**Table S1.** Full Gene Ontology (GO) pathways of WGCNA modules.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Gene Ontology** | | | **Pathway Genes** | | **Adjusted P-Value** |
| **Term** | **Category** | **Name** | **Gene Ratio** | **BG Ratio** |
| **Pathways associated with black module genes** | | | | | |
| GO:0006397 | BP | mRNA processing | 45/412 | 349/10067 | 1.44E-08 |
| GO:0008380 | BP | RNA splicing | 39/412 | 309/10067 | 3.99E-07 |
| GO:0000377 | BP | RNA splicing, via transesterification reactions with bulged adenosine as nucleophile | 31/412 | 233/10067 | 3.69E-06 |
| GO:0000398 | BP | mRNA splicing, via spliceosome | 31/412 | 233/10067 | 3.69E-06 |
| GO:0000375 | BP | RNA splicing, via transesterification reactions | 31/412 | 234/10067 | 3.69E-06 |
| GO:0051028 | BP | mRNA transport | 16/412 | 107/10067 | 2.79E-03 |
| GO:0006473 | BP | protein acetylation | 18/412 | 132/10067 | 2.79E-03 |
| GO:0016569 | BP | covalent chromatin modification | 32/412 | 337/10067 | 2.79E-03 |
| GO:0043543 | BP | protein acylation | 20/412 | 161/10067 | 2.88E-03 |
| GO:0050657 | BP | nucleic acid transport | 18/412 | 137/10067 | 2.93E-03 |
| GO:0050658 | BP | RNA transport | 18/412 | 137/10067 | 2.93E-03 |
| GO:0006913 | BP | nucleocytoplasmic transport | 26/412 | 251/10067 | 2.93E-03 |
| GO:0006405 | BP | RNA export from nucleus | 15/412 | 101/10067 | 2.93E-03 |
| GO:0051169 | BP | nuclear transport | 26/412 | 253/10067 | 2.93E-03 |
| GO:0051236 | BP | establishment of RNA localization | 18/412 | 140/10067 | 3.02E-03 |
| GO:0006406 | BP | mRNA export from nucleus | 13/412 | 81/10067 | 3.60E-03 |
| GO:0071427 | BP | mRNA-containing ribonucleoprotein complex export from nucleus | 13/412 | 81/10067 | 3.60E-03 |
| GO:0071426 | BP | ribonucleoprotein complex export from nucleus | 14/412 | 93/10067 | 3.60E-03 |
| GO:1903311 | BP | regulation of mRNA metabolic process | 24/412 | 230/10067 | 3.60E-03 |
| GO:0071166 | BP | ribonucleoprotein complex localization | 14/412 | 94/10067 | 3.82E-03 |
| GO:0016570 | BP | histone modification | 30/412 | 327/10067 | 3.99E-03 |
| GO:0031503 | BP | protein-containing complex localization | 22/412 | 207/10067 | 5.13E-03 |
| GO:0015931 | BP | nucleobase-containing compound transport | 20/412 | 182/10067 | 6.87E-03 |
| GO:0016607 | CC | nuclear speck | 32/426 | 283/10416 | 6.28E-05 |
| GO:0005681 | CC | spliceosomal complex | 19/426 | 127/10416 | 1.72E-04 |
| GO:0031248 | CC | protein acetyltransferase complex | 11/426 | 65/10416 | 5.54E-03 |
| GO:1902493 | CC | acetyltransferase complex | 11/426 | 65/10416 | 5.54E-03 |
| GO:0005643 | CC | nuclear pore | 10/426 | 57/10416 | 7.01E-03 |
| GO:0003729 | MF | mRNA binding | 22/415 | 196/10268 | 6.48E-03 |
| **Pathways associated with blue module genes** | | | | | |
| GO:0030198 | BP | extracellular matrix organization | 80/889 | 277/10067 | 3.41E-19 |
| GO:0043062 | BP | extracellular structure organization | 80/889 | 278/10067 | 3.41E-19 |
| GO:0001525 | BP | angiogenesis | 85/889 | 387/10067 | 1.23E-12 |
| GO:0048514 | BP | blood vessel morphogenesis | 94/889 | 454/10067 | 1.33E-12 |
| GO:0061448 | BP | connective tissue development | 48/889 | 167/10067 | 5.56E-11 |
| GO:0001501 | BP | skeletal system development | 73/889 | 333/10067 | 8.54E-11 |
| GO:0007507 | BP | heart development | 80/889 | 387/10067 | 1.32E-10 |
| GO:0071363 | BP | cellular response to growth factor stimulus | 87/889 | 454/10067 | 8.55E-10 |
| GO:0070848 | BP | response to growth factor | 89/889 | 472/10067 | 1.03E-09 |
| GO:0048729 | BP | tissue morphogenesis | 85/889 | 442/10067 | 1.03E-09 |
| GO:0002009 | BP | morphogenesis of an epithelium | 76/889 | 380/10067 | 2.00E-09 |
| GO:0030199 | BP | collagen fibril organization | 21/889 | 42/10067 | 2.00E-09 |
| GO:0061061 | BP | muscle structure development | 77/889 | 412/10067 | 3.92E-08 |
| GO:0051216 | BP | cartilage development | 35/889 | 123/10067 | 7.14E-08 |
| GO:0007423 | BP | sensory organ development | 67/889 | 344/10067 | 9.60E-08 |
| GO:1901342 | BP | regulation of vasculature development | 54/889 | 254/10067 | 1.91E-07 |
| GO:0001503 | BP | ossification | 56/889 | 269/10067 | 1.98E-07 |
| GO:0048565 | BP | digestive tract development | 26/889 | 78/10067 | 2.74E-07 |
| GO:0048598 | BP | embryonic morphogenesis | 71/889 | 385/10067 | 2.74E-07 |
| GO:0032989 | BP | cellular component morphogenesis | 84/889 | 493/10067 | 4.18E-07 |
| GO:0009611 | BP | response to wounding | 77/889 | 447/10067 | 1.20E-06 |
| GO:0008285 | BP | negative regulation of cell population proliferation | 77/889 | 451/10067 | 1.72E-06 |
| GO:0055123 | BP | digestive system development | 26/889 | 85/10067 | 1.74E-06 |
| GO:0008015 | BP | blood circulation | 60/889 | 320/10067 | 2.35E-06 |
| GO:0060562 | BP | epithelial tube morphogenesis | 48/889 | 231/10067 | 2.42E-06 |
| GO:0048858 | BP | cell projection morphogenesis | 73/889 | 424/10067 | 2.53E-06 |
| GO:0045596 | BP | negative regulation of cell differentiation | 75/889 | 444/10067 | 3.45E-06 |
| GO:0045765 | BP | regulation of angiogenesis | 47/889 | 227/10067 | 3.45E-06 |
| GO:0051272 | BP | positive regulation of cellular component movement | 70/889 | 404/10067 | 3.51E-06 |
| GO:0120039 | BP | plasma membrane bounded cell projection morphogenesis | 72/889 | 421/10067 | 3.65E-06 |
| GO:0003170 | BP | heart valve development | 19/889 | 51/10067 | 3.65E-06 |
| GO:0030323 | BP | respiratory tube development | 32/889 | 126/10067 | 3.93E-06 |
| GO:0040017 | BP | positive regulation of locomotion | 69/889 | 399/10067 | 4.15E-06 |
| GO:0044057 | BP | regulation of system process | 59/889 | 320/10067 | 4.15E-06 |
| GO:0032990 | BP | cell part morphogenesis | 73/889 | 438/10067 | 7.54E-06 |
| GO:0030324 | BP | lung development | 31/889 | 124/10067 | 8.39E-06 |
| GO:0006935 | BP | chemotaxis | 68/889 | 399/10067 | 8.39E-06 |
| GO:0030335 | BP | positive regulation of cell migration | 66/889 | 383/10067 | 8.39E-06 |
| GO:0060541 | BP | respiratory system development | 34/889 | 144/10067 | 8.39E-06 |
| GO:0007178 | BP | transmembrane receptor protein serine/threonine kinase signaling pathway | 47/889 | 236/10067 | 8.50E-06 |
| GO:2000147 | BP | positive regulation of cell motility | 67/889 | 392/10067 | 8.50E-06 |
| GO:0003013 | BP | circulatory system process | 60/889 | 336/10067 | 8.50E-06 |
| GO:0042330 | BP | taxis | 68/889 | 401/10067 | 9.02E-06 |
| GO:0033002 | BP | muscle cell proliferation | 32/889 | 132/10067 | 9.34E-06 |
| GO:0061564 | BP | axon development | 58/889 | 323/10067 | 1.06E-05 |
| GO:0003179 | BP | heart valve morphogenesis | 17/889 | 45/10067 | 1.06E-05 |
| GO:0030278 | BP | regulation of ossification | 33/889 | 140/10067 | 1.13E-05 |
| GO:0048880 | BP | sensory system development | 46/889 | 233/10067 | 1.28E-05 |
| GO:0001654 | BP | eye development | 45/889 | 226/10067 | 1.33E-05 |
| GO:0090287 | BP | regulation of cellular response to growth factor stimulus | 40/889 | 191/10067 | 1.59E-05 |
| GO:0045165 | BP | cell fate commitment | 29/889 | 116/10067 | 1.59E-05 |
| GO:0003176 | BP | aortic valve development | 13/889 | 28/10067 | 1.71E-05 |
| GO:0048754 | BP | branching morphogenesis of an epithelial tube | 27/889 | 104/10067 | 1.77E-05 |
| GO:0003007 | BP | heart morphogenesis | 37/889 | 171/10067 | 1.80E-05 |
| GO:0003279 | BP | cardiac septum development | 25/889 | 92/10067 | 1.86E-05 |
| GO:0043010 | BP | camera-type eye development | 40/889 | 193/10067 | 1.90E-05 |
| GO:0150063 | BP | visual system development | 45/889 | 230/10067 | 1.92E-05 |
| GO:0001649 | BP | osteoblast differentiation | 34/889 | 151/10067 | 1.92E-05 |
| GO:1905314 | BP | semilunar valve development | 14/889 | 33/10067 | 2.04E-05 |
| GO:0007389 | BP | pattern specification process | 47/889 | 246/10067 | 2.08E-05 |
| GO:0051962 | BP | positive regulation of nervous system development | 58/889 | 332/10067 | 2.10E-05 |
| GO:0035265 | BP | organ growth | 28/889 | 112/10067 | 2.12E-05 |
| GO:0007169 | BP | transmembrane receptor protein tyrosine kinase signaling pathway | 76/889 | 481/10067 | 2.12E-05 |
| GO:0061035 | BP | regulation of cartilage development | 17/889 | 48/10067 | 2.24E-05 |
| GO:0072001 | BP | renal system development | 42/889 | 210/10067 | 2.24E-05 |
| GO:1904018 | BP | positive regulation of vasculature development | 33/889 | 146/10067 | 2.24E-05 |
| GO:0048812 | BP | neuron projection morphogenesis | 67/889 | 407/10067 | 2.24E-05 |
| GO:0007409 | BP | axonogenesis | 53/889 | 294/10067 | 2.24E-05 |
| GO:0001667 | BP | ameboidal-type cell migration | 55/889 | 310/10067 | 2.27E-05 |
| GO:0019932 | BP | second-messenger-mediated signaling | 46/889 | 241/10067 | 2.46E-05 |
| GO:0031589 | BP | cell-substrate adhesion | 50/889 | 273/10067 | 2.83E-05 |
| GO:0003012 | BP | muscle system process | 48/889 | 259/10067 | 3.32E-05 |
| GO:0060485 | BP | mesenchyme development | 38/889 | 185/10067 | 3.67E-05 |
| GO:0061138 | BP | morphogenesis of a branching epithelium | 30/889 | 129/10067 | 3.67E-05 |
| GO:0003180 | BP | aortic valve morphogenesis | 12/889 | 26/10067 | 3.84E-05 |
| GO:0072012 | BP | glomerulus vasculature development | 11/889 | 22/10067 | 4.05E-05 |
| GO:0034330 | BP | cell junction organization | 72/889 | 457/10067 | 4.05E-05 |
| GO:0007411 | BP | axon guidance | 37/889 | 179/10067 | 4.09E-05 |
| GO:0097485 | BP | neuron projection guidance | 37/889 | 179/10067 | 4.09E-05 |
| GO:0048736 | BP | appendage development | 30/889 | 131/10067 | 4.76E-05 |
| GO:0060173 | BP | limb development | 30/889 | 131/10067 | 4.76E-05 |
| GO:0032330 | BP | regulation of chondrocyte differentiation | 14/889 | 36/10067 | 5.28E-05 |
| GO:0003205 | BP | cardiac chamber development | 29/889 | 125/10067 | 5.31E-05 |
| GO:0043009 | BP | chordate embryonic development | 68/889 | 429/10067 | 6.14E-05 |
| GO:0045667 | BP | regulation of osteoblast differentiation | 23/889 | 87/10067 | 6.21E-05 |
| GO:0002062 | BP | chondrocyte differentiation | 20/889 | 69/10067 | 6.25E-05 |
| GO:0032963 | BP | collagen metabolic process | 20/889 | 69/10067 | 6.25E-05 |
| GO:0009792 | BP | embryo development ending in birth or egg hatching | 69/889 | 439/10067 | 6.67E-05 |
| GO:0048568 | BP | embryonic organ development | 50/889 | 283/10067 | 6.84E-05 |
| GO:0072006 | BP | nephron development | 24/889 | 94/10067 | 6.84E-05 |
| GO:0001763 | BP | morphogenesis of a branching structure | 30/889 | 134/10067 | 7.02E-05 |
| GO:0098742 | BP | cell-cell adhesion via plasma-membrane adhesion molecules | 31/889 | 141/10067 | 7.02E-05 |
| GO:0042060 | BP | wound healing | 61/889 | 373/10067 | 7.02E-05 |
| GO:0000904 | BP | cell morphogenesis involved in differentiation | 74/889 | 484/10067 | 7.46E-05 |
| GO:2000027 | BP | regulation of animal organ morphogenesis | 35/889 | 170/10067 | 7.47E-05 |
| GO:1903053 | BP | regulation of extracellular matrix organization | 12/889 | 28/10067 | 8.00E-05 |
| GO:0035107 | BP | appendage morphogenesis | 26/889 | 109/10067 | 9.29E-05 |
| GO:0035108 | BP | limb morphogenesis | 26/889 | 109/10067 | 9.29E-05 |
| GO:0061437 | BP | renal system vasculature development | 11/889 | 24/10067 | 9.29E-05 |
| GO:0061440 | BP | kidney vasculature development | 11/889 | 24/10067 | 9.29E-05 |
| GO:0048667 | BP | cell morphogenesis involved in neuron differentiation | 61/889 | 377/10067 | 9.29E-05 |
| GO:0072210 | BP | metanephric nephron development | 10/889 | 20/10067 | 1.00E-04 |
| GO:0001822 | BP | kidney development | 39/889 | 203/10067 | 1.09E-04 |
| GO:0019935 | BP | cyclic-nucleotide-mediated signaling | 25/889 | 104/10067 | 1.19E-04 |
| GO:0048589 | BP | developmental growth | 66/889 | 423/10067 | 1.24E-04 |
| GO:0090130 | BP | tissue migration | 43/889 | 235/10067 | 1.25E-04 |
| GO:0030336 | BP | negative regulation of cell migration | 38/889 | 197/10067 | 1.28E-04 |
| GO:0001655 | BP | urogenital system development | 42/889 | 228/10067 | 1.34E-04 |
| GO:0090092 | BP | regulation of transmembrane receptor protein serine/threonine kinase signaling pathway | 34/889 | 168/10067 | 1.37E-04 |
| GO:0042692 | BP | muscle cell differentiation | 42/889 | 229/10067 | 1.48E-04 |
| GO:0001502 | BP | cartilage condensation | 7/889 | 10/10067 | 1.60E-04 |
| GO:0060411 | BP | cardiac septum morphogenesis | 18/889 | 62/10067 | 1.61E-04 |
| GO:1903670 | BP | regulation of sprouting angiogenesis | 17/889 | 57/10067 | 1.94E-04 |
| GO:0030326 | BP | embryonic limb morphogenesis | 23/889 | 94/10067 | 1.94E-04 |
| GO:0035113 | BP | embryonic appendage morphogenesis | 23/889 | 94/10067 | 1.94E-04 |
| GO:0006936 | BP | muscle contraction | 38/889 | 202/10067 | 2.19E-04 |
| GO:0051145 | BP | smooth muscle cell differentiation | 14/889 | 41/10067 | 2.26E-04 |
| GO:0032964 | BP | collagen biosynthetic process | 12/889 | 31/10067 | 2.35E-04 |
| GO:0060419 | BP | heart growth | 17/889 | 58/10067 | 2.43E-04 |
| GO:0034329 | BP | cell junction assembly | 48/889 | 283/10067 | 2.67E-04 |
| GO:0048660 | BP | regulation of smooth muscle cell proliferation | 23/889 | 96/10067 | 2.70E-04 |
| GO:0030855 | BP | epithelial cell differentiation | 61/889 | 392/10067 | 2.79E-04 |
| GO:0008217 | BP | regulation of blood pressure | 24/889 | 103/10067 | 2.82E-04 |
| GO:0071772 | BP | response to BMP | 25/889 | 110/10067 | 2.89E-04 |
| GO:0071773 | BP | cellular response to BMP stimulus | 25/889 | 110/10067 | 2.89E-04 |
| GO:0048659 | BP | smooth muscle cell proliferation | 23/889 | 97/10067 | 3.12E-04 |
| GO:2000146 | BP | negative regulation of cell motility | 38/889 | 206/10067 | 3.22E-04 |
| GO:0032835 | BP | glomerulus development | 15/889 | 48/10067 | 3.33E-04 |
| GO:0007264 | BP | small GTPase mediated signal transduction | 59/889 | 378/10067 | 3.40E-04 |
| GO:0098743 | BP | cell aggregation | 7/889 | 11/10067 | 3.46E-04 |
| GO:0055017 | BP | cardiac muscle tissue growth | 16/889 | 54/10067 | 3.54E-04 |
| GO:0003151 | BP | outflow tract morphogenesis | 17/889 | 60/10067 | 3.58E-04 |
| GO:0003281 | BP | ventricular septum development | 17/889 | 60/10067 | 3.58E-04 |
| GO:0061326 | BP | renal tubule development | 17/889 | 60/10067 | 3.58E-04 |
| GO:0010631 | BP | epithelial cell migration | 41/889 | 231/10067 | 3.62E-04 |
| GO:0007517 | BP | muscle organ development | 42/889 | 239/10067 | 3.62E-04 |
| GO:1901888 | BP | regulation of cell junction assembly | 28/889 | 133/10067 | 3.65E-04 |
| GO:0003002 | BP | regionalization | 35/889 | 185/10067 | 3.77E-04 |
| GO:0090132 | BP | epithelium migration | 41/889 | 232/10067 | 3.91E-04 |
| GO:0060021 | BP | roof of mouth development | 19/889 | 73/10067 | 4.07E-04 |
| GO:0010712 | BP | regulation of collagen metabolic process | 11/889 | 28/10067 | 4.09E-04 |
| GO:0010463 | BP | mesenchymal cell proliferation | 12/889 | 33/10067 | 4.16E-04 |
| GO:0120035 | BP | regulation of plasma membrane bounded cell projection organization | 69/889 | 469/10067 | 4.29E-04 |
| GO:0030155 | BP | regulation of cell adhesion | 72/889 | 496/10067 | 4.41E-04 |
| GO:0050769 | BP | positive regulation of neurogenesis | 49/889 | 299/10067 | 4.66E-04 |
| GO:0007160 | BP | cell-matrix adhesion | 33/889 | 172/10067 | 4.66E-04 |
| GO:0045766 | BP | positive regulation of angiogenesis | 27/889 | 128/10067 | 4.69E-04 |
| GO:0061005 | BP | cell differentiation involved in kidney development | 13/889 | 39/10067 | 5.19E-04 |
| GO:0010464 | BP | regulation of mesenchymal cell proliferation | 10/889 | 24/10067 | 5.23E-04 |
| GO:0071559 | BP | response to transforming growth factor beta | 34/889 | 181/10067 | 5.40E-04 |
| GO:0072073 | BP | kidney epithelium development | 22/889 | 95/10067 | 6.06E-04 |
| GO:0031344 | BP | regulation of cell projection organization | 69/889 | 475/10067 | 6.20E-04 |
| GO:0021915 | BP | neural tube development | 26/889 | 123/10067 | 6.21E-04 |
| GO:0090288 | BP | negative regulation of cellular response to growth factor stimulus | 24/889 | 109/10067 | 6.25E-04 |
| GO:0048566 | BP | embryonic digestive tract development | 9/889 | 20/10067 | 6.36E-04 |
| GO:0072109 | BP | glomerular mesangium development | 7/889 | 12/10067 | 6.40E-04 |
| GO:0002040 | BP | sprouting angiogenesis | 22/889 | 96/10067 | 6.94E-04 |
| GO:0007265 | BP | Ras protein signal transduction | 42/889 | 247/10067 | 7.10E-04 |
| GO:0001823 | BP | mesonephros development | 18/889 | 70/10067 | 7.23E-04 |
| GO:0051056 | BP | regulation of small GTPase mediated signal transduction | 42/889 | 248/10067 | 7.74E-04 |
| GO:0072080 | BP | nephron tubule development | 16/889 | 58/10067 | 7.76E-04 |
| GO:0071560 | BP | cellular response to transforming growth factor beta stimulus | 33/889 | 177/10067 | 7.76E-04 |
| GO:0048732 | BP | gland development | 46/889 | 281/10067 | 7.76E-04 |
| GO:0010720 | BP | positive regulation of cell development | 54/889 | 349/10067 | 8.19E-04 |
| GO:0042476 | BP | odontogenesis | 20/889 | 84/10067 | 8.53E-04 |
| GO:0045664 | BP | regulation of neuron differentiation | 62/889 | 419/10067 | 8.56E-04 |
| GO:0032970 | BP | regulation of actin filament-based process | 47/889 | 291/10067 | 8.84E-04 |
| GO:0006816 | BP | calcium ion transport | 39/889 | 226/10067 | 9.17E-04 |
| GO:0042733 | BP | embryonic digit morphogenesis | 14/889 | 47/10067 | 9.17E-04 |
| GO:0060038 | BP | cardiac muscle cell proliferation | 12/889 | 36/10067 | 9.56E-04 |
| GO:0022604 | BP | regulation of cell morphogenesis | 53/889 | 343/10067 | 9.64E-04 |
| GO:0010810 | BP | regulation of cell-substrate adhesion | 31/889 | 164/10067 | 9.64E-04 |
| GO:0007224 | BP | smoothened signaling pathway | 22/889 | 99/10067 | 1.05E-03 |
| GO:0050673 | BP | epithelial cell proliferation | 44/889 | 269/10067 | 1.10E-03 |
| GO:0010632 | BP | regulation of epithelial cell migration | 33/889 | 181/10067 | 1.15E-03 |
| GO:1903522 | BP | regulation of blood circulation | 30/889 | 158/10067 | 1.15E-03 |
| GO:0060537 | BP | muscle tissue development | 41/889 | 245/10067 | 1.16E-03 |
| GO:0003206 | BP | cardiac chamber morphogenesis | 21/889 | 93/10067 | 1.17E-03 |
| GO:1901343 | BP | negative regulation of vasculature development | 21/889 | 93/10067 | 1.17E-03 |
| GO:0072163 | BP | mesonephric epithelium development | 17/889 | 67/10067 | 1.28E-03 |
| GO:0072164 | BP | mesonephric tubule development | 17/889 | 67/10067 | 1.28E-03 |
| GO:0010634 | BP | positive regulation of epithelial cell migration | 25/889 | 122/10067 | 1.29E-03 |
| GO:0051017 | BP | actin filament bundle assembly | 25/889 | 122/10067 | 1.29E-03 |
| GO:0022612 | BP | gland morphogenesis | 20/889 | 87/10067 | 1.31E-03 |
| GO:0060401 | BP | cytosolic calcium ion transport | 23/889 | 108/10067 | 1.33E-03 |
| GO:0090049 | BP | regulation of cell migration involved in sprouting angiogenesis | 11/889 | 32/10067 | 1.33E-03 |
| GO:1903672 | BP | positive regulation of sprouting angiogenesis | 11/889 | 32/10067 | 1.33E-03 |
| GO:0040013 | BP | negative regulation of locomotion | 39/889 | 231/10067 | 1.36E-03 |
| GO:0001656 | BP | metanephros development | 15/889 | 55/10067 | 1.36E-03 |
| GO:0061333 | BP | renal tubule morphogenesis | 14/889 | 49/10067 | 1.36E-03 |
| GO:0008589 | BP | regulation of smoothened signaling pathway | 16/889 | 62/10067 | 1.60E-03 |
| GO:0061572 | BP | actin filament bundle organization | 25/889 | 124/10067 | 1.63E-03 |
| GO:0002011 | BP | morphogenesis of an epithelial sheet | 13/889 | 44/10067 | 1.67E-03 |
| GO:0002042 | BP | cell migration involved in sprouting angiogenesis | 13/889 | 44/10067 | 1.67E-03 |
| GO:0048251 | BP | elastic fiber assembly | 6/889 | 10/10067 | 1.69E-03 |
| GO:0043542 | BP | endothelial cell migration | 31/889 | 170/10067 | 1.73E-03 |
| GO:0019933 | BP | cAMP-mediated signaling | 20/889 | 89/10067 | 1.73E-03 |
| GO:0051271 | BP | negative regulation of cellular component movement | 39/889 | 234/10067 | 1.73E-03 |
| GO:0085029 | BP | extracellular matrix assembly | 11/889 | 33/10067 | 1.73E-03 |
| GO:0007204 | BP | positive regulation of cytosolic calcium ion concentration | 32/889 | 178/10067 | 1.73E-03 |
| GO:0007186 | BP | G protein-coupled receptor signaling pathway | 61/889 | 423/10067 | 1.76E-03 |
| GO:0043410 | BP | positive regulation of MAPK cascade | 53/889 | 353/10067 | 1.79E-03 |
| GO:0001569 | BP | branching involved in blood vessel morphogenesis | 9/889 | 23/10067 | 1.84E-03 |
| GO:0032965 | BP | regulation of collagen biosynthetic process | 9/889 | 23/10067 | 1.84E-03 |
| GO:0070838 | BP | divalent metal ion transport | 41/889 | 252/10067 | 1.92E-03 |
| GO:1902893 | BP | regulation of pri-miRNA transcription by RNA polymerase II | 12/889 | 39/10067 | 1.92E-03 |
| GO:0040008 | BP | regulation of growth | 62/889 | 434/10067 | 1.97E-03 |
| GO:0043408 | BP | regulation of MAPK cascade | 67/889 | 479/10067 | 1.97E-03 |
| GO:0009953 | BP | dorsal/ventral pattern formation | 13/889 | 45/10067 | 2.01E-03 |
| GO:1905114 | BP | cell surface receptor signaling pathway involved in cell-cell signaling | 58/889 | 399/10067 | 2.02E-03 |
| GO:0043583 | BP | ear development | 27/889 | 142/10067 | 2.21E-03 |
| GO:0060412 | BP | ventricular septum morphogenesis | 11/889 | 34/10067 | 2.21E-03 |
| GO:0070588 | BP | calcium ion transmembrane transport | 31/889 | 173/10067 | 2.23E-03 |
| GO:0051480 | BP | regulation of cytosolic calcium ion concentration | 34/889 | 197/10067 | 2.26E-03 |
| GO:0048738 | BP | cardiac muscle tissue development | 26/889 | 135/10067 | 2.33E-03 |
| GO:0002043 | BP | blood vessel endothelial cell proliferation involved in sprouting angiogenesis | 8/889 | 19/10067 | 2.35E-03 |
| GO:0003177 | BP | pulmonary valve development | 8/889 | 19/10067 | 2.35E-03 |
| GO:0031128 | BP | developmental induction | 8/889 | 19/10067 | 2.35E-03 |
| GO:0035148 | BP | tube formation | 22/889 | 106/10067 | 2.45E-03 |
| GO:0061036 | BP | positive regulation of cartilage development | 9/889 | 24/10067 | 2.50E-03 |
| GO:0110111 | BP | negative regulation of animal organ morphogenesis | 9/889 | 24/10067 | 2.50E-03 |
| GO:0003231 | BP | cardiac ventricle development | 20/889 | 92/10067 | 2.50E-03 |
| GO:0032956 | BP | regulation of actin cytoskeleton organization | 41/889 | 256/10067 | 2.51E-03 |
| GO:1902903 | BP | regulation of supramolecular fiber organization | 41/889 | 256/10067 | 2.51E-03 |
| GO:0072511 | BP | divalent inorganic cation transport | 41/889 | 257/10067 | 2.72E-03 |
| GO:0007015 | BP | actin filament organization | 47/889 | 308/10067 | 2.72E-03 |
| GO:0048762 | BP | mesenchymal cell differentiation | 28/889 | 152/10067 | 2.74E-03 |
| GO:0048705 | BP | skeletal system morphogenesis | 26/889 | 137/10067 | 2.83E-03 |
| GO:0060395 | BP | SMAD protein signal transduction | 14/889 | 53/10067 | 2.89E-03 |
| GO:0061614 | BP | pri-miRNA transcription by RNA polymerase II | 12/889 | 41/10067 | 2.93E-03 |
| GO:0043536 | BP | positive regulation of blood vessel endothelial cell migration | 13/889 | 47/10067 | 2.93E-03 |
| GO:0046579 | BP | positive regulation of Ras protein signal transduction | 13/889 | 47/10067 | 2.93E-03 |
| GO:0001657 | BP | ureteric bud development | 16/889 | 66/10067 | 2.93E-03 |
| GO:0045778 | BP | positive regulation of ossification | 16/889 | 66/10067 | 2.93E-03 |
| GO:0016331 | BP | morphogenesis of embryonic epithelium | 22/889 | 108/10067 | 3.05E-03 |
| GO:0048562 | BP | embryonic organ morphogenesis | 31/889 | 177/10067 | 3.10E-03 |
| GO:1905330 | BP | regulation of morphogenesis of an epithelium | 24/889 | 123/10067 | 3.12E-03 |
| GO:0003158 | BP | endothelium development | 20/889 | 94/10067 | 3.19E-03 |
| GO:0003181 | BP | atrioventricular valve morphogenesis | 8/889 | 20/10067 | 3.30E-03 |
| GO:0090596 | BP | sensory organ morphogenesis | 29/889 | 162/10067 | 3.32E-03 |
| GO:0090504 | BP | epiboly | 9/889 | 25/10067 | 3.32E-03 |
| GO:0055024 | BP | regulation of cardiac muscle tissue development | 14/889 | 54/10067 | 3.39E-03 |
| GO:0072028 | BP | nephron morphogenesis | 13/889 | 48/10067 | 3.55E-03 |
| GO:0043534 | BP | blood vessel endothelial cell migration | 20/889 | 95/10067 | 3.62E-03 |
| GO:0110053 | BP | regulation of actin filament organization | 33/889 | 196/10067 | 4.02E-03 |
| GO:0030509 | BP | BMP signaling pathway | 21/889 | 103/10067 | 4.02E-03 |
| GO:0035850 | BP | epithelial cell differentiation involved in kidney development | 10/889 | 31/10067 | 4.03E-03 |
| GO:0003018 | BP | vascular process in circulatory system | 23/889 | 118/10067 | 4.12E-03 |
| GO:0043535 | BP | regulation of blood vessel endothelial cell migration | 17/889 | 75/10067 | 4.15E-03 |
| GO:0060840 | BP | artery development | 17/889 | 75/10067 | 4.15E-03 |
| GO:0032967 | BP | positive regulation of collagen biosynthetic process | 7/889 | 16/10067 | 4.17E-03 |
| GO:0060973 | BP | cell migration involved in heart development | 7/889 | 16/10067 | 4.17E-03 |
| GO:0060420 | BP | regulation of heart growth | 12/889 | 43/10067 | 4.41E-03 |
| GO:0010594 | BP | regulation of endothelial cell migration | 25/889 | 134/10067 | 4.45E-03 |
| GO:0031214 | BP | biomineral tissue development | 21/889 | 104/10067 | 4.45E-03 |
| GO:0110148 | BP | biomineralization | 21/889 | 104/10067 | 4.45E-03 |
| GO:0051150 | BP | regulation of smooth muscle cell differentiation | 8/889 | 21/10067 | 4.56E-03 |
| GO:0060348 | BP | bone development | 26/889 | 142/10067 | 4.56E-03 |
| GO:0072009 | BP | nephron epithelium development | 16/889 | 69/10067 | 4.60E-03 |
| GO:0035051 | BP | cardiocyte differentiation | 19/889 | 90/10067 | 4.69E-03 |
| GO:0032331 | BP | negative regulation of chondrocyte differentiation | 6/889 | 12/10067 | 4.71E-03 |
| GO:0035791 | BP | platelet-derived growth factor receptor-beta signaling pathway | 6/889 | 12/10067 | 4.71E-03 |
| GO:1903587 | BP | regulation of blood vessel endothelial cell proliferation involved in sprouting angiogenesis | 6/889 | 12/10067 | 4.71E-03 |
| GO:0014706 | BP | striated muscle tissue development | 37/889 | 232/10067 | 4.88E-03 |
| GO:0050678 | BP | regulation of epithelial cell proliferation | 37/889 | 232/10067 | 4.88E-03 |
| GO:0043114 | BP | regulation of vascular permeability | 10/889 | 32/10067 | 5.02E-03 |
| GO:0061045 | BP | negative regulation of wound healing | 13/889 | 50/10067 | 5.04E-03 |
| GO:0045666 | BP | positive regulation of neuron differentiation | 38/889 | 241/10067 | 5.08E-03 |
| GO:0007188 | BP | adenylate cyclase-modulating G protein-coupled receptor signaling pathway | 20/889 | 98/10067 | 5.09E-03 |
| GO:0014855 | BP | striated muscle cell proliferation | 12/889 | 44/10067 | 5.18E-03 |
| GO:0072132 | BP | mesenchyme morphogenesis | 12/889 | 44/10067 | 5.18E-03 |
| GO:0003197 | BP | endocardial cushion development | 11/889 | 38/10067 | 5.18E-03 |
| GO:1904705 | BP | regulation of vascular associated smooth muscle cell proliferation | 11/889 | 38/10067 | 5.18E-03 |
| GO:1990874 | BP | vascular associated smooth muscle cell proliferation | 11/889 | 38/10067 | 5.18E-03 |
| GO:0030178 | BP | negative regulation of Wnt signaling pathway | 25/889 | 136/10067 | 5.24E-03 |
| GO:0050804 | BP | modulation of chemical synaptic transmission | 38/889 | 242/10067 | 5.37E-03 |
| GO:0007162 | BP | negative regulation of cell adhesion | 33/889 | 201/10067 | 5.73E-03 |
| GO:0099177 | BP | regulation of trans-synaptic signaling | 38/889 | 243/10067 | 5.80E-03 |
| GO:1901890 | BP | positive regulation of cell junction assembly | 15/889 | 64/10067 | 5.80E-03 |
| GO:0002053 | BP | positive regulation of mesenchymal cell proliferation | 7/889 | 17/10067 | 5.80E-03 |
| GO:0003184 | BP | pulmonary valve morphogenesis | 7/889 | 17/10067 | 5.80E-03 |
| GO:0010714 | BP | positive regulation of collagen metabolic process | 7/889 | 17/10067 | 5.80E-03 |
| GO:0061037 | BP | negative regulation of cartilage development | 7/889 | 17/10067 | 5.80E-03 |
| GO:0062009 | BP | secondary palate development | 7/889 | 17/10067 | 5.80E-03 |
| GO:0031032 | BP | actomyosin structure organization | 26/889 | 145/10067 | 5.80E-03 |
| GO:0051057 | BP | positive regulation of small GTPase mediated signal transduction | 13/889 | 51/10067 | 5.81E-03 |
| GO:0016055 | BP | Wnt signaling pathway | 50/889 | 348/10067 | 5.89E-03 |
| GO:0003171 | BP | atrioventricular valve development | 8/889 | 22/10067 | 5.90E-03 |
| GO:0003272 | BP | endocardial cushion formation | 8/889 | 22/10067 | 5.90E-03 |
| GO:0007187 | BP | G protein-coupled receptor signaling pathway, coupled to cyclic nucleotide second messenger | 21/889 | 107/10067 | 5.91E-03 |
| GO:0045669 | BP | positive regulation of osteoblast differentiation | 12/889 | 45/10067 | 6.05E-03 |
| GO:0048008 | BP | platelet-derived growth factor receptor signaling pathway | 12/889 | 45/10067 | 6.05E-03 |
| GO:0072078 | BP | nephron tubule morphogenesis | 12/889 | 45/10067 | 6.05E-03 |
| GO:0198738 | BP | cell-cell signaling by wnt | 50/889 | 349/10067 | 6.13E-03 |
| GO:0010718 | BP | positive regulation of epithelial to mesenchymal transition | 11/889 | 39/10067 | 6.13E-03 |
| GO:0055021 | BP | regulation of cardiac muscle tissue growth | 11/889 | 39/10067 | 6.13E-03 |
| GO:0060976 | BP | coronary vasculature development | 11/889 | 39/10067 | 6.13E-03 |
| GO:0010975 | BP | regulation of neuron projection development | 49/889 | 341/10067 | 6.46E-03 |
| GO:0032526 | BP | response to retinoic acid | 15/889 | 65/10067 | 6.48E-03 |
| GO:0046620 | BP | regulation of organ growth | 15/889 | 65/10067 | 6.48E-03 |
| GO:0045446 | BP | endothelial cell differentiation | 17/889 | 79/10067 | 6.63E-03 |
| GO:0010002 | BP | cardioblast differentiation | 6/889 | 13/10067 | 6.95E-03 |
| GO:0043116 | BP | negative regulation of vascular permeability | 6/889 | 13/10067 | 6.95E-03 |
| GO:0086014 | BP | atrial cardiac muscle cell action potential | 6/889 | 13/10067 | 6.95E-03 |
| GO:0086026 | BP | atrial cardiac muscle cell to AV node cell signaling | 6/889 | 13/10067 | 6.95E-03 |
| GO:0086066 | BP | atrial cardiac muscle cell to AV node cell communication | 6/889 | 13/10067 | 6.95E-03 |
| GO:0061351 | BP | neural precursor cell proliferation | 19/889 | 94/10067 | 7.11E-03 |
| GO:0072088 | BP | nephron epithelium morphogenesis | 12/889 | 46/10067 | 7.15E-03 |
| GO:0006897 | BP | endocytosis | 54/889 | 388/10067 | 7.15E-03 |
| GO:1903035 | BP | negative regulation of response to wounding | 14/889 | 59/10067 | 7.15E-03 |
| GO:0050680 | BP | negative regulation of epithelial cell proliferation | 18/889 | 87/10067 | 7.28E-03 |
| GO:0046578 | BP | regulation of Ras protein signal transduction | 25/889 | 140/10067 | 7.28E-03 |
| GO:0046622 | BP | positive regulation of organ growth | 10/889 | 34/10067 | 7.36E-03 |
| GO:0007156 | BP | homophilic cell adhesion via plasma membrane adhesion molecules | 17/889 | 80/10067 | 7.39E-03 |
| GO:0030282 | BP | bone mineralization | 17/889 | 80/10067 | 7.39E-03 |
| GO:0070252 | BP | actin-mediated cell contraction | 16/889 | 73/10067 | 7.43E-03 |
| GO:0003148 | BP | outflow tract septum morphogenesis | 8/889 | 23/10067 | 7.57E-03 |
| GO:0045879 | BP | negative regulation of smoothened signaling pathway | 8/889 | 23/10067 | 7.57E-03 |
| GO:0090184 | BP | positive regulation of kidney development | 8/889 | 23/10067 | 7.57E-03 |
| GO:0007219 | BP | Notch signaling pathway | 24/889 | 133/10067 | 7.71E-03 |
| GO:0008016 | BP | regulation of heart contraction | 24/889 | 133/10067 | 7.71E-03 |
| GO:0086019 | BP | cell-cell signaling involved in cardiac conduction | 7/889 | 18/10067 | 7.71E-03 |
| GO:0090050 | BP | positive regulation of cell migration involved in sprouting angiogenesis | 7/889 | 18/10067 | 7.71E-03 |
| GO:0060402 | BP | calcium ion transport into cytosol | 19/889 | 95/10067 | 7.71E-03 |
| GO:0072175 | BP | epithelial tube formation | 19/889 | 95/10067 | 7.71E-03 |
| GO:0007179 | BP | transforming growth factor beta receptor signaling pathway | 25/889 | 141/10067 | 7.78E-03 |
| GO:0060560 | BP | developmental growth involved in morphogenesis | 27/889 | 157/10067 | 7.81E-03 |
| GO:0010595 | BP | positive regulation of endothelial cell migration | 18/889 | 88/10067 | 7.97E-03 |
| GO:0097553 | BP | calcium ion transmembrane import into cytosol | 18/889 | 88/10067 | 7.97E-03 |
| GO:0060993 | BP | kidney morphogenesis | 14/889 | 60/10067 | 8.07E-03 |
| GO:0045860 | BP | positive regulation of protein kinase activity | 52/889 | 373/10067 | 8.14E-03 |
| GO:0031076 | BP | embryonic camera-type eye development | 9/889 | 29/10067 | 8.52E-03 |
| GO:0060043 | BP | regulation of cardiac muscle cell proliferation | 9/889 | 29/10067 | 8.52E-03 |
| GO:0051493 | BP | regulation of cytoskeleton organization | 54/889 | 392/10067 | 8.52E-03 |
| GO:0060389 | BP | pathway-restricted SMAD protein phosphorylation | 11/889 | 41/10067 | 8.70E-03 |
| GO:0086002 | BP | cardiac muscle cell action potential involved in contraction | 10/889 | 35/10067 | 8.85E-03 |
| GO:0021510 | BP | spinal cord development | 13/889 | 54/10067 | 8.95E-03 |
| GO:0031346 | BP | positive regulation of cell projection organization | 41/889 | 277/10067 | 9.05E-03 |
| GO:0030111 | BP | regulation of Wnt signaling pathway | 38/889 | 251/10067 | 9.05E-03 |
| GO:0007266 | BP | Rho protein signal transduction | 20/889 | 104/10067 | 9.05E-03 |
| GO:0007599 | BP | hemostasis | 36/889 | 234/10067 | 9.14E-03 |
| GO:0060047 | BP | heart contraction | 26/889 | 151/10067 | 9.20E-03 |
| GO:0050808 | BP | synapse organization | 37/889 | 243/10067 | 9.40E-03 |
| GO:0050878 | BP | regulation of body fluid levels | 47/889 | 331/10067 | 9.49E-03 |
| GO:0048167 | BP | regulation of synaptic plasticity | 19/889 | 97/10067 | 9.52E-03 |
| GO:0010092 | BP | specification of animal organ identity | 8/889 | 24/10067 | 9.58E-03 |
| GO:0044319 | BP | wound healing, spreading of cells | 8/889 | 24/10067 | 9.58E-03 |
| GO:0060428 | BP | lung epithelium development | 8/889 | 24/10067 | 9.58E-03 |
| GO:0090505 | BP | epiboly involved in wound healing | 8/889 | 24/10067 | 9.58E-03 |
| GO:0070374 | BP | positive regulation of ERK1 and ERK2 cascade | 22/889 | 120/10067 | 9.58E-03 |
| GO:0001759 | BP | organ induction | 6/889 | 14/10067 | 9.74E-03 |
| GO:0061298 | BP | retina vasculature development in camera-type eye | 6/889 | 14/10067 | 9.74E-03 |
| GO:1903055 | BP | positive regulation of extracellular matrix organization | 6/889 | 14/10067 | 9.74E-03 |
| GO:2000738 | BP | positive regulation of stem cell differentiation | 6/889 | 14/10067 | 9.74E-03 |
| GO:0002576 | BP | platelet degranulation | 18/889 | 90/10067 | 9.79E-03 |
| GO:0001935 | BP | endothelial cell proliferation | 20/889 | 105/10067 | 9.81E-03 |
| GO:0031012 | CC | extracellular matrix | 96/909 | 337/10416 | 2.79E-24 |
| GO:0062023 | CC | collagen-containing extracellular matrix | 81/909 | 272/10416 | 7.32E-22 |
| GO:0015629 | CC | actin cytoskeleton | 66/909 | 354/10416 | 2.67E-07 |
| GO:0005788 | CC | endoplasmic reticulum lumen | 43/909 | 191/10416 | 4.97E-07 |
| GO:0042641 | CC | actomyosin | 21/909 | 61/10416 | 1.47E-06 |
| GO:0005581 | CC | collagen trimer | 19/909 | 51/10416 | 1.47E-06 |
| GO:0005925 | CC | focal adhesion | 59/909 | 321/10416 | 1.47E-06 |
| GO:0030055 | CC | cell-substrate junction | 59/909 | 327/10416 | 2.57E-06 |
| GO:0001725 | CC | stress fiber | 18/909 | 53/10416 | 1.11E-05 |
| GO:0097517 | CC | contractile actin filament bundle | 18/909 | 53/10416 | 1.11E-05 |
| GO:0032432 | CC | actin filament bundle | 19/909 | 59/10416 | 1.22E-05 |
| GO:0005604 | CC | basement membrane | 21/909 | 75/10416 | 3.72E-05 |
| GO:0098644 | CC | complex of collagen trimers | 9/909 | 16/10416 | 6.31E-05 |
| GO:0005583 | CC | fibrillar collagen trimer | 7/909 | 10/10416 | 1.06E-04 |
| GO:0098643 | CC | banded collagen fibril | 7/909 | 10/10416 | 1.06E-04 |
| GO:0030027 | CC | lamellipodium | 33/909 | 164/10416 | 1.13E-04 |
| GO:0009986 | CC | cell surface | 70/909 | 483/10416 | 3.48E-04 |
| GO:0043292 | CC | contractile fiber | 27/909 | 135/10416 | 8.30E-04 |
| GO:0005911 | CC | cell-cell junction | 52/909 | 338/10416 | 8.32E-04 |
| GO:0098978 | CC | glutamatergic synapse | 35/909 | 201/10416 | 1.23E-03 |
| GO:0060170 | CC | ciliary membrane | 12/909 | 38/10416 | 1.23E-03 |
| GO:0030016 | CC | myofibril | 25/909 | 126/10416 | 1.51E-03 |
| GO:0030017 | CC | sarcomere | 23/909 | 113/10416 | 1.84E-03 |
| GO:0030425 | CC | dendrite | 53/909 | 362/10416 | 2.13E-03 |
| GO:0097447 | CC | dendritic tree | 53/909 | 363/10416 | 2.20E-03 |
| GO:0005912 | CC | adherens junction | 24/909 | 123/10416 | 2.32E-03 |
| GO:0031252 | CC | cell leading edge | 48/909 | 323/10416 | 2.69E-03 |
| GO:0030018 | CC | Z disc | 18/909 | 81/10416 | 2.69E-03 |
| GO:0031253 | CC | cell projection membrane | 36/909 | 223/10416 | 3.28E-03 |
| GO:0036477 | CC | somatodendritic compartment | 66/909 | 490/10416 | 3.28E-03 |
| GO:0031674 | CC | I band | 18/909 | 84/10416 | 3.86E-03 |
| GO:0031093 | CC | platelet alpha granule lumen | 12/909 | 44/10416 | 3.86E-03 |
| GO:0098794 | CC | postsynapse | 50/909 | 349/10416 | 4.08E-03 |
| GO:0031091 | CC | platelet alpha granule | 14/909 | 61/10416 | 8.11E-03 |
| GO:0005796 | CC | Golgi lumen | 12/909 | 48/10416 | 8.41E-03 |
| GO:0005201 | MF | extracellular matrix structural constituent | 52/906 | 118/10268 | 1.04E-21 |
| GO:0005198 | MF | structural molecule activity | 81/906 | 375/10268 | 3.96E-12 |
| GO:0048407 | MF | platelet-derived growth factor binding | 10/906 | 10/10268 | 5.98E-09 |
| GO:0019838 | MF | growth factor binding | 32/906 | 99/10268 | 5.98E-09 |
| GO:0030020 | MF | extracellular matrix structural constituent conferring tensile strength | 16/906 | 28/10268 | 1.92E-08 |
| GO:0003779 | MF | actin binding | 61/906 | 309/10268 | 1.40E-07 |
| GO:0005539 | MF | glycosaminoglycan binding | 34/906 | 130/10268 | 4.61E-07 |
| GO:0005518 | MF | collagen binding | 21/906 | 59/10268 | 1.06E-06 |
| GO:0008201 | MF | heparin binding | 27/906 | 96/10268 | 2.69E-06 |
| GO:0005509 | MF | calcium ion binding | 64/906 | 382/10268 | 2.33E-05 |
| GO:0005178 | MF | integrin binding | 27/906 | 108/10268 | 3.09E-05 |
| GO:0051393 | MF | alpha-actinin binding | 9/906 | 16/10268 | 1.23E-04 |
| GO:0050840 | MF | extracellular matrix binding | 16/906 | 49/10268 | 1.37E-04 |
| GO:0030545 | MF | receptor regulator activity | 36/906 | 186/10268 | 2.58E-04 |
| GO:0005125 | MF | cytokine activity | 19/906 | 70/10268 | 3.10E-04 |
| GO:0030546 | MF | signaling receptor activator activity | 34/906 | 174/10268 | 3.31E-04 |
| GO:0042805 | MF | actinin binding | 10/906 | 23/10268 | 4.53E-04 |
| GO:0050839 | MF | cell adhesion molecule binding | 57/906 | 363/10268 | 4.53E-04 |
| GO:0048018 | MF | receptor ligand activity | 33/906 | 171/10268 | 4.99E-04 |
| GO:1901681 | MF | sulfur compound binding | 31/906 | 158/10268 | 6.11E-04 |
| GO:0005262 | MF | calcium channel activity | 16/906 | 59/10268 | 1.15E-03 |
| GO:0005520 | MF | insulin-like growth factor binding | 9/906 | 21/10268 | 1.15E-03 |
| GO:0005200 | MF | structural constituent of cytoskeleton | 16/906 | 60/10268 | 1.37E-03 |
| GO:0008083 | MF | growth factor activity | 19/906 | 81/10268 | 1.82E-03 |
| GO:0046332 | MF | SMAD binding | 16/906 | 62/10268 | 1.95E-03 |
| GO:0015085 | MF | calcium ion transmembrane transporter activity | 17/906 | 71/10268 | 3.09E-03 |
| GO:0019955 | MF | cytokine binding | 20/906 | 92/10268 | 3.26E-03 |
| GO:0051371 | MF | muscle alpha-actinin binding | 6/906 | 11/10268 | 3.66E-03 |
| GO:0099094 | MF | ligand-gated cation channel activity | 12/906 | 41/10268 | 3.66E-03 |
| GO:0005261 | MF | cation channel activity | 25/906 | 130/10268 | 3.66E-03 |
| GO:0072509 | MF | divalent inorganic cation transmembrane transporter activity | 19/906 | 87/10268 | 3.91E-03 |
| GO:0050431 | MF | transforming growth factor beta binding | 7/906 | 17/10268 | 8.22E-03 |
| GO:0051015 | MF | actin filament binding | 26/906 | 147/10268 | 9.90E-03 |
| **Pathways associated with brown module genes** | | | | | |
| GO:0071103 | BP | DNA conformation change | 77/791 | 244/10067 | 3.08E-24 |
| GO:0007059 | BP | chromosome segregation | 72/791 | 226/10067 | 4.65E-23 |
| GO:0098813 | BP | nuclear chromosome segregation | 61/791 | 179/10067 | 4.39E-21 |
| GO:0000819 | BP | sister chromatid segregation | 53/791 | 140/10067 | 1.22E-20 |
| GO:0140014 | BP | mitotic nuclear division | 65/791 | 211/10067 | 4.62E-20 |
| GO:0000280 | BP | nuclear division | 76/791 | 280/10067 | 4.69E-20 |
| GO:0051301 | BP | cell division | 96/791 | 419/10067 | 5.42E-20 |
| GO:0000070 | BP | mitotic sister chromatid segregation | 48/791 | 124/10067 | 2.65E-19 |
| GO:0006260 | BP | DNA replication | 60/791 | 197/10067 | 2.43E-18 |
| GO:0048285 | BP | organelle fission | 77/791 | 310/10067 | 5.41E-18 |
| GO:0065004 | BP | protein-DNA complex assembly | 52/791 | 156/10067 | 9.92E-18 |
| GO:0006261 | BP | DNA-dependent DNA replication | 44/791 | 116/10067 | 2.49E-17 |
| GO:0071824 | BP | protein-DNA complex subunit organization | 54/791 | 179/10067 | 2.70E-16 |
| GO:0006323 | BP | DNA packaging | 48/791 | 153/10067 | 3.90E-15 |
| GO:0044770 | BP | cell cycle phase transition | 89/791 | 442/10067 | 8.26E-15 |
| GO:0044772 | BP | mitotic cell cycle phase transition | 85/791 | 416/10067 | 1.69E-14 |
| GO:0051983 | BP | regulation of chromosome segregation | 34/791 | 83/10067 | 1.84E-14 |
| GO:0006334 | BP | nucleosome assembly | 35/791 | 89/10067 | 2.82E-14 |
| GO:0000075 | BP | cell cycle checkpoint | 47/791 | 161/10067 | 1.50E-13 |
| GO:0006302 | BP | double-strand break repair | 51/791 | 192/10067 | 5.95E-13 |
| GO:0007346 | BP | regulation of mitotic cell cycle | 85/791 | 449/10067 | 1.49E-12 |
| GO:0032392 | BP | DNA geometric change | 33/791 | 90/10067 | 1.96E-12 |
| GO:0007088 | BP | regulation of mitotic nuclear division | 38/791 | 118/10067 | 2.36E-12 |
| GO:0034728 | BP | nucleosome organization | 37/791 | 113/10067 | 2.80E-12 |
| GO:0051783 | BP | regulation of nuclear division | 39/791 | 129/10067 | 1.00E-11 |
| GO:0031497 | BP | chromatin assembly | 38/791 | 124/10067 | 1.26E-11 |
| GO:0006281 | BP | DNA repair | 76/791 | 394/10067 | 1.26E-11 |
| GO:0033045 | BP | regulation of sister chromatid segregation | 27/791 | 66/10067 | 1.85E-11 |
| GO:0007093 | BP | mitotic cell cycle checkpoint | 38/791 | 126/10067 | 1.99E-11 |
| GO:0033260 | BP | nuclear DNA replication | 23/791 | 49/10067 | 3.27E-11 |
| GO:0032508 | BP | DNA duplex unwinding | 30/791 | 83/10067 | 3.58E-11 |
| GO:0044786 | BP | cell cycle DNA replication | 23/791 | 52/10067 | 1.48E-10 |
| GO:0006270 | BP | DNA replication initiation | 17/791 | 28/10067 | 1.68E-10 |
| GO:0006333 | BP | chromatin assembly or disassembly | 39/791 | 143/10067 | 2.77E-10 |
| GO:0051304 | BP | chromosome separation | 26/791 | 68/10067 | 2.77E-10 |
| GO:0010965 | BP | regulation of mitotic sister chromatid separation | 22/791 | 49/10067 | 2.82E-10 |
| GO:0033047 | BP | regulation of mitotic sister chromatid segregation | 24/791 | 59/10067 | 3.79E-10 |
| GO:1905818 | BP | regulation of chromosome separation | 22/791 | 51/10067 | 7.21E-10 |
| GO:0051306 | BP | mitotic sister chromatid separation | 22/791 | 52/10067 | 1.13E-09 |
| GO:0007091 | BP | metaphase/anaphase transition of mitotic cell cycle | 21/791 | 48/10067 | 1.45E-09 |
| GO:0044784 | BP | metaphase/anaphase transition of cell cycle | 21/791 | 48/10067 | 1.45E-09 |
| GO:0051321 | BP | meiotic cell cycle | 37/791 | 139/10067 | 1.86E-09 |
| GO:0031570 | BP | DNA integrity checkpoint | 33/791 | 115/10067 | 2.51E-09 |
| GO:1901987 | BP | regulation of cell cycle phase transition | 62/791 | 326/10067 | 3.25E-09 |
| GO:0030071 | BP | regulation of mitotic metaphase/anaphase transition | 20/791 | 46/10067 | 4.59E-09 |
| GO:1902099 | BP | regulation of metaphase/anaphase transition of cell cycle | 20/791 | 46/10067 | 4.59E-09 |
| GO:0090068 | BP | positive regulation of cell cycle process | 44/791 | 192/10067 | 4.91E-09 |
| GO:1901990 | BP | regulation of mitotic cell cycle phase transition | 59/791 | 306/10067 | 5.13E-09 |
| GO:2001251 | BP | negative regulation of chromosome organization | 31/791 | 106/10067 | 5.19E-09 |
| GO:0045930 | BP | negative regulation of mitotic cell cycle | 48/791 | 228/10067 | 1.44E-08 |
| GO:0000724 | BP | double-strand break repair via homologous recombination | 30/791 | 105/10067 | 1.89E-08 |
| GO:0000725 | BP | recombinational repair | 30/791 | 105/10067 | 1.89E-08 |
| GO:0045132 | BP | meiotic chromosome segregation | 20/791 | 50/10067 | 2.47E-08 |
| GO:1903046 | BP | meiotic cell cycle process | 30/791 | 107/10067 | 3.02E-08 |
| GO:0140013 | BP | meiotic nuclear division | 28/791 | 96/10067 | 4.15E-08 |
| GO:0033044 | BP | regulation of chromosome organization | 50/791 | 251/10067 | 4.15E-08 |
| GO:0006310 | BP | DNA recombination | 43/791 | 199/10067 | 4.90E-08 |
| GO:0007052 | BP | mitotic spindle organization | 25/791 | 80/10067 | 6.77E-08 |
| GO:0032200 | BP | telomere organization | 32/791 | 124/10067 | 7.32E-08 |
| GO:1902850 | BP | microtubule cytoskeleton organization involved in mitosis | 28/791 | 100/10067 | 1.09E-07 |
| GO:0033046 | BP | negative regulation of sister chromatid segregation | 16/791 | 35/10067 | 1.21E-07 |
| GO:0051985 | BP | negative regulation of chromosome segregation | 16/791 | 35/10067 | 1.21E-07 |
| GO:1905819 | BP | negative regulation of chromosome separation | 15/791 | 31/10067 | 1.41E-07 |
| GO:2000816 | BP | negative regulation of mitotic sister chromatid separation | 15/791 | 31/10067 | 1.41E-07 |
| GO:0034508 | BP | centromere complex assembly | 17/791 | 40/10067 | 1.43E-07 |
| GO:0008608 | BP | attachment of spindle microtubules to kinetochore | 14/791 | 28/10067 | 2.75E-07 |
| GO:0045787 | BP | positive regulation of cell cycle | 48/791 | 250/10067 | 2.77E-07 |
| GO:0000281 | BP | mitotic cytokinesis | 18/791 | 47/10067 | 3.44E-07 |
| GO:0045814 | BP | negative regulation of gene expression, epigenetic | 25/791 | 87/10067 | 3.97E-07 |
| GO:0045786 | BP | negative regulation of cell cycle | 68/791 | 423/10067 | 4.27E-07 |
| GO:0022616 | BP | DNA strand elongation | 12/791 | 21/10067 | 4.35E-07 |
| GO:0007094 | BP | mitotic spindle assembly checkpoint | 14/791 | 29/10067 | 4.35E-07 |
| GO:0031577 | BP | spindle checkpoint | 14/791 | 29/10067 | 4.35E-07 |
| GO:0071173 | BP | spindle assembly checkpoint | 14/791 | 29/10067 | 4.35E-07 |
| GO:0071174 | BP | mitotic spindle checkpoint | 14/791 | 29/10067 | 4.35E-07 |
| GO:0045839 | BP | negative regulation of mitotic nuclear division | 17/791 | 43/10067 | 4.64E-07 |
| GO:0033048 | BP | negative regulation of mitotic sister chromatid segregation | 15/791 | 34/10067 | 5.78E-07 |
| GO:0051383 | BP | kinetochore organization | 11/791 | 18/10067 | 6.74E-07 |
| GO:0051784 | BP | negative regulation of nuclear division | 17/791 | 44/10067 | 6.74E-07 |
| GO:0045841 | BP | negative regulation of mitotic metaphase/anaphase transition | 14/791 | 30/10067 | 7.01E-07 |
| GO:1902100 | BP | negative regulation of metaphase/anaphase transition of cell cycle | 14/791 | 30/10067 | 7.01E-07 |
| GO:0050000 | BP | chromosome localization | 19/791 | 55/10067 | 7.81E-07 |
| GO:0051303 | BP | establishment of chromosome localization | 19/791 | 55/10067 | 7.81E-07 |
| GO:0051310 | BP | metaphase plate congression | 17/791 | 45/10067 | 9.45E-07 |
| GO:0000910 | BP | cytokinesis | 27/791 | 105/10067 | 1.12E-06 |
| GO:0061640 | BP | cytoskeleton-dependent cytokinesis | 20/791 | 62/10067 | 1.20E-06 |
| GO:0007051 | BP | spindle organization | 31/791 | 133/10067 | 1.25E-06 |
| GO:0044843 | BP | cell cycle G1/S phase transition | 40/791 | 202/10067 | 1.72E-06 |
| GO:0031055 | BP | chromatin remodeling at centromere | 14/791 | 32/10067 | 1.78E-06 |
| GO:0000076 | BP | DNA replication checkpoint | 9/791 | 13/10067 | 2.73E-06 |
| GO:0000082 | BP | G1/S transition of mitotic cell cycle | 38/791 | 190/10067 | 2.78E-06 |
| GO:0097549 | BP | chromatin organization involved in negative regulation of transcription | 25/791 | 97/10067 | 3.27E-06 |
| GO:0034502 | BP | protein localization to chromosome | 19/791 | 61/10067 | 4.69E-06 |
| GO:0000077 | BP | DNA damage checkpoint | 26/791 | 106/10067 | 5.20E-06 |
| GO:0044839 | BP | cell cycle G2/M phase transition | 38/791 | 196/10067 | 6.23E-06 |
| GO:0034401 | BP | chromatin organization involved in regulation of transcription | 26/791 | 107/10067 | 6.23E-06 |
| GO:0006336 | BP | DNA replication-independent nucleosome assembly | 14/791 | 35/10067 | 6.37E-06 |
| GO:0034724 | BP | DNA replication-independent nucleosome organization | 14/791 | 35/10067 | 6.37E-06 |
| GO:0051052 | BP | regulation of DNA metabolic process | 44/791 | 245/10067 | 6.41E-06 |
| GO:0006275 | BP | regulation of DNA replication | 21/791 | 75/10067 | 7.28E-06 |
| GO:0010948 | BP | negative regulation of cell cycle process | 42/791 | 230/10067 | 7.51E-06 |
| GO:1901988 | BP | negative regulation of cell cycle phase transition | 35/791 | 176/10067 | 9.57E-06 |
| GO:0044774 | BP | mitotic DNA integrity checkpoint | 21/791 | 78/10067 | 1.47E-05 |
| GO:1901991 | BP | negative regulation of mitotic cell cycle phase transition | 33/791 | 164/10067 | 1.56E-05 |
| GO:0034080 | BP | CENP-A containing nucleosome assembly | 12/791 | 28/10067 | 1.89E-05 |
| GO:0061641 | BP | CENP-A containing chromatin organization | 12/791 | 28/10067 | 1.89E-05 |
| GO:0070192 | BP | chromosome organization involved in meiotic cell cycle | 14/791 | 38/10067 | 1.94E-05 |
| GO:0007080 | BP | mitotic metaphase plate congression | 13/791 | 33/10067 | 2.00E-05 |
| GO:0000086 | BP | G2/M transition of mitotic cell cycle | 35/791 | 183/10067 | 2.39E-05 |
| GO:1902749 | BP | regulation of cell cycle G2/M phase transition | 31/791 | 152/10067 | 2.44E-05 |
| GO:0061982 | BP | meiosis I cell cycle process | 18/791 | 62/10067 | 2.76E-05 |
| GO:0006271 | BP | DNA strand elongation involved in DNA replication | 9/791 | 16/10067 | 2.83E-05 |
| GO:0090329 | BP | regulation of DNA-dependent DNA replication | 14/791 | 40/10067 | 3.81E-05 |
| GO:0006335 | BP | DNA replication-dependent nucleosome assembly | 10/791 | 21/10067 | 4.91E-05 |
| GO:0034723 | BP | DNA replication-dependent nucleosome organization | 10/791 | 21/10067 | 4.91E-05 |
| GO:0000729 | BP | DNA double-strand break processing | 9/791 | 17/10067 | 5.40E-05 |
| GO:0043486 | BP | histone exchange | 13/791 | 36/10067 | 5.96E-05 |
| GO:0051984 | BP | positive regulation of chromosome segregation | 11/791 | 26/10067 | 5.99E-05 |
| GO:0045931 | BP | positive regulation of mitotic cell cycle | 24/791 | 106/10067 | 5.99E-05 |
| GO:0000723 | BP | telomere maintenance | 25/791 | 114/10067 | 6.78E-05 |
| GO:0032201 | BP | telomere maintenance via semi-conservative replication | 10/791 | 22/10067 | 7.89E-05 |
| GO:0006338 | BP | chromatin remodeling | 30/791 | 153/10067 | 7.89E-05 |
| GO:0030261 | BP | chromosome condensation | 12/791 | 32/10067 | 9.00E-05 |
| GO:0000083 | BP | regulation of transcription involved in G1/S transition of mitotic cell cycle | 11/791 | 27/10067 | 9.00E-05 |
| GO:0007062 | BP | sister chromatid cohesion | 14/791 | 43/10067 | 9.31E-05 |
| GO:0010639 | BP | negative regulation of organelle organization | 46/791 | 292/10067 | 1.23E-04 |
| GO:0010389 | BP | regulation of G2/M transition of mitotic cell cycle | 28/791 | 141/10067 | 1.26E-04 |
| GO:0051054 | BP | positive regulation of DNA metabolic process | 28/791 | 141/10067 | 1.26E-04 |
| GO:0000727 | BP | double-strand break repair via break-induced replication | 7/791 | 11/10067 | 1.46E-04 |
| GO:0051302 | BP | regulation of cell division | 24/791 | 112/10067 | 1.54E-04 |
| GO:0032465 | BP | regulation of cytokinesis | 16/791 | 57/10067 | 1.57E-04 |
| GO:0031572 | BP | G2 DNA damage checkpoint | 10/791 | 24/10067 | 1.90E-04 |
| GO:0032506 | BP | cytokinetic process | 10/791 | 24/10067 | 1.90E-04 |
| GO:1901989 | BP | positive regulation of cell cycle phase transition | 17/791 | 65/10067 | 2.24E-04 |
| GO:0007127 | BP | meiosis I | 16/791 | 59/10067 | 2.49E-04 |
| GO:0045143 | BP | homologous chromosome segregation | 11/791 | 30/10067 | 2.76E-04 |
| GO:0000226 | BP | microtubule cytoskeleton organization | 58/791 | 414/10067 | 2.86E-04 |
| GO:0044773 | BP | mitotic DNA damage checkpoint | 18/791 | 73/10067 | 2.89E-04 |
| GO:1902969 | BP | mitotic DNA replication | 7/791 | 12/10067 | 3.03E-04 |
| GO:0072331 | BP | signal transduction by p53 class mediator | 33/791 | 191/10067 | 3.82E-04 |
| GO:0044818 | BP | mitotic G2/M transition checkpoint | 9/791 | 21/10067 | 4.02E-04 |
| GO:0043044 | BP | ATP-dependent chromatin remodeling | 15/791 | 58/10067 | 8.41E-04 |
| GO:0040029 | BP | regulation of gene expression, epigenetic | 27/791 | 148/10067 | 8.44E-04 |
| GO:0045005 | BP | DNA-dependent DNA replication maintenance of fidelity | 11/791 | 34/10067 | 1.02E-03 |
| GO:0051988 | BP | regulation of attachment of spindle microtubules to kinetochore | 6/791 | 10/10067 | 1.07E-03 |
| GO:0051315 | BP | attachment of mitotic spindle microtubules to kinetochore | 7/791 | 14/10067 | 1.09E-03 |
| GO:0051225 | BP | spindle assembly | 18/791 | 82/10067 | 1.47E-03 |
| GO:0000183 | BP | rDNA heterochromatin assembly | 10/791 | 30/10067 | 1.69E-03 |
| GO:0045840 | BP | positive regulation of mitotic nuclear division | 11/791 | 36/10067 | 1.79E-03 |
| GO:0034501 | BP | protein localization to kinetochore | 7/791 | 15/10067 | 1.85E-03 |
| GO:0006282 | BP | regulation of DNA repair | 20/791 | 99/10067 | 1.97E-03 |
| GO:0032467 | BP | positive regulation of cytokinesis | 8/791 | 20/10067 | 2.08E-03 |
| GO:0031297 | BP | replication fork processing | 9/791 | 26/10067 | 2.74E-03 |
| GO:0042769 | BP | DNA damage response, detection of DNA damage | 9/791 | 26/10067 | 2.74E-03 |
| GO:0051785 | BP | positive regulation of nuclear division | 12/791 | 44/10067 | 2.77E-03 |
| GO:0071897 | BP | DNA biosynthetic process | 24/791 | 134/10067 | 2.87E-03 |
| GO:0006342 | BP | chromatin silencing | 13/791 | 51/10067 | 3.03E-03 |
| GO:1901992 | BP | positive regulation of mitotic cell cycle phase transition | 14/791 | 58/10067 | 3.14E-03 |
| GO:0000018 | BP | regulation of DNA recombination | 17/791 | 80/10067 | 3.35E-03 |
| GO:0060249 | BP | anatomical structure homeostasis | 44/791 | 316/10067 | 3.40E-03 |
| GO:0031507 | BP | heterochromatin assembly | 13/791 | 52/10067 | 3.66E-03 |
| GO:0071459 | BP | protein localization to chromosome, centromeric region | 7/791 | 17/10067 | 4.50E-03 |
| GO:1901796 | BP | regulation of signal transduction by p53 class mediator | 22/791 | 123/10067 | 5.36E-03 |
| GO:1901976 | BP | regulation of cell cycle checkpoint | 8/791 | 23/10067 | 6.06E-03 |
| GO:2000779 | BP | regulation of double-strand break repair | 15/791 | 69/10067 | 6.11E-03 |
| GO:0006268 | BP | DNA unwinding involved in DNA replication | 6/791 | 13/10067 | 6.16E-03 |
| GO:0051382 | BP | kinetochore assembly | 6/791 | 13/10067 | 6.16E-03 |
| GO:0062033 | BP | positive regulation of mitotic sister chromatid segregation | 7/791 | 18/10067 | 6.63E-03 |
| GO:0006305 | BP | DNA alkylation | 11/791 | 42/10067 | 7.18E-03 |
| GO:0006306 | BP | DNA methylation | 11/791 | 42/10067 | 7.18E-03 |
| GO:0090307 | BP | mitotic spindle assembly | 11/791 | 42/10067 | 7.18E-03 |
| GO:2001252 | BP | positive regulation of chromosome organization | 22/791 | 126/10067 | 7.25E-03 |
| GO:0070828 | BP | heterochromatin organization | 13/791 | 57/10067 | 9.11E-03 |
| GO:1902751 | BP | positive regulation of cell cycle G2/M phase transition | 7/791 | 19/10067 | 9.45E-03 |
| GO:0098687 | CC | chromosomal region | 74/818 | 248/10416 | 2.21E-22 |
| GO:0000793 | CC | condensed chromosome | 49/818 | 149/10416 | 1.59E-16 |
| GO:0000775 | CC | chromosome, centromeric region | 47/818 | 142/10416 | 4.16E-16 |
| GO:0044815 | CC | DNA packaging complex | 33/818 | 74/10416 | 1.16E-15 |
| GO:0000779 | CC | condensed chromosome, centromeric region | 34/818 | 94/10416 | 6.40E-13 |
| GO:0000776 | CC | kinetochore | 35/818 | 102/10416 | 1.36E-12 |
| GO:0000786 | CC | nucleosome | 28/818 | 67/10416 | 1.42E-12 |
| GO:0000777 | CC | condensed chromosome kinetochore | 31/818 | 82/10416 | 1.42E-12 |
| GO:0032993 | CC | protein-DNA complex | 40/818 | 132/10416 | 1.42E-12 |
| GO:0005819 | CC | spindle | 58/818 | 274/10416 | 7.82E-11 |
| GO:0005657 | CC | replication fork | 23/818 | 56/10416 | 3.34E-10 |
| GO:0005813 | CC | centrosome | 71/818 | 445/10416 | 1.87E-07 |
| GO:0000794 | CC | condensed nuclear chromosome | 21/818 | 63/10416 | 2.13E-07 |
| GO:0000922 | CC | spindle pole | 29/818 | 122/10416 | 1.62E-06 |
| GO:0000940 | CC | condensed chromosome outer kinetochore | 8/818 | 10/10416 | 1.80E-06 |
| GO:0000784 | CC | nuclear chromosome, telomeric region | 23/818 | 84/10416 | 2.19E-06 |
| GO:0000781 | CC | chromosome, telomeric region | 27/818 | 113/10416 | 3.45E-06 |
| GO:0030496 | CC | midbody | 29/818 | 129/10416 | 4.61E-06 |
| GO:0051233 | CC | spindle midzone | 12/818 | 28/10416 | 1.23E-05 |
| GO:0000788 | CC | nuclear nucleosome | 10/818 | 22/10416 | 5.63E-05 |
| GO:0043596 | CC | nuclear replication fork | 12/818 | 32/10416 | 5.94E-05 |
| GO:0000780 | CC | condensed nuclear chromosome, centromeric region | 11/818 | 27/10416 | 5.94E-05 |
| GO:0072686 | CC | mitotic spindle | 23/818 | 102/10416 | 6.41E-05 |
| GO:0042555 | CC | MCM complex | 6/818 | 10/10416 | 7.55E-04 |
| GO:0005876 | CC | spindle microtubule | 13/818 | 47/10416 | 8.49E-04 |
| GO:0035861 | CC | site of double-strand break | 13/818 | 47/10416 | 8.49E-04 |
| GO:0000778 | CC | condensed nuclear chromosome kinetochore | 7/818 | 16/10416 | 2.00E-03 |
| GO:0005874 | CC | microtubule | 42/818 | 297/10416 | 2.28E-03 |
| GO:0090734 | CC | site of DNA damage | 14/818 | 59/10416 | 2.44E-03 |
| GO:1990023 | CC | mitotic spindle midzone | 5/818 | 10/10416 | 8.75E-03 |
| GO:0140097 | MF | catalytic activity, acting on DNA | 39/789 | 150/10268 | 4.20E-09 |
| GO:0003697 | MF | single-stranded DNA binding | 27/789 | 81/10268 | 5.27E-09 |
| GO:0008094 | MF | DNA-dependent ATPase activity | 27/789 | 81/10268 | 5.27E-09 |
| GO:0003678 | MF | DNA helicase activity | 23/789 | 62/10268 | 1.01E-08 |
| GO:0017116 | MF | single-stranded DNA helicase activity | 10/789 | 13/10268 | 2.23E-07 |
| GO:0003688 | MF | DNA replication origin binding | 11/789 | 19/10268 | 2.60E-06 |
| GO:0046982 | MF | protein heterodimerization activity | 37/789 | 190/10268 | 1.07E-05 |
| GO:0016887 | MF | ATPase activity | 49/789 | 302/10268 | 3.40E-05 |
| GO:0004386 | MF | helicase activity | 27/789 | 127/10268 | 7.42E-05 |
| GO:0000217 | MF | DNA secondary structure binding | 11/789 | 29/10268 | 3.49E-04 |
| GO:0003777 | MF | microtubule motor activity | 14/789 | 51/10268 | 1.27E-03 |
| GO:0043138 | MF | 3'-5' DNA helicase activity | 8/789 | 19/10268 | 2.44E-03 |
| GO:0003774 | MF | motor activity | 18/789 | 84/10268 | 2.95E-03 |
| GO:0003684 | MF | damaged DNA binding | 13/789 | 51/10268 | 4.59E-03 |
| **Pathways associated with green module genes** | | | | | |
| GO:0070603 | CC | SWI/SNF superfamily-type complex | 12/449 | 52/10416 | 5.36E-04 |
| GO:1904949 | CC | ATPase complex | 12/449 | 54/10416 | 5.36E-04 |
| GO:0003712 | MF | transcription coregulator activity | 44/451 | 349/10268 | 1.24E-07 |
| GO:0003713 | MF | transcription coactivator activity | 30/451 | 190/10268 | 2.69E-07 |
| GO:0003682 | MF | chromatin binding | 35/451 | 394/10268 | 8.70E-03 |
| GO:0008134 | MF | transcription factor binding | 38/451 | 443/10268 | 8.70E-03 |
| GO:0070577 | MF | lysine-acetylated histone binding | 6/451 | 18/10268 | 8.70E-03 |
| GO:0140033 | MF | acetylation-dependent protein binding | 6/451 | 18/10268 | 8.70E-03 |
| GO:0042800 | MF | histone methyltransferase activity (H3-K4 specific) | 5/451 | 12/10268 | 8.90E-03 |
| **Pathways associated with greenyellow module genes** | | | | | |
| GO:0045087 | BP | innate immune response | 104/372 | 495/10067 | 2.38E-48 |
| GO:0002274 | BP | myeloid leukocyte activation | 91/372 | 436/10067 | 1.68E-41 |
| GO:0002366 | BP | leukocyte activation involved in immune response | 90/372 | 466/10067 | 3.20E-38 |
| GO:0002263 | BP | cell activation involved in immune response | 90/372 | 469/10067 | 4.17E-38 |
| GO:0050778 | BP | positive regulation of immune response | 82/372 | 389/10067 | 1.29E-37 |
| GO:0043299 | BP | leukocyte degranulation | 76/372 | 362/10067 | 1.69E-34 |
| GO:0006954 | BP | inflammatory response | 83/372 | 449/10067 | 9.96E-34 |
| GO:0002275 | BP | myeloid cell activation involved in immune response | 75/372 | 369/10067 | 4.27E-33 |
| GO:0002444 | BP | myeloid leukocyte mediated immunity | 73/372 | 375/10067 | 7.41E-31 |
| GO:0001817 | BP | regulation of cytokine production | 76/372 | 458/10067 | 2.05E-27 |
| GO:0002253 | BP | activation of immune response | 59/372 | 274/10067 | 6.00E-27 |
| GO:0036230 | BP | granulocyte activation | 65/372 | 338/10067 | 6.26E-27 |
| GO:0042119 | BP | neutrophil activation | 64/372 | 335/10067 | 2.46E-26 |
| GO:0043312 | BP | neutrophil degranulation | 63/372 | 326/10067 | 3.27E-26 |
| GO:0002283 | BP | neutrophil activation involved in immune response | 63/372 | 328/10067 | 4.39E-26 |
| GO:0001819 | BP | positive regulation of cytokine production | 58/372 | 280/10067 | 1.15E-25 |
| GO:0002446 | BP | neutrophil mediated immunity | 63/372 | 335/10067 | 1.36E-25 |
| GO:0002250 | BP | adaptive immune response | 54/372 | 242/10067 | 1.70E-25 |
| GO:0031347 | BP | regulation of defense response | 69/372 | 411/10067 | 3.43E-25 |
| GO:0046649 | BP | lymphocyte activation | 70/372 | 433/10067 | 1.39E-24 |
| GO:0019221 | BP | cytokine-mediated signaling pathway | 72/372 | 475/10067 | 1.34E-23 |
| GO:0032103 | BP | positive regulation of response to external stimulus | 57/372 | 298/10067 | 1.91E-23 |
| GO:0002764 | BP | immune response-regulating signaling pathway | 51/372 | 244/10067 | 1.15E-22 |
| GO:0050865 | BP | regulation of cell activation | 62/372 | 369/10067 | 1.66E-22 |
| GO:0002694 | BP | regulation of leukocyte activation | 59/372 | 337/10067 | 2.72E-22 |
| GO:0002697 | BP | regulation of immune effector process | 51/372 | 249/10067 | 2.74E-22 |
| GO:0002768 | BP | immune response-regulating cell surface receptor signaling pathway | 50/372 | 242/10067 | 5.11E-22 |
| GO:0002429 | BP | immune response-activating cell surface receptor signaling pathway | 48/372 | 222/10067 | 5.11E-22 |
| GO:0002757 | BP | immune response-activating signal transduction | 48/372 | 222/10067 | 5.11E-22 |
| GO:0009617 | BP | response to bacterium | 59/372 | 343/10067 | 5.86E-22 |
| GO:0050900 | BP | leukocyte migration | 52/372 | 279/10067 | 7.99E-21 |
| GO:0050867 | BP | positive regulation of cell activation | 45/372 | 217/10067 | 8.34E-20 |
| GO:0042110 | BP | T cell activation | 51/372 | 294/10067 | 5.86E-19 |
| GO:0002696 | BP | positive regulation of leukocyte activation | 43/372 | 208/10067 | 7.75E-19 |
| GO:0046651 | BP | lymphocyte proliferation | 38/372 | 165/10067 | 2.95E-18 |
| GO:0032943 | BP | mononuclear cell proliferation | 38/372 | 167/10067 | 4.51E-18 |
| GO:0006909 | BP | phagocytosis | 40/372 | 190/10067 | 8.86E-18 |
| GO:0031349 | BP | positive regulation of defense response | 42/372 | 214/10067 | 1.57E-17 |
| GO:0070661 | BP | leukocyte proliferation | 39/372 | 183/10067 | 1.57E-17 |
| GO:0034341 | BP | response to interferon-gamma | 32/372 | 122/10067 | 4.32E-17 |
| GO:0002831 | BP | regulation of response to biotic stimulus | 44/372 | 247/10067 | 1.00E-16 |
| GO:0030595 | BP | leukocyte chemotaxis | 32/372 | 131/10067 | 4.15E-16 |
| GO:0002703 | BP | regulation of leukocyte mediated immunity | 32/372 | 133/10067 | 6.56E-16 |
| GO:0007159 | BP | leukocyte cell-cell adhesion | 41/372 | 225/10067 | 6.56E-16 |
| GO:0002521 | BP | leukocyte differentiation | 50/372 | 335/10067 | 8.37E-16 |
| GO:0002449 | BP | lymphocyte mediated immunity | 34/372 | 154/10067 | 9.86E-16 |
| GO:0097529 | BP | myeloid leukocyte migration | 31/372 | 128/10067 | 1.62E-15 |
| GO:0051249 | BP | regulation of lymphocyte activation | 45/372 | 278/10067 | 1.62E-15 |
| GO:0045088 | BP | regulation of innate immune response | 36/372 | 180/10067 | 2.97E-15 |
| GO:0042116 | BP | macrophage activation | 23/372 | 67/10067 | 4.99E-15 |
| GO:0009615 | BP | response to virus | 38/372 | 206/10067 | 6.36E-15 |
| GO:0050670 | BP | regulation of lymphocyte proliferation | 30/372 | 130/10067 | 2.10E-14 |
| GO:0032944 | BP | regulation of mononuclear cell proliferation | 30/372 | 131/10067 | 2.58E-14 |
| GO:0060326 | BP | cell chemotaxis | 35/372 | 182/10067 | 2.73E-14 |
| GO:0050727 | BP | regulation of inflammatory response | 39/372 | 228/10067 | 3.30E-14 |
| GO:1903039 | BP | positive regulation of leukocyte cell-cell adhesion | 31/372 | 143/10067 | 4.05E-14 |
| GO:0042742 | BP | defense response to bacterium | 26/372 | 99/10067 | 6.69E-14 |
| GO:0002699 | BP | positive regulation of immune effector process | 30/372 | 137/10067 | 8.76E-14 |
| GO:0071346 | BP | cellular response to interferon-gamma | 27/372 | 110/10067 | 1.14E-13 |
| GO:0002237 | BP | response to molecule of bacterial origin | 37/372 | 214/10067 | 1.25E-13 |
| GO:0022409 | BP | positive regulation of cell-cell adhesion | 33/372 | 170/10067 | 1.31E-13 |
| GO:0042098 | BP | T cell proliferation | 28/372 | 120/10067 | 1.32E-13 |
| GO:0051607 | BP | defense response to virus | 32/372 | 160/10067 | 1.41E-13 |
| GO:0070663 | BP | regulation of leukocyte proliferation | 30/372 | 140/10067 | 1.49E-13 |
| GO:0150076 | BP | neuroinflammatory response | 18/372 | 43/10067 | 1.59E-13 |
| GO:0002833 | BP | positive regulation of response to biotic stimulus | 30/372 | 141/10067 | 1.77E-13 |
| GO:0002460 | BP | adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains | 33/372 | 174/10067 | 2.45E-13 |
| GO:1903037 | BP | regulation of leukocyte cell-cell adhesion | 35/372 | 197/10067 | 2.79E-13 |
| GO:0097530 | BP | granulocyte migration | 23/372 | 80/10067 | 3.00E-13 |
| GO:1902105 | BP | regulation of leukocyte differentiation | 34/372 | 188/10067 | 3.91E-13 |
| GO:0002683 | BP | negative regulation of immune system process | 42/372 | 288/10067 | 6.21E-13 |
| GO:0051251 | BP | positive regulation of lymphocyte activation | 33/372 | 180/10067 | 6.39E-13 |
| GO:0050870 | BP | positive regulation of T cell activation | 28/372 | 130/10067 | 9.96E-13 |
| GO:0001774 | BP | microglial cell activation | 15/372 | 30/10067 | 1.11E-12 |
| GO:0002269 | BP | leukocyte activation involved in inflammatory response | 15/372 | 30/10067 | 1.11E-12 |
| GO:0032635 | BP | interleukin-6 production | 24/372 | 95/10067 | 1.69E-12 |
| GO:0022407 | BP | regulation of cell-cell adhesion | 40/372 | 273/10067 | 2.16E-12 |
| GO:0042102 | BP | positive regulation of T cell proliferation | 19/372 | 56/10067 | 2.16E-12 |
| GO:0050671 | BP | positive regulation of lymphocyte proliferation | 22/372 | 79/10067 | 2.16E-12 |
| GO:0032946 | BP | positive regulation of mononuclear cell proliferation | 22/372 | 80/10067 | 2.83E-12 |
| GO:0050851 | BP | antigen receptor-mediated signaling pathway | 29/372 | 146/10067 | 2.83E-12 |
| GO:0050863 | BP | regulation of T cell activation | 34/372 | 202/10067 | 3.03E-12 |
| GO:0032675 | BP | regulation of interleukin-6 production | 23/372 | 89/10067 | 3.15E-12 |
| GO:0060337 | BP | type I interferon signaling pathway | 20/372 | 65/10067 | 3.50E-12 |
| GO:0071357 | BP | cellular response to type I interferon | 20/372 | 65/10067 | 3.50E-12 |
| GO:0071621 | BP | granulocyte chemotaxis | 20/372 | 65/10067 | 3.50E-12 |
| GO:0045576 | BP | mast cell activation | 17/372 | 44/10067 | 3.54E-12 |
| GO:0030593 | BP | neutrophil chemotaxis | 18/372 | 51/10067 | 4.09E-12 |
| GO:0034340 | BP | response to type I interferon | 20/372 | 69/10067 | 1.21E-11 |
| GO:0070665 | BP | positive regulation of leukocyte proliferation | 22/372 | 86/10067 | 1.29E-11 |
| GO:0061900 | BP | glial cell activation | 15/372 | 35/10067 | 1.62E-11 |
| GO:0032496 | BP | response to lipopolysaccharide | 33/372 | 203/10067 | 1.77E-11 |
| GO:0045089 | BP | positive regulation of innate immune response | 25/372 | 116/10067 | 2.01E-11 |
| GO:1990266 | BP | neutrophil migration | 19/372 | 64/10067 | 2.81E-11 |
| GO:0001818 | BP | negative regulation of cytokine production | 30/372 | 179/10067 | 9.28E-11 |
| GO:0042129 | BP | regulation of T cell proliferation | 22/372 | 96/10067 | 1.35E-10 |
| GO:0006935 | BP | chemotaxis | 46/372 | 399/10067 | 1.46E-10 |
| GO:0032729 | BP | positive regulation of interferon-gamma production | 15/372 | 40/10067 | 1.57E-10 |
| GO:0042330 | BP | taxis | 46/372 | 401/10067 | 1.70E-10 |
| GO:0060333 | BP | interferon-gamma-mediated signaling pathway | 18/372 | 64/10067 | 2.99E-10 |
| GO:1903706 | BP | regulation of hemopoiesis | 40/372 | 321/10067 | 3.48E-10 |
| GO:0001906 | BP | cell killing | 19/372 | 73/10067 | 3.48E-10 |
| GO:0002705 | BP | positive regulation of leukocyte mediated immunity | 20/372 | 82/10067 | 3.60E-10 |
| GO:0032755 | BP | positive regulation of interleukin-6 production | 17/372 | 57/10067 | 3.87E-10 |
| GO:0002224 | BP | toll-like receptor signaling pathway | 22/372 | 102/10067 | 4.52E-10 |
| GO:0030098 | BP | lymphocyte differentiation | 33/372 | 231/10067 | 6.05E-10 |
| GO:0071216 | BP | cellular response to biotic stimulus | 26/372 | 146/10067 | 6.09E-10 |
| GO:0045730 | BP | respiratory burst | 12/372 | 25/10067 | 6.09E-10 |
| GO:0050663 | BP | cytokine secretion | 15/372 | 44/10067 | 7.04E-10 |
| GO:1902107 | BP | positive regulation of leukocyte differentiation | 22/372 | 105/10067 | 7.95E-10 |
| GO:0030217 | BP | T cell differentiation | 27/372 | 160/10067 | 8.76E-10 |
| GO:0032612 | BP | interleukin-1 production | 18/372 | 69/10067 | 1.08E-09 |
| GO:0071219 | BP | cellular response to molecule of bacterial origin | 24/372 | 129/10067 | 1.36E-09 |
| GO:0032611 | BP | interleukin-1 beta production | 17/372 | 62/10067 | 1.58E-09 |
| GO:0001909 | BP | leukocyte mediated cytotoxicity | 16/372 | 54/10067 | 1.60E-09 |
| GO:0006959 | BP | humoral immune response | 22/372 | 110/10067 | 1.99E-09 |
| GO:0032677 | BP | regulation of interleukin-8 production | 15/372 | 48/10067 | 2.72E-09 |
| GO:0002819 | BP | regulation of adaptive immune response | 22/372 | 112/10067 | 2.83E-09 |
| GO:0002285 | BP | lymphocyte activation involved in immune response | 22/372 | 113/10067 | 3.37E-09 |
| GO:0032609 | BP | interferon-gamma production | 17/372 | 66/10067 | 4.46E-09 |
| GO:0002440 | BP | production of molecular mediator of immune response | 24/372 | 137/10067 | 4.71E-09 |
| GO:0032637 | BP | interleukin-8 production | 15/372 | 51/10067 | 6.89E-09 |
| GO:0002706 | BP | regulation of lymphocyte mediated immunity | 19/372 | 87/10067 | 7.87E-09 |
| GO:0032652 | BP | regulation of interleukin-1 production | 16/372 | 60/10067 | 8.59E-09 |
| GO:0002279 | BP | mast cell activation involved in immune response | 13/372 | 37/10067 | 8.82E-09 |
| GO:0043303 | BP | mast cell degranulation | 13/372 | 37/10067 | 8.82E-09 |
| GO:0019882 | BP | antigen processing and presentation | 24/372 | 142/10067 | 9.71E-09 |
| GO:0031348 | BP | negative regulation of defense response | 24/372 | 143/10067 | 1.12E-08 |
| GO:0050729 | BP | positive regulation of inflammatory response | 19/372 | 89/10067 | 1.14E-08 |
| GO:1903708 | BP | positive regulation of hemopoiesis | 23/372 | 132/10067 | 1.19E-08 |
| GO:0031341 | BP | regulation of cell killing | 14/372 | 46/10067 | 1.55E-08 |
| GO:0032651 | BP | regulation of interleukin-1 beta production | 15/372 | 54/10067 | 1.56E-08 |
| GO:0002221 | BP | pattern recognition receptor signaling pathway | 23/372 | 134/10067 | 1.59E-08 |
| GO:0002821 | BP | positive regulation of adaptive immune response | 17/372 | 72/10067 | 1.72E-08 |
| GO:0002456 | BP | T cell mediated immunity | 16/372 | 63/10067 | 1.72E-08 |
| GO:0032649 | BP | regulation of interferon-gamma production | 16/372 | 63/10067 | 1.72E-08 |
| GO:0002448 | BP | mast cell mediated immunity | 13/372 | 39/10067 | 1.72E-08 |
| GO:0043300 | BP | regulation of leukocyte degranulation | 13/372 | 39/10067 | 1.72E-08 |
| GO:0002886 | BP | regulation of myeloid leukocyte mediated immunity | 14/372 | 47/10067 | 2.02E-08 |
| GO:0050764 | BP | regulation of phagocytosis | 16/372 | 64/10067 | 2.17E-08 |
| GO:0032733 | BP | positive regulation of interleukin-10 production | 10/372 | 21/10067 | 2.63E-08 |
| GO:0045785 | BP | positive regulation of cell adhesion | 34/372 | 284/10067 | 2.87E-08 |
| GO:0032613 | BP | interleukin-10 production | 12/372 | 34/10067 | 3.58E-08 |
| GO:0002695 | BP | negative regulation of leukocyte activation | 21/372 | 118/10067 | 4.22E-08 |
| GO:0002431 | BP | Fc receptor mediated stimulatory signaling pathway | 16/372 | 67/10067 | 4.36E-08 |
| GO:0030155 | BP | regulation of cell adhesion | 47/372 | 496/10067 | 4.85E-08 |
| GO:0002685 | BP | regulation of leukocyte migration | 22/372 | 131/10067 | 5.27E-08 |
| GO:0002824 | BP | positive regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains | 16/372 | 68/10067 | 5.40E-08 |
| GO:0071222 | BP | cellular response to lipopolysaccharide | 21/372 | 121/10067 | 6.56E-08 |
| GO:0002573 | BP | myeloid leukocyte differentiation | 22/372 | 133/10067 | 6.94E-08 |
| GO:0001910 | BP | regulation of leukocyte mediated cytotoxicity | 12/372 | 36/10067 | 7.25E-08 |
| GO:0002822 | BP | regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains | 19/372 | 101/10067 | 9.24E-08 |
| GO:0050866 | BP | negative regulation of cell activation | 22/372 | 137/10067 | 1.21E-07 |
| GO:0042554 | BP | superoxide anion generation | 10/372 | 24/10067 | 1.21E-07 |
| GO:0032680 | BP | regulation of tumor necrosis factor production | 16/372 | 72/10067 | 1.26E-07 |
| GO:0032623 | BP | interleukin-2 production | 12/372 | 38/10067 | 1.39E-07 |
| GO:0032655 | BP | regulation of interleukin-12 production | 12/372 | 38/10067 | 1.39E-07 |
| GO:0046635 | BP | positive regulation of alpha-beta T cell activation | 12/372 | 38/10067 | 1.39E-07 |
| GO:0050853 | BP | B cell receptor signaling pathway | 12/372 | 38/10067 | 1.39E-07 |
| GO:0032602 | BP | chemokine production | 13/372 | 46/10067 | 1.47E-07 |
| GO:0032653 | BP | regulation of interleukin-10 production | 11/372 | 31/10067 | 1.47E-07 |
| GO:0032633 | BP | interleukin-4 production | 9/372 | 19/10067 | 1.71E-07 |
| GO:0032673 | BP | regulation of interleukin-4 production | 9/372 | 19/10067 | 1.71E-07 |
| GO:0046631 | BP | alpha-beta T cell activation | 17/372 | 84/10067 | 1.80E-07 |
| GO:1903555 | BP | regulation of tumor necrosis factor superfamily cytokine production | 16/372 | 74/10067 | 1.81E-07 |
| GO:0033003 | BP | regulation of mast cell activation | 11/372 | 32/10067 | 2.10E-07 |
| GO:0032640 | BP | tumor necrosis factor production | 16/372 | 75/10067 | 2.20E-07 |
| GO:0038093 | BP | Fc receptor signaling pathway | 20/372 | 119/10067 | 2.47E-07 |
| GO:0050852 | BP | T cell receptor signaling pathway | 20/372 | 119/10067 | 2.47E-07 |
| GO:0032615 | BP | interleukin-12 production | 12/372 | 40/10067 | 2.51E-07 |
| GO:0045619 | BP | regulation of lymphocyte differentiation | 20/372 | 120/10067 | 2.83E-07 |
| GO:0006968 | BP | cellular defense response | 9/372 | 20/10067 | 2.85E-07 |
| GO:0071706 | BP | tumor necrosis factor superfamily cytokine production | 16/372 | 77/10067 | 3.17E-07 |
| GO:0002286 | BP | T cell activation involved in immune response | 14/372 | 58/10067 | 3.30E-07 |
| GO:0032753 | BP | positive regulation of interleukin-4 production | 8/372 | 15/10067 | 3.39E-07 |
| GO:0006801 | BP | superoxide metabolic process | 13/372 | 50/10067 | 4.06E-07 |
| GO:0050707 | BP | regulation of cytokine secretion | 11/372 | 34/10067 | 4.09E-07 |
| GO:0045582 | BP | positive regulation of T cell differentiation | 14/372 | 59/10067 | 4.09E-07 |
| GO:0099024 | BP | plasma membrane invagination | 12/372 | 42/10067 | 4.42E-07 |
| GO:0002367 | BP | cytokine production involved in immune response | 15/372 | 70/10067 | 5.53E-07 |
| GO:0045621 | BP | positive regulation of lymphocyte differentiation | 15/372 | 70/10067 | 5.53E-07 |
| GO:0002700 | BP | regulation of production of molecular mediator of immune response | 17/372 | 91/10067 | 5.76E-07 |
| GO:0048002 | BP | antigen processing and presentation of peptide antigen | 20/372 | 126/10067 | 6.23E-07 |
| GO:0042100 | BP | B cell proliferation | 13/372 | 52/10067 | 6.50E-07 |
| GO:0032102 | BP | negative regulation of response to external stimulus | 29/372 | 248/10067 | 6.59E-07 |
| GO:0060627 | BP | regulation of vesicle-mediated transport | 35/372 | 340/10067 | 6.59E-07 |
| GO:0007204 | BP | positive regulation of cytosolic calcium ion concentration | 24/372 | 178/10067 | 6.81E-07 |
| GO:0042113 | BP | B cell activation | 23/372 | 165/10067 | 6.99E-07 |
| GO:0032732 | BP | positive regulation of interleukin-1 production | 11/372 | 36/10067 | 7.52E-07 |
| GO:0038094 | BP | Fc-gamma receptor signaling pathway | 14/372 | 63/10067 | 9.42E-07 |
| GO:0006911 | BP | phagocytosis, engulfment | 11/372 | 37/10067 | 1.02E-06 |
| GO:0002407 | BP | dendritic cell chemotaxis | 8/372 | 17/10067 | 1.09E-06 |
| GO:0050777 | BP | negative regulation of immune response | 17/372 | 96/10067 | 1.23E-06 |
| GO:0002687 | BP | positive regulation of leukocyte migration | 16/372 | 85/10067 | 1.23E-06 |
| GO:0050864 | BP | regulation of B cell activation | 16/372 | 85/10067 | 1.23E-06 |
| GO:0071674 | BP | mononuclear cell migration | 12/372 | 46/10067 | 1.24E-06 |
| GO:0070374 | BP | positive regulation of ERK1 and ERK2 cascade | 19/372 | 120/10067 | 1.34E-06 |
| GO:0002688 | BP | regulation of leukocyte chemotaxis | 15/372 | 75/10067 | 1.35E-06 |
| GO:0002702 | BP | positive regulation of production of molecular mediator of immune response | 14/372 | 65/10067 | 1.37E-06 |
| GO:0045580 | BP | regulation of T cell differentiation | 17/372 | 97/10067 | 1.40E-06 |
| GO:0051250 | BP | negative regulation of lymphocyte activation | 17/372 | 97/10067 | 1.40E-06 |
| GO:0002718 | BP | regulation of cytokine production involved in immune response | 13/372 | 56/10067 | 1.54E-06 |
| GO:0010324 | BP | membrane invagination | 12/372 | 47/10067 | 1.56E-06 |
| GO:0002720 | BP | positive regulation of cytokine production involved in immune response | 11/372 | 39/10067 | 1.75E-06 |
| GO:0045071 | BP | negative regulation of viral genome replication | 11/372 | 39/10067 | 1.75E-06 |
| GO:0002761 | BP | regulation of myeloid leukocyte differentiation | 15/372 | 77/10067 | 1.88E-06 |
| GO:0046634 | BP | regulation of alpha-beta T cell activation | 13/372 | 57/10067 | 1.88E-06 |
| GO:0007186 | BP | G protein-coupled receptor signaling pathway | 39/372 | 423/10067 | 1.90E-06 |
| GO:0002218 | BP | activation of innate immune response | 15/372 | 79/10067 | 2.64E-06 |
| GO:0002708 | BP | positive regulation of lymphocyte mediated immunity | 13/372 | 59/10067 | 2.87E-06 |
| GO:0072678 | BP | T cell migration | 11/372 | 41/10067 | 3.00E-06 |
| GO:0032731 | BP | positive regulation of interleukin-1 beta production | 10/372 | 33/10067 | 3.08E-06 |
| GO:0030168 | BP | platelet activation | 18/372 | 115/10067 | 3.29E-06 |
| GO:0072503 | BP | cellular divalent inorganic cation homeostasis | 29/372 | 269/10067 | 3.40E-06 |
| GO:0032418 | BP | lysosome localization | 13/372 | 60/10067 | 3.46E-06 |
| GO:0030888 | BP | regulation of B cell proliferation | 11/372 | 42/10067 | 3.84E-06 |
| GO:0098581 | BP | detection of external biotic stimulus | 7/372 | 14/10067 | 4.03E-06 |
| GO:0032757 | BP | positive regulation of interleukin-8 production | 10/372 | 34/10067 | 4.09E-06 |
| GO:0051480 | BP | regulation of cytosolic calcium ion concentration | 24/372 | 197/10067 | 4.09E-06 |
| GO:0051046 | BP | regulation of secretion | 36/372 | 388/10067 | 4.87E-06 |
| GO:0032642 | BP | regulation of chemokine production | 11/372 | 43/10067 | 4.87E-06 |
| GO:0002548 | BP | monocyte chemotaxis | 9/372 | 27/10067 | 4.87E-06 |
| GO:0002755 | BP | MyD88-dependent toll-like receptor signaling pathway | 9/372 | 27/10067 | 4.87E-06 |
| GO:0002433 | BP | immune response-regulating cell surface receptor signaling pathway involved in phagocytosis | 13/372 | 62/10067 | 4.98E-06 |
| GO:0038096 | BP | Fc-gamma receptor signaling pathway involved in phagocytosis | 13/372 | 62/10067 | 4.98E-06 |
| GO:1903305 | BP | regulation of regulated secretory pathway | 16/372 | 95/10067 | 5.33E-06 |
| GO:0032663 | BP | regulation of interleukin-2 production | 10/372 | 35/10067 | 5.34E-06 |
| GO:0070371 | BP | ERK1 and ERK2 cascade | 23/372 | 186/10067 | 5.37E-06 |
| GO:1903901 | BP | negative regulation of viral life cycle | 12/372 | 53/10067 | 5.77E-06 |
| GO:0030003 | BP | cellular cation homeostasis | 35/372 | 376/10067 | 6.39E-06 |
| GO:0032743 | BP | positive regulation of interleukin-2 production | 8/372 | 21/10067 | 6.65E-06 |
| GO:0036336 | BP | dendritic cell migration | 8/372 | 21/10067 | 6.65E-06 |
| GO:0031343 | BP | positive regulation of cell killing | 9/372 | 28/10067 | 6.65E-06 |
| GO:0072507 | BP | divalent inorganic cation homeostasis | 29/372 | 279/10067 | 6.76E-06 |
| GO:0043030 | BP | regulation of macrophage activation | 10/372 | 36/10067 | 6.91E-06 |
| GO:0051092 | BP | positive regulation of NF-kappaB transcription factor activity | 17/372 | 110/10067 | 7.84E-06 |
| GO:0070372 | BP | regulation of ERK1 and ERK2 cascade | 22/372 | 177/10067 | 8.54E-06 |
| GO:0006873 | BP | cellular ion homeostasis | 35/372 | 382/10067 | 9.00E-06 |
| GO:0032722 | BP | positive regulation of chemokine production | 9/372 | 29/10067 | 9.06E-06 |
| GO:0046638 | BP | positive regulation of alpha-beta T cell differentiation | 9/372 | 29/10067 | 9.06E-06 |
| GO:0051090 | BP | regulation of DNA-binding transcription factor activity | 29/372 | 284/10067 | 9.52E-06 |
| GO:0072676 | BP | lymphocyte migration | 12/372 | 56/10067 | 1.03E-05 |
| GO:0018108 | BP | peptidyl-tyrosine phosphorylation | 26/372 | 239/10067 | 1.09E-05 |
| GO:0032928 | BP | regulation of superoxide anion generation | 7/372 | 16/10067 | 1.12E-05 |
| GO:0006874 | BP | cellular calcium ion homeostasis | 27/372 | 255/10067 | 1.13E-05 |
| GO:1903900 | BP | regulation of viral life cycle | 16/372 | 101/10067 | 1.15E-05 |
| GO:0050766 | BP | positive regulation of phagocytosis | 11/372 | 47/10067 | 1.15E-05 |
| GO:0072593 | BP | reactive oxygen species metabolic process | 23/372 | 195/10067 | 1.15E-05 |
| GO:0016064 | BP | immunoglobulin mediated immune response | 14/372 | 78/10067 | 1.19E-05 |
| GO:0002690 | BP | positive regulation of leukocyte chemotaxis | 12/372 | 57/10067 | 1.23E-05 |
| GO:0006897 | BP | endocytosis | 35/372 | 388/10067 | 1.23E-05 |
| GO:0018212 | BP | peptidyl-tyrosine modification | 26/372 | 242/10067 | 1.34E-05 |
| GO:0009595 | BP | detection of biotic stimulus | 8/372 | 23/10067 | 1.37E-05 |
| GO:0032735 | BP | positive regulation of interleukin-12 production | 8/372 | 23/10067 | 1.37E-05 |
| GO:0055074 | BP | calcium ion homeostasis | 27/372 | 260/10067 | 1.59E-05 |
| GO:0019724 | BP | B cell mediated immunity | 14/372 | 80/10067 | 1.59E-05 |
| GO:0006875 | BP | cellular metal ion homeostasis | 31/372 | 326/10067 | 1.72E-05 |
| GO:0043367 | BP | CD4-positive, alpha-beta T cell differentiation | 11/372 | 49/10067 | 1.73E-05 |
| GO:0050730 | BP | regulation of peptidyl-tyrosine phosphorylation | 20/372 | 158/10067 | 1.92E-05 |
| GO:0050728 | BP | negative regulation of inflammatory response | 15/372 | 93/10067 | 1.92E-05 |
| GO:0055080 | BP | cation homeostasis | 36/372 | 414/10067 | 1.97E-05 |
| GO:0002526 | BP | acute inflammatory response | 11/372 | 50/10067 | 2.11E-05 |
| GO:0045123 | BP | cellular extravasation | 11/372 | 50/10067 | 2.11E-05 |
| GO:0002577 | BP | regulation of antigen processing and presentation | 6/372 | 12/10067 | 2.54E-05 |
| GO:0098771 | BP | inorganic ion homeostasis | 36/372 | 419/10067 | 2.57E-05 |
| GO:0006956 | BP | complement activation | 10/372 | 42/10067 | 2.89E-05 |
| GO:0031663 | BP | lipopolysaccharide-mediated signaling pathway | 10/372 | 42/10067 | 2.89E-05 |
| GO:0052548 | BP | regulation of endopeptidase activity | 26/372 | 253/10067 | 2.94E-05 |
| GO:0007229 | BP | integrin-mediated signaling pathway | 14/372 | 85/10067 | 3.23E-05 |
| GO:0048525 | BP | negative regulation of viral process | 12/372 | 63/10067 | 3.50E-05 |
| GO:0002704 | BP | negative regulation of leukocyte mediated immunity | 9/372 | 34/10067 | 3.57E-05 |
| GO:0050854 | BP | regulation of antigen receptor-mediated signaling pathway | 10/372 | 43/10067 | 3.57E-05 |
| GO:0002888 | BP | positive regulation of myeloid leukocyte mediated immunity | 8/372 | 26/10067 | 3.65E-05 |
| GO:0033006 | BP | regulation of mast cell activation involved in immune response | 8/372 | 26/10067 | 3.65E-05 |
| GO:0043304 | BP | regulation of mast cell degranulation | 8/372 | 26/10067 | 3.65E-05 |
| GO:0090322 | BP | regulation of superoxide metabolic process | 8/372 | 26/10067 | 3.65E-05 |
| GO:0042590 | BP | antigen processing and presentation of exogenous peptide antigen via MHC class I | 11/372 | 53/10067 | 3.70E-05 |
| GO:0002478 | BP | antigen processing and presentation of exogenous peptide antigen | 16/372 | 111/10067 | 3.73E-05 |
| GO:0043302 | BP | positive regulation of leukocyte degranulation | 7/372 | 19/10067 | 3.91E-05 |
| GO:0043372 | BP | positive regulation of CD4-positive, alpha-beta T cell differentiation | 7/372 | 19/10067 | 3.91E-05 |
| GO:0046632 | BP | alpha-beta T cell differentiation | 12/372 | 64/10067 | 4.01E-05 |
| GO:1903530 | BP | regulation of secretion by cell | 32/372 | 359/10067 | 4.27E-05 |
| GO:0046641 | BP | positive regulation of alpha-beta T cell proliferation | 6/372 | 13/10067 | 4.27E-05 |
| GO:0002709 | BP | regulation of T cell mediated immunity | 10/372 | 44/10067 | 4.27E-05 |
| GO:0050830 | BP | defense response to Gram-positive bacterium | 10/372 | 44/10067 | 4.27E-05 |
| GO:0007249 | BP | I-kappaB kinase/NF-kappaB signaling | 23/372 | 212/10067 | 4.30E-05 |
| GO:0032760 | BP | positive regulation of tumor necrosis factor production | 9/372 | 35/10067 | 4.39E-05 |
| GO:0019884 | BP | antigen processing and presentation of exogenous antigen | 16/372 | 113/10067 | 4.57E-05 |
| GO:0043269 | BP | regulation of ion transport | 31/372 | 344/10067 | 4.75E-05 |
| GO:0030099 | BP | myeloid cell differentiation | 28/372 | 294/10067 | 4.93E-05 |
| GO:0055065 | BP | metal ion homeostasis | 32/372 | 362/10067 | 4.93E-05 |
| GO:0034121 | BP | regulation of toll-like receptor signaling pathway | 10/372 | 45/10067 | 5.18E-05 |
| GO:0002763 | BP | positive regulation of myeloid leukocyte differentiation | 9/372 | 36/10067 | 5.52E-05 |
| GO:1903557 | BP | positive regulation of tumor necrosis factor superfamily cytokine production | 9/372 | 36/10067 | 5.52E-05 |
| GO:0150077 | BP | regulation of neuroinflammatory response | 7/372 | 20/10067 | 5.53E-05 |
| GO:0035710 | BP | CD4-positive, alpha-beta T cell activation | 11/372 | 56/10067 | 6.12E-05 |
| GO:0045069 | BP | regulation of viral genome replication | 12/372 | 67/10067 | 6.26E-05 |
| GO:0002369 | BP | T cell cytokine production | 8/372 | 28/10067 | 6.30E-05 |
| GO:0030101 | BP | natural killer cell activation | 9/372 | 37/10067 | 6.95E-05 |
| GO:0045637 | BP | regulation of myeloid cell differentiation | 20/372 | 174/10067 | 7.50E-05 |
| GO:0050921 | BP | positive regulation of chemotaxis | 14/372 | 92/10067 | 7.56E-05 |
| GO:0032945 | BP | negative regulation of mononuclear cell proliferation | 10/372 | 47/10067 | 7.59E-05 |
| GO:0050672 | BP | negative regulation of lymphocyte proliferation | 10/372 | 47/10067 | 7.59E-05 |
| GO:0051091 | BP | positive regulation of DNA-binding transcription factor activity | 20/372 | 175/10067 | 8.07E-05 |
| GO:1902622 | BP | regulation of neutrophil migration | 8/372 | 29/10067 | 8.23E-05 |
| GO:0002532 | BP | production of molecular mediator involved in inflammatory response | 10/372 | 48/10067 | 9.19E-05 |
| GO:0060759 | BP | regulation of response to cytokine stimulus | 16/372 | 120/10067 | 9.49E-05 |
| GO:0050801 | BP | ion homeostasis | 37/372 | 467/10067 | 1.05E-04 |
| GO:0001911 | BP | negative regulation of leukocyte mediated cytotoxicity | 6/372 | 15/10067 | 1.06E-04 |
| GO:0032930 | BP | positive regulation of superoxide anion generation | 6/372 | 15/10067 | 1.06E-04 |
| GO:0043032 | BP | positive regulation of macrophage activation | 6/372 | 15/10067 | 1.06E-04 |
| GO:0002920 | BP | regulation of humoral immune response | 9/372 | 39/10067 | 1.06E-04 |
| GO:0019932 | BP | second-messenger-mediated signaling | 24/372 | 241/10067 | 1.06E-04 |
| GO:0001912 | BP | positive regulation of leukocyte mediated cytotoxicity | 7/372 | 22/10067 | 1.06E-04 |
| GO:0090022 | BP | regulation of neutrophil chemotaxis | 7/372 | 22/10067 | 1.06E-04 |
| GO:2000516 | BP | positive regulation of CD4-positive, alpha-beta T cell activation | 7/372 | 22/10067 | 1.06E-04 |
| GO:0052547 | BP | regulation of peptidase activity | 26/372 | 274/10067 | 1.07E-04 |
| GO:0050920 | BP | regulation of chemotaxis | 18/372 | 150/10067 | 1.13E-04 |
| GO:0055082 | BP | cellular chemical homeostasis | 37/372 | 471/10067 | 1.23E-04 |
| GO:0017157 | BP | regulation of exocytosis | 16/372 | 123/10067 | 1.25E-04 |
| GO:0002479 | BP | antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent | 10/372 | 50/10067 | 1.28E-04 |
| GO:0070664 | BP | negative regulation of leukocyte proliferation | 10/372 | 50/10067 | 1.28E-04 |
| GO:0045824 | BP | negative regulation of innate immune response | 9/372 | 40/10067 | 1.28E-04 |
| GO:0046637 | BP | regulation of alpha-beta T cell differentiation | 9/372 | 40/10067 | 1.28E-04 |
| GO:0014068 | BP | positive regulation of phosphatidylinositol 3-kinase signaling | 11/372 | 61/10067 | 1.32E-04 |
| GO:0042267 | BP | natural killer cell mediated cytotoxicity | 8/372 | 31/10067 | 1.32E-04 |
| GO:0043370 | BP | regulation of CD4-positive, alpha-beta T cell differentiation | 8/372 | 31/10067 | 1.32E-04 |
| GO:0002724 | BP | regulation of T cell cytokine production | 7/372 | 23/10067 | 1.43E-04 |
| GO:0045639 | BP | positive regulation of myeloid cell differentiation | 11/372 | 62/10067 | 1.54E-04 |
| GO:0031342 | BP | negative regulation of cell killing | 6/372 | 16/10067 | 1.54E-04 |
| GO:0071624 | BP | positive regulation of granulocyte chemotaxis | 6/372 | 16/10067 | 1.54E-04 |
| GO:0090023 | BP | positive regulation of neutrophil chemotaxis | 6/372 | 16/10067 | 1.54E-04 |
| GO:0090025 | BP | regulation of monocyte chemotaxis | 6/372 | 16/10067 | 1.54E-04 |
| GO:0007596 | BP | blood coagulation | 23/372 | 231/10067 | 1.54E-04 |
| GO:0050817 | BP | coagulation | 23/372 | 231/10067 | 1.54E-04 |
| GO:0019079 | BP | viral genome replication | 13/372 | 86/10067 | 1.56E-04 |
| GO:0050731 | BP | positive regulation of peptidyl-tyrosine phosphorylation | 15/372 | 112/10067 | 1.57E-04 |
| GO:0050792 | BP | regulation of viral process | 17/372 | 140/10067 | 1.60E-04 |
| GO:0002228 | BP | natural killer cell mediated immunity | 8/372 | 32/10067 | 1.63E-04 |
| GO:0030449 | BP | regulation of complement activation | 8/372 | 32/10067 | 1.63E-04 |
| GO:0032720 | BP | negative regulation of tumor necrosis factor production | 8/372 | 32/10067 | 1.63E-04 |
| GO:0071675 | BP | regulation of mononuclear cell migration | 8/372 | 32/10067 | 1.63E-04 |
| GO:0043410 | BP | positive regulation of MAPK cascade | 30/372 | 353/10067 | 1.83E-04 |
| GO:0007599 | BP | hemostasis | 23/372 | 234/10067 | 1.85E-04 |
| GO:0009620 | BP | response to fungus | 7/372 | 24/10067 | 1.85E-04 |
| GO:0046633 | BP | alpha-beta T cell proliferation | 7/372 | 24/10067 | 1.85E-04 |
| GO:0050829 | BP | defense response to Gram-negative bacterium | 7/372 | 24/10067 | 1.85E-04 |
| GO:2000116 | BP | regulation of cysteine-type endopeptidase activity | 19/372 | 172/10067 | 1.95E-04 |
| GO:0006898 | BP | receptor-mediated endocytosis | 19/372 | 174/10067 | 2.29E-04 |
| GO:0050871 | BP | positive regulation of B cell activation | 10/372 | 54/10067 | 2.41E-04 |
| GO:0019722 | BP | calcium-mediated signaling | 16/372 | 131/10067 | 2.55E-04 |
| GO:1903556 | BP | negative regulation of tumor necrosis factor superfamily cytokine production | 8/372 | 34/10067 | 2.57E-04 |
| GO:0090026 | BP | positive regulation of monocyte chemotaxis | 5/372 | 11/10067 | 2.60E-04 |
| GO:0098543 | BP | detection of other organism | 5/372 | 11/10067 | 2.60E-04 |
| GO:0098883 | BP | synapse pruning | 5/372 | 11/10067 | 2.60E-04 |
| GO:1902563 | BP | regulation of neutrophil activation | 5/372 | 11/10067 | 2.60E-04 |
| GO:0002474 | BP | antigen processing and presentation of peptide antigen via MHC class I | 11/372 | 66/10067 | 2.63E-04 |
| GO:0043123 | BP | positive regulation of I-kappaB kinase/NF-kappaB signaling | 17/372 | 147/10067 | 2.88E-04 |
| GO:0019058 | BP | viral life cycle | 22/372 | 225/10067 | 2.93E-04 |
| GO:0032479 | BP | regulation of type I interferon production | 13/372 | 92/10067 | 3.06E-04 |
| GO:0002790 | BP | peptide secretion | 26/372 | 293/10067 | 3.07E-04 |
| GO:0032691 | BP | negative regulation of interleukin-1 beta production | 6/372 | 18/10067 | 3.08E-04 |
| GO:0043903 | BP | regulation of symbiotic process | 17/372 | 148/10067 | 3.10E-04 |
| GO:0045454 | BP | cell redox homeostasis | 9/372 | 45/10067 | 3.13E-04 |
| GO:0050798 | BP | activated T cell proliferation | 7/372 | 26/10067 | 3.13E-04 |
| GO:0032606 | BP | type I interferon production | 13/372 | 93/10067 | 3.39E-04 |
| GO:0051897 | BP | positive regulation of protein kinase B signaling | 14/372 | 107/10067 | 3.62E-04 |
| GO:0030890 | BP | positive regulation of B cell proliferation | 7/372 | 27/10067 | 4.06E-04 |
| GO:0001562 | BP | response to protozoan | 5/372 | 12/10067 | 4.13E-04 |
| GO:0002830 | BP | positive regulation of type 2 immune response | 5/372 | 12/10067 | 4.13E-04 |
| GO:0042832 | BP | defense response to protozoan | 5/372 | 12/10067 | 4.13E-04 |
| GO:0043301 | BP | negative regulation of leukocyte degranulation | 5/372 | 12/10067 | 4.13E-04 |
| GO:0050690 | BP | regulation of defense response to virus by virus | 6/372 | 19/10067 | 4.24E-04 |
| GO:0048872 | BP | homeostasis of number of cells | 19/372 | 183/10067 | 4.34E-04 |
| GO:0038061 | BP | NIK/NF-kappaB signaling | 14/372 | 109/10067 | 4.37E-04 |
| GO:1903307 | BP | positive regulation of regulated secretory pathway | 8/372 | 37/10067 | 4.62E-04 |
| GO:2000514 | BP | regulation of CD4-positive, alpha-beta T cell activation | 8/372 | 37/10067 | 4.62E-04 |
| GO:0009611 | BP | response to wounding | 34/372 | 447/10067 | 4.62E-04 |
| GO:0002698 | BP | negative regulation of immune effector process | 12/372 | 83/10067 | 4.65E-04 |
| GO:0001959 | BP | regulation of cytokine-mediated signaling pathway | 14/372 | 111/10067 | 5.28E-04 |
| GO:0070098 | BP | chemokine-mediated signaling pathway | 8/372 | 38/10067 | 5.61E-04 |
| GO:0009306 | BP | protein secretion | 24/372 | 270/10067 | 5.66E-04 |
| GO:0035592 | BP | establishment of protein localization to extracellular region | 24/372 | 270/10067 | 5.66E-04 |
| GO:0002715 | BP | regulation of natural killer cell mediated immunity | 6/372 | 20/10067 | 5.66E-04 |
| GO:0002828 | BP | regulation of type 2 immune response | 6/372 | 20/10067 | 5.66E-04 |
| GO:0032692 | BP | negative regulation of interleukin-1 production | 6/372 | 20/10067 | 5.66E-04 |
| GO:0042269 | BP | regulation of natural killer cell mediated cytotoxicity | 6/372 | 20/10067 | 5.66E-04 |
| GO:0007200 | BP | phospholipase C-activating G protein-coupled receptor signaling pathway | 9/372 | 49/10067 | 5.97E-04 |
| GO:0071677 | BP | positive regulation of mononuclear cell migration | 5/372 | 13/10067 | 6.23E-04 |
| GO:0002377 | BP | immunoglobulin production | 11/372 | 73/10067 | 6.31E-04 |
| GO:0062207 | BP | regulation of pattern recognition receptor signaling pathway | 10/372 | 61/10067 | 6.46E-04 |
| GO:0045670 | BP | regulation of osteoclast differentiation | 8/372 | 39/10067 | 6.64E-04 |
| GO:1901222 | BP | regulation of NIK/NF-kappaB signaling | 11/372 | 74/10067 | 7.12E-04 |
| GO:0014066 | BP | regulation of phosphatidylinositol 3-kinase signaling | 12/372 | 87/10067 | 7.17E-04 |
| GO:0071692 | BP | protein localization to extracellular region | 24/372 | 275/10067 | 7.37E-04 |
| GO:0046640 | BP | regulation of alpha-beta T cell proliferation | 6/372 | 21/10067 | 7.48E-04 |
| GO:1902624 | BP | positive regulation of neutrophil migration | 6/372 | 21/10067 | 7.48E-04 |
| GO:0002711 | BP | positive regulation of T cell mediated immunity | 7/372 | 30/10067 | 7.81E-04 |
| GO:0051051 | BP | negative regulation of transport | 23/372 | 259/10067 | 7.88E-04 |
| GO:0001776 | BP | leukocyte homeostasis | 10/372 | 63/10067 | 8.38E-04 |
| GO:0010818 | BP | T cell chemotaxis | 5/372 | 14/10067 | 9.09E-04 |
| GO:0044546 | BP | NLRP3 inflammasome complex assembly | 5/372 | 14/10067 | 9.09E-04 |
| GO:0071622 | BP | regulation of granulocyte chemotaxis | 7/372 | 31/10067 | 9.65E-04 |
| GO:0048017 | BP | inositol lipid-mediated signaling | 15/372 | 133/10067 | 1.00E-03 |
| GO:0051651 | BP | maintenance of location in cell | 16/372 | 149/10067 | 1.07E-03 |
| GO:1901224 | BP | positive regulation of NIK/NF-kappaB signaling | 9/372 | 53/10067 | 1.08E-03 |
| GO:0030316 | BP | osteoclast differentiation | 10/372 | 65/10067 | 1.08E-03 |
| GO:0030225 | BP | macrophage differentiation | 7/372 | 32/10067 | 1.18E-03 |
| GO:0046456 | BP | icosanoid biosynthetic process | 7/372 | 32/10067 | 1.18E-03 |
| GO:0002832 | BP | negative regulation of response to biotic stimulus | 10/372 | 66/10067 | 1.22E-03 |
| GO:0008154 | BP | actin polymerization or depolymerization | 16/372 | 151/10067 | 1.23E-03 |
| GO:0042092 | BP | type 2 immune response | 6/372 | 23/10067 | 1.24E-03 |
| GO:0045058 | BP | T cell selection | 6/372 | 23/10067 | 1.24E-03 |
| GO:0045742 | BP | positive regulation of epidermal growth factor receptor signaling pathway | 6/372 | 23/10067 | 1.24E-03 |
| GO:0048247 | BP | lymphocyte chemotaxis | 6/372 | 23/10067 | 1.24E-03 |
| GO:0055094 | BP | response to lipoprotein particle | 6/372 | 23/10067 | 1.24E-03 |
| GO:0097028 | BP | dendritic cell differentiation | 6/372 | 23/10067 | 1.24E-03 |
| GO:0050855 | BP | regulation of B cell receptor signaling pathway | 5/372 | 15/10067 | 1.27E-03 |
| GO:1902106 | BP | negative regulation of leukocyte differentiation | 10/372 | 68/10067 | 1.54E-03 |
| GO:0051924 | BP | regulation of calcium ion transport | 15/372 | 139/10067 | 1.58E-03 |
| GO:0002707 | BP | negative regulation of lymphocyte mediated immunity | 6/372 | 24/10067 | 1.58E-03 |
| GO:0097242 | BP | amyloid-beta clearance | 6/372 | 24/10067 | 1.58E-03 |
| GO:1901186 | BP | positive regulation of ERBB signaling pathway | 6/372 | 24/10067 | 1.58E-03 |
| GO:0043408 | BP | regulation of MAPK cascade | 34/372 | 479/10067 | 1.59E-03 |
| GO:0043122 | BP | regulation of I-kappaB kinase/NF-kappaB signaling | 18/372 | 187/10067 | 1.60E-03 |
| GO:0006690 | BP | icosanoid metabolic process | 9/372 | 56/10067 | 1.60E-03 |
| GO:0030335 | BP | positive regulation of cell migration | 29/372 | 383/10067 | 1.61E-03 |
| GO:0002726 | BP | positive regulation of T cell cytokine production | 5/372 | 16/10067 | 1.73E-03 |
| GO:0006691 | BP | leukotriene metabolic process | 5/372 | 16/10067 | 1.73E-03 |
| GO:0050857 | BP | positive regulation of antigen receptor-mediated signaling pathway | 5/372 | 16/10067 | 1.73E-03 |
| GO:1903306 | BP | negative regulation of regulated secretory pathway | 5/372 | 16/10067 | 1.73E-03 |
| GO:1904894 | BP | positive regulation of receptor signaling pathway via STAT | 8/372 | 45/10067 | 1.73E-03 |
| GO:1990868 | BP | response to chemokine | 8/372 | 45/10067 | 1.73E-03 |
| GO:1990869 | BP | cellular response to chemokine | 8/372 | 45/10067 | 1.73E-03 |
| GO:0050878 | BP | regulation of body fluid levels | 26/372 | 331/10067 | 1.91E-03 |
| GO:0033674 | BP | positive regulation of kinase activity | 31/372 | 426/10067 | 1.93E-03 |
| GO:0001913 | BP | T cell mediated cytotoxicity | 6/372 | 25/10067 | 1.95E-03 |
| GO:0014002 | BP | astrocyte development | 6/372 | 25/10067 | 1.95E-03 |
| GO:0071402 | BP | cellular response to lipoprotein particle stimulus | 6/372 | 25/10067 | 1.95E-03 |
| GO:1904645 | BP | response to amyloid-beta | 7/372 | 35/10067 | 1.99E-03 |
| GO:2000106 | BP | regulation of leukocyte apoptotic process | 9/372 | 58/10067 | 2.03E-03 |
| GO:0002791 | BP | regulation of peptide secretion | 20/372 | 226/10067 | 2.14E-03 |
| GO:0071396 | BP | cellular response to lipid | 28/372 | 372/10067 | 2.20E-03 |
| GO:0051047 | BP | positive regulation of secretion | 18/372 | 193/10067 | 2.26E-03 |
| GO:2000147 | BP | positive regulation of cell motility | 29/372 | 392/10067 | 2.28E-03 |
| GO:0045860 | BP | positive regulation of protein kinase activity | 28/372 | 373/10067 | 2.29E-03 |
| GO:0050715 | BP | positive regulation of cytokine secretion | 5/372 | 17/10067 | 2.30E-03 |
| GO:0150146 | BP | cell junction disassembly | 5/372 | 17/10067 | 2.30E-03 |
| GO:0050868 | BP | negative regulation of T cell activation | 10/372 | 72/10067 | 2.33E-03 |
| GO:0009593 | BP | detection of chemical stimulus | 6/372 | 26/10067 | 2.39E-03 |
| GO:0032715 | BP | negative regulation of interleukin-6 production | 6/372 | 26/10067 | 2.39E-03 |
| GO:0048015 | BP | phosphatidylinositol-mediated signaling | 14/372 | 130/10067 | 2.45E-03 |
| GO:0010959 | BP | regulation of metal ion transport | 19/372 | 212/10067 | 2.52E-03 |
| GO:0002679 | BP | respiratory burst involved in defense response | 4/372 | 10/10067 | 2.53E-03 |
| GO:0002887 | BP | negative regulation of myeloid leukocyte mediated immunity | 4/372 | 10/10067 | 2.53E-03 |
| GO:0019370 | BP | leukotriene biosynthetic process | 4/372 | 10/10067 | 2.53E-03 |
| GO:1903978 | BP | regulation of microglial cell activation | 4/372 | 10/10067 | 2.53E-03 |
| GO:0051896 | BP | regulation of protein kinase B signaling | 15/372 | 147/10067 | 2.68E-03 |
| GO:2000377 | BP | regulation of reactive oxygen species metabolic process | 14/372 | 132/10067 | 2.82E-03 |
| GO:0002714 | BP | positive regulation of B cell mediated immunity | 6/372 | 27/10067 | 2.91E-03 |
| GO:0002891 | BP | positive regulation of immunoglobulin mediated immune response | 6/372 | 27/10067 | 2.91E-03 |
| GO:0061756 | BP | leukocyte adhesion to vascular endothelial cell | 6/372 | 27/10067 | 2.91E-03 |
| GO:0040017 | BP | positive regulation of locomotion | 29/372 | 399/10067 | 2.95E-03 |
| GO:0034162 | BP | toll-like receptor 9 signaling pathway | 5/372 | 18/10067 | 2.98E-03 |
| GO:0030041 | BP | actin filament polymerization | 14/372 | 133/10067 | 3.01E-03 |
| GO:0043491 | BP | protein kinase B signaling | 16/372 | 165/10067 | 3.02E-03 |
| GO:0030162 | BP | regulation of proteolysis | 31/372 | 439/10067 | 3.04E-03 |
| GO:0002758 | BP | innate immune response-activating signal transduction | 9/372 | 62/10067 | 3.20E-03 |
| GO:0014065 | BP | phosphatidylinositol 3-kinase signaling | 12/372 | 104/10067 | 3.34E-03 |
| GO:2000379 | BP | positive regulation of reactive oxygen species metabolic process | 10/372 | 76/10067 | 3.48E-03 |
| GO:0043405 | BP | regulation of MAP kinase activity | 20/372 | 236/10067 | 3.53E-03 |
| GO:0051272 | BP | positive regulation of cellular component movement | 29/372 | 404/10067 | 3.55E-03 |
| GO:0002495 | BP | antigen processing and presentation of peptide antigen via MHC class II | 9/372 | 63/10067 | 3.58E-03 |
| GO:0070997 | BP | neuron death | 20/372 | 237/10067 | 3.67E-03 |
| GO:0060760 | BP | positive regulation of response to cytokine stimulus | 7/372 | 39/10067 | 3.67E-03 |
| GO:0002281 | BP | macrophage activation involved in immune response | 4/372 | 11/10067 | 3.67E-03 |
| GO:0002438 | BP | acute inflammatory response to antigenic stimulus | 4/372 | 11/10067 | 3.67E-03 |
| GO:0002716 | BP | negative regulation of natural killer cell mediated immunity | 4/372 | 11/10067 | 3.67E-03 |
| GO:0045953 | BP | negative regulation of natural killer cell mediated cytotoxicity | 4/372 | 11/10067 | 3.67E-03 |
| GO:0046629 | BP | gamma-delta T cell activation | 4/372 | 11/10067 | 3.67E-03 |
| GO:1900017 | BP | positive regulation of cytokine production involved in inflammatory response | 4/372 | 11/10067 | 3.67E-03 |
| GO:0002504 | BP | antigen processing and presentation of peptide or polysaccharide antigen via MHC class II | 9/372 | 64/10067 | 3.95E-03 |
| GO:0002455 | BP | humoral immune response mediated by circulating immunoglobulin | 6/372 | 29/10067 | 4.18E-03 |
| GO:1900015 | BP | regulation of cytokine production involved in inflammatory response | 6/372 | 29/10067 | 4.18E-03 |
| GO:1901214 | BP | regulation of neuron death | 18/372 | 205/10067 | 4.30E-03 |
| GO:0030838 | BP | positive regulation of actin filament polymerization | 9/372 | 65/10067 | 4.40E-03 |
| GO:1904892 | BP | regulation of receptor signaling pathway via STAT | 9/372 | 65/10067 | 4.40E-03 |
| GO:0051048 | BP | negative regulation of secretion | 11/372 | 93/10067 | 4.47E-03 |
| GO:0042060 | BP | wound healing | 27/372 | 373/10067 | 4.71E-03 |
| GO:0043281 | BP | regulation of cysteine-type endopeptidase activity involved in apoptotic process | 15/372 | 156/10067 | 4.73E-03 |
| GO:0045920 | BP | negative regulation of exocytosis | 5/372 | 20/10067 | 4.80E-03 |
| GO:1902905 | BP | positive regulation of supramolecular fiber organization | 14/372 | 140/10067 | 4.80E-03 |
| GO:0002437 | BP | inflammatory response to antigenic stimulus | 6/372 | 30/10067 | 4.96E-03 |
| GO:1904646 | BP | cellular response to amyloid-beta | 6/372 | 30/10067 | 4.96E-03 |
| GO:1903038 | BP | negative regulation of leukocyte cell-cell adhesion | 10/372 | 80/10067 | 5.00E-03 |
| GO:0010950 | BP | positive regulation of endopeptidase activity | 13/372 | 125/10067 | 5.08E-03 |
| GO:0051656 | BP | establishment of organelle localization | 23/372 | 299/10067 | 5.09E-03 |
| GO:0034765 | BP | regulation of ion transmembrane transport | 20/372 | 244/10067 | 5.11E-03 |
| GO:0001773 | BP | myeloid dendritic cell activation | 4/372 | 12/10067 | 5.14E-03 |
| GO:0030852 | BP | regulation of granulocyte differentiation | 4/372 | 12/10067 | 5.14E-03 |
| GO:0032695 | BP | negative regulation of interleukin-12 production | 4/372 | 12/10067 | 5.14E-03 |
| GO:0045921 | BP | positive regulation of exocytosis | 8/372 | 54/10067 | 5.41E-03 |
| GO:1903409 | BP | reactive oxygen species biosynthetic process | 10/372 | 81/10067 | 5.43E-03 |
| GO:0050708 | BP | regulation of protein secretion | 18/372 | 210/10067 | 5.50E-03 |
| GO:0002292 | BP | T cell differentiation involved in immune response | 7/372 | 42/10067 | 5.57E-03 |
| GO:2001056 | BP | positive regulation of cysteine-type endopeptidase activity | 12/372 | 111/10067 | 5.61E-03 |
| GO:0002534 | BP | cytokine production involved in inflammatory response | 6/372 | 31/10067 | 5.81E-03 |
| GO:0006958 | BP | complement activation, classical pathway | 5/372 | 21/10067 | 5.87E-03 |
| GO:0030851 | BP | granulocyte differentiation | 5/372 | 21/10067 | 5.87E-03 |
| GO:0032814 | BP | regulation of natural killer cell activation | 5/372 | 21/10067 | 5.87E-03 |
| GO:0062208 | BP | positive regulation of pattern recognition receptor signaling pathway | 5/372 | 21/10067 | 5.87E-03 |
| GO:0097696 | BP | receptor signaling pathway via STAT | 10/372 | 82/10067 | 5.88E-03 |
| GO:0046427 | BP | positive regulation of receptor signaling pathway via JAK-STAT | 7/372 | 43/10067 | 6.34E-03 |
| GO:0008064 | BP | regulation of actin polymerization or depolymerization | 13/372 | 129/10067 | 6.60E-03 |
| GO:0051347 | BP | positive regulation of transferase activity | 32/372 | 483/10067 | 6.66E-03 |
| GO:0043254 | BP | regulation of protein-containing complex assembly | 23/372 | 306/10067 | 6.72E-03 |
| GO:0032481 | BP | positive regulation of type I interferon production | 8/372 | 56/10067 | 6.72E-03 |
| GO:0002686 | BP | negative regulation of leukocyte migration | 6/372 | 32/10067 | 6.79E-03 |
| GO:0002675 | BP | positive regulation of acute inflammatory response | 4/372 | 13/10067 | 6.87E-03 |
| GO:0030889 | BP | negative regulation of B cell proliferation | 4/372 | 13/10067 | 6.87E-03 |
| GO:0034134 | BP | toll-like receptor 2 signaling pathway | 4/372 | 13/10067 | 6.87E-03 |
| GO:0045061 | BP | thymic T cell selection | 4/372 | 13/10067 | 6.87E-03 |
| GO:0048143 | BP | astrocyte activation | 4/372 | 13/10067 | 6.87E-03 |
| GO:1900225 | BP | regulation of NLRP3 inflammasome complex assembly | 4/372 | 13/10067 | 6.87E-03 |
| GO:1904996 | BP | positive regulation of leukocyte adhesion to vascular endothelial cell | 4/372 | 13/10067 | 6.87E-03 |
| GO:0090087 | BP | regulation of peptide transport | 29/372 | 424/10067 | 6.88E-03 |
| GO:0030832 | BP | regulation of actin filament length | 13/372 | 130/10067 | 6.91E-03 |
| GO:0032607 | BP | interferon-alpha production | 5/372 | 22/10067 | 7.11E-03 |
| GO:0032647 | BP | regulation of interferon-alpha production | 5/372 | 22/10067 | 7.11E-03 |
| GO:0045589 | BP | regulation of regulatory T cell differentiation | 5/372 | 22/10067 | 7.11E-03 |
| GO:0007015 | BP | actin filament organization | 23/372 | 308/10067 | 7.13E-03 |
| GO:1903532 | BP | positive regulation of secretion by cell | 16/372 | 181/10067 | 7.28E-03 |
| GO:1903531 | BP | negative regulation of secretion by cell | 10/372 | 86/10067 | 8.20E-03 |
| GO:0002262 | BP | myeloid cell homeostasis | 12/372 | 117/10067 | 8.47E-03 |
| GO:0048010 | BP | vascular endothelial growth factor receptor signaling pathway | 9/372 | 72/10067 | 8.49E-03 |
| GO:0002673 | BP | regulation of acute inflammatory response | 5/372 | 23/10067 | 8.66E-03 |
| GO:0035666 | BP | TRIF-dependent toll-like receptor signaling pathway | 5/372 | 23/10067 | 8.66E-03 |
| GO:0045066 | BP | regulatory T cell differentiation | 5/372 | 23/10067 | 8.66E-03 |
| GO:0050869 | BP | negative regulation of B cell activation | 5/372 | 23/10067 | 8.66E-03 |
| GO:0072511 | BP | divalent inorganic cation transport | 20/372 | 257/10067 | 8.95E-03 |
| GO:0030833 | BP | regulation of actin filament polymerization | 12/372 | 118/10067 | 8.99E-03 |
| GO:0043406 | BP | positive regulation of MAP kinase activity | 16/372 | 185/10067 | 8.99E-03 |
| GO:0043277 | BP | apoptotic cell clearance | 6/372 | 34/10067 | 8.99E-03 |
| GO:0002230 | BP | positive regulation of defense response to virus by host | 4/372 | 14/10067 | 8.99E-03 |
| GO:0033005 | BP | positive regulation of mast cell activation | 4/372 | 14/10067 | 8.99E-03 |
| GO:0048708 | BP | astrocyte differentiation | 7/372 | 46/10067 | 8.99E-03 |
| GO:0046209 | BP | nitric oxide metabolic process | 8/372 | 59/10067 | 8.99E-03 |
| GO:1900407 | BP | regulation of cellular response to oxidative stress | 8/372 | 59/10067 | 8.99E-03 |
| GO:0031334 | BP | positive regulation of protein-containing complex assembly | 15/372 | 169/10067 | 9.61E-03 |
| GO:0030141 | CC | secretory granule | 70/388 | 497/10416 | 2.33E-20 |
| GO:0098552 | CC | side of membrane | 54/388 | 319/10416 | 3.06E-19 |
| GO:0009897 | CC | external side of plasma membrane | 41/388 | 194/10416 | 4.32E-18 |
| GO:0030659 | CC | cytoplasmic vesicle membrane | 64/388 | 490/10416 | 3.00E-17 |
| GO:0030667 | CC | secretory granule membrane | 38/388 | 197/10416 | 1.77E-15 |
| GO:0009986 | CC | cell surface | 60/388 | 483/10416 | 3.48E-15 |
| GO:0070820 | CC | tertiary granule | 28/388 | 111/10416 | 1.59E-14 |
| GO:0070821 | CC | tertiary granule membrane | 18/388 | 51/10416 | 5.00E-12 |
| GO:0045335 | CC | phagocytic vesicle | 22/388 | 104/10416 | 9.03E-10 |
| GO:0030139 | CC | endocytic vesicle | 30/388 | 208/10416 | 5.20E-09 |
| GO:0035579 | CC | specific granule membrane | 16/388 | 71/10416 | 1.55E-07 |
| GO:0030666 | CC | endocytic vesicle membrane | 19/388 | 112/10416 | 7.63E-07 |
| GO:0042581 | CC | specific granule | 19/388 | 113/10416 | 8.18E-07 |
| GO:0034774 | CC | secretory granule lumen | 25/388 | 199/10416 | 2.21E-06 |
| GO:0060205 | CC | cytoplasmic vesicle lumen | 25/388 | 201/10416 | 2.41E-06 |
| GO:0098797 | CC | plasma membrane protein complex | 31/388 | 290/10416 | 2.41E-06 |
| GO:0031983 | CC | vesicle lumen | 25/388 | 203/10416 | 2.70E-06 |
| GO:0101003 | CC | ficolin-1-rich granule membrane | 11/388 | 42/10416 | 4.79E-06 |
| GO:0042629 | CC | mast cell granule | 7/388 | 16/10416 | 1.46E-05 |
| GO:0030670 | CC | phagocytic vesicle membrane | 12/388 | 59/10416 | 2.37E-05 |
| GO:0005767 | CC | secondary lysosome | 6/388 | 16/10416 | 2.45E-04 |
| GO:0045121 | CC | membrane raft | 22/388 | 219/10416 | 3.35E-04 |
| GO:0042611 | CC | MHC protein complex | 6/388 | 17/10416 | 3.35E-04 |
| GO:0098857 | CC | membrane microdomain | 22/388 | 220/10416 | 3.37E-04 |
| GO:0098589 | CC | membrane region | 22/388 | 226/10416 | 4.91E-04 |
| GO:0031234 | CC | extrinsic component of cytoplasmic side of plasma membrane | 10/388 | 57/10416 | 5.45E-04 |
| GO:0005766 | CC | primary lysosome | 13/388 | 95/10416 | 5.60E-04 |
| GO:0042582 | CC | azurophil granule | 13/388 | 95/10416 | 5.60E-04 |
| GO:0098802 | CC | plasma membrane signaling receptor complex | 13/388 | 95/10416 | 5.60E-04 |
| GO:0001772 | CC | immunological synapse | 6/388 | 20/10416 | 7.30E-04 |
| GO:0035578 | CC | azurophil granule lumen | 9/388 | 53/10416 | 1.44E-03 |
| GO:1904724 | CC | tertiary granule lumen | 7/388 | 34/10416 | 2.27E-03 |
| GO:0043235 | CC | receptor complex | 20/388 | 222/10416 | 2.42E-03 |
| GO:0101002 | CC | ficolin-1-rich granule | 11/388 | 84/10416 | 2.62E-03 |
| GO:1904813 | CC | ficolin-1-rich granule lumen | 11/388 | 84/10416 | 2.62E-03 |
| GO:0005884 | CC | actin filament | 11/388 | 86/10416 | 3.14E-03 |
| GO:0019898 | CC | extrinsic component of membrane | 17/388 | 183/10416 | 4.40E-03 |
| GO:0061702 | CC | inflammasome complex | 4/388 | 11/10416 | 4.59E-03 |
| GO:0001891 | CC | phagocytic cup | 5/388 | 20/10416 | 6.00E-03 |
| GO:0019897 | CC | extrinsic component of plasma membrane | 11/388 | 96/10416 | 7.32E-03 |
| GO:0005775 | CC | vacuolar lumen | 12/388 | 114/10416 | 8.81E-03 |
| GO:0098562 | CC | cytoplasmic side of membrane | 12/388 | 114/10416 | 8.81E-03 |
| GO:0004888 | MF | transmembrane signaling receptor activity | 52/377 | 399/10268 | 3.26E-13 |
| GO:0140375 | MF | immune receptor activity | 23/377 | 78/10268 | 6.89E-13 |
| GO:0019865 | MF | immunoglobulin binding | 7/377 | 10/10268 | 1.56E-06 |
| GO:0004896 | MF | cytokine receptor activity | 14/377 | 62/10268 | 4.67E-06 |
| GO:0035325 | MF | Toll-like receptor binding | 7/377 | 12/10268 | 5.79E-06 |
| GO:0038187 | MF | pattern recognition receptor activity | 7/377 | 14/10268 | 1.96E-05 |
| GO:0001540 | MF | amyloid-beta binding | 12/377 | 54/10268 | 3.08E-05 |
| GO:0004930 | MF | G protein-coupled receptor activity | 18/377 | 171/10268 | 3.18E-03 |
| GO:0003823 | MF | antigen binding | 8/377 | 38/10268 | 3.18E-03 |
| GO:0016493 | MF | C-C chemokine receptor activity | 5/377 | 14/10268 | 4.52E-03 |
| GO:0050664 | MF | oxidoreductase activity, acting on NAD(P)H, oxygen as acceptor | 5/377 | 14/10268 | 4.52E-03 |
| GO:0019957 | MF | C-C chemokine binding | 5/377 | 15/10268 | 6.03E-03 |
| GO:0038024 | MF | cargo receptor activity | 9/377 | 56/10268 | 6.81E-03 |
| GO:0001637 | MF | G protein-coupled chemoattractant receptor activity | 5/377 | 16/10268 | 6.81E-03 |
| GO:0004950 | MF | chemokine receptor activity | 5/377 | 16/10268 | 6.81E-03 |
| GO:0004715 | MF | non-membrane spanning protein tyrosine kinase activity | 7/377 | 35/10268 | 7.38E-03 |
| GO:0003924 | MF | GTPase activity | 17/377 | 180/10268 | 9.78E-03 |
| **Pathways associated with grey60 module genes** | | | | | |
| GO:0006397 | BP | mRNA processing | 16/72 | 349/10067 | 4.12E-06 |
| GO:1903311 | BP | regulation of mRNA metabolic process | 12/72 | 230/10067 | 6.59E-05 |
| GO:0008380 | BP | RNA splicing | 13/72 | 309/10067 | 1.47E-04 |
| GO:0050684 | BP | regulation of mRNA processing | 8/72 | 105/10067 | 3.49E-04 |
| GO:0034243 | BP | regulation of transcription elongation from RNA polymerase II promoter | 4/72 | 18/10067 | 2.58E-03 |
| GO:1901522 | BP | positive regulation of transcription from RNA polymerase II promoter involved in cellular response to chemical stimulus | 4/72 | 20/10067 | 3.37E-03 |
| GO:1902369 | BP | negative regulation of RNA catabolic process | 5/72 | 46/10067 | 4.80E-03 |
| GO:0043488 | BP | regulation of mRNA stability | 7/72 | 121/10067 | 5.13E-03 |
| GO:0016569 | BP | covalent chromatin modification | 11/72 | 337/10067 | 5.13E-03 |
| GO:0043487 | BP | regulation of RNA stability | 7/72 | 128/10067 | 5.47E-03 |
| GO:0034248 | BP | regulation of cellular amide metabolic process | 10/72 | 290/10067 | 5.47E-03 |
| GO:0000377 | BP | RNA splicing, via transesterification reactions with bulged adenosine as nucleophile | 9/72 | 233/10067 | 5.47E-03 |
| GO:0000398 | BP | mRNA splicing, via spliceosome | 9/72 | 233/10067 | 5.47E-03 |
| GO:0000375 | BP | RNA splicing, via transesterification reactions | 9/72 | 234/10067 | 5.47E-03 |
| GO:1902275 | BP | regulation of chromatin organization | 7/72 | 137/10067 | 5.76E-03 |
| GO:0006402 | BP | mRNA catabolic process | 9/72 | 242/10067 | 5.76E-03 |
| GO:0061013 | BP | regulation of mRNA catabolic process | 7/72 | 138/10067 | 5.76E-03 |
| GO:0010608 | BP | posttranscriptional regulation of gene expression | 12/72 | 439/10067 | 5.76E-03 |
| GO:0006417 | BP | regulation of translation | 9/72 | 245/10067 | 5.76E-03 |
| GO:0032784 | BP | regulation of DNA-templated transcription, elongation | 4/72 | 31/10067 | 6.19E-03 |
| GO:0016570 | BP | histone modification | 10/72 | 327/10067 | 9.05E-03 |
| GO:0034250 | BP | positive regulation of cellular amide metabolic process | 6/72 | 106/10067 | 9.05E-03 |
| GO:0006401 | BP | RNA catabolic process | 9/72 | 268/10067 | 9.49E-03 |
| GO:0036464 | CC | cytoplasmic ribonucleoprotein granule | 8/72 | 156/10416 | 1.32E-03 |
| GO:0035770 | CC | ribonucleoprotein granule | 8/72 | 163/10416 | 1.32E-03 |
| GO:0010494 | CC | cytoplasmic stress granule | 5/72 | 48/10416 | 1.32E-03 |
| GO:0071013 | CC | catalytic step 2 spliceosome | 5/72 | 54/10416 | 1.77E-03 |
| GO:0016607 | CC | nuclear speck | 9/72 | 283/10416 | 4.82E-03 |
| GO:0042788 | CC | polysomal ribosome | 3/72 | 15/10416 | 4.82E-03 |
| GO:0070717 | MF | poly-purine tract binding | 5/71 | 24/10268 | 1.13E-04 |
| GO:0003729 | MF | mRNA binding | 10/71 | 196/10268 | 1.13E-04 |
| GO:0008187 | MF | poly-pyrimidine tract binding | 4/71 | 20/10268 | 6.17E-04 |
| GO:0048027 | MF | mRNA 5'-UTR binding | 4/71 | 20/10268 | 6.17E-04 |
| GO:0003682 | MF | chromatin binding | 12/71 | 394/10268 | 7.49E-04 |
| GO:0003727 | MF | single-stranded RNA binding | 5/71 | 57/10268 | 1.91E-03 |
| GO:0003730 | MF | mRNA 3'-UTR binding | 5/71 | 60/10268 | 2.10E-03 |
| GO:0008143 | MF | poly(A) binding | 3/71 | 18/10268 | 7.04E-03 |
| GO:0008266 | MF | poly(U) RNA binding | 3/71 | 18/10268 | 7.04E-03 |
| **Pathways associated with lightcyan module genes** | | | | | |
| GO:0030198 | BP | extracellular matrix organization | 25/299 | 277/10067 | 1.29E-03 |
| GO:0043062 | BP | extracellular structure organization | 25/299 | 278/10067 | 1.29E-03 |
| GO:0031012 | CC | extracellular matrix | 37/311 | 337/10416 | 7.99E-10 |
| GO:0062023 | CC | collagen-containing extracellular matrix | 33/311 | 272/10416 | 7.99E-10 |
| GO:0005788 | CC | endoplasmic reticulum lumen | 21/311 | 191/10416 | 2.57E-05 |
| GO:0009986 | CC | cell surface | 36/311 | 483/10416 | 2.71E-05 |
| GO:0005796 | CC | Golgi lumen | 10/311 | 48/10416 | 7.00E-05 |
| GO:0009897 | CC | external side of plasma membrane | 20/311 | 194/10416 | 7.00E-05 |
| GO:0098552 | CC | side of membrane | 23/311 | 319/10416 | 3.77E-03 |
| GO:0005539 | MF | glycosaminoglycan binding | 20/299 | 130/10268 | 4.70E-07 |
| GO:0008201 | MF | heparin binding | 14/299 | 96/10268 | 1.61E-04 |
| GO:1901681 | MF | sulfur compound binding | 17/299 | 158/10268 | 5.51E-04 |
| GO:0030246 | MF | carbohydrate binding | 16/299 | 148/10268 | 7.57E-04 |
| GO:0005201 | MF | extracellular matrix structural constituent | 14/299 | 118/10268 | 7.90E-04 |
| GO:0004888 | MF | transmembrane signaling receptor activity | 28/299 | 399/10268 | 1.18E-03 |
| GO:0030021 | MF | extracellular matrix structural constituent conferring compression resistance | 5/299 | 14/10268 | 2.31E-03 |
| GO:0005518 | MF | collagen binding | 9/299 | 59/10268 | 2.89E-03 |
| GO:0004653 | MF | polypeptide N-acetylgalactosaminyltransferase activity | 4/299 | 10/10268 | 7.10E-03 |
| GO:0016757 | MF | transferase activity, transferring glycosyl groups | 15/299 | 175/10268 | 8.18E-03 |
| GO:0008194 | MF | UDP-glycosyltransferase activity | 10/299 | 86/10268 | 8.18E-03 |
| GO:0005501 | MF | retinoid binding | 4/299 | 11/10268 | 8.18E-03 |
| **Pathways associated with lightgreen module genes** | | | | | |
| GO:0006614 | BP | SRP-dependent cotranslational protein targeting to membrane | 33/300 | 51/10067 | 3.09E-35 |
| GO:0006613 | BP | cotranslational protein targeting to membrane | 33/300 | 52/10067 | 4.12E-35 |
| GO:0045047 | BP | protein targeting to ER | 34/300 | 62/10067 | 2.65E-33 |
| GO:0072599 | BP | establishment of protein localization to endoplasmic reticulum | 34/300 | 65/10067 | 1.78E-32 |
| GO:0000184 | BP | nuclear-transcribed mRNA catabolic process, nonsense-mediated decay | 32/300 | 68/10067 | 1.31E-28 |
| GO:0070972 | BP | protein localization to endoplasmic reticulum | 34/300 | 81/10067 | 1.75E-28 |
| GO:0006413 | BP | translational initiation | 34/300 | 91/10067 | 1.72E-26 |
| GO:0006612 | BP | protein targeting to membrane | 37/300 | 118/10067 | 7.81E-26 |
| GO:0019083 | BP | viral transcription | 35/300 | 107/10067 | 4.12E-25 |
| GO:0006119 | BP | oxidative phosphorylation | 33/300 | 97/10067 | 2.89E-24 |
| GO:0019080 | BP | viral gene expression | 35/300 | 114/10067 | 3.98E-24 |
| GO:0006401 | BP | RNA catabolic process | 50/300 | 268/10067 | 4.08E-24 |
| GO:0006402 | BP | mRNA catabolic process | 47/300 | 242/10067 | 2.24E-23 |
| GO:0042773 | BP | ATP synthesis coupled electron transport | 27/300 | 67/10067 | 4.69E-22 |
| GO:0022904 | BP | respiratory electron transport chain | 28/300 | 80/10067 | 6.04E-21 |
| GO:0042775 | BP | mitochondrial ATP synthesis coupled electron transport | 26/300 | 66/10067 | 6.04E-21 |
| GO:0000956 | BP | nuclear-transcribed mRNA catabolic process | 34/300 | 137/10067 | 3.21E-20 |
| GO:0006412 | BP | translation | 54/300 | 386/10067 | 4.23E-20 |
| GO:0044270 | BP | cellular nitrogen compound catabolic process | 54/300 | 390/10067 | 6.59E-20 |
| GO:0022900 | BP | electron transport chain | 33/300 | 131/10067 | 7.00E-20 |
| GO:0045333 | BP | cellular respiration | 32/300 | 122/10067 | 7.48E-20 |
| GO:0090150 | BP | establishment of protein localization to membrane | 40/300 | 208/10067 | 1.08E-19 |
| GO:0034655 | BP | nucleobase-containing compound catabolic process | 52/300 | 367/10067 | 1.20E-19 |
| GO:0043043 | BP | peptide biosynthetic process | 54/300 | 401/10067 | 1.98E-19 |
| GO:0046700 | BP | heterocycle catabolic process | 53/300 | 387/10067 | 2.14E-19 |
| GO:0019439 | BP | aromatic compound catabolic process | 53/300 | 398/10067 | 7.68E-19 |
| GO:1901361 | BP | organic cyclic compound catabolic process | 54/300 | 414/10067 | 8.05E-19 |
| GO:0006518 | BP | peptide metabolic process | 59/300 | 497/10067 | 1.13E-18 |
| GO:0006605 | BP | protein targeting | 42/300 | 271/10067 | 3.79E-17 |
| GO:0046034 | BP | ATP metabolic process | 36/300 | 202/10067 | 1.38E-16 |
| GO:0043604 | BP | amide biosynthetic process | 55/300 | 496/10067 | 5.96E-16 |
| GO:0015980 | BP | energy derivation by oxidation of organic compounds | 32/300 | 181/10067 | 1.48E-14 |
| GO:0072594 | BP | establishment of protein localization to organelle | 44/300 | 358/10067 | 3.73E-14 |
| GO:0006091 | BP | generation of precursor metabolites and energy | 43/300 | 358/10067 | 1.87E-13 |
| GO:0033108 | BP | mitochondrial respiratory chain complex assembly | 20/300 | 75/10067 | 1.99E-12 |
| GO:0072657 | BP | protein localization to membrane | 45/300 | 423/10067 | 3.43E-12 |
| GO:0010257 | BP | NADH dehydrogenase complex assembly | 16/300 | 47/10067 | 1.05E-11 |
| GO:0032981 | BP | mitochondrial respiratory chain complex I assembly | 16/300 | 47/10067 | 1.05E-11 |
| GO:0009060 | BP | aerobic respiration | 17/300 | 56/10067 | 1.52E-11 |
| GO:0006120 | BP | mitochondrial electron transport, NADH to ubiquinone | 14/300 | 36/10067 | 3.98E-11 |
| GO:0007005 | BP | mitochondrion organization | 41/300 | 387/10067 | 5.21E-11 |
| GO:0006521 | BP | regulation of cellular amino acid metabolic process | 13/300 | 33/10067 | 2.12E-10 |
| GO:0022613 | BP | ribonucleoprotein complex biogenesis | 34/300 | 293/10067 | 4.13E-10 |
| GO:0002181 | BP | cytoplasmic translation | 15/300 | 53/10067 | 1.10E-09 |
| GO:0070125 | BP | mitochondrial translational elongation | 13/300 | 38/10067 | 1.63E-09 |
| GO:0061418 | BP | regulation of transcription from RNA polymerase II promoter in response to hypoxia | 14/300 | 47/10067 | 2.28E-09 |
| GO:0042255 | BP | ribosome assembly | 13/300 | 39/10067 | 2.28E-09 |
| GO:0022618 | BP | ribonucleoprotein complex assembly | 21/300 | 121/10067 | 2.55E-09 |
| GO:0033238 | BP | regulation of cellular amine metabolic process | 13/300 | 40/10067 | 3.16E-09 |
| GO:0071826 | BP | ribonucleoprotein complex subunit organization | 21/300 | 124/10067 | 3.96E-09 |
| GO:0070126 | BP | mitochondrial translational termination | 13/300 | 41/10067 | 4.33E-09 |
| GO:0042273 | BP | ribosomal large subunit biogenesis | 13/300 | 42/10067 | 5.98E-09 |
| GO:0006414 | BP | translational elongation | 16/300 | 70/10067 | 6.68E-09 |
| GO:0006415 | BP | translational termination | 14/300 | 51/10067 | 6.71E-09 |
| GO:0031145 | BP | anaphase-promoting complex-dependent catabolic process | 14/300 | 52/10067 | 8.78E-09 |
| GO:0042254 | BP | ribosome biogenesis | 26/300 | 207/10067 | 1.89E-08 |
| GO:0006123 | BP | mitochondrial electron transport, cytochrome c to oxygen | 8/300 | 14/10067 | 5.90E-08 |
| GO:0019646 | BP | aerobic electron transport chain | 8/300 | 14/10067 | 5.90E-08 |
| GO:0010499 | BP | proteasomal ubiquitin-independent protein catabolic process | 8/300 | 16/10067 | 2.36E-07 |
| GO:0043618 | BP | regulation of transcription from RNA polymerase II promoter in response to stress | 14/300 | 67/10067 | 2.97E-07 |
| GO:1902750 | BP | negative regulation of cell cycle G2/M phase transition | 14/300 | 68/10067 | 3.59E-07 |
| GO:0010972 | BP | negative regulation of G2/M transition of mitotic cell cycle | 13/300 | 58/10067 | 4.04E-07 |
| GO:0032543 | BP | mitochondrial translation | 14/300 | 71/10067 | 6.26E-07 |
| GO:0002479 | BP | antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent | 12/300 | 50/10067 | 6.36E-07 |
| GO:1902600 | BP | proton transmembrane transport | 16/300 | 97/10067 | 8.41E-07 |
| GO:0043620 | BP | regulation of DNA-templated transcription in response to stress | 14/300 | 73/10067 | 8.70E-07 |
| GO:0042590 | BP | antigen processing and presentation of exogenous peptide antigen via MHC class I | 12/300 | 53/10067 | 1.23E-06 |
| GO:1902036 | BP | regulation of hematopoietic stem cell differentiation | 11/300 | 44/10067 | 1.51E-06 |
| GO:0031146 | BP | SCF-dependent proteasomal ubiquitin-dependent protein catabolic process | 12/300 | 55/10067 | 1.82E-06 |
| GO:0002474 | BP | antigen processing and presentation of peptide antigen via MHC class I | 13/300 | 66/10067 | 1.82E-06 |
| GO:0070498 | BP | interleukin-1-mediated signaling pathway | 13/300 | 66/10067 | 1.82E-06 |
| GO:0000028 | BP | ribosomal small subunit assembly | 7/300 | 14/10067 | 1.82E-06 |
| GO:0044106 | BP | cellular amine metabolic process | 13/300 | 69/10067 | 3.13E-06 |
| GO:0002478 | BP | antigen processing and presentation of exogenous peptide antigen | 16/300 | 111/10067 | 5.21E-06 |
| GO:0140053 | BP | mitochondrial gene expression | 15/300 | 98/10067 | 5.56E-06 |
| GO:0048002 | BP | antigen processing and presentation of peptide antigen | 17/300 | 126/10067 | 5.56E-06 |
| GO:0019884 | BP | antigen processing and presentation of exogenous antigen | 16/300 | 113/10067 | 6.45E-06 |
| GO:0060218 | BP | hematopoietic stem cell differentiation | 11/300 | 51/10067 | 6.79E-06 |
| GO:0009308 | BP | amine metabolic process | 13/300 | 74/10067 | 6.85E-06 |
| GO:1901532 | BP | regulation of hematopoietic progenitor cell differentiation | 11/300 | 53/10067 | 1.00E-05 |
| GO:1902749 | BP | regulation of cell cycle G2/M phase transition | 18/300 | 152/10067 | 1.67E-05 |
| GO:0010389 | BP | regulation of G2/M transition of mitotic cell cycle | 17/300 | 141/10067 | 2.64E-05 |
| GO:0019882 | BP | antigen processing and presentation | 17/300 | 142/10067 | 2.88E-05 |
| GO:0002223 | BP | stimulatory C-type lectin receptor signaling pathway | 11/300 | 60/10067 | 3.57E-05 |
| GO:0002220 | BP | innate immune response activating cell surface receptor signaling pathway | 11/300 | 61/10067 | 4.19E-05 |
| GO:0042776 | BP | mitochondrial ATP synthesis coupled proton transport | 6/300 | 14/10067 | 4.46E-05 |
| GO:0002758 | BP | innate immune response-activating signal transduction | 11/300 | 62/10067 | 4.85E-05 |
| GO:0015985 | BP | energy coupled proton transport, down electrochemical gradient | 6/300 | 15/10067 | 7.01E-05 |
| GO:0015986 | BP | ATP synthesis coupled proton transport | 6/300 | 15/10067 | 7.01E-05 |
| GO:0060071 | BP | Wnt signaling pathway, planar cell polarity pathway | 12/300 | 78/10067 | 7.59E-05 |
| GO:0090175 | BP | regulation of establishment of planar polarity | 12/300 | 78/10067 | 7.59E-05 |
| GO:0038095 | BP | Fc-epsilon receptor signaling pathway | 11/300 | 68/10067 | 1.18E-04 |
| GO:1901988 | BP | negative regulation of cell cycle phase transition | 18/300 | 176/10067 | 1.23E-04 |
| GO:0010565 | BP | regulation of cellular ketone metabolic process | 14/300 | 111/10067 | 1.25E-04 |
| GO:0010608 | BP | posttranscriptional regulation of gene expression | 31/300 | 439/10067 | 1.68E-04 |
| GO:0016072 | BP | rRNA metabolic process | 17/300 | 164/10067 | 1.82E-04 |
| GO:1901991 | BP | negative regulation of mitotic cell cycle phase transition | 17/300 | 164/10067 | 1.82E-04 |
| GO:0006122 | BP | mitochondrial electron transport, ubiquinol to cytochrome c | 5/300 | 11/10067 | 2.16E-04 |
| GO:0032984 | BP | protein-containing complex disassembly | 19/300 | 202/10067 | 2.16E-04 |
| GO:0071456 | BP | cellular response to hypoxia | 15/300 | 133/10067 | 2.19E-04 |
| GO:0071347 | BP | cellular response to interleukin-1 | 13/300 | 103/10067 | 2.53E-04 |
| GO:0043624 | BP | cellular protein complex disassembly | 15/300 | 135/10067 | 2.58E-04 |
| GO:0042180 | BP | cellular ketone metabolic process | 16/300 | 152/10067 | 2.61E-04 |
| GO:0001736 | BP | establishment of planar polarity | 12/300 | 89/10067 | 2.68E-04 |
| GO:0007164 | BP | establishment of tissue polarity | 12/300 | 89/10067 | 2.68E-04 |
| GO:2000736 | BP | regulation of stem cell differentiation | 11/300 | 75/10067 | 2.72E-04 |
| GO:0090263 | BP | positive regulation of canonical Wnt signaling pathway | 13/300 | 106/10067 | 3.27E-04 |
| GO:0045653 | BP | negative regulation of megakaryocyte differentiation | 5/300 | 12/10067 | 3.29E-04 |
| GO:0006364 | BP | rRNA processing | 16/300 | 156/10067 | 3.43E-04 |
| GO:0010948 | BP | negative regulation of cell cycle process | 20/300 | 230/10067 | 3.64E-04 |
| GO:1990542 | BP | mitochondrial transmembrane transport | 10/300 | 64/10067 | 3.66E-04 |
| GO:0038061 | BP | NIK/NF-kappaB signaling | 13/300 | 109/10067 | 4.23E-04 |
| GO:0002218 | BP | activation of innate immune response | 11/300 | 79/10067 | 4.23E-04 |
| GO:0044839 | BP | cell cycle G2/M phase transition | 18/300 | 196/10067 | 4.48E-04 |
| GO:0036294 | BP | cellular response to decreased oxygen levels | 15/300 | 143/10067 | 4.59E-04 |
| GO:0043487 | BP | regulation of RNA stability | 14/300 | 128/10067 | 5.33E-04 |
| GO:0000086 | BP | G2/M transition of mitotic cell cycle | 17/300 | 183/10067 | 6.38E-04 |
| GO:0000387 | BP | spliceosomal snRNP assembly | 7/300 | 32/10067 | 6.86E-04 |
| GO:0000715 | BP | nucleotide-excision repair, DNA damage recognition | 5/300 | 14/10067 | 7.19E-04 |
| GO:0070555 | BP | response to interleukin-1 | 13/300 | 118/10067 | 9.26E-04 |
| GO:0071453 | BP | cellular response to oxygen levels | 15/300 | 153/10067 | 9.68E-04 |
| GO:0000027 | BP | ribosomal large subunit assembly | 5/300 | 15/10067 | 1.02E-03 |
| GO:0006839 | BP | mitochondrial transport | 16/300 | 172/10067 | 1.02E-03 |
| GO:0043488 | BP | regulation of mRNA stability | 13/300 | 121/10067 | 1.17E-03 |
| GO:0001738 | BP | morphogenesis of a polarized epithelium | 12/300 | 106/10067 | 1.33E-03 |
| GO:0035567 | BP | non-canonical Wnt signaling pathway | 12/300 | 107/10067 | 1.45E-03 |
| GO:0042274 | BP | ribosomal small subunit biogenesis | 8/300 | 49/10067 | 1.63E-03 |
| GO:0034470 | BP | ncRNA processing | 21/300 | 283/10067 | 2.00E-03 |
| GO:1901987 | BP | regulation of cell cycle phase transition | 23/300 | 326/10067 | 2.02E-03 |
| GO:1901990 | BP | regulation of mitotic cell cycle phase transition | 22/300 | 306/10067 | 2.14E-03 |
| GO:0070646 | BP | protein modification by small protein removal | 16/300 | 184/10067 | 2.14E-03 |
| GO:0033209 | BP | tumor necrosis factor-mediated signaling pathway | 11/300 | 98/10067 | 2.72E-03 |
| GO:0045930 | BP | negative regulation of mitotic cell cycle | 18/300 | 228/10067 | 2.77E-03 |
| GO:0045089 | BP | positive regulation of innate immune response | 12/300 | 116/10067 | 2.95E-03 |
| GO:0090090 | BP | negative regulation of canonical Wnt signaling pathway | 12/300 | 116/10067 | 2.95E-03 |
| GO:0007346 | BP | regulation of mitotic cell cycle | 28/300 | 449/10067 | 2.96E-03 |
| GO:0030177 | BP | positive regulation of Wnt signaling pathway | 13/300 | 134/10067 | 3.01E-03 |
| GO:0030178 | BP | negative regulation of Wnt signaling pathway | 13/300 | 136/10067 | 3.47E-03 |
| GO:0038093 | BP | Fc receptor signaling pathway | 12/300 | 119/10067 | 3.65E-03 |
| GO:0061013 | BP | regulation of mRNA catabolic process | 13/300 | 138/10067 | 3.95E-03 |
| GO:0016579 | BP | protein deubiquitination | 15/300 | 176/10067 | 4.04E-03 |
| GO:1905330 | BP | regulation of morphogenesis of an epithelium | 12/300 | 123/10067 | 4.87E-03 |
| GO:0006283 | BP | transcription-coupled nucleotide-excision repair | 7/300 | 45/10067 | 5.48E-03 |
| GO:0007007 | BP | inner mitochondrial membrane organization | 6/300 | 34/10067 | 7.22E-03 |
| GO:0034660 | BP | ncRNA metabolic process | 22/300 | 338/10067 | 7.83E-03 |
| GO:0002244 | BP | hematopoietic progenitor cell differentiation | 11/300 | 113/10067 | 8.59E-03 |
| GO:0006754 | BP | ATP biosynthetic process | 6/300 | 36/10067 | 9.74E-03 |
| GO:0044391 | CC | ribosomal subunit | 44/311 | 90/10416 | 4.28E-41 |
| GO:0005840 | CC | ribosome | 47/311 | 120/10416 | 1.05E-38 |
| GO:0022626 | CC | cytosolic ribosome | 32/311 | 54/10416 | 1.77E-33 |
| GO:0005743 | CC | mitochondrial inner membrane | 62/311 | 313/10416 | 2.80E-32 |
| GO:0019866 | CC | organelle inner membrane | 62/311 | 355/10416 | 4.44E-29 |
| GO:0098798 | CC | mitochondrial protein complex | 43/311 | 152/10416 | 8.04E-29 |
| GO:1990904 | CC | ribonucleoprotein complex | 66/311 | 423/10416 | 3.21E-28 |
| GO:0031966 | CC | mitochondrial membrane | 69/311 | 477/10416 | 1.36E-27 |
| GO:0015934 | CC | large ribosomal subunit | 27/311 | 54/10416 | 8.67E-26 |
| GO:0070469 | CC | respirasome | 28/311 | 68/10416 | 7.73E-24 |
| GO:0022625 | CC | cytosolic large ribosomal subunit | 19/311 | 24/10416 | 7.90E-24 |
| GO:0098800 | CC | inner mitochondrial membrane protein complex | 30/311 | 87/10416 | 5.99E-23 |
| GO:0098803 | CC | respiratory chain complex | 24/311 | 56/10416 | 5.60E-21 |
| GO:0005746 | CC | mitochondrial respirasome | 24/311 | 58/10416 | 1.45E-20 |
| GO:0015935 | CC | small ribosomal subunit | 18/311 | 38/10416 | 1.08E-16 |
| GO:0022627 | CC | cytosolic small ribosomal subunit | 14/311 | 27/10416 | 1.13E-13 |
| GO:1990204 | CC | oxidoreductase complex | 20/311 | 69/10416 | 1.19E-13 |
| GO:0005747 | CC | mitochondrial respiratory chain complex I | 14/311 | 32/10416 | 1.85E-12 |
| GO:0030964 | CC | NADH dehydrogenase complex | 14/311 | 32/10416 | 1.85E-12 |
| GO:0045271 | CC | respiratory chain complex I | 14/311 | 32/10416 | 1.85E-12 |
| GO:0005759 | CC | mitochondrial matrix | 37/311 | 313/10416 | 9.43E-12 |
| GO:1905369 | CC | endopeptidase complex | 13/311 | 38/10416 | 5.59E-10 |
| GO:0070069 | CC | cytochrome complex | 10/311 | 21/10416 | 2.12E-09 |
| GO:1905368 | CC | peptidase complex | 14/311 | 51/10416 | 2.53E-09 |
| GO:0000313 | CC | organellar ribosome | 13/311 | 43/10416 | 2.79E-09 |
| GO:0005761 | CC | mitochondrial ribosome | 13/311 | 43/10416 | 2.79E-09 |
| GO:0005839 | CC | proteasome core complex | 8/311 | 13/10416 | 9.19E-09 |
| GO:0000502 | CC | proteasome complex | 11/311 | 34/10416 | 2.97E-08 |
| GO:0005844 | CC | polysome | 11/311 | 40/10416 | 1.97E-07 |
| GO:0042788 | CC | polysomal ribosome | 7/311 | 15/10416 | 1.31E-06 |
| GO:0005753 | CC | mitochondrial proton-transporting ATP synthase complex | 6/311 | 12/10416 | 6.57E-06 |
| GO:0045259 | CC | proton-transporting ATP synthase complex | 6/311 | 13/10416 | 1.12E-05 |
| GO:0045277 | CC | respiratory chain complex IV | 6/311 | 13/10416 | 1.12E-05 |
| GO:0000315 | CC | organellar large ribosomal subunit | 8/311 | 29/10416 | 1.56E-05 |
| GO:0005762 | CC | mitochondrial large ribosomal subunit | 8/311 | 29/10416 | 1.56E-05 |
| GO:0071005 | CC | U2-type precatalytic spliceosome | 7/311 | 33/10416 | 4.57E-04 |
| GO:0005758 | CC | mitochondrial intermembrane space | 9/311 | 58/10416 | 5.07E-04 |
| GO:0071011 | CC | precatalytic spliceosome | 7/311 | 34/10416 | 5.31E-04 |
| GO:0044815 | CC | DNA packaging complex | 10/311 | 74/10416 | 6.27E-04 |
| GO:0031970 | CC | organelle envelope lumen | 9/311 | 65/10416 | 1.17E-03 |
| GO:0005750 | CC | mitochondrial respiratory chain complex III | 4/311 | 10/10416 | 1.28E-03 |
| GO:0045275 | CC | respiratory chain complex III | 4/311 | 10/10416 | 1.28E-03 |
| GO:0000786 | CC | nucleosome | 9/311 | 67/10416 | 1.38E-03 |
| GO:0120114 | CC | Sm-like protein family complex | 8/311 | 54/10416 | 1.57E-03 |
| GO:0005684 | CC | U2-type spliceosomal complex | 8/311 | 56/10416 | 1.99E-03 |
| GO:0097525 | CC | spliceosomal snRNP complex | 7/311 | 43/10416 | 2.09E-03 |
| GO:0016469 | CC | proton-transporting two-sector ATPase complex | 6/311 | 31/10416 | 2.14E-03 |
| GO:0000314 | CC | organellar small ribosomal subunit | 4/311 | 12/10416 | 2.43E-03 |
| GO:0005763 | CC | mitochondrial small ribosomal subunit | 4/311 | 12/10416 | 2.43E-03 |
| GO:0034719 | CC | SMN-Sm protein complex | 4/311 | 12/10416 | 2.43E-03 |
| GO:0000788 | CC | nuclear nucleosome | 5/311 | 22/10416 | 2.97E-03 |
| GO:0030532 | CC | small nuclear ribonucleoprotein complex | 7/311 | 47/10416 | 3.26E-03 |
| GO:0005685 | CC | U1 snRNP | 4/311 | 15/10416 | 5.88E-03 |
| GO:0046540 | CC | U4/U6 x U5 tri-snRNP complex | 5/311 | 26/10416 | 6.23E-03 |
| GO:0097526 | CC | spliceosomal tri-snRNP complex | 5/311 | 26/10416 | 6.23E-03 |
| GO:0005697 | CC | telomerase holoenzyme complex | 4/311 | 16/10416 | 7.24E-03 |
| GO:0005689 | CC | U12-type spliceosomal complex | 4/311 | 17/10416 | 9.09E-03 |
| GO:0003735 | MF | structural constituent of ribosome | 42/310 | 74/10268 | 1.38E-42 |
| GO:0005198 | MF | structural molecule activity | 47/310 | 375/10268 | 7.92E-15 |
| GO:0009055 | MF | electron transfer activity | 21/310 | 82/10268 | 2.95E-12 |
| GO:0003954 | MF | NADH dehydrogenase activity | 13/310 | 30/10268 | 7.11E-11 |
| GO:0008137 | MF | NADH dehydrogenase (ubiquinone) activity | 13/310 | 30/10268 | 7.11E-11 |
| GO:0050136 | MF | NADH dehydrogenase (quinone) activity | 13/310 | 30/10268 | 7.11E-11 |
| GO:0004129 | MF | cytochrome-c oxidase activity | 10/310 | 18/10268 | 8.96E-10 |
| GO:0015002 | MF | heme-copper terminal oxidase activity | 10/310 | 18/10268 | 8.96E-10 |
| GO:0016676 | MF | oxidoreductase activity, acting on a heme group of donors, oxygen as acceptor | 10/310 | 18/10268 | 8.96E-10 |
| GO:0016675 | MF | oxidoreductase activity, acting on a heme group of donors | 10/310 | 19/10268 | 1.66E-09 |
| GO:0016655 | MF | oxidoreductase activity, acting on NAD(P)H, quinone or similar compound as acceptor | 13/310 | 40/10268 | 2.97E-09 |
| GO:0016491 | MF | oxidoreductase activity | 42/310 | 475/10268 | 9.36E-09 |
| GO:0019843 | MF | rRNA binding | 12/310 | 37/10268 | 1.41E-08 |
| GO:0004298 | MF | threonine-type endopeptidase activity | 8/310 | 14/10268 | 4.84E-08 |
| GO:0070003 | MF | threonine-type peptidase activity | 8/310 | 17/10268 | 3.38E-07 |
| GO:0016651 | MF | oxidoreductase activity, acting on NAD(P)H | 14/310 | 74/10268 | 9.10E-07 |
| GO:0015078 | MF | proton transmembrane transporter activity | 14/310 | 76/10268 | 1.22E-06 |
| GO:0051539 | MF | 4 iron, 4 sulfur cluster binding | 7/310 | 36/10268 | 1.95E-03 |
| GO:0051536 | MF | iron-sulfur cluster binding | 8/310 | 51/10268 | 2.71E-03 |
| GO:0051540 | MF | metal cluster binding | 8/310 | 51/10268 | 2.71E-03 |
| GO:0015252 | MF | proton channel activity | 4/310 | 11/10268 | 4.54E-03 |
| **Pathways associated with red module genes** | | | | | |
| GO:0006487 | BP | protein N-linked glycosylation | 23/944 | 53/10067 | 3.23E-07 |
| GO:0034976 | BP | response to endoplasmic reticulum stress | 45/944 | 191/10067 | 8.45E-06 |
| GO:0006888 | BP | endoplasmic reticulum to Golgi vesicle-mediated transport | 34/944 | 124/10067 | 8.45E-06 |
| GO:0018279 | BP | protein N-linked glycosylation via asparagine | 12/944 | 19/10067 | 1.34E-05 |
| GO:0018196 | BP | peptidyl-asparagine modification | 12/944 | 20/10067 | 2.45E-05 |
| GO:0070085 | BP | glycosylation | 41/944 | 177/10067 | 2.51E-05 |
| GO:0006486 | BP | protein glycosylation | 39/944 | 169/10067 | 4.54E-05 |
| GO:0043413 | BP | macromolecule glycosylation | 39/944 | 169/10067 | 4.54E-05 |
| GO:0009100 | BP | glycoprotein metabolic process | 52/944 | 269/10067 | 1.48E-04 |
| GO:0036503 | BP | ERAD pathway | 21/944 | 68/10067 | 2.46E-04 |
| GO:0035966 | BP | response to topologically incorrect protein | 32/944 | 135/10067 | 2.52E-04 |
| GO:0035967 | BP | cellular response to topologically incorrect protein | 28/944 | 110/10067 | 2.52E-04 |
| GO:0009101 | BP | glycoprotein biosynthetic process | 45/944 | 226/10067 | 2.76E-04 |
| GO:0006643 | BP | membrane lipid metabolic process | 32/944 | 138/10067 | 3.37E-04 |
| GO:0006511 | BP | ubiquitin-dependent protein catabolic process | 67/944 | 397/10067 | 3.45E-04 |
| GO:0048193 | BP | Golgi vesicle transport | 47/944 | 244/10067 | 3.45E-04 |
| GO:0007033 | BP | vacuole organization | 30/944 | 128/10067 | 4.68E-04 |
| GO:0019941 | BP | modification-dependent protein catabolic process | 67/944 | 402/10067 | 4.68E-04 |
| GO:0030433 | BP | ubiquitin-dependent ERAD pathway | 17/944 | 51/10067 | 4.77E-04 |
| GO:0016236 | BP | macroautophagy | 42/944 | 212/10067 | 4.79E-04 |
| GO:0051603 | BP | proteolysis involved in cellular protein catabolic process | 74/944 | 467/10067 | 8.04E-04 |
| GO:0043632 | BP | modification-dependent macromolecule catabolic process | 67/944 | 412/10067 | 9.17E-04 |
| GO:0031647 | BP | regulation of protein stability | 39/944 | 197/10067 | 9.78E-04 |
| GO:0006664 | BP | glycolipid metabolic process | 20/944 | 72/10067 | 1.19E-03 |
| GO:1903509 | BP | liposaccharide metabolic process | 20/944 | 73/10067 | 1.43E-03 |
| GO:1901137 | BP | carbohydrate derivative biosynthetic process | 72/944 | 462/10067 | 1.60E-03 |
| GO:0006986 | BP | response to unfolded protein | 27/944 | 119/10067 | 1.85E-03 |
| GO:0030968 | BP | endoplasmic reticulum unfolded protein response | 21/944 | 82/10067 | 2.40E-03 |
| GO:0034620 | BP | cellular response to unfolded protein | 23/944 | 95/10067 | 2.51E-03 |
| GO:0045851 | BP | pH reduction | 13/944 | 37/10067 | 2.55E-03 |
| GO:0010498 | BP | proteasomal protein catabolic process | 52/944 | 310/10067 | 3.27E-03 |
| GO:0010256 | BP | endomembrane system organization | 50/944 | 295/10067 | 3.39E-03 |
| GO:0006914 | BP | autophagy | 60/944 | 376/10067 | 3.39E-03 |
| GO:0061919 | BP | process utilizing autophagic mechanism | 60/944 | 376/10067 | 3.39E-03 |
| GO:0036507 | BP | protein demannosylation | 8/944 | 16/10067 | 4.78E-03 |
| GO:0036508 | BP | protein alpha-1,2-demannosylation | 8/944 | 16/10067 | 4.78E-03 |
| GO:0051452 | BP | intracellular pH reduction | 12/944 | 36/10067 | 7.95E-03 |
| GO:0046467 | BP | membrane lipid biosynthetic process | 22/944 | 97/10067 | 8.49E-03 |
| GO:0043161 | BP | proteasome-mediated ubiquitin-dependent protein catabolic process | 45/944 | 268/10067 | 8.97E-03 |
| GO:0005774 | CC | vacuolar membrane | 72/982 | 317/10416 | 3.77E-10 |
| GO:0005765 | CC | lysosomal membrane | 64/982 | 279/10416 | 1.59E-09 |
| GO:0098852 | CC | lytic vacuole membrane | 64/982 | 279/10416 | 1.59E-09 |
| GO:0005793 | CC | endoplasmic reticulum-Golgi intermediate compartment | 30/982 | 88/10416 | 2.08E-08 |
| GO:0033116 | CC | endoplasmic reticulum-Golgi intermediate compartment membrane | 20/982 | 50/10416 | 8.24E-07 |
| GO:0031300 | CC | intrinsic component of organelle membrane | 52/982 | 265/10416 | 1.91E-05 |
| GO:0031301 | CC | integral component of organelle membrane | 49/982 | 251/10416 | 4.31E-05 |
| GO:0031227 | CC | intrinsic component of endoplasmic reticulum membrane | 28/982 | 112/10416 | 7.37E-05 |
| GO:0030176 | CC | integral component of endoplasmic reticulum membrane | 26/982 | 107/10416 | 2.55E-04 |
| GO:0005766 | CC | primary lysosome | 24/982 | 95/10416 | 2.55E-04 |
| GO:0042582 | CC | azurophil granule | 24/982 | 95/10416 | 2.55E-04 |
| GO:0044322 | CC | endoplasmic reticulum quality control compartment | 9/982 | 17/10416 | 3.07E-04 |
| GO:0005798 | CC | Golgi-associated vesicle | 26/982 | 111/10416 | 3.94E-04 |
| GO:0030134 | CC | COPII-coated ER to Golgi transport vesicle | 18/982 | 63/10416 | 4.85E-04 |
| GO:0031985 | CC | Golgi cisterna | 19/982 | 73/10416 | 1.13E-03 |
| GO:0033176 | CC | proton-transporting V-type ATPase complex | 8/982 | 16/10416 | 1.31E-03 |
| GO:0042470 | CC | melanosome | 18/982 | 69/10416 | 1.46E-03 |
| GO:0048770 | CC | pigment granule | 18/982 | 69/10416 | 1.46E-03 |
| GO:0030173 | CC | integral component of Golgi membrane | 14/982 | 49/10416 | 3.26E-03 |
| GO:0005775 | CC | vacuolar lumen | 24/982 | 114/10416 | 3.46E-03 |
| GO:0010008 | CC | endosome membrane | 54/982 | 349/10416 | 4.33E-03 |
| GO:0031228 | CC | intrinsic component of Golgi membrane | 14/982 | 51/10416 | 4.51E-03 |
| GO:0005770 | CC | late endosome | 34/982 | 192/10416 | 5.22E-03 |
| GO:0030659 | CC | cytoplasmic vesicle membrane | 70/982 | 490/10416 | 5.40E-03 |
| GO:0043202 | CC | lysosomal lumen | 17/982 | 72/10416 | 6.30E-03 |
| GO:0031902 | CC | late endosome membrane | 22/982 | 107/10416 | 7.06E-03 |
| GO:0032580 | CC | Golgi cisterna membrane | 14/982 | 54/10416 | 7.06E-03 |
| GO:0031984 | CC | organelle subcompartment | 43/982 | 269/10416 | 7.24E-03 |
| GO:0035577 | CC | azurophil granule membrane | 11/982 | 37/10416 | 7.83E-03 |
| **Pathways associated with tan module genes** | | | | | |
| GO:0019751 | BP | polyol metabolic process | 10/160 | 91/10067 | 4.22E-03 |
| GO:0006735 | BP | NADH regeneration | 5/160 | 21/10067 | 8.32E-03 |
| GO:0061621 | BP | canonical glycolysis | 5/160 | 21/10067 | 8.32E-03 |
| GO:0061718 | BP | glucose catabolic process to pyruvate | 5/160 | 21/10067 | 8.32E-03 |
| GO:0019674 | BP | NAD metabolic process | 6/160 | 35/10067 | 8.32E-03 |
| GO:0061620 | BP | glycolytic process through glucose-6-phosphate | 5/160 | 22/10067 | 8.43E-03 |
| GO:0061615 | BP | glycolytic process through fructose-6-phosphate | 5/160 | 23/10067 | 8.43E-03 |
| GO:0006090 | BP | pyruvate metabolic process | 9/160 | 99/10067 | 8.43E-03 |
| **Pathways associated with turquoise module genes** | | | | | |
| GO:0008380 | BP | RNA splicing | 60/733 | 309/10067 | 4.57E-09 |
| GO:0006397 | BP | mRNA processing | 62/733 | 349/10067 | 5.23E-08 |
| GO:0000377 | BP | RNA splicing, via transesterification reactions with bulged adenosine as nucleophile | 43/733 | 233/10067 | 9.13E-06 |
| GO:0000398 | BP | mRNA splicing, via spliceosome | 43/733 | 233/10067 | 9.13E-06 |
| GO:0000375 | BP | RNA splicing, via transesterification reactions | 43/733 | 234/10067 | 9.13E-06 |
| GO:0043484 | BP | regulation of RNA splicing | 26/733 | 109/10067 | 3.00E-05 |
| GO:0003341 | BP | cilium movement | 17/733 | 65/10067 | 1.42E-03 |
| GO:0007099 | BP | centriole replication | 10/733 | 27/10067 | 5.16E-03 |
| GO:0098534 | BP | centriole assembly | 10/733 | 28/10067 | 6.26E-03 |
| GO:0048024 | BP | regulation of mRNA splicing, via spliceosome | 17/733 | 74/10067 | 6.26E-03 |
| GO:0050684 | BP | regulation of mRNA processing | 21/733 | 105/10067 | 6.26E-03 |
| GO:0016607 | CC | nuclear speck | 46/765 | 283/10416 | 1.09E-04 |