**Table S3 GSEA results showing all gene sets which displayed A) decreased and B) increased expression in hESC-VCMs relative to hF-VCMs.** FDR indicates the false discovery date and FDR<0.05 was considered significant. Size = number of genes present within gene sets.

A

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| NAME | SIZE | FDR q-val |
| MITOTIC\_PROMETAPHASE(GO-0000236) | 68 | 0 |
| M\_PHASE\_OF\_MITOTIC\_CELL\_CYCLE(GO-0000087) | 133 | 0 |
| MITOSIS(GO-0007067) | 127 | 0 |
| CELLULAR\_RESPIRATION(GO-0045333) | 105 | 0 |
| ACETYL-COA\_METABOLIC\_PROCESS(GO-0006084) | 25 | 0 |
| AEROBIC\_RESPIRATION(GO-0009060) | 30 | 0 |
| STRIATED\_MUSCLE\_CONTRACTION(GO-0006941) | 27 | 0 |
| ELECTRON\_TRANSPORT\_CHAIN(GO-0022900) | 78 | 0 |
| RESPIRATORY\_ELECTRON\_TRANSPORT\_CHAIN(GO-0022904) | 78 | 0 |
| REGULATION\_OF\_CHROMOSOME\_SEGREGATION(GO-0051983) | 17 | 0 |
| TRICARBOXYLIC\_ACID\_CYCLE(GO-0006099) | 20 | 0 |
| MITOTIC\_CELL\_CYCLE(GO-0000278) | 389 | 0 |
| MUSCLE\_CONTRACTION(GO-0006936) | 135 | 0 |
| DNA\_STRAND\_ELONGATION(GO-0022616) | 27 | 4.55E-05 |
| MUSCLE\_FILAMENT\_SLIDING(GO-0030049) | 34 | 1.66E-04 |
| DNA\_STRAND\_ELONGATION\_INVOLVED\_IN\_DNA\_REPLICATION(GO-0006271) | 25 | 1.94E-04 |
| ACTIN-MYOSIN\_FILAMENT\_SLIDING(GO-0033275) | 34 | 2.56E-04 |
| SPINDLE\_CHECKPOINT(GO-0031577) | 32 | 3.82E-04 |
| CHROMOSOME\_SEGREGATION(GO-0007059) | 61 | 3.62E-04 |
| DNA-DEPENDENT\_DNA\_REPLICATION(GO-0006261) | 46 | 3.75E-04 |
| MUSCLE\_SYSTEM\_PROCESS(GO-0003012) | 146 | 6.22E-04 |
| SISTER\_CHROMATID\_SEGREGATION(GO-0000819) | 25 | 7.37E-04 |
| MITOTIC\_SISTER\_CHROMATID\_SEGREGATION(GO-0000070) | 24 | 0.001011 |
| MICROTUBULE\_CYTOSKELETON\_ORGANIZATION(GO-0000226) | 107 | 9.96E-04 |
| ACTIN\_FILAMENT-BASED\_MOVEMENT(GO-0030048) | 43 | 0.001587 |
| CELLULAR\_RESPONSE\_TO\_REACTIVE\_OXYGEN\_SPECIES(GO-0034614) | 36 | 0.001599 |
| CELLULAR\_RESPONSE\_TO\_HYDROGEN\_PEROXIDE(GO-0070301) | 24 | 0.002145 |
| SPINDLE\_ASSEMBLY\_CHECKPOINT(GO-0071173) | 27 | 0.002114 |
| MITOTIC\_CELL\_CYCLE\_SPINDLE\_ASSEMBLY\_CHECKPOINT(GO-0007094) | 26 | 0.00213 |
| MITOTIC\_CELL\_CYCLE\_SPINDLE\_CHECKPOINT(GO-0071174) | 29 | 0.002393 |
| MITOTIC\_RECOMBINATION(GO-0006312) | 26 | 0.002517 |
| MICROTUBULE\_ORGANIZING\_CENTER\_ORGANIZATION(GO-0031023) | 40 | 0.002497 |
| DNA\_PACKAGING(GO-0006323) | 41 | 0.002632 |
| HEART\_CONTRACTION(GO-0060047) | 15 | 0.003057 |
| NEGATIVE\_REGULATION\_OF\_MITOSIS(GO-0045839) | 32 | 0.003255 |
| CARDIAC\_MUSCLE\_TISSUE\_MORPHOGENESIS(GO-0055008) | 27 | 0.00332 |
| MUSCLE\_ORGAN\_MORPHOGENESIS(GO-0048644) | 29 | 0.003281 |
| TELOMERE\_MAINTENANCE\_VIA\_SEMI-CONSERVATIVE\_REPLICATION(GO-0032201) | 20 | 0.003228 |
| GENERATION\_OF\_PRECURSOR\_METABOLITES\_AND\_ENERGY(GO-0006091) | 273 | 0.003339 |
| BRANCHED\_CHAIN\_FAMILY\_AMINO\_ACID\_CATABOLIC\_PROCESS(GO-0009083) | 17 | 0.003317 |
| DETERMINATION\_OF\_HEART\_LEFT-RIGHT\_ASYMMETRY(GO-0061371) | 24 | 0.003436 |
| CENTROSOME\_ORGANIZATION(GO-0051297) | 35 | 0.003428 |
| CARBOXYLIC\_ACID\_CATABOLIC\_PROCESS(GO-0046395) | 118 | 0.003757 |
| EMBRYONIC\_HEART\_TUBE\_MORPHOGENESIS(GO-0003143) | 23 | 0.003899 |
| TELOMERE\_MAINTENANCE\_VIA\_RECOMBINATION(GO-0000722) | 22 | 0.003813 |
| DNA\_REPLICATION(GO-0006260) | 94 | 0.003975 |
| MICROTUBULE-BASED\_PROCESS(GO-0007017) | 143 | 0.004116 |
| ENERGY\_DERIVATION\_BY\_OXIDATION\_OF\_ORGANIC\_COMPOUNDS(GO-0015980) | 225 | 0.004225 |
| MUSCLE\_TISSUE\_MORPHOGENESIS(GO-0060415) | 29 | 0.004293 |
| MITOTIC\_SPINDLE\_ORGANIZATION(GO-0007052) | 20 | 0.005069 |
| CENTROSOME\_CYCLE(GO-0007098) | 23 | 0.005822 |
| STEROID\_HORMONE\_MEDIATED\_SIGNALING\_PATHWAY(GO-0043401) | 15 | 0.006183 |
| REGULATION\_OF\_CELL\_CYCLE\_PROCESS(GO-0010564) | 305 | 0.006386 |
| HYDROGEN\_PEROXIDE\_METABOLIC\_PROCESS(GO-0042743) | 15 | 0.007155 |
| INTERPHASE\_OF\_MITOTIC\_CELL\_CYCLE(GO-0051329) | 258 | 0.008077 |
| POSITIVE\_REGULATION\_OF\_CELL-SUBSTRATE\_ADHESION(GO-0010811) | 18 | 0.008123 |
| VENTRICULAR\_CARDIAC\_MUSCLE\_TISSUE\_MORPHOGENESIS(GO-0055010) | 20 | 0.008159 |
| HEART\_DEVELOPMENT(GO-0007507) | 148 | 0.009074 |
| HEART\_LOOPING(GO-0001947) | 22 | 0.009037 |
| MUSCLE\_FIBER\_DEVELOPMENT(GO-0048747) | 18 | 0.009429 |
| RESPONSE\_TO\_HYDROGEN\_PEROXIDE(GO-0042542) | 30 | 0.009565 |
| HISTONE\_EXCHANGE(GO-0043486) | 17 | 0.009421 |
| CELLULAR\_LIPID\_CATABOLIC\_PROCESS(GO-0044242) | 69 | 0.00985 |
| REGULATION\_OF\_MUSCLE\_CONTRACTION(GO-0006937) | 41 | 0.009775 |
| INTERPHASE(GO-0051325) | 262 | 0.009856 |
| M-G1\_TRANSITION\_OF\_MITOTIC\_CELL\_CYCLE(GO-0000216) | 70 | 0.011359 |
| FATTY\_ACID\_OXIDATION(GO-0019395) | 41 | 0.011698 |
| CHROMOSOME\_ORGANIZATION(GO-0051276) | 316 | 0.012103 |
| ATP-DEPENDENT\_CHROMATIN\_REMODELING(GO-0043044) | 19 | 0.012084 |
| FATTY\_ACID\_CATABOLIC\_PROCESS(GO-0009062) | 37 | 0.011955 |
| FATTY\_ACID\_TRANSPORT(GO-0015908) | 25 | 0.011938 |
| REGULATION\_OF\_STRIATED\_MUSCLE\_CONTRACTION(GO-0006942) | 20 | 0.012174 |
| ESTABLISHMENT\_OF\_CHROMOSOME\_LOCALIZATION(GO-0051303) | 15 | 0.012016 |
| EMBRYONIC\_HEART\_TUBE\_DEVELOPMENT(GO-0035050) | 26 | 0.012229 |
| FATTY\_ACID\_BETA-OXIDATION(GO-0006635) | 32 | 0.012613 |
| CELL\_CYCLE\_CHECKPOINT(GO-0000075) | 186 | 0.012498 |
| CYTOKINESIS(GO-0000910) | 58 | 0.013471 |
| REGULATION\_OF\_MITOTIC\_METAPHASE-ANAPHASE\_TRANSITION(GO-0030071) | 32 | 0.013346 |
| SPINDLE\_ORGANIZATION(GO-0007051) | 34 | 0.013226 |
| REGULATION\_OF\_CELL\_CYCLE\_ARREST(GO-0071156) | 205 | 0.013169 |
| CARDIAC\_MUSCLE\_TISSUE\_DEVELOPMENT(GO-0048738) | 47 | 0.013146 |
| DNA\_CONFORMATION\_CHANGE(GO-0071103) | 67 | 0.013937 |
| VASCULOGENESIS(GO-0001570) | 23 | 0.015183 |
| REGULATION\_OF\_MICROTUBULE-BASED\_PROCESS(GO-0032886) | 56 | 0.015345 |
| PROTEIN-DNA\_COMPLEX\_ASSEMBLY(GO-0065004) | 30 | 0.015245 |
| MUSCLE\_CELL\_DEVELOPMENT(GO-0055001) | 39 | 0.015487 |
| DNA\_RECOMBINATION(GO-0006310) | 81 | 0.016076 |
| RESPONSE\_TO\_REACTIVE\_OXYGEN\_SPECIES(GO-0000302) | 49 | 0.01667 |
| POSITIVE\_REGULATION\_OF\_CELL-MATRIX\_ADHESION(GO-0001954) | 16 | 0.016956 |
| HEART\_MORPHOGENESIS(GO-0003007) | 84 | 0.01681 |
| NUCLEOTIDE-EXCISION\_REPAIR\_\_DNA\_GAP\_FILLING(GO-0006297) | 19 | 0.016729 |
| REGULATION\_OF\_MICROTUBULE\_CYTOSKELETON\_ORGANIZATION(GO-0070507) | 48 | 0.018741 |
| ACTIVATION\_OF\_PROTEIN\_KINASE\_A\_ACTIVITY(GO-0034199) | 16 | 0.01873 |
| TRANSLATIONAL\_ELONGATION(GO-0006414) | 91 | 0.019484 |
| MUSCLE\_TISSUE\_DEVELOPMENT(GO-0060537) | 87 | 0.019412 |
| CENTROSOME\_DUPLICATION(GO-0051298) | 16 | 0.020953 |
| LIPID\_OXIDATION(GO-0034440) | 42 | 0.022546 |
| REGULATION\_OF\_CYTOKINESIS(GO-0032465) | 19 | 0.02263 |
| LIPID\_CATABOLIC\_PROCESS(GO-0016042) | 84 | 0.022471 |
| LONG-CHAIN\_FATTY\_ACID\_TRANSPORT(GO-0015909) | 21 | 0.022726 |
| CARDIAC\_VENTRICLE\_MORPHOGENESIS(GO-0003208) | 35 | 0.023027 |
| G1-S\_TRANSITION\_OF\_MITOTIC\_CELL\_CYCLE(GO-0000082) | 132 | 0.027002 |
| ACTOMYOSIN\_STRUCTURE\_ORGANIZATION(GO-0031032) | 22 | 0.029589 |
| MUSCLE\_ORGAN\_DEVELOPMENT(GO-0007517) | 103 | 0.033745 |
| REACTIVE\_OXYGEN\_SPECIES\_METABOLIC\_PROCESS(GO-0072593) | 42 | 0.035551 |
| POSITIVE\_REGULATION\_OF\_CELL\_DIVISION(GO-0051781) | 19 | 0.036732 |
| REGULATION\_OF\_ATPASE\_ACTIVITY(GO-0043462) | 21 | 0.037018 |
| CELL\_DIVISION(GO-0051301) | 73 | 0.038581 |
| STRIATED\_MUSCLE\_CELL\_DEVELOPMENT(GO-0055002) | 32 | 0.03848 |
| CARDIAC\_MUSCLE\_CELL\_DIFFERENTIATION(GO-0055007) | 20 | 0.040211 |
| CHROMATIN\_ASSEMBLY\_OR\_DISASSEMBLY(GO-0006333) | 43 | 0.039855 |
| S\_PHASE\_OF\_MITOTIC\_CELL\_CYCLE(GO-0000084) | 97 | 0.042255 |
| VIRAL\_TRANSCRIPTION(GO-0019083) | 81 | 0.042273 |
| DETERMINATION\_OF\_LEFT-RIGHT\_SYMMETRY(GO-0007368) | 35 | 0.042718 |
| TRANSLATIONAL\_TERMINATION(GO-0006415) | 83 | 0.045539 |
| PYRUVATE\_METABOLIC\_PROCESS(GO-0006090) | 21 | 0.045962 |
| DNA\_METABOLIC\_PROCESS(GO-0006259) | 396 | 0.04595 |
| CELLULAR\_PROTEIN\_COMPLEX\_DISASSEMBLY(GO-0043624) | 92 | 0.046882 |
| OXIDATION-REDUCTION\_PROCESS(GO-0055114) | 372 | 0.048087 |

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| NAME | SIZE | FDR q-val |
| CELLULAR\_RESPONSE\_TO\_TYPE\_I\_INTERFERON(GO-0071357) | 62 | 0 |
| RESPONSE\_TO\_TYPE\_I\_INTERFERON(GO-0034340) | 64 | 0 |
| TYPE\_I\_INTERFERON-MEDIATED\_SIGNALING\_PATHWAY(GO-0060337) | 62 | 0 |
| RESPONSE\_TO\_CYTOKINE\_STIMULUS(GO-0034097) | 314 | 0 |
| CELLULAR\_RESPONSE\_TO\_CYTOKINE\_STIMULUS(GO-0071345) | 272 | 0 |
| CYTOKINE-MEDIATED\_SIGNALING\_PATHWAY(GO-0019221) | 232 | 0 |
| INNATE\_IMMUNE\_RESPONSE(GO-0045087) | 324 | 0 |
| RESPONSE\_TO\_ENDOPLASMIC\_RETICULUM\_STRESS(GO-0034976) | 80 | 0 |
| REGULATION\_OF\_RESPONSE\_TO\_STRESS(GO-0080134) | 446 | 0 |
| REGULATION\_OF\_CYTOKINE\_PRODUCTION(GO-0001817) | 226 | 0 |
| RESPONSE\_TO\_INTERFERON-GAMMA(GO-0034341) | 88 | 0 |
| ENDOPLASMIC\_RETICULUM\_UNFOLDED\_PROTEIN\_RESPONSE(GO-0030968) | 71 | 0 |
| REGULATION\_OF\_I-KAPPAB\_KINASE-NF-KAPPAB\_CASCADE(GO-0043122) | 132 | 0 |
| RESPONSE\_TO\_BIOTIC\_STIMULUS(GO-0009607) | 206 | 0 |
| ACTIVATION\_OF\_SIGNALING\_PROTEIN\_ACTIVITY\_INVOLVED\_IN\_UNFOLDED\_PROTEIN\_RESPONSE(GO-0006987) | 61 | 0 |
| REGULATION\_OF\_WOUND\_HEALING(GO-0061041) | 53 | 0 |
| CELLULAR\_RESPONSE\_TO\_TOPOLOGICALLY\_INCORRECT\_PROTEIN(GO-0035967) | 76 | 0 |
| REGULATION\_OF\_CELL\_MIGRATION(GO-0030334) | 237 | 0 |
| NEGATIVE\_REGULATION\_OF\_SIGNAL\_TRANSDUCTION(GO-0009968) | 334 | 0 |
| NEGATIVE\_REGULATION\_OF\_IMMUNE\_SYSTEM\_PROCESS(GO-0002683) | 81 | 0 |
| REGULATION\_OF\_CYTOKINE\_BIOSYNTHETIC\_PROCESS(GO-0042035) | 52 | 0 |
| REGULATION\_OF\_BLOOD\_COAGULATION(GO-0030193) | 42 | 0 |
| POSITIVE\_REGULATION\_OF\_LOCOMOTION(GO-0040017) | 152 | 0 |
| REGULATION\_OF\_CYTOKINE-MEDIATED\_SIGNALING\_PATHWAY(GO-0001959) | 59 | 0 |
| CELLULAR\_RESPONSE\_TO\_INTERFERON-GAMMA(GO-0071346) | 76 | 0 |
| POSITIVE\_REGULATION\_OF\_I-KAPPAB\_KINASE-NF-KAPPAB\_CASCADE(GO-0043123) | 113 | 0 |
| REGULATION\_OF\_CHEMOTAXIS(GO-0050920) | 62 | 0 |
| RESPONSE\_TO\_VIRUS(GO-0009615) | 98 | 0 |
| SKELETAL\_SYSTEM\_DEVELOPMENT(GO-0001501) | 155 | 0 |
| POSITIVE\_REGULATION\_OF\_CELLULAR\_COMPONENT\_MOVEMENT(GO-0051272) | 154 | 0 |
| POSITIVE\_REGULATION\_OF\_CELL\_MOTILITY(GO-2000147) | 148 | 0 |
| POSITIVE\_REGULATION\_OF\_CELL\_MIGRATION(GO-0030335) | 145 | 0 |
| RESPONSE\_TO\_MOLECULE\_OF\_BACTERIAL\_ORIGIN(GO-0002237) | 69 | 0 |
| POSITIVE\_REGULATION\_OF\_CYTOKINE\_BIOSYNTHETIC\_PROCESS(GO-0042108) | 34 | 0 |
| REGULATION\_OF\_INTERLEUKIN-6\_PRODUCTION(GO-0032675) | 37 | 0 |
| ACTIVATION\_OF\_PRO-APOPTOTIC\_GENE\_PRODUCTS(GO-0008633) | 30 | 0 |
| CELLULAR\_RESPONSE\_TO\_MOLECULE\_OF\_BACTERIAL\_ORIGIN(GO-0071219) | 38 | 0 |
| REGULATION\_OF\_LOCOMOTION(GO-0040012) | 267 | 0 |
| RESPONSE\_TO\_UNFOLDED\_PROTEIN(GO-0006986) | 90 | 0 |
| POSITIVE\_REGULATION\_OF\_BEHAVIOR(GO-0048520) | 52 | 0 |
| OLIGOSACCHARIDE\_BIOSYNTHETIC\_PROCESS(GO-0009312) | 35 | 0 |
| NEGATIVE\_REGULATION\_OF\_PEPTIDASE\_ACTIVITY(GO-0010466) | 76 | 0 |
| POSITIVE\_REGULATION\_OF\_CHEMOTAXIS(GO-0050921) | 47 | 0 |
| REGULATION\_OF\_CELLULAR\_COMPONENT\_MOVEMENT(GO-0051270) | 266 | 0 |
| POSITIVE\_REGULATION\_OF\_NUCLEASE\_ACTIVITY(GO-0032075) | 63 | 2.57E-05 |
| NEGATIVE\_REGULATION\_OF\_ENDOPEPTIDASE\_ACTIVITY(GO-0010951) | 73 | 2.62E-05 |
| RESPONSE\_TO\_BACTERIUM(GO-0009617) | 103 | 2.68E-05 |
| POSITIVE\_REGULATION\_OF\_REACTIVE\_OXYGEN\_SPECIES\_METABOLIC\_PROCESS(GO-2000379) | 17 | 2.74E-05 |
| REGULATION\_OF\_CELL\_MOTILITY(GO-2000145) | 254 | 2.80E-05 |
| POSITIVE\_REGULATION\_OF\_LEUKOCYTE\_CHEMOTAXIS(GO-0002690) | 37 | 2.86E-05 |
| INFLAMMATORY\_RESPONSE(GO-0006954) | 137 | 6.89E-05 |
| POSITIVE\_REGULATION\_OF\_LEUKOCYTE\_MIGRATION(GO-0002687) | 41 | 7.01E-05 |
| POSITIVE\_REGULATION\_OF\_CYTOKINE\_PRODUCTION(GO-0001819) | 116 | 7.14E-05 |
| NEGATIVE\_REGULATION\_OF\_HYDROLASE\_ACTIVITY(GO-0051346) | 136 | 7.27E-05 |
| REGULATION\_OF\_ENDOPEPTIDASE\_ACTIVITY(GO-0052548) | 156 | 7.41E-05 |
| CELLULAR\_RESPONSE\_TO\_LIPOPOLYSACCHARIDE(GO-0071222) | 34 | 7.55E-05 |
| EPIDERMIS\_DEVELOPMENT(GO-0008544) | 93 | 7.70E-05 |
| INTERFERON-GAMMA-MEDIATED\_SIGNALING\_PATHWAY(GO-0060333) | 68 | 8.95E-05 |
| ANTI-APOPTOSIS(GO-0006916) | 151 | 1.49E-04 |
| POSITIVE\_REGULATION\_OF\_SIGNAL\_TRANSDUCTION(GO-0009967) | 452 | 1.49E-04 |
| REGULATION\_OF\_PROTEIN\_SECRETION(GO-0050708) | 73 | 1.51E-04 |
| POSITIVE\_REGULATION\_OF\_STRESS-ACTIVATED\_PROTEIN\_KINASE\_SIGNALING\_CASCADE(GO-0070304) | 33 | 1.51E-04 |
| NEGATIVE\_REGULATION\_OF\_CYTOKINE\_PRODUCTION(GO-0001818) | 80 | 1.53E-04 |
| DOLICHOL-LINKED\_OLIGOSACCHARIDE\_BIOSYNTHETIC\_PROCESS(GO-0006488) | 29 | 1.54E-04 |
| CELL\_MOTILITY(GO-0048870) | 343 | 1.55E-04 |
| REGULATION\_OF\_PEPTIDASE\_ACTIVITY(GO-0052547) | 163 | 1.58E-04 |
| NEGATIVE\_REGULATION\_OF\_APOPTOTIC\_PROCESS(GO-0043066) | 336 | 1.60E-04 |
| REGULATION\_OF\_BEHAVIOR(GO-0050795) | 77 | 1.62E-04 |
| NEGATIVE\_REGULATION\_OF\_TYPE\_I\_INTERFERON\_PRODUCTION(GO-0032480) | 27 | 1.65E-04 |
| NEGATIVE\_REGULATION\_OF\_PROGRAMMED\_CELL\_DEATH(GO-0043069) | 337 | 1.68E-04 |
| RESPONSE\_TO\_LIPOPOLYSACCHARIDE(GO-0032496) | 59 | 1.84E-04 |
| REGULATION\_OF\_INTRACELLULAR\_PROTEIN\_KINASE\_CASCADE(GO-0010627) | 377 | 2.19E-04 |
| NEGATIVE\_REGULATION\_OF\_IMMUNE\_RESPONSE(GO-0050777) | 25 | 2.28E-04 |
| NEUTRAL\_AMINO\_ACID\_TRANSPORT(GO-0015804) | 16 | 2.31E-04 |
| NEGATIVE\_REGULATION\_OF\_COAGULATION(GO-0050819) | 28 | 2.34E-04 |
| REGULATION\_OF\_INNATE\_IMMUNE\_RESPONSE(GO-0045088) | 166 | 2.78E-04 |
| RESPONSE\_TO\_INTERLEUKIN-1(GO-0070555) | 38 | 2.93E-04 |
| REGULATION\_OF\_INFLAMMATORY\_RESPONSE(GO-0050727) | 63 | 2.97E-04 |
| POSITIVE\_REGULATION\_OF\_PROTEIN\_TRANSPORT(GO-0051222) | 92 | 3.01E-04 |
| POSITIVE\_REGULATION\_OF\_NF-KAPPAB\_TRANSCRIPTION\_FACTOR\_ACTIVITY(GO-0051092) | 82 | 3.05E-04 |
| CELL\_MIGRATION(GO-0016477) | 319 | 3.09E-04 |
| LEUKOCYTE\_MIGRATION(GO-0050900) | 152 | 3.48E-04 |
| NEGATIVE\_REGULATION\_OF\_BLOOD\_COAGULATION(GO-0030195) | 26 | 3.53E-04 |
| CHEMOTAXIS(GO-0006935) | 380 | 3.60E-04 |
| VESICLE\_TARGETING\_\_TO\_\_FROM\_OR\_WITHIN\_GOLGI(GO-0048199) | 20 | 3.87E-04 |
| POSITIVE\_REGULATION\_OF\_INTRACELLULAR\_PROTEIN\_KINASE\_CASCADE(GO-0010740) | 260 | 4.35E-04 |
| POSITIVE\_REGULATION\_OF\_TRANSCRIPTION\_FACTOR\_IMPORT\_INTO\_NUCLEUS(GO-0042993) | 21 | 4.40E-04 |
| NEGATIVE\_REGULATION\_OF\_CELL\_DEATH(GO-0060548) | 345 | 4.45E-04 |
| LIPOPOLYSACCHARIDE-MEDIATED\_SIGNALING\_PATHWAY(GO-0031663) | 17 | 4.69E-04 |
| REGULATION\_OF\_CELL\_ADHESION\_MEDIATED\_BY\_INTEGRIN(GO-0033628) | 24 | 4.75E-04 |
| EXTRACELLULAR\_MATRIX\_ORGANIZATION(GO-0030198) | 40 | 5.50E-04 |
| CELL\_MORPHOGENESIS\_INVOLVED\_IN\_DIFFERENTIATION(GO-0000904) | 356 | 5.72E-04 |
| TRANSFERRIN\_TRANSPORT(GO-0033572) | 29 | 6.09E-04 |
| POSITIVE\_REGULATION\_OF\_SEQUENCE-SPECIFIC\_DNA\_BINDING\_TRANSCRIPTION\_FACTOR\_ACTIVITY(GO-0051091) | 135 | 6.38E-04 |
| EXTRACELLULAR\_STRUCTURE\_ORGANIZATION(GO-0043062) | 40 | 6.45E-04 |
| REGULATION\_OF\_CELL\_PROJECTION\_ASSEMBLY(GO-0060491) | 28 | 6.45E-04 |
| POSITIVE\_REGULATION\_OF\_SECRETION(GO-0051047) | 102 | 6.52E-04 |
| POSITIVE\_REGULATION\_OF\_STRESS-ACTIVATED\_MAPK\_CASCADE(GO-0032874) | 32 | 6.59E-04 |
| RESPONSE\_TO\_DSRNA(GO-0043331) | 16 | 7.85E-04 |
| POSITIVE\_REGULATION\_OF\_INFLAMMATORY\_RESPONSE(GO-0050729) | 26 | 8.04E-04 |
| POSITIVE\_REGULATION\_OF\_OXIDOREDUCTASE\_ACTIVITY(GO-0051353) | 26 | 8.76E-04 |
| POSITIVE\_REGULATION\_OF\_JNK\_CASCADE(GO-0046330) | 28 | 8.85E-04 |
| REGULATION\_OF\_CELL-CELL\_ADHESION(GO-0022407) | 45 | 8.98E-04 |
| REGULATION\_OF\_VESICLE-MEDIATED\_TRANSPORT(GO-0060627) | 114 | 9.06E-04 |
| REGULATION\_OF\_PROTEOLYSIS(GO-0030162) | 85 | 9.52E-04 |
| POSITIVE\_REGULATION\_OF\_PROTEIN\_IMPORT\_INTO\_NUCLEUS(GO-0042307) | 38 | 9.70E-04 |
| REGULATION\_OF\_JNK\_CASCADE(GO-0046328) | 75 | 9.77E-04 |
| REGULATION\_OF\_SEQUENCE-SPECIFIC\_DNA\_BINDING\_TRANSCRIPTION\_FACTOR\_ACTIVITY(GO-0051090) | 218 | 9.79E-04 |
| POSITIVE\_REGULATION\_OF\_NUCLEOCYTOPLASMIC\_TRANSPORT(GO-0046824) | 44 | 9.86E-04 |
| POSITIVE\_REGULATION\_OF\_ENDOCYTOSIS(GO-0045807) | 34 | 0.001004 |
| BONE\_DEVELOPMENT(GO-0060348) | 34 | 0.001007 |
| NEGATIVE\_REGULATION\_OF\_CELL\_ADHESION(GO-0007162) | 51 | 0.00101 |
| REGULATION\_OF\_VASCULAR\_ENDOTHELIAL\_GROWTH\_FACTOR\_PRODUCTION(GO-0010574) | 16 | 0.001015 |
| DEFENSE\_RESPONSE\_TO\_VIRUS(GO-0051607) | 29 | 0.001024 |
| REGULATION\_OF\_CELL\_PROJECTION\_ORGANIZATION(GO-0031344) | 111 | 0.001029 |
| PEPTIDE\_TRANSPORT(GO-0015833) | 18 | 0.001032 |
| NEGATIVE\_REGULATION\_OF\_VIRAL\_REPRODUCTION(GO-0048525) | 17 | 0.001057 |
| NEGATIVE\_REGULATION\_OF\_CELL\_MIGRATION(GO-0030336) | 71 | 0.00107 |
| CELL\_MORPHOGENESIS(GO-0000902) | 417 | 0.001098 |
| NEGATIVE\_REGULATION\_OF\_RESPONSE\_TO\_CYTOKINE\_STIMULUS(GO-0060761) | 17 | 0.001106 |
| REGULATION\_OF\_SECRETION(GO-0051046) | 227 | 0.001108 |
| ACTIVATION\_OF\_INNATE\_IMMUNE\_RESPONSE(GO-0002218) | 92 | 0.001121 |
| NEGATIVE\_REGULATION\_OF\_CELLULAR\_COMPONENT\_MOVEMENT(GO-0051271) | 78 | 0.001188 |
| REGULATION\_OF\_PROTEIN\_TRANSPORT(GO-0051223) | 156 | 0.001254 |
| RESPONSE\_TO\_GLUCOSE\_STIMULUS(GO-0009749) | 26 | 0.001254 |
| GOLGI\_VESICLE\_TRANSPORT(GO-0048193) | 102 | 0.001264 |
| CELL\_ACTIVATION(GO-0001775) | 302 | 0.001274 |
| REGULATION\_OF\_ENDOCYTOSIS(GO-0030100) | 70 | 0.001295 |
| REGULATION\_OF\_MAP\_KINASE\_ACTIVITY(GO-0043405) | 151 | 0.001316 |
| SENSORY\_ORGAN\_DEVELOPMENT(GO-0007423) | 109 | 0.001326 |
| POSITIVE\_REGULATION\_OF\_NITRIC\_OXIDE\_BIOSYNTHETIC\_PROCESS(GO-0045429) | 15 | 0.001326 |
| LEUKOCYTE\_ACTIVATION(GO-0045321) | 119 | 0.001335 |
| INNATE\_IMMUNE\_RESPONSE-ACTIVATING\_SIGNAL\_TRANSDUCTION(GO-0002758) | 91 | 0.001355 |
| NEGATIVE\_REGULATION\_OF\_VIRAL\_GENOME\_REPLICATION(GO-0045071) | 17 | 0.001365 |
| NEGATIVE\_REGULATION\_OF\_CELL\_MOTILITY(GO-2000146) | 73 | 0.001384 |
| GLYCOPROTEIN\_METABOLIC\_PROCESS(GO-0009100) | 195 | 0.001403 |
| REGULATION\_OF\_CELL\_MORPHOGENESIS(GO-0022604) | 152 | 0.00145 |
| DIGESTIVE\_TRACT\_DEVELOPMENT(GO-0048565) | 34 | 0.001526 |
| CELL\_AGING(GO-0007569) | 33 | 0.001528 |
| POSITIVE\_REGULATION\_OF\_INTERLEUKIN-8\_PRODUCTION(GO-0032757) | 16 | 0.001539 |
| REGULATION\_OF\_DEFENSE\_RESPONSE\_TO\_VIRUS(GO-0050688) | 47 | 0.001543 |
| POSITIVE\_REGULATION\_OF\_INNATE\_IMMUNE\_RESPONSE(GO-0045089) | 112 | 0.00155 |
| REGULATION\_OF\_STRESS-ACTIVATED\_MAPK\_CASCADE(GO-0032872) | 87 | 0.001554 |
| POST-TRANSLATIONAL\_PROTEIN\_MODIFICATION(GO-0043687) | 160 | 0.001561 |
| PATTERN\_RECOGNITION\_RECEPTOR\_SIGNALING\_PATHWAY(GO-0002221) | 88 | 0.001563 |
| NEGATIVE\_REGULATION\_OF\_ENDOTHELIAL\_CELL\_PROLIFERATION(GO-0001937) | 18 | 0.001569 |
| NEGATIVE\_REGULATION\_OF\_PROTEIN\_KINASE\_ACTIVITY(GO-0006469) | 91 | 0.001618 |
| RESPONSE\_TO\_NUTRIENT(GO-0007584) | 71 | 0.001629 |
| CELLULAR\_RESPONSE\_TO\_MECHANICAL\_STIMULUS(GO-0071260) | 43 | 0.001649 |
| NEGATIVE\_REGULATION\_OF\_CELL\_DIFFERENTIATION(GO-0045596) | 179 | 0.00166 |
| SECRETION\_BY\_CELL(GO-0032940) | 197 | 0.001751 |
| REGULATION\_OF\_INTERFERON-GAMMA\_PRODUCTION(GO-0032649) | 34 | 0.001751 |
| NEGATIVE\_REGULATION\_OF\_CELL-CELL\_ADHESION(GO-0022408) | 18 | 0.001762 |
| MORPHOGENESIS\_OF\_A\_BRANCHING\_EPITHELIUM(GO-0061138) | 31 | 0.001763 |
| REGULATION\_OF\_MAPK\_CASCADE(GO-0043408) | 191 | 0.001765 |
| RESPONSE\_TO\_EXTRACELLULAR\_STIMULUS(GO-0009991) | 123 | 0.001774 |
| REGULATION\_OF\_ACTIN\_POLYMERIZATION\_OR\_DEPOLYMERIZATION(GO-0008064) | 32 | 0.001799 |
| ANTERIOR-POSTERIOR\_PATTERN\_SPECIFICATION(GO-0009952) | 26 | 0.00181 |
| CELLULAR\_RESPONSE\_TO\_EXTRACELLULAR\_STIMULUS(GO-0031668) | 81 | 0.001845 |
| AXON\_GUIDANCE(GO-0007411) | 270 | 0.001865 |
| POSITIVE\_REGULATION\_OF\_INTRACELLULAR\_PROTEIN\_TRANSPORT(GO-0090316) | 46 | 0.001907 |
| POSITIVE\_REGULATION\_OF\_EXOCYTOSIS(GO-0045921) | 19 | 0.001911 |
| MORPHOGENESIS\_OF\_A\_BRANCHING\_STRUCTURE(GO-0001763) | 41 | 0.001981 |
| REGULATION\_OF\_REACTIVE\_OXYGEN\_SPECIES\_METABOLIC\_PROCESS(GO-2000377) | 34 | 0.001985 |
| REGULATION\_OF\_INTERLEUKIN-12\_PRODUCTION(GO-0032655) | 23 | 0.001992 |
| REGULATION\_OF\_PROTEIN\_CATABOLIC\_PROCESS(GO-0042176) | 87 | 0.001993 |
| NEGATIVE\_REGULATION\_OF\_KINASE\_ACTIVITY(GO-0033673) | 98 | 0.001996 |
| POSITIVE\_REGULATION\_OF\_MONONUCLEAR\_CELL\_PROLIFERATION(GO-0032946) | 51 | 0.001997 |
| RESPONSE\_TO\_TUMOR\_NECROSIS\_FACTOR(GO-0034612) | 53 | 0.002 |
| REGULATION\_OF\_CELL\_DIFFERENTIATION(GO-0045595) | 442 | 0.002005 |
| REGULATION\_OF\_T\_CELL\_PROLIFERATION(GO-0042129) | 47 | 0.002165 |
| TOLL-LIKE\_RECEPTOR\_SIGNALING\_PATHWAY(GO-0002224) | 79 | 0.00217 |
| AXONOGENESIS(GO-0007409) | 302 | 0.00228 |
| OLIGOSACCHARIDE\_METABOLIC\_PROCESS(GO-0009311) | 49 | 0.002282 |
| EMBRYONIC\_DIGESTIVE\_TRACT\_DEVELOPMENT(GO-0048566) | 17 | 0.002361 |
| ANTIGEN\_PROCESSING\_AND\_PRESENTATION\_OF\_PEPTIDE\_ANTIGEN(GO-0048002) | 89 | 0.002379 |
| LEUKOCYTE\_ACTIVATION\_INVOLVED\_IN\_IMMUNE\_RESPONSE(GO-0002366) | 31 | 0.002393 |
| AGING(GO-0007568) | 40 | 0.002521 |
| LIPOPROTEIN\_METABOLIC\_PROCESS(GO-0042157) | 56 | 0.002566 |
| NEURON\_PROJECTION\_MORPHOGENESIS(GO-0048812) | 316 | 0.002624 |
| REGULATION\_OF\_BLOOD\_VESSEL\_ENDOTHELIAL\_CELL\_MIGRATION(GO-0043535) | 27 | 0.002654 |
| SECRETION(GO-0046903) | 222 | 0.002676 |
| AMINO\_ACID\_TRANSPORT(GO-0006865) | 72 | 0.002762 |
| NEURON\_PROJECTION\_DEVELOPMENT(GO-0031175) | 340 | 0.002781 |
| REGULATION\_OF\_KINASE\_ACTIVITY(GO-0043549) | 427 | 0.002789 |
| INDUCTION\_OF\_APOPTOSIS(GO-0006917) | 267 | 0.002822 |
| REGULATION\_OF\_CELL\_ADHESION(GO-0030155) | 140 | 0.002828 |
| CARBOHYDRATE\_BIOSYNTHETIC\_PROCESS(GO-0016051) | 116 | 0.002841 |
| REGULATION\_OF\_PROTEIN\_KINASE\_ACTIVITY(GO-0045859) | 408 | 0.002847 |
| POSITIVE\_REGULATION\_OF\_INTRACELLULAR\_TRANSPORT(GO-0032388) | 51 | 0.00286 |
| CELLULAR\_RESPONSE\_TO\_INTERLEUKIN-1(GO-0071347) | 25 | 0.003038 |
| CELL\_CHEMOTAXIS(GO-0060326) | 72 | 0.003063 |
| REGULATION\_OF\_SMOOTH\_MUSCLE\_CELL\_MIGRATION(GO-0014910) | 17 | 0.003147 |
| REGULATION\_OF\_TOLL-LIKE\_RECEPTOR\_SIGNALING\_PATHWAY(GO-0034121) | 18 | 0.003163 |
| POSITIVE\_REGULATION\_OF\_PROGRAMMED\_CELL\_DEATH(GO-0043068) | 369 | 0.003239 |
| POSITIVE\_REGULATION\_OF\_PROTEIN\_SECRETION(GO-0050714) | 51 | 0.003242 |
| NEGATIVE\_REGULATION\_OF\_CATALYTIC\_ACTIVITY(GO-0043086) | 370 | 0.003252 |
| POSITIVE\_REGULATION\_OF\_T\_CELL\_PROLIFERATION(GO-0042102) | 34 | 0.003295 |
| DEVELOPMENT\_OF\_PRIMARY\_SEXUAL\_CHARACTERISTICS(GO-0045137) | 59 | 0.003345 |
| BRANCHING\_MORPHOGENESIS\_OF\_A\_TUBE(GO-0048754) | 35 | 0.003355 |
| NEGATIVE\_REGULATION\_OF\_LIPID\_TRANSPORT(GO-0032369) | 17 | 0.003371 |
| NEGATIVE\_REGULATION\_OF\_TRANSFERASE\_ACTIVITY(GO-0051348) | 106 | 0.003433 |
| PROTEIN\_KINASE\_B\_SIGNALING\_CASCADE(GO-0043491) | 15 | 0.003455 |
| REGULATION\_OF\_CYTOKINE\_PRODUCTION\_INVOLVED\_IN\_IMMUNE\_RESPONSE(GO-0002718) | 26 | 0.003484 |
| POSITIVE\_REGULATION\_OF\_APOPTOTIC\_PROCESS(GO-0043065) | 367 | 0.003551 |
| EAR\_DEVELOPMENT(GO-0043583) | 35 | 0.003617 |
| URETERIC\_BUD\_MORPHOGENESIS(GO-0060675) | 19 | 0.003709 |
| MESENCHYME\_DEVELOPMENT(GO-0060485) | 56 | 0.003799 |
| POSITIVE\_REGULATION\_OF\_LYMPHOCYTE\_PROLIFERATION(GO-0050671) | 50 | 0.003806 |
| ANTIGEN\_PROCESSING\_AND\_PRESENTATION\_OF\_PEPTIDE\_ANTIGEN\_VIA\_MHC\_CLASS\_I(GO-0002474) | 86 | 0.003902 |
| ADHERENS\_JUNCTION\_ORGANIZATION(GO-0034332) | 35 | 0.00392 |
| CELLULAR\_RESPONSE\_TO\_NUTRIENT\_LEVELS(GO-0031669) | 77 | 0.004069 |
| T\_CELL\_ACTIVATION(GO-0042110) | 60 | 0.004069 |
| NEGATIVE\_REGULATION\_OF\_INTRACELLULAR\_PROTEIN\_KINASE\_CASCADE(GO-0010741) | 68 | 0.004082 |
| URETERIC\_BUD\_DEVELOPMENT(GO-0001657) | 27 | 0.004216 |
| POSITIVE\_REGULATION\_OF\_CELL\_DEVELOPMENT(GO-0010720) | 71 | 0.004219 |
| NERVE\_DEVELOPMENT(GO-0021675) | 15 | 0.00422 |
| CELLULAR\_MEMBRANE\_ORGANIZATION(GO-0016044) | 309 | 0.00423 |
| RESPONSE\_TO\_MECHANICAL\_STIMULUS(GO-0009612) | 55 | 0.004234 |
| REGULATION\_OF\_EPITHELIAL\_TO\_MESENCHYMAL\_TRANSITION(GO-0010717) | 31 | 0.004371 |
| IMMUNE\_RESPONSE-REGULATING\_SIGNALING\_PATHWAY(GO-0002764) | 175 | 0.004385 |
| NEGATIVE\_REGULATION\_OF\_SEQUENCE-SPECIFIC\_DNA\_BINDING\_TRANSCRIPTION\_FACTOR\_ACTIVITY(GO-0043433) | 79 | 0.004399 |
| LIPID\_BIOSYNTHETIC\_PROCESS(GO-0008610) | 242 | 0.00445 |
| NEURON\_DEVELOPMENT(GO-0048666) | 370 | 0.004458 |
| NEGATIVE\_REGULATION\_OF\_EPITHELIAL\_CELL\_PROLIFERATION(GO-0050680) | 45 | 0.004478 |
| POSITIVE\_REGULATION\_OF\_BLOOD\_VESSEL\_ENDOTHELIAL\_CELL\_MIGRATION(GO-0043536) | 17 | 0.004567 |
| REGULATION\_OF\_CYSTEINE-TYPE\_ENDOPEPTIDASE\_ACTIVITY\_INVOLVED\_IN\_APOPTOTIC\_PROCESS(GO-0043281) | 114 | 0.004581 |
| EYE\_DEVELOPMENT(GO-0001654) | 82 | 0.004656 |
| REGULATION\_OF\_LEUKOCYTE\_MEDIATED\_CYTOTOXICITY(GO-0001910) | 17 | 0.004827 |
| POSITIVE\_REGULATION\_OF\_CELL\_PROLIFERATION(GO-0008284) | 328 | 0.005006 |
| SEX\_DIFFERENTIATION(GO-0007548) | 73 | 0.00511 |
| REGULATION\_OF\_CHEMOKINE\_PRODUCTION(GO-0032642) | 29 | 0.005241 |
| NEGATIVE\_REGULATION\_OF\_PROTEIN\_COMPLEX\_ASSEMBLY(GO-0031333) | 23 | 0.005359 |
| POSITIVE\_REGULATION\_OF\_T\_CELL\_ACTIVATION(GO-0050870) | 120 | 0.005366 |
| REGULATION\_OF\_T\_CELL\_ACTIVATION(GO-0050863) | 145 | 0.005376 |
| POSITIVE\_REGULATION\_OF\_IMMUNE\_RESPONSE(GO-0050778) | 230 | 0.005521 |
| REGULATION\_OF\_VIRAL\_GENOME\_REPLICATION(GO-0045069) | 24 | 0.005642 |
| STEROID\_METABOLIC\_PROCESS(GO-0008202) | 146 | 0.005735 |
| NEURON\_DIFFERENTIATION(GO-0030182) | 422 | 0.005836 |
| LEUKOCYTE\_CHEMOTAXIS(GO-0030595) | 49 | 0.005854 |
| RESPONSE\_TO\_CARBOHYDRATE\_STIMULUS(GO-0009743) | 30 | 0.005948 |
| GONAD\_DEVELOPMENT(GO-0008406) | 53 | 0.005983 |
| PROTEIN\_N-LINKED\_GLYCOSYLATION\_VIA\_ASPARAGINE(GO-0018279) | 77 | 0.006039 |
| APOPTOTIC\_MITOCHONDRIAL\_CHANGES(GO-0008637) | 18 | 0.006122 |
| POSITIVE\_REGULATION\_OF\_PROTEIN\_CATABOLIC\_PROCESS(GO-0045732) | 47 | 0.006124 |
| GLYCOPROTEIN\_BIOSYNTHETIC\_PROCESS(GO-0009101) | 166 | 0.006128 |
| TOLL-LIKE\_RECEPTOR\_4\_SIGNALING\_PATHWAY(GO-0034142) | 72 | 0.006142 |
| CELL\_DEATH(GO-0008219) | 436 | 0.006278 |
| REGULATION\_OF\_PROTEIN\_BINDING(GO-0043393) | 52 | 0.006343 |
| REGULATION\_OF\_INSULIN\_RECEPTOR\_SIGNALING\_PATHWAY(GO-0046626) | 16 | 0.006905 |
| POSITIVE\_REGULATION\_OF\_CYTOKINE\_SECRETION(GO-0050715) | 36 | 0.007057 |
| REPRODUCTIVE\_STRUCTURE\_DEVELOPMENT(GO-0048608) | 61 | 0.007061 |
| ANTIGEN\_PROCESSING\_AND\_PRESENTATION\_OF\_EXOGENOUS\_PEPTIDE\_ANTIGEN\_VIA\_MHC\_CLASS\_I\_\_TAP-DEPENDENT(GO-0002479) | 70 | 0.007085 |
| POSITIVE\_REGULATION\_OF\_PROTEIN\_KINASE\_ACTIVITY(GO-0045860) | 289 | 0.007144 |
| TRNA\_AMINOACYLATION\_FOR\_PROTEIN\_TRANSLATION(GO-0006418) | 33 | 0.007199 |
| POSITIVE\_REGULATION\_OF\_ANGIOGENESIS(GO-0045766) | 53 | 0.007204 |
| FEMALE\_PREGNANCY(GO-0007565) | 42 | 0.007211 |
| REGULATION\_OF\_ANGIOGENESIS(GO-0045765) | 97 | 0.007232 |
| PROTEIN\_N-LINKED\_GLYCOSYLATION(GO-0006487) | 81 | 0.007255 |
| INTRACELLULAR\_PROTEIN\_KINASE\_CASCADE(GO-0007243) | 259 | 0.007375 |
| POSITIVE\_REGULATION\_OF\_RECEPTOR-MEDIATED\_ENDOCYTOSIS(GO-0048260) | 21 | 0.007381 |
| VESICLE-MEDIATED\_TRANSPORT(GO-0016192) | 426 | 0.007383 |
| REGULATION\_OF\_CYSTEINE-TYPE\_ENDOPEPTIDASE\_ACTIVITY(GO-2000116) | 118 | 0.007398 |
| DIGESTIVE\_TRACT\_MORPHOGENESIS(GO-0048546) | 17 | 0.007405 |
| SIGNAL\_TRANSDUCTION\_BY\_P53\_CLASS\_MEDIATOR\_RESULTING\_IN\_INDUCTION\_OF\_APOPTOSIS(GO-0072332) | 19 | 0.007421 |
| REGULATION\_OF\_BINDING(GO-0051098) | 96 | 0.007449 |
| REGULATION\_OF\_ENDOTHELIAL\_CELL\_MIGRATION(GO-0010594) | 54 | 0.007472 |
| NEGATIVE\_REGULATION\_OF\_CANONICAL\_WNT\_RECEPTOR\_SIGNALING\_PATHWAY(GO-0090090) | 54 | 0.007567 |
| NEGATIVE\_REGULATION\_OF\_PROTEIN\_BINDING(GO-0032091) | 24 | 0.007619 |
| GLYCOSAMINOGLYCAN\_METABOLIC\_PROCESS(GO-0030203) | 36 | 0.007633 |
| REGULATION\_OF\_CELLULAR\_RESPONSE\_TO\_INSULIN\_STIMULUS(GO-1900076) | 17 | 0.007664 |
| ANTIGEN\_PROCESSING\_AND\_PRESENTATION\_OF\_EXOGENOUS\_PEPTIDE\_ANTIGEN\_VIA\_MHC\_CLASS\_I(GO-0042590) | 73 | 0.007776 |
| AMINE\_TRANSPORT(GO-0015837) | 87 | 0.007874 |
| REGULATION\_OF\_EXOCYTOSIS(GO-0017157) | 37 | 0.007949 |
| NEGATIVE\_REGULATION\_OF\_EPIDERMAL\_GROWTH\_FACTOR\_RECEPTOR\_SIGNALING\_PATHWAY(GO-0042059) | 35 | 0.007958 |
| PROTEIN\_LIPIDATION(GO-0006497) | 30 | 0.007987 |
| TOLL\_SIGNALING\_PATHWAY(GO-0008063) | 72 | 0.007993 |
| REGULATION\_OF\_ACTIN\_FILAMENT\_POLYMERIZATION(GO-0030833) | 26 | 0.008011 |
| CELL\_PROJECTION\_ORGANIZATION(GO-0030030) | 417 | 0.008012 |
| 'DE\_NOVO'\_PROTEIN\_FOLDING(GO-0006458) | 33 | 0.008454 |
| SYNAPSE\_ASSEMBLY(GO-0007416) | 27 | 0.008575 |
| ANTIGEN\_PROCESSING\_AND\_PRESENTATION(GO-0019882) | 92 | 0.008605 |
| REGULATION\_OF\_DNA\_DAMAGE\_RESPONSE\_\_SIGNAL\_TRANSDUCTION\_BY\_P53\_CLASS\_MEDIATOR(GO-0043516) | 20 | 0.008651 |
| NEUTROPHIL\_CHEMOTAXIS(GO-0030593) | 17 | 0.008654 |
| REGULATION\_OF\_BMP\_SIGNALING\_PATHWAY(GO-0030510) | 32 | 0.008695 |
| ANGIOGENESIS(GO-0001525) | 92 | 0.00873 |
| POSITIVE\_REGULATION\_OF\_TRANSCRIPTION\_FROM\_RNA\_POLYMERASE\_II\_PROMOTER(GO-0045944) | 337 | 0.00873 |
| POSITIVE\_REGULATION\_OF\_PEPTIDYL-SERINE\_PHOSPHORYLATION(GO-0033138) | 26 | 0.008745 |
| EYE\_MORPHOGENESIS(GO-0048592) | 44 | 0.008751 |
| PROGRAMMED\_CELL\_DEATH(GO-0012501) | 415 | 0.008824 |
| POSITIVE\_REGULATION\_OF\_KINASE\_ACTIVITY(GO-0033674) | 301 | 0.008841 |
| POSITIVE\_REGULATION\_OF\_CELL\_DEATH(GO-0010942) | 377 | 0.009345 |
| APOPTOTIC\_PROCESS(GO-0006915) | 412 | 0.009444 |
| REGULATION\_OF\_PLATELET\_ACTIVATION(GO-0010543) | 16 | 0.009599 |
| NEGATIVE\_REGULATION\_OF\_CELL\_PROLIFERATION(GO-0008285) | 301 | 0.009655 |
| REGULATION\_OF\_LYMPHOCYTE\_MIGRATION(GO-2000401) | 17 | 0.009667 |
| MACROMOLECULE\_GLYCOSYLATION(GO-0043413) | 147 | 0.00967 |
| TRANSFORMING\_GROWTH\_FACTOR\_BETA\_RECEPTOR\_SIGNALING\_PATHWAY(GO-0007179) | 48 | 0.00983 |
| MESENCHYMAL\_CELL\_DIFFERENTIATION(GO-0048762) | 46 | 0.009863 |
| POSITIVE\_REGULATION\_OF\_MAP\_KINASE\_ACTIVITY(GO-0043406) | 112 | 0.010055 |
| ACTIVATION\_OF\_CYSTEINE-TYPE\_ENDOPEPTIDASE\_ACTIVITY\_INVOLVED\_IN\_APOPTOTIC\_PROCESS(GO-0006919) | 61 | 0.010197 |
| POSITIVE\_REGULATION\_OF\_TRANSFERASE\_ACTIVITY(GO-0051347) | 307 | 0.010392 |
| REGULATION\_OF\_CELLULAR\_LOCALIZATION(GO-0060341) | 338 | 0.010675 |
| TRNA\_AMINOACYLATION(GO-0043039) | 34 | 0.010693 |
| PHOSPHOLIPID\_TRANSPORT(GO-0015914) | 15 | 0.010865 |
| LONG-CHAIN\_FATTY-ACYL-COA\_BIOSYNTHETIC\_PROCESS(GO-0035338) | 17 | 0.011223 |
| REGULATION\_OF\_T\_CELL\_DIFFERENTIATION(GO-0045580) | 39 | 0.011229 |
| NEGATIVE\_REGULATION\_OF\_PROTEIN\_PHOSPHORYLATION(GO-0001933) | 36 | 0.011566 |
| VESICLE\_LOCALIZATION(GO-0051648) | 45 | 0.011593 |
| NEGATIVE\_REGULATION\_OF\_WNT\_RECEPTOR\_SIGNALING\_PATHWAY(GO-0030178) | 71 | 0.011605 |
| MYD88-INDEPENDENT\_TOLL-LIKE\_RECEPTOR\_SIGNALING\_PATHWAY(GO-0002756) | 62 | 0.011688 |
| REGULATION\_OF\_PROTEIN\_LOCALIZATION(GO-0032880) | 195 | 0.011735 |
| ENDOCRINE\_PANCREAS\_DEVELOPMENT(GO-0031018) | 26 | 0.011744 |
| REGULATION\_OF\_ACTIN\_CYTOSKELETON\_ORGANIZATION(GO-0032956) | 86 | 0.011756 |
| VISUAL\_PERCEPTION(GO-0007601) | 90 | 0.011778 |
| PANCREAS\_DEVELOPMENT(GO-0031016) | 30 | 0.012594 |
| MAPK\_CASCADE(GO-0000165) | 134 | 0.012596 |
| PROTEIN\_GLYCOSYLATION(GO-0006486) | 146 | 0.012609 |
| VACUOLE\_ORGANIZATION(GO-0007033) | 28 | 0.012633 |
| GPI\_ANCHOR\_BIOSYNTHETIC\_PROCESS(GO-0006506) | 26 | 0.01287 |
| METANEPHROS\_DEVELOPMENT(GO-0001656) | 36 | 0.012897 |
| CELL\_MATURATION(GO-0048469) | 25 | 0.012912 |
| NEGATIVE\_REGULATION\_OF\_PHOSPHORYLATION(GO-0042326) | 50 | 0.012931 |
| NEGATIVE\_REGULATION\_OF\_PROTEIN\_SECRETION(GO-0050709) | 23 | 0.012993 |
| POSITIVE\_REGULATION\_OF\_INTERFERON-GAMMA\_PRODUCTION(GO-0032729) | 17 | 0.013068 |
| POSITIVE\_REGULATION\_OF\_SMOOTH\_MUSCLE\_CELL\_PROLIFERATION(GO-0048661) | 18 | 0.013217 |
| DNA\_DAMAGE\_RESPONSE\_\_SIGNAL\_TRANSDUCTION\_RESULTING\_IN\_INDUCTION\_OF\_APOPTOSIS(GO-0008630) | 25 | 0.013246 |
| REGULATION\_OF\_CELL\_GROWTH(GO-0001558) | 129 | 0.013282 |
| POSITIVE\_REGULATION\_OF\_ANTI-APOPTOSIS(GO-0045768) | 19 | 0.013309 |
| G1-S\_TRANSITION\_CHECKPOINT(GO-0071779) | 77 | 0.013594 |
| TOLL-LIKE\_RECEPTOR\_3\_SIGNALING\_PATHWAY(GO-0034138) | 59 | 0.013596 |
| POSITIVE\_REGULATION\_OF\_LIPID\_CATABOLIC\_PROCESS(GO-0050996) | 16 | 0.013599 |
| OSTEOBLAST\_DIFFERENTIATION(GO-0001649) | 30 | 0.013621 |
| REGULATION\_OF\_RECEPTOR\_ACTIVITY(GO-0010469) | 48 | 0.013644 |
| CELLULAR\_SENESCENCE(GO-0090398) | 20 | 0.013674 |
| POSITIVE\_REGULATION\_OF\_MAPK\_CASCADE(GO-0043410) | 101 | 0.013756 |
| REGULATION\_OF\_EMBRYONIC\_DEVELOPMENT(GO-0045995) | 34 | 0.013788 |
| POSITIVE\_REGULATION\_OF\_NEUROGENESIS(GO-0050769) | 43 | 0.013789 |
| 'DE\_NOVO'\_POSTTRANSLATIONAL\_PROTEIN\_FOLDING(GO-0051084) | 29 | 0.013813 |
| EXOCYTOSIS(GO-0006887) | 123 | 0.013929 |
| VESICLE\_ORGANIZATION(GO-0016050) | 41 | 0.013939 |
| POSITIVE\_REGULATION\_OF\_PROTEOLYSIS(GO-0045862) | 47 | 0.014148 |
| EMBRYONIC\_ORGAN\_DEVELOPMENT(GO-0048568) | 73 | 0.014304 |
| SENSORY\_PERCEPTION\_OF\_LIGHT\_STIMULUS(GO-0050953) | 90 | 0.014331 |
| REGULATION\_OF\_WNT\_RECEPTOR\_SIGNALING\_PATHWAY(GO-0030111) | 110 | 0.014444 |
| BRANCHING\_INVOLVED\_IN\_URETERIC\_BUD\_MORPHOGENESIS(GO-0001658) | 17 | 0.014445 |
| CHOLESTEROL\_EFFLUX(GO-0033344) | 20 | 0.014452 |
| FEMALE\_GONAD\_DEVELOPMENT(GO-0008585) | 15 | 0.014483 |
| JAK-STAT\_CASCADE(GO-0007259) | 43 | 0.014683 |
| NEGATIVE\_REGULATION\_OF\_CELL-SUBSTRATE\_ADHESION(GO-0010812) | 20 | 0.014716 |
| SIGNAL\_TRANSDUCTION\_BY\_P53\_CLASS\_MEDIATOR(GO-0072331) | 92 | 0.014809 |
| POSITIVE\_REGULATION\_OF\_ORGANELLE\_ORGANIZATION(GO-0010638) | 127 | 0.014856 |
| CELLULAR\_RESPONSE\_TO\_STARVATION(GO-0009267) | 36 | 0.014887 |
| EPITHELIAL\_CELL\_DIFFERENTIATION(GO-0030855) | 79 | 0.014971 |
| RETROGRADE\_VESICLE-MEDIATED\_TRANSPORT\_\_GOLGI\_TO\_ER(GO-0006890) | 18 | 0.014977 |
| NEGATIVE\_REGULATION\_OF\_SECRETION(GO-0051048) | 51 | 0.015229 |
| EMBRYONIC\_SKELETAL\_SYSTEM\_DEVELOPMENT(GO-0048706) | 26 | 0.015305 |
| AMINE\_METABOLIC\_PROCESS(GO-0009308) | 330 | 0.015318 |
| REGULATION\_OF\_NEURON\_PROJECTION\_DEVELOPMENT(GO-0010975) | 85 | 0.015521 |
| REGULATION\_OF\_AXONOGENESIS(GO-0050770) | 40 | 0.015684 |
| POSITIVE\_REGULATION\_OF\_ENDOPEPTIDASE\_ACTIVITY(GO-0010950) | 77 | 0.015713 |
| BLOOD\_VESSEL\_DEVELOPMENT(GO-0001568) | 144 | 0.015717 |
| REGULATION\_OF\_ADAPTIVE\_IMMUNE\_RESPONSE(GO-0002819) | 43 | 0.015732 |
| SERINE\_FAMILY\_AMINO\_ACID\_METABOLIC\_PROCESS(GO-0009069) | 17 | 0.015761 |
| STEROID\_BIOSYNTHETIC\_PROCESS(GO-0006694) | 73 | 0.01582 |
| SENSORY\_PERCEPTION(GO-0007600) | 175 | 0.015905 |
| MITOTIC\_CELL\_CYCLE\_G1-S\_TRANSITION\_CHECKPOINT(GO-0031575) | 75 | 0.016115 |
| BLOOD\_VESSEL\_MORPHOGENESIS(GO-0048514) | 125 | 0.016271 |
| CARTILAGE\_DEVELOPMENT(GO-0051216) | 39 | 0.016272 |
| GLYCOSAMINOGLYCAN\_BIOSYNTHETIC\_PROCESS(GO-0006024) | 26 | 0.016315 |
| REGULATION\_OF\_MORPHOGENESIS\_OF\_A\_BRANCHING\_STRUCTURE(GO-0060688) | 19 | 0.016352 |
| PROTEIN\_FOLDING(GO-0006457) | 82 | 0.016429 |
| NEGATIVE\_REGULATION\_OF\_MAP\_KINASE\_ACTIVITY(GO-0043407) | 39 | 0.016564 |
| DEFENSE\_RESPONSE\_TO\_BACTERIUM(GO-0042742) | 39 | 0.016592 |
| NEGATIVE\_REGULATION\_OF\_NF-KAPPAB\_TRANSCRIPTION\_FACTOR\_ACTIVITY(GO-0032088) | 38 | 0.01669 |
| TRANSMEMBRANE\_RECEPTOR\_PROTEIN\_SERINE-THREONINE\_KINASE\_SIGNALING\_PATHWAY(GO-0007178) | 79 | 0.016873 |
| REGULATION\_OF\_PROTEIN\_IMPORT\_INTO\_NUCLEUS(GO-0042306) | 70 | 0.016928 |
| WOUND\_HEALING(GO-0042060) | 458 | 0.016972 |
| CELLULAR\_RESPONSE\_TO\_TUMOR\_NECROSIS\_FACTOR(GO-0071356) | 38 | 0.016993 |
| ACUTE\_INFLAMMATORY\_RESPONSE(GO-0002526) | 18 | 0.017686 |
| LEUKOCYTE\_CELL-CELL\_ADHESION(GO-0007159) | 22 | 0.017694 |
| REGULATION\_OF\_BODY\_FLUID\_LEVELS(GO-0050878) | 455 | 0.017726 |
| REGULATION\_OF\_ACTIN\_FILAMENT-BASED\_PROCESS(GO-0032970) | 90 | 0.017753 |
| REGULATION\_OF\_TYPE\_I\_INTERFERON-MEDIATED\_SIGNALING\_PATHWAY(GO-0060338) | 29 | 0.017834 |
| REGULATION\_OF\_PHAGOCYTOSIS(GO-0050764) | 18 | 0.018049 |
| UROGENITAL\_SYSTEM\_DEVELOPMENT(GO-0001655) | 96 | 0.018068 |
| REGULATION\_OF\_PROTEIN\_COMPLEX\_DISASSEMBLY(GO-0043244) | 28 | 0.018183 |
| EPITHELIAL\_TO\_MESENCHYMAL\_TRANSITION(GO-0001837) | 26 | 0.018529 |
| POSITIVE\_REGULATION\_OF\_CYSTEINE-TYPE\_ENDOPEPTIDASE\_ACTIVITY\_INVOLVED\_IN\_APOPTOTIC\_PROCESS(GO-0043280) | 73 | 0.018563 |
| POSITIVE\_REGULATION\_OF\_BINDING(GO-0051099) | 41 | 0.018567 |
| NEGATIVE\_REGULATION\_OF\_CYSTEINE-TYPE\_ENDOPEPTIDASE\_ACTIVITY\_INVOLVED\_IN\_APOPTOTIC\_PROCESS(GO-0043154) | 39 | 0.018607 |
| POSITIVE\_REGULATION\_OF\_FIBROBLAST\_PROLIFERATION(GO-0048146) | 23 | 0.018635 |
| REGULATION\_OF\_INTRACELLULAR\_PROTEIN\_TRANSPORT(GO-0033157) | 83 | 0.018669 |
| REGULATION\_OF\_PROTEIN\_COMPLEX\_ASSEMBLY(GO-0043254) | 90 | 0.018718 |
| IRON\_ION\_TRANSPORT(GO-0006826) | 37 | 0.01883 |
| REGULATION\_OF\_FAT\_CELL\_DIFFERENTIATION(GO-0045598) | 26 | 0.019008 |
| GPI\_ANCHOR\_METABOLIC\_PROCESS(GO-0006505) | 27 | 0.019319 |
| OSSIFICATION(GO-0001503) | 58 | 0.019507 |
| CAMERA-TYPE\_EYE\_DEVELOPMENT(GO-0043010) | 60 | 0.019511 |
| UNSATURATED\_FATTY\_ACID\_BIOSYNTHETIC\_PROCESS(GO-0006636) | 27 | 0.019526 |
| RESPONSE\_TO\_STARVATION(GO-0042594) | 38 | 0.019548 |
| REGULATION\_OF\_EPITHELIAL\_CELL\_MIGRATION(GO-0010632) | 16 | 0.019571 |
| CENTRAL\_NERVOUS\_SYSTEM\_DEVELOPMENT(GO-0007417) | 206 | 0.01961 |
| CHOLESTEROL\_HOMEOSTASIS(GO-0042632) | 37 | 0.019805 |
| BLOOD\_COAGULATION(GO-0007596) | 421 | 0.019867 |
| POSITIVE\_REGULATION\_OF\_PROTEIN\_SERINE-THREONINE\_KINASE\_ACTIVITY(GO-0071902) | 140 | 0.02022 |
| TRIF-DEPENDENT\_TOLL-LIKE\_RECEPTOR\_SIGNALING\_PATHWAY(GO-0035666) | 58 | 0.020235 |
| RENAL\_SYSTEM\_DEVELOPMENT(GO-0072001) | 91 | 0.020267 |
| SIGNAL\_TRANSDUCTION\_IN\_RESPONSE\_TO\_DNA\_DAMAGE(GO-0042770) | 101 | 0.020413 |
| CAMERA-TYPE\_EYE\_MORPHOGENESIS(GO-0048593) | 33 | 0.020423 |
| LYMPHOCYTE\_MIGRATION(GO-0072676) | 15 | 0.020425 |
| POSITIVE\_REGULATION\_OF\_HYDROLASE\_ACTIVITY(GO-0051345) | 377 | 0.02064 |
| REGULATION\_OF\_G-PROTEIN\_COUPLED\_RECEPTOR\_PROTEIN\_SIGNALING\_PATHWAY(GO-0008277) | 52 | 0.020741 |
| EMBRYONIC\_ORGAN\_MORPHOGENESIS(GO-0048562) | 46 | 0.020803 |
| STEROL\_HOMEOSTASIS(GO-0055092) | 37 | 0.020955 |
| POSITIVE\_REGULATION\_OF\_CELL\_GROWTH(GO-0030307) | 47 | 0.021044 |
| C21-STEROID\_HORMONE\_METABOLIC\_PROCESS(GO-0008207) | 22 | 0.021544 |
| REGULATION\_OF\_CATENIN\_IMPORT\_INTO\_NUCLEUS(GO-0035412) | 15 | 0.021737 |
| NEGATIVE\_REGULATION\_OF\_G-PROTEIN\_COUPLED\_RECEPTOR\_PROTEIN\_SIGNALING\_PATHWAY(GO-0045744) | 21 | 0.021744 |
| POSITIVE\_REGULATION\_OF\_EPITHELIAL\_TO\_MESENCHYMAL\_TRANSITION(GO-0010718) | 19 | 0.021803 |
| MRNA\_CAPPING(GO-0006370) | 28 | 0.021852 |
| NEGATIVE\_REGULATION\_OF\_MAPK\_CASCADE(GO-0043409) | 42 | 0.022115 |
| POSITIVE\_REGULATION\_OF\_GROWTH(GO-0045927) | 63 | 0.022181 |
| INDUCTION\_OF\_APOPTOSIS\_BY\_INTRACELLULAR\_SIGNALS(GO-0008629) | 67 | 0.022183 |
| REGULATION\_OF\_OXIDOREDUCTASE\_ACTIVITY(GO-0051341) | 54 | 0.022184 |
| PLATELET\_ACTIVATION(GO-0030168) | 187 | 0.022188 |
| REGULATION\_OF\_CANONICAL\_WNT\_RECEPTOR\_SIGNALING\_PATHWAY(GO-0060828) | 80 | 0.0222 |
| DEVELOPMENTAL\_PROCESS\_INVOLVED\_IN\_REPRODUCTION(GO-0003006) | 117 | 0.022205 |
| C-TERMINAL\_PROTEIN\_LIPIDATION(GO-0006501) | 23 | 0.022215 |
| CELL-CELL\_JUNCTION\_ORGANIZATION(GO-0045216) | 84 | 0.022232 |
| POSITIVE\_REGULATION\_OF\_ADAPTIVE\_IMMUNE\_RESPONSE(GO-0002821) | 21 | 0.022264 |
| CELL\_PROLIFERATION(GO-0008283) | 307 | 0.022325 |
| VASCULATURE\_DEVELOPMENT(GO-0001944) | 155 | 0.022368 |
| HEMOSTASIS(GO-0007599) | 425 | 0.022432 |
| CALCIUM-MEDIATED\_SIGNALING(GO-0019722) | 30 | 0.02266 |
| OVULATION\_CYCLE(GO-0042698) | 17 | 0.023653 |
| LYSOSOME\_ORGANIZATION(GO-0007040) | 18 | 0.02366 |
| POSITIVE\_REGULATION\_OF\_INTERLEUKIN-12\_PRODUCTION(GO-0032735) | 16 | 0.023886 |
| CELL\_ADHESION(GO-0007155) | 251 | 0.023898 |
| CARBOHYDRATE\_METABOLIC\_PROCESS(GO-0005975) | 384 | 0.024059 |
| ANATOMICAL\_STRUCTURE\_FORMATION\_INVOLVED\_IN\_MORPHOGENESIS(GO-0048646) | 234 | 0.02407 |
| LEARNING(GO-0007612) | 21 | 0.024492 |
| ER\_TO\_GOLGI\_VESICLE-MEDIATED\_TRANSPORT(GO-0006888) | 21 | 0.024586 |
| POSITIVE\_REGULATION\_OF\_PEPTIDASE\_ACTIVITY(GO-0010952) | 82 | 0.024728 |
| POSITIVE\_REGULATION\_OF\_WNT\_RECEPTOR\_SIGNALING\_PATHWAY(GO-0030177) | 39 | 0.024729 |
| NEGATIVE\_REGULATION\_OF\_CELLULAR\_PROTEIN\_METABOLIC\_PROCESS(GO-0032269) | 185 | 0.02476 |
| DENDRITE\_DEVELOPMENT(GO-0016358) | 22 | 0.024764 |
| POSITIVE\_REGULATION\_OF\_ENDOTHELIAL\_CELL\_MIGRATION(GO-0010595) | 36 | 0.0248 |
| VESICLE\_TARGETING(GO-0006903) | 27 | 0.024837 |
| PLATELET\_DEGRANULATION(GO-0002576) | 79 | 0.024844 |
| PROTEIN\_TRIMERIZATION(GO-0070206) | 17 | 0.024863 |
| POSITIVE\_REGULATION\_OF\_PROTEASOMAL\_UBIQUITIN-DEPENDENT\_PROTEIN\_CATABOLIC\_PROCESS(GO-0032436) | 26 | 0.024943 |
| RESPONSE\_TO\_RETINOIC\_ACID(GO-0032526) | 44 | 0.025057 |
| CHOLESTEROL\_BIOSYNTHETIC\_PROCESS(GO-0006695) | 24 | 0.025185 |
| REGULATION\_OF\_LYMPHOCYTE\_DIFFERENTIATION(GO-0045619) | 44 | 0.025498 |
| REGULATION\_OF\_PROTEIN\_TYROSINE\_KINASE\_ACTIVITY(GO-0061097) | 34 | 0.025878 |
| NEGATIVE\_REGULATION\_OF\_PROTEIN\_SERINE-THREONINE\_KINASE\_ACTIVITY(GO-0071901) | 56 | 0.025891 |
| AMINE\_BIOSYNTHETIC\_PROCESS(GO-0009309) | 74 | 0.026101 |
| REGULATION\_OF\_PROTEASOMAL\_PROTEIN\_CATABOLIC\_PROCESS(GO-0061136) | 46 | 0.026355 |
| NEGATIVE\_REGULATION\_OF\_CYSTEINE-TYPE\_ENDOPEPTIDASE\_ACTIVITY(GO-2000117) | 41 | 0.026398 |
| POSITIVE\_REGULATION\_OF\_CELL-CELL\_ADHESION(GO-0022409) | 17 | 0.026432 |
| PROSTAGLANDIN\_METABOLIC\_PROCESS(GO-0006693) | 15 | 0.026461 |
| POLYSACCHARIDE\_METABOLIC\_PROCESS(GO-0005976) | 63 | 0.026503 |
| REGULATION\_OF\_INTERFERON-BETA\_PRODUCTION(GO-0032648) | 19 | 0.026514 |
| ICOSANOID\_BIOSYNTHETIC\_PROCESS(GO-0046456) | 24 | 0.02673 |
| DETECTION\_OF\_BIOTIC\_STIMULUS(GO-0009595) | 18 | 0.027231 |
| REGULATION\_OF\_EPIDERMAL\_GROWTH\_FACTOR\_RECEPTOR\_SIGNALING\_PATHWAY(GO-0042058) | 51 | 0.02729 |
| TRIGLYCERIDE\_BIOSYNTHETIC\_PROCESS(GO-0019432) | 28 | 0.027321 |
| POSITIVE\_REGULATION\_OF\_PROTEIN\_METABOLIC\_PROCESS(GO-0051247) | 394 | 0.027359 |
| NUCLEOTIDE-BINDING\_DOMAIN\_\_LEUCINE\_RICH\_REPEAT\_CONTAINING\_RECEPTOR\_SIGNALING\_PATHWAY(GO-0035872) | 39 | 0.0274 |
| BRAIN\_DEVELOPMENT(GO-0007420) | 124 | 0.027418 |
| POSITIVE\_REGULATION\_OF\_PHOSPHORYLATION(GO-0042327) | 175 | 0.027534 |
| PROTEOGLYCAN\_METABOLIC\_PROCESS(GO-0006029) | 24 | 0.027998 |
| REGULATION\_OF\_OSTEOCLAST\_DIFFERENTIATION(GO-0045670) | 18 | 0.028043 |
| REGULATION\_OF\_NEURON\_APOPTOSIS(GO-0043523) | 55 | 0.028047 |
| NEGATIVE\_REGULATION\_OF\_PROTEOLYSIS(GO-0045861) | 18 | 0.02817 |
| POST-GOLGI\_VESICLE-MEDIATED\_TRANSPORT(GO-0006892) | 54 | 0.028174 |
| SKELETAL\_SYSTEM\_MORPHOGENESIS(GO-0048705) | 39 | 0.028194 |
| REGULATION\_OF\_CELL\_SHAPE(GO-0008360) | 50 | 0.02886 |
| REGULATION\_OF\_ERK1\_AND\_ERK2\_CASCADE(GO-0070372) | 76 | 0.02888 |
| GOLGI\_ORGANIZATION(GO-0007030) | 22 | 0.02894 |
| REGULATION\_OF\_PHOSPHATIDYLINOSITOL\_3-KINASE\_CASCADE(GO-0014066) | 35 | 0.029566 |
| MYELOID\_CELL\_DIFFERENTIATION(GO-0030099) | 58 | 0.029707 |
| CELL\_JUNCTION\_ASSEMBLY(GO-0034329) | 110 | 0.030249 |
| REGULATION\_OF\_NUCLEOCYTOPLASMIC\_TRANSPORT(GO-0046822) | 83 | 0.030673 |
| BONE\_MORPHOGENESIS(GO-0060349) | 18 | 0.030827 |
| CELLULAR\_HOMEOSTASIS(GO-0019725) | 297 | 0.030963 |
| REGULATION\_OF\_VIRAL\_TRANSCRIPTION(GO-0046782) | 62 | 0.031008 |
| SYNAPSE\_ORGANIZATION(GO-0050808) | 40 | 0.031353 |
| KIDNEY\_DEVELOPMENT(GO-0001822) | 87 | 0.031399 |
| NUCLEAR\_IMPORT(GO-0051170) | 49 | 0.031483 |
| REGULATION\_OF\_FIBROBLAST\_PROLIFERATION(GO-0048145) | 37 | 0.031684 |
| ACTIN\_FILAMENT\_BUNDLE\_ASSEMBLY(GO-0051017) | 15 | 0.031741 |
| MYD88-DEPENDENT\_TOLL-LIKE\_RECEPTOR\_SIGNALING\_PATHWAY(GO-0002755) | 69 | 0.032163 |
| HORMONE\_BIOSYNTHETIC\_PROCESS(GO-0042446) | 27 | 0.032193 |
| NUCLEOTIDE\_METABOLIC\_PROCESS(GO-0009117) | 308 | 0.032642 |
| CYTOKINE\_PRODUCTION(GO-0001816) | 34 | 0.032644 |
| CELLULAR\_MEMBRANE\_FUSION(GO-0006944) | 35 | 0.032707 |
| GLIOGENESIS(GO-0042063) | 27 | 0.032714 |
| DNA\_DAMAGE\_RESPONSE\_\_SIGNAL\_TRANSDUCTION\_BY\_P53\_CLASS\_MEDIATOR(GO-0030330) | 86 | 0.032919 |
| LEARNING\_OR\_MEMORY(GO-0007611) | 38 | 0.033189 |
| NEGATIVE\_REGULATION\_OF\_BINDING(GO-0051100) | 43 | 0.033447 |
| REGULATION\_OF\_ANTI-APOPTOSIS(GO-0045767) | 25 | 0.03349 |
| TOLL-LIKE\_RECEPTOR\_2\_SIGNALING\_PATHWAY(GO-0034134) | 65 | 0.033556 |
| NEGATIVE\_REGULATION\_OF\_NEURON\_PROJECTION\_DEVELOPMENT(GO-0010977) | 15 | 0.033858 |
| ALCOHOL\_METABOLIC\_PROCESS(GO-0006066) | 243 | 0.033889 |
| REGULATION\_OF\_EPIDERMAL\_GROWTH\_FACTOR-ACTIVATED\_RECEPTOR\_ACTIVITY(GO-0007176) | 18 | 0.034032 |
| AUTOPHAGY(GO-0006914) | 23 | 0.034058 |
| REGULATION\_OF\_CHOLESTEROL\_TRANSPORT(GO-0032374) | 22 | 0.034101 |
| ION\_HOMEOSTASIS(GO-0050801) | 283 | 0.034694 |
| REGULATION\_OF\_EPIDERMIS\_DEVELOPMENT(GO-0045682) | 16 | 0.034739 |
| PHENOL-CONTAINING\_COMPOUND\_METABOLIC\_PROCESS(GO-0018958) | 19 | 0.034975 |
| NUCLEOBASE-CONTAINING\_SMALL\_MOLECULE\_METABOLIC\_PROCESS(GO-0055086) | 356 | 0.034979 |
| NEGATIVE\_REGULATION\_OF\_T\_CELL\_ACTIVATION(GO-0050868) | 26 | 0.03504 |
| STEROL\_BIOSYNTHETIC\_PROCESS(GO-0016126) | 25 | 0.03508 |
| REGULATION\_OF\_NEUROGENESIS(GO-0050767) | 147 | 0.03513 |
| POSITIVE\_REGULATION\_OF\_CYTOSKELETON\_ORGANIZATION(GO-0051495) | 58 | 0.035225 |
| CARBOXYLIC\_ACID\_TRANSPORT(GO-0046942) | 120 | 0.035233 |
| TISSUE\_DEVELOPMENT(GO-0009888) | 387 | 0.035541 |
| KIDNEY\_MORPHOGENESIS(GO-0060993) | 18 | 0.03597 |
| POSTTRANSCRIPTIONAL\_REGULATION\_OF\_GENE\_EXPRESSION(GO-0010608) | 178 | 0.036075 |
| REGULATION\_OF\_MITOCHONDRION\_ORGANIZATION(GO-0010821) | 24 | 0.036094 |
| NEGATIVE\_REGULATION\_OF\_TRANSPORT(GO-0051051) | 132 | 0.036595 |
| REGULATION\_OF\_CELLULAR\_AMINO\_ACID\_METABOLIC\_PROCESS(GO-0006521) | 53 | 0.038192 |
| NEGATIVE\_REGULATION\_OF\_PROTEIN\_COMPLEX\_DISASSEMBLY(GO-0043242) | 18 | 0.038225 |
| MITOTIC\_CELL\_CYCLE\_G1-S\_TRANSITION\_DNA\_DAMAGE\_CHECKPOINT(GO-0031571) | 69 | 0.038696 |
| I-KAPPAB\_KINASE-NF-KAPPAB\_CASCADE(GO-0007249) | 31 | 0.039494 |
| LONG-CHAIN\_FATTY-ACYL-COA\_METABOLIC\_PROCESS(GO-0035336) | 19 | 0.039504 |
| REGULATION\_OF\_SMOOTH\_MUSCLE\_CELL\_PROLIFERATION(GO-0048660) | 32 | 0.03983 |
| RESPIRATORY\_SYSTEM\_DEVELOPMENT(GO-0060541) | 31 | 0.040057 |
| HUMORAL\_IMMUNE\_RESPONSE(GO-0006959) | 53 | 0.040079 |
| C21-STEROID\_HORMONE\_BIOSYNTHETIC\_PROCESS(GO-0006700) | 16 | 0.040223 |
| TOLL-LIKE\_RECEPTOR\_1\_SIGNALING\_PATHWAY(GO-0034130) | 65 | 0.040259 |
| NEGATIVE\_REGULATION\_OF\_CYTOKINE\_BIOSYNTHETIC\_PROCESS(GO-0042036) | 16 | 0.040472 |
| CELLULAR\_AMINO\_ACID\_METABOLIC\_PROCESS(GO-0006520) | 239 | 0.040973 |
| CELLULAR\_RESPONSE\_TO\_INORGANIC\_SUBSTANCE(GO-0071241) | 43 | 0.041663 |
| CELLULAR\_CATION\_HOMEOSTASIS(GO-0030003) | 190 | 0.041698 |
| POSITIVE\_REGULATION\_OF\_CELL\_CYCLE(GO-0045787) | 72 | 0.042063 |
| MALE\_SEX\_DIFFERENTIATION(GO-0046661) | 41 | 0.042223 |
| RESPONSE\_TO\_HYPOXIA(GO-0001666) | 76 | 0.042698 |
| EAR\_MORPHOGENESIS(GO-0042471) | 24 | 0.04275 |
| REGULATION\_OF\_PH(GO-0006885) | 16 | 0.042819 |
| COGNITION(GO-0050890) | 50 | 0.043292 |
| PHOSPHATIDYLINOSITOL-MEDIATED\_SIGNALING(GO-0048015) | 51 | 0.043376 |
| CELLULAR\_ION\_HOMEOSTASIS(GO-0006873) | 265 | 0.04345 |
| NEGATIVE\_REGULATION\_OF\_GROWTH(GO-0045926) | 97 | 0.043794 |
| PHAGOCYTOSIS(GO-0006909) | 32 | 0.044561 |
| CELLULAR\_RESPONSE\_TO\_NUTRIENT(GO-0031670) | 41 | 0.045309 |
| VITAMIN\_METABOLIC\_PROCESS(GO-0006766) | 84 | 0.045388 |
| NEGATIVE\_REGULATION\_OF\_ANGIOGENESIS(GO-0016525) | 37 | 0.045428 |
| REGULATION\_OF\_RESPONSE\_TO\_INTERFERON-GAMMA(GO-0060330) | 20 | 0.04602 |
| RESPONSE\_TO\_ABIOTIC\_STIMULUS(GO-0009628) | 239 | 0.046075 |
| ODONTOGENESIS(GO-0042476) | 25 | 0.046322 |
| GTP\_CATABOLIC\_PROCESS(GO-0006184) | 121 | 0.046331 |
| NEGATIVE\_REGULATION\_OF\_ENDOTHELIAL\_CELL\_MIGRATION(GO-0010596) | 18 | 0.046343 |
| DEVELOPMENTAL\_GROWTH\_INVOLVED\_IN\_MORPHOGENESIS(GO-0060560) | 22 | 0.046376 |
| POSITIVE\_REGULATION\_OF\_T\_CELL\_DIFFERENTIATION(GO-0045582) | 25 | 0.046389 |
| HEMOPOIESIS(GO-0030097) | 137 | 0.046859 |
| NEGATIVE\_REGULATION\_OF\_I-KAPPAB\_KINASE-NF-KAPPAB\_CASCADE(GO-0043124) | 15 | 0.047071 |
| NEGATIVE\_REGULATION\_OF\_INFLAMMATORY\_RESPONSE(GO-0050728) | 16 | 0.047155 |
| POSITIVE\_REGULATION\_OF\_TRANSLATION(GO-0045727) | 28 | 0.047416 |
| REGULATION\_OF\_DEFENSE\_RESPONSE\_TO\_VIRUS\_BY\_VIRUS(GO-0050690) | 28 | 0.04762 |
| RESPONSE\_TO\_METAL\_ION(GO-0010038) | 86 | 0.047936 |
| POSITIVE\_REGULATION\_OF\_CELL\_DIFFERENTIATION(GO-0045597) | 225 | 0.048051 |
| INNER\_EAR\_DEVELOPMENT(GO-0048839) | 25 | 0.048358 |
| ADAPTIVE\_IMMUNE\_RESPONSE(GO-0002250) | 41 | 0.048849 |
| POSITIVE\_REGULATION\_OF\_SMALL\_GTPASE\_MEDIATED\_SIGNAL\_TRANSDUCTION(GO-0051057) | 15 | 0.04893 |
| HETEROCYCLE\_METABOLIC\_PROCESS(GO-0046483) | 434 | 0.04915 |
| PHOSPHOLIPID\_BIOSYNTHETIC\_PROCESS(GO-0008654) | 67 | 0.049573 |
| REGULATION\_OF\_ORGAN\_MORPHOGENESIS(GO-2000027) | 46 | 0.049959 |
| CELL\_CYCLE\_ARREST(GO-0007050) | 90 | 0.049987 |