## MF
| ID | Description | setSize | enrichmentScore | NES | pvalue | p.adjust | qvalues |
| --- | --- | --- | --- | --- | --- | --- | --- |
| GO:0005125 | cytokine activity | 61 | 0.647525 | 2.280870 | 0.001815 | 0.027475 | 0.021717 |
| GO:0005126 | cytokine receptor binding | 64 | 0.635307 | 2.272182 | 0.001733 | 0.027475 | 0.021717 |
| GO:0005179 | hormone activity | 65 | 0.599166 | 2.150213 | 0.001845 | 0.027475 | 0.021717 |
| GO:0019838 | growth factor binding | 37 | 0.629458 | 2.035215 | 0.001894 | 0.027475 | 0.021717 |
| GO:0005520 | insulin-like growth factor binding | 29 | 0.665244 | 2.028451 | 0.001894 | 0.027475 | 0.021717 |
| GO:0005102 | receptor binding | 396 | 0.427237 | 1.943823 | 0.001667 | 0.027475 | 0.021717 |
| GO:0005164 | tumor necrosis factor receptor binding | 11 | 0.815942 | 1.921328 | 0.002033 | 0.027475 | 0.021717 |
| GO:0008009 | chemokine activity | 18 | 0.675792 | 1.863312 | 0.003854 | 0.034033 | 0.026900 |
| GO:0042379 | chemokine receptor binding | 18 | 0.675792 | 1.863312 | 0.003854 | 0.034033 | 0.026900 |
| GO:0004896 | cytokine receptor activity | 44 | 0.566828 | 1.856067 | 0.001894 | 0.027475 | 0.021717 |
| GO:0000978 | RNA polymerase II core promoter proximal region sequence-specific DNA binding | 44 | 0.558467 | 1.845382 | 0.003630 | 0.033837 | 0.026746 |
| GO:0032813 | tumor necrosis factor receptor superfamily binding | 13 | 0.745930 | 1.832641 | 0.002045 | 0.027475 | 0.021717 |
| GO:0031625 | ubiquitin protein ligase binding | 37 | 0.547616 | 1.795250 | 0.003839 | 0.034033 | 0.026900 |
| GO:0044389 | ubiquitin-like protein ligase binding | 37 | 0.547616 | 1.795250 | 0.003839 | 0.034033 | 0.026900 |
| GO:0001664 | G-protein coupled receptor binding | 87 | 0.447665 | 1.689036 | 0.001825 | 0.027475 | 0.021717 |
| GO:0019899 | enzyme binding | 232 | 0.391668 | 1.685565 | 0.001626 | 0.027475 | 0.021717 |
| GO:0046982 | protein heterodimerization activity | 87 | 0.452660 | 1.684589 | 0.001808 | 0.027475 | 0.021717 |
| GO:0035091 | phosphatidylinositol binding | 91 | 0.429732 | 1.643945 | 0.005300 | 0.041561 | 0.032850 |
| GO:0005525 | GTP binding | 384 | 0.356487 | 1.610624 | 0.001695 | 0.027475 | 0.021717 |
| GO:0008528 | G-protein coupled peptide receptor activity | 64 | 0.454567 | 1.578346 | 0.003824 | 0.034033 | 0.026900 |
| GO:0004197 | cysteine-type endopeptidase activity | 101 | 0.405646 | 1.554556 | 0.003604 | 0.033837 | 0.026746 |
| GO:0019001 | guanyl nucleotide binding | 395 | 0.335597 | 1.522881 | 0.001672 | 0.027475 | 0.021717 |
| GO:0032561 | guanyl ribonucleotide binding | 394 | 0.333535 | 1.515855 | 0.001661 | 0.027475 | 0.021717 |
| GO:0005515 | protein binding | 1905 | 0.278196 | 1.397212 | 0.001353 | 0.027475 | 0.021717 |
| GO:0004175 | endopeptidase activity | 317 | 0.300135 | 1.348667 | 0.004762 | 0.037691 | 0.029791 |
| GO:0097367 | carbohydrate derivative binding | 1627 | 0.243118 | 1.214059 | 0.005666 | 0.043275 | 0.034205 |
| GO:0035639 | purine ribonucleoside triphosphate binding | 1524 | 0.242295 | 1.207225 | 0.004267 | 0.035416 | 0.027993 |
| GO:0001883 | purine nucleoside binding | 1525 | 0.241994 | 1.205984 | 0.005674 | 0.043275 | 0.034205 |
| GO:0032550 | purine ribonucleoside binding | 1525 | 0.241994 | 1.205984 | 0.005674 | 0.043275 | 0.034205 |
| GO:0046872 | metal ion binding | 2608 | -0.215397 | -1.146392 | 0.004184 | 0.035416 | 0.027993 |
| GO:0043169 | cation binding | 2657 | -0.219928 | -1.169537 | 0.004329 | 0.035416 | 0.027993 |
| GO:0003677 | DNA binding | 1207 | -0.228489 | -1.173719 | 0.006211 | 0.046528 | 0.036777 |
| GO:0016491 | oxidoreductase activity | 649 | -0.284052 | -1.400471 | 0.002793 | 0.027475 | 0.021717 |
| GO:0005509 | calcium ion binding | 490 | -0.297562 | -1.440617 | 0.002833 | 0.027475 | 0.021717 |
| GO:0043565 | sequence-specific DNA binding | 597 | -0.297825 | -1.456168 | 0.002632 | 0.027475 | 0.021717 |
| GO:0004497 | monooxygenase activity | 121 | -0.389285 | -1.601077 | 0.002247 | 0.027475 | 0.021717 |
| GO:0004252 | serine-type endopeptidase activity | 99 | -0.420127 | -1.656134 | 0.004396 | 0.035461 | 0.028029 |
| GO:0008236 | serine-type peptidase activity | 115 | -0.417584 | -1.678216 | 0.002299 | 0.027475 | 0.021717 |
| GO:0017171 | serine hydrolase activity | 115 | -0.417584 | -1.678216 | 0.002299 | 0.027475 | 0.021717 |
| GO:0016701 | oxidoreductase activity, acting on single donors with incorporation of molecular oxygen | 25 | -0.567269 | -1.707614 | 0.006276 | 0.046599 | 0.036833 |
| GO:0030594 | neurotransmitter receptor activity | 51 | -0.484770 | -1.712123 | 0.004338 | 0.035416 | 0.027993 |
| GO:0005506 | iron ion binding | 162 | -0.400689 | -1.713280 | 0.002331 | 0.027475 | 0.021717 |
| GO:0015020 | glucuronosyltransferase activity | 63 | -0.476222 | -1.760022 | 0.006787 | 0.049952 | 0.039483 |
| GO:0046906 | tetrapyrrole binding | 116 | -0.437587 | -1.767501 | 0.002404 | 0.027475 | 0.021717 |
| GO:0005198 | structural molecule activity | 342 | -0.379236 | -1.770909 | 0.002710 | 0.027475 | 0.021717 |
| GO:0015171 | amino acid transmembrane transporter activity | 59 | -0.492728 | -1.786621 | 0.004651 | 0.037165 | 0.029376 |
| GO:0004553 | hydrolase activity, hydrolyzing O-glycosyl compounds | 113 | -0.439600 | -1.786990 | 0.002247 | 0.027475 | 0.021717 |
| GO:0015085 | calcium ion transmembrane transporter activity | 80 | -0.470785 | -1.794915 | 0.002247 | 0.027475 | 0.021717 |
| GO:0004879 | RNA polymerase II transcription factor activity, ligand-activated sequence-specific DNA binding | 45 | -0.512288 | -1.795365 | 0.002174 | 0.027475 | 0.021717 |
| GO:0098531 | transcription factor activity, direct ligand regulated sequence-specific DNA binding | 45 | -0.512288 | -1.795365 | 0.002174 | 0.027475 | 0.021717 |
| GO:0022892 | substrate-specific transporter activity | 770 | -0.359195 | -1.801985 | 0.002849 | 0.027475 | 0.021717 |
| GO:0020037 | heme binding | 111 | -0.450437 | -1.807592 | 0.002375 | 0.027475 | 0.021717 |
| GO:0005245 | voltage-gated calcium channel activity | 32 | -0.572087 | -1.810616 | 0.004348 | 0.035416 | 0.027993 |
| GO:0016798 | hydrolase activity, acting on glycosyl bonds | 127 | -0.437452 | -1.811068 | 0.002273 | 0.027475 | 0.021717 |
| GO:0005310 | dicarboxylic acid transmembrane transporter activity | 22 | -0.634443 | -1.821366 | 0.004115 | 0.035231 | 0.027847 |
| GO:0008519 | ammonium transmembrane transporter activity | 16 | -0.678609 | -1.830484 | 0.002041 | 0.027475 | 0.021717 |
| GO:0015297 | antiporter activity | 66 | -0.493280 | -1.842764 | 0.002160 | 0.027475 | 0.021717 |
| GO:0004869 | cysteine-type endopeptidase inhibitor activity | 21 | -0.634828 | -1.851379 | 0.001984 | 0.027475 | 0.021717 |
| GO:0017153 | sodium:dicarboxylate symporter activity | 15 | -0.715162 | -1.858855 | 0.004065 | 0.035231 | 0.027847 |
| GO:0005326 | neurotransmitter transporter activity | 24 | -0.622709 | -1.865586 | 0.002092 | 0.027475 | 0.021717 |
| GO:0005328 | neurotransmitter:sodium symporter activity | 24 | -0.622709 | -1.865586 | 0.002092 | 0.027475 | 0.021717 |
| GO:0008227 | G-protein coupled amine receptor activity | 30 | -0.598919 | -1.866433 | 0.006160 | 0.046528 | 0.036777 |
| GO:0016712 | oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, reduced flavin or flavoprotein as one donor, and incorporation of one atom of oxygen | 37 | -0.574983 | -1.880074 | 0.004107 | 0.035231 | 0.027847 |
| GO:0015368 | calcium:cation antiporter activity | 14 | -0.734983 | -1.884207 | 0.002024 | 0.027475 | 0.021717 |
| GO:0005215 | transporter activity | 909 | -0.378705 | -1.916069 | 0.003021 | 0.028804 | 0.022767 |
| GO:0015298 | solute:cation antiporter activity | 26 | -0.639064 | -1.932292 | 0.002045 | 0.027475 | 0.021717 |
| GO:0015296 | anion:cation symporter activity | 47 | -0.557670 | -1.934187 | 0.002075 | 0.027475 | 0.021717 |
| GO:0009881 | photoreceptor activity | 22 | -0.676355 | -1.973639 | 0.002123 | 0.027475 | 0.021717 |
| GO:0008509 | anion transmembrane transporter activity | 196 | -0.449941 | -1.974895 | 0.002381 | 0.027475 | 0.021717 |
| GO:0015491 | cation:cation antiporter activity | 25 | -0.657935 | -1.977590 | 0.002012 | 0.027475 | 0.021717 |
| GO:0022891 | substrate-specific transmembrane transporter activity | 662 | -0.398597 | -1.978327 | 0.002747 | 0.027475 | 0.021717 |
| GO:0022857 | transmembrane transporter activity | 725 | -0.397293 | -1.980127 | 0.002849 | 0.027475 | 0.021717 |
| GO:0005244 | voltage-gated ion channel activity | 139 | -0.476858 | -1.994254 | 0.002217 | 0.027475 | 0.021717 |
| GO:0005231 | excitatory extracellular ligand-gated ion channel activity | 57 | -0.541718 | -1.997837 | 0.002304 | 0.027475 | 0.021717 |
| GO:0022832 | voltage-gated channel activity | 142 | -0.474624 | -1.998954 | 0.002212 | 0.027475 | 0.021717 |
| GO:0005251 | delayed rectifier potassium channel activity | 23 | -0.683761 | -2.009035 | 0.002020 | 0.027475 | 0.021717 |
| GO:0022829 | wide pore channel activity | 13 | -0.787611 | -2.019229 | 0.001984 | 0.027475 | 0.021717 |
| GO:0015276 | ligand-gated ion channel activity | 116 | -0.494796 | -2.020398 | 0.002299 | 0.027475 | 0.021717 |
| GO:0022834 | ligand-gated channel activity | 116 | -0.494796 | -2.020398 | 0.002299 | 0.027475 | 0.021717 |
| GO:0046943 | carboxylic acid transmembrane transporter activity | 102 | -0.505926 | -2.021238 | 0.002222 | 0.027475 | 0.021717 |
| GO:0005343 | organic acid:sodium symporter activity | 30 | -0.642321 | -2.024870 | 0.002105 | 0.027475 | 0.021717 |
| GO:0005249 | voltage-gated potassium channel activity | 74 | -0.546296 | -2.043760 | 0.002132 | 0.027475 | 0.021717 |
| GO:0005342 | organic acid transmembrane transporter activity | 103 | -0.511478 | -2.045363 | 0.002237 | 0.027475 | 0.021717 |
| GO:0003707 | steroid hormone receptor activity | 65 | -0.550225 | -2.046177 | 0.002155 | 0.027475 | 0.021717 |
| GO:0005230 | extracellular ligand-gated ion channel activity | 72 | -0.538143 | -2.050377 | 0.002315 | 0.027475 | 0.021717 |
| GO:0015075 | ion transmembrane transporter activity | 624 | -0.414773 | -2.051820 | 0.002725 | 0.027475 | 0.021717 |
| GO:0008324 | cation transmembrane transporter activity | 460 | -0.429613 | -2.070596 | 0.002564 | 0.027475 | 0.021717 |
| GO:0004970 | ionotropic glutamate receptor activity | 25 | -0.684320 | -2.075166 | 0.002155 | 0.027475 | 0.021717 |
| GO:0005234 | extracellular-glutamate-gated ion channel activity | 25 | -0.684320 | -2.075166 | 0.002155 | 0.027475 | 0.021717 |
| GO:0008514 | organic anion transmembrane transporter activity | 115 | -0.512396 | -2.083995 | 0.002212 | 0.027475 | 0.021717 |
| GO:0019825 | oxygen binding | 41 | -0.620487 | -2.098351 | 0.002070 | 0.027475 | 0.021717 |
| GO:0022838 | substrate-specific channel activity | 297 | -0.459718 | -2.113492 | 0.002618 | 0.027475 | 0.021717 |
| GO:0005267 | potassium channel activity | 90 | -0.545717 | -2.117065 | 0.002137 | 0.027475 | 0.021717 |
| GO:0005216 | ion channel activity | 287 | -0.463103 | -2.121628 | 0.002604 | 0.027475 | 0.021717 |
| GO:0022804 | active transmembrane transporter activity | 251 | -0.467460 | -2.123778 | 0.002336 | 0.027475 | 0.021717 |
| GO:1901618 | organic hydroxy compound transmembrane transporter activity | 31 | -0.674295 | -2.132748 | 0.002096 | 0.027475 | 0.021717 |
| GO:0022890 | inorganic cation transmembrane transporter activity | 378 | -0.453942 | -2.135074 | 0.002506 | 0.027475 | 0.021717 |
| GO:0008392 | arachidonic acid epoxygenase activity | 20 | -0.764264 | -2.135124 | 0.002070 | 0.027475 | 0.021717 |
| GO:0008391 | arachidonic acid monooxygenase activity | 21 | -0.756264 | -2.135685 | 0.002049 | 0.027475 | 0.021717 |
| GO:0015267 | channel activity | 314 | -0.461929 | -2.145991 | 0.002584 | 0.027475 | 0.021717 |
| GO:0022803 | passive transmembrane transporter activity | 314 | -0.461929 | -2.145991 | 0.002584 | 0.027475 | 0.021717 |
| GO:0005261 | cation channel activity | 204 | -0.486117 | -2.147637 | 0.002415 | 0.027475 | 0.021717 |
| GO:0015079 | potassium ion transmembrane transporter activity | 117 | -0.528801 | -2.149145 | 0.002132 | 0.027475 | 0.021717 |
| GO:0022836 | gated channel activity | 246 | -0.477715 | -2.153181 | 0.002506 | 0.027475 | 0.021717 |
| GO:0046873 | metal ion transmembrane transporter activity | 293 | -0.475552 | -2.176099 | 0.002375 | 0.027475 | 0.021717 |
| GO:0015294 | solute:cation symporter activity | 84 | -0.572051 | -2.188001 | 0.002247 | 0.027475 | 0.021717 |
| GO:0015293 | symporter activity | 95 | -0.557710 | -2.213873 | 0.002183 | 0.027475 | 0.021717 |
| GO:0008066 | glutamate receptor activity | 31 | -0.694245 | -2.221014 | 0.002165 | 0.027475 | 0.021717 |
| GO:0015291 | secondary active transmembrane transporter activity | 163 | -0.524570 | -2.242548 | 0.002326 | 0.027475 | 0.021717 |
| GO:0022843 | voltage-gated cation channel activity | 117 | -0.555435 | -2.254193 | 0.002151 | 0.027475 | 0.021717 |
| GO:0005201 | extracellular matrix structural constituent | 22 | -0.775573 | -2.276553 | 0.002049 | 0.027475 | 0.021717 |
| GO:0015370 | solute:sodium symporter activity | 44 | -0.678379 | -2.291141 | 0.002212 | 0.027475 | 0.021717 |
| GO:0015081 | sodium ion transmembrane transporter activity | 103 | -0.576386 | -2.295807 | 0.002294 | 0.027475 | 0.021717 |
| GO:0015077 | monovalent inorganic cation transmembrane transporter activity | 286 | -0.507014 | -2.310284 | 0.002469 | 0.027475 | 0.021717 |

## CC
| ID | Description | setSize | enrichmentScore | NES | pvalue | p.adjust | qvalues |
| --- | --- | --- | --- | --- | --- | --- | --- |
| GO:0000502 | proteasome complex | 50 | 0.651706 | 2.248633 | 0.001873 | 0.021692 | 0.016351 |
| GO:0005838 | proteasome regulatory particle | 15 | 0.797857 | 2.039911 | 0.001934 | 0.021692 | 0.016351 |
| GO:0022624 | proteasome accessory complex | 20 | 0.701984 | 1.958386 | 0.001953 | 0.021692 | 0.016351 |
| GO:0008540 | proteasome regulatory particle, base subcomplex | 12 | 0.794080 | 1.953618 | 0.001984 | 0.021692 | 0.016351 |
| GO:0005885 | Arp2/3 protein complex | 14 | 0.764071 | 1.950978 | 0.001988 | 0.021692 | 0.016351 |
| GO:0030135 | coated vesicle | 39 | 0.593257 | 1.905281 | 0.003883 | 0.029862 | 0.022509 |
| GO:0008305 | integrin complex | 25 | 0.635686 | 1.896690 | 0.001894 | 0.021692 | 0.016351 |
| GO:0098636 | protein complex involved in cell adhesion | 25 | 0.635686 | 1.896690 | 0.001894 | 0.021692 | 0.016351 |
| GO:0005768 | endosome | 160 | 0.439041 | 1.823519 | 0.001916 | 0.021692 | 0.016351 |
| GO:0030117 | membrane coat | 44 | 0.538531 | 1.788808 | 0.001905 | 0.021692 | 0.016351 |
| GO:0048475 | coated membrane | 44 | 0.538531 | 1.788808 | 0.001905 | 0.021692 | 0.016351 |
| GO:0044440 | endosomal part | 68 | 0.477666 | 1.740978 | 0.001890 | 0.021692 | 0.016351 |
| GO:0030684 | preribosome | 40 | 0.533023 | 1.739770 | 0.005618 | 0.036131 | 0.027235 |
| GO:0010008 | endosome membrane | 64 | 0.479660 | 1.734885 | 0.005629 | 0.036131 | 0.027235 |
| GO:0005924 | cell-substrate adherens junction | 14 | 0.672655 | 1.722664 | 0.006098 | 0.036770 | 0.027716 |
| GO:0005925 | focal adhesion | 14 | 0.672655 | 1.722664 | 0.006098 | 0.036770 | 0.027716 |
| GO:0030055 | cell-substrate junction | 14 | 0.672655 | 1.722664 | 0.006098 | 0.036770 | 0.027716 |
| GO:0005615 | extracellular space | 271 | 0.381268 | 1.670894 | 0.001742 | 0.021692 | 0.016351 |
| GO:0005730 | nucleolus | 140 | 0.406385 | 1.668819 | 0.001799 | 0.021692 | 0.016351 |
| GO:0005783 | endoplasmic reticulum | 429 | 0.347667 | 1.594474 | 0.001608 | 0.021692 | 0.016351 |
| GO:0044421 | extracellular region part | 338 | 0.352908 | 1.580107 | 0.001698 | 0.021692 | 0.016351 |
| GO:0044432 | endoplasmic reticulum part | 277 | 0.356517 | 1.573395 | 0.001695 | 0.021692 | 0.016351 |
| GO:0005576 | extracellular region | 607 | 0.325873 | 1.545935 | 0.001563 | 0.021692 | 0.016351 |
| GO:0000323 | lytic vacuole | 104 | 0.387025 | 1.514815 | 0.008772 | 0.049875 | 0.037594 |
| GO:0042175 | nuclear outer membrane-endoplasmic reticulum membrane network | 263 | 0.342119 | 1.498169 | 0.001751 | 0.021692 | 0.016351 |
| GO:0005789 | endoplasmic reticulum membrane | 259 | 0.340057 | 1.483159 | 0.001783 | 0.021692 | 0.016351 |
| GO:0012505 | endomembrane system | 987 | 0.303886 | 1.481395 | 0.001555 | 0.021692 | 0.016351 |
| GO:0031981 | nuclear lumen | 478 | 0.320551 | 1.480688 | 0.001650 | 0.021692 | 0.016351 |
| GO:0005773 | vacuole | 147 | 0.351297 | 1.439452 | 0.008475 | 0.048882 | 0.036846 |
| GO:0044428 | nuclear part | 699 | 0.298629 | 1.428927 | 0.001580 | 0.021692 | 0.016351 |
| GO:0070013 | intracellular organelle lumen | 583 | 0.300189 | 1.407421 | 0.001616 | 0.021692 | 0.016351 |
| GO:0031974 | membrane-enclosed lumen | 600 | 0.298644 | 1.403419 | 0.001592 | 0.021692 | 0.016351 |
| GO:0043233 | organelle lumen | 584 | 0.297430 | 1.396078 | 0.001600 | 0.021692 | 0.016351 |
| GO:0005654 | nucleoplasm | 272 | 0.322505 | 1.393071 | 0.006780 | 0.040273 | 0.030357 |
| GO:0005737 | cytoplasm | 3626 | 0.240867 | 1.241887 | 0.001266 | 0.021692 | 0.016351 |
| GO:0044444 | cytoplasmic part | 2355 | 0.232226 | 1.180963 | 0.003968 | 0.029862 | 0.022509 |
| GO:0016020 | membrane | 3709 | -0.205795 | -1.111274 | 0.005464 | 0.036131 | 0.027235 |
| GO:0016021 | integral component of membrane | 2531 | -0.233578 | -1.246099 | 0.004673 | 0.032368 | 0.024398 |
| GO:0031224 | intrinsic component of membrane | 2570 | -0.234000 | -1.249299 | 0.004717 | 0.032368 | 0.024398 |
| GO:0071944 | cell periphery | 1387 | -0.275162 | -1.426767 | 0.003425 | 0.028203 | 0.021259 |
| GO:0005886 | plasma membrane | 1350 | -0.281101 | -1.455850 | 0.003472 | 0.028203 | 0.021259 |
| GO:0098797 | plasma membrane protein complex | 263 | -0.324627 | -1.465182 | 0.004963 | 0.033478 | 0.025234 |
| GO:0098590 | plasma membrane region | 152 | -0.348712 | -1.470094 | 0.006961 | 0.040740 | 0.030708 |
| GO:0044459 | plasma membrane part | 827 | -0.320918 | -1.619615 | 0.002865 | 0.024264 | 0.018289 |
| GO:0031226 | intrinsic component of plasma membrane | 597 | -0.348200 | -1.709848 | 0.002710 | 0.023448 | 0.017674 |
| GO:0005887 | integral component of plasma membrane | 575 | -0.355421 | -1.741886 | 0.002653 | 0.023448 | 0.017674 |
| GO:0031513 | nonmotile primary cilium | 20 | -0.616788 | -1.752089 | 0.006048 | 0.036770 | 0.027716 |
| GO:0044456 | synapse part | 155 | -0.412938 | -1.753237 | 0.002347 | 0.021692 | 0.016351 |
| GO:0045177 | apical part of cell | 33 | -0.545179 | -1.757198 | 0.003906 | 0.029862 | 0.022509 |
| GO:0034704 | calcium channel complex | 27 | -0.596585 | -1.796209 | 0.004167 | 0.029862 | 0.022509 |
| GO:0005891 | voltage-gated calcium channel complex | 25 | -0.610116 | -1.807723 | 0.004016 | 0.029862 | 0.022509 |
| GO:0005922 | connexon complex | 24 | -0.610701 | -1.819667 | 0.002132 | 0.021692 | 0.016351 |
| GO:0098794 | postsynapse | 79 | -0.473988 | -1.823186 | 0.002165 | 0.021692 | 0.016351 |
| GO:0045211 | postsynaptic membrane | 67 | -0.496945 | -1.823292 | 0.002315 | 0.021692 | 0.016351 |
| GO:0043005 | neuron projection | 142 | -0.439978 | -1.834225 | 0.002288 | 0.021692 | 0.016351 |
| GO:0045202 | synapse | 207 | -0.414602 | -1.836811 | 0.002375 | 0.021692 | 0.016351 |
| GO:0097060 | synaptic membrane | 76 | -0.493480 | -1.859169 | 0.002398 | 0.021692 | 0.016351 |
| GO:0005921 | gap junction | 30 | -0.597872 | -1.865718 | 0.002193 | 0.021692 | 0.016351 |
| GO:0032281 | AMPA glutamate receptor complex | 21 | -0.648875 | -1.869082 | 0.004124 | 0.029862 | 0.022509 |
| GO:0097458 | neuron part | 227 | -0.420197 | -1.883833 | 0.002370 | 0.021692 | 0.016351 |
| GO:0005581 | collagen trimer | 48 | -0.590909 | -2.058711 | 0.002128 | 0.021692 | 0.016351 |
| GO:0008076 | voltage-gated potassium channel complex | 33 | -0.652874 | -2.082948 | 0.002092 | 0.021692 | 0.016351 |
| GO:0034705 | potassium channel complex | 33 | -0.652874 | -2.082948 | 0.002092 | 0.021692 | 0.016351 |
| GO:0008328 | ionotropic glutamate receptor complex | 39 | -0.627492 | -2.093183 | 0.004202 | 0.029862 | 0.022509 |
| GO:0045111 | intermediate filament cytoskeleton | 51 | -0.604601 | -2.167281 | 0.002151 | 0.021692 | 0.016351 |
| GO:0005882 | intermediate filament | 50 | -0.608799 | -2.171338 | 0.002179 | 0.021692 | 0.016351 |
| GO:0034702 | ion channel complex | 140 | -0.524338 | -2.182346 | 0.002320 | 0.021692 | 0.016351 |
| GO:1902495 | transmembrane transporter complex | 155 | -0.519616 | -2.192232 | 0.002364 | 0.021692 | 0.016351 |
| GO:1990351 | transporter complex | 155 | -0.519616 | -2.192232 | 0.002364 | 0.021692 | 0.016351 |
| GO:0034703 | cation channel complex | 72 | -0.610583 | -2.306739 | 0.002169 | 0.021692 | 0.016351 |

## BP
| ID | Description | setSize | enrichmentScore | NES | pvalue | p.adjust | qvalues |
| --- | --- | --- | --- | --- | --- | --- | --- |
| GO:0006954 | inflammatory response | 74 | 0.723217 | 2.593119 | 0.001739 | 0.027820 | 0.021530 |
| GO:0006952 | defense response | 162 | 0.627301 | 2.582557 | 0.001664 | 0.027820 | 0.021530 |
| GO:0043207 | response to external biotic stimulus | 106 | 0.657455 | 2.542325 | 0.001748 | 0.027820 | 0.021530 |
| GO:0051707 | response to other organism | 106 | 0.657455 | 2.542325 | 0.001748 | 0.027820 | 0.021530 |
| GO:0009617 | response to bacterium | 59 | 0.721025 | 2.514872 | 0.001818 | 0.027820 | 0.021530 |
| GO:0009607 | response to biotic stimulus | 114 | 0.618781 | 2.408526 | 0.001733 | 0.027820 | 0.021530 |
| GO:0034097 | response to cytokine | 72 | 0.656034 | 2.383597 | 0.001786 | 0.027820 | 0.021530 |
| GO:0060326 | cell chemotaxis | 38 | 0.742505 | 2.374605 | 0.001812 | 0.027820 | 0.021530 |
| GO:0050900 | leukocyte migration | 36 | 0.741021 | 2.354340 | 0.001745 | 0.027820 | 0.021530 |
| GO:0051704 | multi-organism process | 176 | 0.559328 | 2.328217 | 0.001706 | 0.027820 | 0.021530 |
| GO:0097529 | myeloid leukocyte migration | 31 | 0.737776 | 2.291463 | 0.001754 | 0.027820 | 0.021530 |
| GO:0030595 | leukocyte chemotaxis | 30 | 0.748962 | 2.281087 | 0.001821 | 0.027820 | 0.021530 |
| GO:0006955 | immune response | 195 | 0.528102 | 2.218671 | 0.001779 | 0.027820 | 0.021530 |
| GO:0019221 | cytokine-mediated signaling pathway | 56 | 0.641947 | 2.211717 | 0.001799 | 0.027820 | 0.021530 |
| GO:0032496 | response to lipopolysaccharide | 15 | 0.868246 | 2.200235 | 0.001838 | 0.027820 | 0.021530 |
| GO:0097530 | granulocyte migration | 26 | 0.744753 | 2.199226 | 0.001828 | 0.027820 | 0.021530 |
| GO:0071345 | cellular response to cytokine stimulus | 58 | 0.630219 | 2.197970 | 0.001802 | 0.027820 | 0.021530 |
| GO:0009611 | response to wounding | 177 | 0.521710 | 2.164213 | 0.001681 | 0.027820 | 0.021530 |
| GO:0002237 | response to molecule of bacterial origin | 17 | 0.825044 | 2.157962 | 0.001842 | 0.027820 | 0.021530 |
| GO:1990266 | neutrophil migration | 25 | 0.740370 | 2.155973 | 0.001838 | 0.027820 | 0.021530 |
| GO:0043331 | response to dsRNA | 11 | 0.893329 | 2.130020 | 0.001838 | 0.027820 | 0.021530 |
| GO:0009615 | response to virus | 27 | 0.712457 | 2.128343 | 0.001828 | 0.027820 | 0.021530 |
| GO:0071621 | granulocyte chemotaxis | 23 | 0.733535 | 2.122628 | 0.001828 | 0.027820 | 0.021530 |
| GO:0002376 | immune system process | 471 | 0.453705 | 2.103904 | 0.001634 | 0.027820 | 0.021530 |
| GO:0045087 | innate immune response | 90 | 0.563528 | 2.101973 | 0.001821 | 0.027820 | 0.021530 |
| GO:0006950 | response to stress | 858 | 0.431759 | 2.099819 | 0.001447 | 0.027820 | 0.021530 |
| GO:1903706 | regulation of hemopoiesis | 22 | 0.736208 | 2.089896 | 0.001859 | 0.027820 | 0.021530 |
| GO:0002682 | regulation of immune system process | 91 | 0.559645 | 2.086423 | 0.001757 | 0.027820 | 0.021530 |
| GO:0098542 | defense response to other organism | 46 | 0.621670 | 2.071157 | 0.001808 | 0.027820 | 0.021530 |
| GO:0030163 | protein catabolic process | 287 | 0.468878 | 2.070406 | 0.001661 | 0.027820 | 0.021530 |
| GO:0030593 | neutrophil chemotaxis | 22 | 0.728272 | 2.061185 | 0.001873 | 0.027820 | 0.021530 |
| GO:0042742 | defense response to bacterium | 26 | 0.695073 | 2.048250 | 0.001802 | 0.027820 | 0.021530 |
| GO:0044257 | cellular protein catabolic process | 267 | 0.463300 | 2.042608 | 0.001631 | 0.027820 | 0.021530 |
| GO:0034314 | Arp2/3 complex-mediated actin nucleation | 24 | 0.700812 | 2.041745 | 0.001818 | 0.027820 | 0.021530 |
| GO:0051603 | proteolysis involved in cellular protein catabolic process | 264 | 0.463670 | 2.037784 | 0.001650 | 0.027820 | 0.021530 |
| GO:0043632 | modification-dependent macromolecule catabolic process | 246 | 0.467453 | 2.031240 | 0.001669 | 0.027820 | 0.021530 |
| GO:0019941 | modification-dependent protein catabolic process | 241 | 0.467315 | 2.024304 | 0.001692 | 0.027820 | 0.021530 |
| GO:0007596 | blood coagulation | 48 | 0.596941 | 2.020039 | 0.001815 | 0.027820 | 0.021530 |
| GO:0007599 | hemostasis | 48 | 0.596941 | 2.020039 | 0.001815 | 0.027820 | 0.021530 |
| GO:0048870 | cell motility | 360 | 0.450332 | 2.018862 | 0.001621 | 0.027820 | 0.021530 |
| GO:0051674 | localization of cell | 360 | 0.450332 | 2.018862 | 0.001621 | 0.027820 | 0.021530 |
| GO:0016477 | cell migration | 343 | 0.450098 | 2.013662 | 0.001597 | 0.027820 | 0.021530 |
| GO:0030225 | macrophage differentiation | 14 | 0.780073 | 2.008675 | 0.001957 | 0.027820 | 0.021530 |
| GO:0052547 | regulation of peptidase activity | 62 | 0.565233 | 2.007397 | 0.001828 | 0.027820 | 0.021530 |
| GO:0031347 | regulation of defense response | 40 | 0.612664 | 1.995075 | 0.001852 | 0.027820 | 0.021530 |
| GO:0006511 | ubiquitin-dependent protein catabolic process | 237 | 0.461248 | 1.989019 | 0.001704 | 0.027820 | 0.021530 |
| GO:0050727 | regulation of inflammatory response | 17 | 0.740686 | 1.978130 | 0.001898 | 0.027820 | 0.021530 |
| GO:0006826 | iron ion transport | 20 | 0.722079 | 1.971139 | 0.001912 | 0.027820 | 0.021530 |
| GO:0031638 | zymogen activation | 16 | 0.756183 | 1.966810 | 0.001919 | 0.027820 | 0.021530 |
| GO:0050817 | coagulation | 51 | 0.578229 | 1.966781 | 0.001848 | 0.027820 | 0.021530 |
| GO:0032103 | positive regulation of response to external stimulus | 13 | 0.782812 | 1.963633 | 0.001972 | 0.027820 | 0.021530 |
| GO:1903034 | regulation of response to wounding | 32 | 0.632283 | 1.938117 | 0.001890 | 0.027820 | 0.021530 |
| GO:0043254 | regulation of protein complex assembly | 81 | 0.519709 | 1.934398 | 0.001802 | 0.027820 | 0.021530 |
| GO:0010942 | positive regulation of cell death | 66 | 0.541698 | 1.930311 | 0.001898 | 0.027820 | 0.021530 |
| GO:0043065 | positive regulation of apoptotic process | 66 | 0.541698 | 1.930311 | 0.001898 | 0.027820 | 0.021530 |
| GO:0043068 | positive regulation of programmed cell death | 66 | 0.541698 | 1.930311 | 0.001898 | 0.027820 | 0.021530 |
| GO:0031334 | positive regulation of protein complex assembly | 58 | 0.555258 | 1.926833 | 0.001873 | 0.027820 | 0.021530 |
| GO:0046456 | icosanoid biosynthetic process | 13 | 0.778639 | 1.925607 | 0.003738 | 0.035306 | 0.027325 |
| GO:1901570 | fatty acid derivative biosynthetic process | 13 | 0.778639 | 1.925607 | 0.003738 | 0.035306 | 0.027325 |
| GO:0050878 | regulation of body fluid levels | 54 | 0.558575 | 1.916547 | 0.001862 | 0.027820 | 0.021530 |
| GO:0030162 | regulation of proteolysis | 139 | 0.469018 | 1.903262 | 0.001748 | 0.027820 | 0.021530 |
| GO:0007229 | integrin-mediated signaling pathway | 36 | 0.611471 | 1.896012 | 0.001848 | 0.027820 | 0.021530 |
| GO:0044265 | cellular macromolecule catabolic process | 340 | 0.422032 | 1.893839 | 0.001600 | 0.027820 | 0.021530 |
| GO:0052548 | regulation of endopeptidase activity | 53 | 0.545318 | 1.890119 | 0.001805 | 0.027820 | 0.021530 |
| GO:0030010 | establishment of cell polarity | 33 | 0.599063 | 1.885495 | 0.001815 | 0.027820 | 0.021530 |
| GO:0009605 | response to external stimulus | 444 | 0.411239 | 1.881728 | 0.001543 | 0.027820 | 0.021530 |
| GO:0030168 | platelet activation | 20 | 0.675220 | 1.868973 | 0.001984 | 0.027820 | 0.021530 |
| GO:0007249 | I-kappaB kinase/NF-kappaB signaling | 21 | 0.652193 | 1.863563 | 0.005929 | 0.045678 | 0.035351 |
| GO:0046916 | cellular transition metal ion homeostasis | 23 | 0.656357 | 1.862237 | 0.005660 | 0.044648 | 0.034554 |
| GO:0002573 | myeloid leukocyte differentiation | 34 | 0.593776 | 1.861087 | 0.001805 | 0.027820 | 0.021530 |
| GO:0007162 | negative regulation of cell adhesion | 11 | 0.771000 | 1.861016 | 0.005894 | 0.045560 | 0.035260 |
| GO:0002683 | negative regulation of immune system process | 11 | 0.769658 | 1.856100 | 0.005814 | 0.045092 | 0.034898 |
| GO:0006879 | cellular iron ion homeostasis | 21 | 0.678395 | 1.854204 | 0.003861 | 0.035815 | 0.027718 |
| GO:0010952 | positive regulation of peptidase activity | 24 | 0.633304 | 1.830699 | 0.003683 | 0.035306 | 0.027325 |
| GO:0044089 | positive regulation of cellular component biogenesis | 64 | 0.514340 | 1.821324 | 0.001866 | 0.027820 | 0.021530 |
| GO:0006399 | tRNA metabolic process | 105 | 0.466122 | 1.819289 | 0.001757 | 0.027820 | 0.021530 |
| GO:0060973 | cell migration involved in heart development | 21 | 0.654533 | 1.818992 | 0.001927 | 0.027820 | 0.021530 |
| GO:0009226 | nucleotide-sugar biosynthetic process | 14 | 0.721661 | 1.818452 | 0.003960 | 0.036016 | 0.027874 |
| GO:0048645 | organ formation | 21 | 0.638829 | 1.815147 | 0.003731 | 0.035306 | 0.027325 |
| GO:0009620 | response to fungus | 26 | 0.624041 | 1.812915 | 0.003824 | 0.035615 | 0.027563 |
| GO:0051346 | negative regulation of hydrolase activity | 50 | 0.528150 | 1.810275 | 0.005495 | 0.044121 | 0.034146 |
| GO:0010498 | proteasomal protein catabolic process | 172 | 0.431717 | 1.808106 | 0.001712 | 0.027820 | 0.021530 |
| GO:0007264 | small GTPase mediated signal transduction | 362 | 0.403454 | 1.806899 | 0.001626 | 0.027820 | 0.021530 |
| GO:0042060 | wound healing | 133 | 0.451577 | 1.805758 | 0.001764 | 0.027820 | 0.021530 |
| GO:0010466 | negative regulation of peptidase activity | 37 | 0.556162 | 1.803596 | 0.005587 | 0.044216 | 0.034220 |
| GO:0008154 | actin polymerization or depolymerization | 73 | 0.494448 | 1.802804 | 0.001828 | 0.027820 | 0.021530 |
| GO:0007034 | vacuolar transport | 36 | 0.569471 | 1.802486 | 0.003906 | 0.036016 | 0.027874 |
| GO:0006888 | ER to Golgi vesicle-mediated transport | 38 | 0.557293 | 1.794994 | 0.003766 | 0.035353 | 0.027360 |
| GO:0006919 | activation of cysteine-type endopeptidase activity involved in apoptotic process | 12 | 0.735711 | 1.794524 | 0.005792 | 0.045069 | 0.034880 |
| GO:0097202 | activation of cysteine-type endopeptidase activity | 12 | 0.735711 | 1.794524 | 0.005792 | 0.045069 | 0.034880 |
| GO:0006636 | unsaturated fatty acid biosynthetic process | 14 | 0.706235 | 1.787570 | 0.005545 | 0.044121 | 0.034146 |
| GO:0051336 | regulation of hydrolase activity | 156 | 0.434704 | 1.783891 | 0.001692 | 0.027820 | 0.021530 |
| GO:0090504 | epiboly | 41 | 0.546511 | 1.780671 | 0.003676 | 0.035306 | 0.027325 |
| GO:0000910 | cytokinesis | 40 | 0.537784 | 1.779763 | 0.003623 | 0.035306 | 0.027325 |
| GO:0080134 | regulation of response to stress | 118 | 0.453561 | 1.777103 | 0.001783 | 0.027820 | 0.021530 |
| GO:0010941 | regulation of cell death | 328 | 0.396229 | 1.774594 | 0.001661 | 0.027820 | 0.021530 |
| GO:0040011 | locomotion | 476 | 0.383515 | 1.769013 | 0.001531 | 0.027820 | 0.021530 |
| GO:0001558 | regulation of cell growth | 80 | 0.473874 | 1.768419 | 0.003676 | 0.035306 | 0.027325 |
| GO:0001878 | response to yeast | 23 | 0.619403 | 1.768114 | 0.005758 | 0.045069 | 0.034880 |
| GO:0030833 | regulation of actin filament polymerization | 66 | 0.491766 | 1.767973 | 0.003610 | 0.035306 | 0.027325 |
| GO:0071824 | protein-DNA complex subunit organization | 61 | 0.494429 | 1.767096 | 0.001969 | 0.027820 | 0.021530 |
| GO:0055113 | epiboly involved in gastrulation with mouth forming second | 33 | 0.564131 | 1.765895 | 0.005386 | 0.043979 | 0.034037 |
| GO:0032101 | regulation of response to external stimulus | 61 | 0.500564 | 1.763916 | 0.001773 | 0.027820 | 0.021530 |
| GO:0043161 | proteasome-mediated ubiquitin-dependent protein catabolic process | 169 | 0.424377 | 1.763643 | 0.001736 | 0.027820 | 0.021530 |
| GO:0032271 | regulation of protein polymerization | 67 | 0.487685 | 1.759452 | 0.001812 | 0.027820 | 0.021530 |
| GO:0010950 | positive regulation of endopeptidase activity | 23 | 0.614671 | 1.753659 | 0.001869 | 0.027820 | 0.021530 |
| GO:0043280 | positive regulation of cysteine-type endopeptidase activity involved in apoptotic process | 23 | 0.614671 | 1.753659 | 0.001869 | 0.027820 | 0.021530 |
| GO:2001056 | positive regulation of cysteine-type endopeptidase activity | 23 | 0.614671 | 1.753659 | 0.001869 | 0.027820 | 0.021530 |
| GO:0034470 | ncRNA processing | 171 | 0.422539 | 1.748574 | 0.001748 | 0.027820 | 0.021530 |
| GO:0008064 | regulation of actin polymerization or depolymerization | 69 | 0.480546 | 1.747852 | 0.001799 | 0.027820 | 0.021530 |
| GO:0030832 | regulation of actin filament length | 69 | 0.480546 | 1.747852 | 0.001799 | 0.027820 | 0.021530 |
| GO:0065004 | protein-DNA complex assembly | 50 | 0.510646 | 1.744136 | 0.001976 | 0.027820 | 0.021530 |
| GO:0030041 | actin filament polymerization | 56 | 0.497844 | 1.743866 | 0.003597 | 0.035306 | 0.027325 |
| GO:0007067 | mitotic nuclear division | 123 | 0.439508 | 1.737044 | 0.001745 | 0.027820 | 0.021530 |
| GO:0051301 | cell division | 168 | 0.417900 | 1.734742 | 0.001742 | 0.027820 | 0.021530 |
| GO:0042176 | regulation of protein catabolic process | 81 | 0.459197 | 1.729529 | 0.001799 | 0.027820 | 0.021530 |
| GO:0030838 | positive regulation of actin filament polymerization | 48 | 0.510169 | 1.727077 | 0.005515 | 0.044121 | 0.034146 |
| GO:0032273 | positive regulation of protein polymerization | 49 | 0.504698 | 1.714827 | 0.003690 | 0.035306 | 0.027325 |
| GO:1901699 | cellular response to nitrogen compound | 65 | 0.477500 | 1.714220 | 0.003591 | 0.035306 | 0.027325 |
| GO:0032956 | regulation of actin cytoskeleton organization | 89 | 0.452813 | 1.710697 | 0.003571 | 0.035306 | 0.027325 |
| GO:0002684 | positive regulation of immune system process | 53 | 0.503641 | 1.709484 | 0.005495 | 0.044121 | 0.034146 |
| GO:2000145 | regulation of cell motility | 86 | 0.454820 | 1.700728 | 0.001818 | 0.027820 | 0.021530 |
| GO:0044801 | single-organism membrane fusion | 65 | 0.472245 | 1.694178 | 0.003781 | 0.035353 | 0.027360 |
| GO:0032970 | regulation of actin filament-based process | 91 | 0.445951 | 1.693897 | 0.003559 | 0.035306 | 0.027325 |
| GO:0009057 | macromolecule catabolic process | 378 | 0.373904 | 1.691672 | 0.001613 | 0.027820 | 0.021530 |
| GO:0034660 | ncRNA metabolic process | 219 | 0.396887 | 1.688645 | 0.001757 | 0.027820 | 0.021530 |
| GO:0042981 | regulation of apoptotic process | 308 | 0.380657 | 1.688289 | 0.001695 | 0.027820 | 0.021530 |
| GO:1902532 | negative regulation of intracellular signal transduction | 68 | 0.470660 | 1.685550 | 0.003546 | 0.035306 | 0.027325 |
| GO:0016050 | vesicle organization | 99 | 0.436188 | 1.685042 | 0.003711 | 0.035306 | 0.027325 |
| GO:0032270 | positive regulation of cellular protein metabolic process | 190 | 0.398245 | 1.684905 | 0.003384 | 0.035306 | 0.027325 |
| GO:0008033 | tRNA processing | 64 | 0.475972 | 1.678743 | 0.003745 | 0.035306 | 0.027325 |
| GO:0000041 | transition metal ion transport | 46 | 0.495217 | 1.678314 | 0.005556 | 0.044121 | 0.034146 |
| GO:0043067 | regulation of programmed cell death | 310 | 0.376155 | 1.671213 | 0.001686 | 0.027820 | 0.021530 |
| GO:0006935 | chemotaxis | 179 | 0.399284 | 1.670329 | 0.001681 | 0.027820 | 0.021530 |
| GO:0030036 | actin cytoskeleton organization | 253 | 0.384405 | 1.669335 | 0.001653 | 0.027820 | 0.021530 |
| GO:0051495 | positive regulation of cytoskeleton organization | 52 | 0.483121 | 1.668741 | 0.005525 | 0.044121 | 0.034146 |
| GO:0051247 | positive regulation of protein metabolic process | 194 | 0.393264 | 1.667097 | 0.003373 | 0.035306 | 0.027325 |
| GO:0030334 | regulation of cell migration | 79 | 0.451568 | 1.662051 | 0.001786 | 0.027820 | 0.021530 |
| GO:0030029 | actin filament-based process | 256 | 0.381383 | 1.661491 | 0.001637 | 0.027820 | 0.021530 |
| GO:0051130 | positive regulation of cellular component organization | 114 | 0.421076 | 1.654247 | 0.001848 | 0.027820 | 0.021530 |
| GO:0040008 | regulation of growth | 99 | 0.426664 | 1.649565 | 0.005556 | 0.044121 | 0.034146 |
| GO:0007015 | actin filament organization | 129 | 0.412102 | 1.648762 | 0.001724 | 0.027820 | 0.021530 |
| GO:1901698 | response to nitrogen compound | 116 | 0.419121 | 1.648561 | 0.005357 | 0.043979 | 0.034037 |
| GO:0048584 | positive regulation of response to stimulus | 229 | 0.380378 | 1.646580 | 0.001634 | 0.027820 | 0.021530 |
| GO:0035556 | intracellular signal transduction | 855 | 0.339999 | 1.642337 | 0.001499 | 0.027820 | 0.021530 |
| GO:0042330 | taxis | 185 | 0.393150 | 1.640869 | 0.001715 | 0.027820 | 0.021530 |
| GO:0055076 | transition metal ion homeostasis | 35 | 0.529644 | 1.630832 | 0.005682 | 0.044665 | 0.034567 |
| GO:0032268 | regulation of cellular protein metabolic process | 444 | 0.352677 | 1.626288 | 0.001572 | 0.027820 | 0.021530 |
| GO:0044087 | regulation of cellular component biogenesis | 117 | 0.414133 | 1.625519 | 0.003623 | 0.035306 | 0.027325 |
| GO:0071417 | cellular response to organonitrogen compound | 58 | 0.467696 | 1.624405 | 0.003697 | 0.035306 | 0.027325 |
| GO:0048285 | organelle fission | 163 | 0.389827 | 1.622340 | 0.001718 | 0.027820 | 0.021530 |
| GO:0016049 | cell growth | 117 | 0.406577 | 1.617367 | 0.003578 | 0.035306 | 0.027325 |
| GO:0051246 | regulation of protein metabolic process | 455 | 0.350274 | 1.615834 | 0.001570 | 0.027820 | 0.021530 |
| GO:0008283 | cell proliferation | 223 | 0.374491 | 1.615263 | 0.001739 | 0.027820 | 0.021530 |
| GO:0000280 | nuclear division | 148 | 0.395173 | 1.610480 | 0.001751 | 0.027820 | 0.021530 |
| GO:0030099 | myeloid cell differentiation | 122 | 0.399543 | 1.608231 | 0.003663 | 0.035306 | 0.027325 |
| GO:0008219 | cell death | 436 | 0.348631 | 1.603795 | 0.001626 | 0.027820 | 0.021530 |
| GO:0016265 | death | 436 | 0.348631 | 1.603795 | 0.001626 | 0.027820 | 0.021530 |
| GO:0006928 | movement of cell or subcellular component | 548 | 0.340912 | 1.596618 | 0.001538 | 0.027820 | 0.021530 |
| GO:0042127 | regulation of cell proliferation | 161 | 0.384707 | 1.596279 | 0.003565 | 0.035306 | 0.027325 |
| GO:0045184 | establishment of protein localization | 485 | 0.342953 | 1.594445 | 0.001600 | 0.027820 | 0.021530 |
| GO:0016485 | protein processing | 62 | 0.443194 | 1.591408 | 0.005282 | 0.043979 | 0.034037 |
| GO:0034622 | cellular macromolecular complex assembly | 329 | 0.353516 | 1.580093 | 0.001684 | 0.027820 | 0.021530 |
| GO:0001944 | vasculature development | 314 | 0.351887 | 1.579184 | 0.001653 | 0.027820 | 0.021530 |
| GO:0010638 | positive regulation of organelle organization | 77 | 0.427654 | 1.576263 | 0.005484 | 0.044121 | 0.034146 |
| GO:0007265 | Ras protein signal transduction | 197 | 0.379935 | 1.574790 | 0.003490 | 0.035306 | 0.027325 |
| GO:0015031 | protein transport | 469 | 0.338402 | 1.568016 | 0.001608 | 0.027820 | 0.021530 |
| GO:0040007 | growth | 267 | 0.356992 | 1.567593 | 0.001754 | 0.027820 | 0.021530 |
| GO:0006915 | apoptotic process | 409 | 0.340077 | 1.557768 | 0.001616 | 0.027820 | 0.021530 |
| GO:0030097 | hemopoiesis | 243 | 0.352652 | 1.539289 | 0.001721 | 0.027820 | 0.021530 |
| GO:0051128 | regulation of cellular component organization | 402 | 0.336791 | 1.537789 | 0.001610 | 0.027820 | 0.021530 |
| GO:0012501 | programmed cell death | 412 | 0.335529 | 1.536489 | 0.001626 | 0.027820 | 0.021530 |
| GO:0060548 | negative regulation of cell death | 130 | 0.378006 | 1.535777 | 0.005300 | 0.043979 | 0.034037 |
| GO:0009894 | regulation of catabolic process | 136 | 0.373277 | 1.531929 | 0.005348 | 0.043979 | 0.034037 |
| GO:1903047 | mitotic cell cycle process | 185 | 0.364641 | 1.525959 | 0.005146 | 0.043154 | 0.033398 |
| GO:0031401 | positive regulation of protein modification process | 133 | 0.377191 | 1.524190 | 0.005155 | 0.043154 | 0.033398 |
| GO:0046907 | intracellular transport | 523 | 0.323256 | 1.523844 | 0.001558 | 0.027820 | 0.021530 |
| GO:0008104 | protein localization | 579 | 0.322801 | 1.522528 | 0.001595 | 0.027820 | 0.021530 |
| GO:0050896 | response to stimulus | 3210 | 0.293605 | 1.508645 | 0.001208 | 0.027820 | 0.021530 |
| GO:0031329 | regulation of cellular catabolic process | 131 | 0.367542 | 1.506051 | 0.005329 | 0.043979 | 0.034037 |
| GO:0022402 | cell cycle process | 276 | 0.343281 | 1.505598 | 0.001701 | 0.027820 | 0.021530 |
| GO:0006886 | intracellular protein transport | 332 | 0.335181 | 1.504819 | 0.001650 | 0.027820 | 0.021530 |
| GO:0048518 | positive regulation of biological process | 871 | 0.309765 | 1.502091 | 0.001479 | 0.027820 | 0.021530 |
| GO:0010033 | response to organic substance | 546 | 0.319921 | 1.501679 | 0.001548 | 0.027820 | 0.021530 |
| GO:1902531 | regulation of intracellular signal transduction | 297 | 0.340133 | 1.501229 | 0.001642 | 0.027820 | 0.021530 |
| GO:0001568 | blood vessel development | 277 | 0.338452 | 1.497969 | 0.001692 | 0.027820 | 0.021530 |
| GO:0048522 | positive regulation of cellular process | 738 | 0.312172 | 1.490331 | 0.001560 | 0.027820 | 0.021530 |
| GO:0048534 | hematopoietic or lymphoid organ development | 252 | 0.339825 | 1.488223 | 0.001712 | 0.027820 | 0.021530 |
| GO:0050790 | regulation of catalytic activity | 326 | 0.334779 | 1.487908 | 0.001550 | 0.027820 | 0.021530 |
| GO:0048583 | regulation of response to stimulus | 750 | 0.311743 | 1.487906 | 0.001508 | 0.027820 | 0.021530 |
| GO:0002520 | immune system development | 260 | 0.333838 | 1.474239 | 0.001692 | 0.027820 | 0.021530 |
| GO:0007169 | transmembrane receptor protein tyrosine kinase signaling pathway | 202 | 0.341018 | 1.472442 | 0.005076 | 0.042806 | 0.033129 |
| GO:0016192 | vesicle-mediated transport | 444 | 0.319066 | 1.472305 | 0.003140 | 0.033399 | 0.025848 |
| GO:0034613 | cellular protein localization | 428 | 0.316761 | 1.461754 | 0.001608 | 0.027820 | 0.021530 |
| GO:0070727 | cellular macromolecule localization | 431 | 0.315789 | 1.457603 | 0.001608 | 0.027820 | 0.021530 |
| GO:0007049 | cell cycle | 456 | 0.314772 | 1.451134 | 0.001623 | 0.027820 | 0.021530 |
| GO:1902582 | single-organism intracellular transport | 341 | 0.317419 | 1.439133 | 0.003328 | 0.035238 | 0.027272 |
| GO:0006508 | proteolysis | 677 | 0.300162 | 1.434663 | 0.001499 | 0.027820 | 0.021530 |
| GO:0042221 | response to chemical | 831 | 0.292269 | 1.409110 | 0.001466 | 0.027820 | 0.021530 |
| GO:0007165 | signal transduction | 2230 | 0.274823 | 1.392200 | 0.001294 | 0.027820 | 0.021530 |
| GO:0007167 | enzyme linked receptor protein signaling pathway | 317 | 0.307904 | 1.386192 | 0.004967 | 0.042191 | 0.032653 |
| GO:0051716 | cellular response to stimulus | 2712 | 0.269388 | 1.379155 | 0.001227 | 0.027820 | 0.021530 |
| GO:0007166 | cell surface receptor signaling pathway | 828 | 0.285415 | 1.375246 | 0.001466 | 0.027820 | 0.021530 |
| GO:0072358 | cardiovascular system development | 587 | 0.291881 | 1.374561 | 0.003096 | 0.033086 | 0.025606 |
| GO:0072359 | circulatory system development | 587 | 0.291881 | 1.374561 | 0.003096 | 0.033086 | 0.025606 |
| GO:0009966 | regulation of signal transduction | 627 | 0.289857 | 1.374281 | 0.001490 | 0.027820 | 0.021530 |
| GO:0033036 | macromolecule localization | 699 | 0.286187 | 1.366464 | 0.003072 | 0.033086 | 0.025606 |
| GO:0071310 | cellular response to organic substance | 445 | 0.289547 | 1.336751 | 0.004695 | 0.040175 | 0.031092 |
| GO:0070887 | cellular response to chemical stimulus | 550 | 0.284099 | 1.332694 | 0.006202 | 0.046998 | 0.036373 |
| GO:0051649 | establishment of localization in cell | 678 | 0.278323 | 1.332052 | 0.003086 | 0.033086 | 0.025606 |
| GO:0048519 | negative regulation of biological process | 817 | 0.273209 | 1.329171 | 0.001502 | 0.027820 | 0.021530 |
| GO:0051641 | cellular localization | 766 | 0.274345 | 1.324229 | 0.004637 | 0.039973 | 0.030936 |
| GO:1902589 | single-organism organelle organization | 889 | 0.271556 | 1.319892 | 0.002933 | 0.032022 | 0.024782 |
| GO:0006996 | organelle organization | 1240 | 0.263793 | 1.306811 | 0.002809 | 0.030959 | 0.023960 |
| GO:0048523 | negative regulation of cellular process | 768 | 0.268505 | 1.299643 | 0.006088 | 0.046291 | 0.035826 |
| GO:0048646 | anatomical structure formation involved in morphogenesis | 625 | 0.274394 | 1.299333 | 0.004687 | 0.040175 | 0.031092 |
| GO:0044700 | single organism signaling | 2381 | 0.253876 | 1.290433 | 0.001276 | 0.027820 | 0.021530 |
| GO:0023052 | signaling | 2386 | 0.252981 | 1.285978 | 0.001277 | 0.027820 | 0.021530 |
| GO:0022607 | cellular component assembly | 748 | 0.267503 | 1.285322 | 0.006070 | 0.046291 | 0.035826 |
| GO:0044085 | cellular component biogenesis | 874 | 0.263307 | 1.270863 | 0.004615 | 0.039937 | 0.030908 |
| GO:0007154 | cell communication | 2450 | 0.246192 | 1.252057 | 0.001267 | 0.027820 | 0.021530 |
| GO:0044267 | cellular protein metabolic process | 2067 | 0.238878 | 1.211815 | 0.001332 | 0.027820 | 0.021530 |
| GO:0050789 | regulation of biological process | 4442 | 0.226609 | 1.176661 | 0.001159 | 0.027820 | 0.021530 |
| GO:0050794 | regulation of cellular process | 4275 | 0.226478 | 1.175542 | 0.001163 | 0.027820 | 0.021530 |
| GO:0065007 | biological regulation | 4773 | 0.225595 | 1.173523 | 0.001142 | 0.027820 | 0.021530 |
| GO:0006810 | transport | 1926 | -0.227507 | -1.193829 | 0.003597 | 0.035306 | 0.027325 |
| GO:0044281 | small molecule metabolic process | 841 | -0.256509 | -1.290751 | 0.005376 | 0.043979 | 0.034037 |
| GO:1902578 | single-organism localization | 1536 | -0.251905 | -1.308088 | 0.003413 | 0.035306 | 0.027325 |
| GO:0044765 | single-organism transport | 1476 | -0.260158 | -1.348127 | 0.003460 | 0.035306 | 0.027325 |
| GO:0007399 | nervous system development | 923 | -0.267935 | -1.360830 | 0.002941 | 0.032022 | 0.024782 |
| GO:0019752 | carboxylic acid metabolic process | 402 | -0.291528 | -1.370650 | 0.004878 | 0.041589 | 0.032187 |
| GO:0006082 | organic acid metabolic process | 449 | -0.290193 | -1.380245 | 0.005025 | 0.042530 | 0.032915 |
| GO:0055114 | oxidation-reduction process | 569 | -0.284799 | -1.389925 | 0.002597 | 0.029098 | 0.022520 |
| GO:0006091 | generation of precursor metabolites and energy | 120 | -0.345118 | -1.426453 | 0.006466 | 0.048523 | 0.037553 |
| GO:0032787 | monocarboxylic acid metabolic process | 198 | -0.331193 | -1.456488 | 0.004608 | 0.039937 | 0.030908 |
| GO:0072521 | purine-containing compound metabolic process | 229 | -0.333991 | -1.506475 | 0.002315 | 0.027820 | 0.021530 |
| GO:0021510 | spinal cord development | 53 | -0.445643 | -1.571652 | 0.004115 | 0.036989 | 0.028627 |
| GO:0006816 | calcium ion transport | 105 | -0.389238 | -1.584191 | 0.006593 | 0.049323 | 0.038172 |
| GO:0030001 | metal ion transport | 340 | -0.340619 | -1.591809 | 0.002481 | 0.028070 | 0.021724 |
| GO:0003008 | system process | 401 | -0.337552 | -1.605321 | 0.002817 | 0.030959 | 0.023960 |
| GO:0098662 | inorganic cation transmembrane transport | 233 | -0.361170 | -1.615164 | 0.002421 | 0.027863 | 0.021564 |
| GO:0016052 | carbohydrate catabolic process | 58 | -0.445524 | -1.618819 | 0.004386 | 0.038527 | 0.029817 |
| GO:0006812 | cation transport | 468 | -0.335581 | -1.621217 | 0.002525 | 0.028427 | 0.022001 |
| GO:0098660 | inorganic ion transmembrane transport | 261 | -0.360282 | -1.632273 | 0.002375 | 0.027820 | 0.021530 |
| GO:0071383 | cellular response to steroid hormone stimulus | 88 | -0.419171 | -1.639030 | 0.002273 | 0.027820 | 0.021530 |
| GO:0048545 | response to steroid hormone | 91 | -0.421511 | -1.643945 | 0.002299 | 0.027820 | 0.021530 |
| GO:0034765 | regulation of ion transmembrane transport | 107 | -0.408633 | -1.652567 | 0.004474 | 0.039007 | 0.030189 |
| GO:0044724 | single-organism carbohydrate catabolic process | 56 | -0.463640 | -1.663097 | 0.002188 | 0.027820 | 0.021530 |
| GO:0034762 | regulation of transmembrane transport | 108 | -0.410692 | -1.666093 | 0.004474 | 0.039007 | 0.030189 |
| GO:0006836 | neurotransmitter transport | 93 | -0.424533 | -1.668835 | 0.002268 | 0.027820 | 0.021530 |
| GO:0098656 | anion transmembrane transport | 96 | -0.428024 | -1.692246 | 0.004301 | 0.038317 | 0.029654 |
| GO:0042391 | regulation of membrane potential | 93 | -0.434765 | -1.706783 | 0.002179 | 0.027820 | 0.021530 |
| GO:0098655 | cation transmembrane transport | 268 | -0.376149 | -1.707147 | 0.002439 | 0.027863 | 0.021564 |
| GO:0071705 | nitrogen compound transport | 152 | -0.403631 | -1.707501 | 0.002273 | 0.027820 | 0.021530 |
| GO:0021536 | diencephalon development | 59 | -0.480760 | -1.718345 | 0.002183 | 0.027820 | 0.021530 |
| GO:0006865 | amino acid transport | 50 | -0.495434 | -1.718507 | 0.006263 | 0.047309 | 0.036614 |
| GO:0009416 | response to light stimulus | 78 | -0.448073 | -1.719394 | 0.002070 | 0.027820 | 0.021530 |
| GO:0021854 | hypothalamus development | 16 | -0.654087 | -1.726892 | 0.006036 | 0.046198 | 0.035754 |
| GO:0021761 | limbic system development | 17 | -0.648012 | -1.733589 | 0.006000 | 0.046073 | 0.035657 |
| GO:1901565 | organonitrogen compound catabolic process | 104 | -0.427341 | -1.741561 | 0.002208 | 0.027820 | 0.021530 |
| GO:0070588 | calcium ion transmembrane transport | 75 | -0.460857 | -1.743377 | 0.002252 | 0.027820 | 0.021530 |
| GO:0071804 | cellular potassium ion transport | 77 | -0.460565 | -1.755757 | 0.002294 | 0.027820 | 0.021530 |
| GO:0071805 | potassium ion transmembrane transport | 77 | -0.460565 | -1.755757 | 0.002294 | 0.027820 | 0.021530 |
| GO:0071466 | cellular response to xenobiotic stimulus | 67 | -0.480758 | -1.767043 | 0.002217 | 0.027820 | 0.021530 |
| GO:0048663 | neuron fate commitment | 26 | -0.582338 | -1.770309 | 0.003953 | 0.036016 | 0.027874 |
| GO:0015850 | organic hydroxy compound transport | 48 | -0.518478 | -1.780148 | 0.004367 | 0.038504 | 0.029800 |
| GO:0034220 | ion transmembrane transport | 401 | -0.375052 | -1.783555 | 0.002392 | 0.027863 | 0.021564 |
| GO:0009410 | response to xenobiotic stimulus | 74 | -0.472179 | -1.783692 | 0.002174 | 0.027820 | 0.021530 |
| GO:0007193 | adenylate cyclase-inhibiting G-protein coupled receptor signaling pathway | 27 | -0.585442 | -1.794792 | 0.002062 | 0.027820 | 0.021530 |
| GO:0006814 | sodium ion transport | 95 | -0.460515 | -1.795034 | 0.002222 | 0.027820 | 0.021530 |
| GO:0042493 | response to drug | 51 | -0.515117 | -1.796067 | 0.004283 | 0.038317 | 0.029654 |
| GO:1903825 | organic acid transmembrane transport | 42 | -0.533234 | -1.804311 | 0.003953 | 0.036016 | 0.027874 |
| GO:0006811 | ion transport | 742 | -0.360995 | -1.806359 | 0.002688 | 0.029827 | 0.023084 |
| GO:0017144 | drug metabolic process | 34 | -0.573715 | -1.818690 | 0.004008 | 0.036166 | 0.027990 |
| GO:0055085 | transmembrane transport | 666 | -0.368060 | -1.824141 | 0.002681 | 0.029827 | 0.023084 |
| GO:0098742 | cell-cell adhesion via plasma-membrane adhesion molecules | 102 | -0.459849 | -1.828780 | 0.002169 | 0.027820 | 0.021530 |
| GO:0018298 | protein-chromophore linkage | 21 | -0.635393 | -1.832517 | 0.002119 | 0.027820 | 0.021530 |
| GO:0006820 | anion transport | 219 | -0.417089 | -1.833991 | 0.002342 | 0.027820 | 0.021530 |
| GO:0009072 | aromatic amino acid family metabolic process | 18 | -0.671892 | -1.840570 | 0.003914 | 0.036016 | 0.027874 |
| GO:0009581 | detection of external stimulus | 48 | -0.536516 | -1.868070 | 0.004329 | 0.038317 | 0.029654 |
| GO:0009582 | detection of abiotic stimulus | 48 | -0.536516 | -1.868070 | 0.004329 | 0.038317 | 0.029654 |
| GO:0035235 | ionotropic glutamate receptor signaling pathway | 20 | -0.669864 | -1.881060 | 0.004008 | 0.036166 | 0.027990 |
| GO:0042737 | drug catabolic process | 31 | -0.610494 | -1.886058 | 0.002041 | 0.027820 | 0.021530 |
| GO:0042738 | exogenous drug catabolic process | 31 | -0.610494 | -1.886058 | 0.002041 | 0.027820 | 0.021530 |
| GO:0048167 | regulation of synaptic plasticity | 12 | -0.765494 | -1.895865 | 0.002268 | 0.027820 | 0.021530 |
| GO:0007156 | homophilic cell adhesion via plasma membrane adhesion molecules | 95 | -0.483452 | -1.904440 | 0.002105 | 0.027820 | 0.021530 |
| GO:0009583 | detection of light stimulus | 30 | -0.606920 | -1.918426 | 0.006356 | 0.047855 | 0.037036 |
| GO:0007267 | cell-cell signaling | 287 | -0.415695 | -1.921897 | 0.002427 | 0.027863 | 0.021564 |
| GO:0006805 | xenobiotic metabolic process | 38 | -0.586576 | -1.925353 | 0.002024 | 0.027820 | 0.021530 |
| GO:0051606 | detection of stimulus | 56 | -0.540485 | -1.934238 | 0.002217 | 0.027820 | 0.021530 |
| GO:0009755 | hormone-mediated signaling pathway | 73 | -0.509459 | -1.946957 | 0.002203 | 0.027820 | 0.021530 |
| GO:0015711 | organic anion transport | 134 | -0.483946 | -1.991070 | 0.002320 | 0.027820 | 0.021530 |
| GO:0007602 | phototransduction | 21 | -0.687363 | -1.995143 | 0.002114 | 0.027820 | 0.021530 |
| GO:0015672 | monovalent inorganic cation transport | 251 | -0.446898 | -2.020197 | 0.002358 | 0.027820 | 0.021530 |
| GO:0035249 | synaptic transmission, glutamatergic | 29 | -0.662544 | -2.039245 | 0.002024 | 0.027820 | 0.021530 |
| GO:0050803 | regulation of synapse structure or activity | 16 | -0.770555 | -2.047994 | 0.002304 | 0.027820 | 0.021530 |
| GO:0007606 | sensory perception of chemical stimulus | 26 | -0.677207 | -2.052133 | 0.002114 | 0.027820 | 0.021530 |
| GO:0043401 | steroid hormone mediated signaling pathway | 63 | -0.547380 | -2.058858 | 0.002165 | 0.027820 | 0.021530 |
| GO:0015718 | monocarboxylic acid transport | 29 | -0.667024 | -2.078156 | 0.002024 | 0.027820 | 0.021530 |
| GO:0006813 | potassium ion transport | 115 | -0.512538 | -2.086886 | 0.002342 | 0.027820 | 0.021530 |
| GO:0007215 | glutamate receptor signaling pathway | 44 | -0.621256 | -2.137319 | 0.002041 | 0.027820 | 0.021530 |
| GO:0015849 | organic acid transport | 91 | -0.548875 | -2.152780 | 0.002160 | 0.027820 | 0.021530 |
| GO:0046942 | carboxylic acid transport | 91 | -0.548875 | -2.152780 | 0.002160 | 0.027820 | 0.021530 |
| GO:0007268 | synaptic transmission | 218 | -0.483567 | -2.156038 | 0.002457 | 0.027930 | 0.021616 |
| GO:0050804 | modulation of synaptic transmission | 34 | -0.673564 | -2.210599 | 0.002273 | 0.027820 | 0.021530 |
| GO:0007270 | neuron-neuron synaptic transmission | 40 | -0.664695 | -2.224843 | 0.002016 | 0.027820 | 0.021530 |
| GO:0050953 | sensory perception of light stimulus | 59 | -0.650362 | -2.366345 | 0.002370 | 0.027820 | 0.021530 |
| GO:0007601 | visual perception | 58 | -0.653012 | -2.372085 | 0.002342 | 0.027820 | 0.021530 |
| GO:0050877 | neurological system process | 180 | -0.577351 | -2.504916 | 0.002433 | 0.027863 | 0.021564 |
| GO:0007600 | sensory perception | 113 | -0.623912 | -2.565508 | 0.002309 | 0.027820 | 0.021530 |

## BPRevigo
| term\_ID | description | frequency | plot\_X | plot\_Y | plot\_size | value | uniqueness | dispensability | representative | eliminated |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| GO:0002376 | immune system process | 0.02833 | 1.584 | -2.189 | 2.952 | 0.4537 | 0.994 | 0.000 | 2376 | 0 |
| GO:0023052 | signaling | 0.20103 | -1.845 | -3.233 | 3.803 | 0.2530 | 0.995 | 0.000 | 23052 | 0 |
| GO:0030225 | macrophage differentiation | 0.00032 | -2.075 | -7.084 | 1.041 | 0.7801 | 0.834 | 0.000 | 30225 | 0 |
| GO:0048534 | hematopoietic or lymphoid organ development | 0.00807 | NaN | NaN | 2.408 | 0.3398 | 0.815 | 0.980 | 30225 | 1 |
| GO:0030099 | myeloid cell differentiation | 0.00345 | NaN | NaN | 2.041 | 0.3995 | 0.803 | 0.704 | 30225 | 1 |
| GO:0030097 | hemopoiesis | 0.00769 | NaN | NaN | 2.387 | 0.3527 | 0.816 | 0.907 | 30225 | 1 |
| GO:0002573 | myeloid leukocyte differentiation | 0.00098 | NaN | NaN | 1.505 | 0.5938 | 0.820 | 0.824 | 30225 | 1 |
| GO:0040007 | growth | 0.01092 | -0.978 | -0.016 | 2.539 | 0.3570 | 0.994 | 0.000 | 40007 | 0 |
| GO:0040011 | locomotion | 0.02099 | -0.506 | -0.891 | 2.822 | 0.3835 | 0.994 | 0.000 | 40011 | 0 |
| GO:0043331 | response to dsRNA | 0.00070 | 5.855 | -4.536 | 1.362 | 0.8933 | 0.853 | 0.000 | 43331 | 0 |
| GO:1901698 | response to nitrogen compound | 0.00212 | NaN | NaN | 1.833 | 0.4191 | 0.856 | 0.469 | 43331 | 1 |
| GO:1901699 | cellular response to nitrogen compound | 0.00146 | NaN | NaN | 1.672 | 0.4775 | 0.831 | 0.925 | 43331 | 1 |
| GO:0043207 | response to external biotic stimulus | 0.00488 | NaN | NaN | 2.190 | 0.6575 | 0.826 | 0.974 | 43331 | 1 |
| GO:0030334 | regulation of cell migration | 0.00364 | NaN | NaN | 2.064 | 0.4516 | 0.730 | 0.840 | 43331 | 1 |
| GO:0060973 | cell migration involved in heart development | 0.00060 | NaN | NaN | 1.301 | 0.6545 | 0.756 | 0.641 | 43331 | 1 |
| GO:0050900 | leukocyte migration | 0.00114 | NaN | NaN | 1.568 | 0.7410 | 0.775 | 0.674 | 43331 | 1 |
| GO:0051707 | response to other organism | 0.00488 | NaN | NaN | 2.190 | 0.6575 | 0.825 | 0.871 | 43331 | 1 |
| GO:0048545 | response to steroid hormone | 0.00877 | NaN | NaN | 2.444 | -0.4215 | 0.824 | 0.960 | 43331 | 1 |
| GO:0042493 | response to drug | 0.00073 | NaN | NaN | 1.380 | -0.5151 | 0.867 | 0.413 | 43331 | 1 |
| GO:0009582 | detection of abiotic stimulus | 0.00282 | NaN | NaN | 1.954 | -0.5365 | 0.888 | 0.787 | 43331 | 1 |
| GO:0009581 | detection of external stimulus | 0.00282 | NaN | NaN | 1.954 | -0.5365 | 0.840 | 0.748 | 43331 | 1 |
| GO:0009583 | detection of light stimulus | 0.00218 | NaN | NaN | 1.845 | -0.6069 | 0.838 | 0.946 | 43331 | 1 |
| GO:0019221 | cytokine-mediated signaling pathway | 0.00446 | NaN | NaN | 2.152 | 0.6419 | 0.721 | 0.629 | 43331 | 1 |
| GO:2000145 | regulation of cell motility | 0.00393 | NaN | NaN | 2.097 | 0.4548 | 0.728 | 0.977 | 43331 | 1 |
| GO:0070887 | cellular response to chemical stimulus | 0.02732 | NaN | NaN | 2.937 | 0.2841 | 0.796 | 0.821 | 43331 | 1 |
| GO:0071383 | cellular response to steroid hormone stimulus | 0.00864 | NaN | NaN | 2.438 | -0.4192 | 0.800 | 0.979 | 43331 | 1 |
| GO:0009620 | response to fungus | 0.00089 | NaN | NaN | 1.462 | 0.6240 | 0.846 | 0.764 | 43331 | 1 |
| GO:0009617 | response to bacterium | 0.00263 | NaN | NaN | 1.924 | 0.7210 | 0.833 | 0.941 | 43331 | 1 |
| GO:0009615 | response to virus | 0.00155 | NaN | NaN | 1.699 | 0.7125 | 0.840 | 0.898 | 43331 | 1 |
| GO:0050727 | regulation of inflammatory response | 0.00101 | NaN | NaN | 1.519 | 0.7407 | 0.765 | 0.870 | 43331 | 1 |
| GO:0071310 | cellular response to organic substance | 0.02251 | NaN | NaN | 2.852 | 0.2895 | 0.788 | 0.832 | 43331 | 1 |
| GO:0010033 | response to organic substance | 0.02504 | NaN | NaN | 2.899 | 0.3199 | 0.821 | 0.658 | 43331 | 1 |
| GO:0001878 | response to yeast | 0.00076 | NaN | NaN | 1.398 | 0.6194 | 0.848 | 0.756 | 43331 | 1 |
| GO:0071345 | cellular response to cytokine stimulus | 0.00453 | NaN | NaN | 2.158 | 0.6302 | 0.814 | 0.994 | 43331 | 1 |
| GO:0032496 | response to lipopolysaccharide | 0.00044 | NaN | NaN | 1.176 | 0.8682 | 0.811 | 0.814 | 43331 | 1 |
| GO:0098542 | defense response to other organism | 0.00222 | NaN | NaN | 1.851 | 0.6217 | 0.808 | 0.927 | 43331 | 1 |
| GO:0097529 | myeloid leukocyte migration | 0.00063 | NaN | NaN | 1.322 | 0.7378 | 0.775 | 0.916 | 43331 | 1 |
| GO:0097530 | granulocyte migration | 0.00060 | NaN | NaN | 1.301 | 0.7448 | 0.774 | 0.985 | 43331 | 1 |
| GO:0009755 | hormone-mediated signaling pathway | 0.00874 | NaN | NaN | 2.442 | -0.5095 | 0.708 | 0.939 | 43331 | 1 |
| GO:1990266 | neutrophil migration | 0.00054 | NaN | NaN | 1.255 | 0.7404 | 0.776 | 0.977 | 43331 | 1 |
| GO:0042330 | taxis | 0.01029 | NaN | NaN | 2.513 | 0.3931 | 0.790 | 0.855 | 43331 | 1 |
| GO:0002237 | response to molecule of bacterial origin | 0.00108 | NaN | NaN | 1.544 | 0.8250 | 0.802 | 0.510 | 43331 | 1 |
| GO:0034097 | response to cytokine | 0.00453 | NaN | NaN | 2.158 | 0.6560 | 0.840 | 0.665 | 43331 | 1 |
| GO:0043401 | steroid hormone mediated signaling pathway | 0.00788 | NaN | NaN | 2.398 | -0.5474 | 0.708 | 0.751 | 43331 | 1 |
| GO:0007602 | phototransduction | 0.00193 | NaN | NaN | 1.792 | -0.6874 | 0.736 | 0.635 | 43331 | 1 |
| GO:0032101 | regulation of response to external stimulus | 0.00237 | NaN | NaN | 1.881 | 0.5006 | 0.782 | 0.647 | 43331 | 1 |
| GO:0032103 | positive regulation of response to external stimulus | 0.00095 | NaN | NaN | 1.491 | 0.7828 | 0.755 | 0.551 | 43331 | 1 |
| GO:0048870 | cell motility | 0.01482 | NaN | NaN | 2.671 | 0.4503 | 0.761 | 0.979 | 43331 | 1 |
| GO:0071621 | granulocyte chemotaxis | 0.00054 | NaN | NaN | 1.255 | 0.7335 | 0.650 | 0.985 | 43331 | 1 |
| GO:0071417 | cellular response to organonitrogen compound | 0.00117 | NaN | NaN | 1.580 | 0.4677 | 0.829 | 0.876 | 43331 | 1 |
| GO:0060326 | cell chemotaxis | 0.00329 | NaN | NaN | 2.021 | 0.7425 | 0.642 | 0.606 | 43331 | 1 |
| GO:0009416 | response to light stimulus | 0.00386 | NaN | NaN | 2.090 | -0.4481 | 0.888 | 0.909 | 43331 | 1 |
| GO:0009410 | response to xenobiotic stimulus | 0.00136 | NaN | NaN | 1.643 | -0.4722 | 0.861 | 0.433 | 43331 | 1 |
| GO:0006935 | chemotaxis | 0.01013 | NaN | NaN | 2.507 | 0.3993 | 0.746 | 0.879 | 43331 | 1 |
| GO:0042742 | defense response to bacterium | 0.00095 | NaN | NaN | 1.491 | 0.6951 | 0.818 | 0.859 | 43331 | 1 |
| GO:0030595 | leukocyte chemotaxis | 0.00060 | NaN | NaN | 1.301 | 0.7490 | 0.648 | 0.898 | 43331 | 1 |
| GO:0030593 | neutrophil chemotaxis | 0.00047 | NaN | NaN | 1.204 | 0.7283 | 0.653 | 0.680 | 43331 | 1 |
| GO:0016477 | cell migration | 0.01399 | NaN | NaN | 2.646 | 0.4501 | 0.763 | 0.831 | 43331 | 1 |
| GO:0050896 | response to stimulus | 0.24906 | -1.862 | -2.226 | 3.896 | 0.2936 | 0.995 | 0.000 | 50896 | 0 |
| GO:0051704 | multi-organism process | 0.00804 | 2.723 | -2.806 | 2.407 | 0.5593 | 0.994 | 0.000 | 51704 | 0 |
| GO:0065007 | biological regulation | 0.35587 | 0.657 | -1.772 | 4.051 | 0.2256 | 0.996 | 0.000 | 65007 | 0 |
| GO:0007162 | negative regulation of cell adhesion | 0.00047 | 3.987 | 5.353 | 1.204 | 0.7710 | 0.893 | 0.017 | 7162 | 0 |
| GO:0048523 | negative regulation of cellular process | 0.02688 | NaN | NaN | 2.929 | 0.2685 | 0.860 | 0.707 | 7162 | 1 |
| GO:0002520 | immune system development | 0.00833 | NaN | NaN | 2.422 | 0.3338 | 0.822 | 0.788 | 7162 | 1 |
| GO:0007265 | Ras protein signal transduction | 0.01406 | NaN | NaN | 2.648 | 0.3799 | 0.753 | 0.682 | 7162 | 1 |
| GO:0007264 | small GTPase mediated signal transduction | 0.03198 | NaN | NaN | 3.005 | 0.4035 | 0.732 | 0.555 | 7162 | 1 |
| GO:0007156 | homophilic cell adhesion via plasma membrane adhesion molecules | 0.01304 | NaN | NaN | 2.616 | -0.4835 | 0.984 | 0.550 | 7162 | 1 |
| GO:0002684 | positive regulation of immune system process | 0.00557 | NaN | NaN | 2.248 | 0.5036 | 0.798 | 0.740 | 7162 | 1 |
| GO:0002683 | negative regulation of immune system process | 0.00032 | NaN | NaN | 1.041 | 0.7697 | 0.866 | 0.434 | 7162 | 1 |
| GO:0002682 | regulation of immune system process | 0.00715 | NaN | NaN | 2.356 | 0.5596 | 0.845 | 0.533 | 7162 | 1 |
| GO:1902531 | regulation of intracellular signal transduction | 0.02207 | NaN | NaN | 2.844 | 0.3401 | 0.719 | 0.724 | 7162 | 1 |
| GO:1902532 | negative regulation of intracellular signal transduction | 0.00241 | NaN | NaN | 1.886 | 0.4707 | 0.760 | 0.514 | 7162 | 1 |
| GO:0009966 | regulation of signal transduction | 0.03476 | NaN | NaN | 3.041 | 0.2899 | 0.711 | 0.891 | 7162 | 1 |
| GO:0006955 | immune response | 0.01827 | NaN | NaN | 2.762 | 0.5281 | 0.822 | 0.774 | 7162 | 1 |
| GO:0098742 | cell-cell adhesion via plasma-membrane adhesion molecules | 0.01339 | NaN | NaN | 2.627 | -0.4598 | 0.984 | 0.984 | 7162 | 1 |
| GO:0006826 | iron ion transport | 0.00158 | -5.645 | -3.381 | 1.708 | 0.7221 | 0.820 | 0.034 | 6826 | 0 |
| GO:0055085 | transmembrane transport | 0.06582 | NaN | NaN | 3.318 | -0.3681 | 0.742 | 0.591 | 6826 | 1 |
| GO:0015031 | protein transport | 0.02770 | NaN | NaN | 2.943 | 0.3384 | 0.823 | 0.673 | 6826 | 1 |
| GO:0006820 | anion transport | 0.01326 | NaN | NaN | 2.623 | -0.4171 | 0.791 | 0.500 | 6826 | 1 |
| GO:0006813 | potassium ion transport | 0.00890 | NaN | NaN | 2.450 | -0.5125 | 0.789 | 0.640 | 6826 | 1 |
| GO:0006814 | sodium ion transport | 0.00503 | NaN | NaN | 2.204 | -0.4605 | 0.800 | 0.762 | 6826 | 1 |
| GO:0006816 | calcium ion transport | 0.00836 | NaN | NaN | 2.423 | -0.3892 | 0.790 | 0.961 | 6826 | 1 |
| GO:0006810 | transport | 0.14072 | NaN | NaN | 3.648 | -0.2275 | 0.813 | 0.731 | 6826 | 1 |
| GO:0006811 | ion transport | 0.05746 | NaN | NaN | 3.259 | -0.3610 | 0.774 | 0.746 | 6826 | 1 |
| GO:0006812 | cation transport | 0.03910 | NaN | NaN | 3.092 | -0.3356 | 0.765 | 0.846 | 6826 | 1 |
| GO:0071805 | potassium ion transmembrane transport | 0.00801 | NaN | NaN | 2.405 | -0.4606 | 0.765 | 0.799 | 6826 | 1 |
| GO:0071804 | cellular potassium ion transport | 0.00801 | NaN | NaN | 2.405 | -0.4606 | 0.768 | 0.970 | 6826 | 1 |
| GO:0044765 | single-organism transport | 0.09928 | NaN | NaN | 3.497 | -0.2602 | 0.759 | 0.815 | 6826 | 1 |
| GO:0006865 | amino acid transport | 0.00222 | NaN | NaN | 1.851 | -0.4954 | 0.810 | 0.935 | 6826 | 1 |
| GO:0006886 | intracellular protein transport | 0.01637 | NaN | NaN | 2.714 | 0.3352 | 0.819 | 0.902 | 6826 | 1 |
| GO:0046942 | carboxylic acid transport | 0.00437 | NaN | NaN | 2.143 | -0.5489 | 0.798 | 0.891 | 6826 | 1 |
| GO:0008104 | protein localization | 0.03109 | NaN | NaN | 2.993 | 0.3228 | 0.839 | 0.891 | 6826 | 1 |
| GO:0000041 | transition metal ion transport | 0.00294 | NaN | NaN | 1.973 | 0.4952 | 0.815 | 0.677 | 6826 | 1 |
| GO:0034762 | regulation of transmembrane transport | 0.00674 | NaN | NaN | 2.330 | -0.4107 | 0.729 | 0.878 | 6826 | 1 |
| GO:0098662 | inorganic cation transmembrane transport | 0.02450 | NaN | NaN | 2.889 | -0.3612 | 0.743 | 0.821 | 6826 | 1 |
| GO:0034765 | regulation of ion transmembrane transport | 0.00671 | NaN | NaN | 2.328 | -0.4086 | 0.716 | 0.577 | 6826 | 1 |
| GO:0098656 | anion transmembrane transport | 0.00491 | NaN | NaN | 2.193 | -0.4280 | 0.779 | 0.818 | 6826 | 1 |
| GO:0098655 | cation transmembrane transport | 0.03118 | NaN | NaN | 2.994 | -0.3761 | 0.737 | 0.868 | 6826 | 1 |
| GO:0098660 | inorganic ion transmembrane transport | 0.02729 | NaN | NaN | 2.936 | -0.3603 | 0.746 | 0.800 | 6826 | 1 |
| GO:0015850 | organic hydroxy compound transport | 0.00057 | NaN | NaN | 1.279 | -0.5185 | 0.847 | 0.429 | 6826 | 1 |
| GO:0015849 | organic acid transport | 0.00443 | NaN | NaN | 2.149 | -0.5489 | 0.819 | 0.502 | 6826 | 1 |
| GO:1902578 | single-organism localization | 0.10204 | NaN | NaN | 3.508 | -0.2519 | 0.786 | 0.620 | 6826 | 1 |
| GO:0070588 | calcium ion transmembrane transport | 0.00706 | NaN | NaN | 2.350 | -0.4609 | 0.769 | 0.738 | 6826 | 1 |
| GO:0030001 | metal ion transport | 0.02558 | NaN | NaN | 2.908 | -0.3406 | 0.770 | 0.873 | 6826 | 1 |
| GO:0015672 | monovalent inorganic cation transport | 0.02032 | NaN | NaN | 2.808 | -0.4469 | 0.776 | 0.723 | 6826 | 1 |
| GO:0034220 | ion transmembrane transport | 0.04388 | NaN | NaN | 3.142 | -0.3751 | 0.735 | 0.767 | 6826 | 1 |
| GO:0034613 | cellular protein localization | 0.01909 | NaN | NaN | 2.781 | 0.3168 | 0.834 | 0.962 | 6826 | 1 |
| GO:0015718 | monocarboxylic acid transport | 0.00127 | NaN | NaN | 1.613 | -0.6670 | 0.818 | 0.410 | 6826 | 1 |
| GO:0015711 | organic anion transport | 0.00602 | NaN | NaN | 2.281 | -0.4839 | 0.795 | 0.724 | 6826 | 1 |
| GO:0045184 | establishment of protein localization | 0.02805 | NaN | NaN | 2.948 | 0.3430 | 0.833 | 0.939 | 6826 | 1 |
| GO:0044801 | single-organism membrane fusion | 0.00111 | -4.125 | -0.563 | 1.556 | 0.4722 | 0.882 | 0.037 | 44801 | 0 |
| GO:0008283 | cell proliferation | 0.00671 | 1.903 | -0.677 | 2.328 | 0.3745 | 0.945 | 0.043 | 8283 | 0 |
| GO:0016265 | death | 0.01779 | 0.560 | -3.758 | 2.751 | 0.3486 | 0.940 | 0.054 | 16265 | 0 |
| GO:0046456 | icosanoid biosynthetic process | 0.00054 | -4.949 | 2.995 | 1.255 | 0.7786 | 0.887 | 0.054 | 46456 | 0 |
| GO:0032787 | monocarboxylic acid metabolic process | 0.00839 | NaN | NaN | 2.425 | -0.3312 | 0.868 | 0.653 | 46456 | 1 |
| GO:0019752 | carboxylic acid metabolic process | 0.02520 | NaN | NaN | 2.901 | -0.2915 | 0.853 | 0.842 | 46456 | 1 |
| GO:0009072 | aromatic amino acid family metabolic process | 0.00203 | NaN | NaN | 1.813 | -0.6719 | 0.875 | 0.523 | 46456 | 1 |
| GO:1901570 | fatty acid derivative biosynthetic process | 0.00054 | NaN | NaN | 1.255 | 0.7786 | 0.918 | 0.971 | 46456 | 1 |
| GO:0009226 | nucleotide-sugar biosynthetic process | 0.00044 | NaN | NaN | 1.176 | 0.7217 | 0.893 | 0.432 | 46456 | 1 |
| GO:0006636 | unsaturated fatty acid biosynthetic process | 0.00057 | NaN | NaN | 1.279 | 0.7062 | 0.890 | 0.646 | 46456 | 1 |
| GO:0030010 | establishment of cell polarity | 0.00076 | 0.214 | -0.001 | 1.398 | 0.5991 | 0.930 | 0.058 | 30010 | 0 |
| GO:0000910 | cytokinesis | 0.00199 | -1.897 | 1.199 | 1.806 | 0.5378 | 0.907 | 0.063 | 910 | 0 |
| GO:0000280 | nuclear division | 0.00655 | NaN | NaN | 2.318 | 0.3952 | 0.823 | 0.958 | 910 | 1 |
| GO:0007067 | mitotic nuclear division | 0.00526 | NaN | NaN | 2.223 | 0.4395 | 0.815 | 0.767 | 910 | 1 |
| GO:1903047 | mitotic cell cycle process | 0.00772 | NaN | NaN | 2.389 | 0.3646 | 0.901 | 0.919 | 910 | 1 |
| GO:0022402 | cell cycle process | 0.01320 | NaN | NaN | 2.621 | 0.3433 | 0.898 | 0.680 | 910 | 1 |
| GO:0051301 | cell division | 0.01168 | 2.346 | 2.296 | 2.568 | 0.4179 | 0.912 | 0.079 | 51301 | 0 |
| GO:0042737 | drug catabolic process | 0.01055 | -3.397 | 3.626 | 2.524 | -0.6105 | 0.899 | 0.086 | 42737 | 0 |
| GO:0044724 | single-organism carbohydrate catabolic process | 0.00434 | NaN | NaN | 2.140 | -0.4636 | 0.871 | 0.473 | 42737 | 1 |
| GO:0031329 | regulation of cellular catabolic process | 0.02241 | NaN | NaN | 2.851 | 0.3675 | 0.789 | 0.598 | 42737 | 1 |
| GO:0016052 | carbohydrate catabolic process | 0.00446 | NaN | NaN | 2.152 | -0.4455 | 0.923 | 0.620 | 42737 | 1 |
| GO:0009057 | macromolecule catabolic process | 0.01577 | NaN | NaN | 2.698 | 0.3739 | 0.907 | 0.543 | 42737 | 1 |
| GO:0044257 | cellular protein catabolic process | 0.01007 | NaN | NaN | 2.504 | 0.4633 | 0.852 | 0.970 | 42737 | 1 |
| GO:0043161 | proteasome-mediated ubiquitin-dependent protein catabolic process | 0.00155 | NaN | NaN | 1.699 | 0.4244 | 0.859 | 0.840 | 42737 | 1 |
| GO:0044265 | cellular macromolecule catabolic process | 0.01358 | NaN | NaN | 2.633 | 0.4220 | 0.865 | 0.927 | 42737 | 1 |
| GO:0019941 | modification-dependent protein catabolic process | 0.00848 | NaN | NaN | 2.430 | 0.4673 | 0.838 | 0.989 | 42737 | 1 |
| GO:0043632 | modification-dependent macromolecule catabolic process | 0.00852 | NaN | NaN | 2.431 | 0.4675 | 0.869 | 0.888 | 42737 | 1 |
| GO:1901565 | organonitrogen compound catabolic process | 0.05081 | NaN | NaN | 3.206 | -0.4273 | 0.893 | 0.698 | 42737 | 1 |
| GO:0042738 | exogenous drug catabolic process | 0.00025 | NaN | NaN | 0.954 | -0.6105 | 0.816 | 0.427 | 42737 | 1 |
| GO:0042176 | regulation of protein catabolic process | 0.00054 | NaN | NaN | 1.255 | 0.4592 | 0.811 | 0.725 | 42737 | 1 |
| GO:0010498 | proteasomal protein catabolic process | 0.00165 | NaN | NaN | 1.724 | 0.4317 | 0.859 | 0.815 | 42737 | 1 |
| GO:0030163 | protein catabolic process | 0.01095 | NaN | NaN | 2.540 | 0.4689 | 0.877 | 0.878 | 42737 | 1 |
| GO:0009894 | regulation of catabolic process | 0.02260 | NaN | NaN | 2.854 | 0.3733 | 0.814 | 0.622 | 42737 | 1 |
| GO:0051603 | proteolysis involved in cellular protein catabolic process | 0.00997 | NaN | NaN | 2.500 | 0.4637 | 0.836 | 0.969 | 42737 | 1 |
| GO:0072521 | purine-containing compound metabolic process | 0.05578 | NaN | NaN | 3.246 | -0.3340 | 0.917 | 0.770 | 42737 | 1 |
| GO:0006511 | ubiquitin-dependent protein catabolic process | 0.00833 | NaN | NaN | 2.422 | 0.4612 | 0.838 | 0.534 | 42737 | 1 |
| GO:0050803 | regulation of synapse structure and activity | 0.00060 | 6.807 | 3.721 | 1.301 | -0.7706 | 0.825 | 0.088 | 50803 | 0 |
| GO:0055076 | transition metal ion homeostasis | 0.00231 | NaN | NaN | 1.869 | 0.5296 | 0.880 | 0.895 | 50803 | 1 |
| GO:0032271 | regulation of protein polymerization | 0.00212 | NaN | NaN | 1.833 | 0.4877 | 0.802 | 0.982 | 50803 | 1 |
| GO:0032273 | positive regulation of protein polymerization | 0.00070 | NaN | NaN | 1.362 | 0.5047 | 0.787 | 0.987 | 50803 | 1 |
| GO:0030832 | regulation of actin filament length | 0.00212 | NaN | NaN | 1.833 | 0.4805 | 0.740 | 0.952 | 50803 | 1 |
| GO:0030833 | regulation of actin filament polymerization | 0.00184 | NaN | NaN | 1.771 | 0.4918 | 0.725 | 0.941 | 50803 | 1 |
| GO:0071824 | protein-DNA complex subunit organization | 0.00275 | NaN | NaN | 1.944 | 0.4944 | 0.899 | 0.476 | 50803 | 1 |
| GO:0050878 | regulation of body fluid levels | 0.00380 | NaN | NaN | 2.083 | 0.5586 | 0.806 | 0.538 | 50803 | 1 |
| GO:0031334 | positive regulation of protein complex assembly | 0.00073 | NaN | NaN | 1.380 | 0.5553 | 0.790 | 0.848 | 50803 | 1 |
| GO:0016049 | cell growth | 0.00491 | NaN | NaN | 2.193 | 0.4066 | 0.909 | 0.824 | 50803 | 1 |
| GO:0006879 | cellular iron ion homeostasis | 0.00193 | NaN | NaN | 1.792 | 0.6784 | 0.838 | 0.466 | 50803 | 1 |
| GO:0034314 | Arp2/3 complex-mediated actin nucleation | 0.00032 | NaN | NaN | 1.041 | 0.7008 | 0.730 | 0.411 | 50803 | 1 |
| GO:0010638 | positive regulation of organelle organization | 0.00136 | NaN | NaN | 1.643 | 0.4277 | 0.776 | 0.859 | 50803 | 1 |
| GO:0022607 | cellular component assembly | 0.03106 | NaN | NaN | 2.992 | 0.2675 | 0.878 | 0.820 | 50803 | 1 |
| GO:0007268 | synaptic transmission | 0.00589 | NaN | NaN | 2.272 | -0.4836 | 0.871 | 0.795 | 50803 | 1 |
| GO:0050804 | regulation of synaptic transmission | 0.00089 | NaN | NaN | 1.462 | -0.6736 | 0.839 | 0.707 | 50803 | 1 |
| GO:0007270 | neuron-neuron synaptic transmission | 0.00101 | NaN | NaN | 1.519 | -0.6647 | 0.887 | 0.733 | 50803 | 1 |
| GO:0008154 | actin polymerization or depolymerization | 0.00326 | NaN | NaN | 2.017 | 0.4944 | 0.809 | 0.747 | 50803 | 1 |
| GO:0046916 | cellular transition metal ion homeostasis | 0.00203 | NaN | NaN | 1.813 | 0.6564 | 0.837 | 0.973 | 50803 | 1 |
| GO:0044089 | positive regulation of cellular component biogenesis | 0.00044 | NaN | NaN | 1.176 | 0.5143 | 0.816 | 0.817 | 50803 | 1 |
| GO:0008064 | regulation of actin polymerization or depolymerization | 0.00212 | NaN | NaN | 1.833 | 0.4805 | 0.734 | 0.986 | 50803 | 1 |
| GO:0032970 | regulation of actin filament-based process | 0.00355 | NaN | NaN | 2.053 | 0.4460 | 0.825 | 0.751 | 50803 | 1 |
| GO:0044087 | regulation of cellular component biogenesis | 0.00342 | NaN | NaN | 2.037 | 0.4141 | 0.834 | 0.470 | 50803 | 1 |
| GO:0032956 | regulation of actin cytoskeleton organization | 0.00351 | NaN | NaN | 2.049 | 0.4528 | 0.754 | 0.820 | 50803 | 1 |
| GO:0065004 | protein-DNA complex assembly | 0.00253 | NaN | NaN | 1.908 | 0.5106 | 0.889 | 0.619 | 50803 | 1 |
| GO:0030838 | positive regulation of actin filament polymerization | 0.00063 | NaN | NaN | 1.322 | 0.5102 | 0.717 | 0.942 | 50803 | 1 |
| GO:0051495 | positive regulation of cytoskeleton organization | 0.00098 | NaN | NaN | 1.505 | 0.4831 | 0.776 | 0.880 | 50803 | 1 |
| GO:0035249 | synaptic transmission, glutamatergic | 0.00089 | NaN | NaN | 1.462 | -0.6625 | 0.888 | 0.726 | 50803 | 1 |
| GO:0001558 | regulation of cell growth | 0.00317 | NaN | NaN | 2.004 | 0.4739 | 0.771 | 0.610 | 50803 | 1 |
| GO:0007015 | actin filament organization | 0.00564 | NaN | NaN | 2.253 | 0.4121 | 0.804 | 0.898 | 50803 | 1 |
| GO:0042391 | regulation of membrane potential | 0.00304 | NaN | NaN | 1.987 | -0.4348 | 0.882 | 0.560 | 50803 | 1 |
| GO:0048167 | regulation of synaptic plasticity | 0.00051 | NaN | NaN | 1.230 | -0.7655 | 0.817 | 0.680 | 50803 | 1 |
| GO:0040008 | regulation of growth | 0.00396 | NaN | NaN | 2.100 | 0.4267 | 0.902 | 0.792 | 50803 | 1 |
| GO:0030036 | actin cytoskeleton organization | 0.01314 | NaN | NaN | 2.619 | 0.3844 | 0.799 | 0.856 | 50803 | 1 |
| GO:0051130 | positive regulation of cellular component organization | 0.00260 | NaN | NaN | 1.919 | 0.4211 | 0.795 | 0.720 | 50803 | 1 |
| GO:0034622 | cellular macromolecular complex assembly | 0.01228 | NaN | NaN | 2.590 | 0.3535 | 0.876 | 0.745 | 50803 | 1 |
| GO:0030041 | actin filament polymerization | 0.00215 | NaN | NaN | 1.839 | 0.4978 | 0.805 | 0.868 | 50803 | 1 |
| GO:0043254 | regulation of protein complex assembly | 0.00218 | NaN | NaN | 1.845 | 0.5197 | 0.805 | 0.798 | 50803 | 1 |
| GO:0030029 | actin filament-based process | 0.01320 | 0.400 | 1.423 | 2.621 | 0.3814 | 0.910 | 0.096 | 30029 | 0 |
| GO:0006919 | activation of cysteine-type endopeptidase activity involved in apoptotic process | 0.00032 | 1.657 | 6.912 | 1.041 | 0.7357 | 0.760 | 0.099 | 6919 | 0 |
| GO:0048522 | positive regulation of cellular process | 0.02067 | NaN | NaN | 2.816 | 0.3122 | 0.821 | 0.814 | 6919 | 1 |
| GO:0032270 | positive regulation of cellular protein metabolic process | 0.00307 | NaN | NaN | 1.991 | 0.3982 | 0.770 | 0.977 | 6919 | 1 |
| GO:0032268 | regulation of cellular protein metabolic process | 0.01209 | NaN | NaN | 2.583 | 0.3527 | 0.790 | 0.827 | 6919 | 1 |
| GO:0051247 | positive regulation of protein metabolic process | 0.00320 | NaN | NaN | 2.009 | 0.3933 | 0.790 | 0.786 | 6919 | 1 |
| GO:0048584 | positive regulation of response to stimulus | 0.00899 | NaN | NaN | 2.455 | 0.3804 | 0.765 | 0.638 | 6919 | 1 |
| GO:0060548 | negative regulation of cell death | 0.00367 | NaN | NaN | 2.068 | 0.3780 | 0.808 | 0.877 | 6919 | 1 |
| GO:0050790 | regulation of catalytic activity | 0.04375 | NaN | NaN | 3.141 | 0.3348 | 0.831 | 0.884 | 6919 | 1 |
| GO:0043065 | positive regulation of apoptotic process | 0.00193 | NaN | NaN | 1.792 | 0.5417 | 0.786 | 0.624 | 6919 | 1 |
| GO:0043067 | regulation of programmed cell death | 0.01108 | NaN | NaN | 2.545 | 0.3762 | 0.800 | 0.984 | 6919 | 1 |
| GO:0043068 | positive regulation of programmed cell death | 0.00193 | NaN | NaN | 1.792 | 0.5417 | 0.786 | 0.998 | 6919 | 1 |
| GO:0051336 | regulation of hydrolase activity | 0.03042 | NaN | NaN | 2.983 | 0.4347 | 0.836 | 0.518 | 6919 | 1 |
| GO:0051346 | negative regulation of hydrolase activity | 0.00820 | NaN | NaN | 2.415 | 0.5281 | 0.851 | 0.919 | 6919 | 1 |
| GO:0012501 | programmed cell death | 0.01722 | NaN | NaN | 2.736 | 0.3355 | 0.858 | 0.973 | 6919 | 1 |
| GO:0031401 | positive regulation of protein modification process | 0.00263 | NaN | NaN | 1.924 | 0.3772 | 0.773 | 0.708 | 6919 | 1 |
| GO:0010942 | positive regulation of cell death | 0.00193 | NaN | NaN | 1.792 | 0.5417 | 0.787 | 0.710 | 6919 | 1 |
| GO:0010941 | regulation of cell death | 0.01127 | NaN | NaN | 2.553 | 0.3962 | 0.803 | 0.880 | 6919 | 1 |
| GO:0010466 | negative regulation of peptidase activity | 0.00788 | NaN | NaN | 2.398 | 0.5562 | 0.796 | 0.797 | 6919 | 1 |
| GO:0042981 | regulation of apoptotic process | 0.01099 | NaN | NaN | 2.542 | 0.3807 | 0.800 | 0.828 | 6919 | 1 |
| GO:0010950 | positive regulation of endopeptidase activity | 0.00082 | NaN | NaN | 1.431 | 0.6147 | 0.824 | 0.960 | 6919 | 1 |
| GO:0052547 | regulation of peptidase activity | 0.00902 | NaN | NaN | 2.456 | 0.5652 | 0.795 | 0.970 | 6919 | 1 |
| GO:0052548 | regulation of endopeptidase activity | 0.00801 | NaN | NaN | 2.405 | 0.5453 | 0.797 | 0.965 | 6919 | 1 |
| GO:0010952 | positive regulation of peptidase activity | 0.00104 | NaN | NaN | 1.531 | 0.6333 | 0.828 | 0.625 | 6919 | 1 |
| GO:0030162 | regulation of proteolysis | 0.00937 | NaN | NaN | 2.473 | 0.4690 | 0.807 | 0.652 | 6919 | 1 |
| GO:0008219 | cell death | 0.01779 | NaN | NaN | 2.751 | 0.3486 | 0.857 | 0.978 | 6919 | 1 |
| GO:0031638 | zymogen activation | 0.00041 | NaN | NaN | 1.146 | 0.7562 | 0.934 | 0.779 | 6919 | 1 |
| GO:0097202 | activation of cysteine-type endopeptidase activity | 0.00032 | NaN | NaN | 1.041 | 0.7357 | 0.824 | 0.967 | 6919 | 1 |
| GO:2001056 | positive regulation of cysteine-type endopeptidase activity | 0.00076 | NaN | NaN | 1.398 | 0.6147 | 0.824 | 0.988 | 6919 | 1 |
| GO:0016485 | protein processing | 0.00206 | NaN | NaN | 1.820 | 0.4432 | 0.927 | 0.881 | 6919 | 1 |
| GO:0043280 | positive regulation of cysteine-type endopeptidase activity involved in apoptotic process | 0.00076 | NaN | NaN | 1.398 | 0.6147 | 0.755 | 0.942 | 6919 | 1 |
| GO:0006915 | apoptotic process | 0.01710 | NaN | NaN | 2.733 | 0.3401 | 0.858 | 0.930 | 6919 | 1 |
| GO:0006928 | cellular component movement | 0.02590 | 0.346 | 1.825 | 2.913 | 0.3409 | 0.904 | 0.106 | 6928 | 0 |
| GO:0006091 | generation of precursor metabolites and energy | 0.00785 | -2.398 | 2.859 | 2.396 | -0.3451 | 0.946 | 0.110 | 6091 | 0 |
| GO:0006399 | tRNA metabolic process | 0.00817 | -1.647 | 6.112 | 2.413 | 0.4661 | 0.914 | 0.110 | 6399 | 0 |
| GO:0008033 | tRNA processing | 0.00418 | NaN | NaN | 2.124 | 0.4760 | 0.915 | 0.858 | 6399 | 1 |
| GO:0034470 | ncRNA processing | 0.00712 | NaN | NaN | 2.354 | 0.4225 | 0.911 | 0.905 | 6399 | 1 |
| GO:0007049 | cell cycle | 0.02526 | 1.121 | 3.142 | 2.903 | 0.3148 | 0.904 | 0.115 | 7049 | 0 |
| GO:0042127 | regulation of cell proliferation | 0.00431 | 4.774 | 6.255 | 2.137 | 0.3847 | 0.871 | 0.119 | 42127 | 0 |
| GO:0017144 | drug metabolic process | 0.05520 | -3.268 | 4.435 | 3.242 | -0.5737 | 0.935 | 0.139 | 17144 | 0 |
| GO:0048518 | positive regulation of biological process | 0.02742 | 5.296 | 6.529 | 2.938 | 0.3098 | 0.894 | 0.156 | 48518 | 0 |
| GO:0006954 | inflammatory response | 0.00307 | 6.281 | -3.639 | 1.991 | 0.7232 | 0.866 | 0.160 | 6954 | 0 |
| GO:0031347 | regulation of defense response | 0.00180 | NaN | NaN | 1.763 | 0.6127 | 0.806 | 0.846 | 6954 | 1 |
| GO:0042060 | wound healing | 0.00560 | NaN | NaN | 2.250 | 0.4516 | 0.862 | 0.896 | 6954 | 1 |
| GO:0009611 | response to wounding | 0.00725 | NaN | NaN | 2.362 | 0.5217 | 0.866 | 0.633 | 6954 | 1 |
| GO:0045087 | innate immune response | 0.00215 | NaN | NaN | 1.839 | 0.5635 | 0.817 | 0.853 | 6954 | 1 |
| GO:0007596 | blood coagulation | 0.00323 | NaN | NaN | 2.013 | 0.5969 | 0.715 | 0.892 | 6954 | 1 |
| GO:0030168 | platelet activation | 0.00085 | NaN | NaN | 1.447 | 0.6752 | 0.732 | 0.495 | 6954 | 1 |
| GO:0007599 | hemostasis | 0.00326 | NaN | NaN | 2.017 | 0.5969 | 0.803 | 0.969 | 6954 | 1 |
| GO:1903034 | regulation of response to wounding | 0.00136 | NaN | NaN | 1.643 | 0.6323 | 0.812 | 0.716 | 6954 | 1 |
| GO:0006952 | defense response | 0.00598 | NaN | NaN | 2.279 | 0.6273 | 0.869 | 0.583 | 6954 | 1 |
| GO:0080134 | regulation of response to stress | 0.00415 | NaN | NaN | 2.121 | 0.4536 | 0.805 | 0.600 | 6954 | 1 |
| GO:0007154 | cell communication | 0.20480 | 3.040 | 3.291 | 3.811 | 0.2462 | 0.877 | 0.162 | 7154 | 0 |
| GO:0018298 | protein-chromophore linkage | 0.00237 | -1.464 | 7.415 | 1.881 | -0.6354 | 0.917 | 0.175 | 18298 | 0 |
| GO:0035235 | ionotropic glutamate receptor signaling pathway | 0.00218 | 7.518 | 0.049 | 1.845 | -0.6699 | 0.792 | 0.189 | 35235 | 0 |
| GO:0009607 | response to biotic stimulus | 0.00545 | 7.034 | -4.190 | 2.238 | 0.6188 | 0.898 | 0.190 | 9607 | 0 |
| GO:0007249 | I-kappaB kinase/NF-kappaB signaling | 0.00054 | 7.512 | -0.948 | 1.255 | 0.6522 | 0.812 | 0.193 | 7249 | 0 |
| GO:0048519 | negative regulation of biological process | 0.02982 | 5.536 | 6.520 | 2.975 | 0.2732 | 0.893 | 0.199 | 48519 | 0 |
| GO:0051606 | detection of stimulus | 0.01023 | 6.844 | -3.761 | 2.511 | -0.5405 | 0.892 | 0.213 | 51606 | 0 |
| GO:0007267 | cell-cell signaling | 0.00804 | 6.932 | 1.976 | 2.407 | -0.4157 | 0.885 | 0.234 | 7267 | 0 |
| GO:0006950 | response to stress | 0.03685 | 6.986 | -3.251 | 3.066 | 0.4318 | 0.877 | 0.265 | 6950 | 0 |
| GO:0007034 | vacuolar transport | 0.00025 | -4.299 | -3.650 | 0.954 | 0.5695 | 0.850 | 0.282 | 7034 | 0 |
| GO:0070727 | cellular macromolecule localization | 0.01912 | NaN | NaN | 2.782 | 0.3158 | 0.835 | 0.860 | 7034 | 1 |
| GO:1902582 | single-organism intracellular transport | 0.00972 | NaN | NaN | 2.489 | 0.3174 | 0.798 | 0.816 | 7034 | 1 |
| GO:0006888 | ER to Golgi vesicle-mediated transport | 0.00149 | NaN | NaN | 1.681 | 0.5573 | 0.829 | 0.620 | 7034 | 1 |
| GO:0046907 | intracellular transport | 0.02283 | NaN | NaN | 2.859 | 0.3233 | 0.833 | 0.667 | 7034 | 1 |
| GO:0051649 | establishment of localization in cell | 0.02919 | NaN | NaN | 2.965 | 0.2783 | 0.829 | 0.910 | 7034 | 1 |
| GO:0009605 | response to external stimulus | 0.02061 | 7.396 | -3.775 | 2.814 | 0.4112 | 0.884 | 0.291 | 9605 | 0 |
| GO:0051674 | localization of cell | 0.01482 | -4.132 | -3.903 | 2.671 | 0.4503 | 0.864 | 0.291 | 51674 | 0 |
| GO:0007600 | sensory perception | 0.01282 | -1.616 | -6.791 | 2.609 | -0.6239 | 0.872 | 0.297 | 7600 | 0 |
| GO:0007399 | nervous system development | 0.03112 | NaN | NaN | 2.993 | -0.2679 | 0.853 | 0.670 | 7600 | 1 |
| GO:0003008 | system process | 0.02419 | NaN | NaN | 2.884 | -0.3376 | 0.876 | 0.456 | 7600 | 1 |
| GO:0072358 | cardiovascular system development | 0.02112 | NaN | NaN | 2.825 | 0.2919 | 0.853 | 0.915 | 7600 | 1 |
| GO:0072359 | circulatory system development | 0.02112 | NaN | NaN | 2.825 | 0.2919 | 0.859 | 0.586 | 7600 | 1 |
| GO:0050877 | neurological system process | 0.01428 | NaN | NaN | 2.655 | -0.5774 | 0.873 | 0.844 | 7600 | 1 |
| GO:0001944 | vasculature development | 0.01228 | NaN | NaN | 2.590 | 0.3519 | 0.861 | 0.847 | 7600 | 1 |
| GO:0050953 | sensory perception of light stimulus | 0.00364 | NaN | NaN | 2.064 | -0.6504 | 0.885 | 0.840 | 7600 | 1 |
| GO:0007606 | sensory perception of chemical stimulus | 0.00801 | NaN | NaN | 2.405 | -0.6772 | 0.877 | 0.912 | 7600 | 1 |
| GO:0001568 | blood vessel development | 0.01089 | NaN | NaN | 2.538 | 0.3385 | 0.862 | 0.415 | 7600 | 1 |
| GO:0007601 | visual perception | 0.00361 | NaN | NaN | 2.061 | -0.6530 | 0.885 | 0.839 | 7600 | 1 |
| GO:0007193 | adenylate cyclase-inhibiting G-protein coupled receptor signaling pathway | 0.00082 | 7.679 | -0.406 | 1.431 | -0.5854 | 0.807 | 0.313 | 7193 | 0 |
| GO:0051246 | regulation of protein metabolic process | 0.02150 | 2.772 | 7.092 | 2.833 | 0.3503 | 0.831 | 0.313 | 51246 | 0 |
| GO:0048583 | regulation of response to stimulus | 0.04296 | 8.194 | 0.727 | 3.133 | 0.3117 | 0.804 | 0.324 | 48583 | 0 |
| GO:0042221 | response to chemical | 0.04375 | 7.359 | -3.488 | 3.141 | 0.2923 | 0.874 | 0.333 | 42221 | 0 |
| GO:0071705 | nitrogen compound transport | 0.00658 | -4.990 | -3.997 | 2.320 | -0.4036 | 0.868 | 0.336 | 71705 | 0 |
| GO:0016050 | vesicle organization | 0.00155 | -4.320 | -0.532 | 1.699 | 0.4362 | 0.889 | 0.344 | 16050 | 0 |
| GO:1902589 | single-organism organelle organization | 0.03922 | NaN | NaN | 3.093 | 0.2716 | 0.798 | 0.690 | 16050 | 1 |
| GO:0044085 | cellular component biogenesis | 0.03527 | NaN | NaN | 3.047 | 0.2633 | 0.893 | 0.585 | 16050 | 1 |
| GO:0048285 | organelle fission | 0.00703 | NaN | NaN | 2.348 | 0.3898 | 0.875 | 0.495 | 16050 | 1 |
| GO:0006996 | organelle organization | 0.05091 | NaN | NaN | 3.207 | 0.2638 | 0.861 | 0.734 | 16050 | 1 |
| GO:0051128 | regulation of cellular component organization | 0.01393 | NaN | NaN | 2.644 | 0.3368 | 0.824 | 0.425 | 16050 | 1 |
| GO:0006836 | neurotransmitter transport | 0.00361 | -5.708 | -3.576 | 2.061 | -0.4245 | 0.830 | 0.345 | 6836 | 0 |
| GO:0007215 | glutamate receptor signaling pathway | 0.00285 | 7.575 | 0.291 | 1.959 | -0.6213 | 0.788 | 0.345 | 7215 | 0 |
| GO:0035556 | intracellular signal transduction | 0.06097 | 7.174 | 1.420 | 3.285 | 0.3400 | 0.719 | 0.352 | 35556 | 0 |
| GO:0044700 | single organism signaling | 0.20103 | NaN | NaN | 3.803 | 0.2539 | 0.869 | 0.791 | 35556 | 1 |
| GO:0051716 | cellular response to stimulus | 0.21620 | NaN | NaN | 3.834 | 0.2694 | 0.821 | 0.659 | 35556 | 1 |
| GO:0007166 | cell surface receptor signaling pathway | 0.10036 | NaN | NaN | 3.501 | 0.2854 | 0.702 | 0.652 | 35556 | 1 |
| GO:0007165 | signal transduction | 0.19486 | NaN | NaN | 3.789 | 0.2748 | 0.676 | 0.578 | 35556 | 1 |
| GO:0007229 | integrin-mediated signaling pathway | 0.00298 | 7.929 | 0.298 | 1.978 | 0.6115 | 0.787 | 0.354 | 7229 | 0 |
| GO:0050794 | regulation of cellular process | 0.31918 | 5.706 | 5.581 | 4.004 | 0.2265 | 0.833 | 0.359 | 50794 | 0 |
| GO:0050789 | regulation of biological process | 0.34153 | NaN | NaN | 4.033 | 0.2266 | 0.862 | 0.601 | 50794 | 1 |
| GO:0021854 | hypothalamus development | 0.00044 | -1.342 | -6.550 | 1.176 | -0.6541 | 0.887 | 0.362 | 21854 | 0 |
| GO:0021536 | diencephalon development | 0.00180 | NaN | NaN | 1.763 | -0.4808 | 0.875 | 0.818 | 21854 | 1 |
| GO:0021510 | spinal cord development | 0.00152 | NaN | NaN | 1.690 | -0.4456 | 0.879 | 0.598 | 21854 | 1 |
| GO:0048663 | neuron fate commitment | 0.00095 | NaN | NaN | 1.491 | -0.5823 | 0.864 | 0.458 | 21854 | 1 |
| GO:0021761 | limbic system development | 0.00047 | NaN | NaN | 1.204 | -0.6480 | 0.886 | 0.744 | 21854 | 1 |
| GO:0050817 | coagulation | 0.00348 | -2.146 | -7.240 | 2.045 | 0.5782 | 0.896 | 0.368 | 50817 | 0 |
| GO:0006805 | xenobiotic metabolic process | 0.00013 | 6.452 | -5.067 | 0.699 | -0.5866 | 0.845 | 0.368 | 6805 | 0 |
| GO:0071466 | cellular response to xenobiotic stimulus | 0.00108 | NaN | NaN | 1.544 | -0.4808 | 0.837 | 0.834 | 6805 | 1 |
| GO:0006508 | proteolysis | 0.05930 | -0.793 | 6.975 | 3.273 | 0.3002 | 0.922 | 0.369 | 6508 | 0 |
| GO:0044267 | cellular protein metabolic process | 0.15902 | NaN | NaN | 3.701 | 0.2389 | 0.879 | 0.528 | 6508 | 1 |
| GO:0048645 | organ formation | 0.00044 | -1.364 | -6.699 | 1.176 | 0.6388 | 0.892 | 0.370 | 48645 | 0 |
| GO:0006082 | organic acid metabolic process | 0.02593 | -2.967 | 4.573 | 2.914 | -0.2902 | 0.860 | 0.380 | 6082 | 0 |
| GO:0016192 | vesicle-mediated transport | 0.02248 | -4.798 | -3.994 | 2.852 | 0.3191 | 0.850 | 0.387 | 16192 | 0 |
| GO:0033036 | macromolecule localization | 0.03809 | NaN | NaN | 3.081 | 0.2862 | 0.849 | 0.439 | 16192 | 1 |
| GO:0051641 | cellular localization | 0.03213 | NaN | NaN | 3.007 | 0.2743 | 0.852 | 0.463 | 16192 | 1 |
| GO:0034660 | ncRNA metabolic process | 0.01149 | -1.690 | 6.111 | 2.561 | 0.3969 | 0.918 | 0.390 | 34660 | 0 |
| GO:0055114 | oxidation-reduction process | 0.05651 | -5.195 | 3.483 | 3.252 | -0.2848 | 0.901 | 0.393 | 55114 | 0 |
| GO:0044281 | small molecule metabolic process | 0.09561 | NaN | NaN | 3.480 | -0.2565 | 0.894 | 0.491 | 55114 | 1 |
| GO:0055113 | epiboly involved in gastrulation with mouth forming second | 0.00111 | -2.244 | -7.322 | 1.556 | 0.5641 | 0.889 | 0.397 | 55113 | 0 |
| GO:0090504 | epiboly | 0.00127 | NaN | NaN | 1.613 | 0.5465 | 0.906 | 0.955 | 55113 | 1 |
| GO:0048646 | anatomical structure formation involved in morphogenesis | 0.02257 | NaN | NaN | 2.854 | 0.2744 | 0.932 | 0.544 | 55113 | 1 |
| GO:0007169 | transmembrane receptor protein tyrosine kinase signaling pathway | 0.01048 | 7.420 | 0.753 | 2.521 | 0.3410 | 0.762 | 0.399 | 7169 | 0 |
| GO:0007167 | enzyme linked receptor protein signaling pathway | 0.01573 | NaN | NaN | 2.697 | 0.3079 | 0.752 | 0.475 | 7169 | 1 |

## BPRevigoCollapsedForEM
| GO.ID | Description | p.Val | FDR | Phenotype |
| --- | --- | --- | --- | --- |
| GO:0000910 | cytokinesis | 0.003623 | 0.027325 | 1.779763 |
| GO:0002376 | immune system process | 0.001634 | 0.021530 | 2.103904 |
| GO:0006082 | organic acid metabolic process | 0.005025 | 0.032915 | -1.380245 |
| GO:0006091 | generation of precursor metabolites and energy | 0.006466 | 0.037553 | -1.426453 |
| GO:0006399 | tRNA metabolic process | 0.001757 | 0.021530 | 1.819289 |
| GO:0006508 | proteolysis | 0.001499 | 0.021530 | 1.434663 |
| GO:0006805 | xenobiotic metabolic process | 0.002024 | 0.021530 | -1.925353 |
| GO:0006826 | iron ion transport | 0.001912 | 0.021530 | 1.971139 |
| GO:0006836 | neurotransmitter transport | 0.002268 | 0.021530 | -1.668835 |
| GO:0006919 | activation of cysteine-type endopeptidase activity involved in apoptotic process | 0.005792 | 0.034880 | 1.794524 |
| GO:0006928 | movement of cell or subcellular component | 0.001538 | 0.021530 | 1.596618 |
| GO:0006950 | response to stress | 0.001447 | 0.021530 | 2.099819 |
| GO:0006954 | inflammatory response | 0.001739 | 0.021530 | 2.593119 |
| GO:0007034 | vacuolar transport | 0.003906 | 0.027874 | 1.802486 |
| GO:0007049 | cell cycle | 0.001623 | 0.021530 | 1.451134 |
| GO:0007154 | cell communication | 0.001267 | 0.021530 | 1.252057 |
| GO:0007162 | negative regulation of cell adhesion | 0.005894 | 0.035260 | 1.861016 |
| GO:0007169 | transmembrane receptor protein tyrosine kinase signaling pathway | 0.005076 | 0.033129 | 1.472442 |
| GO:0007193 | adenylate cyclase-inhibiting G-protein coupled receptor signaling pathway | 0.002062 | 0.021530 | -1.794792 |
| GO:0007215 | glutamate receptor signaling pathway | 0.002041 | 0.021530 | -2.137319 |
| GO:0007229 | integrin-mediated signaling pathway | 0.001848 | 0.021530 | 1.896012 |
| GO:0007249 | I-kappaB kinase/NF-kappaB signaling | 0.005929 | 0.035351 | 1.863563 |
| GO:0007267 | cell-cell signaling | 0.002427 | 0.021564 | -1.921897 |
| GO:0007600 | sensory perception | 0.002309 | 0.021530 | -2.565508 |
| GO:0008283 | cell proliferation | 0.001739 | 0.021530 | 1.615263 |
| GO:0009605 | response to external stimulus | 0.001543 | 0.021530 | 1.881728 |
| GO:0009607 | response to biotic stimulus | 0.001733 | 0.021530 | 2.408526 |
| GO:0016050 | vesicle organization | 0.003711 | 0.027325 | 1.685042 |
| GO:0016192 | vesicle-mediated transport | 0.003140 | 0.025848 | 1.472305 |
| GO:0016265 | death | 0.001626 | 0.021530 | 1.603795 |
| GO:0017144 | drug metabolic process | 0.004008 | 0.027990 | -1.818690 |
| GO:0018298 | protein-chromophore linkage | 0.002119 | 0.021530 | -1.832517 |
| GO:0021854 | hypothalamus development | 0.006036 | 0.035754 | -1.726892 |
| GO:0023052 | signaling | 0.001277 | 0.021530 | 1.285978 |
| GO:0030010 | establishment of cell polarity | 0.001815 | 0.021530 | 1.885495 |
| GO:0030029 | actin filament-based process | 0.001637 | 0.021530 | 1.661491 |
| GO:0030225 | macrophage differentiation | 0.001957 | 0.021530 | 2.008675 |
| GO:0034660 | ncRNA metabolic process | 0.001757 | 0.021530 | 1.688645 |
| GO:0035235 | ionotropic glutamate receptor signaling pathway | 0.004008 | 0.027990 | -1.881060 |
| GO:0035556 | intracellular signal transduction | 0.001499 | 0.021530 | 1.642337 |
| GO:0040007 | growth | 0.001754 | 0.021530 | 1.567593 |
| GO:0040011 | locomotion | 0.001531 | 0.021530 | 1.769013 |
| GO:0042127 | regulation of cell proliferation | 0.003565 | 0.027325 | 1.596279 |
| GO:0042221 | response to chemical | 0.001466 | 0.021530 | 1.409110 |
| GO:0042737 | drug catabolic process | 0.002041 | 0.021530 | -1.886058 |
| GO:0043331 | response to dsRNA | 0.001838 | 0.021530 | 2.130020 |
| GO:0044801 | single-organism membrane fusion | 0.003781 | 0.027360 | 1.694178 |
| GO:0046456 | icosanoid biosynthetic process | 0.003738 | 0.027325 | 1.925607 |
| GO:0048518 | positive regulation of biological process | 0.001479 | 0.021530 | 1.502091 |
| GO:0048519 | negative regulation of biological process | 0.001502 | 0.021530 | 1.329171 |
| GO:0048583 | regulation of response to stimulus | 0.001508 | 0.021530 | 1.487906 |
| GO:0048645 | organ formation | 0.003731 | 0.027325 | 1.815147 |
| GO:0050794 | regulation of cellular process | 0.001163 | 0.021530 | 1.175542 |
| GO:0050803 | regulation of synapse structure or activity | 0.002304 | 0.021530 | -2.047994 |
| GO:0050817 | coagulation | 0.001848 | 0.021530 | 1.966781 |
| GO:0050896 | response to stimulus | 0.001208 | 0.021530 | 1.508645 |
| GO:0051246 | regulation of protein metabolic process | 0.001570 | 0.021530 | 1.615834 |
| GO:0051301 | cell division | 0.001742 | 0.021530 | 1.734742 |
| GO:0051606 | detection of stimulus | 0.002217 | 0.021530 | -1.934238 |
| GO:0051674 | localization of cell | 0.001621 | 0.021530 | 2.018862 |
| GO:0051704 | multi-organism process | 0.001706 | 0.021530 | 2.328217 |
| GO:0055113 | epiboly involved in gastrulation with mouth forming second | 0.005386 | 0.034037 | 1.765895 |
| GO:0055114 | oxidation-reduction process | 0.002597 | 0.022520 | -1.389925 |
| GO:0065007 | biological regulation | 0.001142 | 0.021530 | 1.173523 |
| GO:0071705 | nitrogen compound transport | 0.002273 | 0.021530 | -1.707501 |