycle | 34 | 71 | 1.42E-09 |
| GO:0019941~modification-dependent protein catabolic process | 140 | 574 | 1.63E-09 |
| GO:0043632~modification-dependent macromolecule catabolic process | 140 | 574 | 1.63E-09 |
| GO:0016874~ligase activity | 105 | 390 | 1.51E-09 |
| GO:0043234~protein complex | 470 | 2588 | 1.82E-09 |
| GO:0005829~cytosol | 268 | 1330 | 2.26E-09 |
| GO:0031396~regulation of protein ubiquitination | 41 | 100 | 4.44E-09 |
| GO:0051340~regulation of ligase activity | 36 | 81 | 4.73E-09 |
| GO:0005643~nuclear pore | 35 | 79 | 4.65E-09 |
| GO:0051438~regulation of ubiquitin-protein ligase activity | 35 | 78 | 6.39E-09 |
| GO:0006119~oxidative phosphorylation | 40 | 98 | 8.89E-09 |
| GO:0030163~protein catabolic process | 146 | 622 | 1.09E-08 |
| GO:0051603~proteolysis involved in cellular protein catabolic process | 141 | 600 | 2.05E-08 |
| GO:0046930~pore complex | 38 | 95 | 2.36E-08 |
| GO:0044257~cellular protein catabolic process | 141 | 603 | 2.93E-08 |
| GO:0060255~regulation of macromolecule metabolic process | 573 | 3259 | 4E-08 |
| GO:0008033~tRNA processing | 33 | 76 | 6.05E-08 |
| GO:0008380~RNA splicing | 79 | 284 | 7.73E-08 |
| GO:0045333~cellular respiration | 38 | 97 | 9.83E-08 |
| GO:0015980~energy derivation by oxidation of organic compounds | 49 | 144 | 1.08E-07 |
| GO:0006888~ER to Golgi vesicle-mediated transport | 23 | 42 | 1.25E-07 |
| GO:0006397~mRNA processing | 85 | 321 | 2.34E-07 |
| GO:0005681~spliceosome | 45 | 132 | 2.07E-07 |
| GO:0006511~ubiquitin-dependent protein catabolic process | 69 | 242 | 2.81E-07 |
| GO:0022625~cytosolic large ribosomal subunit | 21 | 38 | 3.18E-07 |
| GO:0022613~ribonucleoprotein complex biogenesis | 55 | 180 | 7.83E-07 |
| GO:0016591~DNA-directed RNA polymerase II, holoenzyme | 32 | 81 | 7.94E-07 |
| GO:0080090~regulation of primary metabolic process | 567 | 3291 | 1.21E-06 |
| GO:0008137~NADH dehydrogenase (ubiquinone) activity | 22 | 43 | 1.3E-06 |
| GO:0003954~NADH dehydrogenase activity | 22 | 43 | 1.3E-06 |
| GO:0050136~NADH dehydrogenase (quinone) activity | 22 | 43 | 1.3E-06 |
| GO:0005730~nucleolus | 149 | 698 | 1.27E-06 |
| GO:0000278~mitotic cell cycle | 91 | 370 | 2.89E-06 |
| GO:0045271~respiratory chain complex I | 21 | 42 | 2.76E-06 |
| GO:0005747~mitochondrial respiratory chain complex I | 21 | 42 | 2.76E-06 |
| GO:0030964~NADH dehydrogenase complex | 21 | 42 | 2.76E-06 |
| GO:0016887~ATPase activity | 84 | 334 | 3.54E-06 |
| GO:0000502~proteasome complex | 26 | 61 | 3.25E-06 |
| GO:0006120~mitochondrial electron transport, NADH to ubiquinone | 21 | 42 | 4.71E-06 |
| GO:0044451~nucleoplasm part | 122 | 555 | 4.26E-06 |
| GO:0032269~negative regulation of cellular protein metabolic process | 53 | 180 | 5.26E-06 |
| GO:0010468~regulation of gene expression | 495 | 2856 | 6.33E-06 |
| GO:0051248~negative regulation of protein metabolic process | 54 | 187 | 7.91E-06 |
| GO:0016818~hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides | 159 | 760 | 8.26E-06 |
| GO:0042254~ribosome biogenesis | 40 | 122 | 9.63E-06 |
| GO:0005815~microtubule organizing center | 66 | 253 | 8.39E-06 |
| GO:0008565~protein transporter activity | 32 | 87 | 9.71E-06 |
| GO:0070647~protein modification by small protein conjugation or removal | 48 | 160 | 1.14E-05 |
| GO:0016462~pyrophosphatase activity | 158 | 757 | 1.05E-05 |
| GO:0016817~hydrolase activity, acting on acid anhydrides | 159 | 764 | 1.16E-05 |
| GO:0031400~negative regulation of protein modification process | 39 | 119 | 1.38E-05 |
| GO:0005813~centrosome | 60 | 224 | 1.14E-05 |
| GO:0005777~peroxisome | 35 | 103 | 1.15E-05 |
| GO:0042579~microbody | 35 | 103 | 1.15E-05 |
| GO:0010556~regulation of macromolecule biosynthetic process | 488 | 2830 | 1.45E-05 |
| GO:0050658~RNA transport | 34 | 97 | 1.47E-05 |
| GO:0051236~establishment of RNA localization | 34 | 97 | 1.47E-05 |
| GO:0050657~nucleic acid transport | 34 | 97 | 1.47E-05 |
| GO:0042775~mitochondrial ATP synthesis coupled electron transport | 24 | 56 | 1.65E-05 |
| GO:0042773~ATP synthesis coupled electron transport | 24 | 56 | 1.65E-05 |
| GO:0042623~ATPase activity, coupled | 70 | 272 | 1.66E-05 |
| GO:0019222~regulation of metabolic process | 607 | 3621 | 2.12E-05 |
| GO:0016655~oxidoreductase activity, acting on NADH or NADPH, quinone or similar compound as acceptor | 22 | 49 | 2.03E-05 |
| GO:0031323~regulation of cellular metabolic process | 583 | 3464 | 2.4E-05 |
| GO:0015931~nucleobase, nucleoside, nucleotide and nucleic acid transport | 37 | 113 | 2.85E-05 |
| GO:0070469~respiratory chain | 28 | 75 | 2.33E-05 |
| GO:0033365~protein localization in organelle | 44 | 146 | 3.13E-05 |
| GO:0006403~RNA localization | 34 | 100 | 3.21E-05 |
| GO:0015935~small ribosomal subunit | 25 | 63 | 2.75E-05 |
| GO:0022900~electron transport chain | 37 | 114 | 3.6E-05 |
| GO:0003677~DNA binding | 409 | 2331 | 4.16E-05 |
| GO:0005761~mitochondrial ribosome | 21 | 48 | 3.86E-05 |
| GO:0000313~organellar ribosome | 21 | 48 | 3.86E-05 |
| GO:0043228~non-membrane-bounded organelle | 440 | 2596 | 5.03E-05 |
| GO:0043232~intracellular non-membrane-bounded organelle | 440 | 2596 | 5.03E-05 |
| GO:0006367~transcription initiation from RNA polymerase II promoter | 26 | 68 | 6.39E-05 |
| GO:0022904~respiratory electron transport chain | 25 | 64 | 6.66E-05 |
| GO:0016787~hydrolase activity | 400 | 2283 | 6.38E-05 |
| GO:0012505~endomembrane system | 155 | 782 | 7.03E-05 |

**Cluster6**

|  |  |  |  |
| --- | --- | --- | --- |
| Term | Count | Pop Hits | FDR |
| GO:0005634~nucleus | 1070 | 5077 | 2.16E-27 |
| GO:0005622~intracellular | 2009 | 10995 | 1.83E-24 |
| GO:0044424~intracellular part | 1953 | 10624 | 2.25E-24 |
| GO:0043226~organelle | 1669 | 8989 | 1.7E-18 |
| GO:0043231~intracellular membrane-bounded organelle | 1507 | 7982 | 2.32E-18 |
| GO:0043229~intracellular organelle | 1666 | 8977 | 2.61E-18 |
| GO:0043227~membrane-bounded organelle | 1507 | 7989 | 3.58E-18 |
| GO:0044428~nuclear part | 433 | 1822 | 1.13E-17 |
| GO:0009987~cellular process | 1932 | 10541 | 1.3E-16 |
| GO:0034641~cellular nitrogen compound metabolic process | 769 | 3670 | 3.05E-13 |
| GO:0031981~nuclear lumen | 344 | 1450 | 2.63E-13 |
| GO:0044260~cellular macromolecule metabolic process | 1036 | 5214 | 2.52E-12 |
| GO:0006139~nucleobase, nucleoside, nucleotide and nucleic acid metabolic process | 716 | 3409 | 2.82E-12 |
| GO:0006807~nitrogen compound metabolic process | 780 | 3778 | 7.16E-12 |
| GO:0044237~cellular metabolic process | 1275 | 6636 | 1.05E-11 |
| GO:0005488~binding | 2232 | 12531 | 1.61E-11 |
| GO:0044464~cell part | 2492 | 14826 | 4.31E-11 |
| GO:0005623~cell | 2492 | 14827 | 4.71E-11 |
| GO:0043228~non-membrane-bounded organelle | 545 | 2596 | 6.43E-11 |
| GO:0043232~intracellular non-membrane-bounded organelle | 545 | 2596 | 6.43E-11 |
| GO:0007049~cell cycle | 205 | 776 | 8.66E-11 |
| GO:0005654~nucleoplasm | 220 | 882 | 2.15E-10 |
| GO:0044427~chromosomal part | 116 | 386 | 2.24E-10 |
| GO:0070013~intracellular organelle lumen | 392 | 1779 | 2.67E-10 |
| GO:0005694~chromosome | 132 | 460 | 2.85E-10 |
| GO:0043233~organelle lumen | 398 | 1820 | 5.17E-10 |
| GO:0031974~membrane-enclosed lumen | 403 | 1856 | 1.04E-09 |
| GO:0043170~macromolecule metabolic process | 1102 | 5710 | 1.38E-09 |
| GO:0022403~cell cycle phase | 122 | 414 | 2.49E-09 |
| GO:0022402~cell cycle process | 154 | 565 | 4.89E-09 |
| GO:0006996~organelle organization | 308 | 1332 | 8.72E-09 |
| GO:0000278~mitotic cell cycle | 110 | 370 | 1.26E-08 |
| GO:0003676~nucleic acid binding | 667 | 3264 | 1.7E-08 |
| GO:0000075~cell cycle checkpoint | 41 | 91 | 2.03E-08 |
| GO:0044446~intracellular organelle part | 814 | 4225 | 1.86E-08 |
| GO:0008152~metabolic process | 1418 | 7647 | 2.82E-08 |
| GO:0010467~gene expression | 614 | 2999 | 4.56E-08 |
| GO:0051276~chromosome organization | 133 | 485 | 6.11E-08 |
| GO:0044422~organelle part | 815 | 4251 | 5.16E-08 |
| GO:0044238~primary metabolic process | 1292 | 6923 | 1.11E-07 |
| GO:0051301~cell division | 90 | 295 | 1.33E-07 |
| GO:0006259~DNA metabolic process | 136 | 506 | 1.57E-07 |
| GO:0000087~M phase of mitotic cell cycle | 73 | 224 | 2.05E-07 |
| GO:0000280~nuclear division | 72 | 220 | 2.14E-07 |
| GO:0007067~mitosis | 72 | 220 | 2.14E-07 |
| GO:0051726~regulation of cell cycle | 97 | 331 | 3.14E-07 |
| GO:0048285~organelle fission | 73 | 229 | 5.71E-07 |
| GO:0034645~cellular macromolecule biosynthetic process | 572 | 2812 | 6.04E-07 |
| GO:0009059~macromolecule biosynthetic process | 575 | 2832 | 7.02E-07 |
| GO:0007093~mitotic cell cycle checkpoint | 24 | 43 | 7.93E-07 |
| GO:0005515~protein binding | 1498 | 8154 | 8.1E-07 |
| GO:0000279~M phase | 95 | 329 | 9.78E-07 |
| GO:0005737~cytoplasm | 1315 | 7319 | 1.21E-06 |
| GO:0006350~transcription | 439 | 2101 | 1.76E-06 |
| GO:0005819~spindle | 50 | 147 | 4.08E-06 |
| GO:0051171~regulation of nitrogen compound metabolic process | 569 | 2839 | 5.81E-06 |
| GO:0044249~cellular biosynthetic process | 676 | 3442 | 6.92E-06 |
| GO:0016043~cellular component organization | 507 | 2498 | 7.25E-06 |
| GO:0005730~nucleolus | 164 | 698 | 7.68E-06 |
| GO:0008270~zinc ion binding | 473 | 2311 | 1.03E-05 |
| GO:0019219~regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process | 561 | 2814 | 1.58E-05 |
| GO:0031323~regulation of cellular metabolic process | 676 | 3464 | 1.83E-05 |
| GO:0009058~biosynthetic process | 689 | 3542 | 2.07E-05 |
| GO:0019222~regulation of metabolic process | 703 | 3621 | 2.17E-05 |
| GO:0000775~chromosome, centromeric region | 43 | 124 | 1.76E-05 |
| GO:0060255~regulation of macromolecule metabolic process | 639 | 3259 | 2.31E-05 |
| GO:0003677~DNA binding | 474 | 2331 | 2.15E-05 |
| GO:0045449~regulation of transcription | 521 | 2601 | 2.58E-05 |
| GO:0080090~regulation of primary metabolic process | 644 | 3291 | 2.6E-05 |
| GO:0000776~kinetochore | 31 | 77 | 2.22E-05 |
| GO:0045786~negative regulation of cell cycle | 32 | 81 | 5.81E-05 |
| GO:0009889~regulation of biosynthetic process | 583 | 2966 | 6.35E-05 |
| GO:0006974~response to DNA damage stimulus | 98 | 373 | 6.74E-05 |
| GO:0031326~regulation of cellular biosynthetic process | 579 | 2947 | 7.1E-05 |
| GO:0010556~regulation of macromolecule biosynthetic process | 558 | 2830 | 7.86E-05 |
| GO:0010468~regulation of gene expression | 562 | 2856 | 8.31E-05 |
| GO:0016772~transferase activity, transferring phosphorus-containing groups | 215 | 964 | 9.56E-05 |

**Cluster7**

|  |  |  |  |
| --- | --- | --- | --- |
| Term | Count | Pop Hits | FDR |
| GO:0005576~extracellular region | 1432 | 2010 | 2.7E-160 |
| GO:0032501~multicellular organismal process | 2513 | 4280 | 1.1E-137 |
| GO:0004872~receptor activity | 1266 | 1838 | 5.2E-129 |
| GO:0004888~transmembrane receptor activity | 966 | 1305 | 7.8E-127 |
| GO:0007186~G-protein coupled receptor protein signaling pathway | 849 | 1123 | 8.5E-118 |
| GO:0004930~G-protein coupled receptor activity | 696 | 873 | 1.5E-116 |
| GO:0060089~molecular transducer activity | 1467 | 2270 | 1.8E-115 |
| GO:0004871~signal transducer activity | 1467 | 2270 | 1.8E-115 |
| GO:0005886~plasma membrane | 2247 | 3777 | 2.5E-115 |
| GO:0007166~cell surface receptor linked signal transduction | 1222 | 1856 | 2.5E-100 |
| GO:0007606~sensory perception of chemical stimulus | 422 | 478 | 9.59E-97 |
| GO:0050896~response to stimulus | 2025 | 3502 | 4.88E-93 |
| GO:0007600~sensory perception | 620 | 810 | 4.8E-88 |
| GO:0003008~system process | 1008 | 1503 | 1.03E-87 |
| GO:0007608~sensory perception of smell | 379 | 431 | 2.22E-85 |
| GO:0044421~extracellular region part | 706 | 960 | 7.04E-84 |
| GO:0050890~cognition | 660 | 909 | 4.94E-77 |
| GO:0004984~olfactory receptor activity | 369 | 431 | 1.07E-76 |
| GO:0005615~extracellular space | 524 | 685 | 2.53E-71 |
| GO:0050877~neurological system process | 795 | 1210 | 1.61E-61 |
| GO:0006952~defense response | 460 | 615 | 4.99E-59 |
| GO:0031224~intrinsic to membrane | 2857 | 5485 | 2.5E-58 |
| GO:0007165~signal transduction | 1599 | 2840 | 1.36E-57 |
| GO:0016021~integral to membrane | 2764 | 5297 | 1.62E-56 |
| GO:0006955~immune response | 486 | 690 | 2.37E-49 |
| GO:0031226~intrinsic to plasma membrane | 761 | 1215 | 5.92E-44 |
| GO:0005887~integral to plasma membrane | 746 | 1188 | 1.28E-43 |
| GO:0009605~response to external stimulus | 595 | 914 | 3.67E-43 |
| GO:0002376~immune system process | 632 | 998 | 3.25E-40 |
| GO:0048513~organ development | 1006 | 1738 | 3.48E-40 |
| GO:0044425~membrane part | 3246 | 6578 | 1.25E-37 |
| GO:0016020~membrane | 3541 | 7266 | 2.28E-36 |
| GO:0007275~multicellular organismal development | 1528 | 2865 | 7.96E-36 |
| GO:0009611~response to wounding | 367 | 530 | 2.52E-34 |
| GO:0044459~plasma membrane part | 1222 | 2203 | 2.85E-34 |
| GO:0032502~developmental process | 1644 | 3148 | 1.86E-32 |
| GO:0048731~system development | 1259 | 2330 | 1.09E-31 |
| GO:0006954~inflammatory response | 244 | 325 | 4.33E-31 |
| GO:0005125~cytokine activity | 163 | 195 | 1.52E-30 |
| GO:0009888~tissue development | 428 | 665 | 6.24E-29 |
| GO:0048856~anatomical structure development | 1337 | 2527 | 1.95E-28 |
| GO:0005509~calcium ion binding | 554 | 919 | 1.05E-27 |
| GO:0045111~intermediate filament cytoskeleton | 155 | 187 | 3.06E-27 |
| GO:0005882~intermediate filament | 152 | 183 | 6.81E-27 |
| GO:0005102~receptor binding | 531 | 886 | 1.18E-25 |
| GO:0022610~biological adhesion | 438 | 701 | 1.5E-25 |
| GO:0007155~cell adhesion | 437 | 700 | 2.24E-25 |
| GO:0030246~carbohydrate binding | 245 | 354 | 4.09E-23 |
| GO:0005578~proteinaceous extracellular matrix | 227 | 320 | 1.79E-22 |
| GO:0031012~extracellular matrix | 241 | 345 | 2.12E-22 |
| GO:0030154~cell differentiation | 885 | 1637 | 2.25E-21 |
| GO:0045095~keratin filament | 82 | 88 | 5.1E-21 |
| GO:0042742~defense response to bacterium | 96 | 112 | 5.86E-19 |
| GO:0050776~regulation of immune response | 165 | 226 | 9.87E-19 |
| GO:0048869~cellular developmental process | 905 | 1706 | 1.08E-18 |
| GO:0051707~response to other organism | 200 | 290 | 4.05E-18 |
| GO:0043565~sequence-specific DNA binding | 366 | 607 | 4.23E-18 |
| GO:0004252~serine-type endopeptidase activity | 120 | 154 | 1.61E-17 |
| GO:0008544~epidermis development | 138 | 184 | 2.8E-17 |
| GO:0005179~hormone activity | 91 | 108 | 3.4E-17 |
| GO:0002682~regulation of immune system process | 249 | 385 | 5.36E-17 |
| GO:0048583~regulation of response to stimulus | 290 | 465 | 1.4E-16 |
| GO:0030414~peptidase inhibitor activity | 118 | 153 | 1.33E-16 |
| GO:0007398~ectoderm development | 145 | 199 | 2.72E-16 |
| GO:0002684~positive regulation of immune system process | 167 | 238 | 3.35E-16 |
| GO:0016337~cell-cell adhesion | 188 | 276 | 3.85E-16 |
| GO:0009653~anatomical structure morphogenesis | 651 | 1197 | 3.89E-16 |
| GO:0030855~epithelial cell differentiation | 108 | 137 | 4.38E-16 |
| GO:0009887~organ morphogenesis | 339 | 564 | 6.22E-16 |
| GO:0051239~regulation of multicellular organismal process | 524 | 937 | 8E-16 |
| GO:0008528~peptide receptor activity, G-protein coupled | 93 | 114 | 8.83E-16 |
| GO:0001653~peptide receptor activity | 93 | 114 | 8.83E-16 |
| GO:0000003~reproduction | 439 | 767 | 4.33E-15 |
| GO:0022414~reproductive process | 436 | 762 | 4.33E-15 |
| GO:0065007~biological regulation | 3442 | 7484 | 8.55E-15 |
| GO:0004866~endopeptidase inhibitor activity | 110 | 145 | 1.93E-14 |
| GO:0006935~chemotaxis | 119 | 160 | 3.01E-14 |
| GO:0042330~taxis | 119 | 160 | 3.01E-14 |
| GO:0009617~response to bacterium | 138 | 193 | 3.01E-14 |
| GO:0009897~external side of plasma membrane | 125 | 170 | 5.12E-14 |
| GO:0065008~regulation of biological quality | 769 | 1469 | 1.74E-13 |
| GO:0005529~sugar binding | 137 | 195 | 1.85E-13 |
| GO:0009986~cell surface | 222 | 348 | 2.11E-13 |
| GO:0040011~locomotion | 263 | 431 | 4.04E-13 |
| GO:0045087~innate immune response | 104 | 138 | 4.9E-13 |
| GO:0051704~multi-organism process | 388 | 681 | 7.27E-13 |
| GO:0008236~serine-type peptidase activity | 126 | 178 | 9.82E-13 |
| GO:0001871~pattern binding | 112 | 154 | 1.49E-12 |
| GO:0030247~polysaccharide binding | 112 | 154 | 1.49E-12 |
| GO:0006959~humoral immune response | 67 | 79 | 1.78E-12 |
| GO:0008015~blood circulation | 130 | 186 | 3.45E-12 |
| GO:0003013~circulatory system process | 130 | 186 | 3.45E-12 |
| GO:0019955~cytokine binding | 85 | 109 | 3.27E-12 |
| GO:0019932~second-messenger-mediated signaling | 157 | 235 | 3.67E-12 |
| GO:0017171~serine hydrolase activity | 126 | 180 | 3.62E-12 |
| GO:0060429~epithelium development | 152 | 227 | 6.95E-12 |
| GO:0009607~response to biotic stimulus | 235 | 384 | 7.09E-12 |
| GO:0042221~response to chemical stimulus | 670 | 1281 | 1.62E-11 |
| GO:0050878~regulation of body fluid levels | 103 | 141 | 1.88E-11 |
| GO:0032101~regulation of response to external stimulus | 113 | 159 | 2.69E-11 |
| GO:0007586~digestion | 73 | 91 | 2.77E-11 |
| GO:0002526~acute inflammatory response | 77 | 98 | 4.33E-11 |
| GO:0004867~serine-type endopeptidase inhibitor activity | 73 | 92 | 4.53E-11 |
| GO:0007601~visual perception | 144 | 216 | 5.09E-11 |
| GO:0050953~sensory perception of light stimulus | 144 | 216 | 5.09E-11 |
| GO:0048878~chemical homeostasis | 296 | 512 | 1.03E-10 |
| GO:0048584~positive regulation of response to stimulus | 154 | 236 | 1.1E-10 |
| GO:0004857~enzyme inhibitor activity | 171 | 270 | 1.34E-10 |
| GO:0005539~glycosaminoglycan binding | 100 | 140 | 2.1E-10 |
| GO:0008217~regulation of blood pressure | 77 | 100 | 2.62E-10 |
| GO:0001775~cell activation | 180 | 287 | 2.66E-10 |
| GO:0050778~positive regulation of immune response | 103 | 145 | 3.06E-10 |
| GO:0006950~response to stress | 850 | 1685 | 3.57E-10 |
| GO:0007610~behavior | 272 | 469 | 5.05E-10 |
| GO:0006936~muscle contraction | 107 | 153 | 5.45E-10 |
| GO:0050865~regulation of cell activation | 119 | 175 | 6.87E-10 |
| GO:0003012~muscle system process | 115 | 168 | 7.95E-10 |
| GO:0007565~female pregnancy | 82 | 110 | 9.27E-10 |
| GO:0009913~epidermal cell differentiation | 59 | 72 | 1.1E-09 |
| GO:0006968~cellular defense response | 52 | 61 | 1.15E-09 |
| GO:0001664~G-protein-coupled receptor binding | 82 | 111 | 1.21E-09 |
| GO:0007267~cell-cell signaling | 335 | 600 | 1.41E-09 |
| GO:0042060~wound healing | 127 | 191 | 1.45E-09 |
| GO:0048732~gland development | 96 | 135 | 1.47E-09 |
| GO:0030216~keratinocyte differentiation | 55 | 66 | 1.64E-09 |
| GO:0045165~cell fate commitment | 98 | 139 | 1.98E-09 |
| GO:0051606~detection of stimulus | 86 | 118 | 2.11E-09 |
| GO:0002694~regulation of leukocyte activation | 112 | 166 | 5.68E-09 |
| GO:0050909~sensory perception of taste | 40 | 44 | 5.81E-09 |
| GO:0050793~regulation of developmental process | 368 | 674 | 6.63E-09 |
| GO:0031347~regulation of defense response | 99 | 143 | 7.89E-09 |
| GO:0008009~chemokine activity | 41 | 46 | 8.8E-09 |
| GO:0004175~endopeptidase activity | 219 | 375 | 9.93E-09 |
| GO:0050727~regulation of inflammatory response | 60 | 76 | 1.18E-08 |
| GO:0008083~growth factor activity | 108 | 161 | 1.16E-08 |
| GO:0050789~regulation of biological process | 3222 | 7106 | 1.71E-08 |
| GO:0001501~skeletal system development | 191 | 319 | 1.77E-08 |
| GO:0007599~hemostasis | 78 | 108 | 3.47E-08 |
| GO:0045177~apical part of cell | 118 | 179 | 2.81E-08 |
| GO:0042379~chemokine receptor binding | 42 | 49 | 6.18E-08 |
| GO:0050817~coagulation | 74 | 102 | 6.96E-08 |
| GO:0007596~blood coagulation | 74 | 102 | 6.96E-08 |
| GO:0007626~locomotory behavior | 166 | 274 | 7.42E-08 |
| GO:0005044~scavenger receptor activity | 40 | 46 | 6.99E-08 |
| GO:0007517~muscle organ development | 133 | 211 | 9.61E-08 |
| GO:0031424~keratinization | 38 | 43 | 1.05E-07 |
| GO:0001817~regulation of cytokine production | 117 | 181 | 1.08E-07 |
| GO:0002253~activation of immune response | 69 | 94 | 1.15E-07 |
| GO:0002697~regulation of immune effector process | 73 | 101 | 1.17E-07 |
| GO:0005201~extracellular matrix structural constituent | 64 | 86 | 1.22E-07 |
| GO:0015267~channel activity | 233 | 412 | 1.47E-07 |
| GO:0030594~neurotransmitter receptor activity | 69 | 95 | 1.53E-07 |
| GO:0035270~endocrine system development | 54 | 69 | 1.73E-07 |
| GO:0016324~apical plasma membrane | 91 | 133 | 1.65E-07 |
| GO:0022803~passive transmembrane transporter activity | 233 | 413 | 1.95E-07 |
| GO:0044420~extracellular matrix part | 82 | 117 | 1.78E-07 |
| GO:0045321~leukocyte activation | 148 | 242 | 2.33E-07 |
| GO:0007154~cell communication | 418 | 795 | 2.39E-07 |
| GO:0050670~regulation of lymphocyte proliferation | 62 | 83 | 2.58E-07 |
| GO:0007156~homophilic cell adhesion | 89 | 131 | 2.78E-07 |
| GO:0048562~embryonic organ morphogenesis | 90 | 133 | 3.07E-07 |
| GO:0051249~regulation of lymphocyte activation | 98 | 148 | 3.58E-07 |
| GO:0055065~metal ion homeostasis | 128 | 205 | 4.37E-07 |
| GO:0070663~regulation of leukocyte proliferation | 62 | 84 | 5.49E-07 |
| GO:0032944~regulation of mononuclear cell proliferation | 62 | 84 | 5.49E-07 |
| GO:0006811~ion transport | 403 | 768 | 6.06E-07 |
| GO:0042035~regulation of cytokine biosynthetic process | 56 | 74 | 6.93E-07 |
| GO:0009581~detection of external stimulus | 56 | 74 | 6.93E-07 |
| GO:0003700~transcription factor activity | 497 | 975 | 6.41E-07 |
| GO:0050801~ion homeostasis | 230 | 409 | 7.52E-07 |
| GO:0050867~positive regulation of cell activation | 77 | 111 | 7.64E-07 |
| GO:0002541~activation of plasma proteins involved in acute inflammatory response | 37 | 43 | 7.66E-07 |
| GO:0030141~secretory granule | 115 | 180 | 6.4E-07 |
| GO:0043292~contractile fiber | 83 | 121 | 6.63E-07 |
| GO:0022838~substrate specific channel activity | 223 | 398 | 8.78E-07 |
| GO:0048545~response to steroid hormone stimulus | 120 | 192 | 1.16E-06 |
| GO:0019935~cyclic-nucleotide-mediated signaling | 87 | 130 | 1.2E-06 |
| GO:0019956~chemokine binding | 26 | 27 | 1.09E-06 |
| GO:0048609~reproductive process in a multicellular organism | 267 | 487 | 1.31E-06 |
| GO:0032504~multicellular organism reproduction | 267 | 487 | 1.31E-06 |
| GO:0007588~excretion | 46 | 58 | 1.36E-06 |
| GO:0044449~contractile fiber part | 78 | 113 | 1.19E-06 |
| GO:0006956~complement activation | 36 | 42 | 1.51E-06 |
| GO:0010817~regulation of hormone levels | 98 | 151 | 1.59E-06 |
| GO:0022857~transmembrane transporter activity | 462 | 906 | 1.94E-06 |
| GO:0020037~heme binding | 81 | 121 | 2.28E-06 |
| GO:0006875~cellular metal ion homeostasis | 121 | 196 | 2.71E-06 |
| GO:0007187~G-protein signaling, coupled to cyclic nucleotide second messenger | 78 | 115 | 2.71E-06 |
| GO:0042277~peptide binding | 124 | 203 | 2.51E-06 |
| GO:0002696~positive regulation of leukocyte activation | 73 | 106 | 2.86E-06 |
| GO:0008201~heparin binding | 71 | 103 | 2.7E-06 |
| GO:0042165~neurotransmitter binding | 71 | 103 | 2.7E-06 |
| GO:0051093~negative regulation of developmental process | 153 | 259 | 3.15E-06 |
| GO:0046906~tetrapyrrole binding | 85 | 129 | 3.09E-06 |
| GO:0051241~negative regulation of multicellular organismal process | 104 | 164 | 3.44E-06 |
| GO:0019953~sexual reproduction | 251 | 458 | 3.49E-06 |
| GO:0007204~elevation of cytosolic calcium ion concentration | 75 | 110 | 3.53E-06 |
| GO:0010517~regulation of phospholipase activity | 53 | 71 | 3.67E-06 |
| GO:0019825~oxygen binding | 36 | 43 | 3.5E-06 |
| GO:0048568~embryonic organ development | 108 | 172 | 4.05E-06 |
| GO:0046649~lymphocyte activation | 122 | 199 | 4.13E-06 |
| GO:0060191~regulation of lipase activity | 62 | 87 | 4.44E-06 |
| GO:0055074~calcium ion homeostasis | 116 | 188 | 5.24E-06 |
| GO:0060193~positive regulation of lipase activity | 55 | 75 | 5.46E-06 |
| GO:0001533~cornified envelope | 22 | 22 | 4.5E-06 |
| GO:0004950~chemokine receptor activity | 24 | 25 | 5.2E-06 |
| GO:0055082~cellular chemical homeostasis | 212 | 380 | 5.98E-06 |
| GO:0006874~cellular calcium ion homeostasis | 113 | 183 | 7.19E-06 |
| GO:0030017~sarcomere | 68 | 98 | 6.76E-06 |
| GO:0030016~myofibril | 75 | 111 | 8.17E-06 |
| GO:0051050~positive regulation of transport | 133 | 223 | 1.04E-05 |
| GO:0030005~cellular di-, tri-valent inorganic cation homeostasis | 135 | 227 | 1.06E-05 |
| GO:0010518~positive regulation of phospholipase activity | 51 | 69 | 1.09E-05 |
| GO:0055066~di-, tri-valent inorganic cation homeostasis | 141 | 239 | 1.11E-05 |
| GO:0051046~regulation of secretion | 122 | 202 | 1.28E-05 |
| GO:0051480~cytosolic calcium ion homeostasis | 78 | 118 | 1.34E-05 |
| GO:0042127~regulation of cell proliferation | 404 | 787 | 1.36E-05 |
| GO:0042592~homeostatic process | 387 | 751 | 1.44E-05 |
| GO:0009615~response to virus | 73 | 109 | 1.52E-05 |
| GO:0007602~phototransduction | 29 | 33 | 1.53E-05 |
| GO:0050871~positive regulation of B cell activation | 29 | 33 | 1.53E-05 |
| GO:0055080~cation homeostasis | 164 | 286 | 1.55E-05 |
| GO:0002703~regulation of leukocyte mediated immunity | 46 | 61 | 1.75E-05 |
| GO:0006873~cellular ion homeostasis | 207 | 374 | 1.79E-05 |
| GO:0004497~monooxygenase activity | 66 | 97 | 1.63E-05 |
| GO:0032879~regulation of localization | 320 | 610 | 1.87E-05 |
| GO:0043235~receptor complex | 77 | 116 | 1.64E-05 |
| GO:0007389~pattern specification process | 154 | 267 | 2.16E-05 |
| GO:0050794~regulation of cellular process | 3061 | 6819 | 2.22E-05 |
| GO:0051251~positive regulation of lymphocyte activation | 66 | 97 | 2.41E-05 |
| GO:0005216~ion channel activity | 211 | 386 | 2.35E-05 |
| GO:0006937~regulation of muscle contraction | 52 | 72 | 2.64E-05 |
| GO:0010863~positive regulation of phospholipase C activity | 48 | 65 | 2.64E-05 |
| GO:0007202~activation of phospholipase C activity | 48 | 65 | 2.64E-05 |
| GO:0030003~cellular cation homeostasis | 147 | 254 | 2.96E-05 |
| GO:0051240~positive regulation of multicellular organismal process | 142 | 244 | 2.96E-05 |
| GO:0008509~anion transmembrane transporter activity | 92 | 147 | 2.78E-05 |
| GO:0022891~substrate-specific transmembrane transporter activity | 418 | 827 | 2.82E-05 |
| GO:0050671~positive regulation of lymphocyte proliferation | 42 | 55 | 3.39E-05 |
| GO:0018149~peptide cross-linking | 24 | 26 | 3.44E-05 |
| GO:0048598~embryonic morphogenesis | 173 | 307 | 3.44E-05 |
| GO:0005496~steroid binding | 47 | 64 | 3.23E-05 |
| GO:0008307~structural constituent of muscle | 34 | 42 | 3.57E-05 |
| GO:0048729~tissue morphogenesis | 109 | 180 | 4.5E-05 |
| GO:0042383~sarcolemma | 49 | 67 | 3.64E-05 |
| GO:0050863~regulation of T cell activation | 76 | 117 | 5.15E-05 |
| GO:0034754~cellular hormone metabolic process | 44 | 59 | 5.26E-05 |
| GO:0042562~hormone binding | 38 | 49 | 4.78E-05 |
| GO:0042445~hormone metabolic process | 70 | 106 | 5.72E-05 |
| GO:0009952~anterior/posterior pattern formation | 88 | 140 | 5.75E-05 |
| GO:0044057~regulation of system process | 173 | 309 | 5.92E-05 |
| GO:0051674~localization of cell | 172 | 307 | 5.98E-05 |
| GO:0048870~cell motility | 172 | 307 | 5.98E-05 |
| GO:0002455~humoral immune response mediated by circulating immunoglobulin | 27 | 31 | 6.04E-05 |
| GO:0009583~detection of light stimulus | 32 | 39 | 6.2E-05 |
| GO:0002460~adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains | 54 | 77 | 6.69E-05 |
| GO:0002250~adaptive immune response | 54 | 77 | 6.69E-05 |
| GO:0007159~leukocyte adhesion | 25 | 28 | 6.82E-05 |
| GO:0032946~positive regulation of mononuclear cell proliferation | 42 | 56 | 7.41E-05 |
| GO:0070665~positive regulation of leukocyte proliferation | 42 | 56 | 7.41E-05 |
| GO:0009566~fertilization | 55 | 79 | 7.55E-05 |
| GO:0001708~cell fate specification | 39 | 51 | 8.3E-05 |
| GO:0050864~regulation of B cell activation | 39 | 51 | 8.3E-05 |
| GO:0009582~detection of abiotic stimulus | 47 | 65 | 9.02E-05 |
| GO:0080134~regulation of response to stress | 155 | 274 | 9.22E-05 |
| GO:0002683~negative regulation of immune system process | 57 | 83 | 9.41E-05 |
| GO:0016712~oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, reduced flavin or flavoprotein as one donor, and incorporation of one atom of oxygen | 26 | 30 | 9.25E-05 |