

| ID | Description | GeneRatio | BgRatio | p value | p-adjust | q value | geneID | Count |
|------------|---|-----------|-----------|-------------|-------------|-------------|--|-------|
| GO:0006959 | humoral immune response | 17/98 | 349/18493 | 3.76828E-12 | 1.90374E-09 | 1.35897E-09 | CD74/C1QA/LYZ/ITREM2/CXCL8/CCL2/S/GAPDH/A2M/S100A8/C3/C1QC/C3AR1/GPR183/RNASE5/VISG4/CD83/S100A8 | 17 |
| GO:003595 | leukocyte chemotaxis | 13/98 | 217/18493 | 3.24604E-10 | 4.47507E-08 | 3.19662E-08 | CD74/DUSP1/FCER1/G/CXCL8/CCL2/S100A8/C3AR1/GPR183/ITGB2/IAIF1/PAD2/S100A8/CXCL16 | 13 |
| GO:0097529 | myeloid leukocyte migration | 11/98 | 199/18493 | 8.4161E-09 | 2.64476E-06 | 1.88919E-06 | CD74/DUSP1/FCER1/G/CXCL8/CCL2/S100A8/C3AR1/CX3CR1/ITGB2/IAIF1/S100A8 | 11 |
| GO:0050900 | leukocyte migration | 15/98 | 478/18493 | 3.15597E-08 | 7.93365E-06 | 5.68713E-06 | CD74/DUSP1/FCER1/G/CXCL8/CCL2/S100A8/C3AR1/RHOA/GPR183/CX3CR1/ITGB2/IAIF1/PAD2/S100A8/CXCL16 | 15 |
| GO:0048052 | antigen processing and presentation of peptide antigen | 11/98 | 239/18493 | 2.2625E-09 | 4.9716E-05 | 3.55129E-05 | CD74/HLA-DRB1/HLA-DRA/FCER1/G/ITREM2/HLA-DRB5/VAMP8/B2M/CTSS | 11 |
| GO:0071216 | cellular response to biotic stimulus | 10/98 | 229/18493 | 3.76725E-07 | 4.32493E-05 | 3.08937E-05 | CD74/ITREM2/CXCL8/CCL2/RHOA/CX3CR1/ZFP36/TXNIP/TNFRSF1B/HSPA5 | 10 |
| GO:0019882 | antigen processing and presentation | 9/98 | 175/18493 | 3.78475E-07 | 4.32493E-05 | 3.08937E-05 | CD74/HLA-DRB1/HLA-DRA/FCER1/G/ITREM2/HLA-DRB5/VAMP8/B2M/CTSS | 9 |
| GO:0022685 | regulation of leukocyte migration | 9/98 | 180/18493 | 3.80396E-07 | 4.9716E-05 | 3.55129E-05 | CD74/DUSP1/CXCL8/CCL2/C3AR1/RHOA/CX3CR1/IAIF1/PAD2 | 9 |
| GO:0032103 | positive regulation of response to external stimulus | 11/98 | 237/18493 | 4.94391E-07 | 4.9716E-05 | 3.55129E-05 | CD74/FCER1/G/TMSB4X/CXCL8/S100A8/C3/C3AR1/VAMP8/ITGB2/IAIF1/S100A8 | 11 |
| GO:0019884 | antigen processing and presentation of exogenous antigen | 9/98 | 134/18493 | 3.60578E-07 | 5.2196E-05 | 3.72844E-05 | CD74/HLA-DRB1/HLA-DRA/FCER1/G/HLA-DRB5/VAMP8/B2M/CTSS | 9 |
| GO:048857 | neural nucleus development | 6/98 | 62/18493 | 5.17845E-07 | 7.44343E-05 | 5.31696E-05 | ACTB/YYH4/RHOA/PAD2/HSPA5/CALM2 | 6 |
| GO:0051235 | maintenance of location | 11/98 | 318/18493 | 6.88945E-07 | 7.61149E-05 | 5.43701E-05 | FTL/TMSB10/SGRN/APOE/TMSB4X/S100A8/C3/ANXA5/S100A8/HSPA5/CALM2 | 11 |
| GO:0020054 | antigen processing and presentation of peptide or polysaccharide antigen via MHC class II | 7/98 | 102/18493 | 1.15697E-06 | 7.90337E-05 | 5.6455E-05 | CD74/HLA-DRB1/HLA-DRA/FCER1/G/ITREM2/HLA-DRB5/CTSS | 7 |
| GO:0050920 | regulation of chemotaxis | 9/98 | 210/18493 | 3.73772E-06 | 0.000112016 | 8.0015E-05 | CD74/DUSP1/TMSB4X/CXCL8/CCL2/C3AR1/GPR183/IAIF1/PAD2 | 9 |
| GO:0072442 | amylol-beta cleavage | 7/98 | 201/18493 | 3.36595E-05 | 0.00201475 | 0.00148917 | APOE/MARCO/ITGB2 | 7 |
| GO:0026997 | regulation of immune effector process | 12/98 | 439/18493 | 3.5388E-06 | 0.00026896 | 0.000147789 | CD74/C1QB/C1QA/FCER1/G/A2M/C3/C1QC/C3AR1/TMBIM6/VAMP8/ITGB2/B2M | 12 |
| GO:0072376 | protein activation cascade | 8/98 | 184/18493 | 8.91962E-06 | 0.00049831 | 0.00035595 | C1QB/C1QA/A2M/C3/C1QC/C3AR1/VISG4 | 8 |
| GO:0030591 | midbrain development | 6/98 | 92/18493 | 3.36891E-06 | 0.000512031 | 0.000369752 | ACTB/YYH4/RHOA/PAD2/HSPA5/CALM2 | 6 |
| GO:0045807 | positive regulation of endocytosis | 7/98 | 141/18493 | 1.00097E-05 | 0.000535415 | 0.000382455 | CD14/FCER1/G/APOE/CCL2/C3/B2M/CD63 | 7 |
| GO:0051651 | maintenance of location in cell | 6/98 | 95/18493 | 1.12742E-05 | 0.000583102 | 0.000416519 | FTL/TMSB10/SGRN/APOE/TMSB4X/HSPA5 | 6 |
| GO:0070997 | neuron death | 10/98 | 335/18493 | 1.13652E-05 | 0.000583102 | 0.000416519 | FOS/APOE/CCL2/GAPDH/RHOA/CX3CR1/ITG2/ITGB2/EGR1/HSPA5 | 10 |
| GO:0001819 | positive regulation of cytokine production | 11/98 | 422/18493 | 1.44701E-05 | 0.000673665 | 0.00049121 | CD74/CD14/FCER1/G/CSF1R/GAPDH/CX3CR1/CYBB/CD63/B2M/EGR1 | 11 |
| GO:0072676 | lymphocyte migration | 6/98 | 105/18493 | 2.00067E-05 | 0.00067187 | 0.000619445 | CD74/RHOA/GPR183/IAIF1/PAD2/CXCL16 | 6 |
| GO:0025523 | leukocyte migration involved in inflammatory response | 3/98 | 11/18493 | 2.30886E-05 | 0.00064362 | 0.000688859 | S100A8/ITGB2/S100A8 | 3 |
| GO:2000257 | regulation of protein activation cascade | 6/98 | 108/18493 | 2.34866E-05 | 0.00064362 | 0.000688859 | C1QB/C1QA/A2M/C3/C1QC/C3AR1 | 6 |
| GO:0006556 | complement activation | 7/98 | 170/18493 | 3.35913E-05 | 0.00127522 | 0.000913983 | C1QB/C1QA/A2M/C3/C1QC/C3AR1/VISG4 | 7 |
| GO:0019730 | antimicrobial humoral response | 6/98 | 118/18493 | 3.67602E-05 | 0.00142622 | 0.001018801 | LYZ/CXCL8/GAPDH/S100A8/RNASE5/S100A8 | 6 |
| GO:0043062 | extracellular structure organization | 10/98 | 402/18493 | 3.76828E-12 | 1.90374E-09 | 1.35897E-09 | SPPI/CTSS/APOE/A2M/ITGB2/TNFRSF1B/TMP1/CTSS/APOC1/LCP1 | 10 |
| GO:0046677 | response to antibiotic | 9/98 | 323/18493 | 4.94523E-05 | 0.00175969 | 0.001256974 | PSP/CD14/DUSP1/RHOA/CYBB/TXNIP/EGR1/S100A8/HSPA5 | 9 |
| GO:0002218 | activation of innate immune response | 9/98 | 252/18493 | 5.81986E-05 | 0.001860312 | 0.001290277 | CD14/FCER1/G/S100A8/MARCO/ITGB2/UBC/CTSS/S100A8 | 9 |
| GO:0051238 | sequestering of metal ion | 3/98 | 15/18493 | 2.26348E-05 | 0.001869973 | 0.001356466 | FTL/S100A8/S100A8 | 3 |
| GO:0070765 | female pregnancy | 5/98 | 100/18493 | 2.03355E-05 | 0.001869973 | 0.001468865 | SPPI/FOS/CTSS/ARHGDB/JUNB/TMP1/H3F3B | 5 |
| GO:0032602 | chemokine production | 5/98 | 82/18493 | 7.4505E-05 | 0.002128474 | 0.001520402 | CD74/CSF1R/S100A8/EGR1/S100A8 | 5 |
| GO:2001746 | negative regulation of cell motility | 9/98 | 339/18493 | 3.78971E-05 | 0.002205924 | 0.001575726 | DUSP1/APOE/CCL2/RHOA/ARHGDB/CX3CR1/IAIF1/PAD2/TMP1 | 9 |
| GO:0031349 | positive regulation of defense response | 7/98 | 222/18493 | 3.87947E-05 | 0.002453075 | 0.00175227 | CD14/FCER1/G/S100A8/C3/MARCO/VAMP8/ITGB2/UBC/CTSS/S100A8 | 7 |
| GO:0026863 | negative regulation of immune system process | 10/98 | 437/18493 | 0.000107422 | 0.00282276 | 0.002036064 | CD74/CD14/DUSP1/FCER1/G/CCL2/A2M/C1QC/ZFP36/TMBIM6/PAD2 | 10 |
| GO:0046697 | deoxidization | 3/98 | 201/18493 | 0.000154087 | 0.003654485 | 0.002610455 | SPPI/CTSS/JUNB | 3 |
| GO:0026596 | regulation of vesicle-mediated transport | 10/98 | 372/18493 | 0.000159408 | 0.003654485 | 0.002610455 | CD74/FCER1/G/CCL2/RHOA/GPR183/VAMP8/ITGB2/CD63/EGR1 | 10 |
| GO:007556 | embryo implantation | 4/98 | 52/18493 | 0.000165169 | 0.003827072 | 0.002733737 | SPPI/ARHGDB/TMP1/H3F3B | 4 |
| GO:0051271 | negative regulation of cellular component movement | 9/98 | 374/18493 | 0.000165931 | 0.003827072 | 0.002733737 | DUSP1/APOE/CCL2/RHOA/ARHGDB/CX3CR1/IAIF1/PAD2/TMP1 | 9 |
| GO:0047706 | multi-molecular organism process | 7/98 | 221/18493 | 0.000174331 | 0.003952636 | 0.002822429 | SPPI/FOS/CTSS/ARHGDB/JUNB/TMP1/H3F3B | 7 |
| GO:0051048 | negative regulation of cell activation | 9/98 | 222/18493 | 0.000179328 | 0.003952636 | 0.002822429 | CD74/SGRN/TMSB4X/TMBIM6/VAMP8/TNFRSF1B/ANXA5 | 9 |
| GO:0050867 | positive regulation of cell activation | 9/98 | 384/18493 | 0.000201987 | 0.004340141 | 0.003100231 | CD74/FCER1/G/CCL2/RHOA/GPR183/VAMP8/ITGB2/CD63/IAIF1 | 9 |
| GO:0040013 | negative regulation of locomotion | 9/98 | 386/18493 | 0.00020993 | 0.004421877 | 0.003158616 | DUSP1/APOE/CCL2/RHOA/ARHGDB/CX3CR1/IAIF1/PAD2/TMP1 | 9 |
| GO:1304708 | positive regulation of morphological development | 6/98 | 228/18493 | 0.000211068 | 0.004421877 | 0.003158616 | CXCL8/CX3CR1/CX3CR1/CYBB/ITGB2/EGR1 | 6 |
| GO:0035821 | modification of morphology or physiology of other organism | 6/98 | 161/18493 | 0.000215718 | 0.004481951 | 0.003201528 | LYZ/APOE/GAPDH/S100A8/HSPA5/CALM2 | 6 |
| GO:0006735 | NADH regeneration | 3/98 | 251/18493 | 0.000304958 | 0.005637245 | 0.004026772 | GAPDH/ENO1/PGK1 | 3 |
| GO:0006027 | regulation of vesicle-mediated transport | 10/98 | 498/18493 | 0.000320241 | 0.00565354 | 0.004040412 | CD14/FCER1/G/APOE/CCL2/C3/VAMP8/ITGB2/B2M/CD63/APOC1 | 10 |
| GO:0050922 | negative regulation of chemotaxis | 4/98 | 62/18493 | 0.00032684 | 0.00562748 | 0.00416266 | SPPI/CCL2/IAIF1/PAD2 | 4 |
| GO:0042026 | protein refolding | 3/98 | 261/18493 | 0.000343414 | 0.00595408 | 0.004253092 | B2M/HSPA5/HSPA5 | 3 |
| GO:0032102 | negative regulation of response to external stimulus | 8/98 | 329/18493 | 0.000361632 | 0.006142657 | 0.004387939 | SPPI/DUSP1/APOE/CCL2/IAIF1/TNFRSF1B/ANXA5/PAD2 | 8 |
| GO:1303489 | reactive oxygen species biosynthetic process | 5/98 | 115/18493 | 0.000363221 | 0.006161997 | 0.004401611 | RHOA/CX3CR1/CYBB/ITGB2/IAIF1 | 5 |
| GO:1303706 | regulation of hemopoiesis | 9/98 | 418/18493 | 0.000376905 | 0.006316927 | 0.00451228 | CD74/FOS/TYR/OBP/C1QC/RHOA/ZFP36/CD63/B2M/H3F3B | 9 |
| GO:0007596 | blood coagulation | 9/98 | 334/18493 | 0.000398144 | 0.00648473 | 0.004603144 | ACTB/FCER1/G/APOE/A2M/F13A1/ACTG1/ANXA5/H3F3B | 9 |
| GO:0050817 | coagulation | 9/98 | 400/18493 | 0.000449698 | 0.007113608 | 0.005081362 | ACTB/FCER1/G/APOE/A2M/F13A1/ACTG1/ANXA5/H3F3B | 9 |
| GO:0026867 | positive regulation of leukocyte migration | 5/98 | 121/18493 | 0.000461377 | 0.007204359 | 0.005148186 | CD74/CXCL8/C3AR1/RHOA/IAIF1 | 5 |
| GO:0001893 | maternal placenta development | 3/98 | 31/18493 | 0.000582419 | 0.008512802 | 0.006080827 | SPPI/CTSS/JUNB | 3 |
| GO:0050504 | response to lipopolysaccharide | 10/98 | 420/18493 | 0.000582419 | 0.008512802 | 0.006080827 | FCER1/G/APOE/ITGB2 | 10 |
| GO:1303531 | negative regulation of secretion by cell | 6/98 | 196/18493 | 0.000615788 | 0.008776038 | 0.006268661 | SGRN/TMSB4X/TMBIM6/VAMP8/TNFRSF1B/ANXA5 | 6 |
| GO:0050921 | positive regulation of chemotaxis | 5/98 | 130/18493 | 0.000639532 | 0.008991527 | 0.006422788 | DUSP1/CXCL8/CXCL8/C3AR1/IAIF1 | 5 |
| GO:0071402 | cellular response to lipoprotein particle stimulus | 3/98 | 331/18493 | 0.000701532 | 0.00894877 | 0.00682155 | FCER1/APOE/ITGB2 | 3 |
| GO:0043993 | regulation of symbiosis, encompassing mutualism through parasitism | 5/98 | 31/18493 | 0.000739699 | 0.00894877 | 0.00682155 | CD74/FCER1/G/CXCL8/C3AR1/PDH/ZFP36/HSPA5 | 5 |
| GO:0071706 | tumor necrosis factor superfamily cytokine production | 5/98 | 135/18493 | 0.000759147 | 0.001044714 | 0.007175098 | CD74/FCER1/G/CX3CR1/VAMP8/ZFP36 | 5 |
| GO:0051088 | regulation of binding | 9/98 | 369/18493 | 0.000769147 | 0.010123749 | 0.007231552 | ACTB/APOE/TMSB4X/TMBIM6/B2M/S100A10/HSPA5/CALM2 | 9 |
| GO:0043900 | regulation of multi-organism process | 3/98 | 371/18493 | 0.000785659 | 0.010123749 | 0.007231552 | CD74/FCER1/G/CXCL8/C3AR1/ARHGDB/ZFP36/HSPA5/TMP1 | 3 |
| GO:0026999 | positive regulation of immune effector process | 6/98 | 209/18493 | 0.000806967 | 0.010995881 | 0.00785453 | CD74/FCER1/G/C3/VAMP8/ITGB2/B2M | 6 |
| GO:0051702 | interaction with symbiont | 4/98 | 80/18493 | 0.00086165 | 0.010995881 | 0.00785453 | APOE/GAPDH/HSPA5/CALM2 | 4 |
| GO:0051092 | positive regulation of NF-kappaB transcription factor activity | 4/98 | 146/18493 | 0.000870363 | 0.010995881 | 0.00785453 | S100A8/CX3CR1/ITGB2/UBC/S100A8 | 4 |
| GO:0071674 | mononuclear cell migration | 4/98 | 85/18493 | 0.001108106 | 0.012880809 | 0.00200963 | DUSP1/CCL2/C3AR1/IAIF1 | 4 |
| GO:0001894 | tissue homeostasis | 9/98 | 221/18493 | 0.001148546 | 0.013367794 | 0.009548824 | SPPI/ACTB/LYZ/CSF1R/ACTG1/B2M | 9 |
| GO:0034447 | very-low-density lipoprotein particle clearance | 2/98 | 10/18493 | 0.001216717 | 0.013675682 | 0.009768753 | APOE/APOC1 | 2 |
| GO:1300272 | negative regulation of long-term synaptic potentiation | 2/98 | 10/18493 | 0.001216717 | 0.013675682 | 0.009768753 | APOE/C3/C2 | 2 |
| GO:0050878 | regulation of body fluid levels | 9/98 | 493/18493 | 0.001218517 | 0.013675682 | 0.009768753 | ACTB/FCER1/G/APOE/A2M/F13A1/ACTG1/VAMP8/ANXA5/H3F3B | 9 |
| GO:0006458 | de novo protein folding | 3/98 | 40/18493 | 0.001236739 | 0.013818497 | 0.009807768 | CD74/HSPA5/HSPA5 | 3 |
| GO:0051051 | negative regulation of transport | 9/98 | 455/18493 | 0.001253207 | 0.013853763 | 0.009917393 | CD74/SGRN/TMSB4X/TMBIM6/VAMP8/TNFRSF1B/ANXA5/APOC1/CALM2 | 9 |
| GO:0030574 | collagen catabolic process | 3/98 | 41/18493 | 0.001329276 | 0.014525666 | 0.010378696 | CTSS/CTSS/CTSS | 3 |
| GO:0051602 | response to electrical stimulus | 3/98 | 41/18493 | 0.001329276 | 0.014525666 | 0.010378696 | CD14/ITGB2/IAIF1 | 3 |
| GO:0051047 | positive regulation of secretion | 8/98 | 420/18493 | 0.001371471 | 0.01486114 | 0.010689576 | SPPI/CD14/FCER1/G/CSF1R/GAPDH/VAMP8/ITGB2/S100A8 | 8 |
| GO:0001666 | response to hypoxia | 7/98 | 314/18493 | 0.001407916 | 0.015127045 | 0.010805484 | RHOA/CYBB/ENO1/TMBIM6/UBC/EGR1/PGK1 | 7 |
| GO:0001558 | regulation of cell growth | 8/98 | 416/18493 | 0.001565321 | 0.017103796 | 0.012217508 | SPPI/APOE/S100A8/RHOA/ENO1/S100A8/CXCL16/H3F3B | 8 |
| GO:0026986 | negative regulation of leukocyte migration | 3/98 | 45/18493 | 0.001742576 | 0.017336116 | 0.012383458 | DUSP1/CCL2/PAD2 | 3 |
| GO:0030307 | positive regulation of cell growth | 2/98 | 163/18493 | 0.001756998 | 0.017336116 | 0.012383458 | S100A8/RHOA/S100A8/CXCL16/H3F3B | 2 |
| GO:0061450 | trophoblast cell migration | 2/98 | 12/18493 | 0.001772228 | 0.017336116 | 0.012383458 | ARHGDB/TMP1 | 2 |
| GO:1301163 | regulation of trophoblast cell migration | 2/98 | 12/18493 | 0.001772228 | 0.017336116 | 0.012383458 | ARHGDB/TMP1 | 2 |
| GO:0069884 | ER-nucleus signaling pathway | 3/98 | 46/18493 | 0.001857034 | 0.017819024 | 0.012723407 | CXCL8/CXCL8/HSPA5 | 3 |
| GO:0045185 | maintenance of protein location | 4/98 | 104/18493 | 0.002274245 | 0.020790734 | 0.014851146 | TMSB10/SGRN/TMSB4X/HSPA5 | 4 |
| GO:0042089 | cytokine biosynthetic process | 4/98 | 105/18493 | 0.002354827 | 0.021331301 | 0.015237282 | CX3CR1/CYBB/ZFP36/EGR1 | 4 |
| GO:0006020 | response to fungus | 3/98 | 51/18493 | 0.002499383 | 0.021712117 | 0.015509304 | GAPDH/S100A8/S100A8 | 3 |
| GO:0070482 | response to oxygen levels | 7/98 | 349/18493 | 0.002557828 | 0.021946689 | 0.015676863 | RHOA/CYBB/ENO1/TMBIM6/UBC/EGR1/PGK1 | 7 |
| GO:0043270 | positive regulation of ion transport | 6/98 | 260/18493 | 0.002609912 | 0.022317412 | | | |