# KEGG Enrichment Analysis Results

| Description | KEGG ID | GeneRatio | RichFactor | Adjust P-value | Count |
| --- | --- | --- | --- | --- | --- |
| Endocytosis | omy04144 | 462/8897 | 0.6989410 | 4.012442e-03 | 462 |
| Cellular senescence | omy04218 | 308/8897 | 0.7758186 | 1.667032e-07 | 308 |
| Protein processing in endoplasmic reticulum | omy04141 | 275/8897 | 0.7217848 | 3.468522e-03 | 275 |
| FoxO signaling pathway | omy04068 | 264/8897 | 0.7292818 | 1.672308e-03 | 264 |
| Cell cycle | omy04110 | 255/8897 | 0.7434402 | 5.054681e-04 | 255 |
| Ubiquitin mediated proteolysis | omy04120 | 232/8897 | 0.7483871 | 5.054681e-04 | 232 |
| Spliceosome | omy03040 | 223/8897 | 0.7433333 | 1.118120e-03 | 223 |
| Ribosome | omy03010 | 205/8897 | 0.7677903 | 1.374895e-04 | 205 |
| C-type lectin receptor signaling pathway | omy04625 | 202/8897 | 0.7292419 | 7.161636e-03 | 202 |
| Oocyte meiosis | omy04114 | 195/8897 | 0.7471264 | 1.575557e-03 | 195 |
| Mitophagy - animal | omy04137 | 193/8897 | 0.7283019 | 9.796915e-03 | 193 |
| Oxidative phosphorylation | omy00190 | 187/8897 | 0.7391304 | 4.012442e-03 | 187 |
| Progesterone-mediated oocyte maturation | omy04914 | 157/8897 | 0.7696078 | 8.196607e-04 | 157 |
| Nucleocytoplasmic transport | omy03013 | 155/8897 | 0.7524272 | 3.468522e-03 | 155 |
| p53 signaling pathway | omy04115 | 128/8897 | 0.7441860 | 1.642726e-02 | 128 |
| Ribosome biogenesis in eukaryotes | omy03008 | 111/8897 | 0.7350993 | 4.950226e-02 | 111 |
| Sphingolipid metabolism | omy00600 | 95/8897 | 0.8050847 | 1.118120e-03 | 95 |
| Glycine, serine and threonine metabolism | omy00260 | 59/8897 | 0.7972973 | 1.971207e-02 | 59 |
| Autophagy - other | omy04136 | 57/8897 | 0.9193548 | 2.715881e-05 | 57 |
| One carbon pool by folate | omy00670 | 56/8897 | 0.8000000 | 2.092222e-02 | 56 |
| Biosynthesis of unsaturated fatty acids | omy01040 | 53/8897 | 0.7910448 | 3.884430e-02 | 53 |
| RNA polymerase | omy03020 | 42/8897 | 0.8400000 | 1.423487e-02 | 42 |

# Gene Ontology Enrichment Analysis Results

| GO Source | GO Term | GO ID | Term Size | Query Size | Adjust P-value | Count |
| --- | --- | --- | --- | --- | --- | --- |
| GO:BP | DNA metabolic process | GO:0006259 | 3683 | 1268 | 5.497552e-04 | 260 |
| GO:BP | DNA integration | GO:0015074 | 3304 | 1268 | 4.194433e-02 | 216 |
| GO:BP | DNA recombination | GO:0006310 | 2286 | 1268 | 7.567125e-03 | 163 |
| GO:BP | transposition | GO:0032196 | 2223 | 1268 | 1.334342e-02 | 157 |
| GO:BP | DNA transposition | GO:0006313 | 2223 | 1268 | 1.334342e-02 | 157 |
| GO:BP | transmembrane transport | GO:0055085 | 1509 | 1268 | 8.257490e-03 | 114 |
| GO:BP | multicellular organismal process | GO:0032501 | 1094 | 1268 | 6.289251e-03 | 88 |
| GO:BP | organelle organization | GO:0006996 | 874 | 1268 | 3.105766e-03 | 75 |
| GO:BP | anatomical structure development | GO:0048856 | 873 | 1268 | 4.743953e-02 | 67 |
| GO:BP | cell cycle | GO:0007049 | 361 | 1268 | 7.558401e-13 | 62 |
| GO:MF | binding | GO:0005488 | 22150 | 1629 | 2.556815e-13 | 1151 |
| GO:MF | organic cyclic compound binding | GO:0097159 | 11581 | 1629 | 2.905729e-07 | 634 |
| GO:MF | catalytic activity | GO:0003824 | 9266 | 1629 | 4.562375e-03 | 480 |
| GO:MF | small molecule binding | GO:0036094 | 7538 | 1629 | 1.953388e-05 | 422 |
| GO:MF | ion binding | GO:0043167 | 7314 | 1629 | 3.171005e-05 | 408 |
| GO:MF | DNA binding | GO:0003677 | 4498 | 1629 | 2.905729e-07 | 285 |
| GO:MF | heterocyclic compound binding | GO:1901363 | 3670 | 1629 | 3.930839e-06 | 234 |
| GO:MF | anion binding | GO:0043168 | 3554 | 1629 | 1.237496e-06 | 231 |
| GO:MF | nucleoside phosphate binding | GO:1901265 | 3520 | 1629 | 1.953388e-05 | 220 |
| GO:MF | nucleotide binding | GO:0000166 | 3505 | 1629 | 1.958613e-05 | 219 |
| GO:CC | membrane | GO:0016020 | 6972 | 791 | 8.785775e-17 | 387 |
| GO:CC | nucleus | GO:0005634 | 3571 | 791 | 2.907332e-02 | 166 |
| GO:CC | cell periphery | GO:0071944 | 1484 | 791 | 3.601206e-06 | 97 |
| GO:CC | plasma membrane | GO:0005886 | 1379 | 791 | 5.200871e-06 | 91 |
| GO:CC | extracellular region | GO:0005576 | 1065 | 791 | 1.857881e-05 | 73 |
| GO:CC | intracellular organelle lumen | GO:0070013 | 797 | 791 | 9.636450e-04 | 53 |
| GO:CC | organelle lumen | GO:0043233 | 797 | 791 | 9.636450e-04 | 53 |
| GO:CC | membrane-enclosed lumen | GO:0031974 | 797 | 791 | 9.636450e-04 | 53 |
| GO:CC | cytoskeleton | GO:0005856 | 787 | 791 | 2.194427e-03 | 51 |
| GO:CC | nuclear lumen | GO:0031981 | 693 | 791 | 9.040712e-04 | 48 |