**Supplementary Table 6.** **Gene sets and pathways enriched in i-GSEA4GWAS.**

|  |  |  |
| --- | --- | --- |
| Pathway ID | P | permuted P |
| GO:0000003\_reproduction | < 1.00E-300 | < 1.00E-06 |
| GO:0002376\_immune\_system\_process | < 1.00E-300 | < 1.00E-06 |
| GO:0003700\_transcription\_factor\_activity | < 1.00E-300 | < 1.00E-06 |
| GO:0004672\_protein\_kinase\_activity | < 1.00E-300 | < 1.00E-06 |
| GO:0005102\_receptor\_binding | < 1.00E-300 | < 1.00E-06 |
| GO:0005509\_calcium\_ion\_binding | < 1.00E-300 | < 1.00E-06 |
| GO:0005624\_membrane\_fraction | < 1.00E-300 | < 1.00E-06 |
| GO:0005626\_insoluble\_fraction | < 1.00E-300 | < 1.00E-06 |
| GO:0005654\_nucleoplasm | < 1.00E-300 | < 1.00E-06 |
| GO:0005783\_endoplasmic\_reticulum | < 1.00E-300 | < 1.00E-06 |
| GO:0005794\_Golgi\_apparatus | < 1.00E-300 | < 1.00E-06 |
| GO:0006357\_regulation\_of\_transcription\_from\_RNA\_polymerase\_II\_promoter | < 1.00E-300 | < 1.00E-06 |
| GO:0006468\_protein\_amino\_acid\_phosphorylation | < 1.00E-300 | < 1.00E-06 |
| GO:0006629\_lipid\_metabolic\_process | < 1.00E-300 | < 1.00E-06 |
| GO:0006793\_phosphorus\_metabolic\_process | < 1.00E-300 | < 1.00E-06 |
| GO:0006796\_phosphate\_metabolic\_process | < 1.00E-300 | < 1.00E-06 |
| GO:0006811\_ion\_transport | < 1.00E-300 | < 1.00E-06 |
| GO:0007155\_cell\_adhesion | < 1.00E-300 | < 1.00E-06 |
| GO:0007267\_cell-cell\_signaling | < 1.00E-300 | < 1.00E-06 |
| GO:0008104\_protein\_localization | < 1.00E-300 | < 1.00E-06 |
| GO:0009605\_response\_to\_external\_stimulus | < 1.00E-300 | < 1.00E-06 |
| GO:0009887\_organ\_morphogenesis | < 1.00E-300 | < 1.00E-06 |
| GO:0009888\_tissue\_development | < 1.00E-300 | < 1.00E-06 |
| GO:0009891\_positive\_regulation\_of\_biosynthetic\_process | < 1.00E-300 | < 1.00E-06 |
| GO:0009893\_positive\_regulation\_of\_metabolic\_process | < 1.00E-300 | < 1.00E-06 |
| GO:0009966\_regulation\_of\_signal\_transduction | < 1.00E-300 | < 1.00E-06 |
| GO:0010033\_response\_to\_organic\_substance | < 1.00E-300 | < 1.00E-06 |
| GO:0010557\_positive\_regulation\_of\_macromolecule\_biosynthetic\_process | < 1.00E-300 | < 1.00E-06 |
| GO:0010604\_positive\_regulation\_of\_macromolecule\_metabolic\_process | < 1.00E-300 | < 1.00E-06 |
| GO:0010941\_regulation\_of\_cell\_death | < 1.00E-300 | < 1.00E-06 |
| GO:0012505\_endomembrane\_system | < 1.00E-300 | < 1.00E-06 |
| GO:0015031\_protein\_transport | < 1.00E-300 | < 1.00E-06 |
| GO:0015075\_ion\_transmembrane\_transporter\_activity | < 1.00E-300 | < 1.00E-06 |
| GO:0016301\_kinase\_activity | < 1.00E-300 | < 1.00E-06 |
| GO:0016310\_phosphorylation | < 1.00E-300 | < 1.00E-06 |
| GO:0016462\_pyrophosphatase\_activity | < 1.00E-300 | < 1.00E-06 |
| GO:0016772\_transferase\_activity\_\_transferring\_phosphorus-containing\_groups | < 1.00E-300 | < 1.00E-06 |
| GO:0016773\_phosphotransferase\_activity\_\_alcohol\_group\_as\_acceptor | < 1.00E-300 | < 1.00E-06 |
| GO:0016817\_hydrolase\_activity\_\_acting\_on\_acid\_anhydrides | < 1.00E-300 | < 1.00E-06 |
| GO:0016818\_hydrolase\_activity\_\_acting\_on\_acid\_anhydrides\_\_in\_phosphorus-containing\_anhydrides | < 1.00E-300 | < 1.00E-06 |
| GO:0022008\_neurogenesis | < 1.00E-300 | < 1.00E-06 |
| GO:0022414\_reproductive\_process | < 1.00E-300 | < 1.00E-06 |
| GO:0022607\_cellular\_component\_assembly | < 1.00E-300 | < 1.00E-06 |
| GO:0022610\_biological\_adhesion | < 1.00E-300 | < 1.00E-06 |
| GO:0022857\_transmembrane\_transporter\_activity | < 1.00E-300 | < 1.00E-06 |
| GO:0022891\_substrate-specific\_transmembrane\_transporter\_activity | < 1.00E-300 | < 1.00E-06 |
| GO:0022892\_substrate-specific\_transporter\_activity | < 1.00E-300 | < 1.00E-06 |
| GO:0030054\_cell\_junction | < 1.00E-300 | < 1.00E-06 |
| GO:0030234\_enzyme\_regulator\_activity | < 1.00E-300 | < 1.00E-06 |
| GO:0031325\_positive\_regulation\_of\_cellular\_metabolic\_process | < 1.00E-300 | < 1.00E-06 |
| GO:0031328\_positive\_regulation\_of\_cellular\_biosynthetic\_process | < 1.00E-300 | < 1.00E-06 |
| GO:0031410\_cytoplasmic\_vesicle | < 1.00E-300 | < 1.00E-06 |
| GO:0031982\_vesicle | < 1.00E-300 | < 1.00E-06 |
| GO:0032879\_regulation\_of\_localization | < 1.00E-300 | < 1.00E-06 |
| GO:0034645\_cellular\_macromolecule\_biosynthetic\_process | < 1.00E-300 | < 1.00E-06 |
| GO:0042127\_regulation\_of\_cell\_proliferation | < 1.00E-300 | < 1.00E-06 |
| GO:0042592\_homeostatic\_process | < 1.00E-300 | < 1.00E-06 |
| GO:0042981\_regulation\_of\_apoptosis | < 1.00E-300 | < 1.00E-06 |
| GO:0042995\_cell\_projection | < 1.00E-300 | < 1.00E-06 |
| GO:0043067\_regulation\_of\_programmed\_cell\_death | < 1.00E-300 | < 1.00E-06 |
| GO:0044085\_cellular\_component\_biogenesis | < 1.00E-300 | < 1.00E-06 |
| GO:0044255\_cellular\_lipid\_metabolic\_process | < 1.00E-300 | < 1.00E-06 |
| GO:0044421\_extracellular\_region\_part | < 1.00E-300 | < 1.00E-06 |
| GO:0044430\_cytoskeletal\_part | < 1.00E-300 | < 1.00E-06 |
| GO:0045184\_establishment\_of\_protein\_localization | < 1.00E-300 | < 1.00E-06 |
| GO:0048468\_cell\_development | < 1.00E-300 | < 1.00E-06 |
| GO:0048699\_generation\_of\_neurons | < 1.00E-300 | < 1.00E-06 |
| GO:0050790\_regulation\_of\_catalytic\_activity | < 1.00E-300 | < 1.00E-06 |
| GO:0050793\_regulation\_of\_developmental\_process | < 1.00E-300 | < 1.00E-06 |
| GO:0051239\_regulation\_of\_multicellular\_organismal\_process | < 1.00E-300 | < 1.00E-06 |
| GO:0051641\_cellular\_localization | < 1.00E-300 | < 1.00E-06 |
| GO:0051649\_establishment\_of\_localization\_in\_cell | < 1.00E-300 | < 1.00E-06 |
| GO:0051716\_cellular\_response\_to\_stimulus | < 1.00E-300 | < 1.00E-06 |
| GO:0065009\_regulation\_of\_molecular\_function | < 1.00E-300 | < 1.00E-06 |
| PANTHER\_BIOLOGICAL\_PROCESS\_Cell\_adhesion | < 1.00E-300 | < 1.00E-06 |
| PANTHER\_BIOLOGICAL\_PROCESS\_Neurogenesis | < 1.00E-300 | < 1.00E-06 |
| PANTHER\_BIOLOGICAL\_PROCESS\_Protein\_phosphorylation | < 1.00E-300 | < 1.00E-06 |
| PANTHER\_BIOLOGICAL\_PROCESS\_Proteolysis | < 1.00E-300 | < 1.00E-06 |
| PC\_EGF\_receptor\_(ErbB1)\_signaling\_pathway | < 1.00E-300 | < 1.00E-06 |
| PC\_ErbB1\_downstream\_signaling | < 1.00E-300 | < 1.00E-06 |
| PC\_ErbB\_receptor\_signaling\_network | < 1.00E-300 | < 1.00E-06 |
| PC\_Glypican\_1\_network | < 1.00E-300 | < 1.00E-06 |
| PC\_Glypican\_pathway | < 1.00E-300 | < 1.00E-06 |
| PC\_Internalization\_of\_ErbB1 | < 1.00E-300 | < 1.00E-06 |
| PC\_Proteogylcan\_syndecan-mediated\_signaling\_events | < 1.00E-300 | < 1.00E-06 |
| PC\_Syndecan-1-mediated\_signaling\_events | < 1.00E-300 | < 1.00E-06 |
| REACTOME\_IMMUNE\_SYSTEM | < 1.00E-300 | < 1.00E-06 |
| GO:0006928\_cell\_motion | 1.30E-297 | < 1.00E-06 |
| PANTHER\_BIOLOGICAL\_PROCESS\_Cation\_transport | 1.48E-297 | < 1.00E-06 |
| GO:0007417\_central\_nervous\_system\_development | 1.96E-280 | < 1.00E-06 |
| GO:0030182\_neuron\_differentiation | 8.24E-279 | < 1.00E-06 |
| GO:0030695\_GTPase\_regulator\_activity | 3.56E-272 | < 1.00E-06 |
| GO:0043005\_neuron\_projection | 4.96E-268 | < 1.00E-06 |
| GO:0030030\_cell\_projection\_organization | 6.79E-266 | < 1.00E-06 |
| GO:0030001\_metal\_ion\_transport | 7.18E-265 | < 1.00E-06 |
| GO:0015267\_channel\_activity | 9.64E-259 | < 1.00E-06 |
| GO:0022803\_passive\_transmembrane\_transporter\_activity | 9.64E-259 | < 1.00E-06 |
| GO:0045202\_synapse | 8.25E-258 | < 1.00E-06 |
| GO:0032989\_cellular\_component\_morphogenesis | 1.09E-255 | < 1.00E-06 |
| GO:0022838\_substrate\_specific\_channel\_activity | 1.47E-254 | < 1.00E-06 |
| GO:0005216\_ion\_channel\_activity | 1.69E-248 | < 1.00E-06 |
| GO:0000902\_cell\_morphogenesis | 7.91E-241 | < 1.00E-06 |
| GO:0019226\_transmission\_of\_nerve\_impulse | 7.27E-231 | < 1.00E-06 |
| GO:0046873\_metal\_ion\_transmembrane\_transporter\_activity | 1.20E-221 | < 1.00E-06 |
| GO:0048666\_neuron\_development | 5.89E-217 | < 1.00E-06 |
| PANTHER\_BIOLOGICAL\_PROCESS\_Cell\_adhesion-mediated\_signaling | 3.75E-215 | < 1.00E-06 |
| GO:0022836\_gated\_channel\_activity | 2.97E-212 | < 1.00E-06 |
| GO:0007268\_synaptic\_transmission | 9.42E-206 | < 1.00E-06 |
| GO:0031175\_neurite\_development | 1.07E-202 | < 1.00E-06 |
| REACTOME\_NEURONAL\_SYSTEM | 1.29E-200 | < 1.00E-06 |
| GO:0005261\_cation\_channel\_activity | 1.97E-197 | < 1.00E-06 |
| GO:0005083\_small\_GTPase\_regulator\_activity | 9.68E-195 | < 1.00E-06 |
| GO:0032990\_cell\_part\_morphogenesis | 2.57E-192 | < 1.00E-06 |
| GO:0048858\_cell\_projection\_morphogenesis | 2.30E-188 | < 1.00E-06 |
| GO:0044456\_synapse\_part | 1.25E-182 | < 1.00E-06 |
| GO:0016337\_cell-cell\_adhesion | 1.31E-181 | < 1.00E-06 |
| GO:0000904\_cell\_morphogenesis\_involved\_in\_differentiation | 3.02E-176 | < 1.00E-06 |
| GO:0048812\_neurite\_morphogenesis | 1.27E-173 | < 1.00E-06 |
| GO:0048667\_cell\_morphogenesis\_involved\_in\_neuron\_differentiation | 5.93E-161 | < 1.00E-06 |
| PANTHER\_MOLECULAR\_FUNCTION\_Other\_receptor | 7.96E-157 | < 1.00E-06 |
| GO:0007409\_axonogenesis | 4.30E-154 | < 1.00E-06 |
| GO:0034702\_ion\_channel\_complex | 1.16E-146 | < 1.00E-06 |
| GO:0005244\_voltage-gated\_ion\_channel\_activity | 1.78E-138 | < 1.00E-06 |
| GO:0030425\_dendrite | 9.45E-127 | < 1.00E-06 |
| GO:0045211\_postsynaptic\_membrane | 1.37E-119 | < 1.00E-06 |
| GO:0034703\_cation\_channel\_complex | 3.02E-115 | < 1.00E-06 |
| GO:0070838\_divalent\_metal\_ion\_transport | 1.12E-111 | < 1.00E-06 |
| GO:0006816\_calcium\_ion\_transport | 2.73E-111 | < 1.00E-06 |
| GO:0030955\_potassium\_ion\_binding | 1.97E-95 | < 1.00E-06 |
| PANTHER\_BIOLOGICAL\_PROCESS\_Calcium\_mediated\_signaling | 9.93E-94 | < 1.00E-06 |
| GO:0007411\_axon\_guidance | 2.10E-90 | < 1.00E-06 |
| GO:0015276\_ligand-gated\_ion\_channel\_activity | 2.69E-88 | < 1.00E-06 |
| GO:0014069\_postsynaptic\_density | 1.45E-77 | < 1.00E-06 |
| GO:0005262\_calcium\_channel\_activity | 2.72E-77 | < 1.00E-06 |
| PANTHER\_MOLECULAR\_FUNCTION\_CAM\_family\_adhesion\_molecule | 1.71E-62 | < 1.00E-06 |
| GO:0008324\_cation\_transmembrane\_transporter\_activity | 4.97E-305 | 2.00E-06 |
| GO:0006812\_cation\_transport | 3.10E-299 | 2.00E-06 |
| GO:0060589\_nucleoside-triphosphatase\_regulator\_activity | 4.91E-273 | 2.00E-06 |
| GO:0007420\_brain\_development | 5.26E-182 | 2.00E-06 |
| GO:0022832\_voltage-gated\_channel\_activity | 1.78E-138 | 2.00E-06 |
| GO:0030424\_axon | 2.27E-128 | 2.00E-06 |
| GO:0015674\_di-\_\_tri-valent\_inorganic\_cation\_transport | 4.64E-123 | 2.00E-06 |
| GO:0006813\_potassium\_ion\_transport | 6.17E-110 | 2.00E-06 |
| GO:0022834\_ligand-gated\_channel\_activity | 2.69E-88 | 2.00E-06 |
| GO:0007612\_learning | 6.44E-60 | 2.00E-06 |
| GO:0045296\_cadherin\_binding | 3.06E-20 | 2.00E-06 |
| GO:0008038\_neuron\_recognition | 7.59E-33 | 4.00E-06 |
| GO:0001964\_startle\_response | 1.68E-21 | 4.00E-06 |
| GO:0007610\_behavior | 1.75E-266 | 6.00E-06 |
| GO:0050839\_cell\_adhesion\_molecule\_binding | 6.13E-34 | 6.00E-06 |
| GO:0008037\_cell\_recognition | 2.14E-54 | 8.00E-06 |
| PANTHER\_BIOLOGICAL\_PROCESS\_Cell\_communication | 6.09E-210 | 1.00E-05 |
| PANTHER\_MOLECULAR\_FUNCTION\_Guanyl-nucleotide\_exchange\_factor | 2.25E-112 | 1.00E-05 |
| PID\_RAC1\_REG\_PATHWAY | 7.25E-44 | 1.00E-05 |
| GO:0031420\_alkali\_metal\_ion\_binding | 4.98E-143 | 1.20E-05 |
| PANTHER\_BIOLOGICAL\_PROCESS\_Neurotransmitter\_release | 3.37E-89 | 1.20E-05 |
| GO:0022843\_voltage-gated\_cation\_channel\_activity | 3.68E-112 | 1.40E-05 |
| GO:0005267\_potassium\_channel\_activity | 8.77E-101 | 1.40E-05 |
| PANTHER\_MOLECULAR\_FUNCTION\_Voltage-gated\_potassium\_channel | 6.61E-80 | 1.40E-05 |
| GO:0031225\_anchored\_to\_membrane | 5.25E-135 | 1.60E-05 |
| REACTOME\_TRANSMISSION\_ACROSS\_CHEMICAL\_SYNAPSES | 3.96E-133 | 1.60E-05 |
| GO:0003012\_muscle\_system\_process | 2.74E-125 | 1.60E-05 |
| PANTHER\_BIOLOGICAL\_PROCESS\_Other\_neuronal\_activity | 1.18E-105 | 1.60E-05 |
| REACTOME\_CELL\_CELL\_COMMUNICATION | 7.13E-100 | 1.60E-05 |
| REACTOME\_POTASSIUM\_CHANNELS | 7.55E-81 | 1.60E-05 |
| GO:0005001\_transmembrane\_receptor\_protein\_tyrosine\_phosphatase\_activity | 1.16E-30 | 2.40E-05 |
| GO:0045595\_regulation\_of\_cell\_differentiation | 6.79E-292 | 2.80E-05 |
| GO:0019198\_transmembrane\_receptor\_protein\_phosphatase\_activity | 1.16E-30 | 3.00E-05 |
| PANTHER\_BIOLOGICAL\_PROCESS\_Sulfur\_metabolism | 2.61E-47 | 3.20E-05 |
| PANTHER\_MOLECULAR\_FUNCTION\_Other\_ligand-gated\_ion\_channel | 4.65E-25 | 3.20E-05 |
| GO:0015629\_actin\_cytoskeleton | 6.64E-167 | 3.60E-05 |
| GO:0046903\_secretion | 1.06E-184 | 3.80E-05 |
| REACTOME\_NEUROTRANSMITTER\_RECEPTOR\_BINDING\_AND\_DOWNSTREAM\_TRANSMISSION\_IN\_THE\_POSTSYNAPTIC\_CELL | 1.17E-96 | 4.00E-05 |
| GO:0034705\_potassium\_channel\_complex | 4.28E-73 | 4.20E-05 |
| PANTHER\_BIOLOGICAL\_PROCESS\_Nerve-nerve\_synaptic\_transmission | 2.42E-56 | 4.20E-05 |
| GO:0007626\_locomotory\_behavior | 1.94E-156 | 4.40E-05 |
| PANTHER\_BIOLOGICAL\_PROCESS\_Developmental\_processes | 1.87E-280 | 4.80E-05 |
| GO:0022037\_metencephalon\_development | 7.62E-37 | 4.80E-05 |
| GO:0030036\_actin\_cytoskeleton\_organization | 2.18E-145 | 5.00E-05 |
| GO:0008076\_voltage-gated\_potassium\_channel\_complex | 4.28E-73 | 5.20E-05 |
| PANTHER\_MOLECULAR\_FUNCTION\_Ion\_channel | 7.11E-87 | 5.40E-05 |
| GO:0006936\_muscle\_contraction | 1.03E-114 | 5.60E-05 |
| GO:0030902\_hindbrain\_development | 5.28E-48 | 6.00E-05 |
| GO:0070161\_anchoring\_junction | 2.41E-132 | 6.40E-05 |
| PANTHER\_BIOLOGICAL\_PROCESS\_Muscle\_contraction | 4.72E-128 | 6.60E-05 |
| GO:0005913\_cell-cell\_adherens\_junction | 9.27E-39 | 7.00E-05 |
| GO:0005217\_intracellular\_ligand-gated\_ion\_channel\_activity | 2.89E-23 | 7.20E-05 |
| GO:0005912\_adherens\_junction | 9.70E-122 | 7.40E-05 |
| GO:0021549\_cerebellum\_development | 5.57E-34 | 7.40E-05 |
| PANTHER\_MOLECULAR\_FUNCTION\_Transmembrane\_receptor\_regulatory/adaptor\_protein | 1.41E-53 | 7.60E-05 |
| GO:0050905\_neuromuscular\_process | 9.47E-49 | 8.40E-05 |
| GO:0005096\_GTPase\_activator\_activity | 5.34E-146 | 9.40E-05 |
| PC\_CDC42\_signaling\_events | 5.05E-136 | 9.80E-05 |
| PANTHER\_BIOLOGICAL\_PROCESS\_Synaptic\_transmission | 1.84E-65 | 9.80E-05 |
| GO:0051674\_localization\_of\_cell | 8.39E-186 | 0.000102 |
| GO:0005099\_Ras\_GTPase\_activator\_activity | 1.21E-61 | 0.000104 |
| GO:0008066\_glutamate\_receptor\_activity | 6.17E-36 | 0.000106 |
| GO:0031012\_extracellular\_matrix | 1.29E-226 | 0.000108 |
| GO:0005911\_cell-cell\_junction | 8.00E-133 | 0.000108 |
| GO:0016323\_basolateral\_plasma\_membrane | 8.12E-141 | 0.00011 |
| GO:0051056\_regulation\_of\_small\_GTPase\_mediated\_signal\_transduction | 1.19E-166 | 0.000118 |
| GO:0034704\_calcium\_channel\_complex | 1.00E-34 | 0.00012 |
| GO:0045664\_regulation\_of\_neuron\_differentiation | 5.03E-95 | 0.000122 |
| GO:0040011\_locomotion | 4.27E-234 | 0.000124 |
| GO:0016917\_GABA\_receptor\_activity | 3.60E-17 | 0.00013 |
| GO:0048870\_cell\_motility | 8.39E-186 | 0.000136 |
| GO:0004114\_3'\_5'-cyclic-nucleotide\_phosphodiesterase\_activity | 1.23E-35 | 0.00014 |
| GO:0004112\_cyclic-nucleotide\_phosphodiesterase\_activity | 8.90E-37 | 0.000146 |
| GO:0050770\_regulation\_of\_axonogenesis | 7.65E-48 | 0.00017 |
| GO:0007611\_learning\_or\_memory | 1.06E-88 | 0.000174 |
| GO:0016477\_cell\_migration | 1.35E-168 | 0.000182 |
| GO:0005085\_guanyl-nucleotide\_exchange\_factor\_activity | 1.33E-119 | 0.000182 |
| GO:0044463\_cell\_projection\_part | 1.74E-161 | 0.000184 |
| REACTOME\_AXON\_GUIDANCE | 2.42E-179 | 0.000188 |
| GO:0006939\_smooth\_muscle\_contraction | 5.42E-34 | 0.000198 |
| GO:0021543\_pallium\_development | 2.34E-41 | 0.000206 |
| GO:0019725\_cellular\_homeostasis | 7.08E-243 | 0.000212 |
| GO:0019717\_synaptosome | 5.33E-62 | 0.000218 |
| GO:0010975\_regulation\_of\_neuron\_projection\_development | 1.16E-55 | 0.000218 |
| PC\_Regulation\_of\_CDC42\_activity | 3.12E-141 | 0.00022 |
| GO:0048813\_dendrite\_morphogenesis | 1.61E-15 | 0.000222 |
| GO:0042383\_sarcolemma | 1.05E-54 | 0.000232 |
| GO:0043025\_cell\_soma | 9.12E-117 | 0.000236 |
| GO:0005097\_Rab\_GTPase\_activator\_activity | 3.93E-35 | 0.000252 |
| GO:0048878\_chemical\_homeostasis | 1.98E-271 | 0.000258 |
| GO:0003001\_generation\_of\_a\_signal\_involved\_in\_cell-cell\_signaling | 4.58E-59 | 0.000262 |
| GO:0032313\_regulation\_of\_Rab\_GTPase\_activity | 2.46E-36 | 0.000276 |
| GO:0032483\_regulation\_of\_Rab\_protein\_signal\_transduction | 2.46E-36 | 0.000276 |
| GO:0032940\_secretion\_by\_cell | 3.67E-134 | 0.000286 |
| GO:0031344\_regulation\_of\_cell\_projection\_organization | 6.26E-65 | 0.000286 |
| GO:0008146\_sulfotransferase\_activity | 6.08E-46 | 0.000286 |
| GO:0005578\_proteinaceous\_extracellular\_matrix | 3.74E-208 | 0.000288 |
| PID\_IL8CXCR1\_PATHWAY | 6.44E-26 | 0.000324 |
| PANTHER\_MOLECULAR\_FUNCTION\_Annexin | 3.99E-61 | 0.000338 |
| GO:0009986\_cell\_surface | 2.34E-203 | 0.000342 |
| GO:0033267\_axon\_part | 4.11E-48 | 0.000346 |
| GO:0021537\_telencephalon\_development | 5.26E-54 | 0.00036 |
| GO:0004725\_protein\_tyrosine\_phosphatase\_activity | 4.02E-69 | 0.000386 |
| GO:0030029\_actin\_filament-based\_process | 2.86E-148 | 4.00E-04 |
| GO:0016358\_dendrite\_development | 2.99E-33 | 4.00E-04 |
| REACTOME\_VOLTAGE\_GATED\_POTASSIUM\_CHANNELS | 1.04E-40 | 0.000406 |
| GO:0005230\_extracellular\_ligand-gated\_ion\_channel\_activity | 1.15E-46 | 0.000416 |
| GO:0015672\_monovalent\_inorganic\_cation\_transport | 8.75E-178 | 0.000424 |
| GO:0006875\_cellular\_metal\_ion\_homeostasis | 4.21E-129 | 0.00044 |
| GO:0005088\_Ras\_guanyl-nucleotide\_exchange\_factor\_activity | 1.11E-75 | 0.00044 |
| PANTHER\_MOLECULAR\_FUNCTION\_Voltage-gated\_calcium\_channel | 5.39E-31 | 0.00044 |
| PANTHER\_MOLECULAR\_FUNCTION\_Phosphodiesterase | 8.65E-42 | 0.00047 |
| PANTHER\_BIOLOGICAL\_PROCESS\_Receptor\_protein\_tyrosine\_kinase\_signaling\_pathway | 6.74E-147 | 0.00048 |
| GO:0045177\_apical\_part\_of\_cell | 1.03E-111 | 5.00E-04 |
| GO:0048706\_embryonic\_skeletal\_system\_development | 1.08E-47 | 5.00E-04 |
| REACTOME\_HS\_GAG\_BIOSYNTHESIS | 2.23E-34 | 5.00E-04 |
| PANTHER\_BIOLOGICAL\_PROCESS\_Neuronal\_activities | 5.46E-95 | 0.000502 |
| GO:0051093\_negative\_regulation\_of\_developmental\_process | 1.12E-150 | 0.000518 |
| REACTOME\_ION\_CHANNEL\_TRANSPORT | 5.40E-41 | 0.00052 |
| GO:0045577\_regulation\_of\_B\_cell\_differentiation | 5.78E-18 | 0.00052 |
| GO:0044057\_regulation\_of\_system\_process | 3.04E-196 | 0.00054 |
| GO:0007010\_cytoskeleton\_organization | 2.81E-233 | 0.00056 |
| GO:0007588\_excretion | 9.78E-48 | 0.00058 |
| GO:0050767\_regulation\_of\_neurogenesis | 5.56E-117 | 6.00E-04 |
| GO:0016529\_sarcoplasmic\_reticulum | 3.32E-35 | 6.00E-04 |
| GO:0030900\_forebrain\_development | 3.31E-100 | 0.00064 |
| REACTOME\_GLYCOSAMINOGLYCAN\_METABOLISM | 5.96E-78 | 0.00064 |
| GO:0043616\_keratinocyte\_proliferation | 1.91E-13 | 0.00064 |
| GO:0050890\_cognition | 2.02E-295 | 0.00066 |
| GO:0016528\_sarcoplasm | 3.32E-35 | 0.00068 |
| GO:0055085\_transmembrane\_transport | 1.62679634441455e-310 | 7.00E-04 |
| PANTHER\_BIOLOGICAL\_PROCESS\_Metabolism\_of\_cyclic\_nucleotides | 1.94E-48 | 7.00E-04 |
| PANTHER\_BIOLOGICAL\_PROCESS\_Cell\_structure | 9.87E-298 | 0.00072 |
| GO:0021953\_central\_nervous\_system\_neuron\_differentiation | 8.25E-39 | 0.00072 |
| GO:0030032\_lamellipodium\_assembly | 6.41E-16 | 0.00072 |
| GO:0007167\_enzyme\_linked\_receptor\_protein\_signaling\_pathway | 9.58E-216 | 0.00074 |
| GO:0005245\_voltage-gated\_calcium\_channel\_activity | 2.74E-30 | 0.00078 |
| GO:0022604\_regulation\_of\_cell\_morphogenesis | 2.26E-97 | 8.00E-04 |
| GO:0005249\_voltage-gated\_potassium\_channel\_activity | 7.15E-74 | 0.00082 |
| PANTHER\_MOLECULAR\_FUNCTION\_Other\_cell\_junction\_protein | 2.28E-30 | 0.00082 |
| GO:0019899\_enzyme\_binding | 4.78E-300 | 0.00086 |
| GO:0050772\_positive\_regulation\_of\_axonogenesis | 1.97E-26 | 0.00086 |
| REACTOME\_DEVELOPMENTAL\_BIOLOGY | 2.16E-242 | 0.00088 |
| GO:0055065\_metal\_ion\_homeostasis | 8.40E-133 | 0.00092 |
| GO:0005891\_voltage-gated\_calcium\_channel\_complex | 1.85E-27 | 0.00092 |
| GO:0016324\_apical\_plasma\_membrane | 1.87E-89 | 0.00094 |
| PID\_IL8CXCR2\_PATHWAY | 4.72E-30 | 0.00096 |
| GO:0021587\_cerebellum\_morphogenesis | 1.57E-22 | 0.00096 |
| REACTOME\_GABA\_A\_RECEPTOR\_ACTIVATION | 4.31E-10 | 0.00096 |
| GO:0060402\_calcium\_ion\_transport\_into\_cytosol | 1.83E-18 | 0.00098 |
| GO:0001501\_skeletal\_system\_development | 2.97E-182 | 0.001 |
| GO:0022603\_regulation\_of\_anatomical\_structure\_morphogenesis | 9.12E-146 | 0.001 |
| GO:0004385\_guanylate\_kinase\_activity | 1.38E-14 | 0.001 |
| GO:0003779\_actin\_binding | 9.59E-208 | 0.00106 |
| PANTHER\_BIOLOGICAL\_PROCESS\_Signal\_transduction | 3.69E-162 | 0.00108 |
| GO:0045121\_membrane\_raft | 5.77E-98 | 0.00108 |
| REACTOME\_HEPARAN\_SULFATE\_HEPARIN\_HS\_GAG\_METABOLISM | 3.42E-42 | 0.00108 |
| PC\_Neuroransmitter\_Receptor\_Binding\_And\_Downstream\_Transmission\_In\_The\_Postsynaptic\_Cell | 1.93E-52 | 0.0011 |
| REACTOME\_NETRIN1\_SIGNALING | 3.51E-43 | 0.00112 |
| PANTHER\_MOLECULAR\_FUNCTION\_GABA\_receptor | 5.88E-13 | 0.00112 |
| GO:0050801\_ion\_homeostasis | 1.04E-219 | 0.00114 |
| GO:0016782\_transferase\_activity\_\_transferring\_sulfur-containing\_groups | 3.36E-51 | 0.00114 |
| GO:0004890\_GABA-A\_receptor\_activity | 5.88E-13 | 0.00114 |
| GO:0060401\_cytosolic\_calcium\_ion\_transport | 1.39E-19 | 0.00116 |
| GO:0007156\_homophilic\_cell\_adhesion | 4.97E-74 | 0.00118 |
| PC\_RAC1\_signaling\_pathway | 8.30E-116 | 0.0012 |
| PC\_Regulation\_of\_RhoA\_activity | 8.30E-116 | 0.00124 |
| PC\_RhoA\_signaling\_pathway | 8.30E-116 | 0.00124 |
| REACTOME\_LIGAND\_GATED\_ION\_CHANNEL\_TRANSPORT | 9.22E-16 | 0.00126 |
| PC\_Regulation\_of\_RAC1\_activity | 8.30E-116 | 0.00128 |
| GO:0010769\_regulation\_of\_cell\_morphogenesis\_involved\_in\_differentiation | 3.90E-57 | 0.00128 |
| PID\_TXA2PATHWAY | 3.47E-44 | 0.00128 |
| GO:0004697\_protein\_kinase\_C\_activity | 2.05E-18 | 0.00128 |
| GO:0021988\_olfactory\_lobe\_development | 3.57E-14 | 0.00136 |
| REACTOME\_TRANSMEMBRANE\_TRANSPORT\_OF\_SMALL\_MOLECULES | 8.80E-243 | 0.00138 |
| GO:0030534\_adult\_behavior | 6.39E-58 | 0.0014 |
| PANTHER\_MOLECULAR\_FUNCTION\_Transcription\_factor | 7.14E-92 | 0.00142 |
| REACTOME\_EFFECTS\_OF\_PIP2\_HYDROLYSIS | 5.20E-28 | 0.00142 |
| GO:0030201\_heparan\_sulfate\_proteoglycan\_metabolic\_process | 1.88E-19 | 0.00142 |
| GO:0006836\_neurotransmitter\_transport | 4.45E-58 | 0.00146 |
| Panther\_B\_cell\_activation | 2.65E-28 | 0.00152 |
| PANTHER\_MOLECULAR\_FUNCTION\_Extracellular\_matrix\_glycoprotein | 5.70E-76 | 0.00164 |
| REACTOME\_DSCAM\_INTERACTIONS | 2.16E-15 | 0.00168 |
| PC\_Synaptic\_Transmission | 3.66E-78 | 0.00172 |
| GO:0004012\_phospholipid-translocating\_ATPase\_activity | 5.32E-23 | 0.0018 |
| GO:0034656\_nucleobase\_\_nucleoside\_and\_nucleotide\_catabolic\_process | 4.96E-18 | 0.0018 |
| GO:0045596\_negative\_regulation\_of\_cell\_differentiation | 1.36E-122 | 0.00182 |
| GO:0051960\_regulation\_of\_nervous\_system\_development | 1.56E-130 | 0.00184 |
| GO:0006873\_cellular\_ion\_homeostasis | 2.28E-199 | 0.00186 |
| GO:0005924\_cell-substrate\_adherens\_junction | 3.69E-79 | 0.0019 |
| GO:0021575\_hindbrain\_morphogenesis | 4.07E-23 | 0.00192 |
| GO:0000122\_negative\_regulation\_of\_transcription\_from\_RNA\_polymerase\_II\_promoter | 9.52E-159 | 0.002 |
| GO:0005516\_calmodulin\_binding | 1.07E-111 | 0.002 |
| GO:0060090\_molecular\_adaptor\_activity | 4.95E-57 | 0.002 |
| REACTOME\_GABA\_RECEPTOR\_ACTIVATION | 2.13E-41 | 0.002 |
| REACTOME\_DAG\_AND\_IP3\_SIGNALING | 3.57E-35 | 0.002 |
| GO:0009791\_post-embryonic\_development | 1.89E-49 | 0.00202 |
| GO:0050954\_sensory\_perception\_of\_mechanical\_stimulus | 1.50E-83 | 0.00204 |
| GO:0005089\_Rho\_guanyl-nucleotide\_exchange\_factor\_activity | 4.11E-64 | 0.0021 |
| PC\_LPA\_receptor\_mediated\_events | 4.23E-63 | 0.0021 |
| REACTOME\_OPIOID\_SIGNALLING | 3.79E-61 | 0.0021 |
| REACTOME\_ADHERENS\_JUNCTIONS\_INTERACTIONS | 7.58E-33 | 0.0021 |
| GO:0021695\_cerebellar\_cortex\_development | 3.65E-20 | 0.0021 |
| REACTOME\_CELL\_JUNCTION\_ORGANIZATION | 3.07E-63 | 0.00214 |
| GO:0055080\_cation\_homeostasis | 1.61E-165 | 0.0022 |
| GO:0021987\_cerebral\_cortex\_development | 6.08E-31 | 0.0022 |
| PID\_REELINPATHWAY | 3.67E-30 | 0.0022 |
| GO:0015247\_aminophospholipid\_transporter\_activity | 5.32E-23 | 0.0022 |
| GO:0034655\_nucleobase\_\_nucleoside\_\_nucleotide\_and\_nucleic\_acid\_catabolic\_process | 4.96E-18 | 0.0022 |
| GO:0051668\_localization\_within\_membrane | 4.04E-15 | 0.00228 |
| GO:0055082\_cellular\_chemical\_homeostasis | 2.28E-199 | 0.0023 |
| GO:0051899\_membrane\_depolarization | 1.07E-33 | 0.0023 |
| GO:0007269\_neurotransmitter\_secretion | 1.34E-26 | 0.0023 |
| GO:0051017\_actin\_filament\_bundle\_formation | 6.81E-20 | 0.0023 |
| GO:0033017\_sarcoplasmic\_reticulum\_membrane | 1.54E-17 | 0.0023 |
| GO:0046578\_regulation\_of\_Ras\_protein\_signal\_transduction | 3.22E-135 | 0.00232 |
| Panther\_Integrin\_signalling\_pathway | 2.40E-91 | 0.00232 |
| PANTHER\_MOLECULAR\_FUNCTION\_G-protein\_modulator | 1.21E-32 | 0.00238 |
| GO:0008284\_positive\_regulation\_of\_cell\_proliferation | 6.48E-237 | 0.0024 |
| GO:0043087\_regulation\_of\_GTPase\_activity | 2.90E-78 | 0.0024 |
| GO:0007215\_glutamate\_signaling\_pathway | 4.07E-29 | 0.0024 |
| BIOCARTA\_EGFR\_SMRTE\_PATHWAY | 4.05E-16 | 0.0024 |
| GO:0045893\_positive\_regulation\_of\_transcription\_\_DNA-dependent | 3.40E-245 | 0.0025 |
| PANTHER\_MOLECULAR\_FUNCTION\_Other\_signaling\_molecule | 8.62E-145 | 0.0025 |
| GO:0030055\_cell-substrate\_junction | 8.53E-80 | 0.0025 |
| PC\_Transmission\_across\_Chemical\_Synapses | 7.38E-75 | 0.0025 |
| GO:0035108\_limb\_morphogenesis | 7.13E-64 | 0.0025 |
| PC\_Reelin\_signaling\_pathway | 3.67E-30 | 0.0025 |
| GO:0051254\_positive\_regulation\_of\_RNA\_metabolic\_process | 2.52E-246 | 0.0026 |
| GO:0006874\_cellular\_calcium\_ion\_homeostasis | 6.37E-115 | 0.0026 |
| GO:0008344\_adult\_locomotory\_behavior | 1.99E-44 | 0.0026 |
| GO:0034483\_heparan\_sulfate\_sulfotransferase\_activity | 1.88E-16 | 0.0026 |
| GO:0010647\_positive\_regulation\_of\_cell\_communication | 5.67E-187 | 0.0028 |
| SIG\_BCR\_SIGNALING\_PATHWAY | 3.89E-42 | 0.0028 |
| GO:0004970\_ionotropic\_glutamate\_receptor\_activity | 2.18E-21 | 0.0028 |
| GO:0043198\_dendritic\_shaft | 1.04E-14 | 0.0028 |
| REACTOME\_PHOSPHOLIPASE\_C\_MEDIATED\_CASCADE | 2.08E-50 | 0.0029 |
| PID\_EPOPATHWAY | 1.44E-33 | 0.0029 |
| GO:0030169\_low-density\_lipoprotein\_binding | 6.78E-26 | 0.0029 |
| GO:0005234\_extracellular-glutamate-gated\_ion\_channel\_activity | 2.18E-21 | 0.0029 |
| GO:0046928\_regulation\_of\_neurotransmitter\_secretion | 1.90E-20 | 0.0029 |
| GO:0015085\_calcium\_ion\_transmembrane\_transporter\_activity | 7.61E-19 | 0.0029 |
| PID\_ENDOTHELINPATHWAY | 1.18E-56 | 0.003 |
| PC\_EPO\_signaling\_pathway | 1.44E-33 | 0.003 |
| GO:0016667\_oxidoreductase\_activity\_\_acting\_on\_sulfur\_group\_of\_donors | 6.74E-30 | 0.003 |
| GO:0003014\_renal\_system\_process | 1.49E-27 | 0.003 |
| GO:0031327\_negative\_regulation\_of\_cellular\_biosynthetic\_process | 8.99E-276 | 0.0032 |
| REACTOME\_SIGNALING\_BY\_PDGF | 1.43E-78 | 0.0032 |
| GO:0002790\_peptide\_secretion | 7.99E-29 | 0.0032 |
| GO:0060284\_regulation\_of\_cell\_development | 7.56E-138 | 0.0033 |
| GO:0007413\_axonal\_fasciculation | 1.59E-13 | 0.0033 |
| GO:0010628\_positive\_regulation\_of\_gene\_expression | 2.12E-292 | 0.0034 |
| REACTOME\_SIGNALING\_BY\_RHO\_GTPASES | 2.15E-85 | 0.0034 |
| REACTOME\_ANTIGEN\_ACTIVATES\_B\_CELL\_RECEPTOR\_LEADING\_TO\_GENERATION\_OF\_SECOND\_MESSENGERS | 8.82E-30 | 0.0034 |
| PC\_CREB\_phosphorylation\_through\_the\_activation\_of\_CaMKII | 3.52E-16 | 0.0035 |
| GO:0045944\_positive\_regulation\_of\_transcription\_from\_RNA\_polymerase\_II\_promoter | 1.42E-188 | 0.0036 |
| GO:0051172\_negative\_regulation\_of\_nitrogen\_compound\_metabolic\_process | 3.25E-260 | 0.0037 |
| GO:0032403\_protein\_complex\_binding | 2.13E-127 | 0.0037 |
| GO:0007605\_sensory\_perception\_of\_sound | 5.35E-78 | 0.0037 |
| GO:0021795\_cerebral\_cortex\_cell\_migration | 1.57E-17 | 0.0037 |
| PC\_Ras\_activation\_uopn\_Ca2+\_infux\_through\_NMDA\_receptor | 2.34E-17 | 0.0037 |
| GO:0005925\_focal\_adhesion | 1.22E-75 | 0.0038 |
| GO:0016566\_specific\_transcriptional\_repressor\_activity | 1.43E-24 | 0.0038 |
| GO:0045885\_positive\_regulation\_of\_survival\_gene\_product\_expression | 9.07E-15 | 0.0038 |
| PC\_Interactions\_of\_the\_immunoglobulin\_superfamily\_(IgSF)\_member\_proteins | 6.22E-28 | 0.0039 |
| PC\_Formation\_of\_Platelet\_plug | 1.24E-119 | 0.004 |
| GO:0035107\_appendage\_morphogenesis | 7.13E-64 | 0.004 |
| GO:0030041\_actin\_filament\_polymerization | 6.17E-12 | 0.004 |
| GO:0060173\_limb\_development | 6.18E-66 | 0.0041 |
| Panther\_PDGF\_signaling\_pathway | 4.33E-34 | 0.0041 |
| REACTOME\_GPCR\_DOWNSTREAM\_SIGNALING | 2.60E-271 | 0.0042 |
| GO:0016481\_negative\_regulation\_of\_transcription | 2.99E-233 | 0.0042 |
| GO:0048646\_anatomical\_structure\_formation\_involved\_in\_morphogenesis | 4.46E-199 | 0.0042 |
| PANTHER\_BIOLOGICAL\_PROCESS\_Cell\_motility | 8.25E-187 | 0.0042 |
| PANTHER\_MOLECULAR\_FUNCTION\_Calmodulin\_related\_protein | 4.39E-94 | 0.0042 |
| PANTHER\_MOLECULAR\_FUNCTION\_Signaling\_molecule | 3.50E-45 | 0.0042 |
| GO:0051020\_GTPase\_binding | 1.59E-83 | 0.0043 |
| GO:0019904\_protein\_domain\_specific\_binding | 5.60E-197 | 0.0044 |
| GO:0030003\_cellular\_cation\_homeostasis | 2.33E-145 | 0.0044 |
| REACTOME\_NEPHRIN\_INTERACTIONS | 6.59E-21 | 0.0044 |
| GO:0001662\_behavioral\_fear\_response | 1.37E-19 | 0.0044 |
| GO:0031674\_I\_band | 5.09E-44 | 0.0045 |
| GO:0022804\_active\_transmembrane\_transporter\_activity | 1.02E-220 | 0.0046 |
| GO:0042578\_phosphoric\_ester\_hydrolase\_activity | 1.15E-197 | 0.0046 |
| GO:0033555\_multicellular\_organismal\_response\_to\_stress | 4.93E-33 | 0.0046 |
| GO:0030288\_outer\_membrane-bounded\_periplasmic\_space | 2.64E-14 | 0.0046 |
| GO:0015291\_secondary\_active\_transmembrane\_transporter\_activity | 2.09E-122 | 0.0047 |
| GO:0050808\_synapse\_organization | 2.37E-42 | 0.0047 |
| PC\_Thromboxane\_A2\_receptor\_signaling | 1.02E-29 | 0.0047 |
| PC\_Unblocking\_of\_NMDA\_receptor,\_glutamate\_binding\_and\_activation | 6.64E-17 | 0.0047 |
| PC\_Class\_C/3\_(Metabotropic\_glutamate/pheromone\_receptors) | 1.55E-87 | 0.0049 |
| GO:0031346\_positive\_regulation\_of\_cell\_projection\_organization | 8.00E-38 | 0.0049 |
| GO:0005834\_heterotrimeric\_G-protein\_complex | 6.22E-27 | 0.0049 |
| GO:0019199\_transmembrane\_receptor\_protein\_kinase\_activity | 3.19E-72 | 0.005 |
| GO:0048736\_appendage\_development | 6.18E-66 | 0.005 |
| REACTOME\_NRAGE\_SIGNALS\_DEATH\_THROUGH\_JNK | 3.14E-36 | 0.005 |
| PANTHER\_MOLECULAR\_FUNCTION\_Glutamate\_receptor | 3.37E-22 | 0.005 |
| GO:0005100\_Rho\_GTPase\_activator\_activity | 5.28E-21 | 0.005 |
| GO:0002209\_behavioral\_defense\_response | 1.37E-19 | 0.005 |
| REACTOME\_SIGNALING\_BY\_GPCR | 8.30277317836215e-320 | 0.0051 |
| GO:0006029\_proteoglycan\_metabolic\_process | 8.06E-41 | 0.0051 |
| GO:0005548\_phospholipid\_transporter\_activity | 2.63E-34 | 0.0051 |
| GO:0009187\_cyclic\_nucleotide\_metabolic\_process | 6.39E-34 | 0.0051 |
| GO:0046879\_hormone\_secretion | 8.97E-32 | 0.0051 |
| GO:0034311\_diol\_metabolic\_process | 4.73E-28 | 0.0051 |
| REACTOME\_EXTRACELLULAR\_MATRIX\_ORGANIZATION | 2.29E-63 | 0.0052 |
| GO:0007214\_gamma-aminobutyric\_acid\_signaling\_pathway | 8.33E-16 | 0.0052 |
| GO:0045934\_negative\_regulation\_of\_nucleobase\_\_nucleoside\_\_nucleotide\_and\_nucleic\_acid\_metabolic\_process | 2.33E-257 | 0.0053 |
| PANTHER\_BIOLOGICAL\_PROCESS\_Extracellular\_matrix\_protein-mediated\_signaling | 3.85E-57 | 0.0053 |
| GO:0008154\_actin\_polymerization\_or\_depolymerization | 4.75E-17 | 0.0053 |
| GO:0007600\_sensory\_perception | 8.20E-237 | 0.0054 |
| GO:0042734\_presynaptic\_membrane | 4.60E-29 | 0.0054 |
| PANTHER\_MOLECULAR\_FUNCTION\_Other\_transferase | 4.71E-74 | 0.0055 |
| REACTOME\_PLATELET\_HOMEOSTASIS | 9.38E-67 | 0.0055 |
| PANTHER\_MOLECULAR\_FUNCTION\_Other\_oxidoreductase | 3.30E-24 | 0.0055 |
| GO:0009890\_negative\_regulation\_of\_biosynthetic\_process | 6.93E-278 | 0.0056 |
| PANTHER\_MOLECULAR\_FUNCTION\_Cadherin | 5.10E-49 | 0.0056 |
| GO:0009712\_catechol\_metabolic\_process | 4.73E-28 | 0.0056 |
| GO:0015914\_phospholipid\_transport | 5.67E-35 | 0.0057 |
| GO:0022029\_telencephalon\_cell\_migration | 3.06E-18 | 0.0057 |
| REACTOME\_CREB\_PHOSPHORYLATION\_THROUGH\_THE\_ACTIVATION\_OF\_CAMKII | 1.03E-16 | 0.0058 |
| REACTOME\_CELL\_EXTRACELLULAR\_MATRIX\_INTERACTIONS | 2.33E-14 | 0.0058 |
| PC\_Platelet\_Activation | 3.36E-117 | 0.0059 |
| GO:0042277\_peptide\_binding | 1.90E-111 | 0.0059 |
| REACTOME\_ION\_TRANSPORT\_BY\_P\_TYPE\_ATPASES | 7.09E-32 | 0.0059 |
| GO:0018958\_phenol\_metabolic\_process | 6.53E-29 | 0.0059 |
| GO:0042417\_dopamine\_metabolic\_process | 4.04E-18 | 0.0059 |
| PC\_Thrombin\_signalling\_through\_proteinase\_activated\_receptors\_(PARs) | 8.80E-78 | 0.006 |
| PC\_Thromboxane\_signalling\_through\_TP\_receptor | 7.54E-74 | 0.006 |
| GO:0021885\_forebrain\_cell\_migration | 3.06E-18 | 0.006 |
| GO:0051347\_positive\_regulation\_of\_transferase\_activity | 4.37E-155 | 0.0061 |
| REACTOME\_DOWNSTREAM\_SIGNALING\_OF\_ACTIVATED\_FGFR | 9.18E-72 | 0.0061 |
| REACTOME\_COLLAGEN\_FORMATION | 9.86E-48 | 0.0061 |
| PID\_ERBB4\_PATHWAY | 5.17E-28 | 0.0063 |
| GO:0008542\_visual\_learning | 5.28E-24 | 0.0064 |
| REACTOME\_UNBLOCKING\_OF\_NMDA\_RECEPTOR\_GLUTAMATE\_BINDING\_AND\_ACTIVATION | 1.29E-15 | 0.0064 |
| GO:0001764\_neuron\_migration | 2.49E-44 | 0.0065 |
| PID\_RHOA\_REG\_PATHWAY | 4.47E-36 | 0.0065 |
| PC\_ErbB4\_signaling\_events | 4.32E-24 | 0.0065 |
| GO:0045941\_positive\_regulation\_of\_transcription | 1.68E-282 | 0.0066 |
| GO:0055074\_calcium\_ion\_homeostasis | 1.25E-118 | 0.0066 |
| GO:0007416\_synaptogenesis | 2.14E-24 | 0.0066 |
| BIOCARTA\_CELL2CELL\_PATHWAY | 8.70E-17 | 0.0066 |
| GO:0045619\_regulation\_of\_lymphocyte\_differentiation | 5.45E-44 | 0.0067 |
| PC\_VEGFR1\_specific\_signals | 1.09E-26 | 0.0067 |
| GO:0006584\_catecholamine\_metabolic\_process | 4.73E-28 | 0.0068 |
| GO:0050848\_regulation\_of\_calcium-mediated\_signaling | 1.58E-19 | 0.0068 |
| PC\_Signal\_amplification | 1.61E-85 | 0.0069 |
| GO:0007204\_elevation\_of\_cytosolic\_calcium\_ion\_concentration | 2.77E-73 | 0.007 |
| GO:0030072\_peptide\_hormone\_secretion | 1.10E-26 | 0.007 |
| Panther\_Axon\_guidance\_mediated\_by\_netrin | 2.66E-20 | 0.007 |
| GO:0009914\_hormone\_transport | 2.00E-32 | 0.0072 |
| GO:0007270\_nerve-nerve\_synaptic\_transmission | 9.43E-28 | 0.0072 |
| GO:0051588\_regulation\_of\_neurotransmitter\_transport | 8.69E-22 | 0.0072 |
| REACTOME\_RAS\_ACTIVATION\_UOPN\_CA2\_INFUX\_THROUGH\_NMDA\_RECEPTOR | 2.40E-20 | 0.0072 |
| GO:0021955\_central\_nervous\_system\_neuron\_axonogenesis | 6.75E-18 | 0.0072 |
| GO:0042597\_periplasmic\_space | 2.64E-14 | 0.0072 |
| GO:0007389\_pattern\_specification\_process | 8.18E-133 | 0.0073 |
| GO:0004857\_enzyme\_inhibitor\_activity | 1.11E-119 | 0.0073 |
| GO:0042596\_fear\_response | 8.68E-22 | 0.0073 |
| GO:0048565\_gut\_development | 1.94E-33 | 0.0074 |
| GO:0008219\_cell\_death | 8.05918745145256e-317 | 0.0075 |
| GO:0051174\_regulation\_of\_phosphorus\_metabolic\_process | 5.74E-244 | 0.0075 |
| GO:0042325\_regulation\_of\_phosphorylation | 7.87E-239 | 0.0075 |
| GO:0005231\_excitatory\_extracellular\_ligand-gated\_ion\_channel\_activity | 1.21E-35 | 0.0075 |
| GO:0009593\_detection\_of\_chemical\_stimulus | 2.64E-25 | 0.0075 |
| GO:0051128\_regulation\_of\_cellular\_component\_organization | 1.57E-238 | 0.0076 |
| GO:0009967\_positive\_regulation\_of\_signal\_transduction | 2.51E-167 | 0.0076 |
| GO:0010817\_regulation\_of\_hormone\_levels | 6.30E-89 | 0.0076 |
| GO:0051705\_behavioral\_interaction\_between\_organisms | 4.03E-25 | 0.0076 |
| REACTOME\_CHONDROITIN\_SULFATE\_DERMATAN\_SULFATE\_METABOLISM | 4.50E-36 | 0.0077 |
| GO:0060048\_cardiac\_muscle\_contraction | 7.59E-18 | 0.0077 |
| GO:0016339\_calcium-dependent\_cell-cell\_adhesion | 8.12E-13 | 0.0077 |
| GO:0044420\_extracellular\_matrix\_part | 3.03E-83 | 0.0078 |
| GO:0032350\_regulation\_of\_hormone\_metabolic\_process | 2.09E-15 | 0.0078 |
| PID\_TCR\_PATHWAY | 1.90E-49 | 0.0079 |
| BIOCARTA\_FMLP\_PATHWAY | 3.30E-31 | 0.0079 |
| GO:0008092\_cytoskeletal\_protein\_binding | 4.08E-300 | 0.008 |
| GO:0007613\_memory | 9.48E-36 | 0.008 |
| GO:0010558\_negative\_regulation\_of\_macromolecule\_biosynthetic\_process | 3.20E-264 | 0.0081 |
| GO:0007169\_transmembrane\_receptor\_protein\_tyrosine\_kinase\_signaling\_pathway | 1.42E-153 | 0.0081 |
| GO:0008015\_blood\_circulation | 4.31E-118 | 0.0081 |
| PC\_CXCR4-mediated\_signaling\_events | 3.05E-98 | 0.0081 |
| GO:0030031\_cell\_projection\_assembly | 1.39E-58 | 0.0082 |
| GO:0045058\_T\_cell\_selection | 5.64E-19 | 0.0082 |
| GO:0044449\_contractile\_fiber\_part | 1.74E-76 | 0.0083 |
| REACTOME\_REGULATION\_OF\_INSULIN\_SECRETION | 3.53E-67 | 0.0083 |
| PID\_LPA4\_PATHWAY | 1.25E-16 | 0.0083 |
| GO:0042805\_actinin\_binding | 4.65E-14 | 0.0083 |
| SIG\_PIP3\_SIGNALING\_IN\_B\_LYMPHOCYTES | 1.95E-34 | 0.0084 |
| GO:0050850\_positive\_regulation\_of\_calcium-mediated\_signaling | 6.42E-18 | 0.0085 |
| REACTOME\_CLASS\_C\_3\_METABOTROPIC\_GLUTAMATE\_PHEROMONE\_RECEPTORS | 1.25E-16 | 0.0085 |
| GO:0051969\_regulation\_of\_transmission\_of\_nerve\_impulse | 8.43E-100 | 0.0086 |
| GO:0043195\_terminal\_button | 1.03E-17 | 0.0086 |
| GO:0051318\_G1\_phase | 1.07E-17 | 0.0086 |
| GO:0050804\_regulation\_of\_synaptic\_transmission | 4.36E-94 | 0.0087 |
| GO:0007015\_actin\_filament\_organization | 3.66E-47 | 0.0088 |
| GO:0016564\_transcription\_repressor\_activity | 2.59E-175 | 0.0089 |
| GO:0033674\_positive\_regulation\_of\_kinase\_activity | 3.03E-149 | 0.0089 |
| GO:0008081\_phosphoric\_diester\_hydrolase\_activity | 3.53E-75 | 0.0089 |
| PANTHER\_BIOLOGICAL\_PROCESS\_Oncogene | 4.48E-66 | 0.0089 |
| GO:0042165\_neurotransmitter\_binding | 4.18E-57 | 0.0089 |
| GO:0043542\_endothelial\_cell\_migration | 1.35E-22 | 0.0089 |
| REACTOME\_CELL\_CELL\_JUNCTION\_ORGANIZATION | 7.40E-46 | 0.009 |
| GO:0035094\_response\_to\_nicotine | 1.06E-18 | 0.009 |
| GO:0045935\_positive\_regulation\_of\_nucleobase\_\_nucleoside\_\_nucleotide\_and\_nucleic\_acid\_metabolic\_process | 1.09338701752984e-312 | 0.0091 |
| GO:0060047\_heart\_contraction | 7.84E-19 | 0.0091 |
| GO:0044462\_external\_encapsulating\_structure\_part | 1.60E-16 | 0.0091 |
| PC\_Prostanoid\_ligand\_receptors | 3.52E-85 | 0.0092 |
| GO:0021696\_cerebellar\_cortex\_morphogenesis | 1.51E-17 | 0.0092 |
| GO:0019220\_regulation\_of\_phosphate\_metabolic\_process | 5.74E-244 | 0.0093 |
| GO:0007218\_neuropeptide\_signaling\_pathway | 2.26E-56 | 0.0093 |
| GO:0003727\_single-stranded\_RNA\_binding | 1.08E-22 | 0.0093 |
| GO:0030313\_cell\_envelope | 1.60E-16 | 0.0093 |
| GO:0031290\_retinal\_ganglion\_cell\_axon\_guidance | 8.29E-18 | 0.0094 |
| GO:0055067\_monovalent\_inorganic\_cation\_homeostasis | 5.39E-33 | 0.0095 |
| GO:0051216\_cartilage\_development | 2.98E-57 | 0.0096 |
| PID\_THROMBIN\_PAR1\_PATHWAY | 3.72E-32 | 0.0096 |
| GO:0003013\_circulatory\_system\_process | 4.31E-118 | 0.0097 |
| GO:0048705\_skeletal\_system\_morphogenesis | 2.09E-64 | 0.0097 |
| GO:0004222\_metalloendopeptidase\_activity | 1.91E-70 | 0.0098 |
| PC\_Muscarinic\_acetylcholine\_receptors | 1.23E-82 | 0.0099 |
| BIOCARTA\_TEL\_PATHWAY | 2.24E-22 | 0.0099 |
| GO:0031324\_negative\_regulation\_of\_cellular\_metabolic\_process | 0.00E+00 | 0.01 |
| GO:0051897\_positive\_regulation\_of\_protein\_kinase\_B\_signaling\_cascade | 3.01E-11 | 0.01 |
| GO:0031644\_regulation\_of\_neurological\_system\_process | 8.02E-102 | 0.0101 |
| GO:0004714\_transmembrane\_receptor\_protein\_tyrosine\_kinase\_activity | 2.90E-58 | 0.0101 |
| GO:0003015\_heart\_process | 7.84E-19 | 0.0101 |
| GO:0005615\_extracellular\_space | 8.75681950689025e-320 | 0.0102 |
| PANTHER\_MOLECULAR\_FUNCTION\_Other\_select\_calcium\_binding\_proteins | 6.86E-32 | 0.0104 |
| REACTOME\_CREB\_PHOSPHORYLATION\_THROUGH\_THE\_ACTIVATION\_OF\_RAS | 1.17E-23 | 0.0104 |
| PC\_GABA\_receptor\_activation | 1.32E-18 | 0.0104 |
| GO:0043209\_myelin\_sheath | 3.77E-15 | 0.0106 |
| GO:0016265\_death | 2.35521192185651e-317 | 0.0107 |
| GO:0060079\_regulation\_of\_excitatory\_postsynaptic\_membrane\_potential | 7.14E-19 | 0.0107 |
| GO:0070491\_transcription\_repressor\_binding | 2.98E-16 | 0.0108 |
| REACTOME\_SIGNALLING\_BY\_NGF | 2.79E-138 | 0.0109 |
| GO:0004713\_protein\_tyrosine\_kinase\_activity | 1.38E-120 | 0.0109 |
| PID\_CDC42\_PATHWAY | 5.44E-49 | 0.0109 |
| GO:0031280\_negative\_regulation\_of\_cyclase\_activity | 5.99E-48 | 0.0109 |
| GO:0051173\_positive\_regulation\_of\_nitrogen\_compound\_metabolic\_process | 4.79243676466009e-322 | 0.011 |
| PANTHER\_MOLECULAR\_FUNCTION\_Protein\_phosphatase | 2.40E-82 | 0.011 |
| BIOCARTA\_CCR3\_PATHWAY | 8.67E-19 | 0.011 |
| GO:0006470\_protein\_amino\_acid\_dephosphorylation | 3.56E-79 | 0.0111 |
| REACTOME\_PLATELET\_CALCIUM\_HOMEOSTASIS | 3.87E-20 | 0.0111 |
| GO:0021533\_cell\_differentiation\_in\_hindbrain | 2.24E-12 | 0.0111 |
| GO:0006937\_regulation\_of\_muscle\_contraction | 1.47E-53 | 0.0112 |
| PANTHER\_BIOLOGICAL\_PROCESS\_G-protein\_mediated\_signaling | 8.94E-304 | 0.0113 |
| PC\_Platelet\_activation\_triggers | 2.05E-97 | 0.0113 |
| GO:0030017\_sarcomere | 9.87E-66 | 0.0114 |
| GO:0007194\_negative\_regulation\_of\_adenylate\_cyclase\_activity | 5.99E-48 | 0.0114 |
| GO:0050864\_regulation\_of\_B\_cell\_activation | 1.25E-31 | 0.0115 |
| GO:0008237\_metallopeptidase\_activity | 2.78E-113 | 0.0118 |
| GO:0015293\_symporter\_activity | 2.79E-91 | 0.0118 |
| GO:0051339\_regulation\_of\_lyase\_activity | 2.03E-73 | 0.0118 |
| GO:0051350\_negative\_regulation\_of\_lyase\_activity | 5.99E-48 | 0.0118 |
| GO:0015297\_antiporter\_activity | 7.09E-42 | 0.0118 |
| GO:0030018\_Z\_disc | 3.38E-35 | 0.0118 |
| GO:0018107\_peptidyl-threonine\_phosphorylation | 1.11E-13 | 0.0118 |
| PANTHER\_MOLECULAR\_FUNCTION\_Other\_transporter | 4.90E-186 | 0.012 |
| GO:0032318\_regulation\_of\_Ras\_GTPase\_activity | 1.12E-65 | 0.0121 |
| GO:0019897\_extrinsic\_to\_plasma\_membrane | 4.57E-42 | 0.0121 |
| GO:0031279\_regulation\_of\_cyclase\_activity | 2.03E-73 | 0.0123 |
| PID\_P38\_MK2PATHWAY | 1.02E-19 | 0.0123 |
| GO:0021952\_central\_nervous\_system\_projection\_neuron\_axonogenesis | 4.74E-15 | 0.0124 |
| GO:0090092\_regulation\_of\_transmembrane\_receptor\_protein\_serine/threonine\_kinase\_signaling\_pathway | 5.25E-58 | 0.0126 |
| PANTHER\_MOLECULAR\_FUNCTION\_Membrane-bound\_signaling\_molecule | 6.63E-80 | 0.0127 |
| GO:0051592\_response\_to\_calcium\_ion | 7.64E-39 | 0.0127 |
| GO:0019201\_nucleotide\_kinase\_activity | 1.54E-18 | 0.0127 |
| GO:0014070\_response\_to\_organic\_cyclic\_substance | 2.16E-86 | 0.0128 |
| ST\_WNT\_CA2\_CYCLIC\_GMP\_PATHWAY | 3.36E-21 | 0.0128 |
| GO:0009790\_embryonic\_development | 5.59E-276 | 0.0129 |
| GO:0004674\_protein\_serine/threonine\_kinase\_activity | 5.58E-231 | 0.0129 |
| REACTOME\_PLATELET\_ACTIVATION\_SIGNALING\_AND\_AGGREGATION | 8.89E-120 | 0.013 |
| GO:0050885\_neuromuscular\_process\_controlling\_balance | 1.36E-24 | 0.0132 |
| GO:0005581\_collagen | 6.08E-27 | 0.0133 |
| GO:0007266\_Rho\_protein\_signal\_transduction | 1.57E-23 | 0.0133 |
| PC\_Serotonin\_receptors | 1.40E-87 | 0.0134 |
| GO:0019098\_reproductive\_behavior | 3.62E-16 | 0.0134 |
| GO:0008047\_enzyme\_activator\_activity | 5.15E-188 | 0.0136 |
| PID\_INTEGRIN4\_PATHWAY | 3.82E-16 | 0.0138 |
| GO:0002062\_chondrocyte\_differentiation | 1.87E-12 | 0.0138 |
| GO:0042101\_T\_cell\_receptor\_complex | 7.05E-11 | 0.0138 |
| GO:0045086\_positive\_regulation\_of\_interleukin-2\_biosynthetic\_process | 1.30E-09 | 0.0138 |
| REACTOME\_DOWNSTREAM\_SIGNAL\_TRANSDUCTION | 5.52E-60 | 0.014 |
| GO:0007292\_female\_gamete\_generation | 3.47E-53 | 0.014 |
| GO:0048041\_focal\_adhesion\_formation | 4.68E-16 | 0.014 |
| REACTOME\_DCC\_MEDIATED\_ATTRACTIVE\_SIGNALING | 6.11E-16 | 0.014 |
| GO:0009395\_phospholipid\_catabolic\_process | 1.07E-19 | 0.0141 |
| REACTOME\_TANDEM\_PORE\_DOMAIN\_POTASSIUM\_CHANNELS | 1.96E-12 | 0.0141 |
| GO:0005070\_SH3/SH2\_adaptor\_activity | 1.21E-38 | 0.0143 |
| GO:0045860\_positive\_regulation\_of\_protein\_kinase\_activity | 1.83E-142 | 0.0144 |
| GO:0034707\_chloride\_channel\_complex | 1.32E-31 | 0.0144 |
| REACTOME\_POST\_NMDA\_RECEPTOR\_ACTIVATION\_EVENTS | 3.08E-29 | 0.0144 |
| GO:0030312\_external\_encapsulating\_structure | 2.56E-17 | 0.0144 |
| PC\_P2Y\_receptors | 3.99E-83 | 0.0145 |
| PC\_ADP\_signalling\_through\_P2Y\_purinoceptor\_1 | 8.29E-69 | 0.0148 |
| REACTOME\_PLC\_BETA\_MEDIATED\_EVENTS | 3.54E-37 | 0.0149 |
| PID\_VEGFR1\_PATHWAY | 2.77E-23 | 0.0149 |
| REACTOME\_G\_ALPHA\_S\_SIGNALLING\_EVENTS | 1.15E-80 | 0.0151 |
| PC\_Cell\_junction\_organization | 3.36E-45 | 0.0152 |
| PID\_EPHA\_FWDPATHWAY | 2.59E-30 | 0.0154 |
| GO:0030315\_T-tubule | 7.34E-21 | 0.0154 |
| GO:0046068\_cGMP\_metabolic\_process | 8.93E-11 | 0.0154 |
| GO:0001816\_cytokine\_production | 7.81E-35 | 0.0155 |
| PID\_RXR\_VDR\_PATHWAY | 1.63E-24 | 0.0155 |
| GO:0002020\_protease\_binding | 3.11E-17 | 0.0155 |
| PANTHER\_MOLECULAR\_FUNCTION\_Extracellular\_matrix\_linker\_protein | 1.17E-25 | 0.0156 |
| REACTOME\_HS\_GAG\_DEGRADATION | 1.59E-18 | 0.0157 |
| GO:0045061\_thymic\_T\_cell\_selection | 1.87E-13 | 0.0157 |
| PID\_RAS\_PATHWAY | 3.37E-23 | 0.0158 |
| REACTOME\_SIGNALING\_BY\_ERBB2 | 1.02E-69 | 0.016 |
| REACTOME\_REGULATION\_OF\_INSULIN\_SECRETION\_BY\_ACETYLCHOLINE | 3.47E-12 | 0.016 |
| GO:0030246\_carbohydrate\_binding | 7.36E-187 | 0.0162 |
| GO:0030005\_cellular\_di-\_\_tri-valent\_inorganic\_cation\_homeostasis | 6.95E-130 | 0.0162 |
| PC\_Eicosanoid\_ligand-binding\_receptors | 3.26E-86 | 0.0163 |
| PANTHER\_MOLECULAR\_FUNCTION\_Extracellular\_matrix | 3.19E-75 | 0.0163 |
| GO:0008093\_cytoskeletal\_adaptor\_activity | 9.66E-21 | 0.0165 |
| PC\_Adrenoceptors | 4.92E-86 | 0.0166 |
| PC\_Lectin\_pathway\_of\_complement\_activation | 2.31E-81 | 0.0166 |
| GO:0055123\_digestive\_system\_development | 3.64E-23 | 0.0166 |
| GO:0035023\_regulation\_of\_Rho\_protein\_signal\_transduction | 9.37E-73 | 0.0168 |
| GO:0015269\_calcium-activated\_potassium\_channel\_activity | 3.07E-18 | 0.0168 |
| GO:0043062\_extracellular\_structure\_organization | 2.95E-99 | 0.0169 |
| GO:0031267\_small\_GTPase\_binding | 1.35E-71 | 0.0169 |
| GO:0048546\_digestive\_tract\_morphogenesis | 3.64E-23 | 0.0169 |
| GO:0005901\_caveola | 1.60E-40 | 0.017 |
| GO:0043679\_nerve\_terminal | 7.81E-16 | 0.0171 |
| GO:0045892\_negative\_regulation\_of\_transcription\_\_DNA-dependent | 1.42E-194 | 0.0172 |
| GO:0008484\_sulfuric\_ester\_hydrolase\_activity | 1.53E-14 | 0.0172 |
| GO:0021761\_limbic\_system\_development | 2.53E-25 | 0.0174 |
| PANTHER\_BIOLOGICAL\_PROCESS\_Other\_developmental\_process | 4.78E-54 | 0.0175 |
| GO:0046483\_heterocycle\_metabolic\_process | 9.39E-194 | 0.0176 |
| GO:0060341\_regulation\_of\_cellular\_localization | 1.67E-162 | 0.0176 |
| PID\_DELTANP63PATHWAY | 4.98E-37 | 0.0176 |
| PC\_Free\_fatty\_acid\_receptors | 4.59E-68 | 0.0177 |
| GO:0030073\_insulin\_secretion | 6.18E-17 | 0.0182 |
| GO:0032102\_negative\_regulation\_of\_response\_to\_external\_stimulus | 2.71E-31 | 0.0184 |
| GO:0030183\_B\_cell\_differentiation | 8.50E-35 | 0.0185 |
| ST\_MYOCYTE\_AD\_PATHWAY | 6.72E-23 | 0.0188 |
| GO:0003777\_microtubule\_motor\_activity | 3.20E-48 | 0.0189 |
| GO:0045786\_negative\_regulation\_of\_cell\_cycle | 7.84E-44 | 0.0189 |
| GO:0008201\_heparin\_binding | 4.08E-78 | 0.0192 |
| PC\_IL2-mediated\_signaling\_events | 1.16E-74 | 0.0193 |
| REACTOME\_ACTIVATION\_OF\_NMDA\_RECEPTOR\_exprON\_GLUTAMATE\_BINDING\_AND\_POSTSYNAPTIC\_EVENTS | 4.67E-30 | 0.0193 |
| GO:0015833\_peptide\_transport | 7.66E-35 | 0.0194 |
| GO:0016234\_inclusion\_body | 1.05E-15 | 0.0194 |
| GO:0003774\_motor\_activity | 2.86E-92 | 0.0195 |
| GO:0001505\_regulation\_of\_neurotransmitter\_levels | 9.38E-44 | 0.0195 |
| GO:0010629\_negative\_regulation\_of\_gene\_expression | 1.57E-244 | 0.02 |
| GO:0043068\_positive\_regulation\_of\_programmed\_cell\_death | 1.71E-227 | 0.02 |
| GO:0048471\_perinuclear\_region\_of\_cytoplasm | 3.00E-182 | 0.02 |
| GO:0009792\_embryonic\_development\_ending\_in\_birth\_or\_egg\_hatching | 6.66E-170 | 0.02 |
| REACTOME\_INTEGRATION\_OF\_ENERGY\_METABOLISM | 5.51E-82 | 0.02 |
| GO:0017016\_Ras\_GTPase\_binding | 2.63E-66 | 0.02 |
| PC\_BCR\_signaling\_pathway | 1.58E-44 | 0.02 |
| PID\_CD8TCRPATHWAY | 3.61E-39 | 0.02 |
| GO:0005884\_actin\_filament | 4.72E-32 | 0.02 |
| GO:0017137\_Rab\_GTPase\_binding | 3.79E-30 | 0.02 |
| REACTOME\_INTERACTION\_BETWEEN\_L1\_AND\_ANKYRINS | 8.58E-28 | 0.02 |
| GO:0007632\_visual\_behavior | 1.94E-25 | 0.02 |
| GO:0035249\_synaptic\_transmission\_\_glutamatergic | 1.31E-18 | 0.02 |
| GO:0018210\_peptidyl-threonine\_modification | 8.18E-16 | 0.02 |
| BIOCARTA\_AKAPCENTROSOME\_PATHWAY | 2.74E-13 | 0.02 |
| GO:0046716\_muscle\_maintenance | 1.06E-10 | 0.02 |
| GO:0014014\_negative\_regulation\_of\_gliogenesis | 4.06E-10 | 0.02 |
| GO:0007628\_adult\_walking\_behavior | 3.33E-24 | 0.0203 |
| PANTHER\_MOLECULAR\_FUNCTION\_Non-motor\_actin\_binding\_protein | 5.31E-102 | 0.0204 |
| PC\_Signaling\_events\_mediated\_by\_Hepatocyte\_Growth\_Factor\_Receptor\_(c-Met) | 3.92633968750039e-320 | 0.0207 |
| GO:0051253\_negative\_regulation\_of\_RNA\_metabolic\_process | 4.41E-195 | 0.0207 |
| PC\_Cell-extracellular\_matrix\_interactions | 1.69E-14 | 0.0207 |
| GO:0060249\_anatomical\_structure\_homeostasis | 3.90E-48 | 0.0209 |
| GO:0012501\_programmed\_cell\_death | 1.06E-254 | 0.021 |
| GO:0006915\_apoptosis | 9.40E-254 | 0.021 |
| REACTOME\_METABOLISM\_OF\_CARBOHYDRATES | 2.35E-128 | 0.021 |
| GO:0050865\_regulation\_of\_cell\_activation | 1.47E-100 | 0.021 |
| REACTOME\_SIGNALING\_BY\_FGFR | 9.35E-79 | 0.021 |
| PANTHER\_BIOLOGICAL\_PROCESS\_Segment\_specification | 2.20E-50 | 0.021 |
| PANTHER\_MOLECULAR\_FUNCTION\_Select\_regulatory\_molecule | 5.91E-47 | 0.021 |
| GO:0045454\_cell\_redox\_homeostasis | 5.37E-40 | 0.021 |
| PID\_SYNDECAN\_1\_PATHWAY | 8.88E-31 | 0.021 |
| GO:0021954\_central\_nervous\_system\_neuron\_development | 3.87E-29 | 0.021 |
| GO:0005227\_calcium\_activated\_cation\_channel\_activity | 2.79E-21 | 0.021 |
| SA\_B\_CELL\_RECEPTOR\_COMPLEXES | 1.26E-19 | 0.021 |
| GO:0048265\_response\_to\_pain | 6.52E-17 | 0.021 |
| GO:0008328\_ionotropic\_glutamate\_receptor\_complex | 6.29E-16 | 0.021 |
| GO:0005537\_mannose\_binding | 3.13E-13 | 0.021 |
| REACTOME\_MYOGENESIS | 5.69E-24 | 0.0211 |
| GO:0016597\_amino\_acid\_binding | 2.86E-41 | 0.0213 |
| PC\_Transport\_of\_inorganic\_cations/anions\_and\_amino\_acids/oligopeptides | 8.13E-48 | 0.0214 |
| PID\_BCR\_5PATHWAY | 1.90E-44 | 0.0214 |
| GO:0030016\_myofibril | 2.03E-74 | 0.0216 |
| GO:0010942\_positive\_regulation\_of\_cell\_death | 3.33E-228 | 0.022 |
| GO:0051338\_regulation\_of\_transferase\_activity | 9.99E-199 | 0.022 |
| GO:0051046\_regulation\_of\_secretion | 1.00E-127 | 0.022 |
| GO:0060348\_bone\_development | 5.16E-73 | 0.022 |
| PC\_Opsins | 4.18E-66 | 0.022 |
| PANTHER\_BIOLOGICAL\_PROCESS\_Extracellular\_transport\_and\_import | 1.18E-50 | 0.022 |
| GO:0050730\_regulation\_of\_peptidyl-tyrosine\_phosphorylation | 6.63E-43 | 0.022 |
| PANTHER\_MOLECULAR\_FUNCTION\_ATP-binding\_cassette\_(ABC)\_transporter | 3.42E-33 | 0.022 |
| REACTOME\_NITRIC\_OXIDE\_STIMULATES\_GUANYLATE\_CYCLASE | 4.49E-29 | 0.022 |
| REACTOME\_ACTIVATION\_OF\_KAINATE\_RECEPTORS\_exprON\_GLUTAMATE\_BINDING | 4.40E-28 | 0.022 |
| GO:0060078\_regulation\_of\_postsynaptic\_membrane\_potential | 2.03E-20 | 0.022 |
| GO:0005251\_delayed\_rectifier\_potassium\_channel\_activity | 1.96E-14 | 0.022 |
| GO:0016079\_synaptic\_vesicle\_exocytosis | 1.21E-10 | 0.022 |
| GO:0030035\_microspike\_assembly | 1.47E-21 | 0.0221 |
| GO:0000080\_G1\_phase\_of\_mitotic\_cell\_cycle | 3.60E-13 | 0.0222 |
| GO:0043954\_cellular\_component\_maintenance | 5.94E-18 | 0.0223 |
| BIOCARTA\_CDMAC\_PATHWAY | 4.65E-18 | 0.0227 |
| GO:0030516\_regulation\_of\_axon\_extension | 5.97E-18 | 0.0227 |
| GO:0043065\_positive\_regulation\_of\_apoptosis | 3.84E-224 | 0.023 |
| GO:0071310\_cellular\_response\_to\_organic\_substance | 2.85E-104 | 0.023 |
| PC\_GPCR\_downstream\_signaling | 4.71E-87 | 0.023 |
| GO:0008509\_anion\_transmembrane\_transporter\_activity | 4.19E-83 | 0.023 |
| GO:0045761\_regulation\_of\_adenylate\_cyclase\_activity | 3.37E-71 | 0.023 |
| PANTHER\_BIOLOGICAL\_PROCESS\_Tumor\_suppressor | 1.42E-54 | 0.023 |
| GO:0009123\_nucleoside\_monophosphate\_metabolic\_process | 7.80E-46 | 0.023 |
| GO:0043279\_response\_to\_alkaloid | 3.13E-45 | 0.023 |
| PANTHER\_MOLECULAR\_FUNCTION\_Cytoskeletal\_protein | 1.05E-43 | 0.023 |
| GO:0005254\_chloride\_channel\_activity | 7.53E-39 | 0.023 |
| PID\_A6B1\_A6B4\_INTEGRIN\_PATHWAY | 4.74E-37 | 0.023 |
| PANTHER\_MOLECULAR\_FUNCTION\_Nuclear\_hormone\_receptor | 2.18E-35 | 0.023 |
| GO:0051262\_protein\_tetramerization | 1.69E-28 | 0.023 |
| GO:0050680\_negative\_regulation\_of\_epithelial\_cell\_proliferation | 1.40E-20 | 0.023 |
| GO:0045930\_negative\_regulation\_of\_mitotic\_cell\_cycle | 9.78E-20 | 0.023 |
| PC\_Nucleotide-like\_(purinergic)\_receptors | 1.05E-87 | 0.0231 |
| GO:0003707\_steroid\_hormone\_receptor\_activity | 1.33E-36 | 0.0238 |
| GO:0007189\_activation\_of\_adenylate\_cyclase\_activity\_by\_G-protein\_signaling\_pathway | 4.58E-32 | 0.0238 |
| PC\_Signaling\_events\_mediated\_by\_focal\_adhesion\_kinase | 1.05808098466187e-310 | 0.024 |
| REACTOME\_G\_ALPHA1213\_SIGNALLING\_EVENTS | 1.33E-53 | 0.024 |
| PC\_Amino\_acid\_and\_oligopeptide\_SLC\_transporters | 8.13E-48 | 0.024 |
| GO:0006940\_regulation\_of\_smooth\_muscle\_contraction | 4.47E-33 | 0.024 |
| PC\_Cell-cell\_junction\_organization | 1.77E-20 | 0.024 |
| GO:0008306\_associative\_learning | 1.84E-15 | 0.024 |
| GO:0004065\_arylsulfatase\_activity | 7.74E-12 | 0.024 |
| GO:0071495\_cellular\_response\_to\_endogenous\_stimulus | 6.53E-93 | 0.0241 |
| GO:0010559\_regulation\_of\_glycoprotein\_biosynthetic\_process | 4.34E-13 | 0.0242 |
| GO:0005529\_sugar\_binding | 9.16E-92 | 0.0243 |
| GO:0045494\_photoreceptor\_cell\_maintenance | 5.94E-18 | 0.0243 |
| GO:0007601\_visual\_perception | 4.68E-118 | 0.025 |
| PC\_Creation\_of\_C4\_and\_C2\_activators | 1.74E-82 | 0.025 |
| GO:0043292\_contractile\_fiber | 1.11E-79 | 0.025 |
| GO:0048704\_embryonic\_skeletal\_system\_morphogenesis | 9.54E-30 | 0.025 |
| GO:0016776\_phosphotransferase\_activity\_\_phosphate\_group\_as\_acceptor | 6.68E-25 | 0.025 |
| GO:0046058\_cAMP\_metabolic\_process | 1.87E-22 | 0.025 |
| GO:0048538\_thymus\_development | 1.84E-16 | 0.025 |
| GO:0048639\_positive\_regulation\_of\_developmental\_growth | 1.96E-14 | 0.025 |
| GO:0004930\_G-protein\_coupled\_receptor\_activity | 7.58E-229 | 0.026 |
| GO:0043009\_chordate\_embryonic\_development | 6.66E-170 | 0.026 |
| PC\_Amine\_ligand-binding\_receptors | 6.30E-94 | 0.026 |
| GO:0030817\_regulation\_of\_cAMP\_biosynthetic\_process | 7.89E-77 | 0.026 |
| GO:0005604\_basement\_membrane | 3.78E-60 | 0.026 |
| PID\_LYSOPHOSPHOLIPID\_PATHWAY | 5.29E-55 | 0.026 |
| PANTHER\_MOLECULAR\_FUNCTION\_Microtubule\_binding\_motor\_protein | 6.81E-41 | 0.026 |
| Panther\_Axon\_guidance\_mediated\_by\_Slit/Robo | 9.22E-18 | 0.026 |
| GO:0005796\_Golgi\_lumen | 3.67E-15 | 0.026 |
| Panther\_VEGF\_signaling\_pathway | 8.59E-13 | 0.026 |
| GO:0060042\_retina\_morphogenesis\_in\_camera-type\_eye | 2.30E-11 | 0.026 |
| PANTHER\_MOLECULAR\_FUNCTION\_Glycosyltransferase | 9.00E-121 | 0.027 |
| PANTHER\_MOLECULAR\_FUNCTION\_Extracellular\_matrix\_structural\_protein | 1.54E-56 | 0.027 |
| GO:0010578\_regulation\_of\_adenylate\_cyclase\_activity\_involved\_in\_G-protein\_signaling | 4.58E-32 | 0.027 |
| GO:0010579\_positive\_regulation\_of\_adenylate\_cyclase\_activity\_by\_G-protein\_signaling\_pathway | 4.58E-32 | 0.027 |
| GO:0005581\_COL8A2\_GO:0005581\_updated\_with\_COL8A2 | 9.00E-28 | 0.027 |
| PC\_GPCR\_ligand\_binding | 6.06E-193 | 0.0279 |
| REACTOME\_SLC\_MEDIATED\_TRANSMEMBRANE\_TRANSPORT | 5.15E-144 | 0.028 |
| PC\_Histamine\_receptors | 3.01E-86 | 0.028 |
| GO:0030155\_regulation\_of\_cell\_adhesion | 6.95E-82 | 0.028 |
| GO:0030808\_regulation\_of\_nucleotide\_biosynthetic\_process | 1.69E-80 | 0.028 |
| GO:0008238\_exopeptidase\_activity | 2.59E-57 | 0.028 |
| GO:0010720\_positive\_regulation\_of\_cell\_development | 1.84E-52 | 0.028 |
| PC\_Organic\_anion\_transporters | 8.13E-48 | 0.028 |
| GO:0030139\_endocytic\_vesicle | 8.87E-40 | 0.028 |
| GO:0030140\_trans-Golgi\_network\_transport\_vesicle | 6.60E-19 | 0.028 |
| PC\_p38\_signaling\_mediated\_by\_MAPKAP\_kinases | 6.08E-18 | 0.028 |
| GO:0006066\_cellular\_alcohol\_metabolic\_process | 1.23E-207 | 0.029 |
| PC\_Signaling\_by\_GPCR | 2.08E-193 | 0.029 |
| GO:0050953\_sensory\_perception\_of\_light\_stimulus | 4.68E-118 | 0.029 |
| PANTHER\_BIOLOGICAL\_PROCESS\_Cell\_surface\_receptor\_mediated\_signal\_transduction | 2.57E-97 | 0.029 |
| GO:0009897\_external\_side\_of\_plasma\_membrane | 1.35E-92 | 0.029 |
| PC\_G\_alpha\_(q)\_signalling\_events | 4.18E-66 | 0.029 |
| GO:0031404\_chloride\_ion\_binding | 2.84E-39 | 0.029 |
| GO:0060041\_retina\_development\_in\_camera-type\_eye | 2.94E-21 | 0.029 |
| PC\_CREB\_phosphorylation\_through\_the\_activation\_of\_Ras | 6.06E-21 | 0.029 |
| GO:0005086\_ARF\_guanyl-nucleotide\_exchange\_factor\_activity | 6.10E-19 | 0.029 |
| GO:0021544\_subpallium\_development | 2.54E-10 | 0.029 |
| GO:0016491\_oxidoreductase\_activity | 2.04E-303 | 0.03 |
| PC\_Axon\_guidance | 9.61E-120 | 0.03 |
| GO:0019900\_kinase\_binding | 5.77E-108 | 0.03 |
| GO:0051480\_cytosolic\_calcium\_ion\_homeostasis | 7.87E-78 | 0.03 |
| GO:0002521\_leukocyte\_differentiation | 1.02E-74 | 0.03 |
| GO:0030098\_lymphocyte\_differentiation | 1.04E-62 | 0.03 |
| GO:0051048\_negative\_regulation\_of\_secretion | 1.82E-44 | 0.03 |
| GO:0004879\_ligand-dependent\_nuclear\_receptor\_activity | 7.80E-39 | 0.03 |
| PID\_NETRIN\_PATHWAY | 9.03E-30 | 0.03 |
| PC\_Activation\_of\_NMDA\_receptor\_upon\_glutamate\_binding\_and\_postsynaptic\_events | 2.89E-24 | 0.03 |
| GO:0031984\_organelle\_subcompartment | 1.61E-23 | 0.03 |
| GO:0051289\_protein\_homotetramerization | 6.42E-21 | 0.03 |
| REACTOME\_IONOTROPIC\_ACTIVITY\_OF\_KAINATE\_RECEPTORS | 7.42E-14 | 0.03 |
| GO:0035004\_phosphoinositide\_3-kinase\_activity | 3.38E-10 | 0.03 |
| GO:0030141\_secretory\_granule | 3.84E-106 | 0.031 |
| REACTOME\_NCAM\_SIGNALING\_FOR\_NEURITE\_OUT\_GROWTH | 2.22E-48 | 0.031 |
| GO:0045580\_regulation\_of\_T\_cell\_differentiation | 4.46E-34 | 0.031 |
| PID\_GLYPICAN\_1PATHWAY | 1.70E-25 | 0.031 |
| BIOCARTA\_SPPA\_PATHWAY | 5.51E-25 | 0.031 |
| GO:0050921\_positive\_regulation\_of\_chemotaxis | 1.06E-24 | 0.031 |
| GO:0043500\_muscle\_adaptation | 1.50E-17 | 0.031 |
| PANTHER\_BIOLOGICAL\_PROCESS\_Intracellular\_signaling\_cascade | 2.60E-141 | 0.032 |
| GO:0001932\_regulation\_of\_protein\_amino\_acid\_phosphorylation | 7.13E-110 | 0.032 |
| GO:0004721\_phosphoprotein\_phosphatase\_activity | 7.24E-91 | 0.032 |
| GO:0016311\_dephosphorylation | 3.19E-88 | 0.032 |
| GO:0032101\_regulation\_of\_response\_to\_external\_stimulus | 9.38E-85 | 0.032 |
| PC\_Formyl\_peptide\_receptors\_bind\_formyl\_peptides\_and\_many\_other\_ligands | 2.08E-74 | 0.032 |
| GO:0008277\_regulation\_of\_G-protein\_coupled\_receptor\_protein\_signaling\_pathway | 5.00E-34 | 0.032 |
| GO:0048863\_stem\_cell\_differentiation | 1.93E-22 | 0.032 |
| GO:0045995\_regulation\_of\_embryonic\_development | 1.60E-16 | 0.032 |
| GO:0050926\_regulation\_of\_positive\_chemotaxis | 5.26E-14 | 0.032 |
| GO:0012502\_induction\_of\_programmed\_cell\_death | 1.63E-177 | 0.033 |
| PC\_Hemostasis | 1.52E-176 | 0.033 |
| PANTHER\_MOLECULAR\_FUNCTION\_Metalloprotease | 2.55E-94 | 0.033 |
| GO:0030814\_regulation\_of\_cAMP\_metabolic\_process | 4.09E-79 | 0.033 |
| GO:0043176\_amine\_binding | 6.83E-72 | 0.033 |
| REACTOME\_TRANSPORT\_OF\_INORGANIC\_CATIONS\_ANIONS\_AND\_AMINO\_ACIDS\_OLIGOPEPTIDES | 3.43E-68 | 0.033 |
| GO:0050920\_regulation\_of\_chemotaxis | 4.91E-27 | 0.033 |
| GO:0019898\_extrinsic\_to\_membrane | 1.96E-276 | 0.034 |
| GO:0006917\_induction\_of\_apoptosis | 5.72E-176 | 0.034 |
| GO:0016791\_phosphatase\_activity | 9.15E-131 | 0.034 |
| GO:0008194\_UDP-glycosyltransferase\_activity | 1.59E-72 | 0.034 |
| PID\_HDAC\_CLASSII\_PATHWAY | 5.64E-25 | 0.034 |
| GO:0022839\_ion\_gated\_channel\_activity | 4.48E-20 | 0.034 |
| GO:0001990\_regulation\_of\_systemic\_arterial\_blood\_pressure\_by\_hormone | 3.80E-15 | 0.034 |
| GO:0016303\_1-phosphatidylinositol-3-kinase\_activity | 3.38E-10 | 0.034 |
| PC\_Signaling\_in\_Immune\_system | 2.43E-217 | 0.035 |
| PC\_Chemokine\_receptors\_bind\_chemokines | 2.23E-83 | 0.035 |
| GO:0001503\_ossification | 2.67E-67 | 0.035 |
| GO:0005253\_anion\_channel\_activity | 2.71E-43 | 0.035 |
| GO:0034329\_cell\_junction\_assembly | 1.29E-41 | 0.035 |
| GO:0016486\_peptide\_hormone\_processing | 1.56E-18 | 0.035 |
| GO:0050664\_oxidoreductase\_activity\_\_acting\_on\_NADH\_or\_NADPH\_\_with\_oxygen\_as\_acceptor | 4.58E-10 | 0.035 |
| GO:0045730\_respiratory\_burst | 4.14E-09 | 0.035 |
| GO:0006461\_protein\_complex\_assembly | 2.76E-227 | 0.036 |
| GO:0031252\_cell\_leading\_edge | 3.87E-96 | 0.036 |
| GO:0030802\_regulation\_of\_cyclic\_nucleotide\_biosynthetic\_process | 1.69E-80 | 0.036 |
| PC\_Activation\_of\_C3\_and\_C5 | 1.00E-77 | 0.036 |
| GO:0035113\_embryonic\_appendage\_morphogenesis | 1.50E-53 | 0.036 |
| PC\_RNA\_Polymerase\_III\_Transcription\_Termination | 1.62E-17 | 0.036 |
| PC\_Complement\_cascade | 2.39E-83 | 0.037 |
| GO:0046700\_heterocycle\_catabolic\_process | 1.02E-60 | 0.037 |
| PANTHER\_MOLECULAR\_FUNCTION\_Tyrosine\_protein\_kinase\_receptor | 2.92E-59 | 0.037 |
| PANTHER\_MOLECULAR\_FUNCTION\_Nucleotide\_kinase | 8.33E-30 | 0.037 |
| REACTOME\_AMINE\_COMPOUND\_SLC\_TRANSPORTERS | 2.55E-24 | 0.037 |
| PID\_EPHA2\_FWDPATHWAY | 7.21E-14 | 0.037 |
| GO:0070887\_cellular\_response\_to\_chemical\_stimulus | 8.42E-155 | 0.038 |
| GO:0007187\_G-protein\_signaling\_\_coupled\_to\_cyclic\_nucleotide\_second\_messenger | 6.31E-75 | 0.038 |
| PANTHER\_MOLECULAR\_FUNCTION\_Cell\_adhesion\_molecule | 1.18E-66 | 0.038 |
| GO:0030414\_peptidase\_inhibitor\_activity | 1.34E-65 | 0.038 |
| GO:0030594\_neurotransmitter\_receptor\_activity | 1.18E-49 | 0.038 |
| GO:0030166\_proteoglycan\_biosynthetic\_process | 1.78E-25 | 0.038 |
| GO:0009798\_axis\_specification | 4.65E-21 | 0.038 |
| GO:0046658\_anchored\_to\_plasma\_membrane | 1.19E-19 | 0.038 |
| GO:0035176\_social\_behavior | 1.25E-13 | 0.038 |
| GO:0045686\_negative\_regulation\_of\_glial\_cell\_differentiation | 4.06E-10 | 0.038 |
| GO:0005539\_glycosaminoglycan\_binding | 1.18E-96 | 0.039 |
| GO:0030326\_embryonic\_limb\_morphogenesis | 1.50E-53 | 0.039 |
| GO:0016209\_antioxidant\_activity | 1.17E-28 | 0.039 |
| GO:0005080\_protein\_kinase\_C\_binding | 4.97E-21 | 0.039 |
| GO:0046631\_alpha-beta\_T\_cell\_activation | 2.92E-16 | 0.039 |
| GO:0001958\_endochondral\_ossification | 2.01E-11 | 0.039 |
| GO:0008593\_regulation\_of\_Notch\_signaling\_pathway | 3.59E-11 | 0.039 |
| GO:0019838\_growth\_factor\_binding | 2.43E-74 | 0.04 |
| PC\_Signaling\_events\_regulated\_by\_Ret\_tyrosine\_kinase | 1.87E-46 | 0.04 |
| GO:0016247\_channel\_regulator\_activity | 2.64E-41 | 0.04 |
| GO:0019902\_phosphatase\_binding | 5.30E-41 | 0.04 |
| REACTOME\_CA\_DEPENDENT\_EVENTS | 2.63E-27 | 0.04 |
| BIOCARTA\_NOS1\_PATHWAY | 4.80E-23 | 0.04 |
| GO:0030512\_negative\_regulation\_of\_transforming\_growth\_factor\_beta\_receptor\_signaling\_pathway | 4.88E-16 | 0.04 |
| GO:0051896\_regulation\_of\_protein\_kinase\_B\_signaling\_cascade | 8.45E-14 | 0.04 |
| GO:0050854\_regulation\_of\_antigen\_receptor-mediated\_signaling\_pathway | 1.49E-13 | 0.04 |
| GO:0009892\_negative\_regulation\_of\_metabolic\_process | 1.92685601878086e-322 | 0.041 |
| GO:0051240\_positive\_regulation\_of\_multicellular\_organismal\_process | 1.86E-133 | 0.041 |
| PC\_G\_alpha\_(i)\_signalling\_events | 1.25E-72 | 0.041 |
| GO:0005342\_organic\_acid\_transmembrane\_transporter\_activity | 2.64E-66 | 0.041 |
| GO:0030278\_regulation\_of\_ossification | 1.55E-57 | 0.041 |
| PID\_TRKRPATHWAY | 1.28E-50 | 0.041 |
| GO:0050769\_positive\_regulation\_of\_neurogenesis | 5.83E-47 | 0.041 |
| PANTHER\_BIOLOGICAL\_PROCESS\_Anion\_transport | 8.63E-41 | 0.041 |
| GO:0040014\_regulation\_of\_multicellular\_organism\_growth | 1.49E-37 | 0.041 |
| BIOCARTA\_NO1\_PATHWAY | 2.25E-34 | 0.041 |
| REACTOME\_NCAM1\_INTERACTIONS | 4.55E-29 | 0.041 |
| PC\_RXR\_and\_RAR\_heterodimerization\_with\_other\_nuclear\_receptor | 2.28E-19 | 0.041 |
| GO:0015850\_organic\_alcohol\_transport | 3.68E-17 | 0.041 |
| PC\_Adherens\_junctions\_interactions | 4.11E-14 | 0.041 |
| GO:0010605\_negative\_regulation\_of\_macromolecule\_metabolic\_process | 1.09E-306 | 0.042 |
| REACTOME\_GASTRIN\_CREB\_SIGNALLING\_PATHWAY\_VIA\_PKC\_AND\_MAPK | 1.84E-119 | 0.042 |
| GO:0051259\_protein\_oligomerization | 1.84E-100 | 0.042 |
| GO:0043168\_anion\_binding | 6.81E-49 | 0.042 |
| GO:0044447\_axoneme\_part | 6.80E-18 | 0.042 |
| GO:0001542\_ovulation\_from\_ovarian\_follicle | 1.97E-17 | 0.042 |
| GO:0050927\_positive\_regulation\_of\_positive\_chemotaxis | 5.26E-14 | 0.042 |
| GO:0043069\_negative\_regulation\_of\_programmed\_cell\_death | 1.18E-192 | 0.043 |
| GO:0030799\_regulation\_of\_cyclic\_nucleotide\_metabolic\_process | 3.97E-83 | 0.043 |
| PID\_IL2\_1PATHWAY | 4.43E-40 | 0.043 |
| GO:0050768\_negative\_regulation\_of\_neurogenesis | 5.56E-32 | 0.043 |
| GO:0043549\_regulation\_of\_kinase\_activity | 7.05E-191 | 0.044 |
| PC\_Initial\_triggering\_of\_complement | 2.39E-83 | 0.044 |
| GO:0007229\_integrin-mediated\_signaling\_pathway | 1.08E-47 | 0.044 |
| GO:0048701\_embryonic\_cranial\_skeleton\_morphogenesis | 3.94E-16 | 0.044 |
| PC\_Myogenesis | 9.55E-15 | 0.044 |
| GO:0043560\_insulin\_receptor\_substrate\_binding | 2.18E-11 | 0.044 |
| GO:0060548\_negative\_regulation\_of\_cell\_death | 1.18E-192 | 0.045 |
| GO:0045165\_cell\_fate\_commitment | 8.56E-81 | 0.045 |
| PANTHER\_BIOLOGICAL\_PROCESS\_T-cell\_mediated\_immunity | 5.15E-69 | 0.045 |
| GO:0051260\_protein\_homooligomerization | 8.94E-59 | 0.045 |
| GO:0033993\_response\_to\_lipid | 4.88E-22 | 0.045 |
| GO:0050886\_endocrine\_process | 1.29E-17 | 0.045 |
| GO:0031294\_lymphocyte\_costimulation | 3.12E-12 | 0.045 |
| GO:0055066\_di-\_\_tri-valent\_inorganic\_cation\_homeostasis | 1.87E-137 | 0.046 |
| PANTHER\_BIOLOGICAL\_PROCESS\_Vision | 2.57E-100 | 0.046 |
| GO:0048511\_rhythmic\_process | 2.78E-89 | 0.046 |
| PC\_Alternative\_complement\_activation | 1.38E-78 | 0.046 |
| PC\_Adenosine\_P1\_receptors | 3.24E-77 | 0.046 |
| GO:0046943\_carboxylic\_acid\_transmembrane\_transporter\_activity | 2.64E-66 | 0.046 |
| GO:0005275\_amine\_transmembrane\_transporter\_activity | 2.64E-57 | 0.046 |
| GO:0030879\_mammary\_gland\_development | 2.76E-42 | 0.046 |
| PC\_Post\_NMDA\_receptor\_activation\_events | 2.89E-24 | 0.046 |
| GO:0045884\_regulation\_of\_survival\_gene\_product\_expression | 3.81E-17 | 0.046 |
| GO:0004407\_histone\_deacetylase\_activity | 9.23E-16 | 0.046 |
| GO:0045921\_positive\_regulation\_of\_exocytosis | 1.49E-12 | 0.046 |
| GO:0006163\_purine\_nucleotide\_metabolic\_process | 9.97E-111 | 0.047 |
| GO:0006690\_icosanoid\_metabolic\_process | 2.51E-36 | 0.047 |
| PC\_Signaling\_events\_mediated\_by\_HDAC\_Class\_II | 1.77E-25 | 0.047 |
| GO:0031985\_Golgi\_cisterna | 5.99E-22 | 0.047 |
| GO:0042058\_regulation\_of\_epidermal\_growth\_factor\_receptor\_signaling\_pathway | 1.22E-20 | 0.047 |
| GO:0033077\_T\_cell\_differentiation\_in\_the\_thymus | 1.92E-19 | 0.047 |
| GO:0030295\_protein\_kinase\_activator\_activity | 6.63E-16 | 0.047 |
| GO:0006949\_syncytium\_formation | 7.87E-16 | 0.047 |
| PC\_Classical\_antibody-mediated\_complement\_activation | 7.49E-79 | 0.048 |
| REACTOME\_INTEGRIN\_CELL\_SURFACE\_INTERACTIONS | 1.95E-56 | 0.048 |
| GO:0019229\_regulation\_of\_vasoconstriction | 1.02E-37 | 0.048 |
| REACTOME\_GABA\_B\_RECEPTOR\_ACTIVATION | 6.03E-32 | 0.048 |
| GO:0043197\_dendritic\_spine | 1.20E-27 | 0.048 |
| GO:0008375\_acetylglucosaminyltransferase\_activity | 2.71E-26 | 0.048 |
| PANTHER\_BIOLOGICAL\_PROCESS\_Antioxidation\_and\_free\_radical\_removal | 2.05E-20 | 0.048 |
| PANTHER\_BIOLOGICAL\_PROCESS\_Sulfur\_redox\_metabolism | 1.86E-19 | 0.048 |
| REACTOME\_DOWNSTREAM\_TCR\_SIGNALING | 3.68E-18 | 0.048 |
| GO:0021766\_hippocampus\_development | 4.92E-17 | 0.048 |
| GO:0007520\_myoblast\_fusion | 8.90E-15 | 0.048 |
| PC\_CDO\_in\_myogenesis | 9.55E-15 | 0.048 |
| GO:0004016\_adenylate\_cyclase\_activity | 1.23E-14 | 0.048 |
| GO:0015035\_protein\_disulfide\_oxidoreductase\_activity | 2.14E-12 | 0.048 |
| GO:0030291\_protein\_serine/threonine\_kinase\_inhibitor\_activity | 2.81E-12 | 0.048 |
| GO:0043235\_receptor\_complex | 8.79E-85 | 0.049 |
| GO:0051924\_regulation\_of\_calcium\_ion\_transport | 9.16E-46 | 0.049 |
| REACTOME\_G\_ALPHA\_Z\_SIGNALLING\_EVENTS | 3.06E-39 | 0.049 |
| GO:0006941\_striated\_muscle\_contraction | 7.91E-30 | 0.049 |
| PC\_Amino\_acid\_transport\_across\_the\_plasma\_membrane | 3.87E-25 | 0.049 |
| GO:0046888\_negative\_regulation\_of\_hormone\_secretion | 8.24E-22 | 0.049 |
| GO:0010811\_positive\_regulation\_of\_cell-substrate\_adhesion | 2.43E-17 | 0.049 |
| GO:0045076\_regulation\_of\_interleukin-2\_biosynthetic\_process | 1.54E-13 | 0.049 |
| GO:0002792\_negative\_regulation\_of\_peptide\_secretion | 1.88E-13 | 0.049 |
| BIOCARTA\_LECTIN\_PATHWAY | 3.28E-11 | 0.049 |
| GO:0005095\_GTPase\_inhibitor\_activity | 4.52E-11 | 0.049 |