

| id | source | term_id | term_name | term_size | intersection_size | p_value |
|----|--------|------------|---|-----------|-------------------|---------|
| 1 | GO:BP | GO:0006270 | DNA replication initiation | 20 | 12 | 5.5e−06 |
| 2 | GO:BP | GO:0006261 | DNA−templated DNA replication | 75 | 20 | 6.4e−04 |
| 3 | GO:MF | GO:0003688 | DNA replication origin binding | 8 | 6 | 8.4e−04 |
| 4 | GO:BP | GO:0006260 | DNA replication | 116 | 25 | 1.5e−03 |
| 5 | GO:MF | GO:0030527 | structural constituent of chromatin | 78 | 16 | 1.7e−03 |
| 6 | GO:BP | GO:0009765 | photosynthesis, light harvesting | 31 | 10 | 3.2e−03 |
| 7 | GO:CC | GO:0042555 | MCM complex | 5 | 5 | 3.6e−03 |
| 8 | GO:MF | GO:0019840 | isoprenoid binding | 24 | 6 | 3.8e−03 |
| 9 | GO:MF | GO:0043178 | alcohol binding | 24 | 6 | 3.8e−03 |
| 10 | GO:MF | GO:0004864 | protein phosphatase inhibitor activity | 25 | 6 | 3.8e−03 |
| 11 | GO:MF | GO:0031492 | nucleosomal DNA binding | 20 | 7 | 3.8e−03 |
| 12 | GO:MF | GO:0010427 | abscisic acid binding | 22 | 6 | 3.8e−03 |
| 13 | GO:MF | GO:0042562 | hormone binding | 25 | 6 | 3.8e−03 |
| 14 | GO:MF | GO:0019212 | phosphatase inhibitor activity | 26 | 6 | 4.2e−03 |
| 15 | GO:BP | GO:0080163 | regulation of protein serine/threonine phosphatase activity | 17 | 6 | 4.9e−03 |
| 16 | GO:MF | GO:0016717 | oxidoreductase activity, acting on paired donors, with oxidation of a pair of donors resulting in the reduction of molecular oxygen to two molecules of water | 22 | 7 | 7.1e−03 |
| 17 | GO:MF | GO:0031491 | nucleosome binding | 24 | 7 | 7.6e−03 |
| 18 | GO:MF | GO:0015333 | peptide:proton symporter activity | 27 | 3 | 9.0e−03 |
| 19 | GO:MF | GO:0042937 | tripeptide transmembrane transporter activity | 6 | 2 | 9.5e−03 |
| 20 | GO:MF | GO:0043891 | glyceraldehyde−3−phosphate dehydrogenase (NAD(P)+) (phosphorylating) activity | 8 | 4 | 9.5e−03 |
| 21 | GO:MF | GO:0004365 | glyceraldehyde−3−phosphate dehydrogenase (NAD+) (phosphorylating) activity | 8 | 4 | 9.5e−03 |
| 22 | GO:MF | GO:0003682 | chromatin binding | 82 | 13 | 9.5e−03 |
| 23 | GO:MF | GO:0071916 | dipeptide transmembrane transporter activity | 6 | 2 | 9.5e−03 |
| 24 | GO:MF | GO:0016762 | xyloglucan:xyloglucosyl transferase activity | 32 | 8 | 1.0e−02 |
| 25 | GO:MF | GO:0005372 | water transmembrane transporter activity | 25 | 7 | 1.0e−02 |
| 26 | GO:MF | GO:0015250 | water channel activity | 25 | 7 | 1.0e−02 |
| 27 | GO:CC | GO:0031298 | replication fork protection complex | 7 | 4 | 1.4e−02 |
| 28 | GO:MF | GO:0031490 | chromatin DNA binding | 30 | 7 | 1.7e−02 |
| 29 | GO:MF | GO:0050661 | NADP binding | 63 | 3 | 1.7e−02 |
| 30 | GO:MF | GO:0033293 | monocarboxylic acid binding | 39 | 6 | 1.7e−02 |
| 31 | GO:BP | GO:1901874 | negative regulation of post−translational protein modification | 5 | 3 | 1.9e−02 |
| 32 | GO:BP | GO:0000076 | DNA replication checkpoint signaling | 9 | 4 | 1.9e−02 |
| 33 | GO:MF | GO:0004124 | cysteine synthase activity | 6 | 3 | 2.5e−02 |
| 34 | GO:MF | GO:1904680 | peptide transmembrane transporter activity | 53 | 3 | 3.0e−02 |
| 35 | GO:MF | GO:0035673 | oligopeptide transmembrane transporter activity | 53 | 3 | 3.0e−02 |
| 36 | GO:MF | GO:0008883 | glutamyl−tRNA reductase activity | 3 | 2 | 3.0e−02 |
| 37 | GO:MF | GO:0015318 | inorganic molecular entity transmembrane transporter activity | 434 | 9 | 3.2e−02 |
| 38 | GO:MF | GO:0015295 | solute:proton symporter activity | 57 | 3 | 3.2e−02 |
| 39 | GO:MF | GO:0042887 | amide transmembrane transporter activity | 57 | 3 | 3.2e−02 |
| 40 | GO:MF | GO:0019888 | protein phosphatase regulator activity | 46 | 6 | 3.2e−02 |
| 41 | GO:MF | GO:0000234 | phosphoethanolamine N−methyltransferase activity | 2 | 2 | 3.4e−02 |
| 42 | GO:MF | GO:0015291 | secondary active transmembrane transporter activity | 214 | 5 | 3.4e−02 |
| 43 | GO:MF | GO:0015294 | solute:monoatomic cation symporter activity | 60 | 3 | 3.4e−02 |
| 44 | GO:MF | GO:0019208 | phosphatase regulator activity | 48 | 6 | 3.5e−02 |
| 45 | GO:MF | GO:0008061 | chitin binding | 25 | 6 | 3.5e−02 |
| 46 | GO:MF | GO:0016835 | carbon−oxygen lyase activity | 149 | 19 | 3.6e−02 |
| 47 | GO:MF | GO:0003855 | 3−dehydroquinate dehydratase activity | 3 | 2 | 3.6e−02 |
| 48 | GO:MF | GO:0015293 | symporter activity | 66 | 3 | 3.9e−02 |
| 49 | GO:MF | GO:0017116 | single−stranded DNA helicase activity | 2 | 1 | 3.9e−02 |
| 50 | GO:BP | GO:0043666 | regulation of phosphoprotein phosphatase activity | 27 | 6 | 4.4e−02 |
| 51 | GO:BP | GO:0006334 | nucleosome assembly | 50 | 11 | 4.4e−02 |
| 52 | GO:BP | GO:0031570 | DNA integrity checkpoint signaling | 15 | 5 | 4.4e−02 |
| 53 | GO:BP | GO:0042938 | dipeptide transport | 6 | 2 | 4.4e−02 |
| 54 | GO:BP | GO:0035304 | regulation of protein dephosphorylation | 28 | 6 | 4.4e−02 |
| 55 | GO:BP | GO:0034728 | nucleosome organization | 51 | 11 | 4.4e−02 |
| 56 | GO:BP | GO:1901988 | negative regulation of cell cycle phase transition | 23 | 6 | 4.5e−02 |
| 57 | GO:BP | GO:0010921 | regulation of phosphatase activity | 30 | 6 | 4.5e−02 |
| 58 | GO:BP | GO:0006269 | DNA replication, synthesis of RNA primer | 3 | 3 | 4.5e−02 |
| 59 | GO:BP | GO:0000075 | cell cycle checkpoint signaling | 23 | 6 | 4.5e−02 |
| 60 | GO:BP | GO:0032508 | DNA duplex unwinding | 20 | 7 | 4.5e−02 |
| 61 | GO:BP | GO:0046364 | monosaccharide biosynthetic process | 14 | 2 | 4.6e−02 |
| 62 | GO:BP | GO:1901873 | regulation of post−translational protein modification | 20 | 4 | 4.6e−02 |
| 63 | GO:MF | GO:0046982 | protein heterodimerization activity | 155 | 15 | 4.7e−02 |
| 64 | GO:MF | GO:0015267 | channel activity | 179 | 8 | 4.7e−02 |
| 65 | GO:MF | GO:0022803 | passive transmembrane transporter activity | 179 | 8 | 4.7e−02 |