| GO:0033108 | BP   | GO:0033108 | mitochondrial respiratory chain complex assembly | 19/207 | 4.10E-19 | 1.40E-15 | 1.08E-15 | 19 |
|----------|------|------------|-----------------------------------------------|--------|-----------|-----------|-----------|----|
| GO:0010257 | BP   | GO:0010257 | NADH dehydrogenase complex assembly            | 15/207 | 3.96E-17 | 4.51E-14 | 3.49E-14 | 15 |
| GO:0032981 | BP   | GO:0032981 | mitochondrial respiratory chain complex I assembly | 15/207 | 3.96E-17 | 4.51E-14 | 3.49E-14 | 15 |
| GO:0006120 | BP   | GO:0006120 | mitochondrial electron transport, NADH to ubiquinone | 12/207 | 2.63E-13 | 2.25E-10 | 1.74E-10 | 12 |
| GO:0019646 | BP   | GO:0019646 | aerobic electron transport chain                | 13/207 | 1.26E-11 | 8.60E-09 | 6.66E-09 | 13 |
| GO:0042773 | BP   | GO:0042773 | ATP synthesis coupled electron transport        | 13/207 | 3.98E-11 | 1.94E-08 | 1.50E-08 | 13 |
| GO:0042775 | BP   | GO:0042775 | mitochondrial ATP synthesis coupled electron transport | 13/207 | 3.98E-11 | 1.94E-08 | 1.50E-08 | 13 |
| GO:0045785 | BP   | GO:0045785 | positive regulation of cell adhesion           | 24/207 | 4.37E-18 | 4.73E-08 | 3.66E-08 | 24 |
| GO:0050900 | BP   | GO:0050900 | leukocyte migration                            | 22/207 | 1.47E-10 | 5.57E-08 | 4.31E-08 | 22 |
| GO:0007159 | BP   | GO:0007159 | leukocyte cell-cell adhesion                    | 22/207 | 1.63E-10 | 5.57E-08 | 4.31E-08 | 22 |
| GO:0022904 | BP   | GO:0022904 | respiratory electron transport chain            | 13/207 | 4.11E-10 | 1.17E-07 | 9.08E-08 | 13 |
| GO:0022409 | BP   | GO:0022409 | positive regulation of cell-cell adhesion       | 19/207 | 4.12E-10 | 1.17E-07 | 9.08E-08 | 19 |
| GO:0006119 | BP   | GO:0006119 | oxidative phosphorylation                      | 14/207 | 5.53E-10 | 1.45E-07 | 1.12E-07 | 14 |
| GO:0010592 | BP   | GO:0010592 | positive regulation of lamellipodium assembly   | 8/207  | 6.86E-10 | 1.67E-07 | 1.29E-07 | 8  |
| GO:1903039 | BP   | GO:1903039 | positive regulation of leukocyte cell-cell adhesion | 17/207 | 1.41E-09 | 3.20E-07 | 2.48E-07 | 17 |
| GO:0009060 | BP   | GO:0009060 | aerobic respiration                            | 15/207 | 3.04E-09 | 6.48E-07 | 5.02E-07 | 15 |
| GO:1902745 | BP   | GO:1902745 | positive regulation of lamellipodium organization | 8/207  | 5.72E-09 | 1.10E-06 | 8.48E-07 | 8  |
| GO:0030183 | BP   | GO:0030183 | B cell differentiation                          | 13/207 | 5.78E-09 | 1.10E-06 | 8.48E-07 | 13 |
| GO:0030098 | BP   | GO:0030098 | lymphocyte differentiation                     | 20/207 | 6.81E-09 | 1.22E-06 | 9.48E-07 | 20 |
| GO          | BP      | Description                              | GO       | BP      | Description                              | GO       | BP      | Description                              | GO       | BP      | Description                              | GO       | BP      | Description                              |
|------------|---------|------------------------------------------|----------|---------|------------------------------------------|----------|---------|------------------------------------------|----------|---------|------------------------------------------|----------|---------|------------------------------------------|----------|---------|------------------------------------------|
| GO:19027   | BP      | regulation of lamellipodium organization | GO:00343 | BP      | Arp2/3 complex-mediated actin nucleation | GO:00299 | BP      | electron transport chain                | GO:19031 | BP      | mononuclear cell differentiation         | GO:00105 | BP      | regulation of lamellipodium organization | GO:0081  | BP      | actin polymerization or depolymerization | GO:00421 | BP      | T cell activation                        | GO:00453 | BP      | cellular respiration                      | GO:00488 | BP      | homeostasis of number of cells           | GO:00450 | BP      | actin nucleation                          | GO:00975 | BP      | lamellipodium organization               | GO:00448 | BP      | regulation of actin filament length       | GO:00508 | BP      | positive regulation of T cell activation | GO:00308 | BP      | positive regulation of actin filament polymerization | GO:01200 | BP      | regulation of plasma membrane bounded cell projection assembly | GO:00080 | BP      | regulation of actin polymerization or depolymerization | GO:00604 | BP      | regulation of cell projection assembly   | GO:00308 | BP      | regulation of actin filament length       | GO:19030 | BP      | regulation of leukocyte cell-cell adhesion |
| GO:0030041 | BP | GO:0030 041 | actin filament polymerization | 13/207 | 191/187 | 2.15E-07 | 1.79E-05 | 1.38E-05 | 13 |
| GO:0002703 | BP | GO:0002 703 | regulation of leukocyte mediated immunity | 14/207 | 226/187 | 2.32E-07 | 1.88E-05 | 1.46E-05 | 14 |
| GO:0002687 | BP | GO:0002 687 | positive regulation of leukocyte migration | 11/207 | 135/187 | 3.13E-07 | 2.48E-05 | 1.92E-05 | 11 |
| GO:0022604 | BP | GO:0022 604 | regulation of cell morphogenesis | 16/207 | 309/187 | 3.62E-07 | 2.80E-05 | 2.17E-05 | 16 |
| GO:0032273 | BP | GO:0032 273 | positive regulation of protein polymerization | 11/207 | 138/187 | 3.91E-07 | 2.96E-05 | 2.30E-05 | 11 |
| GO:0046034 | BP | GO:0046 034 | ATP metabolic process | 15/207 | 277/187 | 4.82E-07 | 3.54E-05 | 2.74E-05 | 15 |
| GO:0002703 | BP | GO:0002 703 | regulation of leukocyte mediated immunity | 14/207 | 226/187 | 2.32E-07 | 1.88E-05 | 1.46E-05 | 14 |
| GO:0030833 | BP | GO:0030 833 | regulation of actin filament polymerization | 12/207 | 172/187 | 4.88E-07 | 3.54E-05 | 2.74E-05 | 12 |
| GO:0110053 | BP | GO:0110 053 | regulation of actin filament organization | 15/207 | 278/187 | 5.04E-07 | 3.58E-05 | 2.78E-05 | 15 |
| GO:0006091 | BP | GO:0006 091 | generation of precursor metabolites and energy | 20/207 | 490/187 | 5.58E-07 | 3.89E-05 | 3.01E-05 | 20 |
| GO:1902905 | BP | GO:1902 905 | positive regulation of supramolecular fiber organization | 13/207 | 209/187 | 6.03E-07 | 4.12E-05 | 3.19E-05 | 13 |
| GO:1903706 | BP | GO:1903 706 | regulation of hemopoiesis | 17/207 | 367/187 | 7.35E-07 | 4.92E-05 | 3.81E-05 | 17 |
| GO:0050863 | BP | GO:0050 863 | regulation of T cell activation | 16/207 | 329/187 | 8.33E-07 | 5.46E-05 | 4.23E-05 | 16 |
| GO:0097529 | BP | GO:0097 529 | myeloid leukocyte migration | 13/207 | 220/187 | 1.08E-06 | 6.94E-05 | 5.37E-05 | 13 |
| GO:0008360 | BP | GO:0008 360 | regulation of cell shape | 11/207 | 154/187 | 1.17E-06 | 7.39E-05 | 5.73E-05 | 11 |
| GO:0002697 | BP | GO:0002 697 | regulation of immune effector process | 16/207 | 339/187 | 1.23E-06 | 7.62E-05 | 5.90E-05 | 16 |
| GO:0030032 | BP | GO:0030 032 | lamellipodium assembly | 8/207 | 72/187 | 1.27E-06 | 7.62E-05 | 5.90E-05 | 8 |
| GO:0033627 | BP | GO:0033 627 | cell adhesion mediated by integrin | 8/207 | 72/187 | 1.27E-06 | 7.62E-05 | 5.90E-05 | 8 |
| GO:0043254 | BP | GO:0043 254 | regulation of protein-containing complex assembly | 18/207 | 428/187 | 1.38E-06 | 8.13E-05 | 6.30E-05 | 18 |
| GO:0051495 | BP | GO:0051 495 | positive regulation of cytoskeleton organization | 13/207 | 226/187 | 1.46E-06 | 8.43E-05 | 6.53E-05 | 13 |
| GO:0071674 | BP | GO:0071 674 | mononuclear cell migration | 12/207 | 196/187 | 1.95E-06 | 0.00011 | 8.55E-05 | 12 |
| GO:0060326 | BP | GO:0060 326 | cell chemotaxis | 15/207 | 310/187 | 1.97E-06 | 0.00011 | 8.55E-05 | 15 |
| GO:0032271 | BP | GO:0032 271 | regulation of protein polymerization | 13/207 | 233/187 | 2.05E-06 | 0.000113 | 8.72E-05 | 13 |
| GO          | BP   | Description                                                                 | Count | FDR  | p-value | Benjamini-Hochberg FDR | Benjamini-Hochberg FDR |
|-------------|------|------------------------------------------------------------------------------|-------|------|---------|------------------------|------------------------|
| GO:00070    | 15   | actin filament organization                                                  | 18/207| 442/187 | 2.18E-06 | 0.000118               | 9.14E-05               |
| GO:00313    | 34   | positive regulation of protein-containing complex assembly                  | 13/207| 237/187 | 2.47E-06 | 0.000129               | 0.0001                 |
| GO:01200    | 34   | positive regulation of plasma membrane bounded cell projection assembly     | 9/207 | 105/187 | 2.49E-06 | 0.000129               | 0.0001                 |
| GO:00329    | 56   | regulation of actin cytoskeleton organization                               | 16/207| 358/187 | 2.50E-06 | 0.000129               | 0.0001                 |
| GO:00706    | 61   | leukocyte proliferation                                                     | 15/207| 318/187 | 2.70E-06 | 0.000138               | 0.000107               |
| GO:00706    | 63   | regulation of leukocyte proliferation                                        | 13/207| 245/187 | 3.56E-06 | 0.000179               | 0.000138               |
| GO:00456    | 19   | regulation of lymphocyte differentiation                                    | 11/207| 174/187 | 3.86E-06 | 0.000191               | 0.000148               |
| GO:00026    | 85   | regulation of leukocyte migration                                           | 12/207| 210/187 | 3.99E-06 | 0.000194               | 0.000151               |
| GO:00466    | 51   | lymphocyte proliferation                                                    | 14/207| 288/187 | 4.14E-06 | 0.000199               | 0.000154               |
| GO:00703    | 71   | ERK1 and ERK2 cascade                                                       | 15/207| 330/187 | 4.24E-06 | 0.000201               | 0.000156               |
| GO:00329    | 43   | mononuclear cell proliferation                                              | 14/207| 291/187 | 4.67E-06 | 0.000218               | 0.000169               |
| GO:00308    | 65   | cortical cytoskeleton organization                                          | 7/207 | 61/1872 | 4.80E-06 | 0.000218               | 0.000169               |
| GO:00341    | 13   | heterotypic cell-cell adhesion                                              | 7/207 | 61/1872 | 4.80E-06 | 0.000218               | 0.000169               |
| GO:00421    | 13   | B cell activation                                                          | 15/207| 334/187 | 4.91E-06 | 0.000222               | 0.000171               |
| GO:00326    | 40   | tumor necrosis factor production                                             | 11/207| 181/187 | 5.64E-06 | 0.000247               | 0.000191               |
| GO:00326    | 80   | regulation of tumor necrosis factor production                              | 11/207| 181/187 | 5.64E-06 | 0.000247               | 0.000191               |
| GO:00512    | 58   | protein polymerization                                                      | 14/207| 297/187 | 5.90E-06 | 0.000255               | 0.000197               |
| GO:00717    | 06   | tumor necrosis factor superfamily cytokine production                       | 11/207| 186/187 | 7.32E-06 | 0.000308               | 0.000239               |
| GO:19035    | 55   | regulation of tumor necrosis factor superfamily cytokine production         | 11/207| 186/187 | 7.32E-06 | 0.000308               | 0.000239               |
| GO:00328    | 68   | response to insulin                                                         | 13/207| 264/187 | 8.01E-06 | 0.000332               | 0.000257               |
| GO       | BP | GO       | Description                                      | Fold Change | p-value  | FDR  | p-value  | FDR  |
|----------|----|----------|--------------------------------------------------|-------------|----------|------|----------|------|
| GO:00506 | 70 | BP       | regulation of lymphocyte proliferation           | 12/207      | 225/187  | 8.07E-06 | 0.000332 | 0.000257 | 12   |
| GO:00329 | 44 | BP       | regulation of mononuclear cell proliferation     | 12/207      | 227/187  | 8.83E-06 | 0.000359 | 0.000278 | 12   |
| GO:00069 | 09 | BP       | phagocytosis                                      | 14/207      | 308/187  | 8.93E-06 | 0.000359 | 0.000278 | 14   |
| GO:00329 | 70 | BP       | regulation of actin filament-based process       | 16/207      | 397/187  | 9.29E-06 | 0.000369 | 0.000285 | 16   |
| GO:00026 | 90 | BP       | positive regulation of leukocyte chemotaxis      | 8/207       | 94/187   | 9.62E-06 | 0.000377 | 0.000292 | 8    |
| GO:00466 | 37 | BP       | regulation of alpha-beta T cell differentiation  | 7/207       | 68/182   | 9.99E-06 | 0.000387 | 0.00023  | 7    |
| GO:00451 | 23 | BP       | cellular extravasation                           | 7/207       | 70/182   | 1.21E-05 | 0.000465 | 0.00036   | 7    |
| GO:00023 | 66 | BP       | leukocyte activation involved in immune response | 13/207      | 275/187  | 1.24E-05 | 0.00047  | 0.000364 | 13   |
| GO:00512 | 51 | BP       | positive regulation of lymphocyte activation     | 15/207      | 362/187  | 1.28E-05 | 0.000482 | 0.000373 | 15   |
| GO:00615 | 15 | BP       | myeloid cell development                         | 7/207       | 71/182   | 1.33E-05 | 0.000493 | 0.000382 | 7    |
| GO:00026 | 96 | BP       | positive regulation of leukocyte activation      | 16/207      | 409/187  | 1.34E-05 | 0.000493 | 0.000382 | 16   |
| GO:00420 | 98 | BP       | T cell proliferation                             | 11/207      | 199/187  | 1.39E-05 | 0.000503 | 0.00039  | 11   |
| GO:00313 | 41 | BP       | regulation of cell killing                       | 8/207       | 99/182   | 1.41E-05 | 0.000503 | 0.00039  | 8    |
| GO:00336 | 28 | BP       | regulation of cell adhesion mediated by integrin | 6/207       | 48/182   | 1.42E-05 | 0.000503 | 0.00039  | 6    |
| GO:00022 | 63 | BP       | cell activation involved in immune response      | 13/207      | 279/187  | 1.45E-05 | 0.000504 | 0.00039  | 13   |
| GO:19021 | 05 | BP       | regulation of leukocyte differentiation          | 13/207      | 279/187  | 1.45E-05 | 0.000504 | 0.00039  | 13   |
| GO:00700 | 85 | BP       | glycosylation                                     | 12/207      | 240/187  | 1.54E-05 | 0.000533 | 0.000412 | 12   |
| GO:00328 | 69 | BP       | cellular response to insulin stimulus            | 11/207      | 203/187  | 1.67E-05 | 0.00057  | 0.000441 | 11   |
| GO:00508 | 67 | BP       | positive regulation of cell activation           | 16/207      | 420/187  | 1.86E-05 | 0.000629 | 0.000487 | 16   |
| GO:00301 | 48 | BP       | sphingolipid biosynthetic process                 | 8/207       | 103/187  | 1.89E-05 | 0.000631 | 0.000489 | 8    |
| GO:00466 | 34 | BP       | regulation of alpha-beta T cell activation       | 8/207       | 104/187  | 2.02E-05 | 0.000671 | 0.00052  | 8    |
| GO:00421 | 29 | BP       | regulation of T cell proliferation               | 10/207      | 171/187  | 2.11E-05 | 0.000693 | 0.000537 | 10   |
| GO:0030099 | BP | GO:0030099 | myeloid cell differentiation | 15/207 | 381/187 | 2.34E-05 | 0.000759 | 0.000588 | 15 |
|-------------|----|------------|----------------------------|--------|---------|-----------|---------|---------|-----|
| GO:1902903 | BP | GO:1902903 | regulation of supramolecular fiber organization | 15/207 | 383/187 | 2.48E-05 | 0.000799 | 0.000619 | 15 |
| GO:0046467 | BP | GO:0046467 | membrane lipid biosynthetic process | 9/207 | 142/187 | 2.91E-05 | 0.000929 | 0.00072 | 9 |
| GO:0035855 | BP | GO:0035855 | megakaryocyte development | 4/207 | 17/187 | 3.09E-05 | 0.000975 | 0.000755 | 4 |
| GO:0002443 | BP | GO:0002443 | leukocyte mediated immunity | 16/207 | 440/187 | 3.27E-05 | 0.001024 | 0.000793 | 16 |
| GO:0002446 | BP | GO:0002446 | neutrophil mediated immunity | 5/207 | 34/187 | 3.37E-05 | 0.001047 | 0.000811 | 5 |
| GO:0007162 | BP | GO:0007162 | negative regulation of cell adhesion | 13/207 | 303/187 | 3.43E-05 | 0.001048 | 0.000811 | 13 |
| GO:0001910 | BP | GO:0001910 | regulation of leukocyte mediated cytotoxicity | 7/207 | 82/187 | 3.44E-05 | 0.001048 | 0.000811 | 7 |
| GO:0003019 | BP | GO:0003019 | megakaryocyte differentiation | 6/207 | 57/187 | 3.85E-05 | 0.001164 | 0.000901 | 6 |
| GO:0009730 | BP | GO:0009730 | granulocyte migration | 9/207 | 148/187 | 4.04E-05 | 0.001209 | 0.000936 | 9 |
| GO:0001776 | BP | GO:0001776 | leukocyte homeostasis | 10/207 | 194/187 | 4.49E-05 | 0.001266 | 0.000981 | 7 |
| GO:0030595 | BP | GO:0030595 | leukocyte chemotaxis | 11/207 | 226/187 | 4.49E-05 | 0.001266 | 0.000981 | 11 |
| GO:0002285 | BP | GO:0002285 | lymphocyte activation involved in immune response | 10/207 | 194/187 | 6.18E-05 | 0.001655 | 0.001281 | 10 |
| GO:0016032 | BP | GO:0016032 | viral process | 15/207 | 415/187 | 6.20E-05 | 0.001655 | 0.001281 | 15 |
| GO:0002688 | BP | GO:0002688 | regulation of leukocyte chemotaxis | 8/207 | 122/187 | 6.39E-05 | 0.001655 | 0.001281 | 8 |
| GO:1990266 | BP | GO:1990266 | neutrophil migration | 8/207 | 122/187 | 6.39E-05 | 0.001655 | 0.001281 | 8 |
| GO:0002262 | BP | GO:0002262 | myeloid cell homeostasis | 9/207 | 157/187 | 6.40E-05 | 0.001655 | 0.001281 | 9 |
| GO:1902107 | BP | GO:1902107 | positive regulation of leukocyte differentiation | 9/207 | 157/187 | 6.40E-05 | 0.001655 | 0.001281 | 9 |
| GO:1903708 | BP | GO:1903708 | positive regulation of hemopoiesis | 9/207 | 157/187 | 6.40E-05 | 0.001655 | 0.001281 | 9 |
| GO:0070302 | BP | GO:0070302 | regulation of stress-activated protein kinase signaling cascade | 10/207 | 195/187 | 6.46E-05 | 0.001655 | 0.001283 | 10 |
| GO:0051051 | BP | GO:0051051 | negative regulation of transport | 16/207 | 470/187 | 7.16E-05 | 0.001812 | 0.001404 | 16 |
| GO:0001909 | BP | GO:0001909 | leukocyte mediated cytotoxicity | 8/207 | 124/187 | 7.17E-05 | 0.001812 | 0.001404 | 8 |
| GO:0003630 | BP | GO:0003630 | positive regulation of cell adhesion mediated by integrin | 4/207 | 21/187 | 7.49E-05 | 0.001881 | 0.001457 | 4 |
| GO:0071621 | BP | GO:0071621 | granulocyte chemotaxis | 8/207 | 125/187 | 7.59E-05 | 0.00189 | 0.001464 | 8 |
| GO:0006487 | BP | GO:0006487 | protein N-linked glycosylation | 6/207 | 65/187 | 8.15E-05 | 0.002002 | 0.00155 | 6 |
| GO:0046513 | BP | GO:0046513 | ceramide biosynthetic process | 6/207 | 65/187 | 8.15E-05 | 0.002002 | 0.00155 | 6 |
| GO:0050764 | BP | GO:0050764 | regulation of phagocytosis | 7/207 | 95/187 | 8.86E-05 | 0.002159 | 0.001672 | 7 |
| GO:0034101 | BP | GO:0034101 | erythrocyte homeostasis | 8/207 | 129/187 | 9.47E-05 | 0.002292 | 0.001775 | 8 |
| GO:0016601 | BP | GO:0016601 | Rac protein signal transduction | 5/207 | 42/187 | 9.60E-05 | 0.002307 | 0.001787 | 5 |
| GO:0002429 | BP | GO:0002429 | immune response-activating cell surface receptor signaling pathway | 12/207 | 291/187 | 23 | 0.0001 | 0.002379 | 0.001842 | 12 |
| GO:0002757 | BP | GO:0002757 | immune response-activating signal transduction | 12/207 | 291/187 | 23 | 0.0001 | 0.002379 | 0.001842 | 12 |
| GO:0001655 | BP | GO:0001655 | urogenital system development | 13/207 | 338/187 | 0.000104 | 0.002453 | 0.0019 | 13 |
| GO:0016266 | BP | GO:0016266 | O-glycan processing | 5/207 | 43/187 | 0.000108 | 0.002486 | 0.001925 | 5 |
| GO:0036230 | BP | GO:0036230 | granulocyte activation | 5/207 | 43/187 | 0.000108 | 0.002486 | 0.001925 | 5 |
| GO:0070301 | BP | GO:0070301 | cellular response to hydrogen peroxide | 7/207 | 98/187 | 0.000108 | 0.002486 | 0.001925 | 7 |
| GO:0050765 65 | BP | GO:0050765 | negative regulation of phagocytosis | 4/2 07 | 23/1 872 | 0.000109 | 0.002496 | 0.001933 | 4 |
| GO:0007219 19 | BP | GO:0007219 | Notch signaling pathway | 9/2 07 | 172/1 87 | 0.000129 | 0.002889 | 0.002237 | 9 |
| GO:0032528 28 | BP | GO:0032528 | microvillus organization | 4/2 07 | 24/1 872 | 0.00013 | 0.002889 | 0.002237 | 4 |
| GO:0032928 28 | BP | GO:0032928 | regulation of superoxide anion generation | 4/2 07 | 24/1 872 | 0.00013 | 0.002889 | 0.002237 | 4 |
| GO:0090023 23 | BP | GO:0090023 | positive regulation of neutrophil chemotaxis | 4/2 07 | 24/1 872 | 0.00013 | 0.002889 | 0.002237 | 4 |
| GO:0042102 02 | BP | GO:0042102 | positive regulation of T cell proliferation | 7/2 07 | 101/1 87 | 0.00013 | 0.002889 | 0.002237 | 7 |
| GO:0030217 17 | BP | GO:0030217 | T cell differentiation | 11/207 | 257/1 87 | 0.000141 | 0.003111 | 0.002409 | 11 |
| GO:0050671 71 | BP | GO:0050671 | positive regulation of lymphocyte proliferation | 8/2 07 | 137/1 87 | 0.000144 | 0.003151 | 0.002441 | 8 |
| GO:0030593 93 | BP | GO:0030593 | neutrophil chemotaxis | 7/2 07 | 103/1 87 | 0.000147 | 0.003204 | 0.002481 | 7 |
| GO:0007157 57 | BP | GO:0007157 | heterophilic cell-cell adhesion via plasma membrane cell adhesion molecules | 5/2 07 | 46/1 872 | 0.000149 | 0.003204 | 0.002481 | 5 |
| GO:0043300 00 | BP | GO:0043300 | regulation of leukocyte degranulation | 5/2 07 | 46/1 872 | 0.000149 | 0.003204 | 0.002481 | 5 |
| GO:2000601 01 | BP | GO:2000601 | positive regulation of Arp2/3 complex-mediated actin nucleation | 3/2 07 | 10/1 872 | 0.000151 | 0.003211 | 0.002487 | 3 |
| GO:0032946 46 | BP | GO:0032946 | positive regulation of mononuclear cell proliferation | 8/2 07 | 138/1 87 | 0.000151 | 0.003211 | 0.002487 | 8 |
| GO:0045621 21 | BP | GO:0045621 | positive regulation of lymphocyte differentiation | 7/2 07 | 104/1 87 | 0.000157 | 0.003299 | 0.002555 | 7 |
| GO:0007163 63 | BP | GO:0007163 | establishment or maintenance of cell polarity | 10/207 | 218/1 87 | 0.000162 | 0.003395 | 0.00263 | 10 |
| GO:0032008 08 | BP | GO:0032008 | positive regulation of TOR signaling | 5/2 07 | 47/1 872 | 0.000166 | 0.003445 | 0.002668 | 5 |
| GO:0034341 41 | BP | GO:0034341 | response to interferon-gamma | 8/2 07 | 141/1 87 | 0.000176 | 0.003612 | 0.002798 | 8 |
| GO:0050921 21 | BP | GO:0050921 | positive regulation of chemotaxis | 8/2 07 | 141/1 87 | 0.000176 | 0.003612 | 0.002798 | 8 |
| GO:0043409 09 | BP | GO:0043409 | negative regulation of MAPK cascade | 9/2 07 | 180/1 87 | 0.000182 | 0.003711 | 0.002874 | 9 |
| GO:1901653 53 | BP | GO:1901653 | cellular response to peptide | 13/207 | 359/1 87 | 0.000189 | 0.003839 | 0.002973 | 13 |
| GO:0002274 | BP | GO:0002274 | myeloid leukocyte activation | 10/207 | 223/187 | 0.000195 | 0.003936 | 0.003048 | 10 |
| GO:0006054 | BP | GO:0006054 | N-acetylneuraminate metabolic process | 3/207 | 111/1872 | 0.000206 | 0.004059 | 0.003144 | 3 |
| GO:0043312 | BP | GO:0043312 | neutrophil degranulation | 3/207 | 111/1872 | 0.000206 | 0.004059 | 0.003144 | 3 |
| GO:0046643 | BP | GO:0046643 | regulation of gamma-delta T cell activation | 3/207 | 111/1872 | 0.000206 | 0.004059 | 0.003144 | 3 |
| GO:0002433 | BP | GO:0002433 | immune response-regulating cell surface receptor signaling pathway involved in phagocytosis | 4/207 | 2718723 | 0.000209 | 0.004059 | 0.003144 | 4 |
| GO:0038096 | BP | GO:0038096 | Fc-gamma receptor signaling pathway involved in phagocytosis | 4/207 | 2718723 | 0.000209 | 0.004059 | 0.003144 | 4 |
| GO:0071624 | BP | GO:0071624 | positive regulation of granulocyte chemotaxis | 4/207 | 2718723 | 0.000209 | 0.004059 | 0.003144 | 4 |
| GO:0002768 | BP | GO:0002768 | immune response-regulating cell surface receptor signaling pathway | 12/207 | 31518723 | 0.000212 | 0.004059 | 0.003144 | 12 |
| GO:0031589 | BP | GO:0031589 | cell-substrate adhesion | 13/207 | 36318723 | 0.000211 | 0.004059 | 0.003144 | 13 |
| GO:0002698 | BP | GO:0002698 | negative regulation of immune effector process | 7/207 | 11018723 | 0.000222 | 0.004059 | 0.003144 | 7 |
| GO:0009101 | BP | GO:0009101 | glycoprotein biosynthetic process | 12/207 | 31718723 | 0.000223 | 0.004059 | 0.003258 | 12 |
| GO:0060337 | BP | GO:0060337 | type I interferon signaling pathway | 5/207 | 501872 | 0.000223 | 0.004059 | 0.003258 | 5 |
| GO:0045580 | BP | GO:0045580 | regulation of T cell differentiation | 8/207 | 146187 | 0.000223 | 0.004059 | 0.003258 | 8 |
| GO:0038094 | BP | GO:0038094 | Fc-gamma receptor signaling pathway | 4/207 | 281872 | 0.000241 | 0.004488 | 0.003475 | 4 |
| GO:1902624 | BP | GO:1902624 | positive regulation of neutrophil migration | 4/207 | 281872 | 0.000241 | 0.004488 | 0.003475 | 4 |
| GO:0071496 | BP | GO:0071496 | cellular response to external stimulus | 12/207 | 32018723 | 0.000243 | 0.004488 | 0.003475 | 12 |
| GO:0043370 | BP | GO:0043370 | regulation of CD4-positive, alpha-beta T cell differentiation | 5/207 | 5118723 | 0.000245 | 0.004488 | 0.003475 | 5 |
| GO:0071622 | BP | GO:0071622 | regulation of granulocyte chemotaxis | 5/207 | 5118723 | 0.000245 | 0.004488 | 0.003475 | 5 |
| GO:0046632 | BP | GO:0046632 | alpha-beta T cell differentiation | 7/207 | 112187 | 0.000248 | 0.004525 | 0.003504 | 7 |
| GO:00019 06 | BP | GO:0001 906 | cell killing | 9/2 07 | 188/187 | 0.000251 | 0.004559 | 0.003531 | 9 |
| GO:00713 57 | BP | GO:0071 357 | cellular response to type I interferon | 5/2 07 | 52/1872 | 0.000268 | 0.004843 | 0.00375 | 5 |
| GO:00726 83 | BP | GO:0072 683 | T cell extravasation | 3/2 07 | 12/1872 | 0.000272 | 0.004865 | 0.003767 | 3 |
| GO:00726 83 | BP | GO:0072 683 | regulation of neutrophil activation | 3/2 07 | 12/1872 | 0.000272 | 0.004865 | 0.003767 | 3 |
| GO:00022 53 | BP | GO:0002 253 | activation of immune response | 13/207 | 375/187 | 0.000288 | 0.005124 | 0.003968 | 13 |
| GO:00713 57 | BP | GO:0071 357 | extrinsic apoptotic signaling pathway via death domain receptors | 6/2 07 | 82/1872 | 0.000296 | 0.005231 | 0.004051 | 6 |
| GO:00321 03 | BP | GO:0032 103 | positive regulation of response to external stimulus | 14/207 | 427/18723 | 0.000298 | 0.005557 | 0.004303 | 4 |
| GO:00455 77 | BP | GO:0045 577 | regulation of B cell differentiation | 4/2 07 | 30/1872 | 0.000317 | 0.005582 | 0.004323 | 5 |
| GO:00028 23 | BP | GO:0002 823 | negative regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains | 5/2 07 | 54/1872 | 0.000321 | 0.005582 | 0.004323 | 5 |
| GO:00066 65 | BP | GO:0006 665 | sphingolipid metabolic process | 8/2 07 | 155/187 | 0.000335 | 0.00577 | 0.004468 | 8 |
| GO:00466 31 | BP | GO:0046 31 | alpha-beta T cell activation | 8/2 07 | 156/187 | 0.00035 | 0.005873 | 0.004548 | 8 |
| GO:00364 62 | BP | GO:0036 462 | TRAIL-activated apoptotic signaling pathway | 3/2 07 | 13/1872 | 0.000351 | 0.005873 | 0.004548 | 3 |
| GO:00424 92 | BP | GO:0042 492 | gamma-delta T cell differentiation | 3/2 07 | 13/1872 | 0.000351 | 0.005873 | 0.004548 | 3 |
| GO:00704 86 | BP | GO:0070 486 | leukocyte aggregation | 3/2 07 | 13/1872 | 0.000351 | 0.005873 | 0.004548 | 3 |
| GO:00302 18 | BP | GO:0030 218 | erythrocyte differentiation | 7/2 07 | 120/187 | 0.000378 | 0.006293 | 0.004873 | 7 |
| GO:00028 86 | BP | GO:0002 886 | regulation of myeloid leukocyte mediated immunity | 5/2 07 | 56/1872 | 0.00038 | 0.006301 | 0.00488 | 5 |
| GO:0071375 | BP | GO:0071375 | cellular response to peptide hormone stimulus | 11/207 | 290/187 | 0.000399 | 0.006578 | 0.005095 | 11 |
| GO:0090022 | BP | GO:0090022 | regulation of neutrophil chemotaxis | 4/207 | 32/187 | 0.000409 | 0.006718 | 0.005203 | 4 |
| GO:0031098 | BP | GO:0031098 | stress-activated protein kinase signaling cascade | 10/207 | 247/187 | 0.00044 | 0.007168 | 0.005551 | 10 |
| GO:0006643 | BP | GO:0006643 | membrane lipid metabolic process | 9/207 | 203/187 | 0.000441 | 0.007168 | 0.005551 | 9 |
| GO:0003376 | BP | GO:0003376 | sphingosine-1-phosphate receptor signaling pathway | 3/207 | 14/187 | 0.000443 | 0.007168 | 0.005551 | 3 |
| GO:0034340 | BP | GO:0034340 | response to type I interferon | 5/207 | 58/187 | 0.000448 | 0.007215 | 0.005587 | 5 |
| GO:0032496 | BP | GO:0032496 | response to lipopolysaccharide | 12/207 | 343/187 | 0.000454 | 0.007272 | 0.005632 | 12 |
| GO:0002431 | BP | GO:0002431 | Fc receptor mediated stimulatory signaling pathway | 4/207 | 33/187 | 0.000462 | 0.007367 | 0.005705 | 4 |
| GO:0060348 | BP | GO:0060348 | bone development | 9/207 | 205/187 | 0.000474 | 0.007522 | 0.005825 | 9 |
| GO:0002820 | BP | GO:0002820 | negative regulation of adaptive immune response | 5/207 | 59/187 | 0.000474 | 0.007522 | 0.005825 | 9 |
| GO:0002822 | BP | GO:0002822 | regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains | 8/207 | 168/187 | 0.000573 | 0.008687 | 0.006727 | 8 |
| GO:20012 33 | BP | GO:2001 233 | regulation of apoptotic signaling pathway | 12/207 | 356/187 23 | 0.000631 | 0.009523 | 0.007375 | 12 |
| GO:00450 89 | BP | GO:0045 089 | positive regulation of innate immune response | 7/207 | 131/187 23 | 0.00064 | 0.009578 | 0.007417 | 7 |
| GO:00508 53 | BP | GO:0050 853 | B cell receptor signaling pathway | 7/207 | 131/187 7 | 0.00064 | 0.009578 | 0.007417 | 7 |
| GO:00603 38 | BP | GO:0060 338 | regulation of type I interferon-mediated signaling pathway | 4/207 | 36/187 3 | 0.000648 | 0.009578 | 0.007417 | 4 |
| GO:00903 22 | BP | GO:0090 322 | regulation of superoxide metabolic process | 4/207 | 36/187 3 | 0.000648 | 0.009578 | 0.007417 | 4 |
| GO:00324 79 | BP | GO:0032 479 | regulation of type I interferon production | 6/207 | 95/187 2 | 0.000652 | 0.009578 | 0.007417 | 6 |
| GO:00326 06 | BP | GO:0032 606 | type I interferon production | 6/207 | 95/187 2 | 0.000652 | 0.009578 | 0.007417 | 6 |
| GO:00027 04 | BP | GO:0002 704 | negative regulation of leukocyte mediated immunity | 5/207 | 63/187 3 | 0.000657 | 0.009578 | 0.007417 | 5 |
| GO:00014 43 | BP | GO:0001 343 | positive regulation of cell killing | 5/207 | 63/187 2 | 0.000657 | 0.009578 | 0.007417 | 5 |
| GO:00075 69 | BP | GO:0007 569 | cell aging | 7/207 | 132/187 | 0.00067 | 0.009578 | 0.007417 | 7 |
| GO:00026 93 | BP | GO:0002 693 | positive regulation of cellular extravasation | 3/207 | 16/187 2 | 0.000671 | 0.009578 | 0.007417 | 3 |
| GO:00300 33 | BP | GO:0030 033 | microvillus assembly | 3/207 | 16/187 2 | 0.000671 | 0.009578 | 0.007417 | 3 |
| GO:00717 32 | BP | GO:0071 732 | cellular response to nitric oxide | 3/207 | 16/187 2 | 0.000671 | 0.009578 | 0.007417 | 3 |
| GO:00905 20 | BP | GO:0090 520 | sphingolipid mediated signaling pathway | 3/207 | 16/187 2 | 0.000671 | 0.009578 | 0.007417 | 3 |
| GO:00308 88 | BP | GO:0030 888 | regulation of B cell proliferation | 5/207 | 64/187 3 | 0.000707 | 0.01001 | 0.007752 | 5 |
| GO:19000 76 | BP | GO:1900 076 | regulation of cellular response to insulin stimulus | 5/207 | 64/187 3 | 0.000707 | 0.01001 | 0.007752 | 5 |
| GO:00434 34 | BP | GO:0043 434 | response to peptide hormone | 13/207 | 414/187 | 0.000731 | 0.01036 | 0.007989 | 13 |
| GO:00450 88 | BP | GO:0045 088 | regulation of innate immune response | 9/207 | 218/187 | 0.000737 | 0.01034 | 0.008008 | 9 |
| GO:00027 64 | BP | GO:0002 764 | immune response-regulating signaling pathway | 14/207 | 468/187 23 | 0.000739 | 0.01034 | 0.008008 | 14 |
| GO:00022 37 | BP | GO:0002 237 | response to molecule of bacterial origin | 12/207 | 363/187 | 0.000748 | 0.010415 | 0.008066 | 12 |
| GO:00716 77 | BP | GO:0071 677 | positive regulation of mononuclear cell migration | 5/207 | 65/187 3 | 0.000759 | 0.01053 | 0.008154 | 5 |
| GO:003537 | BP | GO:0035337 | fatty-acyl-CoA metabolic process | 4/207 | 38/1872 | 0.000798 | 0.010979 | 0.008503 | 4 |
| GO:1903305 | BP | GO:1903305 | regulation of regulated secretory pathway | 7/207 | 136/1872 | 0.0008 | 0.010979 | 0.008503 | 7 |
| GO:0072673 | BP | GO:0072673 | lamellipodium morphogenesis | 3/207 | 17/1872 | 0.000808 | 0.010979 | 0.008503 | 3 |
| GO:00002444 | BP | GO:00002444 | myeloid leukocyte mediated immunity | 6/207 | 99/1872 | 0.000811 | 0.010979 | 0.008503 | 6 |
| GO:0042100 | BP | GO:0042100 | B cell proliferation | 6/207 | 99/1872 | 0.000811 | 0.010979 | 0.008503 | 6 |
| GO:0046626 | BP | GO:0046626 | regulation of insulin receptor signaling pathway | 5/207 | 66/1872 | 0.000814 | 0.010979 | 0.008503 | 5 |
| GO:0072678 | BP | GO:0072678 | T cell migration | 5/207 | 66/1872 | 0.000814 | 0.010979 | 0.008503 | 5 |
| GO:00019058 | BP | GO:00019058 | viral life cycle | 11/207 | 317/187 | 0.000835 | 0.011193 | 0.008668 | 11 |
| GO:0035265 | BP | GO:0035265 | organ growth | 8/207 | 178/187 | 0.000836 | 0.011193 | 0.008668 | 8 |
| GO:0044635 | BP | GO:0044635 | positive regulation of alpha-beta T cell activation | 5/207 | 67/1872 | 0.000872 | 0.011533 | 0.008932 | 5 |
| GO:2000514 | BP | GO:2000514 | regulation of CD4-positive, alpha-beta T cell activation | 5/207 | 67/1872 | 0.000872 | 0.011533 | 0.008932 | 5 |
| GO:0072594 | BP | GO:0072594 | establishment of protein localization to organelle | 13/207 | 422/1872 | 0.000872 | 0.011533 | 0.008932 | 13 |
| GO:0048608 | BP | GO:0048608 | reproductive structure development | 13/207 | 424/1872 | 0.00091 | 0.011995 | 0.00929 | 13 |
| GO:0043410 | BP | GO:0043410 | positive regulation of MAPK cascade | 14/207 | 480/187 | 0.000943 | 0.012383 | 0.00959 | 14 |
| GO:0006672 | BP | GO:0006672 | ceramide metabolic process | 6/207 | 102/187 | 0.000948 | 0.012396 | 0.0096 | 6 |
| GO:0002283 | BP | GO:0002283 | neutrophil activation involved in immune response | 3/207 | 18/1872 | 0.000962 | 0.01243 | 0.009627 | 3 |
| GO:1902170 | BP | GO:1902170 | cellular response to reactive nitrogen species | 3/207 | 18/1872 | 0.000962 | 0.01243 | 0.009627 | 3 |
| GO:2000641 | BP | GO:2000641 | regulation of early endosome to late endosome transport | 3/207 | 18/1872 | 0.000962 | 0.01243 | 0.009627 | 3 |
| GO:0061458 | BP | GO:0061458 | reproductive system development | 13/207 | 427/187 | 0.000971 | 0.012461 | 0.009651 | 13 |
| GO:0030866 | BP | GO:0030866 | cortical actin cytoskeleton organization | 4/207 | 40/1872 | 0.000971 | 0.012461 | 0.009651 | 4 |
| GO:0018108 | BP | GO:0018108 | peptidyl-tyrosine phosphorylation | 12/207 | 375/187 | 0.000991 | 0.012662 | 0.009806 | 12 |
| GO:0032760 | BP  | GO:0032760 | positive regulation of tumor necrosis factor production | 6/2 07 | 103/187 23 | 0.000997 | 0.012694 | 0.009831 | 6 |
|------------|-----|-----------|--------------------------------------------------------|------|-----------|----------|----------|----------|---|
| GO:0002819 | BP  | GO:0002819 | regulation of adaptive immune response                  | 8/2 07 | 183/187   | 0.001    | 0.012694 | 0.009831 | 8 |
| GO:0032006 | BP  | GO:0032006 | regulation of TOR signaling                            | 6/2 07 | 104/187   | 0.001049 | 0.013259 | 0.010268 | 6 |
| GO:0018212 | BP  | GO:0018212 | peptidyl-tyrosine modification                          | 12/207| 378/187   | 0.001061 | 0.013357 | 0.010344 | 12|
| GO:1902622 | BP  | GO:1902622 | regulation of neutrophil migration                     | 4/2 07 | 41/1872   | 0.001067 | 0.013388 | 0.010368 | 4 |
| GO:0002683 | BP  | GO:0002683 | negative regulation of immune system process           | 13/207| 434/187   | 0.001124 | 0.013873 | 0.010744 | 13|
| GO:0014067 | BP  | GO:0014067 | negative regulation of phosphatidylinositol 3-kinase signaling | 3/2 07 | 19/1872   | 0.001133 | 0.013873 | 0.010744 | 3 |
| GO:0030011 | BP  | GO:0030011 | maintenance of cell polarity                           | 3/2 07 | 19/1872   | 0.001133 | 0.013873 | 0.010744 | 3 |
| GO:0030220 | BP  | GO:0030220 | platelet formation                                     | 3/2 07 | 19/1872   | 0.001133 | 0.013873 | 0.010744 | 3 |
| GO:0036344 | BP  | GO:0036344 | platelet morphogenesis                                 | 3/2 07 | 19/1872   | 0.001133 | 0.013873 | 0.010744 | 3 |
| GO:0072074 | BP  | GO:0072074 | kidney mesenchyme development                          | 3/2 07 | 19/1872   | 0.001133 | 0.013873 | 0.010744 | 3 |
| GO:0150116 | BP  | GO:0150116 | regulation of cell-substrate junction organization      | 5/2 07 | 71/1872   | 0.001134 | 0.013873 | 0.010744 | 5 |
| GO:0002695 | BP  | GO:0002695 | negative regulation of leukocyte activation            | 8/2 07 | 187/187   | 0.001157 | 0.014013 | 0.010852 | 8 |
| GO:0046620 | BP  | GO:0046620 | regulation of organ growth                              | 6/2 07 | 106/187   | 0.001158 | 0.014065 | 0.010892 | 6 |
| GO:0006040 | BP  | GO:0006040 | amino sugar metabolic process                          | 4/2 07 | 42/1872   | 0.001169 | 0.014101 | 0.010924 | 4 |
| GO:0030890 | BP  | GO:0030890 | positive regulation of B cell proliferation             | 4/2 07 | 42/1872   | 0.001169 | 0.014101 | 0.010924 | 4 |
| GO:0007160 | BP  | GO:0007160 | cell-matrix adhesion                                   | 9/2 07 | 233/187   | 0.001177 | 0.014144 | 0.010954 | 9 |
| GO:0006470 | BP  | GO:0006470 | protein dephosphorylation                               | 10/207| 281/187   | 0.001183 | 0.014169 | 0.010973 | 10|
| GO:0042542 | BP  | GO:0042542 | response to hydrogen peroxide                          | 7/2 07 | 146/187   | 0.001211 | 0.014406 | 0.011157 | 7 |
| GO:0007229 | BP  | GO:0007229 | integrin-mediated signaling pathway                    | 6/2 07 | 107/187   | 0.001216 | 0.014406 | 0.011157 | 6 |
| GO:1903557 | BP  | GO:1903557 | positive regulation of tumor necrosis factor superfamily cytokine production | 6/2 07 | 107/187   | 0.001216 | 0.014406 | 0.011157 | 6 |
| GO:0043299 | BP  | GO:0043299 | leukocyte degranulation                                 | 5/2 07 | 73/1872   | 0.001285 | 0.015178 | 0.011755 | 5 |
| GO:0009100 | BP | GO:0009100 | glycoprotein metabolic process | 12/207 | 387/187 | 0.001296 | 0.015251 | 0.011811 | 12 |
|----------|----|------------|-------------------------------|-------|-------|------|-------|------|-----|
| GO:0032986 | BP | GO:0032986 | protein-DNA complex disassembly | 3/207 | 20/1872 | 0.001322 | 0.015342 | 0.011882 | 3 |
| GO:0046629 | BP | GO:0046629 | gamma-delta T cell activation | 3/207 | 20/1872 | 0.001322 | 0.015342 | 0.011882 | 3 |
| GO:0071731 | BP | GO:0071731 | response to nitric oxide | 3/207 | 20/1872 | 0.001322 | 0.015342 | 0.011882 | 3 |
| GO:0097503 | BP | GO:0097503 | sialylation | 3/207 | 20/1872 | 0.001322 | 0.015342 | 0.011882 | 3 |
| GO:0002456 | BP | GO:0002456 | T cell mediated immunity | 6/109 | 187 | 0.001338 | 0.015476 | 0.011985 | 6 |
| GO:0032386 | BP | GO:0032386 | regulation of intracellular transport | 11/337 | 187 | 0.001366 | 0.015753 | 0.012199 | 11 |
| GO:0042554 | BP | GO:0042554 | superoxide anion generation | 4/44 | 1872 | 0.001394 | 0.016017 | 0.012404 | 4 |
| GO:0001959 | BP | GO:0001959 | regulation of cytokine-mediated signaling pathway | 7/150 | 18723 | 0.001416 | 0.016217 | 0.012559 | 7 |
| GO:0097193 | BP | GO:0097193 | intrinsic apoptotic signaling pathway | 10/288 | 187 | 0.001422 | 0.016229 | 0.012568 | 10 |
| GO:0007568 | BP | GO:0007568 | aging | 11/339 | 187 | 0.001432 | 0.016291 | 0.012616 | 11 |
| GO:0050851 | BP | GO:0050851 | antigen receptor-mediated signaling pathway | 9/240 | 18723 | 0.001445 | 0.016384 | 0.012688 | 9 |
| GO:0034504 | BP | GO:0034504 | protein localization to nucleus | 10/290 | 187 | 0.001497 | 0.016915 | 0.013099 | 10 |
| GO:0034315 | BP | GO:0034315 | regulation of Arp2/3 complex-mediated actin nucleation | 3/21 | 8723 | 0.001529 | 0.017208 | 0.013327 | 3 |
| GO:0032609 | BP | GO:0032609 | interferon-gamma production | 6/112 | 187 | 0.001538 | 0.017208 | 0.013327 | 6 |
| GO:0032649 | BP | GO:0032649 | regulation of interferon-gamma production | 6/112 | 18723 | 0.001538 | 0.017208 | 0.013327 | 6 |
| GO:0022408 | BP | GO:0022408 | negative regulation of cell-cell adhesion | 8/196 | 187 | 0.00155 | 0.017293 | 0.013392 | 8 |
| GO:0001822 | BP | GO:0001822 | kidney development | 10/293 | 187 | 0.001615 | 0.017955 | 0.013905 | 10 |
| GO:2000107 | BP | GO:2000107 | negative regulation of leukocyte apoptotic process | 4/46 | 18723 | 0.001647 | 0.01825 | 0.014134 | 4 |
| GO:0002286 | BP | GO:0002286 | T cell activation involved in immune response | 6/114 | 18723 | 0.001683 | 0.018594 | 0.0144 | 6 |
| GO:0006606 | BP | GO:0006606 | protein import into nucleus | 7/155 | 187 | 0.001709 | 0.018726 | 0.014502 | 7 |
| GO:0031668 | BP | GO:0031668 | cellular response to extracellular stimulus | 9/246 | 187 | 0.001712 | 0.018726 | 0.014502 | 9 |
| GO:0071216 | BP | GO:0071216 | cellular response to biotic stimulus | 9/2 | 246/187 | 0.001712 | 0.018726 | 0.014502 | 9 |
|------------|----|------------|-------------------------------------|-----|---------|----------|----------|----------|----|
| GO:0070373 | BP | GO:0070373 | negative regulation of ERK1 and ERK2 cascade | 5/2 | 78/1873 | 0.001728 | 0.018842 | 0.014592 | 5 |
| GO:0032069 | BP | GO:0032069 | regulation of nuclease activity | 3/2 | 22/1872 | 0.001757 | 0.018971 | 0.014692 | 3 |
| GO:0043371 | BP | GO:0043371 | negative regulation of CD4-positive, alpha-beta T cell differentiation | 3/2 | 22/1872 | 0.001757 | 0.018971 | 0.014692 | 3 |
| GO:0046628 | BP | GO:0046628 | positive regulation of insulin receptor signaling pathway | 3/2 | 22/1872 | 0.001757 | 0.018971 | 0.014692 | 3 |
| GO:0045646 | BP | GO:0045646 | regulation of erythrocyte differentiation | 4/2 | 47/1872 | 0.001785 | 0.019216 | 0.014881 | 4 |
| GO:0018107 | BP | GO:0018107 | peptidyl-threonine phosphorylation | 6/2 | 116/187 | 0.001839 | 0.019678 | 0.01524 | 6 |
| GO:0043200 | BP | GO:0043200 | response to amino acid | 6/2 | 116/187 | 0.001839 | 0.019678 | 0.01524 | 6 |
| GO:0032388 | BP | GO:0032388 | positive regulation of intracellular transport | 8/2 | 202/187 | 0.001874 | 0.019989 | 0.01548 | 8 |
| GO:0072676 | BP | GO:0072676 | lymphocyte migration | 6/2 | 117/187 | 0.001921 | 0.020426 | 0.015819 | 6 |
| GO:2001238 | BP | GO:2001238 | positive regulation of extrinsic apoptotic signaling pathway | 4/2 | 48/1872 | 0.00193 | 0.020461 | 0.015846 | 4 |
| GO:0051170 | BP | GO:0051170 | import into nucleus | 7/2 | 159/187 | 0.001976 | 0.020875 | 0.016166 | 7 |
| GO:0018279 | BP | GO:0018279 | protein N-linked glycosylation via asparagine | 3/2 | 23/1872 | 0.002004 | 0.021041 | 0.016295 | 3 |
| GO:1903306 | BP | GO:1903306 | negative regulation of regulated secretory pathway | 3/2 | 23/1872 | 0.002004 | 0.021041 | 0.016295 | 3 |
| GO:2000106 | BP | GO:2000106 | regulation of leukocyte apoptotic process | 5/2 | 81/1872 | 0.002042 | 0.021378 | 0.016556 | 5 |
| GO:0035088 | BP | GO:0035088 | establishment or maintenance of apical/basal cell polarity | 4/2 | 49/1872 | 0.002084 | 0.021619 | 0.016743 | 4 |
| GO:0061245 | BP | GO:0061245 | establishment or maintenance of bipolar cell polarity | 4/2 | 49/1872 | 0.002084 | 0.021619 | 0.016743 | 4 |
| GO:1902041 | BP | GO:1902041 | regulation of extrinsic apoptotic signaling pathway via death domain receptors | 4/2 | 49/1872 | 0.002084 | 0.021619 | 0.016743 | 4 |
| GO:0017038 | BP | GO:0017038 | protein import | 8/2 | 206/187 | 0.002118 | 0.021906 | 0.016965 | 8 |
| GO:00023 12 | BP | GO:0002 312 | B cell activation involved in immune response | 5/2 07 | 82/1 872 3 | 0.002155 | 0.022225 | 0.017212 5 |
|---|---|---|---|---|---|---|---|---|
| GO:00607 59 | BP | GO:0060 759 | regulation of response to cytokine stimulus | 7/2 07 | 162/1 872 23 | 0.002196 | 0.022574 | 0.017482 7 |
| GO:00380 93 | BP | GO:0038 093 | Fc receptor signaling pathway | 4/2 07 | 50/1 872 | 0.002246 | 0.022881 | 0.01772 4 |
| GO:00466 38 | BP | GO:0046 638 | positive regulation of alpha-beta T cell differentiation | 4/2 07 | 50/1 872 3 | 0.002246 | 0.022881 | 0.01772 4 |
| GO:19015 70 | BP | GO:1901 570 | fatty acid derivative biosynthetic process | 4/2 07 | 50/1 872 | 0.002246 | 0.022881 | 0.01772 4 |
| GO:00017 79 | BP | GO:0001 779 | natural killer cell differentiation | 3/2 07 | 24/1 872 | 0.002271 | 0.022955 | 0.017777 3 |
| GO:00181 96 | BP | GO:0018 196 | peptidyl-asparagine modification | 3/2 07 | 24/1 872 | 0.002271 | 0.022955 | 0.017777 3 |
| GO:00433 67 | BP | GO:0043 367 | CD4-positive, alpha-beta T cell differentiation | 5/2 07 | 83/1 872 3 | 0.002273 | 0.022955 | 0.017777 5 |
| GO:00712 22 | BP | GO:0071 222 | cellular response to lipopolysaccharide | 8/2 07 | 209/1 187 | 0.002317 | 0.023326 | 0.018064 8 |
| GO:00456 37 | BP | GO:0045 637 | regulation of myeloid cell differentiation | 8/2 07 | 210/1 187 | 0.002386 | 0.023954 | 0.018551 8 |
| GO:00328 73 | BP | GO:0032 873 | negative regulation of stress-activated MAPK cascade | 4/2 07 | 51/1 872 3 | 0.002416 | 0.024112 | 0.018674 4 |
| GO:00703 03 | BP | GO:0070 303 | negative regulation of stress-activated protein kinase signaling cascade | 4/2 07 | 51/1 872 3 | 0.002416 | 0.024112 | 0.018674 4 |
| GO:00326 35 | BP | GO:0032 635 | interleukin-6 production | 7/2 07 | 165/1 187 | 0.002435 | 0.024155 | 0.018707 7 |
| GO:00326 75 | BP | GO:0032 675 | regulation of interleukin-6 production | 7/2 07 | 165/1 187 23 | 0.002435 | 0.024155 | 0.018707 7 |
| GO:00301 68 | BP | GO:0030 168 | platelet activation | 6/2 07 | 123/1 187 | 0.002472 | 0.024384 | 0.018884 6 |
| GO:00508 52 | BP | GO:0050 852 | T cell receptor signaling pathway | 6/2 07 | 123/1 187 | 0.002472 | 0.024384 | 0.018884 6 |
| GO:00027 09 | BP | GO:0002 709 | regulation of T cell mediated immunity | 5/2 07 | 85/1 872 | 0.002523 | 0.024817 | 0.019219 5 |
| GO:00353 36 | BP | GO:0035 336 | long-chain fatty-acyl-CoA metabolic process | 3/2 07 | 25/1 872 3 | 0.00256 | 0.024966 | 0.019334 3 |
| GO:00469 49 | BP | GO:0046 949 | fatty-acyl-CoA biosynthetic process | 3/2 07 | 25/1 872 | 0.00256 | 0.024966 | 0.019334 3 |
| GO:19000 78 | BP | GO:1900 078 | positive regulation of cellular response to insulin stimulus | 3/2 07 | 25/1 872 3 | 0.00256 | 0.024966 | 0.019334 3 |
| GO:00432 77 | BP | GO:0043 277 | apoptotic cell clearance | 4/2 07 | 52/1 872 | 0.002595 | 0.025235 | 0.019543 4 |
| GO          | BP       | Description                                | q-values | Fisher's p-values | False discovery rates | p-values | q-values | FDR p-values | Count |
|-------------|----------|--------------------------------------------|----------|-------------------|-----------------------|----------|----------|--------------|--------|
| GO:0006493  | BP       | protein O-linked glycosylation             | 0.002655 | 0.025637          | 0.019855              | 0.002655 | 0.025637 | 0.019855     | 5      |
| GO:0022406  | BP       | membrane docking                           | 0.002655 | 0.025637          | 0.019855              | 0.002655 | 0.025637 | 0.019855     | 5      |
| GO:0042060  | BP       | wound healing                              | 0.002659 | 0.025637          | 0.019951              | 0.025762 | 0.019855 | 0.019951     | 12     |
| GO:0018210  | BP       | peptidyl-threonine modification            | 0.00268  | 0.025762          | 0.020472              | 0.026147 | 0.019944 | 0.020472     | 10     |
| GO:0002833  | BP       | positive regulation of response to biotic stimulus | 0.002693 | 0.025818          | 0.020472              | 0.026434 | 0.020472 | 0.020472     | 7      |
| GO:0018105  | BP       | peptidyl-serine phosphorylation            | 0.002735 | 0.026147          | 0.020472              | 0.026434 | 0.020472 | 0.020472     | 10     |
| GO:0022406  | BP       | regulation of peptidyl-tyrosine phosphorylation | 0.002757 | 0.026284          | 0.020355              | 0.026784 | 0.020355 | 0.020355     | 9      |
| GO:0002707  | BP       | negative regulation of lymphocyte mediated immunity | 0.002783 | 0.026434          | 0.020472              | 0.027942 | 0.020472 | 0.020472     | 4      |
| GO:0031929  | BP       | TOR signaling                              | 0.002788 | 0.026434          | 0.020472              | 0.028177 | 0.020472 | 0.020472     | 6      |
| GO:0046639  | BP       | negative regulation of alpha-beta T cell differentiation | 0.002817 | 0.027141          | 0.021019              | 0.028177 | 0.021019 | 0.021019     | 3      |
| GO:0070374  | BP       | positive regulation of ERK1 and ERK2 cascade | 0.002919 | 0.027506          | 0.021302              | 0.028177 | 0.021302 | 0.021302     | 8      |
| GO:0031331  | BP       | positive regulation of cellular catabolic process | 0.002926 | 0.027506          | 0.021302              | 0.028177 | 0.021302 | 0.021302     | 12     |
| GO:0070228  | BP       | regulation of lymphocyte apoptotic process | 0.00298  | 0.027942          | 0.02164               | 0.030077 | 0.02164 | 0.02164      | 4      |
| GO:2001020  | BP       | regulation of response to DNA damage stimulus | 0.003087 | 0.028868          | 0.022357              | 0.030077 | 0.022357 | 0.022357     | 8      |
| GO:0034109  | BP       | homotypic cell-cell adhesion                | 0.003234 | 0.030077          | 0.023292              | 0.030077 | 0.023292 | 0.023292     | 5      |
| GO:0035304  | BP       | regulation of protein dephosphorylation     | 0.003234 | 0.030077          | 0.023292              | 0.030077 | 0.023292 | 0.023292     | 5      |
| GO:0010810  | BP       | regulation of cell-substrate adhesion       | 0.003263 | 0.030179          | 0.023372              | 0.030179 | 0.023372 | 0.023372     | 8      |
| GO:0071219  | BP       | cellular response to molecule of bacterial origin | 0.003263 | 0.030179          | 0.023372              | 0.030179 | 0.023372 | 0.023372     | 8      |
| GO:0000302  | BP       | response to reactive oxygen species         | 0.003353 | 0.030933          | 0.023956              | 0.030933 | 0.023956 | 0.023956     | 8      |
| GO:0002275  | BP       | myeloid cell activation involved in immune response | 0.003392 | 0.030965          | 0.023981              | 0.030965 | 0.023981 | 0.023981     | 5      |
| GO:0050878  | BP       | regulation of body fluid levels             | 0.003397 | 0.030965          | 0.023981              | 0.030965 | 0.023981 | 0.023981     | 11     |
| GO:00019    | BP | GO:00019  | positive regulation of leukocyte mediated cytotoxicity | 4/2 | 07 | 56/1 872 3 | 0.003402 | 0.030965 | 0.023981 | 4 |
|-------------|----|-----------|--------------------------------------------------------|-----|----|------------|---------|---------|---------|---|
| GO:00326 08 | BP | GO:00326  | interferon-beta production                              | 4/2 | 07 | 56/1 872 3 | 0.003402 | 0.030965 | 0.023981 | 4 |
| GO:00326 48 | BP | GO:00326  | regulation of interferon-beta production               | 4/2 | 07 | 56/1 872 3 | 0.003402 | 0.030965 | 0.023981 | 4 |
| GO:00509 20 | BP | GO:00509  | regulation of chemotaxis                               | 8/2 | 07 | 223/187    | 0.003446 | 0.03128  | 0.024225 | 8 |
| GO:00023 13 | BP | GO:00023  | mature B cell differentiation involved in immune response | 3/2 | 07 | 28/1 872 3 | 0.003559 | 0.032044 | 0.024816 | 3 |
| GO:00903 44 | BP | GO:00903  | negative regulation of cell aging                     | 3/2 | 07 | 28/1 872 3 | 0.003559 | 0.032044 | 0.024816 | 3 |
| GO:19036 49 | BP | GO:19036  | regulation of cytoplasmic transport                    | 3/2 | 07 | 28/1 872 3 | 0.003559 | 0.032044 | 0.024816 | 3 |
| GO:00028 31 | BP | GO:00028  | regulation of response to biotic stimulus              | 10/2 | 07 | 327/187 23 | 0.003568 | 0.032044 | 0.024816 | 10 |
| GO:00617 56 | BP | GO:00617  | leukocyte adhesion to vascular endothelial cell         | 4/2 | 07 | 57/1 872 3 | 0.003628 | 0.032498 | 0.025168 | 4 |
| GO:00903 98 | BP | GO:00903  | cellular senescence                                    | 5/2 | 07 | 93/1 872 3 | 0.003724 | 0.033275 | 0.025769 | 5 |
| GO:00712 41 | BP | GO:00712  | cellular response to inorganic substance               | 8/2 | 07 | 226/187    | 0.003736 | 0.03329  | 0.025781 | 8 |
| GO:00027 05 | BP | GO:00027  | positive regulation of leukocyte mediated immunity      | 6/2 | 07 | 134/187 23 | 0.00378  | 0.033595 | 0.026017 | 6 |
| GO:00486 38 | BP | GO:00486  | regulation of developmental growth                     | 10/2 | 07 | 330/187 23 | 0.003805 | 0.033727 | 0.026119 | 10 |
| GO:00100 43 | BP | GO:00100  | response to zinc ion                                   | 4/2 | 07 | 58/1 872 3 | 0.003863 | 0.034072 | 0.026386 | 4 |
| GO:00324 81 | BP | GO:00324  | positive regulation of type I interferon production    | 4/2 | 07 | 58/1 872 3 | 0.003863 | 0.034072 | 0.026386 | 4 |
| GO:00017 38 | BP | GO:00017  | morphogenesis of a polarized epithelium                  | 5/2 | 07 | 94/1 872 3 | 0.003899 | 0.034296 | 0.026565 | 5 |
| GO:00011 01 | BP | GO:00011  | response to acid chemical                               | 6/2 | 07 | 135/187    | 0.00392  | 0.034393 | 0.026636 | 6 |
| GO:00190 82 | BP | GO:00190  | viral protein processing                                | 3/2 | 07 | 29/1 872 3 | 0.003938 | 0.034459 | 0.026687 | 3 |
| GO:00331 57 | BP | GO:00331  | regulation of intracellular protein transport           | 8/2 | 07 | 229/187 23 | 0.004044 | 0.035299 | 0.027337 | 8 |
| GO:00085 93 | BP | GO:00085  | regulation of Notch signaling pathway                  | 5/2 | 07 | 95/1 872 3 | 0.004079 | 0.035516 | 0.027505 | 5 |
| GO:00069 79 | BP | GO:00069  | response to oxidative stress                           | 12/2 | 07 | 446/187    | 0.004142 | 0.035975 | 0.027861 | 12 |
| GO:0045471 | BP | GO:0045471 | response to ethanol | 6/2 | 137/187 | 0.004212 | 0.036486 | 0.028256 | 6 |
| GO:1901655 | BP | GO:1901655 | cellular response to ketone | 5/2 | 96/187 | 0.004266 | 0.036856 | 0.028543 | 5 |
| GO:0010800 | BP | GO:0010800 | positive regulation of peptidyl-threonine phosphorylation | 3/2 | 30/187 | 0.00434 | 0.037216 | 0.028822 | 3 |
| GO:0051125 | BP | GO:0051125 | regulation of actin nucleation | 3/2 | 30/187 | 0.00434 | 0.037216 | 0.028822 | 3 |
| GO:0070229 | BP | GO:0070229 | negative regulation of lymphocyte apoptotic process | 3/2 | 30/187 | 0.00434 | 0.037216 | 0.028822 | 3 |
| GO:0018209 | BP | GO:0018209 | peptidyl-serine modification | 10/207 | 338/187 | 0.004497 | 0.038470 | 0.029793 | 10 |
| GO:0002699 | BP | GO:0002699 | positive regulation of immune effector process | 8/207 | 235/187 | 0.004719 | 0.040265 | 0.031183 | 8 |
| GO:0001782 | BP | GO:0001782 | B cell homeostasis | 3/2 | 31/187 | 0.004766 | 0.040364 | 0.031260 | 3 |
| GO:0008045 | BP | GO:0008045 | motor neuron axon guidance | 3/2 | 31/187 | 0.004766 | 0.040364 | 0.031260 | 3 |
| GO:0090183 | BP | GO:0090183 | regulation of kidney development | 3/2 | 31/187 | 0.004766 | 0.040364 | 0.031260 | 3 |
| GO:0002260 | BP | GO:0002260 | lymphocyte homeostasis | 4/2 | 62/187 | 0.004909 | 0.041165 | 0.031880 | 4 |
| GO:0032613 | BP | GO:0032613 | interleukin-10 production | 4/2 | 62/187 | 0.004909 | 0.041165 | 0.031880 | 4 |
| GO:0032653 | BP | GO:0032653 | regulation of interleukin-10 production | 4/2 | 62/187 | 0.004909 | 0.041165 | 0.031880 | 4 |
| GO:0045428 | BP | GO:0045428 | regulation of nitric oxide biosynthetic process | 4/2 | 62/187 | 0.004909 | 0.041165 | 0.031880 | 4 |
| GO:0007346 | BP | GO:0007346 | regulation of mitotic cell cycle | 12/207 | 457/187 | 0.005015 | 0.041951 | 0.032488 | 12 |
| GO:0061640 | BP | GO:0061640 | cytoskeleton-dependent cytokinesis | 5/2 | 100/187 | 0.005071 | 0.042262 | 0.032729 | 5 |
| GO:0001865 | BP | GO:0001865 | NK T cell differentiation | 2/2 | 10/187 | 0.005164 | 0.042262 | 0.032729 | 2 |
| GO:0001915 | BP | GO:0001915 | negative regulation of T cell mediated cytotoxicity | 2/2 | 10/187 | 0.005164 | 0.042262 | 0.032729 | 2 |
| GO:0002291 | BP | GO:0002291 | T cell activation via T cell receptor contact with antigen bound to MHC molecule on antigen presenting cell | 2/2 | 10/187 | 0.005164 | 0.042262 | 0.032729 | 2 |
| GO:0019062 | BP | GO:0019062 | virion attachment to host cell | 2/2 | 10/187 | 0.005164 | 0.042262 | 0.032729 | 2 |
| GO:00309 53 | BP | GO:0030 953 | astral microtubule organization | 2/2 07 | 10/1 872 | 0.005164 | 0.042262 | 0.032729 | 2 |
| GO:00320 70 | BP | GO:0032 070 | regulation of deoxyribonuclease activity | 2/2 07 | 10/1 872 3 | 0.005164 | 0.042262 | 0.032729 | 2 |
| GO:00603 68 | BP | GO:0060 368 | regulation of Fc receptor mediated stimulatory signaling pathway | 2/2 07 | 10/1 872 3 | 0.005164 | 0.042262 | 0.032729 | 2 |
| GO:19029 46 | BP | GO:1902 946 | protein localization to early endosome | 2/2 07 | 10/1 872 | 0.005164 | 0.042262 | 0.032729 | 2 |
| GO:00508 54 | BP | GO:0050 854 | regulation of antigen receptor-mediated signaling pathway | 4/2 07 | 63/1 872 3 | 0.005197 | 0.042393 | 0.032831 | 3 |
| GO:00433 72 | BP | GO:0043 372 | positive regulation of CD4-positive, alpha-beta T cell differentiation | 3/2 07 | 32/1 872 3 | 0.005217 | 0.042393 | 0.032831 | 3 |
| GO:20005 15 | BP | GO:2000 515 | negative regulation of CD4-positive, alpha-beta T cell activation | 3/2 07 | 32/1 872 3 | 0.005217 | 0.042393 | 0.032831 | 3 |
| GO:01501 15 | BP | GO:0150 115 | cell-substrate junction organization | 5/2 07 | 101/187 | 0.005289 | 0.042875 | 0.033204 | 5 |
| GO:00018 85 | BP | GO:0001 885 | endothelial cell development | 4/2 07 | 64/1 872 | 0.005497 | 0.044349 | 0.034346 | 4 |
| GO:00801 64 | BP | GO:0080 164 | regulation of nitric oxide metabolic process | 4/2 07 | 64/1 872 3 | 0.005497 | 0.044349 | 0.034346 | 4 |
| GO:00357 10 | BP | GO:0035 710 | CD4-positive, alpha-beta T cell activation | 5/2 07 | 102/187 | 0.005512 | 0.044373 | 0.034364 | 5 |
| GO:00165 70 | BP | GO:0016 570 | histone modification | 12/207 | 463/187 | 0.005549 | 0.044565 | 0.034512 | 12 |
| GO:00023 35 | BP | GO:0002 335 | mature B cell differentiation | 3/2 07 | 33/1 872 | 0.005692 | 0.045392 | 0.035154 | 3 |
| GO:00341 10 | BP | GO:0034 110 | regulation of homotypic cell-cell adhesion | 3/2 07 | 33/1 872 3 | 0.005692 | 0.045392 | 0.035154 | 3 |
| GO:00459 20 | BP | GO:0045 920 | negative regulation of exocytosis | 3/2 07 | 33/1 872 | 0.005692 | 0.045392 | 0.035154 | 3 |
| GO:00024 49 | BP | GO:0002 449 | lymphocyte mediated immunity | 10/207 | 350/187 | 0.005719 | 0.045501 | 0.035237 | 10 |
| GO:00456 39 | BP | GO:0045 639 | positive regulation of myeloid cell differentiation | 5/2 07 | 103/187 23 | 0.005743 | 0.045582 | 0.035301 | 5 |
| GO:00454 53 | BP | GO:0045 453 | bone resorption | 4/2 07 | 65/1 872 | 0.005807 | 0.045986 | 0.035613 | 4 |
| GO:00507 77 | BP | GO:0050 777 | negative regulation of immune response | 7/2 07 | 194/187 | 0.005908 | 0.046677 | 0.036148 | 7 |
| GO:00336 74 | BP | GO:0033 674 | positive regulation of kinase activity | 12/207 | 467/187 | 0.00593 | 0.046743 | 0.036199 | 12 |
| GO:0031346 | BP | GO:0031346 | positive regulation of cell projection organization | 10/207 | 353/187 | 0.006062 | 0.047308 | 0.036637 | 10 |
| GO:2001056 | BP | GO:2001056 | positive regulation of cysteine-type endopeptidase activity | 6/207 | 148/187 | 0.006113 | 0.047308 | 0.036637 | 6 |
| GO:0002562 | BP | GO:0002562 | somatic diversification of immune receptors via germline recombination within a single locus | 4/207 | 66/1872 | 0.006129 | 0.047308 | 0.036637 | 4 |
| GO:0016444 | BP | GO:0016444 | somatic cell DNA recombination | 4/207 | 66/1872 | 0.006129 | 0.047308 | 0.036637 | 4 |
| GO:0050766 | BP | GO:0050766 | positive regulation of phagocytosis | 4/207 | 66/1872 | 0.006129 | 0.047308 | 0.036637 | 4 |
| GO:0051893 | BP | GO:0051893 | regulation of focal adhesion assembly | 4/207 | 66/1872 | 0.006129 | 0.047308 | 0.036637 | 4 |
| GO:0090109 | BP | GO:0090109 | regulation of cell-substrate junction assembly | 4/207 | 66/1872 | 0.006129 | 0.047308 | 0.036637 | 4 |
| GO:0044319 | BP | GO:0044319 | wound healing, spreading of cells | 3/207 | 34/1872 | 0.006193 | 0.047308 | 0.036637 | 3 |
| GO:0090505 | BP | GO:0090505 | epiboly involved in wound healing | 3/207 | 34/1872 | 0.006193 | 0.047308 | 0.036637 | 3 |
| GO:2001022 | BP | GO:2001022 | positive regulation of response to DNA damage stimulus | 5/207 | 105/1872 | 0.006224 | 0.047308 | 0.036637 | 5 |
| GO:0031032 | BP | GO:0031032 | actomyosin structure organization | 7/207 | 196/187 | 0.00624 | 0.047308 | 0.036637 | 7 |
| GO:0035090 | BP | GO:0035090 | maintenance of apical/basal cell polarity | 2/207 | 11/1872 | 0.006265 | 0.047308 | 0.036637 | 2 |
| GO:0035457 | BP | GO:0035457 | cellular response to interferon-alpha | 2/207 | 11/1872 | 0.006265 | 0.047308 | 0.036637 | 2 |
| GO:0045199 | BP | GO:0045199 | maintenance of epithelial cell apical/basal polarity | 2/207 | 11/1872 | 0.006265 | 0.047308 | 0.036637 | 2 |
| GO:0045654 | BP | GO:0045654 | positive regulation of megakaryocyte differentiation | 2/207 | 11/1872 | 0.006265 | 0.047308 | 0.036637 | 2 |
| GO:0046501 | BP | GO:0046501 | protoporphyrinogen IX metabolic process | 2/207 | 11/1872 | 0.006265 | 0.047308 | 0.036637 | 2 |
| GO:0048096 | BP | GO:0048096 | chromatin-mediated maintenance of transcription | 2/207 | 11/1872 | 0.006265 | 0.047308 | 0.036637 | 2 |
| GO:0060746 | BP | GO:0060746 | parental behavior | 2/207 | 11/1872 | 0.006265 | 0.047308 | 0.036637 | 2 |
| GO:1905668 | BP | GO:1905668 | positive regulation of protein localization to endosome | 2/207 | 11/1872 | 0.006265 | 0.047308 | 0.036637 | 2 |
| GO:0002460 | BP | GO:0002460 | adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains | 10/207 | 356/18723 | 0.00642 | 0.048372 | 0.037461 | 10 |
|---|---|---|---|---|---|---|---|---|---|
| GO:0070527 | BP | GO:0070527 | platelet aggregation | 4/207 | 67/1872 | 0.006463 | 0.04846 | 0.037529 | 4 |
| GO:0042116 | BP | GO:0042116 | macrophage activation | 5/207 | 106/187 | 0.006475 | 0.04846 | 0.037529 | 5 |
| GO:0071887 | BP | GO:0071887 | leukocyte apoptotic process | 5/207 | 106/187 | 0.006475 | 0.04846 | 0.037529 | 5 |
| GO:0001818 | BP | GO:0001818 | negative regulation of cytokine production | 10/207 | 357/187 | 0.006543 | 0.048868 | 0.037845 | 10 |
| GO:0070527 | BP | GO:0070527 | platelet aggregation | 4/207 | 67/1872 | 0.006463 | 0.04846 | 0.037529 | 4 |
| GO:0071887 | BP | GO:0071887 | leukocyte apoptotic process | 5/207 | 106/187 | 0.006475 | 0.04846 | 0.037529 | 5 |
| GO:0001818 | BP | GO:0001818 | negative regulation of cytokine production | 10/207 | 357/187 | 0.006543 | 0.048868 | 0.037845 | 10 |
| GO:0050864 | BP | GO:0050864 | regulation of B cell activation | 7/207 | 198/187 | 0.006585 | 0.049071 | 0.038002 | 7 |
| GO:0031667 | BP | GO:0031667 | response to nutrient levels | 12/207 | 474/187 | 0.006646 | 0.04942 | 0.038273 | 12 |
| GO:0046640 | BP | GO:0046640 | regulation of alpha-beta T cell proliferation | 3/207 | 35/1872 | 0.006719 | 0.049465 | 0.038307 | 3 |
| GO:0048821 | BP | GO:0048821 | erythrocyte development | 3/207 | 35/1872 | 0.006719 | 0.049465 | 0.038307 | 3 |
| GO:0071108 | BP | GO:0071108 | protein K48-linked deubiquitination | 3/207 | 35/1872 | 0.006719 | 0.049465 | 0.038307 | 3 |
| GO:0090504 | BP | GO:0090504 | epiboly | 3/207 | 35/1872 | 0.006719 | 0.049465 | 0.038307 | 3 |
| GO:2001236 | BP | GO:2001236 | regulation of extrinsic apoptotic signaling pathway | 6/207 | 151/187 | 0.006725 | 0.049465 | 0.038307 | 6 |
| GO:0051052 | BP | GO:0051052 | regulation of DNA metabolic process | 10/207 | 359/187 | 0.006795 | 0.049875 | 0.038625 | 10 |
| GO:0005747 | CC | GO:0005747 | mitochondrial respiratory chain complex I | 13/216 | 48/19550 | 3.49E-15 | 3.76E-13 | 2.89E-13 | 13 |
| GO:0030964 | CC | GO:0030964 | NADH dehydrogenase complex | 13/216 | 48/19550 | 3.49E-15 | 3.76E-13 | 2.89E-13 | 13 |
| GO:0045271 | CC | GO:0045271 | respiratory chain complex I | 13/216 | 48/19550 | 3.49E-15 | 3.76E-13 | 2.89E-13 | 13 |
| GO:0070469 | CC | GO:0070469 | respirasome | 15/216 | 100/195 | 3.03E-13 | 2.45E-11 | 1.88E-11 | 15 |
| GO:0005746 | CC | GO:0005746 | mitochondrial respirasome | 14/216 | 89/1955 | 9.73E-13 | 6.14E-11 | 4.73E-11 | 14 |
| GO:0098803 | CC | GO:0098803 | respiratory chain complex | 14/216 | 90/1955 | 1.14E-12 | 6.14E-11 | 4.73E-11 | 14 |
| GO:1990204 | CC | GO:1990204 | oxidoreductase complex | 13/216 | 112/195 | 3.31E-10 | 1.53E-08 | 1.17E-08 | 13 |
| GO:0098800 | CC GO:0098800 | inner mitochondrial membrane protein complex | 14/216 | 147/195 | 9.68E-10 | 3.91E-08 | 3.01E-08 | 14 |
|-----------|----------------|---------------------------------------------|--------|--------|-----------|-----------|-----------|----|
| GO:0005925 | CC GO:0005925 | focal adhesion | 21/216 | 418/195 | 8.56E-09 | 3.07E-07 | 2.36E-07 | 21 |
| GO:0030055 | CC GO:0030055 | cell-substrate junction complex | 21/216 | 425/195 | 1.14E-08 | 3.69E-07 | 2.84E-07 | 21 |
| GO:0005743 | CC GO:0005743 | mitochondrial inner membrane | 22/216 | 495/195 | 3.37E-08 | 9.89E-07 | 7.61E-07 | 22 |
| GO:0031209 | CC GO:0031209 | SCAR complex | 5/2 | 12/1 | 1.17E-07 | 3.15E-06 | 2.42E-06 | 5 |
| GO:0030027 | CC GO:0030027 | lamellipodium | 13/216 | 202/195 | 4.11E-07 | 1.02E-05 | 7.85E-06 | 13 |
| GO:0101002 | CC GO:0101002 | ficolin-1-rich granule | 12/216 | 185/195 | 1.06E-06 | 2.45E-05 | 1.89E-05 | 12 |
| GO:0098798 | CC GO:0098798 | mitochondrial protein-containing complex | 14/216 | 268/195 | 1.80E-06 | 3.88E-05 | 2.98E-05 | 14 |
| GO:0030667 | CC GO:0030667 | secretory granule membrane | 14/216 | 311/195 | 1.00E-05 | 0.000202 | 0.000155 | 14 |
| GO:0070820 | CC GO:0070820 | tertiary granule | 10/216 | 164/195 | 1.47E-05 | 0.000279 | 0.000215 | 10 |
| GO:0031252 | CC GO:0031252 | cell leading edge | 16/216 | 422/195 | 1.98E-05 | 0.000356 | 0.000274 | 16 |
| GO:0030175 | CC GO:0030175 | filopodium | 8/2 | 107/195 | 2.49E-05 | 0.000423 | 0.000326 | 8 |
| GO:0016514 | CC GO:0016514 | SWI/SNF complex | 4/2 | 19/1 | 4.93E-05 | 0.000796 | 0.000613 | 4 |
| GO:1902495 | CC GO:1902495 | transmembrane transporter complex | 14/216 | 366/195 | 6.01E-05 | 0.000924 | 0.000711 | 14 |
| GO:0005902 | CC GO:0005902 | microvillus | 7/2 | 91/1 | 6.73E-05 | 0.000987 | 0.000759 | 7 |
| GO:0098562 | CC GO:0098562 | cytoplasmic side of membrane | 10/216 | 197/195 | 7.04E-05 | 0.000988 | 0.00076 | 10 |
| GO:1990351 | CC GO:1990351 | transporter complex | 14/216 | 381/195 | 9.21E-05 | 0.001187 | 0.000913 | 14 |
| GO:0045121 | CC GO:0045121 | membrane raft | 13/216 | 335/195 | 9.55E-05 | 0.001187 | 0.000913 | 13 |
| GO:0098857 | CC GO:0098857 | membrane microdomain | 13/216 | 335/195 | 9.55E-05 | 0.001187 | 0.000913 | 13 |
| GO:00099998 | CC GO:00099989 | cytoplasmic side of plasma membrane | 9/2 | 172/195 | 0.000129 | 0.001541 | 0.001185 | 9 |
| GO:0035861 | CC GO:0035861 | site of double-strand break | 6/2 | 73/1 | 0.000156 | 0.001737 | 0.001336 | 6 |
| GO:0007021 | CC GO:0007021 | tertiary granule membrane | 6/2 | 73/1 | 0.000156 | 0.001737 | 0.001336 | 6 |
| GO:0098858 | CC GO:0098858 | actin-based cell projection | 10/216 | 221/195 | 0.000181 | 0.001951 | 0.001501 | 10 |
| GO:0031528 | CC GO:0031528 | microvillus membrane | 4/2 | 27/1 | 0.000208 | 0.002171 | 0.00167 | 4 |
| GO:0071564 | CC | GO:0071564 | npBAF complex | 3/2 | 12/1 | 0.000272 | 0.002712 | 0.002086 | 3 |
| GO:0002102 | CC | GO:0002102 | podosome | 4/2 | 29/1 | 0.000277 | 0.002712 | 0.002086 | 4 |
| GO:1990907 | CC | GO:1990907 | beta-catenin-TCF complex | 3/2 | 13/1 | 0.000351 | 0.00333 | 0.002561 | 3 |
| GO:0042581 | CC | GO:0042581 | specific granule membrane | 8/2 | 160/1 | 0.000414 | 0.003819 | 0.002937 | 8 |
| GO:1904813 | CC | GO:1904813 | ficolin-1-rich granule lumen | 7/2 | 124/1 | 0.000460 | 0.004131 | 0.003177 | 7 |
| GO:0035579 | CC | GO:0035579 | specific granule membrane | 6/2 | 91/1 | 0.000518 | 0.004522 | 0.003478 | 6 |
| GO:0071565 | CC | GO:0071565 | nBAF complex | 3/2 | 15/1 | 0.000549 | 0.004664 | 0.003587 | 3 |
| GO:0101003 | CC | GO:0101003 | ficolin-1-rich granule membrane | 5/2 | 61/1 | 0.000566 | 0.004685 | 0.003603 | 5 |
| GO:0090734 | CC | GO:0090734 | site of DNA damage | 6/2 | 97/1 | 0.000727 | 0.005871 | 0.004515 | 6 |
| GO:0032433 | CC | GO:0032433 | filopodium tip | 3/2 | 17/1 | 0.000807 | 0.006355 | 0.004888 | 3 |
| GO:0034774 | CC | GO:0034774 | secretory granule lumen | 11/2 | 322/1 | 0.000948 | 0.00729 | 0.005607 | 11 |
| GO:0060205 | CC | GO:0060205 | cytoplasmic vesicle lumen | 11/2 | 325/1 | 0.001022 | 0.007675 | 0.005903 | 11 |
| GO:0031983 | CC | GO:0031983 | vesicle lumen | 11/2 | 327/1 | 0.001074 | 0.007881 | 0.006061 | 11 |
| GO:0001772 | CC | GO:0001772 | immunological synapse | 4/2 | 44/1 | 0.001392 | 0.00999 | 0.007683 | 4 |
| GO:0005884 | CC | GO:0005884 | actin filament | 6/2 | 114/1 | 0.001681 | 0.011804 | 0.009078 | 6 |
| GO:0097197 | CC | GO:0097197 | tetraspanin-enriched microdomain | 2/2 | 10/1 | 0.005158 | 0.035446 | 0.027262 | 2 |
| GO:0031234 | CC | GO:0031234 | extrinsic component of cytoplasmic side of plasma membrane | 5/2 | 101/1 | 0.005281 | 0.035535 | 0.02733 | 5 |
| GO:0002178 | CC | GO:0002178 | palmitoyltransferase complex | 2/2 | 111/1 | 0.006258 | 0.041253 | 0.031728 | 2 |
| GO:0005759 | CC | GO:0005759 | mitochondrial matrix | 12/2 | 480/1 | 0.00731 | 0.045437 | 0.034946 | 12 |
| GO:0005938 | CC | GO:0005938 | cell cortex | 9/2 | 308/1 | 0.007448 | 0.045437 | 0.034946 | 9 |
| GO:0018995 | CC | GO:0018995 | host cellular component | 2/2 | 12/1 | 0.007456 | 0.045437 | 0.034946 | 2 |
| GO:0043657 | CC | GO:0043657 | host cell | 2/2 | 12/1 | 0.007456 | 0.045437 | 0.034946 | 2 |
| GO:0070663 | CC | GO:0070663 | SWI/SNF superfamily-type complex | 4/2 | 72/1 | 0.008301 | 0.049568 | 0.038123 | 4 |
| GO:1904949 | CC | GO:1904949 | ATPase complex | 4/2 | 73/1 | 0.008708 | 0.049568 | 0.038123 | 4 |
| GO:0001931 | CC | GO:0001931 | uropod | 2/2 | 13/1 | 0.008747 | 0.049568 | 0.038123 | 2 |
| GO:0031254 | CC | GO:0031254 | cell trailing edge | 2/2 | 13/1 | 0.008747 | 0.049568 | 0.038123 | 2 |
| GO:0003954 | MF | GO:0003954 | NADH dehydrogenase activity | 13/212 | 45/18368 | 2.35E-15 | 1.02E-12 | 8.41E-13 | 13 |
| GO:0008137 | MF | GO:0008137 | NADH dehydrogenase (ubiquinone) activity | 12/212 | 42/18368 | 3.34E-14 | 6.59E-12 | 5.46E-12 | 12 |
| GO:0050136 | MF | GO:0050136 | NADH dehydrogenase activity | 12/212 | 43/18368 | 4.58E-14 | 6.59E-12 | 5.46E-12 | 12 |
| GO:0003955 | MF | GO:0003955 | NAD(P)H dehydrogenase (quinone) activity | 12/212 | 45/18368 | 8.42E-14 | 9.09E-12 | 7.53E-12 | 12 |
| GO:0015453 | MF | GO:0015453 | oxidoreduction-driven active transmembrane transporter activity | 13/212 | 72/18368 | 1.74E-12 | 1.32E-10 | 1.09E-10 | 13 |
| GO:0016655 | MF | GO:0016655 | oxidoreductase activity, acting on NAD(P)H, quinone or similar compound as acceptor | 12/212 | 57/18368 | 1.83E-12 | 1.32E-10 | 1.09E-10 | 12 |
| GO:0016651 | MF | GO:0016651 | oxidoreductase activity, acting on NAD(P)H | 13/212 | 88/18368 | 2.50E-11 | 1.54E-09 | 1.28E-09 | 13 |
| GO:0009055 | MF | GO:0009055 | electron transfer activity | 14/212 | 126/183 | 2.14E-10 | 1.16E-08 | 9.57E-09 | 14 |
| GO:00037712 | MF | GO:00037712 | transcription coregulator activity | 24/212 | 489/183 | 2.53E-09 | 1.21E-07 | 1.00E-07 | 24 |
| GO:00153399 | MF | GO:00153399 | primary active transmembrane transporter activity | 13/212 | 181/18368 | 1.88E-07 | 8.13E-06 | 6.73E-06 | 13 |
| GO:00037713 | MF | GO:00037713 | transcription coactivator activity | 15/212 | 262/183 | 4.09E-07 | 1.60E-05 | 1.33E-05 | 15 |
| GO:0051015 | MF | GO:0051015 | actin filament binding | 11/212 | 217/183 | 4.57E-05 | 0.001645 | 0.001363 | 11 |
| GO:0022804 | MF | GO:0022804 | active transmembrane transporter activity | 15/212 | 406/183 | 7.86E-05 | 0.002612 | 0.002164 | 15 |
| GO:0051539 | MF | GO:0051539 | 4 iron, 4 sulfur cluster binding | 5/212 | 42/1836 | 0.000117 | 0.003376 | 0.002797 | 5 |
| GO:0140103 | MF | GO:0140103 | catalytic activity, acting on a glycoprotein | 4/212 | 23/1836 | 0.000129 | 0.003376 | 0.002797 | 4 |
| GO:0051536 | MF | GO:0051536 | iron-sulfur cluster binding | 6/212 | 68/1836 | 0.000133 | 0.003376 | 0.002797 | 6 |
| GO:0051540 | MF | GO:0051540 | metal cluster binding | 6/212 | 68/1836 | 0.000133 | 0.003376 | 0.002797 | 6 |
| GO:00017784 | MF | GO:00017784 | phosphotyrosine residue binding | 5/212 | 44/1836 | 0.000147 | 0.003531 | 0.002925 | 5 |
| GO          | MF      | GO          | Description                                      | Count1 | Count2 | Count3 | Count4 | P-val1 | P-val2 | P-val3 | Rank |
|-------------|---------|-------------|--------------------------------------------------|--------|--------|--------|--------|--------|--------|--------|-------|
| GO:00052    | MF      | GO:00052    | structural constituent of cytoskeleton           | 7/2    | 12     | 103/183| 0.000192| 0.004195| 0.003475| 7     |
| GO:00037    | MF      | GO:00037    | actin binding                                    | 15/212 | 441/183| 0.000195| 0.004195| 0.003475| 15    |
| GO:01402    | MF      | GO:01402    | DNA-binding transcription factor binding         | 14/212 | 394/183| 0.000204| 0.004195| 0.003475| 14    |
| GO:00453    | MF      | GO:00453    | protein phosphorylated amino acid binding        | 5/2    | 12     | 56/1836| 0.000463| 0.00876 | 0.007258| 5     |
| GO:00199    | MF      | GO:00199    | phosphatase binding                              | 9/2    | 12     | 196/183| 0.000466| 0.00876 | 0.007258| 9     |
| GO:00512    | MF      | GO:00512    | phosphoprotein binding                           | 6/2    | 12     | 88/1836| 0.000543| 0.009782| 0.008104| 6     |
| GO:00428    | MF      | GO:00428    | histone deacetylase binding                      | 7/2    | 12     | 127/183| 0.000686| 0.011849| 0.009816| 7     |
| GO:00302    | MF      | GO:00302    | protein kinase activator activity                | 6/2    | 12     | 101/183| 0.001123| 0.01866 | 0.015459| 6     |
| GO:00314    | MF      | GO:00314    | chromatin DNA binding                            | 6/2    | 12     | 103/183| 0.001243| 0.019891| 0.016479| 6     |
| GO:00192    | MF      | GO:00192    | kinase activator activity                        | 6/2    | 12     | 107/183| 0.001513| 0.02334 | 0.019336| 6     |
| GO:00083    | MF      | GO:00083    | sialytransferase activity                        | 3/2    | 12     | 21/1836| 0.001729| 0.025554| 0.021171| 3     |
| GO:00047    | MF      | GO:00047    | non-membrane spanning protein tyrosine kinase activity | 4/2    | 12     | 45/1836| 0.001775| 0.025554| 0.021171| 4     |
| GO:00510    | MF      | GO:00510    | GTPase binding                                   | 10/212 | 291/183| 0.002104| 0.029319| 0.024289| 10    |
| GO:00167    | MF      | GO:00167    | acyltransferase activity                         | 9/2    | 12     | 250/183| 0.002551| 0.033014| 0.027351| 9     |
| GO:00432    | MF      | GO:00432    | phospholipase binding                            | 3/2    | 12     | 24/1836| 0.002566| 0.033014| 0.027351| 3     |
| GO:00198    | MF      | GO:00198    | protein kinase regulator activity                | 8/2    | 12     | 204/183| 0.002598| 0.033014| 0.027351| 8     |
| GO:00312    | MF      | GO:00312    | small GTPase binding                             | 9/2    | 12     | 259/183| 0.003227| 0.039836| 0.033003| 9     |
| GO:00171    | MF      | GO:00171    | SH3 domain binding                               | 6/2    | 12     | 130/183| 0.004015| 0.048179| 0.039915| 6     |