

| GOTERM category    | Term                                                                  | PValue   | Fold Enrichment | Bonferroni | Benjamini | FDR      |
|--------------------|-----------------------------------------------------------------------|----------|-----------------|------------|-----------|----------|
| Biological process | GO:0007155~cell adhesion                                              | 5,07E-16 | 2,15            | 1,85E-12   | 1,85E-12  | 1,01E-12 |
|                    | GO:0022610~biological adhesion                                        | 5,49E-16 | 2,15            | 1,85E-12   | 9,25E-13  | 1,01E-12 |
|                    | GO:0030029~actin filament-based process                               | 8,59E-12 | 2,89            | 2,87E-08   | 9,55E-09  | 1,57E-08 |
|                    | GO:0030030~cell projection organization                               | 9,76E-12 | 2,32            | 3,25E-08   | 8,14E-09  | 1,78E-08 |
|                    | GO:0016337~cell-cell adhesion                                         | 2,95E-11 | 2,54            | 9,83E-08   | 1,97E-08  | 5,37E-08 |
|                    | GO:0007010~cytoskeleton organization                                  | 7,74E-11 | 2,24            | 2,58E-07   | 4,30E-08  | 1,41E-07 |
|                    | GO:0030036~actin cytoskeleton organization                            | 1,29E-10 | 2,83            | 4,31E-07   | 6,16E-08  | 2,36E-07 |
|                    | GO:0043062~extracellular structure organization                       | 1,73E-10 | 2,93            | 5,76E-07   | 7,20E-08  | 3,15E-07 |
|                    | GO:0000902~cell morphogenesis                                         | 3,26E-10 | 2,23            | 1,09E-06   | 1,21E-07  | 5,94E-07 |
|                    | GO:0032989~cellular component morphogenesis                           | 9,69E-10 | 2,11            | 3,23E-06   | 3,23E-07  | 1,77E-06 |
|                    | GO:0030163~protein catabolic process                                  | 1,27E-09 | 1,84            | 4,24E-06   | 3,86E-07  | 2,32E-06 |
|                    | GO:0016477~cell migration                                             | 4,40E-09 | 2,33            | 1,47E-05   | 1,22E-06  | 8,02E-06 |
|                    | GO:0033043~regulation of organelle organization                       | 6,42E-09 | 2,70            | 2,14E-05   | 1,65E-06  | 1,17E-05 |
|                    | GO:0006928~cell motion                                                | 7,23E-09 | 2,02            | 2,41E-05   | 1,72E-06  | 1,32E-05 |
|                    | GO:0044257~cellular protein catabolic process                         | 7,89E-09 | 1,82            | 2,63E-05   | 1,75E-06  | 1,44E-05 |
|                    | GO:0051493~regulation of cytoskeleton organization                    | 1,11E-08 | 3,18            | 3,70E-05   | 2,31E-06  | 2,02E-05 |
|                    | GO:0007156~homophilic cell adhesion                                   | 1,52E-08 | 2,95            | 5,06E-05   | 2,98E-06  | 1,18E-05 |
|                    | GO:0009057~macromolecule catabolic process                            | 1,82E-08 | 1,71            | 6,08E-05   | 3,38E-06  | 3,32E-05 |
|                    | GO:0044265~cellular macromolecule catabolic process                   | 2,12E-08 | 1,73            | 7,08E-05   | 3,73E-06  | 3,87E-05 |
|                    | GO:0051603~proteolysis involved in cellular protein catabolic process | 2,53E-08 | 1,79            | 8,43E-05   | 4,21E-06  | 4,61E-05 |
|                    | GO:0031175~neuron projection development                              | 6,48E-08 | 2,28            | 2,16E-04   | 1,03E-05  | 1,18E-04 |
|                    | GO:0051056~regulation of small GTPase mediated signal transduction    | 1,05E-07 | 2,23            | 3,51E-04   | 1,60E-05  | 1,92E-04 |
|                    | GO:0019941~modification-dependent protein catabolic process           | 1,57E-07 | 1,76            | 5,22E-04   | 2,27E-05  | 2,86E-04 |
|                    | GO:0043632~modification-dependent macromolecule catabolic process     | 1,57E-07 | 1,76            | 5,22E-04   | 2,27E-05  | 2,86E-04 |
|                    | GO:0048858~cell projection morphogenesis                              | 3,14E-07 | 2,26            | 1,05E-03   | 4,36E-05  | 5,71E-04 |
|                    | GO:0048666~neuron development                                         | 3,20E-07 | 2,02            | 1,07E-03   | 4,27E-05  | 5,83E-04 |
|                    | GO:0019226~transmission of nerve impulse                              | 5,27E-07 | 2,16            | 1,76E-03   | 6,76E-05  | 9,61E-04 |
|                    | GO:0051129~negative regulation of cellular component organization     | 6,08E-07 | 2,95            | 2,02E-03   | 7,50E-05  | 1,11E-03 |
|                    | GO:0044087~regulation of cellular component biogenesis                | 9,03E-07 | 2,97            | 3,01E-03   | 1,08E-04  | 1,65E-03 |
|                    | GO:0007268~synaptic transmission                                      | 1,24E-06 | 2,28            | 4,14E-03   | 1,43E-04  | 2,27E-03 |
|                    | GO:0032990~cell part morphogenesis                                    | 1,28E-06 | 2,16            | 4,25E-03   | 1,42E-04  | 2,33E-03 |
|                    | GO:0048870~cell motility                                              | 1,53E-06 | 1,97            | 5,07E-03   | 1,64E-04  | 2,78E-03 |
|                    | GO:0051674~localization of cell                                       | 1,53E-06 | 1,97            | 5,07E-03   | 1,64E-04  | 2,78E-03 |
|                    | GO:0035023~regulation of Rho protein signal transduction              | 1,69E-06 | 2,95            | 5,62E-03   | 1,76E-04  | 3,08E-03 |
|                    | GO:0043242~negative regulation of protein complex disassembly         | 2,37E-06 | 4,35            | 7,86E-03   | 2,39E-04  | 4,31E-03 |
|                    | GO:0032956~regulation of actin cytoskeleton organization              | 2,58E-06 | 3,39            | 8,55E-03   | 2,53E-04  | 4,69E-03 |
|                    | GO:0007267~cell-cell signaling                                        | 2,95E-06 | 1,93            | 9,80E-03   | 2,81E-04  | 5,38E-03 |
|                    | GO:0000904~cell morphogenesis involved in differentiation             | 3,17E-06 | 2,11            | 1,05E-02   | 2,93E-04  | 5,77E-03 |
|                    | GO:0016192~vesicle-mediated transport                                 | 3,33E-06 | 1,70            | 1,11E-02   | 3,00E-04  | 6,07E-03 |
|                    | GO:0032970~regulation of actin filament-based process                 | 3,40E-06 | 3,33            | 1,13E-02   | 2,98E-04  | 6,19E-03 |
|                    | GO:0007015~actin filament organization                                | 3,71E-06 | 3,45            | 1,23E-02   | 3,17E-04  | 6,75E-03 |
|                    | GO:0048812~neuron projection morphogenesis                            | 6,42E-06 | 2,19            | 2,12E-02   | 5,35E-04  | 1,17E-02 |
|                    | GO:0030705~cytoskeleton-dependent intracellular transport             | 6,66E-06 | 4,31            | 2,20E-02   | 5,41E-04  | 1,21E-02 |
|                    | GO:0007409~axonogenesis                                               | 6,93E-06 | 2,24            | 2,29E-02   | 5,50E-04  | 1,26E-02 |
|                    | GO:0051494~negative regulation of cytoskeleton organization           | 7,54E-06 | 3,60            | 2,48E-02   | 5,84E-04  | 1,37E-02 |
|                    | GO:0043254~regulation of protein complex assembly                     | 9,62E-06 | 3,12            | 3,15E-02   | 7,28E-04  | 1,75E-02 |
|                    | GO:0050808~synapse organization                                       | 1,02E-05 | 3,52            | 3,34E-02   | 7,54E-04  | 1,85E-02 |
|                    | GO:0039198~extracellular matrix organization                          | 1,09E-05 | 2,61            | 3,56E-02   | 7,88E-04  | 1,98E-02 |
|                    | GO:0032535~regulation of cellular component size                      | 1,36E-05 | 2,21            | 4,43E-02   | 9,63E-04  | 2,47E-02 |
|                    | GO:0007610~behavior                                                   | 1,38E-05 | 1,71            | 4,50E-02   | 9,59E-04  | 2,51E-02 |
|                    | GO:0048667~cell morphogenesis involved in neuron differentiation      | 1,43E-05 | 2,12            | 4,66E-02   | 9,73E-04  | 2,60E-02 |
|                    | GO:0007626~locomotory behavior                                        | 1,45E-05 | 1,95            | 4,71E-02   | 9,65E-04  | 2,64E-02 |
|                    | GO:003182~neuron differentiation                                      | 1,61E-05 | 1,71            | 5,21E-02   | 1,05E-03  | 2,92E-02 |
|                    | GO:0042592~homeostatic process                                        | 1,70E-05 | 1,57            | 5,51E-02   | 1,09E-03  | 3,10E-02 |
|                    | GO:0030832~regulation of actin filament length                        | 1,80E-05 | 3,39            | 5,84E-02   | 1,13E-03  | 3,29E-02 |
|                    | GO:0016044~membrane organization                                      | 2,11E-05 | 1,87            | 6,79E-02   | 1,30E-03  | 3,84E-02 |
|                    | GO:0046578~regulation of Ras protein signal transduction              | 3,05E-05 | 2,08            | 9,67E-02   | 1,85E-03  | 5,55E-02 |
|                    | GO:0007017~microtubule-based process                                  | 3,62E-05 | 1,97            | 1,14E-01   | 2,15E-03  | 6,59E-02 |
|                    | GO:0006511~ubiquitin-dependent protein catabolic process              | 3,69E-05 | 2,23            | 1,16E-01   | 2,16E-03  | 6,72E-02 |
|                    | GO:0043244~regulation of protein complex disassembly                  | 3,76E-05 | 3,54            | 1,18E-01   | 2,16E-03  | 6,85E-02 |
|                    | GO:0048878~chemical homeostasis                                       | 4,65E-05 | 1,70            | 1,44E-01   | 2,62E-03  | 8,46E-02 |
|                    | GO:0008064~regulation of actin polymerization or depolymerization     | 5,89E-05 | 3,25            | 1,78E-01   | 3,27E-03  | 1,07E-01 |
|                    | GO:0030833~regulation of actin filament polymerization                | 6,64E-05 | 3,39            | 1,99E-01   | 3,62E-03  | 1,21E-01 |
|                    | GO:0010639~negative regulation of organelle organization              | 6,91E-05 | 2,95            | 2,06E-01   | 3,71E-03  | 1,26E-01 |
|                    | GO:0006897~endocytosis                                                | 7,02E-05 | 2,00            | 2,09E-01   | 3,71E-03  | 1,28E-01 |
|                    | GO:0010324~membrane invagination                                      | 7,02E-05 | 2,00            | 2,09E-01   | 3,71E-03  | 1,28E-01 |
|                    | GO:0008283~cell proliferation                                         | 7,18E-05 | 1,85            | 2,13E-01   | 3,73E-03  | 1,31E-01 |
|                    | GO:0032271~regulation of protein polymerization                       | 8,25E-05 | 3,03            | 2,40E-01   | 4,22E-03  | 1,50E-01 |
|                    | GO:0044271~nitrogen compound biosynthetic process                     | 8,42E-05 | 1,75            | 2,45E-01   | 4,25E-03  | 1,53E-01 |
|                    | GO:0006508~proteolysis                                                | 9,37E-05 | 1,37            | 2,68E-01   | 4,65E-03  | 1,71E-01 |
|                    | GO:0055080~cation homeostasis                                         | 1,01E-04 | 1,99            | 2,86E-01   | 4,95E-03  | 1,84E-01 |
|                    | GO:0030031~cell projection assembly                                   | 1,07E-04 | 2,76            | 2,99E-01   | 5,14E-03  | 1,94E-01 |
|                    | GO:0000910~cytokinesis                                                | 1,45E-04 | 4,14            | 3,83E-01   | 6,87E-03  | 2,63E-01 |
|                    | GO:0050801~ion homeostasis                                            | 1,47E-04 | 1,73            | 3,87E-01   | 6,88E-03  | 2,67E-01 |
|                    | GO:0007411~axon guidance                                              | 1,72E-04 | 2,38            | 4,37E-01   | 7,94E-03  | 3,13E-01 |
|                    | GO:0019725~cellular homeostasis                                       | 1,85E-04 | 1,66            | 4,60E-01   | 8,40E-03  | 3,36E-01 |
|                    | GO:0030155~regulation of cell adhesion                                | 2,57E-04 | 2,38            | 5,76E-01   | 1,15E-02  | 4,68E-01 |
|                    | GO:0060249~anatomical structure homeostasis                           | 3,58E-04 | 2,45            | 6,97E-01   | 1,58E-02  | 6,51E-01 |

|                    |                                                                         |          |      |          |          |          |
|--------------------|-------------------------------------------------------------------------|----------|------|----------|----------|----------|
|                    | GO:0022604~regulation of cell morphogenesis                             | 4,05E-04 | 2,30 | 7,41E-01 | 1,76E-02 | 7,36E-01 |
|                    | GO:0007507~heart development                                            | 5,39E-04 | 1,78 | 8,34E-01 | 2,31E-02 | 9,77E-01 |
|                    | GO:0030835~negative regulation of actin filament depolymerization       | 5,42E-04 | 4,35 | 8,36E-01 | 2,29E-02 | 9,83E-01 |
|                    | GO:0032940~secretion by cell                                            | 5,91E-04 | 1,86 | 8,60E-01 | 2,46E-02 | 1,07E+00 |
|                    | GO:0008104~protein localization                                         | 6,76E-04 | 1,38 | 8,95E-01 | 2,78E-02 | 1,22E+00 |
|                    | GO:0010769~regulation of cell morphogenesis involved in differentiation | 8,42E-04 | 2,84 | 9,40E-01 | 3,41E-02 | 1,52E+00 |
|                    | GO:0055082~cellular chemical homeostasis                                | 8,82E-04 | 1,67 | 9,47E-01 | 3,53E-02 | 1,60E+00 |
|                    | GO:0006793~phosphorus metabolic process                                 | 9,49E-04 | 1,34 | 9,58E-01 | 3,74E-02 | 1,72E+00 |
|                    | GO:0006796~phosphate metabolic process                                  | 9,49E-04 | 1,34 | 9,58E-01 | 3,74E-02 | 1,72E+00 |
|                    | GO:0031344~regulation of cell projection organization                   | 9,95E-04 | 2,67 | 9,64E-01 | 3,88E-02 | 1,80E+00 |
|                    | GO:0001764~neuron migration                                             | 1,04E-03 | 2,47 | 9,69E-01 | 3,99E-02 | 1,87E+00 |
|                    | GO:0000226~microtubule cytoskeleton organization                        | 1,06E-03 | 2,10 | 9,71E-01 | 4,03E-02 | 1,92E+00 |
|                    | GO:0044057~regulation of system process                                 | 1,17E-03 | 1,77 | 9,80E-01 | 4,40E-02 | 2,12E+00 |
|                    | GO:0010810~regulation of cell-substrate adhesion                        | 1,26E-03 | 3,05 | 9,85E-01 | 4,68E-02 | 2,28E+00 |
|                    | GO:0032319~regulation of Rho GTPase activity                            | 1,34E-03 | 5,08 | 9,89E-01 | 4,91E-02 | 2,42E+00 |
| Cellular component | GO:0042995~cell projection                                              | 3,26E-27 | 2,55 | 1,59E-24 | 1,59E-24 | 4,67E-24 |
|                    | GO:0043005~neuron projection                                            | 3,70E-24 | 3,41 | 1,80E-21 | 9,01E-22 | 5,31E-21 |
|                    | GO:0005856~cytoskeleton                                                 | 4,44E-21 | 1,89 | 2,16E-18 | 7,21E-19 | 6,37E-18 |
|                    | GO:0030424~axon                                                         | 1,53E-14 | 3,90 | 7,46E-12 | 1,87E-12 | 2,20E-11 |
|                    | GO:0015629~actin cytoskeleton                                           | 6,76E-12 | 2,73 | 3,29E-09 | 6,58E-10 | 9,70E-09 |
|                    | GO:0043232~intracellular non-membrane-bounded organelle                 | 2,52E-11 | 1,44 | 1,23E-08 | 2,05E-09 | 3,62E-08 |
|                    | GO:0043228~non-membrane-bounded organelle                               | 2,52E-11 | 1,44 | 1,23E-08 | 2,05E-09 | 3,62E-08 |
|                    | GO:0045202~synapse                                                      | 5,95E-11 | 2,27 | 2,90E-08 | 4,14E-09 | 8,54E-08 |
|                    | GO:0044430~cytoskeletal part                                            | 7,23E-11 | 1,75 | 3,52E-08 | 4,40E-09 | 1,04E-07 |
|                    | GO:0030425~dendrite                                                     | 1,34E-10 | 3,34 | 6,53E-08 | 7,26E-09 | 1,92E-07 |
|                    | GO:0031252~cell leading edge                                            | 2,35E-10 | 3,28 | 1,14E-07 | 1,14E-08 | 3,37E-07 |
|                    | GO:0030054~cell junction                                                | 2,61E-10 | 1,97 | 1,27E-07 | 1,16E-08 | 3,75E-07 |
|                    | GO:0044420~extracellular matrix part                                    | 3,03E-10 | 3,54 | 1,48E-07 | 1,23E-08 | 4,35E-07 |
|                    | GO:0000267~cell fraction                                                | 1,19E-09 | 1,81 | 5,80E-07 | 4,46E-08 | 1,71E-06 |
|                    | GO:0005604~basement membrane                                            | 1,09E-08 | 3,63 | 5,29E-06 | 3,78E-07 | 1,56E-05 |
|                    | GO:0005626~insoluble fraction                                           | 1,13E-08 | 1,81 | 5,48E-06 | 3,66E-07 | 1,62E-05 |
|                    | GO:0005624~membrane fraction                                            | 1,80E-08 | 1,82 | 8,75E-06 | 5,47E-07 | 2,58E-05 |
|                    | GO:0044459~plasma membrane part                                         | 1,89E-08 | 1,41 | 9,20E-06 | 5,41E-07 | 2,71E-05 |
|                    | GO:0031012~extracellular matrix                                         | 6,89E-08 | 2,04 | 3,36E-05 | 1,86E-06 | 9,88E-05 |
|                    | GO:0030427~site of polarized growth                                     | 1,36E-07 | 4,00 | 6,62E-05 | 3,48E-06 | 1,95E-04 |
|                    | GO:0030426~growth cone                                                  | 1,36E-07 | 4,00 | 6,62E-05 | 3,48E-06 | 1,95E-04 |
|                    | GO:0005886~plasma membrane                                              | 1,56E-07 | 1,26 | 7,61E-05 | 3,80E-06 | 2,24E-04 |
|                    | GO:0005578~proteinaceous extracellular matrix                           | 2,14E-07 | 2,02 | 1,04E-04 | 4,96E-06 | 3,07E-04 |
|                    | GO:0030027~lamellipodium                                                | 2,73E-07 | 3,56 | 1,33E-04 | 6,05E-06 | 3,92E-04 |
|                    | GO:0015630~microtubule cytoskeleton                                     | 7,06E-07 | 1,77 | 3,44E-04 | 1,49E-05 | 1,01E-03 |
|                    | GO:0005912~adherens junction                                            | 7,47E-07 | 2,79 | 3,63E-04 | 1,51E-05 | 1,07E-03 |
|                    | GO:0070161~anchoring junction                                           | 1,90E-06 | 2,57 | 9,23E-04 | 3,69E-05 | 2,72E-03 |
|                    | GO:0043025~cell soma                                                    | 1,97E-06 | 2,61 | 9,61E-04 | 3,70E-05 | 2,83E-03 |
|                    | GO:0044456~synapse part                                                 | 6,87E-06 | 2,07 | 3,34E-03 | 1,24E-04 | 9,85E-03 |
|                    | GO:0030863~cortical cytoskeleton                                        | 7,33E-06 | 3,79 | 3,57E-03 | 1,28E-04 | 1,05E-02 |
|                    | GO:0005938~cell cortex                                                  | 9,54E-06 | 2,43 | 4,63E-03 | 1,60E-04 | 1,37E-02 |
|                    | GO:0005913~cell-cell adherens junction                                  | 1,80E-05 | 4,27 | 8,71E-03 | 2,91E-04 | 2,58E-02 |
|                    | GO:0005829~cytosol                                                      | 2,11E-05 | 1,58 | 1,02E-02 | 3,32E-04 | 3,03E-02 |
|                    | GO:0005581~collagen                                                     | 3,02E-05 | 5,36 | 1,46E-02 | 4,60E-04 | 4,34E-02 |
|                    | GO:0016323~basolateral plasma membrane                                  | 3,42E-05 | 2,24 | 1,65E-02 | 5,04E-04 | 4,90E-02 |
|                    | GO:0031410~cytoplasmic vesicle                                          | 3,68E-05 | 1,58 | 1,78E-02 | 5,27E-04 | 5,28E-02 |
|                    | GO:0044448~cell cortex part                                             | 5,48E-05 | 2,79 | 2,64E-02 | 7,63E-04 | 7,87E-02 |
|                    | GO:0014069~postsynaptic density                                         | 7,27E-05 | 3,20 | 3,48E-02 | 9,83E-04 | 1,04E-01 |
|                    | GO:0031982~vesicle                                                      | 7,70E-05 | 1,55 | 3,68E-02 | 1,01E-03 | 1,10E-01 |
|                    | GO:0016023~cytoplasmic membrane-bounded vesicle                         | 8,38E-05 | 1,62 | 4,00E-02 | 1,07E-03 | 1,20E-01 |
|                    | GO:0031988~membrane-bounded vesicle                                     | 1,28E-04 | 1,60 | 6,06E-02 | 1,60E-03 | 1,84E-01 |
|                    | GO:0005911~cell-cell junction                                           | 1,38E-04 | 2,00 | 6,52E-02 | 1,68E-03 | 1,98E-01 |
|                    | GO:0000151~ubiquitin ligase complex                                     | 1,53E-04 | 2,89 | 7,20E-02 | 1,82E-03 | 2,20E-01 |
|                    | GO:0048770~pigment granule                                              | 1,62E-04 | 2,52 | 7,58E-02 | 1,88E-03 | 2,32E-01 |
|                    | GO:0042470~melanosome                                                   | 1,62E-04 | 2,52 | 7,58E-02 | 1,88E-03 | 2,32E-01 |
|                    | GO:0016459~myosin complex                                               | 1,89E-04 | 2,84 | 8,81E-02 | 2,14E-03 | 2,71E-01 |
|                    | GO:0044463~cell projection part                                         | 2,24E-04 | 1,98 | 1,03E-01 | 2,47E-03 | 3,20E-01 |
|                    | GO:0033267~axon part                                                    | 3,88E-04 | 4,08 | 1,72E-01 | 4,19E-03 | 5,56E-01 |
|                    | GO:0060053~neurofilament cytoskeleton                                   | 3,91E-04 | 7,64 | 1,73E-01 | 4,13E-03 | 5,59E-01 |
|                    | GO:0001726~ruffle                                                       | 4,25E-04 | 3,04 | 1,87E-01 | 4,40E-03 | 6,09E-01 |
|                    | GO:0030055~cell-substrate junction                                      | 4,99E-04 | 2,62 | 2,16E-01 | 5,06E-03 | 7,14E-01 |
|                    | GO:0019717~synaptosome                                                  | 4,99E-04 | 2,62 | 2,16E-01 | 5,06E-03 | 7,14E-01 |
|                    | GO:0048471~perinuclear region of cytoplasm                              | 7,36E-04 | 1,83 | 3,01E-01 | 7,29E-03 | 1,05E+00 |
|                    | GO:0030864~cortical actin cytoskeleton                                  | 7,60E-04 | 4,17 | 3,09E-01 | 7,38E-03 | 1,08E+00 |
|                    | GO:0000502~proteasome complex                                           | 1,15E-03 | 2,64 | 4,30E-01 | 1,09E-02 | 1,64E+00 |
|                    | GO:0044449~contractile fiber part                                       | 1,48E-03 | 2,25 | 5,13E-01 | 1,37E-02 | 2,10E+00 |
|                    | GO:0005783~endoplasmic reticulum                                        | 1,61E-03 | 1,33 | 5,43E-01 | 1,47E-02 | 2,28E+00 |
|                    | GO:0005819~spindle                                                      | 1,88E-03 | 2,06 | 6,01E-01 | 1,69E-02 | 2,67E+00 |
|                    | GO:0005924~cell-substrate adherens junction                             | 1,94E-03 | 2,51 | 6,11E-01 | 1,70E-02 | 2,74E+00 |
|                    | GO:0043292~contractile fiber                                            | 1,94E-03 | 2,15 | 6,11E-01 | 1,67E-02 | 2,75E+00 |
|                    | GO:0005874~microtubule                                                  | 2,03E-03 | 1,66 | 6,28E-01 | 1,72E-02 | 2,80E+00 |
|                    | GO:0030016~myofibril                                                    | 2,86E-03 | 2,13 | 7,52E-01 | 2,37E-02 | 4,02E+00 |
|                    | GO:0005925~focal adhesion                                               | 2,94E-03 | 2,50 | 7,62E-01 | 2,40E-02 | 4,14E+00 |
|                    | GO:0012505~endomembrane system                                          | 3,27E-03 | 1,39 | 7,97E-01 | 2,62E-02 | 4,59E+00 |

|                           |                                                                             |          |      |          |          |          |
|---------------------------|-----------------------------------------------------------------------------|----------|------|----------|----------|----------|
|                           | GO:0030175~filopodium                                                       | 3,89E-03 | 3,71 | 8,51E-01 | 3,07E-02 | 5,44E+00 |
|                           | GO:0031594~neuromuscular junction                                           | 3,89E-03 | 3,71 | 8,51E-01 | 3,07E-02 | 5,44E+00 |
|                           | GO:0045211~postsynaptic membrane                                            | 5,26E-03 | 1,86 | 9,23E-01 | 4,06E-02 | 7,29E+00 |
|                           | GO:0005815~microtubule organizing center                                    | 5,48E-03 | 1,67 | 9,31E-01 | 4,16E-02 | 7,58E+00 |
| <b>Molecular function</b> | GO:0008092~cytoskeletal protein binding                                     | 1,65E-18 | 2,52 | 1,81E-15 | 1,81E-15 | 2,63E-15 |
|                           | GO:0003779~actin binding                                                    | 8,84E-16 | 2,72 | 9,78E-13 | 4,89E-13 | 1,42E-12 |
|                           | GO:0046872~metal ion binding                                                | 1,16E-12 | 1,30 | 1,28E-09 | 4,26E-10 | 1,86E-09 |
|                           | GO:0043167~ion binding                                                      | 3,65E-12 | 1,29 | 4,02E-09 | 1,01E-09 | 5,84E-09 |
|                           | GO:0043169~cation binding                                                   | 3,66E-12 | 1,29 | 4,03E-09 | 8,05E-10 | 5,85E-09 |
|                           | GO:0030695~GTPase regulator activity                                        | 4,07E-10 | 2,14 | 4,48E-07 | 7,47E-08 | 6,51E-07 |
|                           | GO:0005509~calcium ion binding                                              | 5,48E-10 | 1,69 | 6,04E-07 | 8,62E-08 | 8,77E-07 |
|                           | GO:0019899~enzyme binding                                                   | 7,73E-10 | 2,46 | 8,51E-07 | 1,06E-07 | 1,24E-06 |
|                           | GO:0060589~nucleoside-triphosphatase regulator activity                     | 8,79E-10 | 2,11 | 9,68E-07 | 1,08E-07 | 1,41E-06 |
|                           | GO:0032559~adenyl ribonucleotide binding                                    | 1,36E-08 | 1,45 | 1,49E-05 | 1,49E-06 | 2,17E-05 |
|                           | GO:0005524~ATP binding                                                      | 1,45E-08 | 1,46 | 1,59E-05 | 1,45E-06 | 2,31E-05 |
|                           | GO:0030554~adenyl nucleotide binding                                        | 1,06E-07 | 1,41 | 1,16E-04 | 9,70E-06 | 1,69E-04 |
|                           | GO:0005083~small GTPase regulator activity                                  | 1,51E-07 | 2,25 | 1,66E-04 | 1,28E-05 | 2,42E-04 |
|                           | GO:0001883~purine nucleoside binding                                        | 2,05E-07 | 1,40 | 2,25E-04 | 1,61E-05 | 3,28E-04 |
|                           | GO:0005085~guanyl-nucleotide exchange factor activity                       | 2,81E-07 | 2,56 | 3,09E-04 | 2,06E-05 | 4,50E-04 |
|                           | GO:0001882~nucleoside binding                                               | 3,29E-07 | 1,39 | 3,63E-04 | 2,27E-05 | 5,27E-04 |
|                           | GO:0032553~ribonucleotide binding                                           | 5,08E-07 | 1,35 | 5,59E-04 | 3,29E-05 | 8,12E-04 |
|                           | GO:0032555~purine ribonucleotide binding                                    | 5,08E-07 | 1,35 | 5,59E-04 | 3,29E-05 | 8,12E-04 |
|                           | GO:0008270~zinc ion binding                                                 | 1,84E-06 | 1,30 | 2,03E-03 | 1,13E-04 | 2,95E-03 |
|                           | GO:0017076~purine nucleotide binding                                        | 2,54E-06 | 1,32 | 2,79E-03 | 1,47E-04 | 4,06E-03 |
|                           | GO:0000166~nucleotide binding                                               | 2,81E-06 | 1,29 | 3,09E-03 | 1,55E-04 | 4,49E-03 |
|                           | GO:0005089~Rho guanyl-nucleotide exchange factor activity                   | 6,82E-06 | 3,09 | 7,48E-03 | 3,58E-04 | 1,09E-02 |
|                           | GO:0051015~actin filament binding                                           | 7,07E-06 | 3,62 | 7,76E-03 | 3,54E-04 | 1,13E-02 |
|                           | GO:0005088~Ras guanyl-nucleotide exchange factor activity                   | 7,16E-06 | 2,89 | 7,85E-03 | 3,43E-04 | 1,14E-02 |
|                           | GO:0003774~motor activity                                                   | 1,38E-05 | 2,35 | 1,51E-02 | 6,34E-04 | 2,21E-02 |
|                           | GO:0015171~amino acid transmembrane transporter activity                    | 4,24E-05 | 3,34 | 4,56E-02 | 1,86E-03 | 6,77E-02 |
|                           | GO:0015085~calcium ion transmembrane transporter activity                   | 4,93E-05 | 8,13 | 5,29E-02 | 2,09E-03 | 7,88E-02 |
|                           | GO:0048407~platelet-derived growth factor binding                           | 4,93E-05 | 8,13 | 5,29E-02 | 2,09E-03 | 7,88E-02 |
|                           | GO:0005388~calcium-transporting ATPase activity                             | 4,93E-05 | 8,13 | 5,29E-02 | 2,09E-03 | 7,88E-02 |
|                           | GO:0005201~extracellular matrix structural constituent                      | 5,77E-05 | 4,18 | 6,16E-02 | 2,35E-03 | 9,23E-02 |
|                           | GO:0046914~transition metal ion binding                                     | 7,85E-05 | 1,21 | 8,28E-02 | 3,08E-03 | 1,25E-01 |
|                           | GO:0019900~kinase binding                                                   | 1,16E-04 | 2,58 | 1,20E-01 | 4,39E-03 | 1,85E-01 |
|                           | GO:0051020~GTPase binding                                                   | 1,75E-04 | 2,86 | 1,75E-01 | 6,40E-03 | 2,79E-01 |
|                           | GO:0004714~transmembrane receptor protein tyrosine kinase activity          | 1,77E-04 | 2,98 | 1,77E-01 | 6,26E-03 | 2,82E-01 |
|                           | GO:0017016~Ras GTPase binding                                               | 2,19E-04 | 2,93 | 2,14E-01 | 7,51E-03 | 3,50E-01 |
|                           | GO:0015179~L-amino acid transmembrane transporter activity                  | 2,26E-04 | 3,96 | 2,21E-01 | 7,53E-03 | 3,62E-01 |
|                           | GO:0019901~protein kinase binding                                           | 2,95E-04 | 2,65 | 2,78E-01 | 9,52E-03 | 4,71E-01 |
|                           | GO:0050840~extracellular matrix binding                                     | 3,23E-04 | 4,18 | 2,99E-01 | 1,01E-02 | 5,15E-01 |
|                           | GO:0031267~small GTPase binding                                             | 3,30E-04 | 2,83 | 3,05E-01 | 1,00E-02 | 5,26E-01 |
|                           | GO:0016879~ligase activity, forming carbon-nitrogen bonds                   | 3,35E-04 | 1,89 | 3,08E-01 | 9,91E-03 | 5,34E-01 |
|                           | GO:0019838~growth factor binding                                            | 3,53E-04 | 2,61 | 3,22E-01 | 1,02E-02 | 5,63E-01 |
|                           | GO:0005516~calmodulin binding                                               | 4,28E-04 | 2,20 | 3,76E-01 | 1,20E-02 | 6,82E-01 |
|                           | GO:0015082~di-, tri-valent inorganic cation transmembrane transporter activ | 5,59E-04 | 3,59 | 4,60E-01 | 1,53E-02 | 8,90E-01 |
|                           | GO:0015293~symporter activity                                               | 6,66E-04 | 2,06 | 5,20E-01 | 1,77E-02 | 1,06E+00 |
|                           | GO:0005275~amine transmembrane transporter activity                         | 7,02E-04 | 2,65 | 5,38E-01 | 1,82E-02 | 1,12E+00 |
|                           | GO:0004842~ubiquitin-protein ligase activity                                | 7,38E-04 | 2,21 | 5,57E-01 | 1,87E-02 | 1,17E+00 |
|                           | GO:0019992~diacylglycerol binding                                           | 1,08E-03 | 2,66 | 6,97E-01 | 2,68E-02 | 1,72E+00 |
|                           | GO:0017048~Rho GTPase binding                                               | 1,25E-03 | 3,92 | 7,46E-01 | 3,00E-02 | 1,97E+00 |
|                           | GO:0019894~kinesin binding                                                  | 1,33E-03 | 6,27 | 7,68E-01 | 3,13E-02 | 2,10E+00 |