## 8 hpl MF
| ID | Description | setSize | enrichmentScore | pvalue | p.adjust | qvalues |
| --- | --- | --- | --- | --- | --- | --- |
| GO:0016667 | oxidoreductase activity, acting on a sulfur group of donors | 20 | 0.742951 | 0.000999 | 0.018627 | 0.014213 |
| GO:0016830 | carbon-carbon lyase activity | 22 | 0.740422 | 0.000999 | 0.018627 | 0.014213 |
| GO:0016627 | oxidoreductase activity, acting on the CH-CH group of donors | 34 | 0.681050 | 0.000999 | 0.018627 | 0.014213 |
| GO:0008238 | exopeptidase activity | 37 | 0.667916 | 0.000999 | 0.018627 | 0.014213 |
| GO:0050660 | flavin adenine dinucleotide binding | 33 | 0.596317 | 0.002997 | 0.035352 | 0.026976 |
| GO:0016829 | lyase activity | 78 | 0.537740 | 0.000999 | 0.018627 | 0.014213 |
| GO:0050662 | coenzyme binding | 92 | 0.521503 | 0.001998 | 0.026246 | 0.020028 |
| GO:0016614 | oxidoreductase activity, acting on CH-OH group of donors | 61 | 0.518375 | 0.002997 | 0.035352 | 0.026976 |
| GO:0016491 | oxidoreductase activity | 355 | 0.508699 | 0.000999 | 0.018627 | 0.014213 |
| GO:0016779 | nucleotidyltransferase activity | 68 | 0.505033 | 0.003996 | 0.041994 | 0.032045 |
| GO:0048037 | cofactor binding | 126 | 0.495447 | 0.002997 | 0.035352 | 0.026976 |
| GO:0016741 | transferase activity, transferring one-carbon groups | 112 | 0.481836 | 0.001998 | 0.026246 | 0.020028 |
| GO:0008168 | methyltransferase activity | 108 | 0.478565 | 0.002997 | 0.035352 | 0.026976 |
| GO:0003824 | catalytic activity | 2685 | 0.307549 | 0.000999 | 0.018627 | 0.014213 |
| GO:0005509 | calcium ion binding | 228 | -0.288040 | 0.003996 | 0.041994 | 0.032045 |
| GO:0060089 | molecular transducer activity | 395 | -0.290978 | 0.001998 | 0.026246 | 0.020028 |
| GO:0004871 | signal transducer activity | 350 | -0.293596 | 0.001998 | 0.026246 | 0.020028 |
| GO:0005215 | transporter activity | 424 | -0.315090 | 0.000999 | 0.018627 | 0.014213 |
| GO:0004872 | receptor activity | 278 | -0.345029 | 0.000999 | 0.018627 | 0.014213 |
| GO:0022892 | substrate-specific transporter activity | 348 | -0.349360 | 0.000999 | 0.018627 | 0.014213 |
| GO:0038023 | signaling receptor activity | 233 | -0.357156 | 0.000999 | 0.018627 | 0.014213 |
| GO:0008324 | cation transmembrane transporter activity | 195 | -0.358582 | 0.000999 | 0.018627 | 0.014213 |
| GO:0022857 | transmembrane transporter activity | 334 | -0.363256 | 0.000999 | 0.018627 | 0.014213 |
| GO:0022891 | substrate-specific transmembrane transporter activity | 295 | -0.373635 | 0.000999 | 0.018627 | 0.014213 |
| GO:0015075 | ion transmembrane transporter activity | 276 | -0.382492 | 0.000999 | 0.018627 | 0.014213 |
| GO:0022890 | inorganic cation transmembrane transporter activity | 167 | -0.385972 | 0.000999 | 0.018627 | 0.014213 |
| GO:0022804 | active transmembrane transporter activity | 109 | -0.389949 | 0.001998 | 0.026246 | 0.020028 |
| GO:0004888 | transmembrane signaling receptor activity | 181 | -0.394162 | 0.000999 | 0.018627 | 0.014213 |
| GO:0015077 | monovalent inorganic cation transmembrane transporter activity | 126 | -0.402333 | 0.000999 | 0.018627 | 0.014213 |
| GO:0005216 | ion channel activity | 106 | -0.408498 | 0.000999 | 0.018627 | 0.014213 |
| GO:0022836 | gated channel activity | 98 | -0.420395 | 0.000999 | 0.018627 | 0.014213 |
| GO:0005261 | cation channel activity | 57 | -0.424557 | 0.002997 | 0.035352 | 0.026976 |
| GO:0022832 | voltage-gated channel activity | 56 | -0.429254 | 0.003996 | 0.041994 | 0.032045 |
| GO:0015267 | channel activity | 119 | -0.438402 | 0.000999 | 0.018627 | 0.014213 |
| GO:0022803 | passive transmembrane transporter activity | 119 | -0.438402 | 0.000999 | 0.018627 | 0.014213 |
| GO:0022838 | substrate-specific channel activity | 111 | -0.441752 | 0.000999 | 0.018627 | 0.014213 |
| GO:0004930 | G-protein coupled receptor activity | 94 | -0.458123 | 0.000999 | 0.018627 | 0.014213 |
| GO:0046873 | metal ion transmembrane transporter activity | 112 | -0.472699 | 0.000999 | 0.018627 | 0.014213 |
| GO:0072509 | divalent inorganic cation transmembrane transporter activity | 48 | -0.501701 | 0.000999 | 0.018627 | 0.014213 |
| GO:0008509 | anion transmembrane transporter activity | 73 | -0.517560 | 0.000999 | 0.018627 | 0.014213 |
| GO:0015276 | ligand-gated ion channel activity | 46 | -0.529066 | 0.000999 | 0.018627 | 0.014213 |
| GO:0022834 | ligand-gated channel activity | 46 | -0.529066 | 0.000999 | 0.018627 | 0.014213 |
| GO:0015293 | symporter activity | 32 | -0.529241 | 0.003996 | 0.041994 | 0.032045 |
| GO:0008514 | organic anion transmembrane transporter activity | 40 | -0.545476 | 0.001998 | 0.026246 | 0.020028 |
| GO:0015294 | solute:cation symporter activity | 27 | -0.552248 | 0.001998 | 0.026246 | 0.020028 |
| GO:0008146 | sulfotransferase activity | 21 | -0.571778 | 0.003996 | 0.041994 | 0.032045 |
| GO:0015291 | secondary active transmembrane transporter activity | 53 | -0.591465 | 0.000999 | 0.018627 | 0.014213 |
| GO:0015081 | sodium ion transmembrane transporter activity | 40 | -0.626570 | 0.000999 | 0.018627 | 0.014213 |
| GO:0001653 | peptide receptor activity | 17 | -0.659862 | 0.001998 | 0.026246 | 0.020028 |
| GO:0008528 | G-protein coupled peptide receptor activity | 17 | -0.659862 | 0.001998 | 0.026246 | 0.020028 |
| GO:0015370 | solute:sodium symporter activity | 14 | -0.694092 | 0.003996 | 0.041994 | 0.032045 |
| GO:0015297 | antiporter activity | 18 | -0.716798 | 0.001998 | 0.026246 | 0.020028 |
| GO:0015298 | solute:cation antiporter activity | 12 | -0.752155 | 0.001998 | 0.026246 | 0.020028 |
| GO:0015491 | cation:cation antiporter activity | 12 | -0.752155 | 0.001998 | 0.026246 | 0.020028 |
| GO:0009975 | cyclase activity | 11 | -0.804835 | 0.001998 | 0.026246 | 0.020028 |

## 8 hpl BP
| ID | Description | setSize | enrichmentScore | pvalue | p.adjust | qvalues |
| --- | --- | --- | --- | --- | --- | --- |
| GO:0007623 | circadian rhythm | 16 | 0.815454 | 0.000999 | 0.020127 | 0.015535 |
| GO:0042168 | heme metabolic process | 17 | 0.775208 | 0.000999 | 0.020127 | 0.015535 |
| GO:0006690 | icosanoid metabolic process | 12 | 0.756292 | 0.003996 | 0.039723 | 0.030662 |
| GO:1901568 | fatty acid derivative metabolic process | 12 | 0.756292 | 0.003996 | 0.039723 | 0.030662 |
| GO:0048511 | rhythmic process | 24 | 0.747839 | 0.000999 | 0.020127 | 0.015535 |
| GO:0033559 | unsaturated fatty acid metabolic process | 13 | 0.740845 | 0.003996 | 0.039723 | 0.030662 |
| GO:0022904 | respiratory electron transport chain | 18 | 0.728247 | 0.000999 | 0.020127 | 0.015535 |
| GO:0006119 | oxidative phosphorylation | 15 | 0.727011 | 0.004995 | 0.045467 | 0.035095 |
| GO:0022900 | electron transport chain | 20 | 0.723737 | 0.000999 | 0.020127 | 0.015535 |
| GO:0006778 | porphyrin-containing compound metabolic process | 19 | 0.721652 | 0.001998 | 0.027954 | 0.021577 |
| GO:0042440 | pigment metabolic process | 24 | 0.700909 | 0.001998 | 0.027954 | 0.021577 |
| GO:0006400 | tRNA modification | 22 | 0.673172 | 0.002997 | 0.034049 | 0.026282 |
| GO:1901565 | organonitrogen compound catabolic process | 34 | 0.645274 | 0.001998 | 0.027954 | 0.021577 |
| GO:0008202 | steroid metabolic process | 23 | 0.643404 | 0.004995 | 0.045467 | 0.035095 |
| GO:0045333 | cellular respiration | 40 | 0.641360 | 0.000999 | 0.020127 | 0.015535 |
| GO:0033013 | tetrapyrrole metabolic process | 25 | 0.641300 | 0.001998 | 0.027954 | 0.021577 |
| GO:0006633 | fatty acid biosynthetic process | 28 | 0.629394 | 0.000999 | 0.020127 | 0.015535 |
| GO:0045454 | cell redox homeostasis | 30 | 0.604135 | 0.003996 | 0.039723 | 0.030662 |
| GO:0006631 | fatty acid metabolic process | 47 | 0.586740 | 0.000999 | 0.020127 | 0.015535 |
| GO:0072330 | monocarboxylic acid biosynthetic process | 38 | 0.575420 | 0.002997 | 0.034049 | 0.026282 |
| GO:0015980 | energy derivation by oxidation of organic compounds | 51 | 0.572362 | 0.000999 | 0.020127 | 0.015535 |
| GO:0019439 | aromatic compound catabolic process | 54 | 0.556154 | 0.000999 | 0.020127 | 0.015535 |
| GO:0044270 | cellular nitrogen compound catabolic process | 54 | 0.556154 | 0.000999 | 0.020127 | 0.015535 |
| GO:0046700 | heterocycle catabolic process | 56 | 0.543993 | 0.001998 | 0.027954 | 0.021577 |
| GO:0008033 | tRNA processing | 49 | 0.536597 | 0.002997 | 0.034049 | 0.026282 |
| GO:1901361 | organic cyclic compound catabolic process | 57 | 0.535818 | 0.001998 | 0.027954 | 0.021577 |
| GO:0055114 | oxidation-reduction process | 315 | 0.505631 | 0.000999 | 0.020127 | 0.015535 |
| GO:0051186 | cofactor metabolic process | 84 | 0.503012 | 0.000999 | 0.020127 | 0.015535 |
| GO:0006457 | protein folding | 77 | 0.499007 | 0.001998 | 0.027954 | 0.021577 |
| GO:0051188 | cofactor biosynthetic process | 56 | 0.493988 | 0.002997 | 0.034049 | 0.026282 |
| GO:0006281 | DNA repair | 134 | 0.492343 | 0.000999 | 0.020127 | 0.015535 |
| GO:0007005 | mitochondrion organization | 70 | 0.479677 | 0.004995 | 0.045467 | 0.035095 |
| GO:0034470 | ncRNA processing | 125 | 0.472407 | 0.001998 | 0.027954 | 0.021577 |
| GO:0006091 | generation of precursor metabolites and energy | 76 | 0.471715 | 0.003996 | 0.039723 | 0.030662 |
| GO:0006950 | response to stress | 433 | 0.433858 | 0.000999 | 0.020127 | 0.015535 |
| GO:0006259 | DNA metabolic process | 205 | 0.425701 | 0.000999 | 0.020127 | 0.015535 |
| GO:0006974 | cellular response to DNA damage stimulus | 163 | 0.423609 | 0.002997 | 0.034049 | 0.026282 |
| GO:0006629 | lipid metabolic process | 242 | 0.408615 | 0.001998 | 0.027954 | 0.021577 |
| GO:0033554 | cellular response to stress | 274 | 0.384734 | 0.002997 | 0.034049 | 0.026282 |
| GO:0044710 | single-organism metabolic process | 1225 | 0.366908 | 0.000999 | 0.020127 | 0.015535 |
| GO:0008152 | metabolic process | 3523 | 0.285520 | 0.000999 | 0.020127 | 0.015535 |
| GO:0048731 | system development | 1092 | -0.211360 | 0.000999 | 0.020127 | 0.015535 |
| GO:0044767 | single-organism developmental process | 1476 | -0.213139 | 0.000999 | 0.020127 | 0.015535 |
| GO:0065007 | biological regulation | 2475 | -0.213549 | 0.000999 | 0.020127 | 0.015535 |
| GO:0032502 | developmental process | 1489 | -0.213986 | 0.000999 | 0.020127 | 0.015535 |
| GO:0048856 | anatomical structure development | 1371 | -0.214092 | 0.000999 | 0.020127 | 0.015535 |
| GO:0007275 | multicellular organismal development | 1320 | -0.216153 | 0.000999 | 0.020127 | 0.015535 |
| GO:0050794 | regulation of cellular process | 2244 | -0.222260 | 0.000999 | 0.020127 | 0.015535 |
| GO:0050789 | regulation of biological process | 2319 | -0.223323 | 0.000999 | 0.020127 | 0.015535 |
| GO:0044765 | single-organism transport | 728 | -0.226205 | 0.002997 | 0.034049 | 0.026282 |
| GO:1902578 | single-organism localization | 766 | -0.226498 | 0.002997 | 0.034049 | 0.026282 |
| GO:0044707 | single-multicellular organism process | 1451 | -0.227380 | 0.000999 | 0.020127 | 0.015535 |
| GO:0032501 | multicellular organismal process | 1461 | -0.228697 | 0.000999 | 0.020127 | 0.015535 |
| GO:0009790 | embryo development | 433 | -0.245710 | 0.004995 | 0.045467 | 0.035095 |
| GO:0048523 | negative regulation of cellular process | 407 | -0.246746 | 0.003996 | 0.039723 | 0.030662 |
| GO:0009653 | anatomical structure morphogenesis | 758 | -0.247953 | 0.000999 | 0.020127 | 0.015535 |
| GO:0048869 | cellular developmental process | 720 | -0.250639 | 0.000999 | 0.020127 | 0.015535 |
| GO:0009888 | tissue development | 531 | -0.262475 | 0.000999 | 0.020127 | 0.015535 |
| GO:0007154 | cell communication | 1265 | -0.262627 | 0.000999 | 0.020127 | 0.015535 |
| GO:0007165 | signal transduction | 1146 | -0.263236 | 0.000999 | 0.020127 | 0.015535 |
| GO:0044700 | single organism signaling | 1217 | -0.263311 | 0.000999 | 0.020127 | 0.015535 |
| GO:0023052 | signaling | 1221 | -0.263782 | 0.000999 | 0.020127 | 0.015535 |
| GO:0030154 | cell differentiation | 631 | -0.264516 | 0.000999 | 0.020127 | 0.015535 |
| GO:0048646 | anatomical structure formation involved in morphogenesis | 307 | -0.267821 | 0.000999 | 0.020127 | 0.015535 |
| GO:0072358 | cardiovascular system development | 314 | -0.268846 | 0.002997 | 0.034049 | 0.026282 |
| GO:0072359 | circulatory system development | 314 | -0.268846 | 0.002997 | 0.034049 | 0.026282 |
| GO:0048729 | tissue morphogenesis | 247 | -0.271192 | 0.004995 | 0.045467 | 0.035095 |
| GO:0032989 | cellular component morphogenesis | 279 | -0.274539 | 0.001998 | 0.027954 | 0.021577 |
| GO:0009887 | organ morphogenesis | 241 | -0.275571 | 0.004995 | 0.045467 | 0.035095 |
| GO:0007417 | central nervous system development | 221 | -0.276151 | 0.002997 | 0.034049 | 0.026282 |
| GO:0007399 | nervous system development | 489 | -0.277998 | 0.000999 | 0.020127 | 0.015535 |
| GO:0022008 | neurogenesis | 315 | -0.278825 | 0.000999 | 0.020127 | 0.015535 |
| GO:0009605 | response to external stimulus | 208 | -0.282394 | 0.003996 | 0.039723 | 0.030662 |
| GO:0006357 | regulation of transcription from RNA polymerase II promoter | 223 | -0.286118 | 0.001998 | 0.027954 | 0.021577 |
| GO:0048666 | neuron development | 223 | -0.286169 | 0.004995 | 0.045467 | 0.035095 |
| GO:0048699 | generation of neurons | 298 | -0.287224 | 0.001998 | 0.027954 | 0.021577 |
| GO:0060429 | epithelium development | 296 | -0.287268 | 0.000999 | 0.020127 | 0.015535 |
| GO:0048468 | cell development | 411 | -0.289442 | 0.000999 | 0.020127 | 0.015535 |
| GO:0048583 | regulation of response to stimulus | 445 | -0.291049 | 0.000999 | 0.020127 | 0.015535 |
| GO:0060322 | head development | 173 | -0.292838 | 0.003996 | 0.039723 | 0.030662 |
| GO:0009966 | regulation of signal transduction | 394 | -0.294288 | 0.000999 | 0.020127 | 0.015535 |
| GO:0007389 | pattern specification process | 204 | -0.294308 | 0.000999 | 0.020127 | 0.015535 |
| GO:0010646 | regulation of cell communication | 421 | -0.298123 | 0.000999 | 0.020127 | 0.015535 |
| GO:0023051 | regulation of signaling | 422 | -0.298786 | 0.000999 | 0.020127 | 0.015535 |
| GO:0007420 | brain development | 164 | -0.306729 | 0.001998 | 0.027954 | 0.021577 |
| GO:0007507 | heart development | 169 | -0.310687 | 0.001998 | 0.027954 | 0.021577 |
| GO:0040011 | locomotion | 219 | -0.312337 | 0.002997 | 0.034049 | 0.026282 |
| GO:0006928 | movement of cell or subcellular component | 258 | -0.314935 | 0.001998 | 0.027954 | 0.021577 |
| GO:0055085 | transmembrane transport | 288 | -0.317355 | 0.000999 | 0.020127 | 0.015535 |
| GO:0034220 | ion transmembrane transport | 139 | -0.322374 | 0.002997 | 0.034049 | 0.026282 |
| GO:0048667 | cell morphogenesis involved in neuron differentiation | 123 | -0.324157 | 0.001998 | 0.027954 | 0.021577 |
| GO:0006811 | ion transport | 323 | -0.326124 | 0.000999 | 0.020127 | 0.015535 |
| GO:0061564 | axon development | 122 | -0.326358 | 0.002997 | 0.034049 | 0.026282 |
| GO:0007166 | cell surface receptor signaling pathway | 515 | -0.327324 | 0.000999 | 0.020127 | 0.015535 |
| GO:0007409 | axonogenesis | 111 | -0.332508 | 0.004995 | 0.045467 | 0.035095 |
| GO:0000904 | cell morphogenesis involved in differentiation | 146 | -0.336544 | 0.001998 | 0.027954 | 0.021577 |
| GO:0003008 | system process | 153 | -0.336814 | 0.000999 | 0.020127 | 0.015535 |
| GO:0072521 | purine-containing compound metabolic process | 114 | -0.349283 | 0.003996 | 0.039723 | 0.030662 |
| GO:0007267 | cell-cell signaling | 109 | -0.357492 | 0.003996 | 0.039723 | 0.030662 |
| GO:0009968 | negative regulation of signal transduction | 128 | -0.361191 | 0.000999 | 0.020127 | 0.015535 |
| GO:0010648 | negative regulation of cell communication | 128 | -0.361191 | 0.000999 | 0.020127 | 0.015535 |
| GO:0023057 | negative regulation of signaling | 128 | -0.361191 | 0.000999 | 0.020127 | 0.015535 |
| GO:0016055 | Wnt signaling pathway | 91 | -0.361325 | 0.003996 | 0.039723 | 0.030662 |
| GO:0045595 | regulation of cell differentiation | 108 | -0.361684 | 0.001998 | 0.027954 | 0.021577 |
| GO:0048585 | negative regulation of response to stimulus | 134 | -0.364143 | 0.000999 | 0.020127 | 0.015535 |
| GO:0007155 | cell adhesion | 135 | -0.364147 | 0.001998 | 0.027954 | 0.021577 |
| GO:0022610 | biological adhesion | 135 | -0.364147 | 0.001998 | 0.027954 | 0.021577 |
| GO:0007186 | G-protein coupled receptor signaling pathway | 164 | -0.377485 | 0.000999 | 0.020127 | 0.015535 |
| GO:0003007 | heart morphogenesis | 74 | -0.398334 | 0.002997 | 0.034049 | 0.026282 |
| GO:0009260 | ribonucleotide biosynthetic process | 79 | -0.400435 | 0.002997 | 0.034049 | 0.026282 |
| GO:0046390 | ribose phosphate biosynthetic process | 79 | -0.400435 | 0.002997 | 0.034049 | 0.026282 |
| GO:0042330 | taxis | 76 | -0.400750 | 0.003996 | 0.039723 | 0.030662 |
| GO:0007268 | synaptic transmission | 78 | -0.412395 | 0.000999 | 0.020127 | 0.015535 |
| GO:0006820 | anion transport | 84 | -0.426964 | 0.000999 | 0.020127 | 0.015535 |
| GO:0006935 | chemotaxis | 74 | -0.427719 | 0.000999 | 0.020127 | 0.015535 |
| GO:0060284 | regulation of cell development | 74 | -0.436093 | 0.000999 | 0.020127 | 0.015535 |
| GO:0006164 | purine nucleotide biosynthetic process | 71 | -0.440691 | 0.002997 | 0.034049 | 0.026282 |
| GO:0043269 | regulation of ion transport | 53 | -0.441133 | 0.001998 | 0.027954 | 0.021577 |
| GO:0050877 | neurological system process | 76 | -0.442144 | 0.000999 | 0.020127 | 0.015535 |
| GO:0015711 | organic anion transport | 53 | -0.445587 | 0.001998 | 0.027954 | 0.021577 |
| GO:0009152 | purine ribonucleotide biosynthetic process | 70 | -0.447542 | 0.001998 | 0.027954 | 0.021577 |
| GO:0000122 | negative regulation of transcription from RNA polymerase II promoter | 48 | -0.448005 | 0.004995 | 0.045467 | 0.035095 |
| GO:0050953 | sensory perception of light stimulus | 47 | -0.449874 | 0.004995 | 0.045467 | 0.035095 |
| GO:0051960 | regulation of nervous system development | 70 | -0.456930 | 0.000999 | 0.020127 | 0.015535 |
| GO:0048736 | appendage development | 45 | -0.457100 | 0.002997 | 0.034049 | 0.026282 |
| GO:0007600 | sensory perception | 67 | -0.459263 | 0.001998 | 0.027954 | 0.021577 |
| GO:0072522 | purine-containing compound biosynthetic process | 79 | -0.461909 | 0.000999 | 0.020127 | 0.015535 |
| GO:0007601 | visual perception | 46 | -0.462641 | 0.004995 | 0.045467 | 0.035095 |
| GO:0014706 | striated muscle tissue development | 50 | -0.468330 | 0.001998 | 0.027954 | 0.021577 |
| GO:0060537 | muscle tissue development | 50 | -0.468330 | 0.001998 | 0.027954 | 0.021577 |
| GO:0050767 | regulation of neurogenesis | 65 | -0.477821 | 0.000999 | 0.020127 | 0.015535 |
| GO:0007411 | axon guidance | 61 | -0.489758 | 0.000999 | 0.020127 | 0.015535 |
| GO:0097485 | neuron projection guidance | 61 | -0.489758 | 0.000999 | 0.020127 | 0.015535 |
| GO:0015849 | organic acid transport | 36 | -0.495479 | 0.002997 | 0.034049 | 0.026282 |
| GO:0046942 | carboxylic acid transport | 36 | -0.495479 | 0.002997 | 0.034049 | 0.026282 |
| GO:0045664 | regulation of neuron differentiation | 38 | -0.505813 | 0.001998 | 0.027954 | 0.021577 |
| GO:0034762 | regulation of transmembrane transport | 35 | -0.514774 | 0.002997 | 0.034049 | 0.026282 |
| GO:0098656 | anion transmembrane transport | 24 | -0.517239 | 0.003996 | 0.039723 | 0.030662 |
| GO:0033339 | pectoral fin development | 28 | -0.520830 | 0.003996 | 0.039723 | 0.030662 |
| GO:0034765 | regulation of ion transmembrane transport | 34 | -0.524472 | 0.000999 | 0.020127 | 0.015535 |
| GO:0009581 | detection of external stimulus | 31 | -0.527447 | 0.002997 | 0.034049 | 0.026282 |
| GO:0009582 | detection of abiotic stimulus | 31 | -0.527447 | 0.002997 | 0.034049 | 0.026282 |
| GO:0017157 | regulation of exocytosis | 23 | -0.533058 | 0.004995 | 0.045467 | 0.035095 |
| GO:0051606 | detection of stimulus | 35 | -0.533131 | 0.001998 | 0.027954 | 0.021577 |
| GO:0007219 | Notch signaling pathway | 37 | -0.535571 | 0.001998 | 0.027954 | 0.021577 |
| GO:0007156 | homophilic cell adhesion via plasma membrane adhesion molecules | 27 | -0.554381 | 0.004995 | 0.045467 | 0.035095 |
| GO:0035107 | appendage morphogenesis | 28 | -0.559908 | 0.001998 | 0.027954 | 0.021577 |
| GO:0007602 | phototransduction | 20 | -0.573266 | 0.003996 | 0.039723 | 0.030662 |
| GO:0098742 | cell-cell adhesion via plasma-membrane adhesion molecules | 30 | -0.573890 | 0.001998 | 0.027954 | 0.021577 |
| GO:0009583 | detection of light stimulus | 26 | -0.573982 | 0.001998 | 0.027954 | 0.021577 |
| GO:0008277 | regulation of G-protein coupled receptor protein signaling pathway | 27 | -0.577666 | 0.002997 | 0.034049 | 0.026282 |
| GO:0030509 | BMP signaling pathway | 29 | -0.582315 | 0.000999 | 0.020127 | 0.015535 |
| GO:0098609 | cell-cell adhesion | 31 | -0.592672 | 0.000999 | 0.020127 | 0.015535 |
| GO:0045744 | negative regulation of G-protein coupled receptor protein signaling pathway | 23 | -0.601543 | 0.003996 | 0.039723 | 0.030662 |
| GO:0023021 | termination of signal transduction | 22 | -0.602899 | 0.003996 | 0.039723 | 0.030662 |
| GO:0038032 | termination of G-protein coupled receptor signaling pathway | 22 | -0.602899 | 0.003996 | 0.039723 | 0.030662 |
| GO:0008016 | regulation of heart contraction | 22 | -0.605623 | 0.000999 | 0.020127 | 0.015535 |
| GO:0031290 | retinal ganglion cell axon guidance | 19 | -0.620134 | 0.003996 | 0.039723 | 0.030662 |
| GO:0035051 | cardiocyte differentiation | 16 | -0.661469 | 0.000999 | 0.020127 | 0.015535 |
| GO:0001704 | formation of primary germ layer | 16 | -0.668570 | 0.004995 | 0.045467 | 0.035095 |
| GO:0048738 | cardiac muscle tissue development | 23 | -0.683075 | 0.000999 | 0.020127 | 0.015535 |
| GO:0055007 | cardiac muscle cell differentiation | 13 | -0.711822 | 0.001998 | 0.027954 | 0.021577 |
| GO:0050906 | detection of stimulus involved in sensory perception | 12 | -0.726241 | 0.000999 | 0.020127 | 0.015535 |
| GO:0009187 | cyclic nucleotide metabolic process | 20 | -0.827461 | 0.000999 | 0.020127 | 0.015535 |
| GO:0052652 | cyclic purine nucleotide metabolic process | 18 | -0.830379 | 0.000999 | 0.020127 | 0.015535 |
| GO:0009190 | cyclic nucleotide biosynthetic process | 19 | -0.841017 | 0.000999 | 0.020127 | 0.015535 |

## 8 hpl CC
| ID | Description | setSize | enrichmentScore | pvalue | p.adjust | qvalues |
| --- | --- | --- | --- | --- | --- | --- |
| GO:0005758 | mitochondrial intermembrane space | 16 | 0.784245 | 0.001998 | 0.024324 | 0.019203 |
| GO:0031970 | organelle envelope lumen | 16 | 0.784245 | 0.001998 | 0.024324 | 0.019203 |
| GO:0005759 | mitochondrial matrix | 44 | 0.685806 | 0.000999 | 0.015540 | 0.012268 |
| GO:0000313 | organellar ribosome | 17 | 0.672524 | 0.003996 | 0.037296 | 0.029444 |
| GO:0005761 | mitochondrial ribosome | 17 | 0.672524 | 0.003996 | 0.037296 | 0.029444 |
| GO:0046930 | pore complex | 22 | 0.643037 | 0.005994 | 0.046620 | 0.036805 |
| GO:0005739 | mitochondrion | 318 | 0.501146 | 0.000999 | 0.015540 | 0.012268 |
| GO:0044429 | mitochondrial part | 202 | 0.476011 | 0.000999 | 0.015540 | 0.012268 |
| GO:0005740 | mitochondrial envelope | 160 | 0.411418 | 0.005994 | 0.046620 | 0.036805 |
| GO:0005576 | extracellular region | 165 | 0.406567 | 0.004995 | 0.041135 | 0.032475 |
| GO:0031974 | membrane-enclosed lumen | 363 | 0.398566 | 0.000999 | 0.015540 | 0.012268 |
| GO:0070013 | intracellular organelle lumen | 347 | 0.381625 | 0.000999 | 0.015540 | 0.012268 |
| GO:0043233 | organelle lumen | 348 | 0.381464 | 0.000999 | 0.015540 | 0.012268 |
| GO:0044444 | cytoplasmic part | 1376 | 0.298914 | 0.001998 | 0.024324 | 0.019203 |
| GO:0005737 | cytoplasm | 2152 | 0.285060 | 0.003996 | 0.037296 | 0.029444 |
| GO:0016020 | membrane | 1982 | -0.219890 | 0.000999 | 0.015540 | 0.012268 |
| GO:0044425 | membrane part | 1581 | -0.225861 | 0.000999 | 0.015540 | 0.012268 |
| GO:0031224 | intrinsic component of membrane | 1301 | -0.248701 | 0.000999 | 0.015540 | 0.012268 |
| GO:0016021 | integral component of membrane | 1285 | -0.250015 | 0.000999 | 0.015540 | 0.012268 |
| GO:0005856 | cytoskeleton | 311 | -0.269478 | 0.003996 | 0.037296 | 0.029444 |
| GO:0044430 | cytoskeletal part | 228 | -0.275348 | 0.004995 | 0.041135 | 0.032475 |
| GO:0030054 | cell junction | 127 | -0.320985 | 0.000999 | 0.015540 | 0.012268 |
| GO:0071944 | cell periphery | 577 | -0.328859 | 0.000999 | 0.015540 | 0.012268 |
| GO:0005886 | plasma membrane | 563 | -0.334425 | 0.000999 | 0.015540 | 0.012268 |
| GO:0044459 | plasma membrane part | 295 | -0.351082 | 0.000999 | 0.015540 | 0.012268 |
| GO:0005887 | integral component of plasma membrane | 152 | -0.399913 | 0.000999 | 0.015540 | 0.012268 |
| GO:0031226 | intrinsic component of plasma membrane | 160 | -0.401246 | 0.000999 | 0.015540 | 0.012268 |
| GO:0045202 | synapse | 109 | -0.401683 | 0.000999 | 0.015540 | 0.012268 |
| GO:0005874 | microtubule | 71 | -0.416191 | 0.002997 | 0.032275 | 0.025481 |
| GO:0097458 | neuron part | 70 | -0.449815 | 0.000999 | 0.015540 | 0.012268 |
| GO:1902495 | transmembrane transporter complex | 52 | -0.461944 | 0.004995 | 0.041135 | 0.032475 |
| GO:1990351 | transporter complex | 52 | -0.461944 | 0.004995 | 0.041135 | 0.032475 |
| GO:0097060 | synaptic membrane | 39 | -0.507545 | 0.002997 | 0.032275 | 0.025481 |
| GO:0034702 | ion channel complex | 46 | -0.547706 | 0.001998 | 0.024324 | 0.019203 |
| GO:0030425 | dendrite | 22 | -0.597282 | 0.002997 | 0.032275 | 0.025481 |
| GO:0008328 | ionotropic glutamate receptor complex | 19 | -0.635081 | 0.001998 | 0.024324 | 0.019203 |

## 16 hpl MF
| ID | Description | setSize | enrichmentScore | pvalue | p.adjust | qvalues |
| --- | --- | --- | --- | --- | --- | --- |
| GO:0008235 | metalloexopeptidase activity | 13 | 0.844729 | 0.000999 | 0.018044 | 0.015544 |
| GO:0004860 | protein kinase inhibitor activity | 16 | 0.749683 | 0.001998 | 0.027496 | 0.023686 |
| GO:0019210 | kinase inhibitor activity | 16 | 0.749683 | 0.001998 | 0.027496 | 0.023686 |
| GO:0004869 | cysteine-type endopeptidase inhibitor activity | 13 | 0.744965 | 0.002997 | 0.032684 | 0.028155 |
| GO:0019838 | growth factor binding | 14 | 0.728871 | 0.002997 | 0.032684 | 0.028155 |
| GO:0004714 | transmembrane receptor protein tyrosine kinase activity | 28 | 0.695514 | 0.001998 | 0.027496 | 0.023686 |
| GO:0004866 | endopeptidase inhibitor activity | 35 | 0.683776 | 0.000999 | 0.018044 | 0.015544 |
| GO:0005126 | cytokine receptor binding | 29 | 0.678269 | 0.001998 | 0.027496 | 0.023686 |
| GO:0061135 | endopeptidase regulator activity | 37 | 0.675982 | 0.000999 | 0.018044 | 0.015544 |
| GO:0061134 | peptidase regulator activity | 43 | 0.673175 | 0.000999 | 0.018044 | 0.015544 |
| GO:0004857 | enzyme inhibitor activity | 68 | 0.663291 | 0.000999 | 0.018044 | 0.015544 |
| GO:0030414 | peptidase inhibitor activity | 38 | 0.662407 | 0.000999 | 0.018044 | 0.015544 |
| GO:0017016 | Ras GTPase binding | 24 | 0.648917 | 0.002997 | 0.032684 | 0.028155 |
| GO:0004713 | protein tyrosine kinase activity | 49 | 0.648196 | 0.000999 | 0.018044 | 0.015544 |
| GO:0031267 | small GTPase binding | 25 | 0.648129 | 0.003996 | 0.037864 | 0.032616 |
| GO:0051020 | GTPase binding | 25 | 0.648129 | 0.003996 | 0.037864 | 0.032616 |
| GO:0019199 | transmembrane receptor protein kinase activity | 37 | 0.613561 | 0.002997 | 0.032684 | 0.028155 |
| GO:0008238 | exopeptidase activity | 37 | 0.587638 | 0.003996 | 0.037864 | 0.032616 |
| GO:0019207 | kinase regulator activity | 40 | 0.569600 | 0.003996 | 0.037864 | 0.032616 |
| GO:0008237 | metallopeptidase activity | 62 | 0.552568 | 0.001998 | 0.027496 | 0.023686 |
| GO:0030234 | enzyme regulator activity | 227 | 0.373607 | 0.002997 | 0.032684 | 0.028155 |
| GO:0001071 | nucleic acid binding transcription factor activity | 258 | 0.355648 | 0.004995 | 0.045827 | 0.039476 |
| GO:0003700 | sequence-specific DNA binding transcription factor activity | 258 | 0.355648 | 0.004995 | 0.045827 | 0.039476 |
| GO:0046914 | transition metal ion binding | 662 | 0.324950 | 0.002997 | 0.032684 | 0.028155 |
| GO:0022892 | substrate-specific transporter activity | 348 | -0.277888 | 0.003996 | 0.037864 | 0.032616 |
| GO:0022857 | transmembrane transporter activity | 334 | -0.303673 | 0.000999 | 0.018044 | 0.015544 |
| GO:0022891 | substrate-specific transmembrane transporter activity | 295 | -0.316806 | 0.000999 | 0.018044 | 0.015544 |
| GO:0015075 | ion transmembrane transporter activity | 276 | -0.327058 | 0.000999 | 0.018044 | 0.015544 |
| GO:0008324 | cation transmembrane transporter activity | 195 | -0.331374 | 0.002997 | 0.032684 | 0.028155 |
| GO:0004872 | receptor activity | 278 | -0.332147 | 0.000999 | 0.018044 | 0.015544 |
| GO:0038023 | signaling receptor activity | 233 | -0.356483 | 0.000999 | 0.018044 | 0.015544 |
| GO:0004888 | transmembrane signaling receptor activity | 181 | -0.378761 | 0.000999 | 0.018044 | 0.015544 |
| GO:0022890 | inorganic cation transmembrane transporter activity | 167 | -0.400741 | 0.000999 | 0.018044 | 0.015544 |
| GO:0015077 | monovalent inorganic cation transmembrane transporter activity | 126 | -0.416941 | 0.000999 | 0.018044 | 0.015544 |
| GO:0005216 | ion channel activity | 106 | -0.456653 | 0.000999 | 0.018044 | 0.015544 |
| GO:0046873 | metal ion transmembrane transporter activity | 112 | -0.459516 | 0.000999 | 0.018044 | 0.015544 |
| GO:0015267 | channel activity | 119 | -0.460655 | 0.000999 | 0.018044 | 0.015544 |
| GO:0022803 | passive transmembrane transporter activity | 119 | -0.460655 | 0.000999 | 0.018044 | 0.015544 |
| GO:0022838 | substrate-specific channel activity | 111 | -0.467858 | 0.000999 | 0.018044 | 0.015544 |
| GO:0015291 | secondary active transmembrane transporter activity | 53 | -0.477029 | 0.002997 | 0.032684 | 0.028155 |
| GO:0072509 | divalent inorganic cation transmembrane transporter activity | 48 | -0.478417 | 0.002997 | 0.032684 | 0.028155 |
| GO:0015081 | sodium ion transmembrane transporter activity | 40 | -0.497823 | 0.003996 | 0.037864 | 0.032616 |
| GO:0015079 | potassium ion transmembrane transporter activity | 39 | -0.513825 | 0.000999 | 0.018044 | 0.015544 |
| GO:0022836 | gated channel activity | 98 | -0.524852 | 0.000999 | 0.018044 | 0.015544 |
| GO:0022832 | voltage-gated channel activity | 56 | -0.534459 | 0.000999 | 0.018044 | 0.015544 |
| GO:0005244 | voltage-gated ion channel activity | 53 | -0.542786 | 0.000999 | 0.018044 | 0.015544 |
| GO:0005230 | extracellular ligand-gated ion channel activity | 34 | -0.544781 | 0.001998 | 0.027496 | 0.023686 |
| GO:0004930 | G-protein coupled receptor activity | 94 | -0.546874 | 0.000999 | 0.018044 | 0.015544 |
| GO:0005261 | cation channel activity | 57 | -0.556060 | 0.000999 | 0.018044 | 0.015544 |
| GO:0005267 | potassium channel activity | 29 | -0.557111 | 0.003996 | 0.037864 | 0.032616 |
| GO:0015276 | ligand-gated ion channel activity | 46 | -0.563543 | 0.000999 | 0.018044 | 0.015544 |
| GO:0022834 | ligand-gated channel activity | 46 | -0.563543 | 0.000999 | 0.018044 | 0.015544 |
| GO:0015085 | calcium ion transmembrane transporter activity | 32 | -0.570396 | 0.000999 | 0.018044 | 0.015544 |
| GO:0005249 | voltage-gated potassium channel activity | 25 | -0.608338 | 0.001998 | 0.027496 | 0.023686 |
| GO:0019905 | syntaxin binding | 30 | -0.619429 | 0.000999 | 0.018044 | 0.015544 |
| GO:0022843 | voltage-gated cation channel activity | 39 | -0.642020 | 0.000999 | 0.018044 | 0.015544 |
| GO:0001653 | peptide receptor activity | 17 | -0.656103 | 0.002997 | 0.032684 | 0.028155 |
| GO:0008528 | G-protein coupled peptide receptor activity | 17 | -0.656103 | 0.002997 | 0.032684 | 0.028155 |
| GO:0015297 | antiporter activity | 18 | -0.672375 | 0.001998 | 0.027496 | 0.023686 |
| GO:0005262 | calcium channel activity | 14 | -0.692106 | 0.003996 | 0.037864 | 0.032616 |
| GO:0009881 | photoreceptor activity | 20 | -0.742939 | 0.000999 | 0.018044 | 0.015544 |
| GO:0015298 | solute:cation antiporter activity | 12 | -0.771166 | 0.001998 | 0.027496 | 0.023686 |
| GO:0015491 | cation:cation antiporter activity | 12 | -0.771166 | 0.001998 | 0.027496 | 0.023686 |

## 16 hpl BP
| ID | Description | setSize | enrichmentScore | pvalue | p.adjust | qvalues |
| --- | --- | --- | --- | --- | --- | --- |
| GO:0007623 | circadian rhythm | 16 | 0.831812 | 0.000999 | 0.028481 | 0.023174 |
| GO:0002253 | activation of immune response | 13 | 0.821966 | 0.000999 | 0.028481 | 0.023174 |
| GO:0002757 | immune response-activating signal transduction | 13 | 0.821966 | 0.000999 | 0.028481 | 0.023174 |
| GO:0019221 | cytokine-mediated signaling pathway | 18 | 0.817722 | 0.000999 | 0.028481 | 0.023174 |
| GO:0009617 | response to bacterium | 17 | 0.814902 | 0.000999 | 0.028481 | 0.023174 |
| GO:0071345 | cellular response to cytokine stimulus | 20 | 0.806758 | 0.000999 | 0.028481 | 0.023174 |
| GO:0008286 | insulin receptor signaling pathway | 12 | 0.795615 | 0.001998 | 0.040797 | 0.033196 |
| GO:0002764 | immune response-regulating signaling pathway | 14 | 0.790769 | 0.001998 | 0.040797 | 0.033196 |
| GO:0050778 | positive regulation of immune response | 17 | 0.790547 | 0.000999 | 0.028481 | 0.023174 |
| GO:0006879 | cellular iron ion homeostasis | 11 | 0.783220 | 0.002997 | 0.048175 | 0.039199 |
| GO:0034097 | response to cytokine | 28 | 0.714189 | 0.000999 | 0.028481 | 0.023174 |
| GO:0002684 | positive regulation of immune system process | 23 | 0.713664 | 0.000999 | 0.028481 | 0.023174 |
| GO:0040029 | regulation of gene expression, epigenetic | 22 | 0.711032 | 0.001998 | 0.040797 | 0.033196 |
| GO:0048511 | rhythmic process | 24 | 0.700368 | 0.000999 | 0.028481 | 0.023174 |
| GO:0045087 | innate immune response | 26 | 0.673996 | 0.001998 | 0.040797 | 0.033196 |
| GO:0043434 | response to peptide hormone | 20 | 0.669369 | 0.002997 | 0.048175 | 0.039199 |
| GO:0071375 | cellular response to peptide hormone stimulus | 20 | 0.669369 | 0.002997 | 0.048175 | 0.039199 |
| GO:1901653 | cellular response to peptide | 20 | 0.669369 | 0.002997 | 0.048175 | 0.039199 |
| GO:0031123 | RNA 3'-end processing | 26 | 0.664333 | 0.000999 | 0.028481 | 0.023174 |
| GO:0050776 | regulation of immune response | 22 | 0.663045 | 0.001998 | 0.040797 | 0.033196 |
| GO:1901699 | cellular response to nitrogen compound | 32 | 0.661388 | 0.000999 | 0.028481 | 0.023174 |
| GO:0006955 | immune response | 68 | 0.655493 | 0.000999 | 0.028481 | 0.023174 |
| GO:0043207 | response to external biotic stimulus | 41 | 0.645971 | 0.000999 | 0.028481 | 0.023174 |
| GO:0051707 | response to other organism | 41 | 0.645971 | 0.000999 | 0.028481 | 0.023174 |
| GO:0009607 | response to biotic stimulus | 43 | 0.634795 | 0.001998 | 0.040797 | 0.033196 |
| GO:0002682 | regulation of immune system process | 33 | 0.629388 | 0.000999 | 0.028481 | 0.023174 |
| GO:0031099 | regeneration | 61 | 0.628523 | 0.000999 | 0.028481 | 0.023174 |
| GO:0006952 | defense response | 46 | 0.627738 | 0.000999 | 0.028481 | 0.023174 |
| GO:0045596 | negative regulation of cell differentiation | 26 | 0.627234 | 0.001998 | 0.040797 | 0.033196 |
| GO:0007169 | transmembrane receptor protein tyrosine kinase signaling pathway | 93 | 0.591454 | 0.000999 | 0.028481 | 0.023174 |
| GO:1901698 | response to nitrogen compound | 42 | 0.591407 | 0.000999 | 0.028481 | 0.023174 |
| GO:1902532 | negative regulation of intracellular signal transduction | 38 | 0.589944 | 0.001998 | 0.040797 | 0.033196 |
| GO:0042254 | ribosome biogenesis | 93 | 0.578841 | 0.000999 | 0.028481 | 0.023174 |
| GO:0016072 | rRNA metabolic process | 70 | 0.568071 | 0.000999 | 0.028481 | 0.023174 |
| GO:0006364 | rRNA processing | 68 | 0.568061 | 0.000999 | 0.028481 | 0.023174 |
| GO:0034470 | ncRNA processing | 125 | 0.558132 | 0.000999 | 0.028481 | 0.023174 |
| GO:0022613 | ribonucleoprotein complex biogenesis | 132 | 0.549042 | 0.000999 | 0.028481 | 0.023174 |
| GO:0019439 | aromatic compound catabolic process | 54 | 0.540520 | 0.002997 | 0.048175 | 0.039199 |
| GO:0044270 | cellular nitrogen compound catabolic process | 54 | 0.540520 | 0.002997 | 0.048175 | 0.039199 |
| GO:0042127 | regulation of cell proliferation | 80 | 0.532032 | 0.000999 | 0.028481 | 0.023174 |
| GO:0008283 | cell proliferation | 111 | 0.531708 | 0.000999 | 0.028481 | 0.023174 |
| GO:0009611 | response to wounding | 79 | 0.526220 | 0.001998 | 0.040797 | 0.033196 |
| GO:0051247 | positive regulation of protein metabolic process | 61 | 0.516309 | 0.002997 | 0.048175 | 0.039199 |
| GO:0040007 | growth | 142 | 0.510532 | 0.000999 | 0.028481 | 0.023174 |
| GO:0032270 | positive regulation of cellular protein metabolic process | 60 | 0.509055 | 0.002997 | 0.048175 | 0.039199 |
| GO:0051704 | multi-organism process | 76 | 0.505093 | 0.002997 | 0.048175 | 0.039199 |
| GO:0048589 | developmental growth | 110 | 0.496712 | 0.000999 | 0.028481 | 0.023174 |
| GO:0034660 | ncRNA metabolic process | 164 | 0.495055 | 0.000999 | 0.028481 | 0.023174 |
| GO:0001932 | regulation of protein phosphorylation | 73 | 0.479363 | 0.002997 | 0.048175 | 0.039199 |
| GO:0007167 | enzyme linked receptor protein signaling pathway | 159 | 0.476008 | 0.000999 | 0.028481 | 0.023174 |
| GO:0002376 | immune system process | 205 | 0.475149 | 0.000999 | 0.028481 | 0.023174 |
| GO:0048584 | positive regulation of response to stimulus | 110 | 0.474134 | 0.000999 | 0.028481 | 0.023174 |
| GO:0048870 | cell motility | 163 | 0.457973 | 0.000999 | 0.028481 | 0.023174 |
| GO:0051674 | localization of cell | 163 | 0.457973 | 0.000999 | 0.028481 | 0.023174 |
| GO:0016477 | cell migration | 159 | 0.447973 | 0.000999 | 0.028481 | 0.023174 |
| GO:0042325 | regulation of phosphorylation | 98 | 0.443784 | 0.001998 | 0.040797 | 0.033196 |
| GO:0006950 | response to stress | 433 | 0.422473 | 0.000999 | 0.028481 | 0.023174 |
| GO:0071310 | cellular response to organic substance | 191 | 0.414390 | 0.001998 | 0.040797 | 0.033196 |
| GO:0010033 | response to organic substance | 222 | 0.406845 | 0.001998 | 0.040797 | 0.033196 |
| GO:0010605 | negative regulation of macromolecule metabolic process | 165 | 0.400451 | 0.002997 | 0.048175 | 0.039199 |
| GO:0040011 | locomotion | 219 | 0.386746 | 0.001998 | 0.040797 | 0.033196 |
| GO:0070887 | cellular response to chemical stimulus | 225 | 0.376083 | 0.002997 | 0.048175 | 0.039199 |
| GO:0048518 | positive regulation of biological process | 381 | 0.350702 | 0.002997 | 0.048175 | 0.039199 |
| GO:0050896 | response to stimulus | 1630 | 0.299351 | 0.000999 | 0.028481 | 0.023174 |
| GO:0044765 | single-organism transport | 728 | -0.232714 | 0.001998 | 0.040797 | 0.033196 |
| GO:1902578 | single-organism localization | 766 | -0.235006 | 0.000999 | 0.028481 | 0.023174 |
| GO:0055085 | transmembrane transport | 288 | -0.286092 | 0.002997 | 0.048175 | 0.039199 |
| GO:0006811 | ion transport | 323 | -0.302089 | 0.000999 | 0.028481 | 0.023174 |
| GO:0003008 | system process | 153 | -0.351865 | 0.001998 | 0.040797 | 0.033196 |
| GO:0007267 | cell-cell signaling | 109 | -0.408420 | 0.000999 | 0.028481 | 0.023174 |
| GO:0072522 | purine-containing compound biosynthetic process | 79 | -0.426036 | 0.002997 | 0.048175 | 0.039199 |
| GO:0007186 | G-protein coupled receptor signaling pathway | 164 | -0.469886 | 0.000999 | 0.028481 | 0.023174 |
| GO:0007268 | synaptic transmission | 78 | -0.525604 | 0.000999 | 0.028481 | 0.023174 |
| GO:0034762 | regulation of transmembrane transport | 35 | -0.526409 | 0.002997 | 0.048175 | 0.039199 |
| GO:0016052 | carbohydrate catabolic process | 28 | -0.540872 | 0.002997 | 0.048175 | 0.039199 |
| GO:0007600 | sensory perception | 67 | -0.584317 | 0.000999 | 0.028481 | 0.023174 |
| GO:0050877 | neurological system process | 76 | -0.586823 | 0.000999 | 0.028481 | 0.023174 |
| GO:0045744 | negative regulation of G-protein coupled receptor protein signaling pathway | 23 | -0.596679 | 0.001998 | 0.040797 | 0.033196 |
| GO:0023021 | termination of signal transduction | 22 | -0.608322 | 0.001998 | 0.040797 | 0.033196 |
| GO:0038032 | termination of G-protein coupled receptor signaling pathway | 22 | -0.608322 | 0.001998 | 0.040797 | 0.033196 |
| GO:0007270 | neuron-neuron synaptic transmission | 22 | -0.623482 | 0.002997 | 0.048175 | 0.039199 |
| GO:0000819 | sister chromatid segregation | 16 | -0.633374 | 0.002997 | 0.048175 | 0.039199 |
| GO:0050953 | sensory perception of light stimulus | 47 | -0.646116 | 0.000999 | 0.028481 | 0.023174 |
| GO:0007601 | visual perception | 46 | -0.657956 | 0.000999 | 0.028481 | 0.023174 |
| GO:0051606 | detection of stimulus | 35 | -0.671253 | 0.000999 | 0.028481 | 0.023174 |
| GO:0009190 | cyclic nucleotide biosynthetic process | 19 | -0.672727 | 0.002997 | 0.048175 | 0.039199 |
| GO:0000070 | mitotic sister chromatid segregation | 14 | -0.678216 | 0.001998 | 0.040797 | 0.033196 |
| GO:0009187 | cyclic nucleotide metabolic process | 20 | -0.684289 | 0.001998 | 0.040797 | 0.033196 |
| GO:0009581 | detection of external stimulus | 31 | -0.698876 | 0.000999 | 0.028481 | 0.023174 |
| GO:0009582 | detection of abiotic stimulus | 31 | -0.698876 | 0.000999 | 0.028481 | 0.023174 |
| GO:0009583 | detection of light stimulus | 26 | -0.737798 | 0.000999 | 0.028481 | 0.023174 |
| GO:0018298 | protein-chromophore linkage | 17 | -0.755044 | 0.000999 | 0.028481 | 0.023174 |
| GO:0007602 | phototransduction | 20 | -0.776878 | 0.000999 | 0.028481 | 0.023174 |

## 16 hpl CC
| ID | Description | setSize | enrichmentScore | pvalue | p.adjust | qvalues |
| --- | --- | --- | --- | --- | --- | --- |
| GO:0046930 | pore complex | 22 | 0.836827 | 0.000999 | 0.016454 | 0.013052 |
| GO:0000932 | cytoplasmic mRNA processing body | 16 | 0.755579 | 0.000999 | 0.016454 | 0.013052 |
| GO:0035770 | ribonucleoprotein granule | 19 | 0.700248 | 0.002997 | 0.028937 | 0.022953 |
| GO:0036464 | cytoplasmic ribonucleoprotein granule | 19 | 0.700248 | 0.002997 | 0.028937 | 0.022953 |
| GO:0005666 | DNA-directed RNA polymerase III complex | 15 | 0.700152 | 0.004995 | 0.043706 | 0.034669 |
| GO:0044452 | nucleolar part | 27 | 0.680086 | 0.002997 | 0.028937 | 0.022953 |
| GO:0032040 | small-subunit processome | 22 | 0.669231 | 0.001998 | 0.023310 | 0.018490 |
| GO:0030684 | preribosome | 29 | 0.636473 | 0.001998 | 0.023310 | 0.018490 |
| GO:0005730 | nucleolus | 101 | 0.570992 | 0.000999 | 0.016454 | 0.013052 |
| GO:0005615 | extracellular space | 63 | 0.534412 | 0.001998 | 0.023310 | 0.018490 |
| GO:0044421 | extracellular region part | 78 | 0.525405 | 0.001998 | 0.023310 | 0.018490 |
| GO:0005576 | extracellular region | 165 | 0.456112 | 0.000999 | 0.016454 | 0.013052 |
| GO:0030529 | ribonucleoprotein complex | 273 | 0.401177 | 0.000999 | 0.016454 | 0.013052 |
| GO:0031981 | nuclear lumen | 295 | 0.382299 | 0.000999 | 0.016454 | 0.013052 |
| GO:0031974 | membrane-enclosed lumen | 363 | 0.374376 | 0.000999 | 0.016454 | 0.013052 |
| GO:0043233 | organelle lumen | 348 | 0.373452 | 0.000999 | 0.016454 | 0.013052 |
| GO:0070013 | intracellular organelle lumen | 347 | 0.372725 | 0.000999 | 0.016454 | 0.013052 |
| GO:0016020 | membrane | 1982 | -0.215735 | 0.000999 | 0.016454 | 0.013052 |
| GO:0044425 | membrane part | 1581 | -0.223692 | 0.000999 | 0.016454 | 0.013052 |
| GO:0031224 | intrinsic component of membrane | 1301 | -0.236353 | 0.000999 | 0.016454 | 0.013052 |
| GO:0016021 | integral component of membrane | 1285 | -0.237767 | 0.000999 | 0.016454 | 0.013052 |
| GO:0071944 | cell periphery | 577 | -0.254622 | 0.000999 | 0.016454 | 0.013052 |
| GO:0005886 | plasma membrane | 563 | -0.257383 | 0.000999 | 0.016454 | 0.013052 |
| GO:0031966 | mitochondrial membrane | 146 | -0.316446 | 0.002997 | 0.028937 | 0.022953 |
| GO:0045202 | synapse | 109 | -0.364492 | 0.004995 | 0.043706 | 0.034669 |
| GO:0005743 | mitochondrial inner membrane | 91 | -0.373151 | 0.004995 | 0.043706 | 0.034669 |
| GO:0097458 | neuron part | 70 | -0.447245 | 0.001998 | 0.023310 | 0.018490 |
| GO:0005929 | cilium | 54 | -0.480350 | 0.002997 | 0.028937 | 0.022953 |
| GO:0034702 | ion channel complex | 46 | -0.544453 | 0.001998 | 0.023310 | 0.018490 |
| GO:1902495 | transmembrane transporter complex | 52 | -0.550682 | 0.000999 | 0.016454 | 0.013052 |
| GO:1990351 | transporter complex | 52 | -0.550682 | 0.000999 | 0.016454 | 0.013052 |
| GO:0034703 | cation channel complex | 22 | -0.679526 | 0.001998 | 0.023310 | 0.018490 |

## rd1 MF
| ID | Description | setSize | enrichmentScore | pvalue | p.adjust | qvalues |
| --- | --- | --- | --- | --- | --- | --- |
| GO:0004623 | phospholipase A2 activity | 12 | 0.802726 | 0.001672 | 0.457776 | 0.455906 |
| GO:0019825 | oxygen binding | 16 | 0.796284 | 0.001618 | 0.457776 | 0.455906 |
| GO:0001968 | fibronectin binding | 18 | 0.768493 | 0.001667 | 0.457776 | 0.455906 |
| GO:0031420 | alkali metal ion binding | 14 | 0.745008 | 0.006656 | 0.485857 | 0.483872 |
| GO:0043274 | phospholipase binding | 11 | 0.698209 | 0.031469 | 0.868118 | 0.864571 |
| GO:0008483 | transaminase activity | 15 | 0.688925 | 0.012027 | 0.714810 | 0.711890 |
| GO:0015491 | cation:cation antiporter activity | 11 | 0.681205 | 0.034423 | 0.868118 | 0.864571 |
| GO:0016769 | transferase activity, transferring nitrogenous groups | 16 | 0.674854 | 0.008547 | 0.584936 | 0.582546 |
| GO:0005326 | neurotransmitter transporter activity | 12 | 0.666232 | 0.035831 | 0.868118 | 0.864571 |
| GO:0015459 | potassium channel regulator activity | 16 | 0.626104 | 0.024876 | 0.868118 | 0.864571 |
| GO:0030170 | pyridoxal phosphate binding | 33 | 0.617872 | 0.004471 | 0.485857 | 0.483872 |
| GO:0017080 | sodium channel regulator activity | 18 | 0.610783 | 0.045307 | 0.868118 | 0.864571 |
| GO:0016645 | oxidoreductase activity, acting on the CH-NH group of donors | 19 | 0.608254 | 0.030645 | 0.868118 | 0.864571 |
| GO:0046965 | retinoid X receptor binding | 17 | 0.605430 | 0.040783 | 0.868118 | 0.864571 |
| GO:0005310 | dicarboxylic acid transmembrane transporter activity | 16 | 0.599589 | 0.046926 | 0.868118 | 0.864571 |
| GO:0005254 | chloride channel activity | 27 | 0.593964 | 0.012403 | 0.714810 | 0.711890 |
| GO:0016406 | carnitine O-acyltransferase activity | 21 | 0.578227 | 0.037736 | 0.868118 | 0.864571 |
| GO:0042974 | retinoic acid receptor binding | 26 | 0.543628 | 0.033071 | 0.868118 | 0.864571 |
| GO:0015081 | sodium ion transmembrane transporter activity | 52 | 0.526481 | 0.003017 | 0.485857 | 0.483872 |
| GO:0022843 | voltage-gated cation channel activity | 53 | 0.473979 | 0.025680 | 0.868118 | 0.864571 |
| GO:0015079 | potassium ion transmembrane transporter activity | 50 | 0.462459 | 0.034639 | 0.868118 | 0.864571 |
| GO:0008201 | heparin binding | 58 | 0.459129 | 0.028788 | 0.868118 | 0.864571 |
| GO:0015103 | inorganic anion transmembrane transporter activity | 47 | 0.452986 | 0.041860 | 0.868118 | 0.864571 |
| GO:0034212 | peptide N-acetyltransferase activity | 50 | 0.448993 | 0.038462 | 0.868118 | 0.864571 |
| GO:0042393 | histone binding | 126 | 0.447818 | 0.001355 | 0.457776 | 0.455906 |
| GO:0019905 | syntaxin binding | 64 | 0.427062 | 0.033873 | 0.868118 | 0.864571 |
| GO:0022838 | substrate-specific channel activity | 158 | 0.406737 | 0.003937 | 0.485857 | 0.483872 |
| GO:0005216 | ion channel activity | 153 | 0.399674 | 0.006605 | 0.485857 | 0.483872 |
| GO:0022836 | gated channel activity | 113 | 0.395084 | 0.022472 | 0.868118 | 0.864571 |
| GO:0015077 | monovalent inorganic cation transmembrane transporter activity | 154 | 0.393900 | 0.006345 | 0.485857 | 0.483872 |
| GO:0015267 | channel activity | 168 | 0.389960 | 0.005222 | 0.485857 | 0.483872 |
| GO:0022803 | passive transmembrane transporter activity | 168 | 0.389960 | 0.005222 | 0.485857 | 0.483872 |
| GO:0000149 | SNARE binding | 90 | 0.388242 | 0.045961 | 0.868118 | 0.864571 |
| GO:0046873 | metal ion transmembrane transporter activity | 179 | 0.349207 | 0.036036 | 0.868118 | 0.864571 |
| GO:0022890 | inorganic cation transmembrane transporter activity | 243 | 0.330107 | 0.042373 | 0.868118 | 0.864571 |
| GO:0098772 | molecular function regulator | 684 | -0.244560 | 0.012195 | 0.714810 | 0.711890 |
| GO:0030234 | enzyme regulator activity | 522 | -0.252413 | 0.028571 | 0.868118 | 0.864571 |
| GO:0005096 | GTPase activator activity | 153 | -0.307254 | 0.047244 | 0.868118 | 0.864571 |
| GO:0031267 | small GTPase binding | 186 | -0.311342 | 0.024272 | 0.868118 | 0.864571 |
| GO:0004857 | enzyme inhibitor activity | 161 | -0.315512 | 0.022727 | 0.868118 | 0.864571 |
| GO:0017016 | Ras GTPase binding | 174 | -0.317520 | 0.028037 | 0.868118 | 0.864571 |
| GO:0005088 | Ras guanyl-nucleotide exchange factor activity | 80 | -0.358666 | 0.041401 | 0.868118 | 0.864571 |
| GO:0005126 | cytokine receptor binding | 112 | -0.371052 | 0.014706 | 0.741954 | 0.738922 |
| GO:0017137 | Rab GTPase binding | 67 | -0.376188 | 0.033537 | 0.868118 | 0.864571 |
| GO:0005125 | cytokine activity | 59 | -0.411417 | 0.036697 | 0.868118 | 0.864571 |
| GO:0043236 | laminin binding | 22 | -0.500016 | 0.045918 | 0.868118 | 0.864571 |
| GO:0016796 | exonuclease activity, active with either ribo- or deoxyribonucleic acids and producing 5'-phosphomonoesters | 28 | -0.500802 | 0.024390 | 0.868118 | 0.864571 |
| GO:0008028 | monocarboxylic acid transmembrane transporter activity | 22 | -0.574082 | 0.016438 | 0.750000 | 0.746936 |
| GO:0003756 | protein disulfide isomerase activity | 15 | -0.584594 | 0.040670 | 0.868118 | 0.864571 |
| GO:0016864 | intramolecular oxidoreductase activity, transposing S-S bonds | 15 | -0.584594 | 0.040670 | 0.868118 | 0.864571 |
| GO:0051393 | alpha-actinin binding | 13 | -0.604511 | 0.048611 | 0.868118 | 0.864571 |
| GO:0042805 | actinin binding | 21 | -0.607679 | 0.015038 | 0.741954 | 0.738922 |
| GO:0042605 | peptide antigen binding | 15 | -0.617950 | 0.031746 | 0.868118 | 0.864571 |
| GO:1901618 | organic hydroxy compound transmembrane transporter activity | 22 | -0.637951 | 0.005155 | 0.485857 | 0.483872 |
| GO:0050431 | transforming growth factor beta binding | 12 | -0.643357 | 0.014528 | 0.741954 | 0.738922 |
| GO:0005164 | tumor necrosis factor receptor binding | 14 | -0.673199 | 0.025381 | 0.868118 | 0.864571 |
| GO:0008009 | chemokine activity | 11 | -0.711661 | 0.015584 | 0.741954 | 0.738922 |
| GO:0070405 | ammonium ion binding | 19 | -0.735831 | 0.005405 | 0.485857 | 0.483872 |
| GO:0050997 | quaternary ammonium group binding | 12 | -0.907146 | 0.002584 | 0.485857 | 0.483872 |

## rd1 BP
| ID | Description | setSize | enrichmentScore | pvalue | p.adjust | qvalues |
| --- | --- | --- | --- | --- | --- | --- |
| GO:0019882 | antigen processing and presentation | 47 | -0.404534 | 0.044164 | 0.300850 | 0.266551 |
| GO:0071772 | response to BMP | 75 | 0.415151 | 0.036879 | 0.279295 | 0.247453 |
| GO:0071773 | cellular response to BMP stimulus | 75 | 0.415151 | 0.036879 | 0.279295 | 0.247453 |
| GO:0010971 | positive regulation of G2/M transition of mitotic cell cycle | 12 | -0.704399 | 0.017199 | 0.224465 | 0.198875 |
| GO:1902751 | positive regulation of cell cycle G2/M phase transition | 12 | -0.704399 | 0.017199 | 0.224465 | 0.198875 |
| GO:0045168 | cell-cell signaling involved in cell fate commitment | 20 | 0.694647 | 0.001520 | 0.109626 | 0.097128 |
| GO:0001708 | cell fate specification | 45 | 0.487562 | 0.023358 | 0.241946 | 0.214363 |
| GO:0042063 | gliogenesis | 174 | 0.440318 | 0.001297 | 0.109626 | 0.097128 |
| GO:0045165 | cell fate commitment | 139 | 0.425227 | 0.003896 | 0.128681 | 0.114011 |
| GO:0007622 | rhythmic behavior | 19 | 0.607533 | 0.024430 | 0.245202 | 0.217248 |
| GO:0048512 | circadian behavior | 19 | 0.607533 | 0.024430 | 0.245202 | 0.217248 |
| GO:0032613 | interleukin-10 production | 13 | -0.635502 | 0.040872 | 0.293919 | 0.260410 |
| GO:0032640 | tumor necrosis factor production | 57 | -0.446163 | 0.013333 | 0.206216 | 0.182706 |
| GO:0071706 | tumor necrosis factor superfamily cytokine production | 57 | -0.446163 | 0.013333 | 0.206216 | 0.182706 |
| GO:0032760 | positive regulation of tumor necrosis factor production | 34 | -0.446501 | 0.046647 | 0.307613 | 0.272543 |
| GO:1903557 | positive regulation of tumor necrosis factor superfamily cytokine production | 34 | -0.446501 | 0.046647 | 0.307613 | 0.272543 |
| GO:0032680 | regulation of tumor necrosis factor production | 56 | -0.447325 | 0.010000 | 0.178115 | 0.157808 |
| GO:1903555 | regulation of tumor necrosis factor superfamily cytokine production | 56 | -0.447325 | 0.010000 | 0.178115 | 0.157808 |
| GO:0032633 | interleukin-4 production | 16 | 0.623428 | 0.042789 | 0.299173 | 0.265065 |
| GO:0001816 | cytokine production | 289 | -0.280599 | 0.044304 | 0.300850 | 0.266551 |
| GO:0001817 | regulation of cytokine production | 251 | -0.323903 | 0.011561 | 0.193241 | 0.171211 |
| GO:0001819 | positive regulation of cytokine production | 153 | -0.347345 | 0.013100 | 0.205540 | 0.182107 |
| GO:0001818 | negative regulation of cytokine production | 95 | -0.365550 | 0.023166 | 0.241946 | 0.214363 |
| GO:0050663 | cytokine secretion | 63 | -0.392125 | 0.034985 | 0.279295 | 0.247453 |
| GO:0071356 | cellular response to tumor necrosis factor | 55 | -0.401234 | 0.028213 | 0.257515 | 0.228156 |
| GO:0032675 | regulation of interleukin-6 production | 48 | -0.437619 | 0.015432 | 0.219139 | 0.194155 |
| GO:0032635 | interleukin-6 production | 50 | -0.440740 | 0.018750 | 0.230453 | 0.204179 |
| GO:0050707 | regulation of cytokine secretion | 52 | -0.481565 | 0.005935 | 0.152968 | 0.135528 |
| GO:0050715 | positive regulation of cytokine secretion | 33 | -0.488740 | 0.020833 | 0.234852 | 0.208077 |
| GO:0032663 | regulation of interleukin-2 production | 25 | -0.501339 | 0.043716 | 0.299896 | 0.265705 |
| GO:0032732 | positive regulation of interleukin-1 production | 13 | -0.612127 | 0.037406 | 0.279808 | 0.247908 |
| GO:0032653 | regulation of interleukin-10 production | 12 | -0.695103 | 0.015831 | 0.221229 | 0.196007 |
| GO:0014002 | astrocyte development | 15 | 0.681728 | 0.013072 | 0.205540 | 0.182107 |
| GO:0021884 | forebrain neuron development | 16 | 0.676280 | 0.010769 | 0.185707 | 0.164535 |
| GO:0021772 | olfactory bulb development | 19 | 0.588700 | 0.038721 | 0.285704 | 0.253131 |
| GO:0055025 | positive regulation of cardiac muscle tissue development | 21 | 0.586406 | 0.025600 | 0.249741 | 0.221269 |
| GO:0030850 | prostate gland development | 28 | 0.532810 | 0.030441 | 0.264597 | 0.234431 |
| GO:0021766 | hippocampus development | 43 | 0.532491 | 0.006202 | 0.152968 | 0.135528 |
| GO:0001657 | ureteric bud development | 41 | 0.521525 | 0.017595 | 0.225028 | 0.199373 |
| GO:0072163 | mesonephric epithelium development | 41 | 0.521525 | 0.017595 | 0.225028 | 0.199373 |
| GO:0072164 | mesonephric tubule development | 41 | 0.521525 | 0.017595 | 0.225028 | 0.199373 |
| GO:0001823 | mesonephros development | 42 | 0.521278 | 0.016320 | 0.222347 | 0.196998 |
| GO:0021872 | forebrain generation of neurons | 39 | 0.519054 | 0.019578 | 0.234020 | 0.207340 |
| GO:0061035 | regulation of cartilage development | 35 | 0.518346 | 0.025954 | 0.249741 | 0.221269 |
| GO:0060976 | coronary vasculature development | 27 | 0.514961 | 0.037097 | 0.279295 | 0.247453 |
| GO:0003407 | neural retina development | 32 | 0.502093 | 0.038462 | 0.284760 | 0.252295 |
| GO:0060711 | labyrinthine layer development | 34 | 0.498320 | 0.048077 | 0.311603 | 0.276079 |
| GO:0055024 | regulation of cardiac muscle tissue development | 34 | 0.497093 | 0.036164 | 0.279295 | 0.247453 |
| GO:0001656 | metanephros development | 38 | 0.494153 | 0.039574 | 0.289849 | 0.256804 |
| GO:0021761 | limbic system development | 54 | 0.486757 | 0.011817 | 0.193796 | 0.171702 |
| GO:0021549 | cerebellum development | 56 | 0.459106 | 0.024355 | 0.245202 | 0.217248 |
| GO:0021510 | spinal cord development | 47 | 0.458480 | 0.033486 | 0.274742 | 0.243420 |
| GO:0048736 | appendage development | 107 | 0.458367 | 0.002699 | 0.118967 | 0.105404 |
| GO:0060173 | limb development | 107 | 0.458367 | 0.002699 | 0.118967 | 0.105404 |
| GO:0051216 | cartilage development | 99 | 0.449681 | 0.002762 | 0.118967 | 0.105404 |
| GO:0022037 | metencephalon development | 65 | 0.431823 | 0.037196 | 0.279295 | 0.247453 |
| GO:0061448 | connective tissue development | 132 | 0.424684 | 0.004021 | 0.128681 | 0.114011 |
| GO:0051961 | negative regulation of nervous system development | 185 | 0.421607 | 0.001269 | 0.109626 | 0.097128 |
| GO:0030902 | hindbrain development | 89 | 0.396410 | 0.036364 | 0.279295 | 0.247453 |
| GO:0048592 | eye morphogenesis | 108 | 0.382730 | 0.040816 | 0.293919 | 0.260410 |
| GO:0010721 | negative regulation of cell development | 200 | 0.379943 | 0.003759 | 0.127643 | 0.113091 |
| GO:0022008 | neurogenesis | 921 | 0.362691 | 0.001050 | 0.109626 | 0.097128 |
| GO:0030900 | forebrain development | 214 | 0.351295 | 0.017588 | 0.225028 | 0.199373 |
| GO:0001654 | eye development | 228 | 0.347853 | 0.027500 | 0.256065 | 0.226872 |
| GO:0045653 | negative regulation of megakaryocyte differentiation | 13 | 0.864561 | 0.001715 | 0.109626 | 0.097128 |
| GO:1901533 | negative regulation of hematopoietic progenitor cell differentiation | 17 | 0.816110 | 0.001621 | 0.109626 | 0.097128 |
| GO:0045652 | regulation of megakaryocyte differentiation | 19 | 0.752079 | 0.001701 | 0.109626 | 0.097128 |
| GO:0045672 | positive regulation of osteoclast differentiation | 13 | 0.733769 | 0.006667 | 0.152968 | 0.135528 |
| GO:0048712 | negative regulation of astrocyte differentiation | 12 | 0.712486 | 0.014563 | 0.217496 | 0.192700 |
| GO:0021533 | cell differentiation in hindbrain | 14 | 0.673302 | 0.026534 | 0.253443 | 0.224549 |
| GO:0045670 | regulation of osteoclast differentiation | 28 | 0.625402 | 0.004545 | 0.135462 | 0.120019 |
| GO:1901532 | regulation of hematopoietic progenitor cell differentiation | 35 | 0.614870 | 0.001513 | 0.109626 | 0.097128 |
| GO:0030219 | megakaryocyte differentiation | 34 | 0.606075 | 0.001597 | 0.109626 | 0.097128 |
| GO:0035914 | skeletal muscle cell differentiation | 44 | 0.601753 | 0.001497 | 0.109626 | 0.097128 |
| GO:0048709 | oligodendrocyte differentiation | 57 | 0.570866 | 0.001422 | 0.109626 | 0.097128 |
| GO:0048708 | astrocyte differentiation | 51 | 0.569152 | 0.001443 | 0.109626 | 0.097128 |
| GO:0042491 | auditory receptor cell differentiation | 24 | 0.558608 | 0.025000 | 0.247882 | 0.219621 |
| GO:0021522 | spinal cord motor neuron differentiation | 23 | 0.549694 | 0.044234 | 0.300850 | 0.266551 |
| GO:0035315 | hair cell differentiation | 26 | 0.541130 | 0.035937 | 0.279295 | 0.247453 |
| GO:0021782 | glial cell development | 58 | 0.536635 | 0.001511 | 0.109626 | 0.097128 |
| GO:0021879 | forebrain neuron differentiation | 33 | 0.531934 | 0.022455 | 0.239191 | 0.211921 |
| GO:0045668 | negative regulation of osteoblast differentiation | 29 | 0.530038 | 0.036641 | 0.279295 | 0.247453 |
| GO:0010001 | glial cell differentiation | 135 | 0.499859 | 0.001330 | 0.109626 | 0.097128 |
| GO:0045638 | negative regulation of myeloid cell differentiation | 51 | 0.488735 | 0.017725 | 0.225028 | 0.199373 |
| GO:0045637 | regulation of myeloid cell differentiation | 110 | 0.462894 | 0.001385 | 0.109626 | 0.097128 |
| GO:0002062 | chondrocyte differentiation | 52 | 0.453101 | 0.037313 | 0.279593 | 0.247718 |
| GO:0045665 | negative regulation of neuron differentiation | 129 | 0.435434 | 0.001330 | 0.109626 | 0.097128 |
| GO:0021953 | central nervous system neuron differentiation | 102 | 0.389974 | 0.043836 | 0.299896 | 0.265705 |
| GO:0030099 | myeloid cell differentiation | 220 | 0.351018 | 0.018587 | 0.229491 | 0.203327 |
| GO:0045596 | negative regulation of cell differentiation | 381 | 0.348878 | 0.004551 | 0.135462 | 0.120019 |
| GO:0030182 | neuron differentiation | 773 | 0.346101 | 0.001074 | 0.109626 | 0.097128 |
| GO:0048666 | neuron development | 633 | 0.331225 | 0.001094 | 0.109626 | 0.097128 |
| GO:0045664 | regulation of neuron differentiation | 383 | 0.326258 | 0.015258 | 0.219139 | 0.194155 |
| GO:0051960 | regulation of nervous system development | 524 | 0.323571 | 0.007795 | 0.159963 | 0.141726 |
| GO:0045595 | regulation of cell differentiation | 939 | 0.306231 | 0.006270 | 0.152968 | 0.135528 |
| GO:0060284 | regulation of cell development | 571 | 0.300530 | 0.032151 | 0.271883 | 0.240887 |
| GO:0048468 | cell development | 1238 | 0.292691 | 0.004119 | 0.129733 | 0.114943 |
| GO:0030154 | cell differentiation | 2110 | 0.281885 | 0.003021 | 0.118967 | 0.105404 |
| GO:0030098 | lymphocyte differentiation | 174 | -0.315727 | 0.022523 | 0.239322 | 0.212038 |
| GO:0045446 | endothelial cell differentiation | 56 | -0.458875 | 0.005952 | 0.152968 | 0.135528 |
| GO:0045879 | negative regulation of smoothened signaling pathway | 20 | 0.646827 | 0.007776 | 0.159963 | 0.141726 |
| GO:0008589 | regulation of smoothened signaling pathway | 45 | 0.458945 | 0.044444 | 0.300865 | 0.266565 |
| GO:0007224 | smoothened signaling pathway | 78 | 0.435319 | 0.020718 | 0.234852 | 0.208077 |
| GO:0002683 | negative regulation of immune system process | 207 | 0.345583 | 0.036849 | 0.279295 | 0.247453 |
| GO:0002366 | leukocyte activation involved in immune response | 109 | -0.331818 | 0.041199 | 0.294193 | 0.260653 |
| GO:0002263 | cell activation involved in immune response | 111 | -0.338537 | 0.029851 | 0.262868 | 0.232899 |
| GO:0002699 | positive regulation of immune effector process | 81 | -0.384430 | 0.020408 | 0.234020 | 0.207340 |
| GO:0033006 | regulation of mast cell activation involved in immune response | 18 | -0.674373 | 0.009756 | 0.175492 | 0.155485 |
| GO:0006954 | inflammatory response | 239 | -0.298211 | 0.010811 | 0.185707 | 0.164535 |
| GO:0050727 | regulation of inflammatory response | 122 | -0.360561 | 0.011765 | 0.193796 | 0.171702 |
| GO:0050728 | negative regulation of inflammatory response | 55 | -0.435447 | 0.016026 | 0.222347 | 0.196998 |
| GO:0045087 | innate immune response | 237 | -0.274218 | 0.041885 | 0.295986 | 0.262242 |
| GO:0030101 | natural killer cell activation | 35 | -0.517201 | 0.017442 | 0.225028 | 0.199373 |
| GO:0002323 | natural killer cell activation involved in immune response | 12 | -0.712503 | 0.020202 | 0.234020 | 0.207340 |
| GO:0001779 | natural killer cell differentiation | 19 | -0.719148 | 0.002564 | 0.118967 | 0.105404 |
| GO:0033198 | response to ATP | 11 | 0.783687 | 0.001667 | 0.109626 | 0.097128 |
| GO:0070875 | positive regulation of glycogen metabolic process | 12 | 0.779886 | 0.003484 | 0.121143 | 0.107332 |
| GO:0032369 | negative regulation of lipid transport | 17 | 0.754017 | 0.001623 | 0.109626 | 0.097128 |
| GO:0000097 | sulfur amino acid biosynthetic process | 12 | 0.724314 | 0.003656 | 0.126114 | 0.111736 |
| GO:0006730 | one-carbon metabolic process | 18 | 0.695767 | 0.004926 | 0.139927 | 0.123975 |
| GO:0005979 | regulation of glycogen biosynthetic process | 17 | 0.694112 | 0.006579 | 0.152968 | 0.135528 |
| GO:0010962 | regulation of glucan biosynthetic process | 17 | 0.694112 | 0.006579 | 0.152968 | 0.135528 |
| GO:0000096 | sulfur amino acid metabolic process | 23 | 0.692930 | 0.001678 | 0.109626 | 0.097128 |
| GO:0009069 | serine family amino acid metabolic process | 24 | 0.687342 | 0.001621 | 0.109626 | 0.097128 |
| GO:0006760 | folic acid-containing compound metabolic process | 14 | 0.674568 | 0.008711 | 0.167942 | 0.148795 |
| GO:0046189 | phenol-containing compound biosynthetic process | 16 | 0.651247 | 0.012821 | 0.204095 | 0.180827 |
| GO:0005978 | glycogen biosynthetic process | 26 | 0.633055 | 0.006431 | 0.152968 | 0.135528 |
| GO:0009250 | glucan biosynthetic process | 26 | 0.633055 | 0.006431 | 0.152968 | 0.135528 |
| GO:0042987 | amyloid precursor protein catabolic process | 16 | 0.628124 | 0.048622 | 0.313056 | 0.277365 |
| GO:0032885 | regulation of polysaccharide biosynthetic process | 22 | 0.626591 | 0.008052 | 0.159963 | 0.141726 |
| GO:0006536 | glutamate metabolic process | 17 | 0.624769 | 0.025765 | 0.249741 | 0.221269 |
| GO:0042398 | cellular modified amino acid biosynthetic process | 28 | 0.623506 | 0.002915 | 0.118967 | 0.105404 |
| GO:0019369 | arachidonic acid metabolic process | 19 | 0.605406 | 0.030695 | 0.264984 | 0.234774 |
| GO:0015909 | long-chain fatty acid transport | 27 | 0.604248 | 0.009360 | 0.174593 | 0.154688 |
| GO:0009066 | aspartate family amino acid metabolic process | 26 | 0.601254 | 0.016556 | 0.223705 | 0.198201 |
| GO:0005977 | glycogen metabolic process | 47 | 0.587240 | 0.003058 | 0.118967 | 0.105404 |
| GO:0006073 | cellular glucan metabolic process | 47 | 0.587240 | 0.003058 | 0.118967 | 0.105404 |
| GO:0044042 | glucan metabolic process | 47 | 0.587240 | 0.003058 | 0.118967 | 0.105404 |
| GO:0010907 | positive regulation of glucose metabolic process | 27 | 0.586019 | 0.010870 | 0.185981 | 0.164778 |
| GO:0001523 | retinoid metabolic process | 23 | 0.584412 | 0.030063 | 0.263086 | 0.233092 |
| GO:0070873 | regulation of glycogen metabolic process | 21 | 0.583948 | 0.029921 | 0.262868 | 0.232899 |
| GO:0008652 | cellular amino acid biosynthetic process | 46 | 0.571938 | 0.003200 | 0.118967 | 0.105404 |
| GO:0006112 | energy reserve metabolic process | 52 | 0.564442 | 0.003067 | 0.118967 | 0.105404 |
| GO:0016101 | diterpenoid metabolic process | 25 | 0.561456 | 0.041074 | 0.294084 | 0.260556 |
| GO:1901607 | alpha-amino acid biosynthetic process | 44 | 0.548977 | 0.004847 | 0.139490 | 0.123587 |
| GO:0001676 | long-chain fatty acid metabolic process | 39 | 0.546610 | 0.007519 | 0.159963 | 0.141726 |
| GO:0032881 | regulation of polysaccharide metabolic process | 26 | 0.527441 | 0.049521 | 0.313728 | 0.277961 |
| GO:0044275 | cellular carbohydrate catabolic process | 35 | 0.521635 | 0.028846 | 0.260782 | 0.231051 |
| GO:0044264 | cellular polysaccharide metabolic process | 53 | 0.513917 | 0.012158 | 0.197160 | 0.174682 |
| GO:0009063 | cellular amino acid catabolic process | 42 | 0.507009 | 0.018045 | 0.226659 | 0.200818 |
| GO:0033692 | cellular polysaccharide biosynthetic process | 32 | 0.503772 | 0.049521 | 0.313728 | 0.277961 |
| GO:0034754 | cellular hormone metabolic process | 39 | 0.496881 | 0.027607 | 0.256065 | 0.226872 |
| GO:0005976 | polysaccharide metabolic process | 61 | 0.490149 | 0.009050 | 0.170261 | 0.150850 |
| GO:0000271 | polysaccharide biosynthetic process | 40 | 0.482920 | 0.033742 | 0.274809 | 0.243479 |
| GO:0016053 | organic acid biosynthetic process | 154 | 0.480853 | 0.001368 | 0.109626 | 0.097128 |
| GO:0046394 | carboxylic acid biosynthetic process | 154 | 0.480853 | 0.001368 | 0.109626 | 0.097128 |
| GO:0043467 | regulation of generation of precursor metabolites and energy | 57 | 0.476750 | 0.010654 | 0.185707 | 0.164535 |
| GO:1901605 | alpha-amino acid metabolic process | 124 | 0.463974 | 0.002770 | 0.118967 | 0.105404 |
| GO:0042445 | hormone metabolic process | 77 | 0.456814 | 0.007133 | 0.157578 | 0.139613 |
| GO:0006091 | generation of precursor metabolites and energy | 205 | 0.419281 | 0.001253 | 0.109626 | 0.097128 |
| GO:0044724 | single-organism carbohydrate catabolic process | 70 | 0.419000 | 0.046407 | 0.307613 | 0.272543 |
| GO:0006575 | cellular modified amino acid metabolic process | 115 | 0.417782 | 0.008197 | 0.159963 | 0.141726 |
| GO:0006633 | fatty acid biosynthetic process | 88 | 0.414313 | 0.029586 | 0.262868 | 0.232899 |
| GO:0046034 | ATP metabolic process | 128 | 0.395278 | 0.006579 | 0.152968 | 0.135528 |
| GO:0015980 | energy derivation by oxidation of organic compounds | 152 | 0.385569 | 0.011643 | 0.193796 | 0.171702 |
| GO:0006631 | fatty acid metabolic process | 213 | 0.385058 | 0.003745 | 0.127643 | 0.113091 |
| GO:0033500 | carbohydrate homeostasis | 123 | 0.382243 | 0.034247 | 0.276646 | 0.245107 |
| GO:0042593 | glucose homeostasis | 123 | 0.382243 | 0.034247 | 0.276646 | 0.245107 |
| GO:0009144 | purine nucleoside triphosphate metabolic process | 142 | 0.375993 | 0.017083 | 0.224465 | 0.198875 |
| GO:0032787 | monocarboxylic acid metabolic process | 320 | 0.374611 | 0.001186 | 0.109626 | 0.097128 |
| GO:0009205 | purine ribonucleoside triphosphate metabolic process | 137 | 0.373982 | 0.019815 | 0.234020 | 0.207340 |
| GO:0044283 | small molecule biosynthetic process | 275 | 0.365115 | 0.001215 | 0.109626 | 0.097128 |
| GO:0044262 | cellular carbohydrate metabolic process | 171 | 0.362748 | 0.023196 | 0.241946 | 0.214363 |
| GO:0043436 | oxoacid metabolic process | 541 | 0.357864 | 0.001125 | 0.109626 | 0.097128 |
| GO:0006082 | organic acid metabolic process | 547 | 0.355431 | 0.001121 | 0.109626 | 0.097128 |
| GO:0009126 | purine nucleoside monophosphate metabolic process | 145 | 0.353106 | 0.049351 | 0.313728 | 0.277961 |
| GO:0009167 | purine ribonucleoside monophosphate metabolic process | 145 | 0.353106 | 0.049351 | 0.313728 | 0.277961 |
| GO:0046128 | purine ribonucleoside metabolic process | 187 | 0.343090 | 0.030730 | 0.264984 | 0.234774 |
| GO:0042278 | purine nucleoside metabolic process | 190 | 0.338252 | 0.040455 | 0.293030 | 0.259623 |
| GO:1901615 | organic hydroxy compound metabolic process | 248 | 0.329523 | 0.046972 | 0.308282 | 0.273136 |
| GO:0006163 | purine nucleotide metabolic process | 265 | 0.328535 | 0.035409 | 0.279295 | 0.247453 |
| GO:0044255 | cellular lipid metabolic process | 516 | 0.308204 | 0.015608 | 0.220084 | 0.194993 |
| GO:0055114 | oxidation-reduction process | 569 | 0.307723 | 0.011086 | 0.188948 | 0.167407 |
| GO:0044281 | small molecule metabolic process | 1069 | 0.301209 | 0.003058 | 0.118967 | 0.105404 |
| GO:0044712 | single-organism catabolic process | 639 | 0.287745 | 0.043337 | 0.299896 | 0.265705 |
| GO:1901564 | organonitrogen compound metabolic process | 1145 | 0.275607 | 0.043887 | 0.299896 | 0.265705 |
| GO:0051882 | mitochondrial depolarization | 12 | 0.684283 | 0.028862 | 0.260782 | 0.231051 |
| GO:0050768 | negative regulation of neurogenesis | 168 | 0.412696 | 0.001274 | 0.109626 | 0.097128 |
| GO:0007249 | I-kappaB kinase/NF-kappaB signaling | 145 | -0.329701 | 0.020492 | 0.234020 | 0.207340 |
| GO:0043122 | regulation of I-kappaB kinase/NF-kappaB signaling | 130 | -0.332431 | 0.031373 | 0.267869 | 0.237330 |
| GO:0043123 | positive regulation of I-kappaB kinase/NF-kappaB signaling | 95 | -0.349068 | 0.037671 | 0.280341 | 0.248380 |
| GO:0060045 | positive regulation of cardiac muscle cell proliferation | 12 | 0.772195 | 0.004894 | 0.139927 | 0.123975 |
| GO:0060043 | regulation of cardiac muscle cell proliferation | 18 | 0.686751 | 0.003190 | 0.118967 | 0.105404 |
| GO:0060038 | cardiac muscle cell proliferation | 27 | 0.620892 | 0.003030 | 0.118967 | 0.105404 |
| GO:0014855 | striated muscle cell proliferation | 35 | 0.516429 | 0.029630 | 0.262868 | 0.232899 |
| GO:0007405 | neuroblast proliferation | 39 | 0.498236 | 0.045181 | 0.303956 | 0.269303 |
| GO:2000648 | positive regulation of stem cell proliferation | 43 | 0.481641 | 0.045994 | 0.307613 | 0.272543 |
| GO:0072091 | regulation of stem cell proliferation | 69 | 0.418614 | 0.050000 | 0.315385 | 0.279429 |
| GO:0008284 | positive regulation of cell proliferation | 468 | 0.304802 | 0.029050 | 0.261534 | 0.231717 |
| GO:0001936 | regulation of endothelial cell proliferation | 59 | -0.389424 | 0.035928 | 0.279295 | 0.247453 |
| GO:0001935 | endothelial cell proliferation | 68 | -0.441492 | 0.003058 | 0.118967 | 0.105404 |
| GO:0071157 | negative regulation of cell cycle arrest | 11 | -0.658353 | 0.042929 | 0.299173 | 0.265065 |
| GO:0071425 | hematopoietic stem cell proliferation | 13 | -0.659311 | 0.020101 | 0.234020 | 0.207340 |
| GO:0042246 | tissue regeneration | 21 | -0.668192 | 0.002427 | 0.118967 | 0.105404 |
| GO:0051341 | regulation of oxidoreductase activity | 32 | -0.486537 | 0.021390 | 0.236251 | 0.209316 |
| GO:0048103 | somatic stem cell division | 13 | 0.646127 | 0.048544 | 0.313013 | 0.277328 |
| GO:1901032 | negative regulation of response to reactive oxygen species | 14 | 0.706784 | 0.011804 | 0.193796 | 0.171702 |
| GO:1903206 | negative regulation of hydrogen peroxide-induced cell death | 14 | 0.706784 | 0.011804 | 0.193796 | 0.171702 |
| GO:0036474 | cell death in response to hydrogen peroxide | 19 | 0.585608 | 0.039669 | 0.289849 | 0.256804 |
| GO:2001239 | regulation of extrinsic apoptotic signaling pathway in absence of ligand | 29 | 0.571524 | 0.020408 | 0.234020 | 0.207340 |
| GO:0043525 | positive regulation of neuron apoptotic process | 52 | 0.445523 | 0.035661 | 0.279295 | 0.247453 |
| GO:0043523 | regulation of neuron apoptotic process | 162 | 0.433942 | 0.001295 | 0.109626 | 0.097128 |
| GO:0051402 | neuron apoptotic process | 178 | 0.433657 | 0.001274 | 0.109626 | 0.097128 |
| GO:0043524 | negative regulation of neuron apoptotic process | 109 | 0.423724 | 0.009485 | 0.175414 | 0.155415 |
| GO:1901215 | negative regulation of neuron death | 133 | 0.410709 | 0.005284 | 0.145344 | 0.128774 |
| GO:0070997 | neuron death | 232 | 0.396502 | 0.002445 | 0.118967 | 0.105404 |
| GO:1901214 | regulation of neuron death | 208 | 0.396040 | 0.002525 | 0.118967 | 0.105404 |
| GO:0097285 | cell-type specific apoptotic process | 332 | 0.324379 | 0.038005 | 0.282340 | 0.250151 |
| GO:0012501 | programmed cell death | 1121 | 0.282899 | 0.027778 | 0.256310 | 0.227089 |
| GO:0008219 | cell death | 1203 | 0.279483 | 0.027692 | 0.256065 | 0.226872 |
| GO:0006915 | apoptotic process | 1103 | 0.278201 | 0.040206 | 0.292201 | 0.258888 |
| GO:0016265 | death | 1208 | 0.276876 | 0.040984 | 0.293919 | 0.260410 |
| GO:0006952 | defense response | 576 | -0.244549 | 0.033708 | 0.274809 | 0.243479 |
| GO:0009611 | response to wounding | 337 | -0.336415 | 0.006452 | 0.152968 | 0.135528 |
| GO:1903034 | regulation of response to wounding | 194 | -0.338573 | 0.005102 | 0.143055 | 0.126745 |
| GO:0061041 | regulation of wound healing | 65 | -0.413892 | 0.006079 | 0.152968 | 0.135528 |
| GO:0042060 | wound healing | 183 | -0.420141 | 0.004405 | 0.134827 | 0.119455 |
| GO:1903035 | negative regulation of response to wounding | 85 | -0.460736 | 0.003367 | 0.118967 | 0.105404 |
| GO:0072577 | endothelial cell apoptotic process | 29 | -0.509288 | 0.016575 | 0.223705 | 0.198201 |
| GO:0061045 | negative regulation of wound healing | 31 | -0.543346 | 0.008130 | 0.159963 | 0.141726 |
| GO:0006826 | iron ion transport | 19 | -0.549616 | 0.037572 | 0.280084 | 0.248153 |
| GO:0034405 | response to fluid shear stress | 17 | -0.553943 | 0.047847 | 0.311291 | 0.275802 |
| GO:0071498 | cellular response to fluid shear stress | 11 | -0.716190 | 0.012500 | 0.200461 | 0.177607 |
| GO:0071634 | regulation of transforming growth factor beta production | 13 | 0.644243 | 0.047468 | 0.309871 | 0.274544 |
| GO:0010574 | regulation of vascular endothelial growth factor production | 16 | 0.741083 | 0.003241 | 0.118967 | 0.105404 |
| GO:0010575 | positive regulation of vascular endothelial growth factor production | 12 | 0.674156 | 0.048253 | 0.312010 | 0.276438 |
| GO:0035924 | cellular response to vascular endothelial growth factor stimulus | 27 | -0.473551 | 0.046392 | 0.307613 | 0.272543 |
| GO:0048010 | vascular endothelial growth factor receptor signaling pathway | 33 | -0.522204 | 0.014925 | 0.219139 | 0.194155 |
| GO:0060828 | regulation of canonical Wnt signaling pathway | 115 | 0.397765 | 0.028378 | 0.258018 | 0.228602 |
| GO:0030111 | regulation of Wnt signaling pathway | 162 | 0.371869 | 0.018373 | 0.228737 | 0.202659 |
| GO:0019228 | neuronal action potential | 11 | 0.940834 | 0.001577 | 0.109626 | 0.097128 |
| GO:0006336 | DNA replication-independent nucleosome assembly | 22 | 0.827916 | 0.001626 | 0.109626 | 0.097128 |
| GO:0034724 | DNA replication-independent nucleosome organization | 22 | 0.827916 | 0.001626 | 0.109626 | 0.097128 |
| GO:0048820 | hair follicle maturation | 12 | 0.816456 | 0.001629 | 0.109626 | 0.097128 |
| GO:0010863 | positive regulation of phospholipase C activity | 15 | 0.764708 | 0.001608 | 0.109626 | 0.097128 |
| GO:0014046 | dopamine secretion | 12 | 0.760179 | 0.006678 | 0.152968 | 0.135528 |
| GO:0014059 | regulation of dopamine secretion | 12 | 0.760179 | 0.006678 | 0.152968 | 0.135528 |
| GO:0031128 | developmental induction | 19 | 0.758390 | 0.001541 | 0.109626 | 0.097128 |
| GO:0060602 | branch elongation of an epithelium | 11 | 0.732041 | 0.015306 | 0.219139 | 0.194155 |
| GO:0090075 | relaxation of muscle | 15 | 0.726368 | 0.003333 | 0.118967 | 0.105404 |
| GO:0010800 | positive regulation of peptidyl-threonine phosphorylation | 12 | 0.724559 | 0.004992 | 0.140869 | 0.124809 |
| GO:0050860 | negative regulation of T cell receptor signaling pathway | 11 | 0.722675 | 0.020548 | 0.234020 | 0.207340 |
| GO:0061323 | cell proliferation involved in heart morphogenesis | 11 | 0.722521 | 0.030351 | 0.264343 | 0.234206 |
| GO:2000136 | regulation of cell proliferation involved in heart morphogenesis | 11 | 0.722521 | 0.030351 | 0.264343 | 0.234206 |
| GO:0060413 | atrial septum morphogenesis | 11 | 0.716102 | 0.026846 | 0.254059 | 0.225095 |
| GO:0001504 | neurotransmitter uptake | 12 | 0.708680 | 0.017799 | 0.225028 | 0.199373 |
| GO:0050858 | negative regulation of antigen receptor-mediated signaling pathway | 12 | 0.702147 | 0.018771 | 0.230453 | 0.204179 |
| GO:0006335 | DNA replication-dependent nucleosome assembly | 27 | 0.697140 | 0.001585 | 0.109626 | 0.097128 |
| GO:0034723 | DNA replication-dependent nucleosome organization | 27 | 0.697140 | 0.001585 | 0.109626 | 0.097128 |
| GO:0015800 | acidic amino acid transport | 12 | 0.688242 | 0.026711 | 0.254059 | 0.225095 |
| GO:0050974 | detection of mechanical stimulus involved in sensory perception | 15 | 0.688118 | 0.016835 | 0.224465 | 0.198875 |
| GO:0003009 | skeletal muscle contraction | 16 | 0.687451 | 0.006723 | 0.152968 | 0.135528 |
| GO:0019226 | transmission of nerve impulse | 29 | 0.680915 | 0.001495 | 0.109626 | 0.097128 |
| GO:0021697 | cerebellar cortex formation | 15 | 0.680898 | 0.015699 | 0.220084 | 0.194993 |
| GO:0048247 | lymphocyte chemotaxis | 11 | 0.679221 | 0.043478 | 0.299896 | 0.265705 |
| GO:0035640 | exploration behavior | 14 | 0.677079 | 0.016313 | 0.222347 | 0.196998 |
| GO:0010518 | positive regulation of phospholipase activity | 25 | 0.676712 | 0.001541 | 0.109626 | 0.097128 |
| GO:0042220 | response to cocaine | 13 | 0.675056 | 0.021311 | 0.236251 | 0.209316 |
| GO:0014003 | oligodendrocyte development | 22 | 0.672718 | 0.001616 | 0.109626 | 0.097128 |
| GO:0010092 | specification of organ identity | 11 | 0.669344 | 0.049751 | 0.314272 | 0.278443 |
| GO:0015872 | dopamine transport | 18 | 0.668751 | 0.009772 | 0.175492 | 0.155485 |
| GO:0031646 | positive regulation of neurological system process | 11 | 0.668477 | 0.042955 | 0.299173 | 0.265065 |
| GO:0003401 | axis elongation | 19 | 0.667486 | 0.006557 | 0.152968 | 0.135528 |
| GO:0003341 | cilium movement | 21 | 0.665175 | 0.003252 | 0.118967 | 0.105404 |
| GO:1900078 | positive regulation of cellular response to insulin stimulus | 13 | 0.663589 | 0.029126 | 0.261534 | 0.231717 |
| GO:0007129 | synapsis | 11 | 0.663100 | 0.041293 | 0.294193 | 0.260653 |
| GO:0050433 | regulation of catecholamine secretion | 24 | 0.654065 | 0.001572 | 0.109626 | 0.097128 |
| GO:2000826 | regulation of heart morphogenesis | 16 | 0.653776 | 0.018898 | 0.230700 | 0.204398 |
| GO:1903205 | regulation of hydrogen peroxide-induced cell death | 17 | 0.649870 | 0.023179 | 0.241946 | 0.214363 |
| GO:0016339 | calcium-dependent cell-cell adhesion via plasma membrane cell adhesion molecules | 13 | 0.649509 | 0.041600 | 0.294932 | 0.261308 |
| GO:0010573 | vascular endothelial growth factor production | 17 | 0.649299 | 0.020767 | 0.234852 | 0.208077 |
| GO:0033057 | multicellular organismal reproductive behavior | 17 | 0.646366 | 0.018033 | 0.226659 | 0.200818 |
| GO:1900274 | regulation of phospholipase C activity | 17 | 0.645731 | 0.020281 | 0.234020 | 0.207340 |
| GO:0044848 | biological phase | 21 | 0.640247 | 0.014446 | 0.217243 | 0.192476 |
| GO:0035411 | catenin import into nucleus | 19 | 0.637547 | 0.017685 | 0.225028 | 0.199373 |
| GO:0010799 | regulation of peptidyl-threonine phosphorylation | 20 | 0.634106 | 0.009677 | 0.175492 | 0.155485 |
| GO:0055023 | positive regulation of cardiac muscle tissue growth | 17 | 0.630285 | 0.021242 | 0.236105 | 0.209187 |
| GO:0035115 | embryonic forelimb morphogenesis | 17 | 0.628785 | 0.025765 | 0.249741 | 0.221269 |
| GO:0060972 | left/right pattern formation | 17 | 0.626687 | 0.026891 | 0.254059 | 0.225095 |
| GO:0021535 | cell migration in hindbrain | 14 | 0.624909 | 0.035370 | 0.279295 | 0.247453 |
| GO:0010517 | regulation of phospholipase activity | 31 | 0.624321 | 0.001531 | 0.109626 | 0.097128 |
| GO:0050885 | neuromuscular process controlling balance | 44 | 0.622767 | 0.003030 | 0.118967 | 0.105404 |
| GO:0050432 | catecholamine secretion | 27 | 0.622310 | 0.003155 | 0.118967 | 0.105404 |
| GO:0060512 | prostate gland morphogenesis | 17 | 0.620162 | 0.031826 | 0.270146 | 0.239348 |
| GO:0060740 | prostate gland epithelium morphogenesis | 17 | 0.620162 | 0.031826 | 0.270146 | 0.239348 |
| GO:0021904 | dorsal/ventral neural tube patterning | 22 | 0.620007 | 0.020570 | 0.234020 | 0.207340 |
| GO:0021587 | cerebellum morphogenesis | 31 | 0.618158 | 0.001504 | 0.109626 | 0.097128 |
| GO:0060421 | positive regulation of heart growth | 18 | 0.614355 | 0.035058 | 0.279295 | 0.247453 |
| GO:0046850 | regulation of bone remodeling | 21 | 0.613046 | 0.025039 | 0.247882 | 0.219621 |
| GO:0035136 | forelimb morphogenesis | 22 | 0.609520 | 0.012384 | 0.199335 | 0.176609 |
| GO:1903792 | negative regulation of anion transport | 16 | 0.609144 | 0.040783 | 0.293919 | 0.260410 |
| GO:0001941 | postsynaptic membrane organization | 16 | 0.608591 | 0.043551 | 0.299896 | 0.265705 |
| GO:0021983 | pituitary gland development | 18 | 0.607629 | 0.033493 | 0.274742 | 0.243420 |
| GO:0035082 | axoneme assembly | 19 | 0.604926 | 0.026756 | 0.254059 | 0.225095 |
| GO:0051290 | protein heterotetramerization | 28 | 0.599519 | 0.003155 | 0.118967 | 0.105404 |
| GO:0021696 | cerebellar cortex morphogenesis | 22 | 0.599237 | 0.020313 | 0.234020 | 0.207340 |
| GO:0045124 | regulation of bone resorption | 19 | 0.598726 | 0.046326 | 0.307613 | 0.272543 |
| GO:0003254 | regulation of membrane depolarization | 22 | 0.590923 | 0.023438 | 0.241946 | 0.214363 |
| GO:0031644 | regulation of neurological system process | 37 | 0.588346 | 0.003030 | 0.118967 | 0.105404 |
| GO:0045823 | positive regulation of heart contraction | 19 | 0.587089 | 0.039872 | 0.290463 | 0.257348 |
| GO:0090329 | regulation of DNA-dependent DNA replication | 19 | 0.586541 | 0.029126 | 0.261534 | 0.231717 |
| GO:0003156 | regulation of organ formation | 17 | 0.586195 | 0.047923 | 0.311323 | 0.275830 |
| GO:0051937 | catecholamine transport | 34 | 0.584825 | 0.004573 | 0.135462 | 0.120019 |
| GO:0007628 | adult walking behavior | 27 | 0.584820 | 0.006421 | 0.152968 | 0.135528 |
| GO:0090659 | walking behavior | 27 | 0.584820 | 0.006421 | 0.152968 | 0.135528 |
| GO:0035637 | multicellular organismal signaling | 47 | 0.580484 | 0.001458 | 0.109626 | 0.097128 |
| GO:0051954 | positive regulation of amine transport | 24 | 0.580080 | 0.022187 | 0.237876 | 0.210757 |
| GO:0021575 | hindbrain morphogenesis | 33 | 0.578012 | 0.004559 | 0.135462 | 0.120019 |
| GO:0055021 | regulation of cardiac muscle tissue growth | 26 | 0.576510 | 0.011182 | 0.189473 | 0.167872 |
| GO:0045744 | negative regulation of G-protein coupled receptor protein signaling pathway | 19 | 0.576055 | 0.046589 | 0.307613 | 0.272543 |
| GO:0042558 | pteridine-containing compound metabolic process | 18 | 0.575186 | 0.043403 | 0.299896 | 0.265705 |
| GO:0015844 | monoamine transport | 42 | 0.575117 | 0.004392 | 0.134827 | 0.119455 |
| GO:0035176 | social behavior | 25 | 0.574016 | 0.016129 | 0.222347 | 0.196998 |
| GO:0051703 | intraspecies interaction between organisms | 25 | 0.574016 | 0.016129 | 0.222347 | 0.196998 |
| GO:0048011 | neurotrophin TRK receptor signaling pathway | 21 | 0.568391 | 0.039683 | 0.289849 | 0.256804 |
| GO:0034103 | regulation of tissue remodeling | 33 | 0.568383 | 0.006107 | 0.152968 | 0.135528 |
| GO:0021532 | neural tube patterning | 33 | 0.565473 | 0.009245 | 0.173184 | 0.153440 |
| GO:1903053 | regulation of extracellular matrix organization | 21 | 0.562775 | 0.049505 | 0.313728 | 0.277961 |
| GO:0032892 | positive regulation of organic acid transport | 20 | 0.561029 | 0.048110 | 0.311603 | 0.276079 |
| GO:0051705 | multi-organism behavior | 54 | 0.556096 | 0.001515 | 0.109626 | 0.097128 |
| GO:0051952 | regulation of amine transport | 39 | 0.547790 | 0.007740 | 0.159963 | 0.141726 |
| GO:0060193 | positive regulation of lipase activity | 34 | 0.544528 | 0.016820 | 0.224465 | 0.198875 |
| GO:0050905 | neuromuscular process | 71 | 0.541778 | 0.001481 | 0.109626 | 0.097128 |
| GO:1901606 | alpha-amino acid catabolic process | 32 | 0.538135 | 0.024578 | 0.246116 | 0.218057 |
| GO:0015837 | amine transport | 41 | 0.533502 | 0.015480 | 0.219139 | 0.194155 |
| GO:0001658 | branching involved in ureteric bud morphogenesis | 31 | 0.530023 | 0.029940 | 0.262868 | 0.232899 |
| GO:0060042 | retina morphogenesis in camera-type eye | 32 | 0.527885 | 0.030534 | 0.264814 | 0.234623 |
| GO:0060411 | cardiac septum morphogenesis | 36 | 0.522704 | 0.023256 | 0.241946 | 0.214363 |
| GO:0006334 | nucleosome assembly | 73 | 0.521990 | 0.002849 | 0.118967 | 0.105404 |
| GO:0046849 | bone remodeling | 37 | 0.517141 | 0.025836 | 0.249741 | 0.221269 |
| GO:0060675 | ureteric bud morphogenesis | 32 | 0.515788 | 0.031250 | 0.267347 | 0.236868 |
| GO:0072171 | mesonephric tubule morphogenesis | 33 | 0.515164 | 0.028148 | 0.257515 | 0.228156 |
| GO:0034728 | nucleosome organization | 94 | 0.510488 | 0.002762 | 0.118967 | 0.105404 |
| GO:0030534 | adult behavior | 94 | 0.509869 | 0.001362 | 0.109626 | 0.097128 |
| GO:0033619 | membrane protein proteolysis | 32 | 0.509569 | 0.045016 | 0.303318 | 0.268737 |
| GO:0007626 | locomotory behavior | 135 | 0.507726 | 0.001316 | 0.109626 | 0.097128 |
| GO:0030330 | DNA damage response, signal transduction by p53 class mediator | 36 | 0.507575 | 0.038585 | 0.285189 | 0.252676 |
| GO:1903793 | positive regulation of anion transport | 38 | 0.507522 | 0.027157 | 0.255460 | 0.226336 |
| GO:0044070 | regulation of anion transport | 71 | 0.502484 | 0.001486 | 0.109626 | 0.097128 |
| GO:0009953 | dorsal/ventral pattern formation | 62 | 0.500923 | 0.005831 | 0.152968 | 0.135528 |
| GO:0031497 | chromatin assembly | 84 | 0.500630 | 0.001406 | 0.109626 | 0.097128 |
| GO:0072078 | nephron tubule morphogenesis | 35 | 0.499838 | 0.042360 | 0.297891 | 0.263930 |
| GO:0046717 | acid secretion | 46 | 0.497074 | 0.013761 | 0.211333 | 0.187240 |
| GO:0008344 | adult locomotory behavior | 63 | 0.496881 | 0.007123 | 0.157578 | 0.139613 |
| GO:0035107 | appendage morphogenesis | 93 | 0.495949 | 0.002789 | 0.118967 | 0.105404 |
| GO:0035108 | limb morphogenesis | 93 | 0.495949 | 0.002789 | 0.118967 | 0.105404 |
| GO:1900076 | regulation of cellular response to insulin stimulus | 42 | 0.493902 | 0.023881 | 0.245202 | 0.217248 |
| GO:0007215 | glutamate receptor signaling pathway | 35 | 0.493523 | 0.036641 | 0.279295 | 0.247453 |
| GO:0035725 | sodium ion transmembrane transport | 61 | 0.488356 | 0.007289 | 0.158286 | 0.140240 |
| GO:0060349 | bone morphogenesis | 51 | 0.488138 | 0.015221 | 0.219139 | 0.194155 |
| GO:0051588 | regulation of neurotransmitter transport | 44 | 0.486947 | 0.030882 | 0.265772 | 0.235472 |
| GO:0072028 | nephron morphogenesis | 38 | 0.479699 | 0.045317 | 0.304403 | 0.269699 |
| GO:0017156 | calcium ion-dependent exocytosis | 41 | 0.479566 | 0.044586 | 0.301354 | 0.266998 |
| GO:0018107 | peptidyl-threonine phosphorylation | 53 | 0.479031 | 0.015432 | 0.219139 | 0.194155 |
| GO:0001508 | action potential | 48 | 0.478186 | 0.032999 | 0.273687 | 0.242484 |
| GO:0018210 | peptidyl-threonine modification | 56 | 0.475453 | 0.010654 | 0.185707 | 0.164535 |
| GO:0006333 | chromatin assembly or disassembly | 101 | 0.472639 | 0.002774 | 0.118967 | 0.105404 |
| GO:0001942 | hair follicle development | 51 | 0.471499 | 0.022189 | 0.237876 | 0.210757 |
| GO:0022404 | molting cycle process | 51 | 0.471499 | 0.022189 | 0.237876 | 0.210757 |
| GO:0022405 | hair cycle process | 51 | 0.471499 | 0.022189 | 0.237876 | 0.210757 |
| GO:0098773 | skin epidermis development | 52 | 0.471444 | 0.022026 | 0.237876 | 0.210757 |
| GO:0006939 | smooth muscle contraction | 47 | 0.470555 | 0.024781 | 0.247342 | 0.219143 |
| GO:0006835 | dicarboxylic acid transport | 42 | 0.469379 | 0.024961 | 0.247882 | 0.219621 |
| GO:0048704 | embryonic skeletal system morphogenesis | 55 | 0.465554 | 0.019090 | 0.231741 | 0.205321 |
| GO:0072330 | monocarboxylic acid biosynthetic process | 110 | 0.462793 | 0.002899 | 0.118967 | 0.105404 |
| GO:0071824 | protein-DNA complex subunit organization | 132 | 0.462031 | 0.001325 | 0.109626 | 0.097128 |
| GO:0065004 | protein-DNA complex assembly | 110 | 0.462014 | 0.002751 | 0.118967 | 0.105404 |
| GO:0042490 | mechanoreceptor differentiation | 43 | 0.461516 | 0.044709 | 0.301719 | 0.267321 |
| GO:0051262 | protein tetramerization | 99 | 0.456661 | 0.001425 | 0.109626 | 0.097128 |
| GO:0019233 | sensory perception of pain | 53 | 0.453852 | 0.043609 | 0.299896 | 0.265705 |
| GO:0030326 | embryonic limb morphogenesis | 78 | 0.453708 | 0.007072 | 0.157578 | 0.139613 |
| GO:0035113 | embryonic appendage morphogenesis | 78 | 0.453708 | 0.007072 | 0.157578 | 0.139613 |
| GO:0055067 | monovalent inorganic cation homeostasis | 71 | 0.451478 | 0.015692 | 0.220084 | 0.194993 |
| GO:0006941 | striated muscle contraction | 63 | 0.446122 | 0.019034 | 0.231710 | 0.205293 |
| GO:0032846 | positive regulation of homeostatic process | 90 | 0.446061 | 0.008475 | 0.164422 | 0.145677 |
| GO:0006836 | neurotransmitter transport | 113 | 0.445921 | 0.002725 | 0.118967 | 0.105404 |
| GO:0050806 | positive regulation of synaptic transmission | 84 | 0.445286 | 0.007321 | 0.158286 | 0.140240 |
| GO:0042303 | molting cycle | 57 | 0.441075 | 0.027656 | 0.256065 | 0.226872 |
| GO:0042633 | hair cycle | 57 | 0.441075 | 0.027656 | 0.256065 | 0.226872 |
| GO:0050804 | modulation of synaptic transmission | 185 | 0.441066 | 0.001290 | 0.109626 | 0.097128 |
| GO:0006865 | amino acid transport | 66 | 0.438892 | 0.025915 | 0.249741 | 0.221269 |
| GO:0006165 | nucleoside diphosphate phosphorylation | 56 | 0.436911 | 0.044275 | 0.300850 | 0.266551 |
| GO:0021543 | pallium development | 97 | 0.436911 | 0.008208 | 0.159963 | 0.141726 |
| GO:0097479 | synaptic vesicle localization | 86 | 0.436841 | 0.007143 | 0.157578 | 0.139613 |
| GO:0001505 | regulation of neurotransmitter levels | 109 | 0.435727 | 0.002699 | 0.118967 | 0.105404 |
| GO:0007270 | neuron-neuron synaptic transmission | 88 | 0.435413 | 0.015193 | 0.219139 | 0.194155 |
| GO:0008016 | regulation of heart contraction | 81 | 0.434320 | 0.011204 | 0.189473 | 0.167872 |
| GO:0048706 | embryonic skeletal system development | 73 | 0.433607 | 0.024217 | 0.245202 | 0.217248 |
| GO:0019932 | second-messenger-mediated signaling | 106 | 0.432812 | 0.005548 | 0.149757 | 0.132684 |
| GO:0016579 | protein deubiquitination | 70 | 0.432420 | 0.019432 | 0.234020 | 0.207340 |
| GO:0090277 | positive regulation of peptide hormone secretion | 66 | 0.430766 | 0.026125 | 0.250085 | 0.221573 |
| GO:0006520 | cellular amino acid metabolic process | 175 | 0.430688 | 0.001330 | 0.109626 | 0.097128 |
| GO:0048705 | skeletal system morphogenesis | 127 | 0.430634 | 0.004027 | 0.128681 | 0.114011 |
| GO:0098742 | cell-cell adhesion via plasma-membrane adhesion molecules | 67 | 0.428456 | 0.032689 | 0.273090 | 0.241956 |
| GO:0002793 | positive regulation of peptide secretion | 67 | 0.425255 | 0.032164 | 0.271883 | 0.240887 |
| GO:0006323 | DNA packaging | 108 | 0.425228 | 0.011252 | 0.189535 | 0.167927 |
| GO:0021987 | cerebral cortex development | 72 | 0.422769 | 0.032578 | 0.272801 | 0.241700 |
| GO:0048489 | synaptic vesicle transport | 82 | 0.421670 | 0.017143 | 0.224465 | 0.198875 |
| GO:0097480 | establishment of synaptic vesicle localization | 82 | 0.421670 | 0.017143 | 0.224465 | 0.198875 |
| GO:0007601 | visual perception | 77 | 0.421510 | 0.033803 | 0.274809 | 0.243479 |
| GO:0007268 | synaptic transmission | 295 | 0.419920 | 0.001211 | 0.109626 | 0.097128 |
| GO:0050953 | sensory perception of light stimulus | 78 | 0.417729 | 0.036671 | 0.279295 | 0.247453 |
| GO:0007605 | sensory perception of sound | 73 | 0.416454 | 0.046715 | 0.307613 | 0.272543 |
| GO:0048167 | regulation of synaptic plasticity | 91 | 0.416073 | 0.013870 | 0.212244 | 0.188047 |
| GO:0048771 | tissue remodeling | 88 | 0.415980 | 0.030086 | 0.263086 | 0.233092 |
| GO:0042552 | myelination | 75 | 0.414453 | 0.032738 | 0.273090 | 0.241956 |
| GO:0007272 | ensheathment of neurons | 76 | 0.414394 | 0.032496 | 0.272643 | 0.241560 |
| GO:0008366 | axon ensheathment | 76 | 0.414394 | 0.032496 | 0.272643 | 0.241560 |
| GO:0050796 | regulation of insulin secretion | 99 | 0.412627 | 0.023384 | 0.241946 | 0.214363 |
| GO:0050954 | sensory perception of mechanical stimulus | 83 | 0.409691 | 0.048316 | 0.312010 | 0.276438 |
| GO:1903707 | negative regulation of hemopoiesis | 77 | 0.409417 | 0.042254 | 0.297624 | 0.263693 |
| GO:0006936 | muscle contraction | 121 | 0.409095 | 0.004076 | 0.129304 | 0.114563 |
| GO:0097485 | neuron projection guidance | 104 | 0.408147 | 0.015342 | 0.219139 | 0.194155 |
| GO:0050803 | regulation of synapse structure or activity | 148 | 0.405381 | 0.003963 | 0.128681 | 0.114011 |
| GO:0070646 | protein modification by small protein removal | 83 | 0.403990 | 0.029830 | 0.262868 | 0.232899 |
| GO:0006814 | sodium ion transport | 102 | 0.402794 | 0.008186 | 0.159963 | 0.141726 |
| GO:0007269 | neurotransmitter secretion | 88 | 0.400763 | 0.025678 | 0.249741 | 0.221269 |
| GO:0050808 | synapse organization | 123 | 0.400389 | 0.008130 | 0.159963 | 0.141726 |
| GO:0044708 | single-organism behavior | 241 | 0.399057 | 0.001225 | 0.109626 | 0.097128 |
| GO:0032412 | regulation of ion transmembrane transporter activity | 94 | 0.398689 | 0.032922 | 0.273614 | 0.242420 |
| GO:0031345 | negative regulation of cell projection organization | 89 | 0.398039 | 0.046897 | 0.308282 | 0.273136 |
| GO:0060041 | retina development in camera-type eye | 92 | 0.396016 | 0.037088 | 0.279295 | 0.247453 |
| GO:0022898 | regulation of transmembrane transporter activity | 98 | 0.393578 | 0.036986 | 0.279295 | 0.247453 |
| GO:0030073 | insulin secretion | 121 | 0.391896 | 0.025538 | 0.249741 | 0.221269 |
| GO:0001764 | neuron migration | 97 | 0.391622 | 0.033829 | 0.274809 | 0.243479 |
| GO:0051648 | vesicle localization | 126 | 0.388909 | 0.013569 | 0.209109 | 0.185269 |
| GO:0032844 | regulation of homeostatic process | 226 | 0.387412 | 0.001225 | 0.109626 | 0.097128 |
| GO:0007417 | central nervous system development | 460 | 0.386554 | 0.001120 | 0.109626 | 0.097128 |
| GO:0032868 | response to insulin | 125 | 0.386045 | 0.028264 | 0.257515 | 0.228156 |
| GO:0090276 | regulation of peptide hormone secretion | 120 | 0.384814 | 0.019973 | 0.234020 | 0.207340 |
| GO:0007610 | behavior | 412 | 0.384602 | 0.001124 | 0.109626 | 0.097128 |
| GO:0003012 | muscle system process | 169 | 0.384414 | 0.007595 | 0.159963 | 0.141726 |
| GO:0090087 | regulation of peptide transport | 144 | 0.383869 | 0.014925 | 0.219139 | 0.194155 |
| GO:0032409 | regulation of transporter activity | 104 | 0.381969 | 0.049248 | 0.313728 | 0.277961 |
| GO:0002791 | regulation of peptide secretion | 121 | 0.381084 | 0.028075 | 0.257515 | 0.228156 |
| GO:0050877 | neurological system process | 424 | 0.380994 | 0.001136 | 0.109626 | 0.097128 |
| GO:0007548 | sex differentiation | 130 | 0.379783 | 0.027415 | 0.256065 | 0.226872 |
| GO:0007600 | sensory perception | 231 | 0.379700 | 0.006203 | 0.152968 | 0.135528 |
| GO:0015849 | organic acid transport | 137 | 0.377456 | 0.021592 | 0.236375 | 0.209426 |
| GO:0042391 | regulation of membrane potential | 188 | 0.376708 | 0.006211 | 0.152968 | 0.135528 |
| GO:0007267 | cell-cell signaling | 505 | 0.373079 | 0.001111 | 0.109626 | 0.097128 |
| GO:0071103 | DNA conformation change | 139 | 0.371622 | 0.035278 | 0.279295 | 0.247453 |
| GO:0042886 | amide transport | 191 | 0.371007 | 0.005249 | 0.145310 | 0.128744 |
| GO:0051650 | establishment of vesicle localization | 119 | 0.370148 | 0.046512 | 0.307613 | 0.272543 |
| GO:0051480 | cytosolic calcium ion homeostasis | 126 | 0.369326 | 0.041451 | 0.294836 | 0.261223 |
| GO:0015833 | peptide transport | 183 | 0.367317 | 0.010323 | 0.182366 | 0.161575 |
| GO:0019752 | carboxylic acid metabolic process | 504 | 0.365146 | 0.001126 | 0.109626 | 0.097128 |
| GO:0090596 | sensory organ morphogenesis | 176 | 0.361991 | 0.015345 | 0.219139 | 0.194155 |
| GO:0046942 | carboxylic acid transport | 136 | 0.360801 | 0.041555 | 0.294932 | 0.261308 |
| GO:0055080 | cation homeostasis | 318 | 0.359286 | 0.004673 | 0.136185 | 0.120659 |
| GO:0003002 | regionalization | 181 | 0.357760 | 0.036570 | 0.279295 | 0.247453 |
| GO:0009199 | ribonucleoside triphosphate metabolic process | 140 | 0.357685 | 0.041885 | 0.295986 | 0.262242 |
| GO:0030072 | peptide hormone secretion | 150 | 0.356735 | 0.039164 | 0.288001 | 0.255167 |
| GO:0010817 | regulation of hormone levels | 254 | 0.354099 | 0.012255 | 0.197992 | 0.175419 |
| GO:0002790 | peptide secretion | 152 | 0.353870 | 0.047431 | 0.309871 | 0.274544 |
| GO:0015672 | monovalent inorganic cation transport | 265 | 0.353710 | 0.006061 | 0.152968 | 0.135528 |
| GO:0098771 | inorganic ion homeostasis | 325 | 0.353619 | 0.004700 | 0.136185 | 0.120659 |
| GO:0050801 | ion homeostasis | 358 | 0.353521 | 0.004646 | 0.136185 | 0.120659 |
| GO:0072507 | divalent inorganic cation homeostasis | 214 | 0.352993 | 0.020202 | 0.234020 | 0.207340 |
| GO:0034762 | regulation of transmembrane transport | 179 | 0.352451 | 0.035354 | 0.279295 | 0.247453 |
| GO:0034765 | regulation of ion transmembrane transport | 166 | 0.349588 | 0.031172 | 0.267347 | 0.236868 |
| GO:0023061 | signal release | 262 | 0.346782 | 0.014510 | 0.217454 | 0.192663 |
| GO:0044057 | regulation of system process | 244 | 0.342266 | 0.018226 | 0.228271 | 0.202247 |
| GO:0048699 | generation of neurons | 864 | 0.342072 | 0.001054 | 0.109626 | 0.097128 |
| GO:1903706 | regulation of hemopoiesis | 188 | 0.341956 | 0.043590 | 0.299896 | 0.265705 |
| GO:0007399 | nervous system development | 1237 | 0.340988 | 0.001024 | 0.109626 | 0.097128 |
| GO:0060322 | head development | 369 | 0.340427 | 0.004582 | 0.135462 | 0.120019 |
| GO:0001501 | skeletal system development | 270 | 0.340129 | 0.016990 | 0.224465 | 0.198875 |
| GO:0007420 | brain development | 341 | 0.339977 | 0.008111 | 0.159963 | 0.141726 |
| GO:0072503 | cellular divalent inorganic cation homeostasis | 200 | 0.339816 | 0.039900 | 0.290463 | 0.257348 |
| GO:0055065 | metal ion homeostasis | 279 | 0.339344 | 0.020433 | 0.234020 | 0.207340 |
| GO:0098662 | inorganic cation transmembrane transport | 243 | 0.335648 | 0.032218 | 0.271883 | 0.240887 |
| GO:0048608 | reproductive structure development | 244 | 0.335150 | 0.024272 | 0.245202 | 0.217248 |
| GO:0006820 | anion transport | 264 | 0.334861 | 0.024204 | 0.245202 | 0.217248 |
| GO:0061458 | reproductive system development | 246 | 0.330190 | 0.032927 | 0.273614 | 0.242420 |
| GO:0006325 | chromatin organization | 489 | 0.329359 | 0.005624 | 0.149958 | 0.132862 |
| GO:0098660 | inorganic ion transmembrane transport | 268 | 0.328507 | 0.035583 | 0.279295 | 0.247453 |
| GO:0031175 | neuron projection development | 552 | 0.325425 | 0.001116 | 0.109626 | 0.097128 |
| GO:0043269 | regulation of ion transport | 300 | 0.325346 | 0.029586 | 0.262868 | 0.232899 |
| GO:0007186 | G-protein coupled receptor signaling pathway | 275 | 0.324391 | 0.042631 | 0.299173 | 0.265065 |
| GO:0048878 | chemical homeostasis | 546 | 0.323874 | 0.005482 | 0.148917 | 0.131940 |
| GO:0007423 | sensory organ development | 337 | 0.322450 | 0.020286 | 0.234020 | 0.207340 |
| GO:0098655 | cation transmembrane transport | 267 | 0.320310 | 0.044444 | 0.300865 | 0.266565 |
| GO:0055082 | cellular chemical homeostasis | 351 | 0.318424 | 0.030588 | 0.264814 | 0.234623 |
| GO:0032990 | cell part morphogenesis | 497 | 0.318123 | 0.007856 | 0.159963 | 0.141726 |
| GO:0050767 | regulation of neurogenesis | 466 | 0.316322 | 0.020408 | 0.234020 | 0.207340 |
| GO:0071705 | nitrogen compound transport | 420 | 0.315423 | 0.018519 | 0.229292 | 0.203151 |
| GO:0003008 | system process | 740 | 0.312975 | 0.007535 | 0.159963 | 0.141726 |
| GO:0006812 | cation transport | 516 | 0.311542 | 0.013289 | 0.206216 | 0.182706 |
| GO:0048858 | cell projection morphogenesis | 478 | 0.310616 | 0.018370 | 0.228737 | 0.202659 |
| GO:0051046 | regulation of secretion | 388 | 0.310276 | 0.031567 | 0.269001 | 0.238333 |
| GO:0042592 | homeostatic process | 866 | 0.309538 | 0.003112 | 0.118967 | 0.105404 |
| GO:0030001 | metal ion transport | 400 | 0.309335 | 0.032370 | 0.272635 | 0.241553 |
| GO:0046903 | secretion | 565 | 0.305619 | 0.019780 | 0.234020 | 0.207340 |
| GO:0034220 | ion transmembrane transport | 387 | 0.304754 | 0.035632 | 0.279295 | 0.247453 |
| GO:0006811 | ion transport | 728 | 0.289017 | 0.035870 | 0.279295 | 0.247453 |
| GO:0030030 | cell projection organization | 818 | 0.287890 | 0.026059 | 0.250002 | 0.221500 |
| GO:0048731 | system development | 2389 | 0.275911 | 0.004008 | 0.128681 | 0.114011 |
| GO:2000026 | regulation of multicellular organismal development | 1021 | 0.274898 | 0.048857 | 0.313728 | 0.277961 |
| GO:1902578 | single-organism localization | 2164 | 0.273977 | 0.013039 | 0.205540 | 0.182107 |
| GO:0048513 | organ development | 1718 | 0.272882 | 0.025329 | 0.249628 | 0.221169 |
| GO:0023051 | regulation of signaling | 1615 | 0.272123 | 0.023327 | 0.241946 | 0.214363 |
| GO:0048869 | cellular developmental process | 2280 | 0.271986 | 0.013000 | 0.205540 | 0.182107 |
| GO:0010646 | regulation of cell communication | 1650 | 0.271360 | 0.024341 | 0.245202 | 0.217248 |
| GO:0044765 | single-organism transport | 2045 | 0.270781 | 0.015106 | 0.219139 | 0.194155 |
| GO:0065008 | regulation of biological quality | 1839 | 0.267942 | 0.038191 | 0.283239 | 0.250948 |
| GO:0007275 | multicellular organismal development | 2697 | 0.266009 | 0.023000 | 0.241946 | 0.214363 |
| GO:0044707 | single-multicellular organism process | 3287 | 0.263691 | 0.016016 | 0.222347 | 0.196998 |
| GO:0044710 | single-organism metabolic process | 2801 | 0.263269 | 0.020020 | 0.234020 | 0.207340 |
| GO:0032501 | multicellular organismal process | 3362 | 0.260473 | 0.028028 | 0.257515 | 0.228156 |
| GO:0016043 | cellular component organization | 3446 | 0.255881 | 0.049000 | 0.313728 | 0.277961 |
| GO:0007155 | cell adhesion | 720 | -0.240560 | 0.028169 | 0.257515 | 0.228156 |
| GO:0022610 | biological adhesion | 727 | -0.246690 | 0.029851 | 0.262868 | 0.232899 |
| GO:0016477 | cell migration | 674 | -0.248015 | 0.042857 | 0.299173 | 0.265065 |
| GO:0032101 | regulation of response to external stimulus | 436 | -0.250471 | 0.033333 | 0.274742 | 0.243420 |
| GO:0048646 | anatomical structure formation involved in morphogenesis | 701 | -0.250861 | 0.031250 | 0.267347 | 0.236868 |
| GO:0098602 | single organism cell adhesion | 426 | -0.263375 | 0.024390 | 0.245202 | 0.217248 |
| GO:0030155 | regulation of cell adhesion | 348 | -0.267999 | 0.022901 | 0.241946 | 0.214363 |
| GO:0001775 | cell activation | 434 | -0.268987 | 0.027027 | 0.254793 | 0.225745 |
| GO:0072358 | cardiovascular system development | 589 | -0.269824 | 0.010753 | 0.185707 | 0.164535 |
| GO:0072359 | circulatory system development | 589 | -0.269824 | 0.010753 | 0.185707 | 0.164535 |
| GO:0051270 | regulation of cellular component movement | 453 | -0.274497 | 0.008772 | 0.167942 | 0.148795 |
| GO:0022603 | regulation of anatomical structure morphogenesis | 573 | -0.283844 | 0.010309 | 0.182366 | 0.161575 |
| GO:2000145 | regulation of cell motility | 410 | -0.284911 | 0.007194 | 0.157910 | 0.139907 |
| GO:0031589 | cell-substrate adhesion | 194 | -0.285431 | 0.027397 | 0.256065 | 0.226872 |
| GO:0040012 | regulation of locomotion | 448 | -0.294845 | 0.008772 | 0.167942 | 0.148795 |
| GO:0030334 | regulation of cell migration | 387 | -0.295702 | 0.007519 | 0.159963 | 0.141726 |
| GO:0007015 | actin filament organization | 215 | -0.296499 | 0.042105 | 0.297061 | 0.263194 |
| GO:0009617 | response to bacterium | 191 | -0.296617 | 0.037209 | 0.279295 | 0.247453 |
| GO:0032956 | regulation of actin cytoskeleton organization | 188 | -0.299675 | 0.046083 | 0.307613 | 0.272543 |
| GO:2000147 | positive regulation of cell motility | 233 | -0.302160 | 0.010638 | 0.185707 | 0.164535 |
| GO:0051272 | positive regulation of cellular component movement | 240 | -0.305998 | 0.005376 | 0.146953 | 0.130200 |
| GO:0040017 | positive regulation of locomotion | 246 | -0.306034 | 0.011429 | 0.191771 | 0.169907 |
| GO:0030335 | positive regulation of cell migration | 226 | -0.307526 | 0.009756 | 0.175492 | 0.155485 |
| GO:0040013 | negative regulation of locomotion | 150 | -0.308398 | 0.036145 | 0.279295 | 0.247453 |
| GO:0044764 | multi-organism cellular process | 171 | -0.314676 | 0.033333 | 0.274742 | 0.243420 |
| GO:0016050 | vesicle organization | 164 | -0.315900 | 0.020921 | 0.234852 | 0.208077 |
| GO:0006486 | protein glycosylation | 123 | -0.321005 | 0.035156 | 0.279295 | 0.247453 |
| GO:0043413 | macromolecule glycosylation | 123 | -0.321005 | 0.035156 | 0.279295 | 0.247453 |
| GO:0016032 | viral process | 162 | -0.321991 | 0.024291 | 0.245202 | 0.217248 |
| GO:0043547 | positive regulation of GTPase activity | 166 | -0.322704 | 0.012552 | 0.200560 | 0.177695 |
| GO:0043087 | regulation of GTPase activity | 205 | -0.325711 | 0.004367 | 0.134827 | 0.119455 |
| GO:0007266 | Rho protein signal transduction | 101 | -0.326038 | 0.049618 | 0.313888 | 0.278103 |
| GO:0019058 | viral life cycle | 133 | -0.326107 | 0.034351 | 0.276976 | 0.245399 |
| GO:0001667 | ameboidal-type cell migration | 198 | -0.331112 | 0.009434 | 0.175214 | 0.155238 |
| GO:0051495 | positive regulation of cytoskeleton organization | 119 | -0.334612 | 0.021583 | 0.236375 | 0.209426 |
| GO:0070371 | ERK1 and ERK2 cascade | 124 | -0.337894 | 0.022059 | 0.237876 | 0.210757 |
| GO:0032102 | negative regulation of response to external stimulus | 142 | -0.341286 | 0.016393 | 0.222643 | 0.197261 |
| GO:0044403 | symbiosis, encompassing mutualism through parasitism | 186 | -0.341381 | 0.008850 | 0.167948 | 0.148801 |
| GO:0044419 | interspecies interaction between organisms | 186 | -0.341381 | 0.008850 | 0.167948 | 0.148801 |
| GO:0001944 | vasculature development | 384 | -0.345535 | 0.007092 | 0.157578 | 0.139613 |
| GO:0050792 | regulation of viral process | 94 | -0.349758 | 0.039568 | 0.289849 | 0.256804 |
| GO:0008360 | regulation of cell shape | 97 | -0.351557 | 0.034843 | 0.279295 | 0.247453 |
| GO:0001568 | blood vessel development | 365 | -0.352587 | 0.006711 | 0.152968 | 0.135528 |
| GO:0050900 | leukocyte migration | 110 | -0.354346 | 0.034483 | 0.277522 | 0.245883 |
| GO:0010810 | regulation of cell-substrate adhesion | 115 | -0.354713 | 0.003861 | 0.128681 | 0.114011 |
| GO:0010632 | regulation of epithelial cell migration | 107 | -0.358232 | 0.021429 | 0.236251 | 0.209316 |
| GO:0042742 | defense response to bacterium | 85 | -0.360777 | 0.029703 | 0.262868 | 0.232899 |
| GO:1903900 | regulation of viral life cycle | 88 | -0.374772 | 0.020979 | 0.234852 | 0.208077 |
| GO:0070372 | regulation of ERK1 and ERK2 cascade | 113 | -0.377715 | 0.007273 | 0.158286 | 0.140240 |
| GO:0048514 | blood vessel morphogenesis | 316 | -0.380925 | 0.006211 | 0.152968 | 0.135528 |
| GO:0050878 | regulation of body fluid levels | 161 | -0.381346 | 0.004149 | 0.129735 | 0.114945 |
| GO:0010631 | epithelial cell migration | 139 | -0.383587 | 0.008097 | 0.159963 | 0.141726 |
| GO:0090130 | tissue migration | 139 | -0.383587 | 0.008097 | 0.159963 | 0.141726 |
| GO:0090132 | epithelium migration | 139 | -0.383587 | 0.008097 | 0.159963 | 0.141726 |
| GO:0051701 | interaction with host | 60 | -0.386173 | 0.046512 | 0.307613 | 0.272543 |
| GO:0010594 | regulation of endothelial cell migration | 71 | -0.386756 | 0.016287 | 0.222347 | 0.196998 |
| GO:0002685 | regulation of leukocyte migration | 63 | -0.397959 | 0.034921 | 0.279295 | 0.247453 |
| GO:0001570 | vasculogenesis | 55 | -0.401702 | 0.020468 | 0.234020 | 0.207340 |
| GO:0070374 | positive regulation of ERK1 and ERK2 cascade | 64 | -0.405196 | 0.013289 | 0.206216 | 0.182706 |
| GO:0034446 | substrate adhesion-dependent cell spreading | 58 | -0.406552 | 0.021021 | 0.234852 | 0.208077 |
| GO:0030500 | regulation of bone mineralization | 43 | -0.410751 | 0.047486 | 0.309871 | 0.274544 |
| GO:0000041 | transition metal ion transport | 53 | -0.413855 | 0.024169 | 0.245202 | 0.217248 |
| GO:1903729 | regulation of plasma membrane organization | 54 | -0.414293 | 0.022293 | 0.238048 | 0.210908 |
| GO:0001525 | angiogenesis | 263 | -0.416745 | 0.005587 | 0.149872 | 0.132786 |
| GO:0030168 | platelet activation | 59 | -0.416871 | 0.029851 | 0.262868 | 0.232899 |
| GO:0032006 | regulation of TOR signaling | 49 | -0.418086 | 0.040881 | 0.293919 | 0.260410 |
| GO:0030838 | positive regulation of actin filament polymerization | 60 | -0.421542 | 0.024024 | 0.245202 | 0.217248 |
| GO:0045580 | regulation of T cell differentiation | 52 | -0.423170 | 0.029499 | 0.262868 | 0.232899 |
| GO:0051297 | centrosome organization | 62 | -0.425019 | 0.015198 | 0.219139 | 0.194155 |
| GO:0070167 | regulation of biomineral tissue development | 45 | -0.425695 | 0.020057 | 0.234020 | 0.207340 |
| GO:0050817 | coagulation | 93 | -0.429363 | 0.003472 | 0.121143 | 0.107332 |
| GO:0045619 | regulation of lymphocyte differentiation | 70 | -0.430418 | 0.009585 | 0.175492 | 0.155485 |
| GO:0090003 | regulation of establishment of protein localization to plasma membrane | 39 | -0.432297 | 0.040346 | 0.292726 | 0.259353 |
| GO:0002687 | positive regulation of leukocyte migration | 42 | -0.434113 | 0.027356 | 0.256065 | 0.226872 |
| GO:0006493 | protein O-linked glycosylation | 43 | -0.437927 | 0.039039 | 0.287566 | 0.254781 |
| GO:0007596 | blood coagulation | 91 | -0.440054 | 0.003356 | 0.118967 | 0.105404 |
| GO:0043542 | endothelial cell migration | 97 | -0.440789 | 0.003236 | 0.118967 | 0.105404 |
| GO:0051225 | spindle assembly | 46 | -0.440861 | 0.021472 | 0.236251 | 0.209316 |
| GO:1901342 | regulation of vasculature development | 135 | -0.445521 | 0.003953 | 0.128681 | 0.114011 |
| GO:0002444 | myeloid leukocyte mediated immunity | 39 | -0.445904 | 0.046647 | 0.307613 | 0.272543 |
| GO:0070527 | platelet aggregation | 34 | -0.447335 | 0.042857 | 0.299173 | 0.265065 |
| GO:0007599 | hemostasis | 93 | -0.448438 | 0.003344 | 0.118967 | 0.105404 |
| GO:0030260 | entry into host cell | 36 | -0.452949 | 0.036313 | 0.279295 | 0.247453 |
| GO:0044409 | entry into host | 36 | -0.452949 | 0.036313 | 0.279295 | 0.247453 |
| GO:0051806 | entry into cell of other organism involved in symbiotic interaction | 36 | -0.452949 | 0.036313 | 0.279295 | 0.247453 |
| GO:0051828 | entry into other organism involved in symbiotic interaction | 36 | -0.452949 | 0.036313 | 0.279295 | 0.247453 |
| GO:0052126 | movement in host environment | 36 | -0.452949 | 0.036313 | 0.279295 | 0.247453 |
| GO:0052192 | movement in environment of other organism involved in symbiotic interaction | 36 | -0.452949 | 0.036313 | 0.279295 | 0.247453 |
| GO:0045765 | regulation of angiogenesis | 124 | -0.453025 | 0.003831 | 0.128681 | 0.114011 |
| GO:0003158 | endothelium development | 61 | -0.456220 | 0.003125 | 0.118967 | 0.105404 |
| GO:1903076 | regulation of protein localization to plasma membrane | 51 | -0.457081 | 0.006154 | 0.152968 | 0.135528 |
| GO:1904375 | regulation of protein localization to cell periphery | 51 | -0.457081 | 0.006154 | 0.152968 | 0.135528 |
| GO:0045621 | positive regulation of lymphocyte differentiation | 37 | -0.470300 | 0.022222 | 0.237876 | 0.210757 |
| GO:0043299 | leukocyte degranulation | 36 | -0.476387 | 0.033241 | 0.274742 | 0.243420 |
| GO:0043534 | blood vessel endothelial cell migration | 54 | -0.485523 | 0.003067 | 0.118967 | 0.105404 |
| GO:0009311 | oligosaccharide metabolic process | 34 | -0.487599 | 0.022039 | 0.237876 | 0.210757 |
| GO:0045766 | positive regulation of angiogenesis | 69 | -0.488991 | 0.003344 | 0.118967 | 0.105404 |
| GO:0001885 | endothelial cell development | 34 | -0.490001 | 0.020290 | 0.234020 | 0.207340 |
| GO:0016525 | negative regulation of angiogenesis | 44 | -0.490460 | 0.012085 | 0.196703 | 0.174277 |
| GO:1904018 | positive regulation of vasculature development | 75 | -0.492021 | 0.003300 | 0.118967 | 0.105404 |
| GO:2000351 | regulation of endothelial cell apoptotic process | 27 | -0.493480 | 0.040984 | 0.293919 | 0.260410 |
| GO:0046718 | viral entry into host cell | 33 | -0.498321 | 0.014045 | 0.214173 | 0.189756 |
| GO:0043535 | regulation of blood vessel endothelial cell migration | 37 | -0.499883 | 0.022599 | 0.239548 | 0.212238 |
| GO:1901343 | negative regulation of vasculature development | 47 | -0.500064 | 0.003145 | 0.118967 | 0.105404 |
| GO:2000181 | negative regulation of blood vessel morphogenesis | 46 | -0.500078 | 0.003086 | 0.118967 | 0.105404 |
| GO:0001569 | patterning of blood vessels | 33 | -0.510305 | 0.014245 | 0.215063 | 0.190545 |
| GO:0007229 | integrin-mediated signaling pathway | 45 | -0.515707 | 0.002681 | 0.118967 | 0.105404 |
| GO:0010812 | negative regulation of cell-substrate adhesion | 33 | -0.524066 | 0.005952 | 0.152968 | 0.135528 |
| GO:1900024 | regulation of substrate adhesion-dependent cell spreading | 27 | -0.527889 | 0.020566 | 0.234020 | 0.207340 |
| GO:0019068 | virion assembly | 23 | -0.532493 | 0.034031 | 0.275934 | 0.244475 |
| GO:0046605 | regulation of centrosome cycle | 22 | -0.535905 | 0.041262 | 0.294193 | 0.260653 |
| GO:0030195 | negative regulation of blood coagulation | 20 | -0.536028 | 0.049505 | 0.313728 | 0.277961 |
| GO:0050819 | negative regulation of coagulation | 20 | -0.536028 | 0.049505 | 0.313728 | 0.277961 |
| GO:1900047 | negative regulation of hemostasis | 20 | -0.536028 | 0.049505 | 0.313728 | 0.277961 |
| GO:1903305 | regulation of regulated secretory pathway | 26 | -0.543338 | 0.017812 | 0.225028 | 0.199373 |
| GO:0071384 | cellular response to corticosteroid stimulus | 17 | -0.545610 | 0.043257 | 0.299896 | 0.265705 |
| GO:0033003 | regulation of mast cell activation | 22 | -0.552684 | 0.022167 | 0.237876 | 0.210757 |
| GO:0009225 | nucleotide-sugar metabolic process | 20 | -0.558300 | 0.037534 | 0.280084 | 0.248153 |
| GO:0006900 | membrane budding | 49 | -0.559250 | 0.002801 | 0.118967 | 0.105404 |
| GO:0019076 | viral release from host cell | 25 | -0.560915 | 0.008929 | 0.168711 | 0.149477 |
| GO:1902186 | regulation of viral release from host cell | 23 | -0.566694 | 0.017143 | 0.224465 | 0.198875 |
| GO:0043536 | positive regulation of blood vessel endothelial cell migration | 19 | -0.570154 | 0.037037 | 0.279295 | 0.247453 |
| GO:0007080 | mitotic metaphase plate congression | 20 | -0.573654 | 0.037135 | 0.279295 | 0.247453 |
| GO:0002886 | regulation of myeloid leukocyte mediated immunity | 22 | -0.575454 | 0.025974 | 0.249741 | 0.221269 |
| GO:0071353 | cellular response to interleukin-4 | 18 | -0.575654 | 0.020882 | 0.234852 | 0.208077 |
| GO:2000401 | regulation of lymphocyte migration | 17 | -0.578338 | 0.033505 | 0.274742 | 0.243420 |
| GO:0070670 | response to interleukin-4 | 20 | -0.578595 | 0.014252 | 0.215063 | 0.190545 |
| GO:0018196 | peptidyl-asparagine modification | 23 | -0.585616 | 0.016173 | 0.222347 | 0.196998 |
| GO:0046596 | regulation of viral entry into host cell | 17 | -0.589468 | 0.018868 | 0.230700 | 0.204398 |
| GO:0051767 | nitric-oxide synthase biosynthetic process | 13 | -0.596642 | 0.043796 | 0.299896 | 0.265705 |
| GO:0051769 | regulation of nitric-oxide synthase biosynthetic process | 13 | -0.596642 | 0.043796 | 0.299896 | 0.265705 |
| GO:0043300 | regulation of leukocyte degranulation | 24 | -0.597967 | 0.007853 | 0.159963 | 0.141726 |
| GO:0043687 | post-translational protein modification | 29 | -0.598370 | 0.002793 | 0.118967 | 0.105404 |
| GO:0050710 | negative regulation of cytokine secretion | 18 | -0.601636 | 0.017456 | 0.225028 | 0.199373 |
| GO:0018279 | protein N-linked glycosylation via asparagine | 22 | -0.609224 | 0.015385 | 0.219139 | 0.194155 |
| GO:0033363 | secretory granule organization | 16 | -0.612654 | 0.028497 | 0.258559 | 0.229081 |
| GO:0061028 | establishment of endothelial barrier | 21 | -0.612982 | 0.002646 | 0.118967 | 0.105404 |
| GO:0046755 | viral budding | 16 | -0.617329 | 0.025445 | 0.249628 | 0.221169 |
| GO:1902590 | multi-organism organelle organization | 16 | -0.617329 | 0.025445 | 0.249628 | 0.221169 |
| GO:1902592 | multi-organism membrane budding | 16 | -0.617329 | 0.025445 | 0.249628 | 0.221169 |
| GO:1902850 | microtubule cytoskeleton organization involved in mitosis | 25 | -0.622488 | 0.007576 | 0.159963 | 0.141726 |
| GO:0072678 | T cell migration | 18 | -0.623740 | 0.005141 | 0.143234 | 0.126904 |
| GO:0045947 | negative regulation of translational initiation | 14 | -0.630452 | 0.026882 | 0.254059 | 0.225095 |
| GO:0060416 | response to growth hormone | 14 | -0.635942 | 0.007712 | 0.159963 | 0.141726 |
| GO:0009110 | vitamin biosynthetic process | 11 | -0.636682 | 0.046512 | 0.307613 | 0.272543 |
| GO:0045793 | positive regulation of cell size | 12 | -0.637695 | 0.047847 | 0.311291 | 0.275802 |
| GO:0090307 | mitotic spindle assembly | 22 | -0.639327 | 0.007653 | 0.159963 | 0.141726 |
| GO:0016266 | O-glycan processing | 14 | -0.642918 | 0.021164 | 0.235843 | 0.208955 |
| GO:0044803 | multi-organism membrane organization | 19 | -0.646528 | 0.015113 | 0.219139 | 0.194155 |
| GO:0071312 | cellular response to alkaloid | 11 | -0.650022 | 0.047030 | 0.308282 | 0.273136 |
| GO:0002335 | mature B cell differentiation | 12 | -0.659381 | 0.033766 | 0.274809 | 0.243479 |
| GO:1902187 | negative regulation of viral release from host cell | 12 | -0.669269 | 0.018421 | 0.228737 | 0.202659 |
| GO:0000920 | cell separation after cytokinesis | 13 | -0.671591 | 0.014184 | 0.215063 | 0.190545 |
| GO:0001893 | maternal placenta development | 16 | -0.672306 | 0.011990 | 0.195903 | 0.173569 |
| GO:0039702 | viral budding via host ESCRT complex | 13 | -0.672992 | 0.024814 | 0.247342 | 0.219143 |
| GO:0043304 | regulation of mast cell degranulation | 18 | -0.674373 | 0.009756 | 0.175492 | 0.155485 |
| GO:0050892 | intestinal absorption | 14 | -0.681717 | 0.014670 | 0.218341 | 0.193448 |
| GO:0034389 | lipid particle organization | 11 | -0.690151 | 0.017032 | 0.224465 | 0.198875 |
| GO:0010224 | response to UV-B | 11 | -0.691178 | 0.019465 | 0.234020 | 0.207340 |
| GO:0042832 | defense response to protozoan | 12 | -0.692539 | 0.009592 | 0.175492 | 0.155485 |
| GO:2000403 | positive regulation of lymphocyte migration | 11 | -0.702138 | 0.023136 | 0.241946 | 0.214363 |
| GO:1903077 | negative regulation of protein localization to plasma membrane | 15 | -0.708066 | 0.002421 | 0.118967 | 0.105404 |
| GO:1904376 | negative regulation of protein localization to cell periphery | 15 | -0.708066 | 0.002421 | 0.118967 | 0.105404 |
| GO:0045579 | positive regulation of B cell differentiation | 11 | -0.710056 | 0.016827 | 0.224465 | 0.198875 |
| GO:0044406 | adhesion of symbiont to host | 11 | -0.712438 | 0.017812 | 0.225028 | 0.199373 |
| GO:0043403 | skeletal muscle tissue regeneration | 18 | -0.722452 | 0.002392 | 0.118967 | 0.105404 |
| GO:2000404 | regulation of T cell migration | 13 | -0.769908 | 0.002558 | 0.118967 | 0.105404 |
| GO:0043252 | sodium-independent organic anion transport | 11 | -0.808587 | 0.002475 | 0.118967 | 0.105404 |

## rd1 CC
| ID | Description | setSize | enrichmentScore | pvalue | p.adjust | qvalues |
| --- | --- | --- | --- | --- | --- | --- |
| GO:0034364 | high-density lipoprotein particle | 12 | 0.780851 | 0.005190 | 0.111569 | 0.101548 |
| GO:0046658 | anchored component of plasma membrane | 13 | 0.733280 | 0.005245 | 0.111569 | 0.101548 |
| GO:0031527 | filopodium membrane | 11 | 0.679757 | 0.042834 | 0.330701 | 0.300999 |
| GO:0060076 | excitatory synapse | 18 | 0.644940 | 0.018242 | 0.211832 | 0.192806 |
| GO:0070822 | Sin3-type complex | 13 | 0.636827 | 0.039620 | 0.322051 | 0.293126 |
| GO:0000786 | nucleosome | 57 | 0.631211 | 0.001522 | 0.057737 | 0.052551 |
| GO:0044815 | DNA packaging complex | 59 | 0.624425 | 0.001504 | 0.057737 | 0.052551 |
| GO:0036126 | sperm flagellum | 30 | 0.610362 | 0.003200 | 0.096196 | 0.087556 |
| GO:0000788 | nuclear nucleosome | 28 | 0.600959 | 0.006421 | 0.111569 | 0.101548 |
| GO:0034358 | plasma lipoprotein particle | 22 | 0.583755 | 0.035313 | 0.309125 | 0.281360 |
| GO:1990777 | lipoprotein particle | 22 | 0.583755 | 0.035313 | 0.309125 | 0.281360 |
| GO:0008076 | voltage-gated potassium channel complex | 28 | 0.577114 | 0.011200 | 0.163405 | 0.148729 |
| GO:0034705 | potassium channel complex | 28 | 0.577114 | 0.011200 | 0.163405 | 0.148729 |
| GO:0032994 | protein-lipid complex | 24 | 0.575541 | 0.027113 | 0.280499 | 0.255306 |
| GO:0031514 | motile cilium | 51 | 0.564409 | 0.001468 | 0.057737 | 0.052551 |
| GO:0008328 | ionotropic glutamate receptor complex | 28 | 0.543746 | 0.023962 | 0.262196 | 0.238647 |
| GO:0032587 | ruffle membrane | 40 | 0.539473 | 0.013534 | 0.171503 | 0.156099 |
| GO:0034703 | cation channel complex | 56 | 0.520635 | 0.001515 | 0.057737 | 0.052551 |
| GO:0005581 | collagen trimer | 30 | 0.518770 | 0.045802 | 0.338455 | 0.308057 |
| GO:0034702 | ion channel complex | 101 | 0.498419 | 0.001416 | 0.057737 | 0.052551 |
| GO:0031256 | leading edge membrane | 74 | 0.490544 | 0.005626 | 0.111569 | 0.101548 |
| GO:1902495 | transmembrane transporter complex | 118 | 0.480880 | 0.001393 | 0.057737 | 0.052551 |
| GO:1990351 | transporter complex | 121 | 0.471514 | 0.001376 | 0.057737 | 0.052551 |
| GO:0032993 | protein-DNA complex | 107 | 0.461485 | 0.002778 | 0.096196 | 0.087556 |
| GO:0030175 | filopodium | 56 | 0.458095 | 0.025915 | 0.273063 | 0.248538 |
| GO:0072562 | blood microparticle | 56 | 0.455626 | 0.030129 | 0.295577 | 0.269030 |
| GO:0031225 | anchored component of membrane | 60 | 0.438007 | 0.036443 | 0.311184 | 0.283235 |
| GO:0030426 | growth cone | 114 | 0.421589 | 0.004196 | 0.108519 | 0.098772 |
| GO:0030427 | site of polarized growth | 117 | 0.408001 | 0.005579 | 0.111569 | 0.101548 |
| GO:0044297 | cell body | 398 | 0.401145 | 0.001167 | 0.057737 | 0.052551 |
| GO:0043025 | neuronal cell body | 354 | 0.399531 | 0.001175 | 0.057737 | 0.052551 |
| GO:0008021 | synaptic vesicle | 98 | 0.383007 | 0.043539 | 0.330701 | 0.300999 |
| GO:0030424 | axon | 313 | 0.377575 | 0.001167 | 0.057737 | 0.052551 |
| GO:0036477 | somatodendritic compartment | 506 | 0.373173 | 0.001110 | 0.057737 | 0.052551 |
| GO:0097060 | synaptic membrane | 138 | 0.369256 | 0.032938 | 0.307242 | 0.279647 |
| GO:0043005 | neuron projection | 717 | 0.364229 | 0.001079 | 0.057737 | 0.052551 |
| GO:0031253 | cell projection membrane | 148 | 0.357079 | 0.034031 | 0.307900 | 0.280246 |
| GO:0000785 | chromatin | 327 | 0.351972 | 0.003550 | 0.096196 | 0.087556 |
| GO:0097458 | neuron part | 896 | 0.349604 | 0.001047 | 0.057737 | 0.052551 |
| GO:0098797 | plasma membrane protein complex | 234 | 0.342354 | 0.013564 | 0.171503 | 0.156099 |
| GO:0044456 | synapse part | 380 | 0.340287 | 0.003456 | 0.096196 | 0.087556 |
| GO:0045202 | synapse | 511 | 0.335892 | 0.003344 | 0.096196 | 0.087556 |
| GO:0044463 | cell projection part | 618 | 0.335424 | 0.001100 | 0.057737 | 0.052551 |
| GO:0030425 | dendrite | 340 | 0.335076 | 0.010563 | 0.162448 | 0.147857 |
| GO:0000228 | nuclear chromosome | 313 | 0.335023 | 0.012225 | 0.171406 | 0.156011 |
| GO:0042995 | cell projection | 1279 | 0.317596 | 0.001025 | 0.057737 | 0.052551 |
| GO:0031226 | intrinsic component of plasma membrane | 471 | 0.300314 | 0.030752 | 0.296572 | 0.269935 |
| GO:0030054 | cell junction | 759 | -0.238622 | 0.016129 | 0.193801 | 0.176395 |
| GO:0005615 | extracellular space | 589 | -0.247228 | 0.045455 | 0.338455 | 0.308057 |
| GO:0009986 | cell surface | 396 | -0.261459 | 0.036765 | 0.311184 | 0.283235 |
| GO:0005911 | cell-cell junction | 250 | -0.275991 | 0.037736 | 0.311184 | 0.283235 |
| GO:0098552 | side of membrane | 236 | -0.290767 | 0.025000 | 0.268396 | 0.244290 |
| GO:0031012 | extracellular matrix | 202 | -0.293005 | 0.031414 | 0.297906 | 0.271149 |
| GO:0000139 | Golgi membrane | 168 | -0.314746 | 0.020408 | 0.227691 | 0.207241 |
| GO:0005938 | cell cortex | 150 | -0.316564 | 0.034091 | 0.307900 | 0.280246 |
| GO:0030055 | cell-substrate junction | 300 | -0.333489 | 0.006098 | 0.111569 | 0.101548 |
| GO:0005925 | focal adhesion | 295 | -0.335316 | 0.006098 | 0.111569 | 0.101548 |
| GO:0070161 | anchoring junction | 341 | -0.336938 | 0.006410 | 0.111569 | 0.101548 |
| GO:0005912 | adherens junction | 334 | -0.337553 | 0.006667 | 0.111569 | 0.101548 |
| GO:0005924 | cell-substrate adherens junction | 297 | -0.337934 | 0.006369 | 0.111569 | 0.101548 |
| GO:0009897 | external side of plasma membrane | 118 | -0.360664 | 0.007605 | 0.123628 | 0.112525 |
| GO:0044448 | cell cortex part | 89 | -0.368175 | 0.028662 | 0.291231 | 0.265074 |
| GO:0005604 | basement membrane | 68 | -0.373357 | 0.042424 | 0.330701 | 0.300999 |
| GO:0005913 | cell-cell adherens junction | 40 | -0.443650 | 0.037634 | 0.311184 | 0.283235 |
| GO:0030863 | cortical cytoskeleton | 62 | -0.462237 | 0.002899 | 0.096196 | 0.087556 |
| GO:0042641 | actomyosin | 61 | -0.463043 | 0.009288 | 0.146801 | 0.133616 |
| GO:0009925 | basal plasma membrane | 26 | -0.494259 | 0.043590 | 0.330701 | 0.300999 |
| GO:0030864 | cortical actin cytoskeleton | 44 | -0.503861 | 0.016349 | 0.193801 | 0.176395 |
| GO:0032432 | actin filament bundle | 58 | -0.511392 | 0.006515 | 0.111569 | 0.101548 |
| GO:0045178 | basal part of cell | 40 | -0.513121 | 0.013928 | 0.172278 | 0.156805 |
| GO:0001725 | stress fiber | 54 | -0.522445 | 0.006452 | 0.111569 | 0.101548 |
| GO:0005689 | U12-type spliceosomal complex | 21 | -0.575804 | 0.012953 | 0.171406 | 0.156011 |
| GO:0005605 | basal lamina | 15 | -0.604875 | 0.029340 | 0.292884 | 0.266578 |
| GO:0043218 | compact myelin | 14 | -0.627399 | 0.042394 | 0.330701 | 0.300999 |
| GO:0018995 | host | 15 | -0.637983 | 0.012755 | 0.171406 | 0.156011 |
| GO:0043657 | host cell | 15 | -0.637983 | 0.012755 | 0.171406 | 0.156011 |
| GO:0042611 | MHC protein complex | 12 | -0.705712 | 0.019900 | 0.226468 | 0.206127 |

## Rho MF
| ID | Description | setSize | enrichmentScore | pvalue | p.adjust | qvalues |
| --- | --- | --- | --- | --- | --- | --- |
| GO:0044548 | S100 protein binding | 11 | 0.758549 | 0.003367 | 0.248299 | 0.240602 |
| GO:0043236 | laminin binding | 22 | 0.742036 | 0.001742 | 0.211963 | 0.205392 |
| GO:0005161 | platelet-derived growth factor receptor binding | 13 | 0.722239 | 0.019643 | 0.369953 | 0.358484 |
| GO:0050997 | quaternary ammonium group binding | 12 | 0.701415 | 0.025362 | 0.414504 | 0.401653 |
| GO:0003954 | NADH dehydrogenase activity | 21 | 0.700035 | 0.003401 | 0.248299 | 0.240602 |
| GO:0031418 | L-ascorbic acid binding | 13 | 0.692037 | 0.022375 | 0.401653 | 0.389201 |
| GO:0008137 | NADH dehydrogenase (ubiquinone) activity | 20 | 0.691840 | 0.005111 | 0.251898 | 0.244088 |
| GO:0050136 | NADH dehydrogenase (quinone) activity | 20 | 0.691840 | 0.005111 | 0.251898 | 0.244088 |
| GO:0005527 | macrolide binding | 14 | 0.691058 | 0.016453 | 0.343799 | 0.333141 |
| GO:0005528 | FK506 binding | 14 | 0.691058 | 0.016453 | 0.343799 | 0.333141 |
| GO:0043015 | gamma-tubulin binding | 17 | 0.688909 | 0.010309 | 0.328588 | 0.318401 |
| GO:0031420 | alkali metal ion binding | 14 | 0.673743 | 0.028169 | 0.440644 | 0.426983 |
| GO:0050840 | extracellular matrix binding | 35 | 0.672111 | 0.001661 | 0.211963 | 0.205392 |
| GO:0044769 | ATPase activity, coupled to transmembrane movement of ions, rotational mechanism | 19 | 0.667390 | 0.008562 | 0.306620 | 0.297114 |
| GO:0016628 | oxidoreductase activity, acting on the CH-CH group of donors, NAD or NADP as acceptor | 17 | 0.659640 | 0.018083 | 0.353591 | 0.342629 |
| GO:0048029 | monosaccharide binding | 47 | 0.658343 | 0.001631 | 0.211963 | 0.205392 |
| GO:0046961 | proton-transporting ATPase activity, rotational mechanism | 17 | 0.650382 | 0.020979 | 0.382867 | 0.370997 |
| GO:0004364 | glutathione transferase activity | 21 | 0.645979 | 0.013072 | 0.328588 | 0.318401 |
| GO:0036442 | hydrogen-exporting ATPase activity | 21 | 0.640668 | 0.017007 | 0.343799 | 0.333141 |
| GO:0016655 | oxidoreductase activity, acting on NAD(P)H, quinone or similar compound as acceptor | 25 | 0.635965 | 0.008681 | 0.306620 | 0.297114 |
| GO:0004867 | serine-type endopeptidase inhibitor activity | 35 | 0.632233 | 0.001709 | 0.211963 | 0.205392 |
| GO:0019200 | carbohydrate kinase activity | 22 | 0.630709 | 0.012281 | 0.328588 | 0.318401 |
| GO:0005200 | structural constituent of cytoskeleton | 42 | 0.607702 | 0.003339 | 0.248299 | 0.240602 |
| GO:0030551 | cyclic nucleotide binding | 19 | 0.599837 | 0.033043 | 0.484360 | 0.469344 |
| GO:0015078 | hydrogen ion transmembrane transporter activity | 60 | 0.597527 | 0.001582 | 0.211963 | 0.205392 |
| GO:0016684 | oxidoreductase activity, acting on peroxide as acceptor | 31 | 0.575078 | 0.011844 | 0.328588 | 0.318401 |
| GO:0004601 | peroxidase activity | 30 | 0.553717 | 0.023932 | 0.403156 | 0.390657 |
| GO:0005178 | integrin binding | 63 | 0.552746 | 0.003339 | 0.248299 | 0.240602 |
| GO:0019955 | cytokine binding | 37 | 0.535780 | 0.019934 | 0.369953 | 0.358484 |
| GO:0005518 | collagen binding | 34 | 0.530374 | 0.022887 | 0.403156 | 0.390657 |
| GO:0019829 | cation-transporting ATPase activity | 43 | 0.529477 | 0.013333 | 0.328588 | 0.318401 |
| GO:0042625 | ATPase activity, coupled to transmembrane movement of ions | 44 | 0.529393 | 0.014975 | 0.341618 | 0.331027 |
| GO:0016651 | oxidoreductase activity, acting on NAD(P)H | 51 | 0.517090 | 0.013699 | 0.328588 | 0.318401 |
| GO:0002020 | protease binding | 68 | 0.512208 | 0.001623 | 0.211963 | 0.205392 |
| GO:0019842 | vitamin binding | 49 | 0.508120 | 0.010309 | 0.328588 | 0.318401 |
| GO:0016860 | intramolecular oxidoreductase activity | 31 | 0.499305 | 0.049919 | 0.623493 | 0.604163 |
| GO:0061135 | endopeptidase regulator activity | 70 | 0.494465 | 0.006211 | 0.251898 | 0.244088 |
| GO:0061134 | peptidase regulator activity | 92 | 0.475423 | 0.004594 | 0.251898 | 0.244088 |
| GO:0019838 | growth factor binding | 82 | 0.471692 | 0.006504 | 0.254355 | 0.246470 |
| GO:0051082 | unfolded protein binding | 52 | 0.470773 | 0.034768 | 0.500937 | 0.485407 |
| GO:0004866 | endopeptidase inhibitor activity | 65 | 0.466714 | 0.015674 | 0.343799 | 0.333141 |
| GO:0030414 | peptidase inhibitor activity | 66 | 0.465594 | 0.017268 | 0.343799 | 0.333141 |
| GO:0009055 | electron carrier activity | 53 | 0.449968 | 0.048780 | 0.623493 | 0.604163 |
| GO:0008144 | drug binding | 65 | 0.438501 | 0.036335 | 0.516711 | 0.500692 |
| GO:0050839 | cell adhesion molecule binding | 112 | 0.428235 | 0.012539 | 0.328588 | 0.318401 |
| GO:0003735 | structural constituent of ribosome | 123 | 0.418031 | 0.005979 | 0.251898 | 0.244088 |
| GO:0015077 | monovalent inorganic cation transmembrane transporter activity | 154 | 0.399664 | 0.002869 | 0.248299 | 0.240602 |
| GO:0016491 | oxidoreductase activity | 431 | 0.397373 | 0.001287 | 0.211963 | 0.205392 |
| GO:0030246 | carbohydrate binding | 135 | 0.394565 | 0.013804 | 0.328588 | 0.318401 |
| GO:0005198 | structural molecule activity | 326 | 0.383722 | 0.001284 | 0.211963 | 0.205392 |
| GO:0032403 | protein complex binding | 687 | 0.331781 | 0.001189 | 0.211963 | 0.205392 |
| GO:0044877 | macromolecular complex binding | 1029 | 0.287430 | 0.015891 | 0.343799 | 0.333141 |
| GO:0003723 | RNA binding | 1220 | 0.276592 | 0.026696 | 0.423659 | 0.410525 |
| GO:0004872 | receptor activity | 390 | -0.265402 | 0.042735 | 0.584936 | 0.566802 |
| GO:0004871 | signal transducer activity | 477 | -0.270882 | 0.030769 | 0.462329 | 0.447996 |
| GO:0004888 | transmembrane signaling receptor activity | 265 | -0.287332 | 0.045113 | 0.603328 | 0.584623 |
| GO:0008047 | enzyme activator activity | 272 | -0.288895 | 0.036900 | 0.518024 | 0.501965 |
| GO:0000981 | RNA polymerase II transcription factor activity, sequence-specific DNA binding | 364 | -0.292391 | 0.004202 | 0.251898 | 0.244088 |
| GO:0000976 | transcription regulatory region sequence-specific DNA binding | 372 | -0.292607 | 0.023697 | 0.403156 | 0.390657 |
| GO:0000975 | regulatory region DNA binding | 473 | -0.294019 | 0.011236 | 0.328588 | 0.318401 |
| GO:0044212 | transcription regulatory region DNA binding | 473 | -0.294019 | 0.011236 | 0.328588 | 0.318401 |
| GO:0001071 | nucleic acid binding transcription factor activity | 551 | -0.296937 | 0.005714 | 0.251898 | 0.244088 |
| GO:0003700 | transcription factor activity, sequence-specific DNA binding | 551 | -0.296937 | 0.005714 | 0.251898 | 0.244088 |
| GO:0001067 | regulatory region nucleic acid binding | 476 | -0.300800 | 0.011364 | 0.328588 | 0.318401 |
| GO:0043565 | sequence-specific DNA binding | 550 | -0.300815 | 0.005587 | 0.251898 | 0.244088 |
| GO:0000978 | RNA polymerase II core promoter proximal region sequence-specific DNA binding | 197 | -0.306628 | 0.045296 | 0.603328 | 0.584623 |
| GO:0038023 | signaling receptor activity | 314 | -0.307684 | 0.007905 | 0.298487 | 0.289233 |
| GO:0060589 | nucleoside-triphosphatase regulator activity | 187 | -0.319449 | 0.030822 | 0.462329 | 0.447996 |
| GO:0016791 | phosphatase activity | 173 | -0.353028 | 0.006135 | 0.251898 | 0.244088 |
| GO:0001047 | core promoter binding | 103 | -0.356018 | 0.045732 | 0.603328 | 0.584623 |
| GO:0004930 | G-protein coupled receptor activity | 107 | -0.371605 | 0.023810 | 0.403156 | 0.390657 |
| GO:0004721 | phosphoprotein phosphatase activity | 116 | -0.373113 | 0.003030 | 0.248299 | 0.240602 |
| GO:0005088 | Ras guanyl-nucleotide exchange factor activity | 80 | -0.386439 | 0.030812 | 0.462329 | 0.447996 |
| GO:0004725 | protein tyrosine phosphatase activity | 55 | -0.401413 | 0.046322 | 0.603834 | 0.585114 |
| GO:0005089 | Rho guanyl-nucleotide exchange factor activity | 44 | -0.445050 | 0.041775 | 0.579040 | 0.561088 |
| GO:0001046 | core promoter sequence-specific DNA binding | 62 | -0.456266 | 0.011594 | 0.328588 | 0.318401 |
| GO:0035250 | UDP-galactosyltransferase activity | 33 | -0.462106 | 0.049020 | 0.623493 | 0.604163 |
| GO:0000979 | RNA polymerase II core promoter sequence-specific DNA binding | 35 | -0.509759 | 0.018970 | 0.364427 | 0.353129 |
| GO:0019003 | GDP binding | 48 | -0.516795 | 0.005222 | 0.251898 | 0.244088 |
| GO:0008528 | G-protein coupled peptide receptor activity | 24 | -0.545332 | 0.033175 | 0.484360 | 0.469344 |
| GO:0045182 | translation regulator activity | 23 | -0.575146 | 0.025761 | 0.414830 | 0.401969 |
| GO:0036002 | pre-mRNA binding | 20 | -0.614704 | 0.009950 | 0.328588 | 0.318401 |
| GO:0070888 | E-box binding | 20 | -0.617736 | 0.014742 | 0.341618 | 0.331027 |
| GO:0017147 | Wnt-protein binding | 16 | -0.648271 | 0.024831 | 0.411964 | 0.399192 |
| GO:0005109 | frizzled binding | 18 | -0.660020 | 0.016908 | 0.343799 | 0.333141 |
| GO:0004707 | MAP kinase activity | 15 | -0.672795 | 0.013575 | 0.328588 | 0.318401 |
| GO:0005154 | epidermal growth factor receptor binding | 20 | -0.674853 | 0.004902 | 0.251898 | 0.244088 |

## Rho BP
| ID | Description | setSize | enrichmentScore | pvalue | p.adjust | qvalues |
| --- | --- | --- | --- | --- | --- | --- |
| GO:0019884 | antigen processing and presentation of exogenous antigen | 15 | 0.745162 | 0.003552 | 0.157818 | 0.145789 |
| GO:0002474 | antigen processing and presentation of peptide antigen via MHC class I | 20 | 0.656735 | 0.013491 | 0.242276 | 0.223809 |
| GO:0048002 | antigen processing and presentation of peptide antigen | 27 | 0.595315 | 0.022807 | 0.297656 | 0.274967 |
| GO:0030509 | BMP signaling pathway | 71 | -0.394201 | 0.046784 | 0.396460 | 0.366241 |
| GO:0001953 | negative regulation of cell-matrix adhesion | 23 | 0.669784 | 0.001695 | 0.146671 | 0.135491 |
| GO:0000278 | mitotic cell cycle | 505 | -0.271393 | 0.025126 | 0.306730 | 0.283351 |
| GO:0007050 | cell cycle arrest | 90 | -0.405097 | 0.008798 | 0.213290 | 0.197033 |
| GO:0010458 | exit from mitosis | 13 | -0.705206 | 0.016627 | 0.258076 | 0.238405 |
| GO:0007389 | pattern specification process | 246 | -0.362905 | 0.003300 | 0.154291 | 0.142531 |
| GO:0001708 | cell fate specification | 45 | -0.414611 | 0.049020 | 0.403279 | 0.372540 |
| GO:0045165 | cell fate commitment | 139 | -0.428088 | 0.002985 | 0.154291 | 0.142531 |
| GO:0009798 | axis specification | 51 | -0.567382 | 0.002519 | 0.150485 | 0.139014 |
| GO:0001709 | cell fate determination | 21 | -0.573620 | 0.022779 | 0.297656 | 0.274967 |
| GO:0045168 | cell-cell signaling involved in cell fate commitment | 20 | -0.723098 | 0.002342 | 0.150485 | 0.139014 |
| GO:0007622 | rhythmic behavior | 19 | 0.761418 | 0.003257 | 0.154291 | 0.142531 |
| GO:0048512 | circadian behavior | 19 | 0.761418 | 0.003257 | 0.154291 | 0.142531 |
| GO:0032760 | positive regulation of tumor necrosis factor production | 34 | 0.520677 | 0.037300 | 0.358837 | 0.331485 |
| GO:1903557 | positive regulation of tumor necrosis factor superfamily cytokine production | 34 | 0.520677 | 0.037300 | 0.358837 | 0.331485 |
| GO:0032680 | regulation of tumor necrosis factor production | 56 | 0.482020 | 0.016556 | 0.258076 | 0.238405 |
| GO:1903555 | regulation of tumor necrosis factor superfamily cytokine production | 56 | 0.482020 | 0.016556 | 0.258076 | 0.238405 |
| GO:0032640 | tumor necrosis factor production | 57 | 0.481745 | 0.014778 | 0.249909 | 0.230860 |
| GO:0071706 | tumor necrosis factor superfamily cytokine production | 57 | 0.481745 | 0.014778 | 0.249909 | 0.230860 |
| GO:0001818 | negative regulation of cytokine production | 95 | 0.398099 | 0.031104 | 0.338794 | 0.312970 |
| GO:0034097 | response to cytokine | 277 | 0.356513 | 0.006667 | 0.201204 | 0.185867 |
| GO:0071345 | cellular response to cytokine stimulus | 222 | 0.338104 | 0.037736 | 0.358862 | 0.331509 |
| GO:0048821 | erythrocyte development | 22 | 0.586725 | 0.021505 | 0.291600 | 0.269373 |
| GO:0061515 | myeloid cell development | 41 | 0.499426 | 0.035775 | 0.357156 | 0.329932 |
| GO:0007420 | brain development | 341 | -0.286963 | 0.024793 | 0.306730 | 0.283351 |
| GO:0060322 | head development | 369 | -0.287319 | 0.016736 | 0.258848 | 0.239118 |
| GO:0001822 | kidney development | 129 | -0.332480 | 0.049563 | 0.405649 | 0.374729 |
| GO:0060560 | developmental growth involved in morphogenesis | 137 | -0.332720 | 0.048387 | 0.402085 | 0.371437 |
| GO:0014031 | mesenchymal cell development | 102 | -0.367756 | 0.029070 | 0.329842 | 0.304701 |
| GO:0048864 | stem cell development | 105 | -0.376065 | 0.023460 | 0.300764 | 0.277839 |
| GO:0021987 | cerebral cortex development | 72 | -0.396657 | 0.048913 | 0.403279 | 0.372540 |
| GO:0045995 | regulation of embryonic development | 69 | -0.402516 | 0.045198 | 0.389910 | 0.360190 |
| GO:0001892 | embryonic placenta development | 70 | -0.410547 | 0.024194 | 0.306252 | 0.282909 |
| GO:0072073 | kidney epithelium development | 59 | -0.433637 | 0.036939 | 0.358837 | 0.331485 |
| GO:0072006 | nephron development | 63 | -0.443542 | 0.008065 | 0.202919 | 0.187452 |
| GO:0003279 | cardiac septum development | 47 | -0.457521 | 0.027027 | 0.318318 | 0.294055 |
| GO:0060324 | face development | 41 | -0.475178 | 0.028061 | 0.322733 | 0.298133 |
| GO:0021536 | diencephalon development | 37 | -0.478200 | 0.024570 | 0.306252 | 0.282909 |
| GO:0035050 | embryonic heart tube development | 52 | -0.482538 | 0.007673 | 0.202919 | 0.187452 |
| GO:0072009 | nephron epithelium development | 48 | -0.486295 | 0.009901 | 0.222906 | 0.205916 |
| GO:0061053 | somite development | 45 | -0.491410 | 0.012315 | 0.234109 | 0.216265 |
| GO:0061326 | renal tubule development | 49 | -0.500939 | 0.005141 | 0.177337 | 0.163820 |
| GO:0001656 | metanephros development | 38 | -0.506103 | 0.020513 | 0.287537 | 0.265620 |
| GO:0045682 | regulation of epidermis development | 34 | -0.509312 | 0.016867 | 0.259032 | 0.239288 |
| GO:0014032 | neural crest cell development | 37 | -0.527569 | 0.020101 | 0.282708 | 0.261159 |
| GO:0072080 | nephron tubule development | 44 | -0.536142 | 0.005013 | 0.177337 | 0.163820 |
| GO:0021983 | pituitary gland development | 18 | -0.567336 | 0.037471 | 0.358837 | 0.331485 |
| GO:0003197 | endocardial cushion development | 21 | -0.584252 | 0.026066 | 0.312078 | 0.288291 |
| GO:0001823 | mesonephros development | 42 | -0.592828 | 0.002519 | 0.150485 | 0.139014 |
| GO:0001657 | ureteric bud development | 41 | -0.597731 | 0.002519 | 0.150485 | 0.139014 |
| GO:0072163 | mesonephric epithelium development | 41 | -0.597731 | 0.002519 | 0.150485 | 0.139014 |
| GO:0072164 | mesonephric tubule development | 41 | -0.597731 | 0.002519 | 0.150485 | 0.139014 |
| GO:0060438 | trachea development | 14 | -0.675704 | 0.023148 | 0.300105 | 0.277230 |
| GO:0048368 | lateral mesoderm development | 11 | -0.691361 | 0.031915 | 0.343322 | 0.317153 |
| GO:0072170 | metanephric tubule development | 12 | -0.707619 | 0.024664 | 0.306252 | 0.282909 |
| GO:0043584 | nose development | 11 | -0.709172 | 0.017778 | 0.269206 | 0.248687 |
| GO:0060674 | placenta blood vessel development | 21 | -0.712125 | 0.004975 | 0.177337 | 0.163820 |
| GO:0003283 | atrial septum development | 14 | -0.720780 | 0.007353 | 0.202919 | 0.187452 |
| GO:0071696 | ectodermal placode development | 14 | -0.729751 | 0.009281 | 0.218022 | 0.201404 |
| GO:0060716 | labyrinthine layer blood vessel development | 12 | -0.735642 | 0.011876 | 0.232501 | 0.214779 |
| GO:0061311 | cell surface receptor signaling pathway involved in heart development | 12 | -0.749527 | 0.013953 | 0.247459 | 0.228597 |
| GO:0045653 | negative regulation of megakaryocyte differentiation | 13 | 0.789355 | 0.005310 | 0.180282 | 0.166541 |
| GO:0045652 | regulation of megakaryocyte differentiation | 19 | 0.748575 | 0.003361 | 0.154291 | 0.142531 |
| GO:1901533 | negative regulation of hematopoietic progenitor cell differentiation | 17 | 0.597817 | 0.048027 | 0.401470 | 0.370869 |
| GO:0030219 | megakaryocyte differentiation | 34 | 0.563219 | 0.009852 | 0.222906 | 0.205916 |
| GO:0045638 | negative regulation of myeloid cell differentiation | 51 | 0.530601 | 0.004902 | 0.177337 | 0.163820 |
| GO:0045600 | positive regulation of fat cell differentiation | 30 | 0.525248 | 0.046699 | 0.396460 | 0.366241 |
| GO:0030099 | myeloid cell differentiation | 220 | 0.339010 | 0.036517 | 0.358837 | 0.331485 |
| GO:0048762 | mesenchymal cell differentiation | 108 | -0.363734 | 0.035608 | 0.357156 | 0.329932 |
| GO:0001649 | osteoblast differentiation | 131 | -0.373376 | 0.011696 | 0.232102 | 0.214411 |
| GO:0030856 | regulation of epithelial cell differentiation | 77 | -0.395143 | 0.037143 | 0.358837 | 0.331485 |
| GO:0045446 | endothelial cell differentiation | 56 | -0.431054 | 0.026316 | 0.314199 | 0.290250 |
| GO:0045445 | myoblast differentiation | 45 | -0.479127 | 0.018519 | 0.272618 | 0.251838 |
| GO:0002763 | positive regulation of myeloid leukocyte differentiation | 31 | -0.481672 | 0.035714 | 0.357156 | 0.329932 |
| GO:0014033 | neural crest cell differentiation | 40 | -0.548919 | 0.015306 | 0.251971 | 0.232765 |
| GO:0045661 | regulation of myoblast differentiation | 26 | -0.610504 | 0.004950 | 0.177337 | 0.163820 |
| GO:0045662 | negative regulation of myoblast differentiation | 13 | -0.646255 | 0.037915 | 0.359235 | 0.331853 |
| GO:0045672 | positive regulation of osteoclast differentiation | 13 | -0.732275 | 0.006803 | 0.202919 | 0.187452 |
| GO:0021533 | cell differentiation in hindbrain | 14 | 0.665056 | 0.029720 | 0.332407 | 0.307070 |
| GO:0007224 | smoothened signaling pathway | 78 | -0.384459 | 0.038781 | 0.362416 | 0.334792 |
| GO:0008589 | regulation of smoothened signaling pathway | 45 | -0.502552 | 0.010782 | 0.227462 | 0.210124 |
| GO:0045879 | negative regulation of smoothened signaling pathway | 20 | -0.607497 | 0.022613 | 0.297656 | 0.274967 |
| GO:0045880 | positive regulation of smoothened signaling pathway | 18 | -0.624096 | 0.025126 | 0.306730 | 0.283351 |
| GO:0060831 | smoothened signaling pathway involved in dorsal/ventral neural tube patterning | 11 | -0.670393 | 0.047962 | 0.401470 | 0.370869 |
| GO:0002455 | humoral immune response mediated by circulating immunoglobulin | 11 | 0.793218 | 0.007220 | 0.202919 | 0.187452 |
| GO:0070232 | regulation of T cell apoptotic process | 18 | 0.637601 | 0.029565 | 0.332017 | 0.306709 |
| GO:0070231 | T cell apoptotic process | 30 | 0.549294 | 0.026801 | 0.317373 | 0.293182 |
| GO:0016064 | immunoglobulin mediated immune response | 48 | 0.520514 | 0.008013 | 0.202919 | 0.187452 |
| GO:0002449 | lymphocyte mediated immunity | 101 | 0.403122 | 0.022693 | 0.297656 | 0.274967 |
| GO:0002252 | immune effector process | 347 | 0.364512 | 0.002587 | 0.150485 | 0.139014 |
| GO:0006955 | immune response | 477 | 0.322371 | 0.011509 | 0.230497 | 0.212928 |
| GO:0002682 | regulation of immune system process | 594 | 0.298231 | 0.042067 | 0.375940 | 0.347284 |
| GO:0002376 | immune system process | 1101 | 0.294268 | 0.011198 | 0.229256 | 0.211781 |
| GO:0002251 | organ or tissue specific immune response | 15 | -0.636862 | 0.037647 | 0.358837 | 0.331485 |
| GO:0002385 | mucosal immune response | 15 | -0.636862 | 0.037647 | 0.358837 | 0.331485 |
| GO:0035455 | response to interferon-alpha | 12 | 0.747326 | 0.009653 | 0.221002 | 0.204156 |
| GO:0034340 | response to type I interferon | 17 | 0.727569 | 0.007042 | 0.202919 | 0.187452 |
| GO:0060337 | type I interferon signaling pathway | 14 | 0.716024 | 0.012821 | 0.234109 | 0.216265 |
| GO:0071357 | cellular response to type I interferon | 14 | 0.716024 | 0.012821 | 0.234109 | 0.216265 |
| GO:0035456 | response to interferon-beta | 24 | 0.641034 | 0.008834 | 0.213290 | 0.197033 |
| GO:0002526 | acute inflammatory response | 38 | 0.601226 | 0.001639 | 0.146671 | 0.135491 |
| GO:0002673 | regulation of acute inflammatory response | 21 | 0.583105 | 0.048110 | 0.401470 | 0.370869 |
| GO:0034341 | response to interferon-gamma | 30 | 0.528358 | 0.034722 | 0.354232 | 0.327231 |
| GO:0006956 | complement activation | 19 | 0.731135 | 0.001721 | 0.146671 | 0.135491 |
| GO:0045087 | innate immune response | 237 | 0.361009 | 0.014205 | 0.247459 | 0.228597 |
| GO:0002227 | innate immune response in mucosa | 12 | -0.709632 | 0.034562 | 0.353429 | 0.326490 |
| GO:0045104 | intermediate filament cytoskeleton organization | 19 | 0.644350 | 0.018116 | 0.271489 | 0.250796 |
| GO:0045103 | intermediate filament-based process | 20 | 0.641371 | 0.014235 | 0.247459 | 0.228597 |
| GO:0042987 | amyloid precursor protein catabolic process | 16 | 0.710679 | 0.007105 | 0.202919 | 0.187452 |
| GO:0006089 | lactate metabolic process | 13 | 0.702114 | 0.015734 | 0.257072 | 0.237477 |
| GO:0051156 | glucose 6-phosphate metabolic process | 13 | 0.687776 | 0.033628 | 0.351604 | 0.324804 |
| GO:0019320 | hexose catabolic process | 12 | 0.683708 | 0.029982 | 0.332407 | 0.307070 |
| GO:0090322 | regulation of superoxide metabolic process | 12 | 0.667172 | 0.047038 | 0.397721 | 0.367406 |
| GO:0015985 | energy coupled proton transport, down electrochemical gradient | 17 | 0.659811 | 0.010490 | 0.223468 | 0.206434 |
| GO:0015986 | ATP synthesis coupled proton transport | 17 | 0.659811 | 0.010490 | 0.223468 | 0.206434 |
| GO:0009206 | purine ribonucleoside triphosphate biosynthetic process | 37 | 0.658165 | 0.001678 | 0.146671 | 0.135491 |
| GO:0046365 | monosaccharide catabolic process | 14 | 0.656418 | 0.029361 | 0.330577 | 0.305380 |
| GO:0009201 | ribonucleoside triphosphate biosynthetic process | 39 | 0.653802 | 0.001701 | 0.146671 | 0.135491 |
| GO:2000573 | positive regulation of DNA biosynthetic process | 16 | 0.643951 | 0.041367 | 0.375325 | 0.346717 |
| GO:0006754 | ATP biosynthetic process | 31 | 0.628944 | 0.008333 | 0.206811 | 0.191047 |
| GO:0009145 | purine nucleoside triphosphate biosynthetic process | 38 | 0.625732 | 0.003373 | 0.154291 | 0.142531 |
| GO:0050435 | beta-amyloid metabolic process | 19 | 0.623141 | 0.024348 | 0.306252 | 0.282909 |
| GO:0006767 | water-soluble vitamin metabolic process | 20 | 0.599085 | 0.028070 | 0.322733 | 0.298133 |
| GO:0009142 | nucleoside triphosphate biosynthetic process | 47 | 0.567159 | 0.001667 | 0.146671 | 0.135491 |
| GO:0019674 | NAD metabolic process | 24 | 0.554289 | 0.042955 | 0.377903 | 0.349098 |
| GO:0006096 | glycolytic process | 47 | 0.547417 | 0.006525 | 0.198314 | 0.183198 |
| GO:0006757 | ATP generation from ADP | 47 | 0.547417 | 0.006525 | 0.198314 | 0.183198 |
| GO:0046031 | ADP metabolic process | 52 | 0.544393 | 0.003210 | 0.154291 | 0.142531 |
| GO:0022904 | respiratory electron transport chain | 43 | 0.542235 | 0.008375 | 0.206811 | 0.191047 |
| GO:0042451 | purine nucleoside biosynthetic process | 65 | 0.539772 | 0.003221 | 0.154291 | 0.142531 |
| GO:0046129 | purine ribonucleoside biosynthetic process | 65 | 0.539772 | 0.003221 | 0.154291 | 0.142531 |
| GO:0006749 | glutathione metabolic process | 40 | 0.537790 | 0.011765 | 0.232406 | 0.214692 |
| GO:0006081 | cellular aldehyde metabolic process | 37 | 0.526243 | 0.031034 | 0.338794 | 0.312970 |
| GO:0006090 | pyruvate metabolic process | 64 | 0.521090 | 0.001575 | 0.146671 | 0.135491 |
| GO:0042455 | ribonucleoside biosynthetic process | 72 | 0.510476 | 0.004862 | 0.177337 | 0.163820 |
| GO:0009135 | purine nucleoside diphosphate metabolic process | 57 | 0.509939 | 0.004785 | 0.177337 | 0.163820 |
| GO:0009179 | purine ribonucleoside diphosphate metabolic process | 57 | 0.509939 | 0.004785 | 0.177337 | 0.163820 |
| GO:0009127 | purine nucleoside monophosphate biosynthetic process | 44 | 0.508296 | 0.008078 | 0.202919 | 0.187452 |
| GO:0009168 | purine ribonucleoside monophosphate biosynthetic process | 44 | 0.508296 | 0.008078 | 0.202919 | 0.187452 |
| GO:0009199 | ribonucleoside triphosphate metabolic process | 140 | 0.505563 | 0.001456 | 0.146671 | 0.135491 |
| GO:0009205 | purine ribonucleoside triphosphate metabolic process | 137 | 0.503373 | 0.001464 | 0.146671 | 0.135491 |
| GO:0046034 | ATP metabolic process | 128 | 0.494491 | 0.001445 | 0.146671 | 0.135491 |
| GO:0009156 | ribonucleoside monophosphate biosynthetic process | 46 | 0.492668 | 0.009804 | 0.222906 | 0.205916 |
| GO:0009163 | nucleoside biosynthetic process | 74 | 0.491590 | 0.006483 | 0.198314 | 0.183198 |
| GO:1903363 | negative regulation of cellular protein catabolic process | 45 | 0.490613 | 0.027157 | 0.318629 | 0.294342 |
| GO:0046209 | nitric oxide metabolic process | 34 | 0.490008 | 0.048739 | 0.403279 | 0.372540 |
| GO:0009144 | purine nucleoside triphosphate metabolic process | 142 | 0.488993 | 0.001477 | 0.146671 | 0.135491 |
| GO:0022900 | electron transport chain | 46 | 0.481564 | 0.035484 | 0.357156 | 0.329932 |
| GO:0009132 | nucleoside diphosphate metabolic process | 72 | 0.481310 | 0.006339 | 0.198314 | 0.183198 |
| GO:0009141 | nucleoside triphosphate metabolic process | 154 | 0.477268 | 0.001447 | 0.146671 | 0.135491 |
| GO:0009185 | ribonucleoside diphosphate metabolic process | 61 | 0.476776 | 0.012579 | 0.234109 | 0.216265 |
| GO:0072524 | pyridine-containing compound metabolic process | 93 | 0.473430 | 0.006154 | 0.198314 | 0.183198 |
| GO:1901659 | glycosyl compound biosynthetic process | 76 | 0.470889 | 0.011236 | 0.229256 | 0.211781 |
| GO:0009124 | nucleoside monophosphate biosynthetic process | 52 | 0.469444 | 0.024470 | 0.306252 | 0.282909 |
| GO:0046128 | purine ribonucleoside metabolic process | 187 | 0.465249 | 0.001401 | 0.146671 | 0.135491 |
| GO:0042278 | purine nucleoside metabolic process | 190 | 0.464154 | 0.001391 | 0.146671 | 0.135491 |
| GO:0072593 | reactive oxygen species metabolic process | 134 | 0.463962 | 0.003044 | 0.154291 | 0.142531 |
| GO:0009126 | purine nucleoside monophosphate metabolic process | 145 | 0.463532 | 0.001406 | 0.146671 | 0.135491 |
| GO:0009167 | purine ribonucleoside monophosphate metabolic process | 145 | 0.463532 | 0.001406 | 0.146671 | 0.135491 |
| GO:0009161 | ribonucleoside monophosphate metabolic process | 147 | 0.458457 | 0.001404 | 0.146671 | 0.135491 |
| GO:2000377 | regulation of reactive oxygen species metabolic process | 89 | 0.455961 | 0.006192 | 0.198314 | 0.183198 |
| GO:0019362 | pyridine nucleotide metabolic process | 91 | 0.450110 | 0.011024 | 0.228136 | 0.210747 |
| GO:0046496 | nicotinamide nucleotide metabolic process | 91 | 0.450110 | 0.011024 | 0.228136 | 0.210747 |
| GO:0009123 | nucleoside monophosphate metabolic process | 156 | 0.449835 | 0.001381 | 0.146671 | 0.135491 |
| GO:0009119 | ribonucleoside metabolic process | 199 | 0.449273 | 0.001410 | 0.146671 | 0.135491 |
| GO:0044724 | single-organism carbohydrate catabolic process | 70 | 0.442243 | 0.033071 | 0.349698 | 0.323043 |
| GO:1901657 | glycosyl compound metabolic process | 220 | 0.441858 | 0.001393 | 0.146671 | 0.135491 |
| GO:0009116 | nucleoside metabolic process | 210 | 0.439846 | 0.001414 | 0.146671 | 0.135491 |
| GO:0045333 | cellular respiration | 97 | 0.431167 | 0.019374 | 0.277887 | 0.256706 |
| GO:0006733 | oxidoreduction coenzyme metabolic process | 101 | 0.427266 | 0.016975 | 0.259770 | 0.239970 |
| GO:0009152 | purine ribonucleotide biosynthetic process | 126 | 0.407437 | 0.010219 | 0.223468 | 0.206434 |
| GO:0070646 | protein modification by small protein removal | 83 | 0.406319 | 0.036278 | 0.358837 | 0.331485 |
| GO:0072522 | purine-containing compound biosynthetic process | 139 | 0.406269 | 0.010189 | 0.223468 | 0.206434 |
| GO:0009150 | purine ribonucleotide metabolic process | 257 | 0.406205 | 0.001366 | 0.146671 | 0.135491 |
| GO:0006163 | purine nucleotide metabolic process | 265 | 0.405171 | 0.001387 | 0.146671 | 0.135491 |
| GO:0006164 | purine nucleotide biosynthetic process | 132 | 0.402538 | 0.010204 | 0.223468 | 0.206434 |
| GO:0072521 | purine-containing compound metabolic process | 292 | 0.399609 | 0.001326 | 0.146671 | 0.135491 |
| GO:0009259 | ribonucleotide metabolic process | 264 | 0.399464 | 0.001357 | 0.146671 | 0.135491 |
| GO:0046390 | ribose phosphate biosynthetic process | 134 | 0.399385 | 0.011834 | 0.232501 | 0.214779 |
| GO:0019693 | ribose phosphate metabolic process | 273 | 0.395096 | 0.004027 | 0.175007 | 0.161667 |
| GO:0009260 | ribonucleotide biosynthetic process | 131 | 0.394290 | 0.016467 | 0.258076 | 0.238405 |
| GO:0005996 | monosaccharide metabolic process | 142 | 0.391021 | 0.008902 | 0.213748 | 0.197456 |
| GO:0031330 | negative regulation of cellular catabolic process | 93 | 0.390946 | 0.041534 | 0.375940 | 0.347284 |
| GO:0006575 | cellular modified amino acid metabolic process | 115 | 0.389171 | 0.027692 | 0.322733 | 0.298133 |
| GO:0051186 | cofactor metabolic process | 221 | 0.385224 | 0.005517 | 0.184446 | 0.170387 |
| GO:0009165 | nucleotide biosynthetic process | 167 | 0.383279 | 0.014451 | 0.249909 | 0.230860 |
| GO:0006732 | coenzyme metabolic process | 189 | 0.378442 | 0.012535 | 0.234109 | 0.216265 |
| GO:0019318 | hexose metabolic process | 132 | 0.374657 | 0.036982 | 0.358837 | 0.331485 |
| GO:1901293 | nucleoside phosphate biosynthetic process | 172 | 0.371780 | 0.021739 | 0.291600 | 0.269373 |
| GO:0009117 | nucleotide metabolic process | 366 | 0.361787 | 0.002614 | 0.150485 | 0.139014 |
| GO:0006753 | nucleoside phosphate metabolic process | 372 | 0.360965 | 0.002604 | 0.150485 | 0.139014 |
| GO:0055086 | nucleobase-containing small molecule metabolic process | 403 | 0.360015 | 0.002632 | 0.150485 | 0.139014 |
| GO:0006091 | generation of precursor metabolites and energy | 205 | 0.354338 | 0.025000 | 0.306730 | 0.283351 |
| GO:0055114 | oxidation-reduction process | 569 | 0.348768 | 0.001235 | 0.146671 | 0.135491 |
| GO:0006518 | peptide metabolic process | 464 | 0.318543 | 0.017857 | 0.269469 | 0.248930 |
| GO:0019637 | organophosphate metabolic process | 595 | 0.313181 | 0.014652 | 0.249909 | 0.230860 |
| GO:1901564 | organonitrogen compound metabolic process | 1145 | 0.312025 | 0.002247 | 0.150485 | 0.139014 |
| GO:1901135 | carbohydrate derivative metabolic process | 601 | 0.307629 | 0.015912 | 0.258034 | 0.238366 |
| GO:0043603 | cellular amide metabolic process | 544 | 0.307052 | 0.016414 | 0.258076 | 0.238405 |
| GO:0044712 | single-organism catabolic process | 639 | 0.300732 | 0.024600 | 0.306252 | 0.282909 |
| GO:0044710 | single-organism metabolic process | 2801 | 0.299949 | 0.001020 | 0.146671 | 0.135491 |
| GO:1901566 | organonitrogen compound biosynthetic process | 738 | 0.291902 | 0.034360 | 0.353025 | 0.326116 |
| GO:0044281 | small molecule metabolic process | 1069 | 0.284464 | 0.013652 | 0.244161 | 0.225550 |
| GO:0008152 | metabolic process | 6203 | 0.260640 | 0.008016 | 0.202919 | 0.187452 |
| GO:0006635 | fatty acid beta-oxidation | 49 | -0.433369 | 0.037037 | 0.358837 | 0.331485 |
| GO:0006695 | cholesterol biosynthetic process | 34 | -0.499766 | 0.046341 | 0.395678 | 0.365518 |
| GO:1902653 | secondary alcohol biosynthetic process | 34 | -0.499766 | 0.046341 | 0.395678 | 0.365518 |
| GO:0010894 | negative regulation of steroid biosynthetic process | 15 | -0.591360 | 0.047516 | 0.400204 | 0.369700 |
| GO:0045939 | negative regulation of steroid metabolic process | 15 | -0.591360 | 0.047516 | 0.400204 | 0.369700 |
| GO:0033539 | fatty acid beta-oxidation using acyl-CoA dehydrogenase | 16 | -0.608049 | 0.025761 | 0.310133 | 0.286493 |
| GO:0061013 | regulation of mRNA catabolic process | 17 | -0.633917 | 0.021429 | 0.291600 | 0.269373 |
| GO:0051900 | regulation of mitochondrial depolarization | 11 | 0.669968 | 0.042048 | 0.375940 | 0.347284 |
| GO:0051560 | mitochondrial calcium ion homeostasis | 13 | 0.658036 | 0.038664 | 0.362145 | 0.334541 |
| GO:0090201 | negative regulation of release of cytochrome c from mitochondria | 17 | 0.645338 | 0.031250 | 0.339531 | 0.313651 |
| GO:0010823 | negative regulation of mitochondrion organization | 31 | 0.606987 | 0.008000 | 0.202919 | 0.187452 |
| GO:0001836 | release of cytochrome c from mitochondria | 44 | 0.563962 | 0.004926 | 0.177337 | 0.163820 |
| GO:0032543 | mitochondrial translation | 36 | 0.560620 | 0.013311 | 0.241732 | 0.223306 |
| GO:0090199 | regulation of release of cytochrome c from mitochondria | 36 | 0.556518 | 0.011345 | 0.230403 | 0.212841 |
| GO:0046902 | regulation of mitochondrial membrane permeability | 37 | 0.552404 | 0.023411 | 0.300764 | 0.277839 |
| GO:0051881 | regulation of mitochondrial membrane potential | 42 | 0.548902 | 0.010363 | 0.223468 | 0.206434 |
| GO:0007006 | mitochondrial membrane organization | 63 | 0.538336 | 0.003236 | 0.154291 | 0.142531 |
| GO:0007005 | mitochondrion organization | 420 | 0.365709 | 0.001255 | 0.146671 | 0.135491 |
| GO:0001833 | inner cell mass cell proliferation | 11 | 0.766472 | 0.001757 | 0.146884 | 0.135688 |
| GO:0032944 | regulation of mononuclear cell proliferation | 90 | -0.377440 | 0.029940 | 0.332407 | 0.307070 |
| GO:0050670 | regulation of lymphocyte proliferation | 88 | -0.378869 | 0.032353 | 0.346320 | 0.319923 |
| GO:0050680 | negative regulation of epithelial cell proliferation | 91 | -0.420000 | 0.010870 | 0.228136 | 0.210747 |
| GO:0010463 | mesenchymal cell proliferation | 34 | -0.529216 | 0.012755 | 0.234109 | 0.216265 |
| GO:0010464 | regulation of mesenchymal cell proliferation | 29 | -0.537549 | 0.022005 | 0.294256 | 0.271827 |
| GO:0002053 | positive regulation of mesenchymal cell proliferation | 24 | -0.569636 | 0.014151 | 0.247459 | 0.228597 |
| GO:0043616 | keratinocyte proliferation | 20 | -0.584665 | 0.038554 | 0.362145 | 0.334541 |
| GO:0035019 | somatic stem cell population maintenance | 32 | -0.522308 | 0.016867 | 0.259032 | 0.239288 |
| GO:0097284 | hepatocyte apoptotic process | 12 | 0.804287 | 0.001855 | 0.150485 | 0.139014 |
| GO:1902175 | regulation of oxidative stress-induced intrinsic apoptotic signaling pathway | 21 | 0.620012 | 0.025641 | 0.309544 | 0.285950 |
| GO:2000379 | positive regulation of reactive oxygen species metabolic process | 48 | 0.599487 | 0.001639 | 0.146671 | 0.135491 |
| GO:1903428 | positive regulation of reactive oxygen species biosynthetic process | 25 | 0.593369 | 0.018707 | 0.273747 | 0.252881 |
| GO:0008631 | intrinsic apoptotic signaling pathway in response to oxidative stress | 36 | 0.551412 | 0.016393 | 0.258076 | 0.238405 |
| GO:1903426 | regulation of reactive oxygen species biosynthetic process | 34 | 0.546144 | 0.015177 | 0.251754 | 0.232565 |
| GO:0070228 | regulation of lymphocyte apoptotic process | 33 | 0.530162 | 0.027200 | 0.318629 | 0.294342 |
| GO:0008637 | apoptotic mitochondrial changes | 81 | 0.511099 | 0.001560 | 0.146671 | 0.135491 |
| GO:1903409 | reactive oxygen species biosynthetic process | 43 | 0.510298 | 0.021595 | 0.291600 | 0.269373 |
| GO:0033555 | multicellular organismal response to stress | 39 | 0.507665 | 0.042139 | 0.375940 | 0.347284 |
| GO:0070227 | lymphocyte apoptotic process | 45 | 0.496840 | 0.019169 | 0.276777 | 0.255680 |
| GO:0043154 | negative regulation of cysteine-type endopeptidase activity involved in apoptotic process | 57 | 0.484081 | 0.011475 | 0.230497 | 0.212928 |
| GO:0043280 | positive regulation of cysteine-type endopeptidase activity involved in apoptotic process | 74 | 0.482771 | 0.004539 | 0.177337 | 0.163820 |
| GO:0043281 | regulation of cysteine-type endopeptidase activity involved in apoptotic process | 131 | 0.456301 | 0.001451 | 0.146671 | 0.135491 |
| GO:0043149 | stress fiber assembly | 60 | 0.454256 | 0.029260 | 0.330295 | 0.305119 |
| GO:2001243 | negative regulation of intrinsic apoptotic signaling pathway | 64 | 0.453410 | 0.019608 | 0.280315 | 0.258948 |
| GO:2001235 | positive regulation of apoptotic signaling pathway | 124 | 0.397102 | 0.014728 | 0.249909 | 0.230860 |
| GO:2001234 | negative regulation of apoptotic signaling pathway | 145 | 0.395266 | 0.005882 | 0.195150 | 0.180276 |
| GO:0097193 | intrinsic apoptotic signaling pathway | 198 | 0.388232 | 0.012676 | 0.234109 | 0.216265 |
| GO:0043524 | negative regulation of neuron apoptotic process | 109 | 0.385915 | 0.037651 | 0.358837 | 0.331485 |
| GO:2001233 | regulation of apoptotic signaling pathway | 267 | 0.370879 | 0.004104 | 0.176592 | 0.163132 |
| GO:0051402 | neuron apoptotic process | 178 | 0.368390 | 0.025298 | 0.307105 | 0.283696 |
| GO:0097190 | apoptotic signaling pathway | 391 | 0.364329 | 0.001319 | 0.146671 | 0.135491 |
| GO:0043523 | regulation of neuron apoptotic process | 162 | 0.363843 | 0.031343 | 0.339696 | 0.313803 |
| GO:0070997 | neuron death | 232 | 0.347360 | 0.015172 | 0.251754 | 0.232565 |
| GO:1901214 | regulation of neuron death | 208 | 0.340035 | 0.036775 | 0.358837 | 0.331485 |
| GO:0006952 | defense response | 576 | 0.332116 | 0.003636 | 0.159633 | 0.147465 |
| GO:0010942 | positive regulation of cell death | 400 | 0.331568 | 0.012579 | 0.234109 | 0.216265 |
| GO:0043068 | positive regulation of programmed cell death | 377 | 0.329518 | 0.018987 | 0.275983 | 0.254947 |
| GO:0043065 | positive regulation of apoptotic process | 374 | 0.329117 | 0.016582 | 0.258076 | 0.238405 |
| GO:0043066 | negative regulation of apoptotic process | 531 | 0.315422 | 0.017157 | 0.261627 | 0.241685 |
| GO:0043067 | regulation of programmed cell death | 890 | 0.314682 | 0.001120 | 0.146671 | 0.135491 |
| GO:0043069 | negative regulation of programmed cell death | 541 | 0.314408 | 0.015873 | 0.258034 | 0.238366 |
| GO:0042981 | regulation of apoptotic process | 879 | 0.313771 | 0.001125 | 0.146671 | 0.135491 |
| GO:0010941 | regulation of cell death | 962 | 0.306422 | 0.001117 | 0.146671 | 0.135491 |
| GO:0012501 | programmed cell death | 1121 | 0.299317 | 0.001106 | 0.146671 | 0.135491 |
| GO:0060548 | negative regulation of cell death | 595 | 0.299056 | 0.032297 | 0.346320 | 0.319923 |
| GO:0006915 | apoptotic process | 1103 | 0.297366 | 0.002198 | 0.150485 | 0.139014 |
| GO:0016265 | death | 1208 | 0.295181 | 0.001080 | 0.146671 | 0.135491 |
| GO:0008219 | cell death | 1203 | 0.294876 | 0.002157 | 0.150485 | 0.139014 |
| GO:0006950 | response to stress | 1826 | 0.269593 | 0.023555 | 0.301083 | 0.278134 |
| GO:0043620 | regulation of DNA-templated transcription in response to stress | 33 | -0.535052 | 0.010782 | 0.227462 | 0.210124 |
| GO:0010656 | negative regulation of muscle cell apoptotic process | 27 | -0.542512 | 0.034314 | 0.353025 | 0.326116 |
| GO:0043618 | regulation of transcription from RNA polymerase II promoter in response to stress | 30 | -0.545227 | 0.013405 | 0.241732 | 0.223306 |
| GO:0071604 | transforming growth factor beta production | 14 | 0.665647 | 0.036430 | 0.358837 | 0.331485 |
| GO:0030111 | regulation of Wnt signaling pathway | 162 | -0.337444 | 0.021277 | 0.291600 | 0.269373 |
| GO:0060828 | regulation of canonical Wnt signaling pathway | 115 | -0.347002 | 0.031546 | 0.341039 | 0.315044 |
| GO:0030177 | positive regulation of Wnt signaling pathway | 64 | -0.493693 | 0.002717 | 0.153374 | 0.141683 |
| GO:0090263 | positive regulation of canonical Wnt signaling pathway | 41 | -0.605547 | 0.002513 | 0.150485 | 0.139014 |
| GO:0051895 | negative regulation of focal adhesion assembly | 12 | 0.769878 | 0.007246 | 0.202919 | 0.187452 |
| GO:1901889 | negative regulation of cell junction assembly | 13 | 0.758047 | 0.005386 | 0.181454 | 0.167623 |
| GO:0030325 | adrenal gland development | 13 | 0.739948 | 0.014159 | 0.247459 | 0.228597 |
| GO:0032095 | regulation of response to food | 13 | 0.734925 | 0.003521 | 0.157818 | 0.145789 |
| GO:0048070 | regulation of developmental pigmentation | 12 | 0.734188 | 0.013937 | 0.247459 | 0.228597 |
| GO:0001963 | synaptic transmission, dopaminergic | 15 | 0.731089 | 0.005051 | 0.177337 | 0.163820 |
| GO:0070861 | regulation of protein exit from endoplasmic reticulum | 14 | 0.730962 | 0.006981 | 0.202919 | 0.187452 |
| GO:0018126 | protein hydroxylation | 11 | 0.715407 | 0.024436 | 0.306252 | 0.282909 |
| GO:0051882 | mitochondrial depolarization | 12 | 0.712299 | 0.018051 | 0.271445 | 0.250755 |
| GO:0072376 | protein activation cascade | 24 | 0.707535 | 0.001672 | 0.146671 | 0.135491 |
| GO:0071218 | cellular response to misfolded protein | 11 | 0.698990 | 0.033808 | 0.351604 | 0.324804 |
| GO:0072595 | maintenance of protein localization in organelle | 17 | 0.697470 | 0.012069 | 0.233119 | 0.215350 |
| GO:0046835 | carbohydrate phosphorylation | 21 | 0.697203 | 0.001715 | 0.146671 | 0.135491 |
| GO:0042832 | defense response to protozoan | 12 | 0.691922 | 0.029144 | 0.329842 | 0.304701 |
| GO:0046931 | pore complex assembly | 12 | 0.685698 | 0.024390 | 0.306252 | 0.282909 |
| GO:0098815 | modulation of excitatory postsynaptic potential | 14 | 0.681314 | 0.028520 | 0.325909 | 0.301068 |
| GO:0001504 | neurotransmitter uptake | 12 | 0.679229 | 0.036697 | 0.358837 | 0.331485 |
| GO:0050850 | positive regulation of calcium-mediated signaling | 15 | 0.678021 | 0.011945 | 0.232635 | 0.214903 |
| GO:0006336 | DNA replication-independent nucleosome assembly | 22 | 0.676559 | 0.001647 | 0.146671 | 0.135491 |
| GO:0034724 | DNA replication-independent nucleosome organization | 22 | 0.676559 | 0.001647 | 0.146671 | 0.135491 |
| GO:0071800 | podosome assembly | 14 | 0.663871 | 0.030576 | 0.336408 | 0.310766 |
| GO:0001562 | response to protozoan | 15 | 0.661164 | 0.023339 | 0.300764 | 0.277839 |
| GO:0051788 | response to misfolded protein | 13 | 0.659567 | 0.040516 | 0.373440 | 0.344975 |
| GO:1903959 | regulation of anion transmembrane transport | 14 | 0.658571 | 0.045217 | 0.389910 | 0.360190 |
| GO:2000242 | negative regulation of reproductive process | 17 | 0.654211 | 0.018771 | 0.273759 | 0.252892 |
| GO:0098586 | cellular response to virus | 19 | 0.642714 | 0.022727 | 0.297656 | 0.274967 |
| GO:1902017 | regulation of cilium assembly | 16 | 0.633044 | 0.046512 | 0.396352 | 0.366141 |
| GO:0046596 | regulation of viral entry into host cell | 17 | 0.628558 | 0.039724 | 0.368100 | 0.340043 |
| GO:0061098 | positive regulation of protein tyrosine kinase activity | 20 | 0.627797 | 0.020900 | 0.290201 | 0.268081 |
| GO:0001832 | blastocyst growth | 18 | 0.626387 | 0.024263 | 0.306252 | 0.282909 |
| GO:0033057 | multicellular organismal reproductive behavior | 17 | 0.622153 | 0.045217 | 0.389910 | 0.360190 |
| GO:0061077 | chaperone-mediated protein folding | 36 | 0.606274 | 0.003333 | 0.154291 | 0.142531 |
| GO:0044705 | multi-organism reproductive behavior | 23 | 0.598388 | 0.021700 | 0.291600 | 0.269373 |
| GO:0019098 | reproductive behavior | 24 | 0.596845 | 0.021622 | 0.291600 | 0.269373 |
| GO:0003254 | regulation of membrane depolarization | 22 | 0.595882 | 0.025090 | 0.306730 | 0.283351 |
| GO:0032469 | endoplasmic reticulum calcium ion homeostasis | 19 | 0.593876 | 0.043630 | 0.382290 | 0.353151 |
| GO:0014068 | positive regulation of phosphatidylinositol 3-kinase signaling | 32 | 0.593542 | 0.004847 | 0.177337 | 0.163820 |
| GO:0048066 | developmental pigmentation | 24 | 0.588461 | 0.027826 | 0.322733 | 0.298133 |
| GO:0032527 | protein exit from endoplasmic reticulum | 30 | 0.568531 | 0.015254 | 0.251971 | 0.232765 |
| GO:0051339 | regulation of lyase activity | 38 | 0.560714 | 0.015000 | 0.251699 | 0.232514 |
| GO:0060079 | excitatory postsynaptic potential | 35 | 0.558650 | 0.013378 | 0.241732 | 0.223306 |
| GO:0090559 | regulation of membrane permeability | 42 | 0.555006 | 0.015152 | 0.251754 | 0.232565 |
| GO:1902600 | hydrogen ion transmembrane transport | 44 | 0.551670 | 0.006515 | 0.198314 | 0.183198 |
| GO:0048477 | oogenesis | 39 | 0.546330 | 0.016393 | 0.258076 | 0.238405 |
| GO:0010466 | negative regulation of peptidase activity | 106 | 0.545221 | 0.001520 | 0.146671 | 0.135491 |
| GO:0006165 | nucleoside diphosphate phosphorylation | 56 | 0.537719 | 0.004854 | 0.177337 | 0.163820 |
| GO:0015992 | proton transport | 64 | 0.537587 | 0.004754 | 0.177337 | 0.163820 |
| GO:0010951 | negative regulation of endopeptidase activity | 89 | 0.535752 | 0.001541 | 0.146671 | 0.135491 |
| GO:0007029 | endoplasmic reticulum organization | 30 | 0.535423 | 0.032468 | 0.346693 | 0.320267 |
| GO:0006818 | hydrogen transport | 65 | 0.528279 | 0.004658 | 0.177337 | 0.163820 |
| GO:0006378 | mRNA polyadenylation | 28 | 0.527205 | 0.049658 | 0.405661 | 0.374740 |
| GO:0046939 | nucleotide phosphorylation | 62 | 0.523425 | 0.006309 | 0.198314 | 0.183198 |
| GO:0019724 | B cell mediated immunity | 49 | 0.520177 | 0.006359 | 0.198314 | 0.183198 |
| GO:0007589 | body fluid secretion | 46 | 0.517754 | 0.008183 | 0.204395 | 0.188815 |
| GO:0007200 | phospholipase C-activating G-protein coupled receptor signaling pathway | 28 | 0.515688 | 0.040708 | 0.373964 | 0.345459 |
| GO:0032941 | secretion by tissue | 43 | 0.513358 | 0.016234 | 0.258076 | 0.238405 |
| GO:0032507 | maintenance of protein location in cell | 57 | 0.509413 | 0.007974 | 0.202919 | 0.187452 |
| GO:0051899 | membrane depolarization | 44 | 0.503827 | 0.014901 | 0.251001 | 0.231869 |
| GO:0014066 | regulation of phosphatidylinositol 3-kinase signaling | 46 | 0.501618 | 0.022152 | 0.295313 | 0.272804 |
| GO:0043901 | negative regulation of multi-organism process | 75 | 0.501067 | 0.003115 | 0.154291 | 0.142531 |
| GO:0045185 | maintenance of protein location | 62 | 0.499887 | 0.007862 | 0.202919 | 0.187452 |
| GO:0018208 | peptidyl-proline modification | 38 | 0.486945 | 0.049180 | 0.403279 | 0.372540 |
| GO:0052547 | regulation of peptidase activity | 196 | 0.486637 | 0.001393 | 0.146671 | 0.135491 |
| GO:0052548 | regulation of endopeptidase activity | 174 | 0.485164 | 0.001418 | 0.146671 | 0.135491 |
| GO:2000117 | negative regulation of cysteine-type endopeptidase activity | 57 | 0.484081 | 0.011475 | 0.230497 | 0.212928 |
| GO:0051928 | positive regulation of calcium ion transport | 53 | 0.481161 | 0.019769 | 0.281697 | 0.260225 |
| GO:0035821 | modification of morphology or physiology of other organism | 44 | 0.480632 | 0.035831 | 0.357156 | 0.329932 |
| GO:0051817 | modification of morphology or physiology of other organism involved in symbiotic interaction | 44 | 0.480632 | 0.035831 | 0.357156 | 0.329932 |
| GO:1903901 | negative regulation of viral life cycle | 43 | 0.480059 | 0.038143 | 0.360180 | 0.332727 |
| GO:0010952 | positive regulation of peptidase activity | 90 | 0.475712 | 0.001543 | 0.146671 | 0.135491 |
| GO:0048525 | negative regulation of viral process | 45 | 0.473209 | 0.038206 | 0.360180 | 0.332727 |
| GO:0010950 | positive regulation of endopeptidase activity | 85 | 0.472839 | 0.004566 | 0.177337 | 0.163820 |
| GO:0051289 | protein homotetramerization | 51 | 0.470578 | 0.022876 | 0.297660 | 0.274971 |
| GO:0045861 | negative regulation of proteolysis | 164 | 0.467364 | 0.001441 | 0.146671 | 0.135491 |
| GO:2001056 | positive regulation of cysteine-type endopeptidase activity | 79 | 0.457322 | 0.012251 | 0.234109 | 0.216265 |
| GO:0051705 | multi-organism behavior | 54 | 0.453715 | 0.044872 | 0.389247 | 0.359578 |
| GO:0044706 | multi-multicellular organism process | 80 | 0.446752 | 0.004792 | 0.177337 | 0.163820 |
| GO:0031348 | negative regulation of defense response | 81 | 0.444465 | 0.021070 | 0.290695 | 0.268537 |
| GO:0006457 | protein folding | 127 | 0.443713 | 0.007278 | 0.202919 | 0.187452 |
| GO:0090317 | negative regulation of intracellular protein transport | 68 | 0.443546 | 0.035427 | 0.357156 | 0.329932 |
| GO:2000116 | regulation of cysteine-type endopeptidase activity | 136 | 0.442095 | 0.001431 | 0.146671 | 0.135491 |
| GO:0051651 | maintenance of location in cell | 65 | 0.441796 | 0.028571 | 0.325909 | 0.301068 |
| GO:0042177 | negative regulation of protein catabolic process | 74 | 0.430145 | 0.040310 | 0.372740 | 0.344328 |
| GO:0051054 | positive regulation of DNA metabolic process | 99 | 0.423528 | 0.015576 | 0.255452 | 0.235981 |
| GO:0030198 | extracellular matrix organization | 116 | 0.420497 | 0.010309 | 0.223468 | 0.206434 |
| GO:0043062 | extracellular structure organization | 116 | 0.420497 | 0.010309 | 0.223468 | 0.206434 |
| GO:0051262 | protein tetramerization | 99 | 0.416483 | 0.018377 | 0.272618 | 0.251838 |
| GO:0043406 | positive regulation of MAP kinase activity | 106 | 0.397516 | 0.040971 | 0.373964 | 0.345459 |
| GO:0031032 | actomyosin structure organization | 101 | 0.390119 | 0.042386 | 0.375940 | 0.347284 |
| GO:0050714 | positive regulation of protein secretion | 113 | 0.387546 | 0.031915 | 0.343322 | 0.317153 |
| GO:0009615 | response to virus | 169 | 0.387056 | 0.011080 | 0.228223 | 0.210828 |
| GO:0045862 | positive regulation of proteolysis | 190 | 0.385022 | 0.002837 | 0.154291 | 0.142531 |
| GO:0034976 | response to endoplasmic reticulum stress | 157 | 0.378402 | 0.026798 | 0.317373 | 0.293182 |
| GO:0051346 | negative regulation of hydrolase activity | 192 | 0.378392 | 0.008824 | 0.213290 | 0.197033 |
| GO:0051607 | defense response to virus | 149 | 0.371268 | 0.034139 | 0.353025 | 0.326116 |
| GO:0002443 | leukocyte mediated immunity | 138 | 0.369328 | 0.033382 | 0.351604 | 0.324804 |
| GO:0050878 | regulation of body fluid levels | 161 | 0.368069 | 0.021053 | 0.290695 | 0.268537 |
| GO:0030162 | regulation of proteolysis | 405 | 0.365383 | 0.001280 | 0.146671 | 0.135491 |
| GO:0042254 | ribosome biogenesis | 169 | 0.357610 | 0.042336 | 0.375940 | 0.347284 |
| GO:0098542 | defense response to other organism | 231 | 0.356893 | 0.016575 | 0.258076 | 0.238405 |
| GO:0042391 | regulation of membrane potential | 188 | 0.351055 | 0.028329 | 0.324845 | 0.300084 |
| GO:0022613 | ribonucleoprotein complex biogenesis | 263 | 0.343449 | 0.020576 | 0.287537 | 0.265620 |
| GO:0043900 | regulation of multi-organism process | 230 | 0.336080 | 0.042936 | 0.377903 | 0.349098 |
| GO:0015672 | monovalent inorganic cation transport | 265 | 0.335238 | 0.032982 | 0.349604 | 0.322956 |
| GO:0034470 | ncRNA processing | 208 | 0.334846 | 0.048227 | 0.401522 | 0.370917 |
| GO:0043086 | negative regulation of catalytic activity | 388 | 0.334291 | 0.006452 | 0.198314 | 0.183198 |
| GO:0043623 | cellular protein complex assembly | 316 | 0.333790 | 0.018205 | 0.271893 | 0.251169 |
| GO:1902533 | positive regulation of intracellular signal transduction | 475 | 0.329629 | 0.004988 | 0.177337 | 0.163820 |
| GO:0022411 | cellular component disassembly | 256 | 0.326814 | 0.048064 | 0.401470 | 0.370869 |
| GO:0051347 | positive regulation of transferase activity | 304 | 0.318406 | 0.040558 | 0.373440 | 0.344975 |
| GO:0045859 | regulation of protein kinase activity | 404 | 0.309911 | 0.049118 | 0.403279 | 0.372540 |
| GO:0043549 | regulation of kinase activity | 439 | 0.308270 | 0.041045 | 0.373964 | 0.345459 |
| GO:0034622 | cellular macromolecular complex assembly | 544 | 0.302765 | 0.042373 | 0.375940 | 0.347284 |
| GO:0051336 | regulation of hydrolase activity | 542 | 0.300742 | 0.032953 | 0.349604 | 0.322956 |
| GO:0051338 | regulation of transferase activity | 496 | 0.298335 | 0.046798 | 0.396460 | 0.366241 |
| GO:0044711 | single-organism biosynthetic process | 786 | 0.294908 | 0.017503 | 0.265971 | 0.245698 |
| GO:0048584 | positive regulation of response to stimulus | 955 | 0.293194 | 0.014673 | 0.249909 | 0.230860 |
| GO:0006508 | proteolysis | 891 | 0.292258 | 0.016298 | 0.258076 | 0.238405 |
| GO:0006810 | transport | 2533 | 0.288803 | 0.002051 | 0.150485 | 0.139014 |
| GO:0051234 | establishment of localization | 2613 | 0.288294 | 0.002049 | 0.150485 | 0.139014 |
| GO:0050790 | regulation of catalytic activity | 1050 | 0.281699 | 0.030822 | 0.337411 | 0.311692 |
| GO:0051179 | localization | 3208 | 0.280783 | 0.001015 | 0.146671 | 0.135491 |
| GO:0015031 | protein transport | 1134 | 0.278737 | 0.032787 | 0.349245 | 0.322624 |
| GO:1902578 | single-organism localization | 2164 | 0.277004 | 0.009356 | 0.218597 | 0.201935 |
| GO:0044765 | single-organism transport | 2045 | 0.275101 | 0.014599 | 0.249909 | 0.230860 |
| GO:0045184 | establishment of protein localization | 1214 | 0.274605 | 0.043478 | 0.381730 | 0.352634 |
| GO:0044699 | single-organism process | 7115 | 0.271805 | 0.000999 | 0.146671 | 0.135491 |
| GO:0033036 | macromolecule localization | 1693 | 0.269139 | 0.042508 | 0.376252 | 0.347573 |
| GO:1902589 | single-organism organelle organization | 1575 | 0.269114 | 0.048128 | 0.401470 | 0.370869 |
| GO:0071702 | organic substance transport | 1508 | 0.268632 | 0.049093 | 0.403279 | 0.372540 |
| GO:0044085 | cellular component biogenesis | 1575 | 0.268325 | 0.039112 | 0.363985 | 0.336241 |
| GO:0009987 | cellular process | 8034 | 0.257332 | 0.011000 | 0.228136 | 0.210747 |
| GO:0044763 | single-organism cellular process | 6381 | 0.251561 | 0.037000 | 0.358837 | 0.331485 |
| GO:0051254 | positive regulation of RNA metabolic process | 941 | -0.243670 | 0.041322 | 0.375325 | 0.346717 |
| GO:0009719 | response to endogenous stimulus | 649 | -0.257951 | 0.034483 | 0.353429 | 0.326490 |
| GO:0051276 | chromosome organization | 638 | -0.262474 | 0.006329 | 0.198314 | 0.183198 |
| GO:0045944 | positive regulation of transcription from RNA polymerase II promoter | 651 | -0.271280 | 0.025000 | 0.306730 | 0.283351 |
| GO:0001944 | vasculature development | 384 | -0.271614 | 0.033898 | 0.351604 | 0.324804 |
| GO:0006325 | chromatin organization | 489 | -0.273929 | 0.010309 | 0.223468 | 0.206434 |
| GO:1901698 | response to nitrogen compound | 359 | -0.279652 | 0.038627 | 0.362145 | 0.334541 |
| GO:0048514 | blood vessel morphogenesis | 316 | -0.284059 | 0.028000 | 0.322733 | 0.298133 |
| GO:0001568 | blood vessel development | 365 | -0.284778 | 0.016598 | 0.258076 | 0.238405 |
| GO:0009725 | response to hormone | 319 | -0.285325 | 0.041825 | 0.375940 | 0.347284 |
| GO:0014070 | response to organic cyclic compound | 309 | -0.291424 | 0.024000 | 0.305877 | 0.282562 |
| GO:0000280 | nuclear division | 304 | -0.292240 | 0.041667 | 0.375940 | 0.347284 |
| GO:0035239 | tube morphogenesis | 256 | -0.294845 | 0.027027 | 0.318318 | 0.294055 |
| GO:0060627 | regulation of vesicle-mediated transport | 270 | -0.296321 | 0.007692 | 0.202919 | 0.187452 |
| GO:0033993 | response to lipid | 287 | -0.305376 | 0.033708 | 0.351604 | 0.324804 |
| GO:0048568 | embryonic organ development | 281 | -0.307586 | 0.020080 | 0.282708 | 0.261159 |
| GO:0010243 | response to organonitrogen compound | 310 | -0.308053 | 0.012500 | 0.234109 | 0.216265 |
| GO:0001503 | ossification | 224 | -0.308654 | 0.021739 | 0.291600 | 0.269373 |
| GO:0007067 | mitotic nuclear division | 251 | -0.309633 | 0.018450 | 0.272618 | 0.251838 |
| GO:0032870 | cellular response to hormone stimulus | 231 | -0.314821 | 0.030534 | 0.336408 | 0.310766 |
| GO:0060562 | epithelial tube morphogenesis | 227 | -0.324181 | 0.003559 | 0.157818 | 0.145789 |
| GO:0071824 | protein-DNA complex subunit organization | 132 | -0.336600 | 0.026471 | 0.315181 | 0.291157 |
| GO:0065004 | protein-DNA complex assembly | 110 | -0.342917 | 0.037464 | 0.358837 | 0.331485 |
| GO:0030522 | intracellular receptor signaling pathway | 128 | -0.343283 | 0.037356 | 0.358837 | 0.331485 |
| GO:0017157 | regulation of exocytosis | 110 | -0.351192 | 0.035503 | 0.357156 | 0.329932 |
| GO:0016197 | endosomal transport | 175 | -0.361571 | 0.006390 | 0.198314 | 0.183198 |
| GO:0003002 | regionalization | 181 | -0.370867 | 0.003145 | 0.154291 | 0.142531 |
| GO:0031023 | microtubule organizing center organization | 68 | -0.374056 | 0.039370 | 0.365603 | 0.337736 |
| GO:0001843 | neural tube closure | 79 | -0.378281 | 0.042254 | 0.375940 | 0.347284 |
| GO:0060606 | tube closure | 79 | -0.378281 | 0.042254 | 0.375940 | 0.347284 |
| GO:0009799 | specification of symmetry | 69 | -0.381041 | 0.045570 | 0.391394 | 0.361561 |
| GO:0009855 | determination of bilateral symmetry | 69 | -0.381041 | 0.045570 | 0.391394 | 0.361561 |
| GO:0006937 | regulation of muscle contraction | 72 | -0.381414 | 0.050000 | 0.407692 | 0.376617 |
| GO:0009952 | anterior/posterior pattern specification | 112 | -0.381665 | 0.012422 | 0.234109 | 0.216265 |
| GO:0061138 | morphogenesis of a branching epithelium | 127 | -0.389959 | 0.002924 | 0.154291 | 0.142531 |
| GO:0030518 | intracellular steroid hormone receptor signaling pathway | 74 | -0.394890 | 0.025210 | 0.306899 | 0.283507 |
| GO:0030326 | embryonic limb morphogenesis | 78 | -0.407407 | 0.018568 | 0.272618 | 0.251838 |
| GO:0035113 | embryonic appendage morphogenesis | 78 | -0.407407 | 0.018568 | 0.272618 | 0.251838 |
| GO:0001763 | morphogenesis of a branching structure | 137 | -0.409907 | 0.002890 | 0.154291 | 0.142531 |
| GO:0006402 | mRNA catabolic process | 86 | -0.418461 | 0.007792 | 0.202919 | 0.187452 |
| GO:0000956 | nuclear-transcribed mRNA catabolic process | 78 | -0.427526 | 0.007557 | 0.202919 | 0.187452 |
| GO:0043112 | receptor metabolic process | 93 | -0.428983 | 0.008547 | 0.209860 | 0.193864 |
| GO:0014074 | response to purine-containing compound | 56 | -0.429391 | 0.029810 | 0.332407 | 0.307070 |
| GO:0048754 | branching morphogenesis of an epithelial tube | 108 | -0.430688 | 0.002786 | 0.154291 | 0.142531 |
| GO:0022406 | membrane docking | 56 | -0.432065 | 0.042895 | 0.377903 | 0.349098 |
| GO:0014897 | striated muscle hypertrophy | 43 | -0.436744 | 0.038860 | 0.362416 | 0.334792 |
| GO:0051592 | response to calcium ion | 56 | -0.437328 | 0.019886 | 0.282438 | 0.260910 |
| GO:0009612 | response to mechanical stimulus | 71 | -0.450240 | 0.007792 | 0.202919 | 0.187452 |
| GO:0003300 | cardiac muscle hypertrophy | 42 | -0.453743 | 0.028721 | 0.326754 | 0.301848 |
| GO:0048844 | artery morphogenesis | 36 | -0.462876 | 0.037940 | 0.359235 | 0.331853 |
| GO:0006893 | Golgi to plasma membrane transport | 38 | -0.465460 | 0.044776 | 0.389194 | 0.359529 |
| GO:0001570 | vasculogenesis | 55 | -0.472200 | 0.007732 | 0.202919 | 0.187452 |
| GO:0008333 | endosome to lysosome transport | 36 | -0.483033 | 0.036496 | 0.358837 | 0.331485 |
| GO:0046849 | bone remodeling | 37 | -0.483606 | 0.034314 | 0.353025 | 0.326116 |
| GO:0009953 | dorsal/ventral pattern formation | 62 | -0.494585 | 0.002519 | 0.150485 | 0.139014 |
| GO:0043392 | negative regulation of DNA binding | 33 | -0.502603 | 0.033766 | 0.351604 | 0.324804 |
| GO:0007031 | peroxisome organization | 28 | -0.507594 | 0.044289 | 0.386506 | 0.357046 |
| GO:0003143 | embryonic heart tube morphogenesis | 41 | -0.509255 | 0.009662 | 0.221002 | 0.204156 |
| GO:0060420 | regulation of heart growth | 30 | -0.512298 | 0.022500 | 0.297656 | 0.274967 |
| GO:0006939 | smooth muscle contraction | 47 | -0.517599 | 0.007634 | 0.202919 | 0.187452 |
| GO:0016126 | sterol biosynthetic process | 36 | -0.517683 | 0.021429 | 0.291600 | 0.269373 |
| GO:0060042 | retina morphogenesis in camera-type eye | 32 | -0.518670 | 0.033493 | 0.351604 | 0.324804 |
| GO:0031663 | lipopolysaccharide-mediated signaling pathway | 27 | -0.524533 | 0.029885 | 0.332407 | 0.307070 |
| GO:0021587 | cerebellum morphogenesis | 31 | -0.524973 | 0.030769 | 0.337411 | 0.311692 |
| GO:0060425 | lung morphogenesis | 34 | -0.532393 | 0.007335 | 0.202919 | 0.187452 |
| GO:0061333 | renal tubule morphogenesis | 39 | -0.535271 | 0.005051 | 0.177337 | 0.163820 |
| GO:0060711 | labyrinthine layer development | 34 | -0.542597 | 0.007595 | 0.202919 | 0.187452 |
| GO:0060688 | regulation of morphogenesis of a branching structure | 26 | -0.544256 | 0.033898 | 0.351604 | 0.324804 |
| GO:0072028 | nephron morphogenesis | 38 | -0.549285 | 0.005249 | 0.179635 | 0.165943 |
| GO:0072088 | nephron epithelium morphogenesis | 37 | -0.550194 | 0.010390 | 0.223468 | 0.206434 |
| GO:0060411 | cardiac septum morphogenesis | 36 | -0.556306 | 0.007916 | 0.202919 | 0.187452 |
| GO:0071277 | cellular response to calcium ion | 25 | -0.557502 | 0.030457 | 0.336408 | 0.310766 |
| GO:0021575 | hindbrain morphogenesis | 33 | -0.563349 | 0.012755 | 0.234109 | 0.216265 |
| GO:0021532 | neural tube patterning | 33 | -0.568908 | 0.007335 | 0.202919 | 0.187452 |
| GO:0001782 | B cell homeostasis | 21 | -0.578522 | 0.027907 | 0.322733 | 0.298133 |
| GO:0045933 | positive regulation of muscle contraction | 25 | -0.578571 | 0.023202 | 0.300105 | 0.277230 |
| GO:0042446 | hormone biosynthetic process | 30 | -0.582740 | 0.007194 | 0.202919 | 0.187452 |
| GO:0009880 | embryonic pattern specification | 26 | -0.582787 | 0.020000 | 0.282708 | 0.261159 |
| GO:0060993 | kidney morphogenesis | 46 | -0.584750 | 0.002584 | 0.150485 | 0.139014 |
| GO:0001825 | blastocyst formation | 28 | -0.585922 | 0.009547 | 0.221002 | 0.204156 |
| GO:0035137 | hindlimb morphogenesis | 27 | -0.590358 | 0.012594 | 0.234109 | 0.216265 |
| GO:0000578 | embryonic axis specification | 18 | -0.592977 | 0.048499 | 0.402244 | 0.371584 |
| GO:0035115 | embryonic forelimb morphogenesis | 17 | -0.596742 | 0.035461 | 0.357156 | 0.329932 |
| GO:0072078 | nephron tubule morphogenesis | 35 | -0.598312 | 0.005115 | 0.177337 | 0.163820 |
| GO:0050869 | negative regulation of B cell activation | 15 | -0.605929 | 0.044444 | 0.387085 | 0.357581 |
| GO:0048670 | regulation of collateral sprouting | 14 | -0.613623 | 0.035629 | 0.357156 | 0.329932 |
| GO:0038066 | p38MAPK cascade | 17 | -0.614439 | 0.043880 | 0.383706 | 0.354459 |
| GO:0021904 | dorsal/ventral neural tube patterning | 22 | -0.615664 | 0.009662 | 0.221002 | 0.204156 |
| GO:0065005 | protein-lipid complex assembly | 16 | -0.618995 | 0.040909 | 0.373964 | 0.345459 |
| GO:0045022 | early endosome to late endosome transport | 33 | -0.620264 | 0.002387 | 0.150485 | 0.139014 |
| GO:0072171 | mesonephric tubule morphogenesis | 33 | -0.623529 | 0.005141 | 0.177337 | 0.163820 |
| GO:0060675 | ureteric bud morphogenesis | 32 | -0.626312 | 0.005038 | 0.177337 | 0.163820 |
| GO:0060441 | epithelial tube branching involved in lung morphogenesis | 17 | -0.636415 | 0.020737 | 0.288860 | 0.266843 |
| GO:0048668 | collateral sprouting | 18 | -0.637481 | 0.019277 | 0.277412 | 0.256267 |
| GO:0009948 | anterior/posterior axis specification | 25 | -0.638788 | 0.007299 | 0.202919 | 0.187452 |
| GO:0045987 | positive regulation of smooth muscle contraction | 18 | -0.641368 | 0.019093 | 0.276595 | 0.255512 |
| GO:0061014 | positive regulation of mRNA catabolic process | 15 | -0.641562 | 0.026066 | 0.312078 | 0.288291 |
| GO:1900744 | regulation of p38MAPK cascade | 15 | -0.644085 | 0.046083 | 0.395023 | 0.364913 |
| GO:0001658 | branching involved in ureteric bud morphogenesis | 31 | -0.644540 | 0.004890 | 0.177337 | 0.163820 |
| GO:2000678 | negative regulation of transcription regulatory region DNA binding | 13 | -0.651063 | 0.037647 | 0.358837 | 0.331485 |
| GO:0000289 | nuclear-transcribed mRNA poly(A) tail shortening | 14 | -0.662567 | 0.025463 | 0.308251 | 0.284755 |
| GO:0003230 | cardiac atrium development | 21 | -0.664400 | 0.005115 | 0.177337 | 0.163820 |
| GO:0006940 | regulation of smooth muscle contraction | 29 | -0.673120 | 0.002469 | 0.150485 | 0.139014 |
| GO:0045992 | negative regulation of embryonic development | 16 | -0.674921 | 0.009950 | 0.222906 | 0.205916 |
| GO:0006491 | N-glycan processing | 12 | -0.675606 | 0.040816 | 0.373964 | 0.345459 |
| GO:0031128 | developmental induction | 19 | -0.679166 | 0.002288 | 0.150485 | 0.139014 |
| GO:2000826 | regulation of heart morphogenesis | 16 | -0.684034 | 0.009217 | 0.218022 | 0.201404 |
| GO:0031290 | retinal ganglion cell axon guidance | 13 | -0.689367 | 0.027972 | 0.322733 | 0.298133 |
| GO:0060602 | branch elongation of an epithelium | 11 | -0.695024 | 0.022779 | 0.297656 | 0.274967 |
| GO:0051955 | regulation of amino acid transport | 14 | -0.708990 | 0.011990 | 0.232635 | 0.214903 |
| GO:0003209 | cardiac atrium morphogenesis | 18 | -0.727246 | 0.002415 | 0.150485 | 0.139014 |
| GO:0060788 | ectodermal placode formation | 14 | -0.729751 | 0.009281 | 0.218022 | 0.201404 |
| GO:0071697 | ectodermal placode morphogenesis | 14 | -0.729751 | 0.009281 | 0.218022 | 0.201404 |
| GO:2000641 | regulation of early endosome to late endosome transport | 16 | -0.751111 | 0.004640 | 0.177337 | 0.163820 |
| GO:0051957 | positive regulation of amino acid transport | 11 | -0.765926 | 0.011682 | 0.232102 | 0.214411 |
| GO:0015800 | acidic amino acid transport | 12 | -0.767952 | 0.014151 | 0.247459 | 0.228597 |
| GO:0060413 | atrial septum morphogenesis | 11 | -0.822256 | 0.002358 | 0.150485 | 0.139014 |

## Rho CC
| ID | Description | setSize | enrichmentScore | pvalue | p.adjust | qvalues |
| --- | --- | --- | --- | --- | --- | --- |
| GO:0005753 | mitochondrial proton-transporting ATP synthase complex | 15 | 0.771845 | 0.003578 | 0.031320 | 0.026305 |
| GO:0045259 | proton-transporting ATP synthase complex | 16 | 0.721985 | 0.007092 | 0.055280 | 0.046429 |
| GO:0033178 | proton-transporting two-sector ATPase complex, catalytic domain | 12 | 0.691002 | 0.041971 | 0.217545 | 0.182713 |
| GO:0071004 | U2-type prespliceosome | 12 | 0.672181 | 0.035714 | 0.204209 | 0.171512 |
| GO:0005682 | U5 snRNP | 12 | 0.668366 | 0.045455 | 0.228882 | 0.192234 |
| GO:0046930 | pore complex | 12 | 0.667257 | 0.047285 | 0.233960 | 0.196500 |
| GO:0097386 | glial cell projection | 12 | 0.663923 | 0.047038 | 0.233960 | 0.196500 |
| GO:0005685 | U1 snRNP | 15 | 0.662627 | 0.021390 | 0.136754 | 0.114858 |
| GO:0005747 | mitochondrial respiratory chain complex I | 36 | 0.653171 | 0.001653 | 0.016795 | 0.014106 |
| GO:0030964 | NADH dehydrogenase complex | 36 | 0.653171 | 0.001653 | 0.016795 | 0.014106 |
| GO:0045271 | respiratory chain complex I | 36 | 0.653171 | 0.001653 | 0.016795 | 0.014106 |
| GO:0000314 | organellar small ribosomal subunit | 24 | 0.641020 | 0.001783 | 0.017487 | 0.014687 |
| GO:0005763 | mitochondrial small ribosomal subunit | 24 | 0.641020 | 0.001783 | 0.017487 | 0.014687 |
| GO:0016469 | proton-transporting two-sector ATPase complex | 34 | 0.637554 | 0.003328 | 0.030056 | 0.025243 |
| GO:0072562 | blood microparticle | 56 | 0.635668 | 0.001592 | 0.016795 | 0.014106 |
| GO:0071010 | prespliceosome | 18 | 0.629038 | 0.038532 | 0.208807 | 0.175374 |
| GO:0033177 | proton-transporting two-sector ATPase complex, proton-transporting domain | 16 | 0.612452 | 0.035211 | 0.204209 | 0.171512 |
| GO:0070469 | respiratory chain | 61 | 0.607924 | 0.001538 | 0.016795 | 0.014106 |
| GO:0005882 | intermediate filament | 50 | 0.595069 | 0.001642 | 0.016795 | 0.014106 |
| GO:0005746 | mitochondrial respiratory chain | 56 | 0.594840 | 0.001543 | 0.016795 | 0.014106 |
| GO:0030672 | synaptic vesicle membrane | 24 | 0.591020 | 0.027972 | 0.169058 | 0.141989 |
| GO:0098800 | inner mitochondrial membrane protein complex | 86 | 0.588485 | 0.001543 | 0.016795 | 0.014106 |
| GO:0098803 | respiratory chain complex | 53 | 0.586705 | 0.001563 | 0.016795 | 0.014106 |
| GO:0001917 | photoreceptor inner segment | 23 | 0.583657 | 0.037037 | 0.208261 | 0.174916 |
| GO:1990204 | oxidoreductase complex | 70 | 0.570818 | 0.001600 | 0.016795 | 0.014106 |
| GO:0098798 | mitochondrial protein complex | 118 | 0.570084 | 0.001495 | 0.016795 | 0.014106 |
| GO:0005790 | smooth endoplasmic reticulum | 25 | 0.556470 | 0.035889 | 0.204209 | 0.171512 |
| GO:0005793 | endoplasmic reticulum-Golgi intermediate compartment | 40 | 0.535580 | 0.013699 | 0.099930 | 0.083930 |
| GO:0000313 | organellar ribosome | 63 | 0.531298 | 0.001603 | 0.016795 | 0.014106 |
| GO:0005761 | mitochondrial ribosome | 63 | 0.531298 | 0.001603 | 0.016795 | 0.014106 |
| GO:0044455 | mitochondrial membrane part | 132 | 0.522378 | 0.001466 | 0.016795 | 0.014106 |
| GO:0005758 | mitochondrial intermembrane space | 46 | 0.514712 | 0.014286 | 0.101607 | 0.085338 |
| GO:0031970 | organelle envelope lumen | 53 | 0.503398 | 0.007788 | 0.059885 | 0.050296 |
| GO:0031968 | organelle outer membrane | 120 | 0.487133 | 0.001445 | 0.016795 | 0.014106 |
| GO:0031514 | motile cilium | 51 | 0.486754 | 0.018212 | 0.124850 | 0.104860 |
| GO:0019867 | outer membrane | 121 | 0.486670 | 0.001437 | 0.016795 | 0.014106 |
| GO:0015935 | small ribosomal subunit | 63 | 0.479658 | 0.014173 | 0.101607 | 0.085338 |
| GO:0005741 | mitochondrial outer membrane | 111 | 0.477324 | 0.001451 | 0.016795 | 0.014106 |
| GO:0016363 | nuclear matrix | 60 | 0.472620 | 0.019512 | 0.130617 | 0.109703 |
| GO:0045111 | intermediate filament cytoskeleton | 94 | 0.470341 | 0.004800 | 0.040165 | 0.033734 |
| GO:0005743 | mitochondrial inner membrane | 290 | 0.458687 | 0.001335 | 0.016795 | 0.014106 |
| GO:0019866 | organelle inner membrane | 313 | 0.452169 | 0.001295 | 0.016795 | 0.014106 |
| GO:0015934 | large ribosomal subunit | 69 | 0.451554 | 0.018721 | 0.126811 | 0.106507 |
| GO:0044391 | ribosomal subunit | 131 | 0.447142 | 0.001502 | 0.016795 | 0.014106 |
| GO:0005740 | mitochondrial envelope | 426 | 0.446715 | 0.001256 | 0.016795 | 0.014106 |
| GO:0034399 | nuclear periphery | 77 | 0.440669 | 0.024631 | 0.154009 | 0.129350 |
| GO:0031966 | mitochondrial membrane | 397 | 0.440560 | 0.001250 | 0.016795 | 0.014106 |
| GO:0044429 | mitochondrial part | 546 | 0.439465 | 0.001200 | 0.016795 | 0.014106 |
| GO:0005604 | basement membrane | 68 | 0.439041 | 0.042003 | 0.217545 | 0.182713 |
| GO:0000502 | proteasome complex | 67 | 0.434678 | 0.038035 | 0.208807 | 0.175374 |
| GO:0031012 | extracellular matrix | 202 | 0.428451 | 0.001374 | 0.016795 | 0.014106 |
| GO:0005759 | mitochondrial matrix | 170 | 0.416256 | 0.001429 | 0.016795 | 0.014106 |
| GO:0005840 | ribosome | 183 | 0.413527 | 0.001464 | 0.016795 | 0.014106 |
| GO:0098796 | membrane protein complex | 617 | 0.411873 | 0.001182 | 0.016795 | 0.014106 |
| GO:0005578 | proteinaceous extracellular matrix | 164 | 0.405895 | 0.002954 | 0.027112 | 0.022771 |
| GO:0031967 | organelle envelope | 651 | 0.404856 | 0.001182 | 0.016795 | 0.014106 |
| GO:0031975 | envelope | 652 | 0.404751 | 0.001179 | 0.016795 | 0.014106 |
| GO:0098797 | plasma membrane protein complex | 234 | 0.392643 | 0.001427 | 0.016795 | 0.014106 |
| GO:0043209 | myelin sheath | 175 | 0.375794 | 0.016667 | 0.117078 | 0.098332 |
| GO:0044432 | endoplasmic reticulum part | 328 | 0.368982 | 0.002639 | 0.024612 | 0.020671 |
| GO:0042175 | nuclear outer membrane-endoplasmic reticulum membrane network | 271 | 0.368530 | 0.005502 | 0.044724 | 0.037563 |
| GO:0005789 | endoplasmic reticulum membrane | 261 | 0.363460 | 0.004155 | 0.035288 | 0.029637 |
| GO:0031090 | organelle membrane | 1260 | 0.358669 | 0.001094 | 0.016795 | 0.014106 |
| GO:0005739 | mitochondrion | 1247 | 0.353428 | 0.001087 | 0.016795 | 0.014106 |
| GO:0005615 | extracellular space | 589 | 0.348083 | 0.001215 | 0.016795 | 0.014106 |
| GO:0005783 | endoplasmic reticulum | 941 | 0.333673 | 0.001119 | 0.016795 | 0.014106 |
| GO:0065010 | extracellular membrane-bounded organelle | 1858 | 0.328789 | 0.001047 | 0.016795 | 0.014106 |
| GO:0043230 | extracellular organelle | 1868 | 0.328416 | 0.001052 | 0.016795 | 0.014106 |
| GO:0044297 | cell body | 398 | 0.328124 | 0.020513 | 0.135719 | 0.113988 |
| GO:0070062 | extracellular exosome | 1853 | 0.328025 | 0.001049 | 0.016795 | 0.014106 |
| GO:1903561 | extracellular vesicle | 1863 | 0.327654 | 0.001053 | 0.016795 | 0.014106 |
| GO:0031982 | vesicle | 2370 | 0.322580 | 0.001026 | 0.016795 | 0.014106 |
| GO:0031988 | membrane-bounded vesicle | 2191 | 0.321291 | 0.001033 | 0.016795 | 0.014106 |
| GO:0098588 | bounding membrane of organelle | 848 | 0.320714 | 0.003476 | 0.030906 | 0.025957 |
| GO:0044421 | extracellular region part | 2245 | 0.316967 | 0.001030 | 0.016795 | 0.014106 |
| GO:0005576 | extracellular region | 2404 | 0.311146 | 0.001033 | 0.016795 | 0.014106 |
| GO:0043226 | organelle | 7751 | 0.307752 | 0.001002 | 0.016795 | 0.014106 |
| GO:0005737 | cytoplasm | 6515 | 0.307095 | 0.000999 | 0.016795 | 0.014106 |
| GO:0043234 | protein complex | 2804 | 0.305262 | 0.001021 | 0.016795 | 0.014106 |
| GO:0044444 | cytoplasmic part | 4461 | 0.305125 | 0.001006 | 0.016795 | 0.014106 |
| GO:0043227 | membrane-bounded organelle | 7272 | 0.303519 | 0.001001 | 0.016795 | 0.014106 |
| GO:0032991 | macromolecular complex | 3324 | 0.302749 | 0.001014 | 0.016795 | 0.014106 |
| GO:0044422 | organelle part | 4465 | 0.298090 | 0.001001 | 0.016795 | 0.014106 |
| GO:0044446 | intracellular organelle part | 4358 | 0.298005 | 0.001003 | 0.016795 | 0.014106 |
| GO:0030529 | ribonucleoprotein complex | 561 | 0.297891 | 0.045340 | 0.228882 | 0.192234 |
| GO:0044424 | intracellular part | 8094 | 0.296412 | 0.001000 | 0.016795 | 0.014106 |
| GO:0005622 | intracellular | 8160 | 0.293421 | 0.001000 | 0.016795 | 0.014106 |
| GO:0043229 | intracellular organelle | 7180 | 0.291760 | 0.001001 | 0.016795 | 0.014106 |
| GO:0005829 | cytosol | 1089 | 0.291336 | 0.009989 | 0.074785 | 0.062811 |
| GO:0031410 | cytoplasmic vesicle | 690 | 0.289393 | 0.038915 | 0.208893 | 0.175446 |
| GO:0012505 | endomembrane system | 2190 | 0.287743 | 0.002081 | 0.020071 | 0.016857 |
| GO:0043231 | intracellular membrane-bounded organelle | 6611 | 0.284309 | 0.001002 | 0.016795 | 0.014106 |
| GO:0097458 | neuron part | 896 | 0.281944 | 0.044674 | 0.228882 | 0.192234 |
| GO:0044464 | cell part | 8762 | 0.281019 | 0.001003 | 0.016795 | 0.014106 |
| GO:0005623 | cell | 8765 | 0.280628 | 0.001002 | 0.016795 | 0.014106 |
| GO:0044425 | membrane part | 3023 | 0.274960 | 0.005097 | 0.042030 | 0.035301 |
| GO:0016020 | membrane | 4717 | 0.268874 | 0.004028 | 0.034728 | 0.029167 |
| GO:0005694 | chromosome | 557 | -0.267668 | 0.041667 | 0.217545 | 0.182713 |
| GO:0030055 | cell-substrate junction | 300 | -0.286066 | 0.038462 | 0.208807 | 0.175374 |
| GO:0000785 | chromatin | 327 | -0.288700 | 0.028226 | 0.169058 | 0.141989 |
| GO:0000790 | nuclear chromatin | 210 | -0.316143 | 0.021127 | 0.136754 | 0.114858 |
| GO:0032993 | protein-DNA complex | 107 | -0.364120 | 0.032641 | 0.193466 | 0.162489 |
| GO:0005777 | peroxisome | 106 | -0.366959 | 0.025714 | 0.157327 | 0.132137 |
| GO:0042579 | microbody | 106 | -0.366959 | 0.025714 | 0.157327 | 0.132137 |
| GO:0000775 | chromosome, centromeric region | 106 | -0.382938 | 0.022654 | 0.143222 | 0.120290 |
| GO:0044815 | DNA packaging complex | 59 | -0.416522 | 0.037333 | 0.208261 | 0.174916 |
| GO:0000786 | nucleosome | 57 | -0.416587 | 0.034853 | 0.204209 | 0.171512 |
| GO:0043296 | apical junction complex | 88 | -0.444176 | 0.008310 | 0.063047 | 0.052952 |
| GO:0005923 | bicellular tight junction | 78 | -0.451346 | 0.005714 | 0.045159 | 0.037928 |
| GO:0070160 | occluding junction | 78 | -0.451346 | 0.005714 | 0.045159 | 0.037928 |
| GO:0005876 | spindle microtubule | 28 | -0.555128 | 0.021176 | 0.136754 | 0.114858 |
| GO:0030904 | retromer complex | 20 | -0.575331 | 0.042056 | 0.217545 | 0.182713 |
| GO:0035869 | ciliary transition zone | 19 | -0.645526 | 0.016990 | 0.117896 | 0.099019 |
| GO:0000242 | pericentriolar material | 13 | -0.714169 | 0.011601 | 0.085726 | 0.072000 |
| GO:0000788 | nuclear nucleosome | 28 | -0.764727 | 0.002618 | 0.024612 | 0.020671 |

## 8 hpl BP Revigo
| term\_ID | description | frequency | plot\_X | plot\_Y | plot\_size | value | uniqueness | dispensability | representative | eliminated |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| GO:0007623 | circadian rhythm | 0.00082 | 3.342 | 5.510 | 1.431 | 0.8155 | 0.988 | 0.000 | 7623 | 0 |
| GO:0042168 | heme metabolic process | 0.00117 | 3.465 | -6.570 | 1.580 | 0.7752 | 0.798 | 0.205 | 42168 | 0 |
| GO:1901568 | fatty acid derivative metabolic process | 0.00066 | 5.504 | -4.587 | 1.342 | 0.7563 | 0.880 | 0.196 | 1901568 | 0 |
| GO:0006690 | icosanoid metabolic process | 0.00066 | 5.185 | -5.156 | 1.342 | 0.7563 | 0.831 | 0.324 | 6690 | 0 |
| GO:0048511 | rhythmic process | 0.00136 | 2.251 | 2.788 | 1.643 | 0.7478 | 0.988 | 0.000 | 48511 | 0 |
| GO:0022904 | respiratory electron transport chain | 0.00120 | 5.531 | -5.551 | 1.591 | 0.7282 | 0.826 | 0.205 | 22904 | 0 |
| GO:0042440 | pigment metabolic process | 0.00177 | 4.912 | -4.690 | 1.756 | 0.7009 | 0.877 | 0.212 | 42440 | 0 |
| GO:0006400 | tRNA modification | 0.00228 | 1.173 | -6.663 | 1.863 | 0.6732 | 0.870 | 0.205 | 6400 | 0 |
| GO:0033013 | tetrapyrrole metabolic process | 0.00218 | 2.027 | -6.809 | 1.845 | 0.6413 | 0.871 | 0.351 | 33013 | 0 |
| GO:0045454 | cell redox homeostasis | 0.00396 | -5.773 | -0.454 | 2.100 | 0.6041 | 0.859 | 0.075 | 45454 | 0 |
| GO:0055114 | oxidation-reduction process | 0.05651 | 5.505 | -5.877 | 3.252 | 0.5056 | 0.831 | 0.391 | 55114 | 0 |
| GO:0051186 | cofactor metabolic process | 0.00943 | 0.890 | -1.420 | 2.476 | 0.5030 | 0.921 | 0.099 | 51186 | 0 |
| GO:0006457 | protein folding | 0.00823 | 0.227 | -4.830 | 2.417 | 0.4990 | 0.913 | 0.109 | 6457 | 0 |
| GO:0006281 | DNA repair | 0.01241 | -0.090 | -7.252 | 2.594 | 0.4923 | 0.713 | 0.307 | 6281 | 0 |
| GO:0007005 | mitochondrion organization | 0.00266 | 1.264 | -0.651 | 1.929 | 0.4797 | 0.925 | 0.023 | 7005 | 0 |
| GO:0006091 | generation of precursor metabolites and energy | 0.00785 | 2.535 | -2.316 | 2.396 | 0.4717 | 0.922 | 0.109 | 6091 | 0 |
| GO:0006950 | response to stress | 0.03685 | -4.433 | -6.526 | 3.066 | 0.4339 | 0.898 | 0.265 | 6950 | 0 |
| GO:0006629 | lipid metabolic process | 0.02517 | 5.379 | -6.095 | 2.901 | 0.4086 | 0.836 | 0.318 | 6629 | 0 |
| GO:0044710 | single-organism metabolic process | 0.20100 | 4.677 | 0.319 | 3.803 | 0.3669 | 0.871 | 0.093 | 44710 | 0 |
| GO:0040011 | locomotion | 0.02099 | -0.066 | 0.604 | 2.822 | -0.3123 | 0.988 | 0.000 | 40011 | 0 |
| GO:0006928 | cellular component movement | 0.02590 | -2.834 | -0.231 | 2.913 | -0.3149 | 0.872 | 0.092 | 6928 | 0 |
| GO:0007267 | cell-cell signaling | 0.00804 | -7.156 | -1.850 | 2.407 | -0.3575 | 0.843 | 0.257 | 7267 | 0 |
| GO:0016055 | Wnt signaling pathway | 0.01007 | -6.786 | -4.344 | 2.504 | -0.3613 | 0.773 | 0.400 | 16055 | 0 |
| GO:0022610 | biological adhesion | 0.03311 | -0.399 | 2.756 | 3.020 | -0.3641 | 0.988 | 0.000 | 22610 | 0 |
| GO:0007268 | synaptic transmission | 0.00589 | -7.124 | -1.674 | 2.272 | -0.4124 | 0.848 | 0.236 | 7268 | 0 |
| GO:0048736 | appendage development | 0.00263 | -0.809 | 5.891 | 1.924 | -0.4571 | 0.706 | 0.369 | 48736 | 0 |
| GO:0015849 | organic acid transport | 0.00443 | -2.594 | 4.447 | 2.149 | -0.4955 | 0.865 | 0.388 | 15849 | 0 |
| GO:0098656 | anion transmembrane transport | 0.00491 | -2.835 | 4.544 | 2.193 | -0.5172 | 0.821 | 0.328 | 98656 | 0 |
| GO:0017157 | regulation of exocytosis | 0.00063 | -5.570 | 2.393 | 1.322 | -0.5331 | 0.824 | 0.121 | 17157 | 0 |
| GO:0051606 | detection of stimulus | 0.01023 | -4.068 | -6.768 | 2.511 | -0.5331 | 0.910 | 0.221 | 51606 | 0 |
| GO:0007219 | Notch signaling pathway | 0.00307 | -6.469 | -4.410 | 1.991 | -0.5356 | 0.796 | 0.359 | 7219 | 0 |
| GO:0007156 | homophilic cell adhesion via plasma membrane adhesion molecules | 0.01304 | 2.944 | 5.016 | 2.616 | -0.5544 | 0.957 | 0.000 | 7156 | 0 |
| GO:0030509 | BMP signaling pathway | 0.00187 | -4.745 | -6.340 | 1.778 | -0.5823 | 0.725 | 0.344 | 30509 | 0 |
| GO:0038032 | termination of G-protein coupled receptor signaling pathway | 0.00320 | -6.432 | -4.494 | 2.009 | -0.6029 | 0.745 | 0.197 | 38032 | 0 |
| GO:0001704 | formation of primary germ layer | 0.00225 | -0.914 | 6.180 | 1.857 | -0.6686 | 0.695 | 0.356 | 1704 | 0 |
| GO:0048738 | cardiac muscle tissue development | 0.00168 | -0.721 | 5.709 | 1.732 | -0.6831 | 0.678 | 0.328 | 48738 | 0 |
| GO:0050906 | detection of stimulus involved in sensory perception | 0.00785 | -4.917 | -3.044 | 2.396 | -0.7262 | 0.677 | 0.046 | 50906 | 0 |
| GO:0009187 | cyclic nucleotide metabolic process | 0.00310 | 3.821 | -6.340 | 1.996 | -0.8275 | 0.788 | 0.000 | 9187 | 0 |

## 16 hpl BP Revigo
| term\_ID | description | frequency | plot\_X | plot\_Y | plot\_size | value | uniqueness | dispensability | representative | eliminated |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| GO:0007623 | circadian rhythm | 0.00082 | -4.480 | 2.573 | 1.431 | 0.8318 | 0.979 | 0.000 | 7623 | 0 |
| GO:0019221 | cytokine-mediated signaling pathway | 0.00446 | -5.990 | -2.568 | 2.152 | 0.8177 | 0.636 | 0.000 | 19221 | 0 |
| GO:0009617 | response to bacterium | 0.00263 | -5.596 | 4.689 | 1.924 | 0.8149 | 0.775 | 0.184 | 9617 | 0 |
| GO:0002764 | immune response-regulating signaling pathway | 0.00158 | -6.553 | -1.190 | 1.708 | 0.7908 | 0.645 | 0.222 | 2764 | 0 |
| GO:0006879 | cellular iron ion homeostasis | 0.00193 | -2.615 | -5.379 | 1.792 | 0.7832 | 0.878 | 0.114 | 6879 | 0 |
| GO:0040029 | regulation of gene expression, epigenetic | 0.00199 | 5.787 | -4.519 | 1.806 | 0.7110 | 0.856 | 0.122 | 40029 | 0 |
| GO:0048511 | rhythmic process | 0.00136 | 4.573 | 0.825 | 1.643 | 0.7004 | 0.979 | 0.000 | 48511 | 0 |
| GO:0031123 | RNA 3'-end processing | 0.00108 | 6.200 | 3.315 | 1.544 | 0.6643 | 0.882 | 0.258 | 31123 | 0 |
| GO:0009607 | response to biotic stimulus | 0.00545 | -6.461 | 4.341 | 2.238 | 0.6348 | 0.821 | 0.213 | 9607 | 0 |
| GO:0031099 | regeneration | 0.00279 | 1.818 | -4.317 | 1.949 | 0.6285 | 0.932 | 0.043 | 31099 | 0 |
| GO:0006952 | defense response | 0.00598 | -6.099 | 3.619 | 2.279 | 0.6277 | 0.796 | 0.215 | 6952 | 0 |
| GO:0045596 | negative regulation of cell differentiation | 0.00190 | -0.513 | -6.622 | 1.785 | 0.6272 | 0.813 | 0.326 | 45596 | 0 |
| GO:0016072 | rRNA metabolic process | 0.00256 | 5.316 | 4.819 | 1.914 | 0.5681 | 0.875 | 0.283 | 16072 | 0 |
| GO:0022613 | ribonucleoprotein complex biogenesis | 0.00658 | 1.283 | 4.296 | 2.320 | 0.5490 | 0.937 | 0.387 | 22613 | 0 |
| GO:0042127 | regulation of cell proliferation | 0.00431 | -2.488 | -7.892 | 2.137 | 0.5320 | 0.869 | 0.143 | 42127 | 0 |
| GO:0008283 | cell proliferation | 0.00671 | -1.771 | 0.847 | 2.328 | 0.5317 | 0.941 | 0.047 | 8283 | 0 |
| GO:0040007 | growth | 0.01092 | -1.916 | -0.482 | 2.539 | 0.5105 | 0.979 | 0.000 | 40007 | 0 |
| GO:0032270 | positive regulation of cellular protein metabolic process | 0.00307 | 5.300 | -4.635 | 1.991 | 0.5091 | 0.775 | 0.310 | 32270 | 0 |
| GO:0051704 | multi-organism process | 0.00804 | 4.215 | -0.117 | 2.407 | 0.5051 | 0.979 | 0.000 | 51704 | 0 |
| GO:0048589 | developmental growth | 0.00529 | 2.349 | -4.826 | 2.225 | 0.4967 | 0.930 | 0.356 | 48589 | 0 |
| GO:0034660 | ncRNA metabolic process | 0.01149 | 5.871 | 3.734 | 2.561 | 0.4951 | 0.881 | 0.347 | 34660 | 0 |
| GO:0002376 | immune system process | 0.02833 | 0.209 | -0.797 | 2.952 | 0.4751 | 0.979 | 0.000 | 2376 | 0 |
| GO:0051674 | localization of cell | 0.01482 | 0.575 | -6.065 | 2.671 | 0.4580 | 0.918 | 0.366 | 51674 | 0 |
| GO:0016477 | cell migration | 0.01399 | -0.182 | -4.832 | 2.646 | 0.4480 | 0.850 | 0.335 | 16477 | 0 |
| GO:0042325 | regulation of phosphorylation | 0.00909 | 3.393 | -6.534 | 2.459 | 0.4438 | 0.828 | 0.334 | 42325 | 0 |
| GO:0006950 | response to stress | 0.03685 | -6.671 | 3.063 | 3.066 | 0.4225 | 0.789 | 0.265 | 6950 | 0 |
| GO:0040011 | locomotion | 0.02099 | -1.591 | 1.943 | 2.822 | 0.3867 | 0.979 | 0.000 | 40011 | 0 |
| GO:0048518 | positive regulation of biological process | 0.02742 | -1.191 | -8.108 | 2.938 | 0.3507 | 0.888 | 0.165 | 48518 | 0 |
| GO:0003008 | system process | 0.02419 | 1.039 | 6.423 | 2.884 | -0.3519 | 0.906 | 0.394 | 3008 | 0 |
| GO:0007267 | cell-cell signaling | 0.00804 | -7.729 | -2.004 | 2.407 | -0.4084 | 0.866 | 0.250 | 7267 | 0 |
| GO:0072522 | purine-containing compound biosynthetic process | 0.00826 | 4.085 | 5.959 | 2.418 | -0.4260 | 0.899 | 0.348 | 72522 | 0 |
| GO:0034762 | regulation of transmembrane transport | 0.00674 | -0.218 | -7.372 | 2.330 | -0.5264 | 0.807 | 0.149 | 34762 | 0 |
| GO:0016052 | carbohydrate catabolic process | 0.00446 | 2.155 | -0.394 | 2.152 | -0.5409 | 0.931 | 0.075 | 16052 | 0 |
| GO:0007270 | neuron-neuron synaptic transmission | 0.00101 | -6.961 | -2.395 | 1.519 | -0.6235 | 0.872 | 0.208 | 7270 | 0 |
| GO:0007601 | visual perception | 0.00361 | 0.738 | 2.920 | 2.061 | -0.6580 | 0.891 | 0.044 | 7601 | 0 |
| GO:0051606 | detection of stimulus | 0.01023 | -7.119 | 3.513 | 2.511 | -0.6713 | 0.812 | 0.209 | 51606 | 0 |
| GO:0009190 | cyclic nucleotide biosynthetic process | 0.00288 | 4.988 | 4.303 | 1.964 | -0.6727 | 0.857 | 0.087 | 9190 | 0 |
| GO:0000070 | mitotic sister chromatid segregation | 0.00149 | 1.529 | 3.798 | 1.681 | -0.6782 | 0.902 | 0.071 | 70 | 0 |
| GO:0018298 | protein-chromophore linkage | 0.00237 | 7.185 | 1.022 | 1.881 | -0.7550 | 0.913 | 0.024 | 18298 | 0 |