# Online Supplement: GoMiner Analysis Output

| GO ID | Total | Down | Up | Changed | P-Value (Down) | P-Value (Up) | P-Value (Changed) | Term |
|---|---|---|---|---|---|---|---|---|
| 6817 | 26 | 8 | 2 | 10 | 0 | 0.1006 | 0 | phosphate transport |
| 5201 | 39 | 11 | 2 | 13 | 0 | 0.1938 | 0 | extracellular matrix structural constituent |
| 30020 | 10 | 6 | 0 | 6 | 0 | 1 | 0 | extracellular matrix structural constituent conferring tensile strength |
| 5583 | 9 | 7 | 0 | 7 | 0 | 1 | 0 | fibrillar collagen |
| 5581 | 13 | 7 | 0 | 7 | 0 | 1 | 0 | collagen |
| 6631 | 93 | 3 | 12 | 15 | 0.5099 | 0 | 0 | fatty acid metabolism |
| 5588 | 3 | 3 | 0 | 3 | 0 | 1 | 0.0001 | collagen type V |
| 5578 | 194 | 19 | 3 | 22 | 0 | 0.7764 | 0.0002 | extracellular matrix |
| 30198 | 44 | 6 | 3 | 9 | 0.0015 | 0.0623 | 0.0002 | extracellular matrix organization and biogenesis |
| 43062 | 44 | 6 | 3 | 9 | 0.0015 | 0.0623 | 0.0002 | extracellular structure organization and biogenesis |
| 15698 | 77 | 9 | 3 | 12 | 0.0003 | 0.2145 | 0.0004 | inorganic anion transport |
| 6635 | 15 | 0 | 5 | 5 | 1 | 0 | 0.0006 | fatty acid beta-oxidation |
| 6820 | 108 | 10 | 4 | 14 | 0.001 | 0.1857 | 0.0008 | anion transport |
| 5739 | 273 | 8 | 18 | 26 | 0.5414 | 0 | 0.0009 | mitochondrion |
| 1501 | 98 | 13 | 0 | 13 | 0 | 1 | 0.001 | skeletal development |
| 19395 | 17 | 0 | 5 | 5 | 1 | 0 | 0.0011 | fatty acid oxidation |
| 19752 | 206 | 5 | 16 | 21 | 0.7219 | 0 | 0.0012 | carboxylic acid metabolism |
| 6082 | 208 | 5 | 16 | 21 | 0.7299 | 0 | 0.0013 | organic acid metabolism |
| 6975 | 2 | 2 | 0 | 2 | 0.0008 | 1 | 0.0025 | DNA damage induced protein phosphorylation |
| 4312 | 2 | 1 | 1 | 2 | 0.0572 | 0.0411 | 0.0025 | fatty-acid synthase activity |
| 50729 | 2 | 1 | 1 | 2 | 0.0572 | 0.0411 | 0.0025 | positive regulation of inflammatory response |
| 16746 | 49 | 1 | 7 | 8 | 0.7655 | 0.0001 | 0.0025 | transferase activity, transferring acyl groups |
| 4466 | 2 | 0 | 2 | 2 | 1 | 0.0004 | 0.0025 | long-chain-acyl-CoA dehydrogenase activity |
| 5520 | 13 | 2 | 2 | 4 | 0.0528 | 0.0287 | 0.003 | insulin-like growth factor binding |
| 30247 | 52 | 7 | 1 | 8 | 0.0007 | 0.6667 | 0.0037 | polysaccharide binding |
| 5539 | 52 | 7 | 1 | 8 | 0.0007 | 0.6667 | 0.0037 | glycosaminoglycan binding |
| 6084 | 7 | 0 | 3 | 3 | 1 | 0.0003 | 0.0037 | acetyl-CoA metabolism |
| 6811 | 391 | 23 | 8 | 31 | 0.0007 | 0.5735 | 0.0054 | ion transport |
| 1871 | 56 | 7 | 1 | 8 | 0.001 | 0.6939 | 0.0059 | pattern binding |
| 16747 | 45 | 1 | 6 | 7 | 0.7358 | 0.0003 | 0.0062 | transferase activity, transferring groups other than amino-acyl groups |
| 8415 | 45 | 1 | 6 | 7 | 0.7358 | 0.0003 | 0.0062 | acyltransferase activity |
| 47498 | 3 | 2 | 0 | 2 | 0.0025 | 1 | 0.0072 | calcium-dependent phospholipase A2 activity |
| 5584 | 3 | 2 | 0 | 2 | 0.0025 | 1 | 0.0072 | collagen type I |

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|---|---|---|---|---|---|---|---|---|
| 45089 | 3 | 1 | 1 | 2 | 0.0845 | 0.0611 | 0.0072 | positive regulation of innate immune response |
| 16416 | 3 | 0 | 2 | 2 | 1 | 0.0013 | 0.0072 | O-palmitoyltransferase activity |
| 16409 | 3 | 0 | 2 | 2 | 1 | 0.0013 | 0.0072 | palmitoyltransferase activity |
| 4095 | 3 | 0 | 2 | 2 | 1 | 0.0013 | 0.0072 | carnitine O-palmitoyltransferase activity |
| 5518 | 9 | 3 | 0 | 3 | 0.0018 | 1 | 0.0082 | collagen binding |
| 5509 | 229 | 20 | 0 | 20 | 0 | 1 | 0.0091 | calcium ion binding |
| 6629 | 277 | 9 | 14 | 23 | 0.4118 | 0.0015 | 0.0096 | lipid metabolism |
| 43167 | 516 | 29 | 8 | 37 | 0.0003 | 0.8579 | 0.0122 | ion binding |
| 46872 | 516 | 29 | 8 | 37 | 0.0003 | 0.8579 | 0.0122 | metal ion binding |
| 8152 | 2089 | 64 | 56 | 120 | 0.2935 | 0.004 | 0.0131 | metabolism |
| 5198 | 253 | 14 | 7 | 21 | 0.0138 | 0.2712 | 0.0132 | structural molecule activity |
| 4768 | 4 | 2 | 0 | 2 | 0.0048 | 1 | 0.0138 | stearoyl-CoA 9-desaturase activity |
| 16215 | 4 | 2 | 0 | 2 | 0.0048 | 1 | 0.0138 | CoA desaturase activity |
| 9071 | 4 | 2 | 0 | 2 | 0.0048 | 1 | 0.0138 | serine family amino acid catabolism |
| 50930 | 4 | 2 | 0 | 2 | 0.0048 | 1 | 0.0138 | induction of positive chemotaxis |
| 50927 | 4 | 2 | 0 | 2 | 0.0048 | 1 | 0.0138 | positive regulation of positive chemotaxis |
| 50926 | 4 | 2 | 0 | 2 | 0.0048 | 1 | 0.0138 | regulation of positive chemotaxis |
| 50918 | 4 | 2 | 0 | 2 | 0.0048 | 1 | 0.0138 | positive chemotaxis |
| 19903 | 4 | 1 | 1 | 2 | 0.1111 | 0.0806 | 0.0138 | protein phosphatase binding |
| 19902 | 4 | 1 | 1 | 2 | 0.1111 | 0.0806 | 0.0138 | phosphatase binding |
| 50778 | 4 | 1 | 1 | 2 | 0.1111 | 0.0806 | 0.0138 | positive regulation of immune response |
| 16406 | 4 | 0 | 2 | 2 | 1 | 0.0025 | 0.0138 | carnitine O-acyltransferase activity |
| 4623 | 11 | 3 | 0 | 3 | 0.0033 | 1 | 0.0149 | phospholipase A2 activity |
| 8201 | 42 | 5 | 1 | 6 | 0.0068 | 0.5878 | 0.0165 | heparin binding |
| 16830 | 21 | 1 | 3 | 4 | 0.4617 | 0.0088 | 0.0183 | carbon-carbon lyase activity |
| 16324 | 21 | 1 | 3 | 4 | 0.4617 | 0.0088 | 0.0183 | apical plasma membrane |
| 8374 | 12 | 0 | 3 | 3 | 1 | 0.0017 | 0.0191 | O-acyltransferase activity |
| 50808 | 32 | 3 | 2 | 5 | 0.0641 | 0.142 | 0.0195 | synapse organization and biogenesis |
| 16765 | 32 | 2 | 3 | 5 | 0.2371 | 0.0278 | 0.0195 | transferase activity, transferring alkyl or aryl (other than methyl) groups |
| 16829 | 82 | 3 | 6 | 9 | 0.4267 | 0.0067 | 0.0196 | lyase activity |
| 16491 | 264 | 9 | 12 | 21 | 0.3567 | 0.0077 | 0.0205 | oxidoreductase activity |
| 8203 | 33 | 2 | 3 | 5 | 0.248 | 0.0302 | 0.0221 | cholesterol metabolism |
| 30833 | 5 | 2 | 0 | 2 | 0.0079 | 1 | 0.0223 | regulation of actin filament polymerization |
| 50921 | 5 | 2 | 0 | 2 | 0.0079 | 1 | 0.0223 | positive regulation of chemotaxis |
| 50920 | 5 | 2 | 0 | 2 | 0.0079 | 1 | 0.0223 | regulation of chemotaxis |
| 48169 | 5 | 2 | 0 | 2 | 0.0079 | 1 | 0.0223 | regulation of long-term neuronal synaptic plasticity |
| 8147 | 5 | 2 | 0 | 2 | 0.0079 | 1 | 0.0223 | structural constituent of bone |

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|---|---|---|---|---|---|---|---|---|
| 4712 | 5 | 1 | 1 | 2 | 0.1369 | 0.0997 | 0.0223 | protein threonine/tyrosine kinase activity |
| 45445 | 5 | 1 | 1 | 2 | 0.1369 | 0.0997 | 0.0223 | myoblast differentiation |
| 16408 | 5 | 0 | 2 | 2 | 1 | 0.0041 | 0.0223 | C-acyltransferase activity |
| 4300 | 5 | 0 | 2 | 2 | 1 | 0.0041 | 0.0223 | enoyl-CoA hydratase activity |
| 902 | 112 | 8 | 3 | 11 | 0.0152 | 0.4132 | 0.0224 | cellular morphogenesis |
| 43169 | 435 | 27 | 4 | 31 | 0.0001 | 0.9846 | 0.0234 | cation binding |
| 45595 | 58 | 4 | 3 | 7 | 0.0862 | 0.1185 | 0.0237 | regulation of cell differentiation |
| 50793 | 128 | 8 | 4 | 12 | 0.0312 | 0.2749 | 0.0243 | regulation of development |
| 9968 | 23 | 3 | 1 | 4 | 0.0276 | 0.3838 | 0.0251 | negative regulation of signal transduction |
| 7582 | 3385 | 102 | 77 | 179 | 0.2124 | 0.0347 | 0.0282 | physiological process |
| 6066 | 133 | 5 | 7 | 12 | 0.342 | 0.0197 | 0.0317 | alcohol metabolism |
| 4684 | 6 | 2 | 0 | 2 | 0.0116 | 1 | 0.0324 | calmodulin-dependent protein kinase I activity |
| 30041 | 6 | 2 | 0 | 2 | 0.0116 | 1 | 0.0324 | actin filament polymerization |
| 45177 | 6 | 0 | 2 | 2 | 1 | 0.0061 | 0.0324 | apical part of cell |
| 3995 | 6 | 0 | 2 | 2 | 1 | 0.0061 | 0.0324 | acyl-CoA dehydrogenase activity |
| 19866 | 62 | 3 | 4 | 7 | 0.2674 | 0.0389 | 0.0329 | inner membrane |
| 1503 | 37 | 5 | 0 | 5 | 0.0039 | 1 | 0.0346 | ossification |
| 16053 | 37 | 3 | 2 | 5 | 0.0906 | 0.1787 | 0.0346 | organic acid biosynthesis |
| 46394 | 37 | 3 | 2 | 5 | 0.0906 | 0.1787 | 0.0346 | carboxylic acid biosynthesis |
| 7155 | 247 | 14 | 5 | 19 | 0.0113 | 0.5903 | 0.0365 | cell adhesion |
| 9057 | 264 | 13 | 7 | 20 | 0.0405 | 0.3079 | 0.0371 | macromolecule catabolism |
| 16125 | 38 | 2 | 3 | 5 | 0.3022 | 0.0433 | 0.0383 | sterol metabolism |
| 3824 | 1580 | 48 | 43 | 91 | 0.3712 | 0.0159 | 0.0413 | catalytic activity |
| 48168 | 16 | 3 | 0 | 3 | 0.0101 | 1 | 0.0421 | regulation of neuronal synaptic plasticity |
| 30246 | 109 | 9 | 1 | 10 | 0.004 | 0.9017 | 0.0433 | carbohydrate binding |
| 6144 | 7 | 2 | 0 | 2 | 0.0159 | 1 | 0.0439 | purine base metabolism |
| 9894 | 7 | 2 | 0 | 2 | 0.0159 | 1 | 0.0439 | regulation of catabolism |
| 15270 | 7 | 2 | 0 | 2 | 0.0159 | 1 | 0.0439 | dihydropyridine-sensitive calcium channel activity |
| 4697 | 7 | 1 | 1 | 2 | 0.1862 | 0.1368 | 0.0439 | protein kinase C activity |
| 19239 | 7 | 1 | 1 | 2 | 0.1862 | 0.1368 | 0.0439 | deaminase activity |
| 50727 | 7 | 1 | 1 | 2 | 0.1862 | 0.1368 | 0.0439 | regulation of inflammatory response |
| 5315 | 7 | 0 | 2 | 2 | 1 | 0.0084 | 0.0439 | inorganic phosphate transporter activity |
| 50767 | 28 | 4 | 0 | 4 | 0.008 | 1 | 0.0478 | regulation of neurogenesis |
| 9056 | 374 | 17 | 9 | 26 | 0.0399 | 0.3734 | 0.0478 | catabolism |
| 7050 | 28 | 3 | 1 | 4 | 0.046 | 0.4456 | 0.0478 | cell cycle arrest |
| 4683 | 17 | 3 | 0 | 3 | 0.012 | 1 | 0.0493 | calmodulin regulated protein kinase activity |
| 3754 | 17 | 2 | 1 | 3 | 0.0854 | 0.3007 | 0.0493 | chaperone activity |

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|---|---|---|---|---|---|---|---|---|
| 6379 | 1 | 1 | 0 | 1 | 0.029 | 1 | 0.0498 | mRNA cleavage |
| 18223 | 1 | 1 | 0 | 1 | 0.029 | 1 | 0.0498 | protein-cysteine farnesyltransferase activity |
| 6123 | 1 | 1 | 0 | 1 | 0.029 | 1 | 0.0498 | mitochondrial electron transport, cytochrome c to oxygen |
| 4998 | 1 | 1 | 0 | 1 | 0.029 | 1 | 0.0498 | transferrin receptor activity |
| 16931 | 1 | 1 | 0 | 1 | 0.029 | 1 | 0.0498 | vasopressin activated calcium mobilizing receptor activity |
| 16910 | 1 | 1 | 0 | 1 | 0.029 | 1 | 0.0498 | SAP kinase 3 activity |
| 4903 | 1 | 1 | 0 | 1 | 0.029 | 1 | 0.0498 | growth hormone receptor activity |
| 4720 | 1 | 1 | 0 | 1 | 0.029 | 1 | 0.0498 | protein-lysine 6-oxidase activity |
| 4698 | 1 | 1 | 0 | 1 | 0.029 | 1 | 0.0498 | calcium-dependent protein kinase C activity |
| 4686 | 1 | 1 | 0 | 1 | 0.029 | 1 | 0.0498 | eukaryotic elongation factor-2 kinase activity |
| 4586 | 1 | 1 | 0 | 1 | 0.029 | 1 | 0.0498 | ornithine decarboxylase activity |
| 42761 | 1 | 1 | 0 | 1 | 0.029 | 1 | 0.0498 | very-long-chain fatty acid biosynthesis |
| 16420 | 1 | 1 | 0 | 1 | 0.029 | 1 | 0.0498 | malonyltransferase activity |
| 16419 | 1 | 1 | 0 | 1 | 0.029 | 1 | 0.0498 | S-malonyltransferase activity |
| 4367 | 1 | 1 | 0 | 1 | 0.029 | 1 | 0.0498 | glycerol-3-phosphate dehydrogenase (NAD+) activity |
| 4320 | 1 | 1 | 0 | 1 | 0.029 | 1 | 0.0498 | oleoyl-[acyl-carrier protein] hydrolase activity |
| 4314 | 1 | 1 | 0 | 1 | 0.029 | 1 | 0.0498 | [acyl-carrier protein] S-malonyltransferase activity |
| 16297 | 1 | 1 | 0 | 1 | 0.029 | 1 | 0.0498 | acyl-[acyl-carrier protein] hydrolase activity |
| 16296 | 1 | 1 | 0 | 1 | 0.029 | 1 | 0.0498 | palmitoyl-[acyl-carrier protein] hydrolase activity |
| 16295 | 1 | 1 | 0 | 1 | 0.029 | 1 | 0.0498 | myristoyl-[acyl-carrier protein] hydrolase activity |
| 4248 | 1 | 1 | 0 | 1 | 0.029 | 1 | 0.0498 | stromelysin 1 activity |
| 30322 | 1 | 1 | 0 | 1 | 0.029 | 1 | 0.0498 | stabilization of membrane potential |
| 42176 | 1 | 1 | 0 | 1 | 0.029 | 1 | 0.0498 | regulation of protein catabolism |
| 30023 | 1 | 1 | 0 | 1 | 0.029 | 1 | 0.0498 | extracellular matrix constituent conferring elasticity |
| 45917 | 1 | 1 | 0 | 1 | 0.029 | 1 | 0.0498 | positive regulation of complement activation |
| 45669 | 1 | 1 | 0 | 1 | 0.029 | 1 | 0.0498 | positive regulation of osteoblast differentiation |
| 45601 | 1 | 1 | 0 | 1 | 0.029 | 1 | 0.0498 | regulation of endothelial cell differentiation |
| 7170 | 1 | 1 | 0 | 1 | 0.029 | 1 | 0.0498 | transmembrane receptor protein tyrosine kinase ligand binding |
| 45340 | 1 | 1 | 0 | 1 | 0.029 | 1 | 0.0498 | mercury ion binding |
| 5592 | 1 | 1 | 0 | 1 | 0.029 | 1 | 0.0498 | collagen type XI |
| 5586 | 1 | 1 | 0 | 1 | 0.029 | 1 | 0.0498 | collagen type III |
| 5290 | 1 | 1 | 0 | 1 | 0.029 | 1 | 0.0498 | L-histidine transporter activity |
| 17172 | 1 | 1 | 0 | 1 | 0.029 | 1 | 0.0498 | cysteine dioxygenase activity |
| 17147 | 1 | 1 | 0 | 1 | 0.029 | 1 | 0.0498 | Wnt-protein binding |
| 48251 | 1 | 1 | 0 | 1 | 0.029 | 1 | 0.0498 | elastic fiber assembly |
| 48155 | 1 | 1 | 0 | 1 | 0.029 | 1 | 0.0498 | S100 alpha binding |
| 48154 | 1 | 1 | 0 | 1 | 0.029 | 1 | 0.0498 | S100 beta binding |

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|---|---|---|---|---|---|---|---|---|
| 48151 | 1 | 1 | 0 | 1 | 0.029 | 1 | 0.0498 | hyperphosphorylation |
| 48143 | 1 | 1 | 0 | 1 | 0.029 | 1 | 0.0498 | astrocyte activation |
| 164 | 1 | 1 | 0 | 1 | 0.029 | 1 | 0.0498 | protein phosphatase type 1 complex |
| 43149 | 1 | 1 | 0 | 1 | 0.029 | 1 | 0.0498 | stress fiber formation |
| 15817 | 1 | 1 | 0 | 1 | 0.029 | 1 | 0.0498 | L-histidine transport |
| 15732 | 1 | 1 | 0 | 1 | 0.029 | 1 | 0.0498 | prostaglandin transport |
| 15271 | 1 | 1 | 0 | 1 | 0.029 | 1 | 0.0498 | outward rectifier potassium channel activity |
| 46325 | 1 | 1 | 0 | 1 | 0.029 | 1 | 0.0498 | negative regulation of glucose import |
| 10003 | 1 | 0 | 1 | 1 | 1 | 0.0208 | 0.0498 | gastrulation (sensu Mammalia) |
| 6798 | 1 | 0 | 1 | 1 | 1 | 0.0208 | 0.0498 | polyphosphate catabolism |
| 6797 | 1 | 0 | 1 | 1 | 1 | 0.0208 | 0.0498 | polyphosphate metabolism |
| 1762 | 1 | 0 | 1 | 1 | 1 | 0.0208 | 0.0498 | beta-alanine transport |
| 1761 | 1 | 0 | 1 | 1 | 1 | 0.0208 | 0.0498 | beta-alanine transporter activity |
| 1702 | 1 | 0 | 1 | 1 | 1 | 0.0208 | 0.0498 | gastrulation (sensu Deuterostomia) |
| 4940 | 1 | 0 | 1 | 1 | 1 | 0.0208 | 0.0498 | beta1-adrenergic receptor activity |
| 16833 | 1 | 0 | 1 | 1 | 1 | 0.0208 | 0.0498 | oxo-acid-lyase activity |
| 4772 | 1 | 0 | 1 | 1 | 1 | 0.0208 | 0.0498 | sterol O-acyltransferase activity |
| 16724 | 1 | 0 | 1 | 1 | 1 | 0.0208 | 0.0498 | oxidoreductase activity, oxidizing metal ions, oxygen as acceptor |
| 16722 | 1 | 0 | 1 | 1 | 1 | 0.0208 | 0.0498 | oxidoreductase activity, oxidizing metal ions |
| 51041 | 1 | 0 | 1 | 1 | 1 | 0.0208 | 0.0498 | positive regulation of calcium-independent cell-cell adhesion |
| 51040 | 1 | 0 | 1 | 1 | 1 | 0.0208 | 0.0498 | regulation of calcium-independent cell-cell adhesion |
| 30881 | 1 | 0 | 1 | 1 | 1 | 0.0208 | 0.0498 | beta-2-microglobulin binding |
| 16509 | 1 | 0 | 1 | 1 | 1 | 0.0208 | 0.0498 | long-chain-3-hydroxyacyl-CoA dehydrogenase activity |
| 9399 | 1 | 0 | 1 | 1 | 1 | 0.0208 | 0.0498 | nitrogen fixation |
| 4492 | 1 | 0 | 1 | 1 | 1 | 0.0208 | 0.0498 | methylmalonyl-CoA decarboxylase activity |
| 4419 | 1 | 0 | 1 | 1 | 1 | 0.0208 | 0.0498 | hydroxymethylglutaryl-CoA lyase activity |
| 16338 | 1 | 0 | 1 | 1 | 1 | 0.0208 | 0.0498 | calcium-independent cell-cell adhesion |
| 4356 | 1 | 0 | 1 | 1 | 1 | 0.0208 | 0.0498 | glutamate-ammonia ligase activity |
| 4322 | 1 | 0 | 1 | 1 | 1 | 0.0208 | 0.0498 | ferroxidase activity |
| 4316 | 1 | 0 | 1 | 1 | 1 | 0.0208 | 0.0498 | 3-oxoacyl-[acyl-carrier protein] reductase activity |
| 4281 | 1 | 0 | 1 | 1 | 1 | 0.0208 | 0.0498 | pancreatic elastase II activity |
| 4096 | 1 | 0 | 1 | 1 | 1 | 0.0208 | 0.0498 | catalase activity |
| 19433 | 1 | 0 | 1 | 1 | 1 | 0.0208 | 0.0498 | triacylglycerol catabolism |
| 45663 | 1 | 0 | 1 | 1 | 1 | 0.0208 | 0.0498 | positive regulation of myoblast differentiation |
| 45661 | 1 | 0 | 1 | 1 | 1 | 0.0208 | 0.0498 | regulation of myoblast differentiation |
| 19211 | 1 | 0 | 1 | 1 | 1 | 0.0208 | 0.0498 | phosphatase activator activity |
| 45294 | 1 | 0 | 1 | 1 | 1 | 0.0208 | 0.0498 | alpha-catenin binding |

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|---|---|---|---|---|---|---|---|---|
| 45136 | 1 | 0 | 1 | 1 | 1 | 0.0208 | 0.0498 | development of secondary sexual characteristics |
| 5932 | 1 | 0 | 1 | 1 | 1 | 0.0208 | 0.0498 | basal body |
| 5610 | 1 | 0 | 1 | 1 | 1 | 0.0208 | 0.0498 | laminin-5 |
| 50902 | 1 | 0 | 1 | 1 | 1 | 0.0208 | 0.0498 | leukocyte adhesive activation |
| 5476 | 1 | 0 | 1 | 1 | 1 | 0.0208 | 0.0498 | carnitine:acyl carnitine carrier activity |
| 5369 | 1 | 0 | 1 | 1 | 1 | 0.0208 | 0.0498 | taurine:sodium symporter activity |
| 5368 | 1 | 0 | 1 | 1 | 1 | 0.0208 | 0.0498 | taurine transporter activity |
| 48276 | 1 | 0 | 1 | 1 | 1 | 0.0208 | 0.0498 | gastrulation (sensu Vertebrata) |
| 299 | 1 | 0 | 1 | 1 | 1 | 0.0208 | 0.0498 | integral to membrane of membrane fraction |
| 3955 | 1 | 0 | 1 | 1 | 1 | 0.0208 | 0.0498 | NAD(P)H dehydrogenase (quinone) activity |
| 3945 | 1 | 0 | 1 | 1 | 1 | 0.0208 | 0.0498 | N-acetyllactosamine synthase activity |
| 3831 | 1 | 0 | 1 | 1 | 1 | 0.0208 | 0.0498 | beta-N-acetylglucosaminylglycopeptide beta-1,4-galactosyltransferase activity |
| 46951 | 1 | 0 | 1 | 1 | 1 | 0.0208 | 0.0498 | ketone body biosynthesis |
| 46950 | 1 | 0 | 1 | 1 | 1 | 0.0208 | 0.0498 | ketone body metabolism |
| 15734 | 1 | 0 | 1 | 1 | 1 | 0.0208 | 0.0498 | taurine transport |
| 50080 | 1 | 0 | 1 | 1 | 1 | 0.0208 | 0.0498 | malonyl-CoA decarboxylase activity |
| 15679 | 1 | 0 | 1 | 1 | 1 | 0.0208 | 0.0498 | plasma membrane copper ion transport |
| 3692 | 1 | 0 | 1 | 1 | 1 | 0.0208 | 0.0498 | left-handed Z-DNA binding |
| 46503 | 1 | 0 | 1 | 1 | 1 | 0.0208 | 0.0498 | glycerolipid catabolism |
| 46464 | 1 | 0 | 1 | 1 | 1 | 0.0208 | 0.0498 | acylglycerol catabolism |
| 46461 | 1 | 0 | 1 | 1 | 1 | 0.0208 | 0.0498 | neutral lipid catabolism |
| 8160 | 1 | 0 | 1 | 1 | 1 | 0.0208 | 0.0498 | protein tyrosine phosphatase activator activity |
| 46340 | 1 | 0 | 1 | 1 | 1 | 0.0208 | 0.0498 | diacylglycerol catabolism |
| 82 | 29 | 4 | 0 | 4 | 0.0091 | 1 | 0.0534 | G1/S transition of mitotic cell cycle |
| 6633 | 29 | 3 | 1 | 4 | 0.0502 | 0.4572 | 0.0534 | fatty acid biosynthesis |
| 5743 | 55 | 3 | 3 | 6 | 0.2129 | 0.1052 | 0.0538 | mitochondrial inner membrane |
| 16740 | 520 | 18 | 16 | 34 | 0.2434 | 0.0667 | 0.0539 | transferase activity |
| 4685 | 8 | 2 | 0 | 2 | 0.0208 | 1 | 0.0566 | calcium- and calmodulin-dependent protein kinase activity |
| 7613 | 8 | 2 | 0 | 2 | 0.0208 | 1 | 0.0566 | memory |
| 4864 | 8 | 1 | 1 | 2 | 0.2099 | 0.1547 | 0.0566 | protein phosphatase inhibitor activity |
| 45088 | 8 | 1 | 1 | 2 | 0.2099 | 0.1547 | 0.0566 | regulation of innate immune response |
| 30595 | 18 | 2 | 1 | 3 | 0.0943 | 0.3153 | 0.0571 | immune cell chemotaxis |
| 19888 | 18 | 1 | 2 | 3 | 0.4118 | 0.0526 | 0.0571 | protein phosphatase regulator activity |
| 19208 | 18 | 1 | 2 | 3 | 0.4118 | 0.0526 | 0.0571 | phosphatase regulator activity |
| 5604 | 18 | 1 | 2 | 3 | 0.4118 | 0.0526 | 0.0571 | basement membrane |
| 6805 | 18 | 0 | 3 | 3 | 1 | 0.0056 | 0.0571 | xenobiotic metabolism |
| 46849 | 44 | 5 | 0 | 5 | 0.0083 | 1 | 0.0654 | bone remodeling |

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|---|---|---|---|---|---|---|---|---|
| 6928 | 231 | 12 | 5 | 17 | 0.0341 | 0.5293 | 0.0654 | cell motility |
| 45597 | 19 | 2 | 1 | 3 | 0.1035 | 0.3296 | 0.0654 | positive regulation of cell differentiation |
| 16042 | 44 | 3 | 2 | 5 | 0.1339 | 0.2322 | 0.0654 | lipid catabolism |
| 6979 | 44 | 1 | 4 | 5 | 0.7278 | 0.0125 | 0.0654 | response to oxidative stress |
| 16627 | 19 | 0 | 3 | 3 | 1 | 0.0066 | 0.0654 | oxidoreductase activity, acting on the CH-CH group of donors |
| 9410 | 19 | 0 | 3 | 3 | 1 | 0.0066 | 0.0654 | response to xenobiotic stimulus |
| 7416 | 31 | 3 | 1 | 4 | 0.0593 | 0.4797 | 0.0655 | synaptogenesis |
| 5740 | 87 | 4 | 4 | 8 | 0.2445 | 0.1058 | 0.0661 | mitochondrial membrane |
| 4857 | 103 | 5 | 4 | 9 | 0.1777 | 0.1651 | 0.069 | enzyme inhibitor activity |
| 4707 | 9 | 2 | 0 | 2 | 0.0263 | 1 | 0.0705 | MAP kinase activity |
| 9156 | 9 | 2 | 0 | 2 | 0.0263 | 1 | 0.0705 | ribonucleoside monophosphate biosynthesis |
| 5540 | 9 | 2 | 0 | 2 | 0.0263 | 1 | 0.0705 | hyaluronic acid binding |
| 1565 | 9 | 1 | 1 | 2 | 0.2328 | 0.1723 | 0.0705 | phorbol ester receptor activity |
| 16814 | 9 | 1 | 1 | 2 | 0.2328 | 0.1723 | 0.0705 | hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in cyclic amidi |
| 19212 | 9 | 1 | 1 | 2 | 0.2328 | 0.1723 | 0.0705 | phosphatase inhibitor activity |
| 5890 | 9 | 1 | 1 | 2 | 0.2328 | 0.1723 | 0.0705 | sodium:potassium-exchanging ATPase complex |
| 16460 | 9 | 0 | 2 | 2 | 1 | 0.014 | 0.0705 | myosin II |
| 48167 | 20 | 3 | 0 | 3 | 0.0189 | 1 | 0.0742 | regulation of synaptic plasticity |
| 50900 | 20 | 2 | 1 | 3 | 0.1129 | 0.3436 | 0.0742 | immune cell migration |
| 30324 | 20 | 1 | 2 | 3 | 0.4456 | 0.0637 | 0.0742 | lung development |
| 30323 | 20 | 1 | 2 | 3 | 0.4456 | 0.0637 | 0.0742 | respiratory tube development |
| 16323 | 20 | 0 | 3 | 3 | 1 | 0.0076 | 0.0742 | basolateral plasma membrane |
| 19318 | 75 | 3 | 4 | 7 | 0.3715 | 0.0694 | 0.0777 | hexose metabolism |
| 5996 | 75 | 3 | 4 | 7 | 0.3715 | 0.0694 | 0.0777 | monosaccharide metabolism |
| 6091 | 138 | 5 | 6 | 11 | 0.3712 | 0.0658 | 0.0806 | energy pathways |
| null | 47 | 4 | 1 | 5 | 0.046 | 0.6293 | 0.0821 | obsolete_function |
| 30832 | 10 | 2 | 0 | 2 | 0.0322 | 1 | 0.0853 | regulation of actin filament length |
| 9161 | 10 | 2 | 0 | 2 | 0.0322 | 1 | 0.0853 | ribonucleoside monophosphate metabolism |
| 9124 | 10 | 2 | 0 | 2 | 0.0322 | 1 | 0.0853 | nucleoside monophosphate biosynthesis |
| 9112 | 10 | 2 | 0 | 2 | 0.0322 | 1 | 0.0853 | nucleobase metabolism |
| 46777 | 10 | 2 | 0 | 2 | 0.0322 | 1 | 0.0853 | autophosphorylation |
| 8064 | 10 | 2 | 0 | 2 | 0.0322 | 1 | 0.0853 | regulation of actin polymerization and/or depolymerization |
| 5391 | 10 | 1 | 1 | 2 | 0.2551 | 0.1896 | 0.0853 | sodium:potassium-exchanging ATPase activity |
| 7548 | 10 | 0 | 2 | 2 | 1 | 0.0172 | 0.0853 | sex differentiation |
| 5605 | 10 | 0 | 2 | 2 | 1 | 0.0172 | 0.0853 | basal lamina |
| 40007 | 108 | 7 | 2 | 9 | 0.0361 | 0.663 | 0.0872 | growth |
| 16779 | 22 | 2 | 1 | 3 | 0.1323 | 0.3707 | 0.0933 | nucleotidyltransferase activity |

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| 16836 | 22 | 1 | 2 | 3 | 0.4774 | 0.0754 | 0.0933 | hydro-lyase activity |
| 7179 | 35 | 3 | 1 | 4 | 0.0795 | 0.5219 | 0.0937 | transforming growth factor beta receptor signaling pathway |
| 9653 | 789 | 35 | 12 | 47 | 0.0044 | 0.9172 | 0.096 | morphogenesis |
| 15186 | 2 | 1 | 0 | 1 | 0.0572 | 1 | 0.0971 | L-glutamine transporter activity |
| 15079 | 2 | 1 | 0 | 1 | 0.0572 | 1 | 0.0971 | potassium ion transporter activity |
| 6868 | 2 | 1 | 0 | 1 | 0.0572 | 1 | 0.0971 | L-glutamine transport |
| 6546 | 2 | 1 | 0 | 1 | 0.0572 | 1 | 0.0971 | glycine catabolism |
| 1527 | 2 | 1 | 0 | 1 | 0.0572 | 1 | 0.0971 | microfibril |
| 16892 | 2 | 1 | 0 | 1 | 0.0572 | 1 | 0.0971 | endoribonuclease activity, producing 3'-phosphomonoesters |
| 4886 | 2 | 1 | 0 | 1 | 0.0572 | 1 | 0.0971 | retinoid-X receptor activity |
| 4619 | 2 | 1 | 0 | 1 | 0.0572 | 1 | 0.0971 | phosphoglycerate mutase activity |
| 4522 | 2 | 1 | 0 | 1 | 0.0572 | 1 | 0.0971 | pancreatic ribonuclease activity |
| 16417 | 2 | 1 | 0 | 1 | 0.0572 | 1 | 0.0971 | S-acyltransferase activity |
| 42564 | 2 | 1 | 0 | 1 | 0.0572 | 1 | 0.0971 | NLS-dependent protein nuclear import complex |
| 4274 | 2 | 1 | 0 | 1 | 0.0572 | 1 | 0.0971 | dipeptidyl-peptidase IV activity |
| 9093 | 2 | 1 | 0 | 1 | 0.0572 | 1 | 0.0971 | cysteine catabolism |
| 4105 | 2 | 1 | 0 | 1 | 0.0572 | 1 | 0.0971 | choline-phosphate cytidylyltransferase activity |
| 30346 | 2 | 1 | 0 | 1 | 0.0572 | 1 | 0.0971 | protein phosphatase 2B binding |
| 4083 | 2 | 1 | 0 | 1 | 0.0572 | 1 | 0.0971 | bisphosphoglycerate phosphatase activity |
| 19530 | 2 | 1 | 0 | 1 | 0.0572 | 1 | 0.0971 | taurine metabolism |
| 19452 | 2 | 1 | 0 | 1 | 0.0572 | 1 | 0.0971 | L-cysteine catabolism to taurine |
| 19448 | 2 | 1 | 0 | 1 | 0.0572 | 1 | 0.0971 | L-cysteine catabolism |
| 45667 | 2 | 1 | 0 | 1 | 0.0572 | 1 | 0.0971 | regulation of osteoblast differentiation |
| 7150 | 2 | 1 | 0 | 1 | 0.0572 | 1 | 0.0971 | growth pattern |
| 7044 | 2 | 1 | 0 | 1 | 0.0572 | 1 | 0.0971 | cell-substrate junction assembly |
| 5960 | 2 | 1 | 0 | 1 | 0.0572 | 1 | 0.0971 | glycine cleavage complex |
| 5763 | 2 | 1 | 0 | 1 | 0.0572 | 1 | 0.0971 | mitochondrial small ribosomal subunit |
| 314 | 2 | 1 | 0 | 1 | 0.0572 | 1 | 0.0971 | organellar small ribosomal subunit |
| 48156 | 2 | 1 | 0 | 1 | 0.0572 | 1 | 0.0971 | tau protein binding |
| 43205 | 2 | 1 | 0 | 1 | 0.0572 | 1 | 0.0971 | fibril |
| 38 | 2 | 1 | 0 | 1 | 0.0572 | 1 | 0.0971 | very-long-chain fatty acid metabolism |
| 3876 | 2 | 1 | 0 | 1 | 0.0572 | 1 | 0.0971 | AMP deaminase activity |
| 46627 | 2 | 1 | 0 | 1 | 0.0572 | 1 | 0.0971 | negative regulation of insulin receptor signaling pathway |
| 8332 | 2 | 1 | 0 | 1 | 0.0572 | 1 | 0.0971 | low voltage-gated calcium channel activity |
| 8282 | 2 | 1 | 0 | 1 | 0.0572 | 1 | 0.0971 | ATP-sensitive potassium channel complex |
| 8281 | 2 | 1 | 0 | 1 | 0.0572 | 1 | 0.0971 | sulfonylurea receptor activity |
| 46439 | 2 | 1 | 0 | 1 | 0.0572 | 1 | 0.0971 | L-cysteine metabolism |

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|---|---|---|---|---|---|---|---|---|
| 46328 | 2 | 1 | 0 | 1 | 0.0572 | 1 | 0.0971 | regulation of JNK cascade |
| 46324 | 2 | 1 | 0 | 1 | 0.0572 | 1 | 0.0971 | regulation of glucose import |
| 46323 | 2 | 1 | 0 | 1 | 0.0572 | 1 | 0.0971 | glucose import |
| 1798 | 2 | 0 | 1 | 1 | 1 | 0.0411 | 0.0971 | positive regulation of type IIa hypersensitivity |
| 1796 | 2 | 0 | 1 | 1 | 1 | 0.0411 | 0.0971 | regulation of type IIa hypersensitivity |
| 1794 | 2 | 0 | 1 | 1 | 1 | 0.0411 | 0.0971 | type IIa hypersensitivity |
| 6012 | 2 | 0 | 1 | 1 | 1 | 0.0411 | 0.0971 | galactose metabolism |
| 16880 | 2 | 0 | 1 | 1 | 1 | 0.0411 | 0.0971 | acid-ammonia (or amide) ligase activity |
| 4745 | 2 | 0 | 1 | 1 | 1 | 0.0411 | 0.0971 | retinol dehydrogenase activity |
| 16553 | 2 | 0 | 1 | 1 | 1 | 0.0411 | 0.0971 | base conversion or substitution editing |
| 16508 | 2 | 0 | 1 | 1 | 1 | 0.0411 | 0.0971 | long-chain-enoyl-CoA hydratase activity |
| 4478 | 2 | 0 | 1 | 1 | 1 | 0.0411 | 0.0971 | methionine adenosyltransferase activity |
| 4465 | 2 | 0 | 1 | 1 | 1 | 0.0411 | 0.0971 | lipoprotein lipase activity |
| 4461 | 2 | 0 | 1 | 1 | 1 | 0.0411 | 0.0971 | lactose synthase activity |
| 4421 | 2 | 0 | 1 | 1 | 1 | 0.0411 | 0.0971 | hydroxymethylglutaryl-CoA synthase activity |
| 16316 | 2 | 0 | 1 | 1 | 1 | 0.0411 | 0.0971 | phosphatidylinositol-3,4-bisphosphate 4-phosphatase activity |
| 30548 | 2 | 0 | 1 | 1 | 1 | 0.0411 | 0.0971 | acetylcholine receptor regulator activity |
| 16211 | 2 | 0 | 1 | 1 | 1 | 0.0411 | 0.0971 | ammonia ligase activity |
| 4234 | 2 | 0 | 1 | 1 | 1 | 0.0411 | 0.0971 | macrophage elastase activity |
| 4128 | 2 | 0 | 1 | 1 | 1 | 0.0411 | 0.0971 | cytochrome-b5 reductase activity |
| 19864 | 2 | 0 | 1 | 1 | 1 | 0.0411 | 0.0971 | IgG binding |
| 19770 | 2 | 0 | 1 | 1 | 1 | 0.0411 | 0.0971 | IgG receptor activity |
| 45995 | 2 | 0 | 1 | 1 | 1 | 0.0411 | 0.0971 | regulation of embryonic development |
| 45785 | 2 | 0 | 1 | 1 | 1 | 0.0411 | 0.0971 | positive regulation of cell adhesion |
| 5860 | 2 | 0 | 1 | 1 | 1 | 0.0411 | 0.0971 | non-muscle myosin |
| 5010 | 2 | 0 | 1 | 1 | 1 | 0.0411 | 0.0971 | insulin-like growth factor receptor activity |
| 8934 | 2 | 0 | 1 | 1 | 1 | 0.0411 | 0.0971 | inositol-1(or 4)-monophosphatase activity |
| 48009 | 2 | 0 | 1 | 1 | 1 | 0.0411 | 0.0971 | insulin-like growth factor receptor signaling pathway |
| 3969 | 2 | 0 | 1 | 1 | 1 | 0.0411 | 0.0971 | RNA editase activity |
| 8670 | 2 | 0 | 1 | 1 | 1 | 0.0411 | 0.0971 | 2,4-dienoyl-CoA reductase (NADPH) activity |
| 3726 | 2 | 0 | 1 | 1 | 1 | 0.0411 | 0.0971 | double-stranded RNA adenosine deaminase activity |
| 8157 | 2 | 0 | 1 | 1 | 1 | 0.0411 | 0.0971 | protein phosphatase 1 binding |
| 8132 | 2 | 0 | 1 | 1 | 1 | 0.0411 | 0.0971 | pancreatic elastase activity |
| 9123 | 11 | 2 | 0 | 2 | 0.0386 | 1 | 0.1009 | nucleoside monophosphate metabolism |
| 3773 | 11 | 2 | 0 | 2 | 0.0386 | 1 | 0.1009 | heat shock protein activity |
| 15718 | 11 | 1 | 1 | 2 | 0.2768 | 0.2065 | 0.1009 | monocarboxylic acid transport |
| 6810 | 907 | 36 | 17 | 53 | 0.0223 | 0.7266 | 0.1032 | transport |

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|---|---|---|---|---|---|---|---|---|
| 7623 | 23 | 2 | 1 | 3 | 0.1423 | 0.3838 | 0.1036 | circadian rhythm |
| 16616 | 51 | 2 | 3 | 5 | 0.4383 | 0.0885 | 0.1076 | oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as ac |
| 16564 | 37 | 3 | 1 | 4 | 0.0906 | 0.5417 | 0.1096 | transcriptional repressor activity |
| 7605 | 37 | 3 | 1 | 4 | 0.0906 | 0.5417 | 0.1096 | perception of sound |
| 19838 | 37 | 2 | 2 | 4 | 0.2914 | 0.1787 | 0.1096 | growth factor binding |
| 8150 | 3795 | 111 | 83 | 194 | 0.4542 | 0.0641 | 0.1123 | biological_process |
| 5891 | 24 | 3 | 0 | 3 | 0.0309 | 1 | 0.1142 | voltage-gated calcium channel complex |
| 6956 | 24 | 2 | 1 | 3 | 0.1524 | 0.3967 | 0.1142 | complement activation |
| 6959 | 67 | 2 | 4 | 6 | 0.5842 | 0.0495 | 0.1144 | humoral immune response |
| 6469 | 12 | 2 | 0 | 2 | 0.0455 | 1 | 0.1172 | negative regulation of protein kinase activity |
| 5788 | 12 | 2 | 0 | 2 | 0.0455 | 1 | 0.1172 | endoplasmic reticulum lumen |
| 8154 | 12 | 2 | 0 | 2 | 0.0455 | 1 | 0.1172 | actin polymerization and/or depolymerization |
| 6879 | 12 | 1 | 1 | 2 | 0.2978 | 0.223 | 0.1172 | iron ion homeostasis |
| 45637 | 12 | 1 | 1 | 2 | 0.2978 | 0.223 | 0.1172 | regulation of myeloid blood cell differentiation |
| 5178 | 12 | 1 | 1 | 2 | 0.2978 | 0.223 | 0.1172 | integrin binding |
| 1763 | 12 | 0 | 2 | 2 | 1 | 0.0246 | 0.1172 | branching morphogenesis |
| 4437 | 12 | 0 | 2 | 2 | 1 | 0.0246 | 0.1172 | inositol or phosphatidylinositol phosphatase activity |
| 15674 | 83 | 6 | 1 | 7 | 0.0322 | 0.828 | 0.1173 | di-, tri-valent inorganic cation transport |
| 50954 | 38 | 3 | 1 | 4 | 0.0964 | 0.5513 | 0.118 | sensory perception of mechanical stimulus |
| 6800 | 53 | 1 | 4 | 5 | 0.7918 | 0.0235 | 0.1216 | oxygen and reactive oxygen species metabolism |
| 30163 | 218 | 10 | 5 | 15 | 0.0988 | 0.4772 | 0.1236 | protein catabolism |
| 7178 | 39 | 3 | 1 | 4 | 0.1023 | 0.5608 | 0.1267 | transmembrane receptor protein serine/threonine kinase signaling pathway |
| 50982 | 39 | 3 | 1 | 4 | 0.1023 | 0.5608 | 0.1267 | detection of mechanical stimulus |
| 16049 | 69 | 5 | 1 | 6 | 0.0486 | 0.768 | 0.1269 | cell growth |
| 6731 | 69 | 2 | 4 | 6 | 0.6004 | 0.0541 | 0.1269 | coenzyme and prosthetic group metabolism |
| 16614 | 54 | 2 | 3 | 5 | 0.4678 | 0.1009 | 0.1289 | oxidoreductase activity, acting on CH-OH group of donors |
| 8361 | 70 | 5 | 1 | 6 | 0.0511 | 0.7729 | 0.1334 | regulation of cell size |
| 8629 | 13 | 2 | 0 | 2 | 0.0528 | 1 | 0.1342 | induction of apoptosis by intracellular signals |
| 30855 | 13 | 1 | 1 | 2 | 0.3182 | 0.2392 | 0.1342 | epithelial cell differentiation |
| 8286 | 13 | 1 | 1 | 2 | 0.3182 | 0.2392 | 0.1342 | insulin receptor signaling pathway |
| 42995 | 40 | 2 | 2 | 4 | 0.3238 | 0.2014 | 0.1356 | cell projection |
| 5245 | 26 | 3 | 0 | 3 | 0.038 | 1 | 0.1367 | voltage-gated calcium channel activity |
| 16835 | 26 | 1 | 2 | 3 | 0.5357 | 0.1006 | 0.1367 | carbon-oxygen lyase activity |
| 6930 | 3 | 1 | 0 | 1 | 0.0845 | 1 | 0.142 | substrate-bound cell migration, cell extension |
| 6656 | 3 | 1 | 0 | 1 | 0.0845 | 1 | 0.142 | phosphatidylcholine biosynthesis |
| 6636 | 3 | 1 | 0 | 1 | 0.0845 | 1 | 0.142 | fatty acid desaturation |
| 1649 | 3 | 1 | 0 | 1 | 0.0845 | 1 | 0.142 | osteoblast differentiation |

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|---|---|---|---|---|---|---|---|---|
| 16868 | 3 | 1 | 0 | 1 | 0.0845 | 1 | 0.142 | intramolecular transferase activity, phosphotransferases |
| 4862 | 3 | 1 | 0 | 1 | 0.0845 | 1 | 0.142 | cAMP-dependent protein kinase inhibitor activity |
| 16805 | 3 | 1 | 0 | 1 | 0.0845 | 1 | 0.142 | dipeptidase activity |
| 4660 | 3 | 1 | 0 | 1 | 0.0845 | 1 | 0.142 | protein farnesyltransferase activity |
| 42775 | 3 | 1 | 0 | 1 | 0.0845 | 1 | 0.142 | ATP synthesis coupled electron transport (sensu Eukarya) |
| 42773 | 3 | 1 | 0 | 1 | 0.0845 | 1 | 0.142 | ATP synthesis coupled electron transport |
| 4293 | 3 | 1 | 0 | 1 | 0.0845 | 1 | 0.142 | tissue kallikrein activity |
| 4287 | 3 | 1 | 0 | 1 | 0.0845 | 1 | 0.142 | prolyl oligopeptidase activity |
| 30502 | 3 | 1 | 0 | 1 | 0.0845 | 1 | 0.142 | negative regulation of bone mineralization |
| 4047 | 3 | 1 | 0 | 1 | 0.0845 | 1 | 0.142 | aminomethyltransferase activity |
| 30162 | 3 | 1 | 0 | 1 | 0.0845 | 1 | 0.142 | regulation of proteolysis and peptidolysis |
| 30032 | 3 | 1 | 0 | 1 | 0.0845 | 1 | 0.142 | lamellipodium biogenesis |
| 5546 | 3 | 1 | 0 | 1 | 0.0845 | 1 | 0.142 | phosphatidylinositol-4,5-bisphosphate binding |
| 5381 | 3 | 1 | 0 | 1 | 0.0845 | 1 | 0.142 | iron ion transporter activity |
| 8883 | 3 | 1 | 0 | 1 | 0.0845 | 1 | 0.142 | glutamyl-tRNA reductase activity |
| 3708 | 3 | 1 | 0 | 1 | 0.0845 | 1 | 0.142 | retinoic acid receptor activity |
| 46626 | 3 | 1 | 0 | 1 | 0.0845 | 1 | 0.142 | regulation of insulin receptor signaling pathway |
| 15272 | 3 | 1 | 0 | 1 | 0.0845 | 1 | 0.142 | ATP-activated inward rectifier potassium channel activity |
| 6090 | 3 | 0 | 1 | 1 | 1 | 0.0611 | 0.142 | pyruvate metabolism |
| 6086 | 3 | 0 | 1 | 1 | 1 | 0.0611 | 0.142 | acetyl-CoA biosynthesis from pyruvate |
| 9954 | 3 | 0 | 1 | 1 | 1 | 0.0611 | 0.142 | proximal/distal pattern formation |
| 9925 | 3 | 0 | 1 | 1 | 1 | 0.0611 | 0.142 | basal plasma membrane |
| 4939 | 3 | 0 | 1 | 1 | 1 | 0.0611 | 0.142 | beta-adrenergic receptor activity |
| 16803 | 3 | 0 | 1 | 1 | 1 | 0.0611 | 0.142 | ether hydrolase activity |
| 4740 | 3 | 0 | 1 | 1 | 1 | 0.0611 | 0.142 | [pyruvate dehydrogenase (lipoamide)] kinase activity |
| 51020 | 3 | 0 | 1 | 1 | 1 | 0.0611 | 0.142 | GTPase binding |
| 9312 | 3 | 0 | 1 | 1 | 1 | 0.0611 | 0.142 | oligosaccharide biosynthesis |
| 42708 | 3 | 0 | 1 | 1 | 1 | 0.0611 | 0.142 | elastase activity |
| 4463 | 3 | 0 | 1 | 1 | 1 | 0.0611 | 0.142 | leukotriene-A4 hydrolase activity |
| 16312 | 3 | 0 | 1 | 1 | 1 | 0.0611 | 0.142 | inositol bisphosphate phosphatase activity |
| 4332 | 3 | 0 | 1 | 1 | 1 | 0.0611 | 0.142 | fructose-bisphosphate aldolase activity |
| 4301 | 3 | 0 | 1 | 1 | 1 | 0.0611 | 0.142 | epoxide hydrolase activity |
| 4000 | 3 | 0 | 1 | 1 | 1 | 0.0611 | 0.142 | adenosine deaminase activity |
| 30238 | 3 | 0 | 1 | 1 | 1 | 0.0611 | 0.142 | male sex determination |
| 19763 | 3 | 0 | 1 | 1 | 1 | 0.0611 | 0.142 | immunoglobulin receptor activity |
| 45213 | 3 | 0 | 1 | 1 | 1 | 0.0611 | 0.142 | neurotransmitter receptor metabolism |
| 5902 | 3 | 0 | 1 | 1 | 1 | 0.0611 | 0.142 | microvillus |

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| 5697 | 3 | 0 | 1 | 1 | 1 | 0.0611 | 0.142 | telomerase holoenzyme complex |
| 5606 | 3 | 0 | 1 | 1 | 1 | 0.0611 | 0.142 | laminin-1 |
| 3988 | 3 | 0 | 1 | 1 | 1 | 0.0611 | 0.142 | acetyl-CoA C-acyltransferase activity |
| 43027 | 3 | 0 | 1 | 1 | 1 | 0.0611 | 0.142 | caspase inhibitor activity |
| 3720 | 3 | 0 | 1 | 1 | 1 | 0.0611 | 0.142 | telomerase activity |
| 15321 | 3 | 0 | 1 | 1 | 1 | 0.0611 | 0.142 | sodium-dependent phosphate transporter activity |
| 15302 | 3 | 0 | 1 | 1 | 1 | 0.0611 | 0.142 | uncoupling protein activity |
| 46339 | 3 | 0 | 1 | 1 | 1 | 0.0611 | 0.142 | diacylglycerol metabolism |
| 15980 | 88 | 5 | 2 | 7 | 0.1106 | 0.5507 | 0.1465 | energy derivation by oxidation of organic compounds |
| 6112 | 27 | 3 | 0 | 3 | 0.0419 | 1 | 0.1485 | energy reserve metabolism |
| 7622 | 27 | 2 | 1 | 3 | 0.1836 | 0.4338 | 0.1485 | rhythmic behavior |
| 6730 | 14 | 1 | 1 | 2 | 0.338 | 0.255 | 0.1516 | one-carbon compound metabolism |
| 4364 | 14 | 0 | 2 | 2 | 1 | 0.033 | 0.1516 | glutathione transferase activity |
| 6732 | 57 | 1 | 4 | 5 | 0.8152 | 0.0298 | 0.152 | coenzyme metabolism |
| 40008 | 73 | 4 | 2 | 6 | 0.1604 | 0.4511 | 0.1538 | regulation of growth |
| 43170 | 1149 | 44 | 20 | 64 | 0.0194 | 0.8571 | 0.1568 | macromolecule metabolism |
| 1558 | 58 | 4 | 1 | 5 | 0.0862 | 0.7066 | 0.1601 | regulation of cell growth |
| 9260 | 28 | 3 | 0 | 3 | 0.046 | 1 | 0.1606 | ribonucleotide biosynthesis |
| 6096 | 28 | 2 | 1 | 3 | 0.1941 | 0.4456 | 0.1606 | glycolysis |
| 5319 | 28 | 1 | 2 | 3 | 0.5624 | 0.114 | 0.1606 | lipid transporter activity |
| 16310 | 282 | 14 | 4 | 18 | 0.0321 | 0.8481 | 0.1621 | phosphorylation |
| 5262 | 43 | 4 | 0 | 4 | 0.0347 | 1 | 0.1638 | calcium channel activity |
| 16298 | 43 | 3 | 1 | 4 | 0.1274 | 0.5965 | 0.1638 | lipase activity |
| 16064 | 43 | 1 | 3 | 4 | 0.7196 | 0.0589 | 0.1638 | humoral defense mechanism (sensu Vertebrata) |
| 6508 | 212 | 9 | 5 | 14 | 0.1598 | 0.4525 | 0.168 | proteolysis and peptidolysis |
| 16789 | 59 | 4 | 1 | 5 | 0.0905 | 0.7128 | 0.1683 | carboxylic ester hydrolase activity |
| 6006 | 59 | 3 | 2 | 5 | 0.2438 | 0.3481 | 0.1683 | glucose metabolism |
| 6958 | 15 | 1 | 1 | 2 | 0.3573 | 0.2706 | 0.1695 | complement activation, classical pathway |
| 16831 | 15 | 1 | 1 | 2 | 0.3573 | 0.2706 | 0.1695 | carboxy-lyase activity |
| 50776 | 15 | 1 | 1 | 2 | 0.3573 | 0.2706 | 0.1695 | regulation of immune response |
| 46915 | 15 | 1 | 1 | 2 | 0.3573 | 0.2706 | 0.1695 | transition metal ion transporter activity |
| 9636 | 15 | 0 | 2 | 2 | 1 | 0.0376 | 0.1695 | response to toxin |
| 5576 | 1059 | 40 | 19 | 59 | 0.0334 | 0.808 | 0.171 | extracellular |
| 4867 | 29 | 2 | 1 | 3 | 0.2048 | 0.4572 | 0.1729 | serine-type endopeptidase inhibitor activity |
| 51094 | 29 | 2 | 1 | 3 | 0.2048 | 0.4572 | 0.1729 | positive regulation of development |
| 9986 | 44 | 3 | 1 | 4 | 0.1339 | 0.605 | 0.1736 | cell surface |
| 4263 | 44 | 3 | 1 | 4 | 0.1339 | 0.605 | 0.1736 | chymotrypsin activity |

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|---|---|---|---|---|---|---|---|---|
| 5783 | 196 | 7 | 6 | 13 | 0.3407 | 0.221 | 0.1755 | endoplasmic reticulum |
| 6812 | 250 | 13 | 3 | 16 | 0.0276 | 0.9005 | 0.1774 | cation transport |
| 16477 | 93 | 5 | 2 | 7 | 0.1314 | 0.581 | 0.1788 | cell migration |
| 9628 | 215 | 6 | 8 | 14 | 0.5989 | 0.0763 | 0.181 | response to abiotic stimulus |
| 7517 | 77 | 4 | 2 | 6 | 0.1833 | 0.4788 | 0.183 | muscle development |
| 4295 | 45 | 3 | 1 | 4 | 0.1406 | 0.6132 | 0.1836 | trypsin activity |
| 6544 | 4 | 1 | 0 | 1 | 0.1111 | 1 | 0.1848 | glycine metabolism |
| 16866 | 4 | 1 | 0 | 1 | 0.1111 | 1 | 0.1848 | intramolecular transferase activity |
| 4865 | 4 | 1 | 0 | 1 | 0.1111 | 1 | 0.1848 | type 1 serine/threonine specific protein phosphatase inhibitor activity |
| 9649 | 4 | 1 | 0 | 1 | 0.1111 | 1 | 0.1848 | entrainment of circadian clock |
| 16778 | 4 | 1 | 0 | 1 | 0.1111 | 1 | 0.1848 | diphosphotransferase activity |
| 4749 | 4 | 1 | 0 | 1 | 0.1111 | 1 | 0.1848 | ribose-phosphate diphosphokinase activity |
| 4708 | 4 | 1 | 0 | 1 | 0.1111 | 1 | 0.1848 | MAP kinase kinase activity |
| 51017 | 4 | 1 | 0 | 1 | 0.1111 | 1 | 0.1848 | actin filament bundle formation |
| 4396 | 4 | 1 | 0 | 1 | 0.1111 | 1 | 0.1848 | hexokinase activity |
| 30514 | 4 | 1 | 0 | 1 | 0.1111 | 1 | 0.1848 | negative regulation of BMP signaling pathway |
| 30512 | 4 | 1 | 0 | 1 | 0.1111 | 1 | 0.1848 | negative regulation of transforming growth factor beta receptor signaling pathway |
| 30510 | 4 | 1 | 0 | 1 | 0.1111 | 1 | 0.1848 | regulation of BMP signaling pathway |
| 4245 | 4 | 1 | 0 | 1 | 0.1111 | 1 | 0.1848 | neprilysin activity |
| 30279 | 4 | 1 | 0 | 1 | 0.1111 | 1 | 0.1848 | negative regulation of ossification |
| 19841 | 4 | 1 | 0 | 1 | 0.1111 | 1 | 0.1848 | retinol binding |
| 30169 | 4 | 1 | 0 | 1 | 0.1111 | 1 | 0.1848 | low-density lipoprotein binding |
| 45446 | 4 | 1 | 0 | 1 | 0.1111 | 1 | 0.1848 | endothelial cell differentiation |
| 5954 | 4 | 1 | 0 | 1 | 0.1111 | 1 | 0.1848 | calcium- and calmodulin-dependent protein kinase complex |
| 50678 | 4 | 1 | 0 | 1 | 0.1111 | 1 | 0.1848 | regulation of epithelial cell proliferation |
| 17158 | 4 | 1 | 0 | 1 | 0.1111 | 1 | 0.1848 | regulation of calcium ion-dependent exocytosis |
| 5041 | 4 | 1 | 0 | 1 | 0.1111 | 1 | 0.1848 | low-density lipoprotein receptor activity |
| 98 | 4 | 1 | 0 | 1 | 0.1111 | 1 | 0.1848 | sulfur amino acid catabolism |
| 80 | 4 | 1 | 0 | 1 | 0.1111 | 1 | 0.1848 | G1 phase of mitotic cell cycle |
| 46470 | 4 | 1 | 0 | 1 | 0.1111 | 1 | 0.1848 | phosphatidylcholine metabolism |
| 6878 | 4 | 0 | 1 | 1 | 1 | 0.0806 | 0.1848 | copper ion homeostasis |
| 1569 | 4 | 0 | 1 | 1 | 1 | 0.0806 | 0.1848 | patterning of blood vessels |
| 6085 | 4 | 0 | 1 | 1 | 1 | 0.0806 | 0.1848 | acetyl-CoA biosynthesis |
| 16934 | 4 | 0 | 1 | 1 | 1 | 0.0806 | 0.1848 | glycine-gated chloride channel activity |
| 4891 | 4 | 0 | 1 | 1 | 1 | 0.0806 | 0.1848 | glycine-inhibited chloride channel activity |
| 16832 | 4 | 0 | 1 | 1 | 1 | 0.0806 | 0.1848 | aldehyde-lyase activity |
| 16801 | 4 | 0 | 1 | 1 | 1 | 0.0806 | 0.1848 | hydrolase activity, acting on ether bonds |

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| 16547 | 4 | 0 | 1 | 1 | 1 | 0.0806 | 0.1848 | RNA editing |
| 16453 | 4 | 0 | 1 | 1 | 1 | 0.0806 | 0.1848 | C-acetyltransferase activity |
| 30545 | 4 | 0 | 1 | 1 | 1 | 0.0806 | 0.1848 | receptor regulator activity |
| 45884 | 4 | 0 | 1 | 1 | 1 | 0.0806 | 0.1848 | regulation of survival gene product activity |
| 19413 | 4 | 0 | 1 | 1 | 1 | 0.0806 | 0.1848 | acetate biosynthesis |
| 7223 | 4 | 0 | 1 | 1 | 1 | 0.0806 | 0.1848 | frizzled-2 signaling pathway |
| 45123 | 4 | 0 | 1 | 1 | 1 | 0.0806 | 0.1848 | cellular extravasation |
| 5639 | 4 | 0 | 1 | 1 | 1 | 0.0806 | 0.1848 | integral to nuclear inner membrane |
| 781 | 4 | 0 | 1 | 1 | 1 | 0.0806 | 0.1848 | chromosome, telomeric region |
| 303 | 4 | 0 | 1 | 1 | 1 | 0.0806 | 0.1848 | response to superoxide |
| 3985 | 4 | 0 | 1 | 1 | 1 | 0.0806 | 0.1848 | acetyl-CoA C-acetyltransferase activity |
| 3964 | 4 | 0 | 1 | 1 | 1 | 0.0806 | 0.1848 | RNA-directed DNA polymerase activity |
| 43112 | 4 | 0 | 1 | 1 | 1 | 0.0806 | 0.1848 | receptor metabolism |
| 15909 | 4 | 0 | 1 | 1 | 1 | 0.0806 | 0.1848 | long-chain fatty acid transport |
| 46912 | 4 | 0 | 1 | 1 | 1 | 0.0806 | 0.1848 | transferase activity, transferring acyl groups, acyl groups converted into alkyl on trar |
| 8634 | 4 | 0 | 1 | 1 | 1 | 0.0806 | 0.1848 | negative regulation of survival gene product activity |
| 6816 | 61 | 5 | 0 | 5 | 0.0308 | 1 | 0.1852 | calcium ion transport |
| 5244 | 111 | 8 | 0 | 8 | 0.0144 | 1 | 0.1862 | voltage-gated ion channel activity |
| 6119 | 16 | 2 | 0 | 2 | 0.0768 | 1 | 0.1877 | oxidative phosphorylation |
| 16790 | 16 | 2 | 0 | 2 | 0.0768 | 1 | 0.1877 | thiolester hydrolase activity |
| 9069 | 16 | 2 | 0 | 2 | 0.0768 | 1 | 0.1877 | serine family amino acid metabolism |
| 19200 | 16 | 2 | 0 | 2 | 0.0768 | 1 | 0.1877 | carbohydrate kinase activity |
| 7585 | 16 | 1 | 1 | 2 | 0.376 | 0.2858 | 0.1877 | respiratory gaseous exchange |
| 46916 | 16 | 1 | 1 | 2 | 0.376 | 0.2858 | 0.1877 | transition metal ion homeostasis |
| 16684 | 16 | 0 | 2 | 2 | 1 | 0.0424 | 0.1877 | oxidoreductase activity, acting on peroxide as acceptor |
| 4601 | 16 | 0 | 2 | 2 | 1 | 0.0424 | 0.1877 | peroxidase activity |
| 5839 | 16 | 0 | 2 | 2 | 1 | 0.0424 | 0.1877 | proteasome core complex (sensu Eukarya) |
| 5516 | 78 | 3 | 3 | 6 | 0.3953 | 0.2199 | 0.1906 | calmodulin binding |
| 45859 | 46 | 4 | 0 | 4 | 0.043 | 1 | 0.1939 | regulation of protein kinase activity |
| 15405 | 46 | 3 | 1 | 4 | 0.1475 | 0.6214 | 0.1939 | P-P-bond-hydrolysis-driven transporter activity |
| 42803 | 31 | 2 | 1 | 3 | 0.2263 | 0.4797 | 0.1984 | protein homodimerization activity |
| 8238 | 31 | 2 | 1 | 3 | 0.2263 | 0.4797 | 0.1984 | exopeptidase activity |
| 30001 | 219 | 12 | 2 | 14 | 0.0237 | 0.9476 | 0.1991 | metal ion transport |
| 6796 | 329 | 14 | 6 | 20 | 0.0921 | 0.6906 | 0.2013 | phosphate metabolism |
| 6793 | 329 | 14 | 6 | 20 | 0.0921 | 0.6906 | 0.2013 | phosphorus metabolism |
| 15399 | 63 | 4 | 1 | 5 | 0.1087 | 0.7363 | 0.2028 | primary active transporter activity |
| 1666 | 17 | 1 | 1 | 2 | 0.3942 | 0.3007 | 0.2062 | response to hypoxia |

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| 4177 | 17 | 1 | 1 | 2 | 0.3942 | 0.3007 | 0.2062 | aminopeptidase activity |
| 9259 | 32 | 3 | 0 | 3 | 0.0641 | 1 | 0.2115 | ribonucleotide metabolism |
| 6007 | 32 | 2 | 1 | 3 | 0.2371 | 0.4906 | 0.2115 | glucose catabolism |
| 51082 | 32 | 2 | 1 | 3 | 0.2371 | 0.4906 | 0.2115 | unfolded protein binding |
| 16055 | 32 | 1 | 2 | 3 | 0.6113 | 0.142 | 0.2115 | Wnt receptor signaling pathway |
| 8324 | 98 | 5 | 2 | 7 | 0.1538 | 0.6099 | 0.2139 | cation transporter activity |
| 4674 | 188 | 9 | 3 | 12 | 0.0934 | 0.7576 | 0.2243 | protein serine/threonine kinase activity |
| 46873 | 33 | 2 | 1 | 3 | 0.248 | 0.5012 | 0.2247 | metal ion transporter activity |
| 15662 | 33 | 2 | 1 | 3 | 0.248 | 0.5012 | 0.2247 | ATPase activity, coupled to transmembrane movement of ions, phosphorylative mec |
| 5759 | 33 | 1 | 2 | 3 | 0.6227 | 0.1492 | 0.2247 | mitochondrial matrix |
| 6986 | 18 | 2 | 0 | 2 | 0.0943 | 1 | 0.2248 | response to unfolded protein |
| 6941 | 18 | 1 | 1 | 2 | 0.4118 | 0.3153 | 0.2248 | striated muscle contraction |
| 1726 | 5 | 1 | 0 | 1 | 0.1369 | 1 | 0.2254 | ruffles |
| 16909 | 5 | 1 | 0 | 1 | 0.1369 | 1 | 0.2254 | SAP kinase activity |
| 16894 | 5 | 1 | 0 | 1 | 0.1369 | 1 | 0.2254 | endonuclease activity, active with either ribo- or deoxyribonucleic acids and produci |
| 16806 | 5 | 1 | 0 | 1 | 0.1369 | 1 | 0.2254 | dipeptidyl-peptidase and tripeptidyl-peptidase activity |
| 30856 | 5 | 1 | 0 | 1 | 0.1369 | 1 | 0.2254 | regulation of epithelial cell differentiation |
| 16529 | 5 | 1 | 0 | 1 | 0.1369 | 1 | 0.2254 | sarcoplasmic reticulum |
| 16528 | 5 | 1 | 0 | 1 | 0.1369 | 1 | 0.2254 | sarcoplasm |
| 4521 | 5 | 1 | 0 | 1 | 0.1369 | 1 | 0.2254 | endoribonuclease activity |
| 4221 | 5 | 1 | 0 | 1 | 0.1369 | 1 | 0.2254 | ubiquitin thiolesterase activity |
| 30449 | 5 | 1 | 0 | 1 | 0.1369 | 1 | 0.2254 | regulation of complement activation |
| 42391 | 5 | 1 | 0 | 1 | 0.1369 | 1 | 0.2254 | regulation of membrane potential |
| 4024 | 5 | 1 | 0 | 1 | 0.1369 | 1 | 0.2254 | alcohol dehydrogenase activity, zinc-dependent |
| 4022 | 5 | 1 | 0 | 1 | 0.1369 | 1 | 0.2254 | alcohol dehydrogenase activity |
| 30228 | 5 | 1 | 0 | 1 | 0.1369 | 1 | 0.2254 | lipoprotein receptor activity |
| 30199 | 5 | 1 | 0 | 1 | 0.1369 | 1 | 0.2254 | collagen fibril organization |
| 30178 | 5 | 1 | 0 | 1 | 0.1369 | 1 | 0.2254 | negative regulation of Wnt receptor signaling pathway |
| 42102 | 5 | 1 | 0 | 1 | 0.1369 | 1 | 0.2254 | positive regulation of T-cell proliferation |
| 5761 | 5 | 1 | 0 | 1 | 0.1369 | 1 | 0.2254 | mitochondrial ribosome |
| 5744 | 5 | 1 | 0 | 1 | 0.1369 | 1 | 0.2254 | mitochondrial inner membrane presequence translocase complex |
| 50769 | 5 | 1 | 0 | 1 | 0.1369 | 1 | 0.2254 | positive regulation of neurogenesis |
| 50673 | 5 | 1 | 0 | 1 | 0.1369 | 1 | 0.2254 | epithelial cell proliferation |
| 313 | 5 | 1 | 0 | 1 | 0.1369 | 1 | 0.2254 | organellar ribosome |
| 17015 | 5 | 1 | 0 | 1 | 0.1369 | 1 | 0.2254 | regulation of transforming growth factor beta receptor signaling pathway |
| 15802 | 5 | 1 | 0 | 1 | 0.1369 | 1 | 0.2254 | basic amino acid transport |
| 15800 | 5 | 1 | 0 | 1 | 0.1369 | 1 | 0.2254 | acidic amino acid transport |