

GO-Stats Results

Your dataset contains **196** annotated gene products.

You can download a tabulated text output file [here](#), for use with a spreadsheet application.

| Color codes | | | |
|-------------|---------------------------------------------------------------|-----------|------------------------------------------------------------------|
| E | The term is enriched in your gene set. | D | The term is depleted in your gene set. |
| | P-value < 0.01 | | 0.01 < P-value < 0.05 |
| RO | Number of genes annotated for this term in the reference set. | RF | Frequency of genes annotated for this term in the reference set. |
| DO | Number of genes annotated for this term in your gene set. | DF | Frequency of genes annotated for this term in your gene set. |

The terms are ranked according to the P-value column representing their statistical relevance. The 'level' column describes the depth at which a given GO term is found in the GO hierarchy (note that some terms can be found at several levels simultaneously). The last column indicates whether a given GO term is enriched (E) or depleted (D), based on the term frequency ratio (DF/RF). To visualize the hierarchy between these terms, you can click on the radio button close to a GO ID, and all its parent terms in the list are highlighted in orange. When moving the mouse pointer on the GO ID column will make all the genes associated with a given GO term appear in a box. The terms are hyperlinked to the QuickGO EBI browser.

| GO ID | Level | GO Term | RO | RF | DO | DF | P-value | E/D |
|----------------------------------|-------|-----------------------------------------------------------------------------------------------------|------|--------|-----|--------|--------------|-----|
| <input type="radio"/> GO:0009987 | 2 | cellular process | 4654 | 0.7187 | 174 | 0.8878 | 3.819450E-09 | E |
| <input type="radio"/> GO:0065007 | 2 | biological regulation | 948 | 0.1464 | 57 | 0.2908 | 6.063120E-08 | E |
| <input type="radio"/> GO:0007049 | 3 | cell cycle | 458 | 0.0707 | 34 | 0.1735 | 4.677622E-07 | E |
| <input type="radio"/> GO:0006139 | 4 | nucleobase, nucleoside, nucleotide and nucleic acid metabolic process | 1532 | 0.2366 | 76 | 0.3878 | 6.292203E-07 | E |
| <input type="radio"/> GO:0050794 | 4,3 | regulation of cellular process | 738 | 0.1140 | 45 | 0.2296 | 1.401721E-06 | E |
| <input type="radio"/> GO:0022402 | 4,3 | cell cycle process | 439 | 0.0678 | 32 | 0.1633 | 1.540739E-06 | E |
| <input type="radio"/> GO:0050789 | 3 | regulation of biological process | 761 | 0.1175 | 45 | 0.2296 | 3.146809E-06 | E |
| <input type="radio"/> GO:0022403 | 5,4 | cell cycle phase | 353 | 0.0545 | 26 | 0.1327 | 1.275830E-05 | E |
| <input type="radio"/> GO:0006350 | 5 | transcription | 567 | 0.0876 | 35 | 0.1786 | 1.813099E-05 | E |
| <input type="radio"/> GO:0016070 | 5 | RNA metabolic process | 1058 | 0.1634 | 54 | 0.2755 | 2.045086E-05 | E |
| <input type="radio"/> GO:0032774 | 6 | RNA biosynthetic process | 524 | 0.0809 | 32 | 0.1633 | 5.091001E-05 | E |
| <input type="radio"/> GO:0016575 | 11,9 | histone deacetylation | 24 | 0.0037 | 6 | 0.0306 | 5.608761E-05 | E |
| <input type="radio"/> GO:0000279 | 6,5 | M phase | 258 | 0.0398 | 20 | 0.1020 | 6.348182E-05 | E |
| <input type="radio"/> GO:0019219 | 6,5 | regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process | 440 | 0.0679 | 28 | 0.1429 | 7.593252E-05 | E |
| <input type="radio"/> GO:0030952 | 6 | establishment and/or maintenance of cytoskeleton polarity | 9 | 0.0014 | 4 | 0.0204 | 8.826337E-05 | E |
| <input type="radio"/> GO:0030950 | 8,7 | establishment and/or maintenance of actin cytoskeleton polarity | 9 | 0.0014 | 4 | 0.0204 | 8.826337E-05 | E |
| <input type="radio"/> GO:0006476 | 8 | protein amino acid deacetylation | 26 | 0.0040 | 6 | 0.0306 | 9.037161E-05 | E |
| <input type="radio"/> GO:0006351 | 7,6 | transcription, DNA-dependent | 522 | 0.0806 | 31 | 0.1582 | 0.0001085 | E |
| <input type="radio"/> GO:0016071 | 6 | mRNA metabolic process | 210 | 0.0324 | 17 | 0.0867 | 0.0001321 | E |
| <input type="radio"/> GO:0045449 | 7,6 | regulation of transcription | 386 | 0.0596 | 25 | 0.1276 | 0.0001390 | E |
| <input type="radio"/> GO:0031323 | 5,4 | regulation of cellular metabolic process | 507 | 0.0783 | 30 | 0.1531 | 0.0001480 | E |
| <input type="radio"/> GO:0019222 | 4,3 | regulation of metabolic process | 538 | 0.0831 | 31 | 0.1582 | 0.0001813 | E |

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|-----------------------|------------|-------------|------------------------------------------------------------------------------------------------------|------|--------|-----|--------|-----------|---|
| <input type="radio"/> | GO:0016043 | 3 | cellular component organization and biogenesis | 2264 | 0.3496 | 91 | 0.4643 | 0.0002092 | E |
| <input type="radio"/> | GO:0001558 | 5,6,4,8,9 | regulation of cell growth | 11 | 0.0017 | 4 | 0.0204 | 0.0002176 | E |
| <input type="radio"/> | GO:0006259 | 5 | DNA metabolic process | 523 | 0.0808 | 30 | 0.1531 | 0.0002459 | E |
| <input type="radio"/> | GO:0043283 | 4 | biopolymer metabolic process | 2230 | 0.3443 | 89 | 0.4541 | 0.0003259 | E |
| <input type="radio"/> | GO:0040008 | 4,3 | regulation of growth | 13 | 0.0020 | 4 | 0.0204 | 0.0004440 | E |
| <input type="radio"/> | GO:0031929 | 6 | TOR signaling pathway | 13 | 0.0020 | 4 | 0.0204 | 0.0004440 | E |
| <input type="radio"/> | GO:0006355 | 8,7 | regulation of transcription, DNA-dependent | 359 | 0.0554 | 22 | 0.1122 | 0.0006783 | E |
| <input type="radio"/> | GO:0007001 | 6 | chromosome organization and biogenesis (sensu Eukaryota) | 567 | 0.0876 | 30 | 0.1531 | 0.0008510 | E |
| <input type="radio"/> | GO:0006366 | 8,7 | transcription from RNA polymerase II promoter | 343 | 0.0530 | 21 | 0.1071 | 0.0008896 | E |
| <input type="radio"/> | GO:0051276 | 5 | chromosome organization and biogenesis | 572 | 0.0883 | 30 | 0.1531 | 0.0009670 | E |
| <input type="radio"/> | GO:0051327 | 7,5,6 | M phase of meiotic cell cycle | 148 | 0.0229 | 12 | 0.0612 | 0.0011656 | E |
| <input type="radio"/> | GO:0051321 | 4 | meiotic cell cycle | 148 | 0.0229 | 12 | 0.0612 | 0.0011656 | E |
| <input type="radio"/> | GO:0007126 | 8,6,7,5 | meiosis | 148 | 0.0229 | 12 | 0.0612 | 0.0011656 | E |
| <input type="radio"/> | GO:0000375 | 8 | RNA splicing, via transesterification reactions | 110 | 0.0170 | 10 | 0.0510 | 0.0012728 | E |
| <input type="radio"/> | GO:0065008 | 3 | regulation of biological quality | 260 | 0.0401 | 17 | 0.0867 | 0.0013263 | E |
| <input type="radio"/> | GO:0006996 | 4 | organelle organization and biogenesis | 1388 | 0.2143 | 58 | 0.2959 | 0.0015725 | E |
| <input type="radio"/> | GO:0000278 | 4 | mitotic cell cycle | 266 | 0.0411 | 17 | 0.0867 | 0.0016606 | E |
| <input type="radio"/> | GO:0016568 | 8 | chromatin modification | 223 | 0.0344 | 15 | 0.0765 | 0.0018720 | E |
| <input type="radio"/> | GO:0050801 | 6 | ion homeostasis | 119 | 0.0184 | 10 | 0.0510 | 0.0022108 | E |
| <input type="radio"/> | GO:0006325 | 7 | establishment and/or maintenance of chromatin architecture | 253 | 0.0391 | 16 | 0.0816 | 0.0024271 | E |
| <input type="radio"/> | GO:0006323 | 6 | DNA packaging | 253 | 0.0391 | 16 | 0.0816 | 0.0024271 | E |
| <input type="radio"/> | GO:0048878 | 5 | chemical homeostasis | 121 | 0.0187 | 10 | 0.0510 | 0.0024774 | E |
| <input type="radio"/> | GO:0000398 | 8,10 | nuclear mRNA splicing, via spliceosome | 102 | 0.0158 | 9 | 0.0459 | 0.0026072 | E |
| <input type="radio"/> | GO:0000377 | 9 | RNA splicing, via transesterification reactions with bulged adenosine as nucleophile | 103 | 0.0159 | 9 | 0.0459 | 0.0027730 | E |
| <input type="radio"/> | GO:0006357 | 9,8 | regulation of transcription from RNA polymerase II promoter | 221 | 0.0341 | 14 | 0.0714 | 0.0041754 | E |
| <input type="radio"/> | GO:0008380 | 7 | RNA splicing | 132 | 0.0204 | 10 | 0.0510 | 0.0044059 | E |
| <input type="radio"/> | GO:0016569 | 9 | covalent chromatin modification | 91 | 0.0141 | 8 | 0.0408 | 0.0044240 | E |
| <input type="radio"/> | GO:0016570 | 10,8 | histone modification | 91 | 0.0141 | 8 | 0.0408 | 0.0044240 | E |
| <input type="radio"/> | GO:0055072 | 9 | iron ion homeostasis | 38 | 0.0059 | 5 | 0.0255 | 0.0045006 | E |
| <input type="radio"/> | GO:0006879 | 10,8 | cellular iron ion homeostasis | 38 | 0.0059 | 5 | 0.0255 | 0.0045006 | E |
| <input type="radio"/> | GO:0042592 | 4 | homeostatic process | 134 | 0.0207 | 10 | 0.0510 | 0.0048508 | E |
| <input type="radio"/> | GO:0006397 | 7 | mRNA processing | 157 | 0.0242 | 11 | 0.0561 | 0.0050810 | E |
| <input type="radio"/> | GO:0000301 | 9,7,6,8 | retrograde transport, vesicle recycling within Golgi | 4 | 0.0006 | 2 | 0.0102 | 0.0051460 | E |
| <input type="radio"/> | GO:0007010 | 5 | cytoskeleton organization and biogenesis | 227 | 0.0351 | 14 | 0.0714 | 0.0051466 | E |
| <input type="radio"/> | GO:0043170 | 3 | macromolecule metabolic process | 2841 | 0.4387 | 101 | 0.5153 | 0.0053099 | E |
| <input type="radio"/> | GO:0055082 | 6,4 | cellular chemical homeostasis | 115 | 0.0178 | 9 | 0.0459 | 0.0054333 | E |
| <input type="radio"/> | GO:0006873 | 7,5 | cellular ion homeostasis | 115 | 0.0178 | 9 | 0.0459 | 0.0054333 | E |
| <input type="radio"/> | GO:0000070 | 9,7,5,8,6,4 | mitotic sister chromatid segregation | 59 | 0.0091 | 6 | 0.0306 | 0.0065771 | E |
| <input type="radio"/> | GO:0000819 | 7,4 | sister chromatid segregation | 62 | 0.0096 | 6 | 0.0306 | 0.0081997 | E |
| <input type="radio"/> | GO:0055080 | 7 | cation homeostasis | 102 | 0.0158 | 8 | 0.0408 | 0.0082149 | E |
| <input type="radio"/> | GO:0030003 | 8,6 | cellular cation homeostasis | 102 | 0.0158 | 8 | 0.0408 | 0.0082149 | E |
| <input type="radio"/> | GO:0051017 | 9 | actin filament bundle formation | 5 | 0.0008 | 2 | 0.0102 | 0.0083195 | E |

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| <input type="radio"/> | GO:0045011 | 10 | actin cable formation | 5 | 0.0008 | 2 | 0.0102 | 0.0083195 | E |
| <input type="radio"/> | GO:0031110 | 6,9,5 | regulation of microtubule polymerization or depolymerization | 15 | 0.0023 | 3 | 0.0153 | 0.0086397 | E |
| <input type="radio"/> | GO:0030005 | 9,7 | cellular di-, tri-valent inorganic cation homeostasis | 64 | 0.0099 | 6 | 0.0306 | 0.0094166 | E |
| <input type="radio"/> | GO:0055066 | 8 | di-, tri-valent inorganic cation homeostasis | 64 | 0.0099 | 6 | 0.0306 | 0.0094166 | E |
| <input type="radio"/> | GO:0007067 | 8,6,7,5 | mitosis | 127 | 0.0196 | 9 | 0.0459 | 0.0095688 | E |
| <input type="radio"/> | GO:0019725 | 5,3 | cellular homeostasis | 128 | 0.0198 | 9 | 0.0459 | 0.0099893 | E |
| <input type="radio"/> | GO:0031109 | 8 | microtubule polymerization or depolymerization | 16 | 0.0025 | 3 | 0.0153 | 0.0103158 | E |
| <input type="radio"/> | GO:0032502 | 2 | developmental process | 436 | 0.0673 | 21 | 0.1071 | 0.0104190 | E |
| <input type="radio"/> | GO:0000087 | 7,5,6 | M phase of mitotic cell cycle | 129 | 0.0199 | 9 | 0.0459 | 0.0104222 | E |
| <input type="radio"/> | GO:0015892 | 13,11,8,9,5,10,6 | siderophore-iron transport | 6 | 0.0009 | 2 | 0.0102 | 0.0121052 | E |
| <input type="radio"/> | GO:0033214 | 12,10 | iron assimilation by chelation and transport | 6 | 0.0009 | 2 | 0.0102 | 0.0121052 | E |
| <input type="radio"/> | GO:0030029 | 6 | actin filament-based process | 112 | 0.0173 | 8 | 0.0408 | 0.0132009 | E |
| <input type="radio"/> | GO:0031325 | 6,5 | positive regulation of cellular metabolic process | 116 | 0.0179 | 8 | 0.0408 | 0.0156436 | E |
| <input type="radio"/> | GO:0009893 | 5,4 | positive regulation of metabolic process | 116 | 0.0179 | 8 | 0.0408 | 0.0156436 | E |
| <input type="radio"/> | GO:0045913 | 6,5 | positive regulation of carbohydrate metabolic process | 7 | 0.0011 | 2 | 0.0102 | 0.0164391 | E |
| <input type="radio"/> | GO:0045835 | 8,10,9,7 | negative regulation of meiosis | 7 | 0.0011 | 2 | 0.0102 | 0.0164391 | E |
| <input type="radio"/> | GO:0006265 | 6 | DNA topological change | 7 | 0.0011 | 2 | 0.0102 | 0.0164391 | E |
| <input type="radio"/> | GO:0000003 | 2 | reproduction | 323 | 0.0499 | 16 | 0.0816 | 0.0170365 | E |
| <input type="radio"/> | GO:0044238 | 3 | primary metabolic process | 3247 | 0.5014 | 109 | 0.5561 | 0.0172835 | E |
| <input type="radio"/> | GO:0007059 | 3 | chromosome segregation | 119 | 0.0184 | 8 | 0.0408 | 0.0176485 | E |
| <input type="radio"/> | GO:0006826 | 7,8,9 | iron ion transport | 20 | 0.0031 | 3 | 0.0153 | 0.0186001 | E |
| <input type="radio"/> | GO:0016192 | 4,5 | vesicle-mediated transport | 328 | 0.0506 | 16 | 0.0816 | 0.0188873 | E |
| <input type="radio"/> | GO:0044237 | 3 | cellular metabolic process | 3403 | 0.5255 | 113 | 0.5765 | 0.0202258 | E |
| <input type="radio"/> | GO:0006891 | 8,6,5,7 | intra-Golgi vesicle-mediated transport | 21 | 0.0032 | 3 | 0.0153 | 0.0210514 | E |
| <input type="radio"/> | GO:0051179 | 2 | localization | 1051 | 0.1623 | 40 | 0.2041 | 0.0211915 | E |
| <input type="radio"/> | GO:0007323 | 9 | peptide pheromone maturation | 8 | 0.0012 | 2 | 0.0102 | 0.0212614 | E |
| <input type="radio"/> | GO:0033212 | 11,9 | iron assimilation | 8 | 0.0012 | 2 | 0.0102 | 0.0212614 | E |
| <input type="radio"/> | GO:0048522 | 5,4 | positive regulation of cellular process | 124 | 0.0191 | 8 | 0.0408 | 0.0213205 | E |
| <input type="radio"/> | GO:0048518 | 4 | positive regulation of biological process | 124 | 0.0191 | 8 | 0.0408 | 0.0213205 | E |
| <input type="radio"/> | GO:0045941 | 8,7 | positive regulation of transcription | 101 | 0.0156 | 7 | 0.0357 | 0.0217327 | E |
| <input type="radio"/> | GO:0016049 | 5,3,7,8 | cell growth | 102 | 0.0158 | 7 | 0.0357 | 0.0226422 | E |
| <input type="radio"/> | GO:0006402 | 7 | mRNA catabolic process | 60 | 0.0093 | 5 | 0.0255 | 0.0252177 | E |
| <input type="radio"/> | GO:0000393 | 7,6,9,11 | spliceosomal conformational changes to generate catalytic conformation | 9 | 0.0014 | 2 | 0.0102 | 0.0265162 | E |
| <input type="radio"/> | GO:0015891 | 4,5 | siderophore transport | 9 | 0.0014 | 2 | 0.0102 | 0.0265162 | E |
| <input type="radio"/> | GO:0000184 | 8 | mRNA catabolic process, nonsense-mediated decay | 9 | 0.0014 | 2 | 0.0102 | 0.0265162 | E |
| <input type="radio"/> | GO:0030036 | 7 | actin cytoskeleton organization and biogenesis | 107 | 0.0165 | 7 | 0.0357 | 0.0275031 | E |
| <input type="radio"/> | GO:0006457 | 6 | protein folding | 84 | 0.0130 | 6 | 0.0306 | 0.0279486 | E |
| <input type="radio"/> | GO:0045935 | 7,6 | positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process | 108 | 0.0167 | 7 | 0.0357 | 0.0285366 | E |
| <input type="radio"/> | GO:0007154 | 3 | cell communication | 240 | 0.0371 | 12 | 0.0612 | 0.0299052 | E |
| <input type="radio"/> | GO:0051754 | 11,9,8,6,5,10,7,4 | meiotic sister chromatid cohesion, centromeric | 1 | 0.0002 | 1 | 0.0051 | 0.0302656 | E |
| <input type="radio"/> | GO:0009302 | 8,7 | snoRNA transcription | 1 | 0.0002 | 1 | 0.0051 | 0.0302656 | E |

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|-----------------------|------------|-------------------|------------------------------------------------------------------------------|------|--------|-----|--------|-----------|---|
| <input type="radio"/> | GO:0015682 | 8,9,10 | ferric iron transport | 1 | 0.0002 | 1 | 0.0051 | 0.0302656 | E |
| <input type="radio"/> | GO:0042930 | 5,6 | enterobactin transport | 1 | 0.0002 | 1 | 0.0051 | 0.0302656 | E |
| <input type="radio"/> | GO:0008105 | 5 | asymmetric protein localization | 1 | 0.0002 | 1 | 0.0051 | 0.0302656 | E |
| <input type="radio"/> | GO:0015890 | 5,6 | nicotinamide mononucleotide transport | 1 | 0.0002 | 1 | 0.0051 | 0.0302656 | E |
| <input type="radio"/> | GO:0009237 | 5 | siderophore metabolic process | 1 | 0.0002 | 1 | 0.0051 | 0.0302656 | E |
| <input type="radio"/> | GO:0043462 | 6 | regulation of ATPase activity | 1 | 0.0002 | 1 | 0.0051 | 0.0302656 | E |
| <input type="radio"/> | GO:0015685 | 14,12,9,10,6,11,7 | ferric-enterobactin transport | 1 | 0.0002 | 1 | 0.0051 | 0.0302656 | E |
| <input type="radio"/> | GO:0045739 | 9,8,7 | positive regulation of DNA repair | 1 | 0.0002 | 1 | 0.0051 | 0.0302656 | E |
| <input type="radio"/> | GO:0016578 | 11,9,10 | histone deubiquitination | 1 | 0.0002 | 1 | 0.0051 | 0.0302656 | E |
| <input type="radio"/> | GO:0045103 | 6 | intermediate filament-based process | 1 | 0.0002 | 1 | 0.0051 | 0.0302656 | E |
| <input type="radio"/> | GO:0032780 | 7 | negative regulation of ATPase activity | 1 | 0.0002 | 1 | 0.0051 | 0.0302656 | E |
| <input type="radio"/> | GO:0045732 | 7,8,6 | positive regulation of protein catabolic process | 1 | 0.0002 | 1 | 0.0051 | 0.0302656 | E |
| <input type="radio"/> | GO:0009896 | 6,5 | positive regulation of catabolic process | 1 | 0.0002 | 1 | 0.0051 | 0.0302656 | E |
| <input type="radio"/> | GO:0008152 | 2 | metabolic process | 3516 | 0.5429 | 114 | 0.5816 | 0.0317192 | E |
| <input type="radio"/> | GO:0006012 | 7,8 | galactose metabolic process | 10 | 0.0015 | 2 | 0.0102 | 0.0321510 | E |
| <input type="radio"/> | GO:0051234 | 2,3 | establishment of localization | 1004 | 0.1550 | 37 | 0.1888 | 0.0321626 | E |
| <input type="radio"/> | GO:0043687 | 7 | post-translational protein modification | 388 | 0.0599 | 17 | 0.0867 | 0.0327008 | E |
| <input type="radio"/> | GO:0007242 | 5 | intracellular signaling cascade | 137 | 0.0212 | 8 | 0.0408 | 0.0327403 | E |
| <input type="radio"/> | GO:0032506 | 5,3 | cytokinetic process | 88 | 0.0136 | 6 | 0.0306 | 0.0330241 | E |
| <input type="radio"/> | GO:0051301 | 3 | cell division | 246 | 0.0380 | 12 | 0.0612 | 0.0338350 | E |
| <input type="radio"/> | GO:0006810 | 3,4 | transport | 981 | 0.1515 | 36 | 0.1837 | 0.0344976 | E |
| <input type="radio"/> | GO:0015749 | 5,6 | monosaccharide transport | 26 | 0.0040 | 3 | 0.0153 | 0.0353563 | E |
| <input type="radio"/> | GO:0008645 | 6,7 | hexose transport | 26 | 0.0040 | 3 | 0.0153 | 0.0353563 | E |
| <input type="radio"/> | GO:0048193 | 7,5,6 | Golgi vesicle transport | 166 | 0.0256 | 9 | 0.0459 | 0.0354654 | E |
| <input type="radio"/> | GO:0007033 | 5 | vacuole organization and biogenesis | 67 | 0.0103 | 5 | 0.0255 | 0.0360865 | E |
| <input type="radio"/> | GO:0032505 | 4,3 | reproduction of a single-celled organism | 194 | 0.0300 | 10 | 0.0510 | 0.0363443 | E |
| <input type="radio"/> | GO:0000041 | 7,8 | transition metal ion transport | 46 | 0.0071 | 4 | 0.0204 | 0.0373610 | E |
| <input type="radio"/> | GO:0006464 | 6 | protein modification process | 520 | 0.0803 | 21 | 0.1071 | 0.0379609 | E |
| <input type="radio"/> | GO:0030154 | 4 | cell differentiation | 173 | 0.0267 | 9 | 0.0459 | 0.0420427 | E |
| <input type="radio"/> | GO:0048869 | 3 | cellular developmental process | 173 | 0.0267 | 9 | 0.0459 | 0.0420427 | E |
| <input type="radio"/> | GO:0016458 | 5 | gene silencing | 95 | 0.0147 | 6 | 0.0306 | 0.0428670 | E |
| <input type="radio"/> | GO:0031507 | 6,10 | heterochromatin formation | 95 | 0.0147 | 6 | 0.0306 | 0.0428670 | E |
| <input type="radio"/> | GO:0006342 | 10,6,7,11,9 | chromatin silencing | 95 | 0.0147 | 6 | 0.0306 | 0.0428670 | E |
| <input type="radio"/> | GO:0045814 | 5 | negative regulation of gene expression, epigenetic | 95 | 0.0147 | 6 | 0.0306 | 0.0428670 | E |
| <input type="radio"/> | GO:0000083 | 10,9,6,5,7,8,4 | G1/S-specific transcription in mitotic cell cycle | 12 | 0.0019 | 2 | 0.0102 | 0.0443674 | E |
| <input type="radio"/> | GO:0006310 | 6 | DNA recombination | 122 | 0.0188 | 7 | 0.0357 | 0.0449417 | E |
| <input type="radio"/> | GO:0030435 | 5 | sporulation | 123 | 0.0190 | 7 | 0.0357 | 0.0462362 | E |
| <input type="radio"/> | GO:0065004 | 6,5 | protein-DNA complex assembly | 74 | 0.0114 | 5 | 0.0255 | 0.0486985 | E |
| <input type="radio"/> | GO:0006401 | 6 | RNA catabolic process | 74 | 0.0114 | 5 | 0.0255 | 0.0486985 | E |
| <input type="radio"/> | GO:0043488 | 9,8,7 | regulation of mRNA stability | 30 | 0.0046 | 3 | 0.0153 | 0.0488914 | E |
| <input type="radio"/> | GO:0043487 | 8,7 | regulation of RNA stability | 30 | 0.0046 | 3 | 0.0153 | 0.0488914 | E |
| <input type="radio"/> | GO:0051128 | 5,4 | regulation of cellular component organization and biogenesis | 30 | 0.0046 | 3 | 0.0153 | 0.0488914 | E |
| <input type="radio"/> | GO:0051641 | 4,3 | cellular localization | 642 | 0.0991 | 24 | 0.1224 | 0.0495200 | E |
| <input type="radio"/> | GO:0040029 | 4 | regulation of gene expression, epigenetic | 100 | 0.0154 | 6 | 0.0306 | 0.0505457 | E |

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|-----------------------|------------|--------------------|-------------------------------------------------------------------------|-----|--------|----|--------|-----------|---|
| <input type="radio"/> | GO:0007127 | 9,7,6,8,5 | meiosis I | 75 | 0.0116 | 5 | 0.0255 | 0.0506203 | E |
| <input type="radio"/> | GO:0007103 | 6,7,5,8 | spindle pole body duplication in nuclear envelope | 13 | 0.0020 | 2 | 0.0102 | 0.0508605 | E |
| <input type="radio"/> | GO:0007017 | 6 | microtubule-based process | 101 | 0.0156 | 6 | 0.0306 | 0.0521367 | E |
| <input type="radio"/> | GO:0006950 | 3 | response to stress | 488 | 0.0754 | 19 | 0.0969 | 0.0523147 | E |
| <input type="radio"/> | GO:0006338 | 9 | chromatin remodeling | 155 | 0.0239 | 8 | 0.0408 | 0.0523572 | E |
| <input type="radio"/> | GO:0007062 | 7,4 | sister chromatid cohesion | 31 | 0.0048 | 3 | 0.0153 | 0.0525091 | E |
| <input type="radio"/> | GO:0045892 | 9,8 | negative regulation of transcription, DNA-dependent | 156 | 0.0241 | 8 | 0.0408 | 0.0535459 | E |
| <input type="radio"/> | GO:0045045 | 7,5,4,6 | secretory pathway | 243 | 0.0375 | 11 | 0.0561 | 0.0538502 | E |
| <input type="radio"/> | GO:0008361 | 4,6,7 | regulation of cell size | 129 | 0.0199 | 7 | 0.0357 | 0.0542773 | E |
| <input type="radio"/> | GO:0022616 | 6 | DNA strand elongation | 32 | 0.0049 | 3 | 0.0153 | 0.0562059 | E |
| <input type="radio"/> | GO:0006271 | 8,7 | DNA strand elongation during DNA replication | 32 | 0.0049 | 3 | 0.0153 | 0.0562059 | E |
| <input type="radio"/> | GO:0031497 | 5,9 | chromatin assembly | 104 | 0.0161 | 6 | 0.0306 | 0.0570056 | E |
| <input type="radio"/> | GO:0030474 | 5,6,4,7 | spindle pole body duplication | 14 | 0.0022 | 2 | 0.0102 | 0.0575562 | E |
| <input type="radio"/> | GO:0045990 | 9,7,8,5 | regulation of transcription by carbon catabolites | 14 | 0.0022 | 2 | 0.0102 | 0.0575562 | E |
| <input type="radio"/> | GO:0006825 | 8,9 | copper ion transport | 14 | 0.0022 | 2 | 0.0102 | 0.0575562 | E |
| <input type="radio"/> | GO:0050896 | 2 | response to stimulus | 763 | 0.1178 | 27 | 0.1378 | 0.0579717 | E |
| <input type="radio"/> | GO:0048856 | 3 | anatomical structure development | 248 | 0.0383 | 11 | 0.0561 | 0.0582209 | E |
| <input type="radio"/> | GO:0000902 | 5,6 | cell morphogenesis | 248 | 0.0383 | 11 | 0.0561 | 0.0582209 | E |
| <input type="radio"/> | GO:0032989 | 4,5 | cellular structure morphogenesis | 248 | 0.0383 | 11 | 0.0561 | 0.0582209 | E |
| <input type="radio"/> | GO:0009653 | 4,3 | anatomical structure morphogenesis | 248 | 0.0383 | 11 | 0.0561 | 0.0582209 | E |
| <input type="radio"/> | GO:0015757 | 7,8 | galactose transport | 2 | 0.0003 | 1 | 0.0051 | 0.0587082 | E |
| <input type="radio"/> | GO:0031087 | 11,9,10 | deadenylation-independent decapping | 2 | 0.0003 | 1 | 0.0051 | 0.0587082 | E |
| <input type="radio"/> | GO:0006467 | 7,8 | protein thiol-disulfide exchange | 2 | 0.0003 | 1 | 0.0051 | 0.0587082 | E |
| <input type="radio"/> | GO:0051292 | 8,7 | nuclear pore complex assembly | 2 | 0.0003 | 1 | 0.0051 | 0.0587082 | E |
| <input type="radio"/> | GO:0043146 | 9,8,12,10,7 | spindle stabilization | 2 | 0.0003 | 1 | 0.0051 | 0.0587082 | E |
| <input type="radio"/> | GO:0006434 | 9,8,10,7 | seryl-tRNA aminoacylation | 2 | 0.0003 | 1 | 0.0051 | 0.0587082 | E |
| <input type="radio"/> | GO:0031086 | 10,8,9 | mRNA catabolic process, deadenylation-independent decay | 2 | 0.0003 | 1 | 0.0051 | 0.0587082 | E |
| <input type="radio"/> | GO:0006282 | 8,7,6 | regulation of DNA repair | 2 | 0.0003 | 1 | 0.0051 | 0.0587082 | E |
| <input type="radio"/> | GO:0051177 | 10,8,7,5,9,6,4 | meiotic sister chromatid cohesion | 2 | 0.0003 | 1 | 0.0051 | 0.0587082 | E |
| <input type="radio"/> | GO:0051865 | 10 | protein autoubiquitination | 2 | 0.0003 | 1 | 0.0051 | 0.0587082 | E |
| <input type="radio"/> | GO:0043148 | 10,9,6,5,4,13,11,8 | mitotic spindle stabilization | 2 | 0.0003 | 1 | 0.0051 | 0.0587082 | E |
| <input type="radio"/> | GO:0006269 | 8,6,7 | DNA replication, synthesis of RNA primer | 2 | 0.0003 | 1 | 0.0051 | 0.0587082 | E |
| <input type="radio"/> | GO:0007131 | 10,8,7,5,9,6,4 | meiotic recombination | 55 | 0.0085 | 4 | 0.0204 | 0.0594289 | E |
| <input type="radio"/> | GO:0032940 | 6,4,5 | secretion by cell | 250 | 0.0386 | 11 | 0.0561 | 0.0599859 | E |
| <input type="radio"/> | GO:0046903 | 3,4 | secretion | 250 | 0.0386 | 11 | 0.0561 | 0.0599859 | E |
| <input type="radio"/> | GO:0022607 | 4 | cellular component assembly | 471 | 0.0727 | 18 | 0.0918 | 0.0601657 | E |
| <input type="radio"/> | GO:0016481 | 8,7 | negative regulation of transcription | 162 | 0.0250 | 8 | 0.0408 | 0.0608288 | E |
| <input type="radio"/> | GO:0051649 | 5,3,4 | establishment of cellular localization | 606 | 0.0936 | 22 | 0.1122 | 0.0617892 | E |
| <input type="radio"/> | GO:0051640 | 5,4 | organelle localization | 56 | 0.0086 | 4 | 0.0204 | 0.0620866 | E |
| <input type="radio"/> | GO:0030437 | 7,6 | sporulation (sensu Fungi) | 108 | 0.0167 | 6 | 0.0306 | 0.0636889 | E |
| <input type="radio"/> | GO:0048622 | 6,5 | reproductive sporulation | 108 | 0.0167 | 6 | 0.0306 | 0.0636889 | E |
| <input type="radio"/> | GO:0015674 | 6,7 | di-, tri-valent inorganic cation transport | 34 | 0.0053 | 3 | 0.0153 | 0.0638084 | E |
| <input type="radio"/> | GO:0046907 | 6,4,5 | intracellular transport | 545 | 0.0842 | 20 | 0.1020 | 0.0642779 | E |
| <input type="radio"/> | GO:0009894 | 5,4 | regulation of catabolic process | 15 | 0.0023 | 2 | 0.0102 | 0.0644172 | E |

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|-----------------------|------------|--------------|--------------------------------------------------------------------------------------------------------------|-----|--------|----|--------|-----------|---|
| <input type="radio"/> | GO:0000910 | 4 | cytokinesis | 109 | 0.0168 | 6 | 0.0306 | 0.0653880 | E |
| <input type="radio"/> | GO:0051726 | 5,4 | regulation of cell cycle | 167 | 0.0258 | 8 | 0.0408 | 0.0670471 | E |
| <input type="radio"/> | GO:0000074 | 6,5 | regulation of progression through cell cycle | 167 | 0.0258 | 8 | 0.0408 | 0.0670471 | E |
| <input type="radio"/> | GO:0000086 | 8,5,6,7,4 | G2/M transition of mitotic cell cycle | 35 | 0.0054 | 3 | 0.0153 | 0.0676996 | E |
| <input type="radio"/> | GO:0051704 | 2 | multi-organism process | 139 | 0.0215 | 7 | 0.0357 | 0.0684649 | E |
| <input type="radio"/> | GO:0051325 | 6,5 | interphase | 112 | 0.0173 | 6 | 0.0306 | 0.0705384 | E |
| <input type="radio"/> | GO:0051329 | 7,5,6 | interphase of mitotic cell cycle | 112 | 0.0173 | 6 | 0.0306 | 0.0705384 | E |
| <input type="radio"/> | GO:0006396 | 6 | RNA processing | 491 | 0.0758 | 18 | 0.0918 | 0.0705584 | E |
| <input type="radio"/> | GO:0007047 | 5 | cell wall organization and biogenesis | 200 | 0.0309 | 9 | 0.0459 | 0.0706700 | E |
| <input type="radio"/> | GO:0045229 | 4 | external encapsulating structure organization and biogenesis | 200 | 0.0309 | 9 | 0.0459 | 0.0706700 | E |
| <input type="radio"/> | GO:0043412 | 5 | biopolymer modification | 664 | 0.1025 | 23 | 0.1173 | 0.0711952 | E |
| <input type="radio"/> | GO:0040007 | 2 | growth | 141 | 0.0218 | 7 | 0.0357 | 0.0713768 | E |
| <input type="radio"/> | GO:0051300 | 5,4,6 | spindle pole body organization and biogenesis | 16 | 0.0025 | 2 | 0.0102 | 0.0714091 | E |
| <input type="radio"/> | GO:0031023 | 5 | microtubule organizing center organization and biogenesis | 16 | 0.0025 | 2 | 0.0102 | 0.0714091 | E |
| <input type="radio"/> | GO:0051252 | 7,6 | regulation of RNA metabolic process | 36 | 0.0056 | 3 | 0.0153 | 0.0716411 | E |
| <input type="radio"/> | GO:0009991 | 4 | response to extracellular stimulus | 37 | 0.0057 | 3 | 0.0153 | 0.0756259 | E |
| <input type="radio"/> | GO:0031667 | 5 | response to nutrient levels | 37 | 0.0057 | 3 | 0.0153 | 0.0756259 | E |
| <input type="radio"/> | GO:0009605 | 3 | response to external stimulus | 37 | 0.0057 | 3 | 0.0153 | 0.0756259 | E |
| <input type="radio"/> | GO:0030001 | 6,7 | metal ion transport | 62 | 0.0096 | 4 | 0.0204 | 0.0785873 | E |
| <input type="radio"/> | GO:0048523 | 5,4 | negative regulation of cellular process | 239 | 0.0369 | 10 | 0.0510 | 0.0787887 | E |
| <input type="radio"/> | GO:0006260 | 6 | DNA replication | 117 | 0.0181 | 6 | 0.0306 | 0.0792432 | E |
| <input type="radio"/> | GO:0009892 | 5,4 | negative regulation of metabolic process | 208 | 0.0321 | 9 | 0.0459 | 0.0795193 | E |
| <input type="radio"/> | GO:0008643 | 4,5 | carbohydrate transport | 38 | 0.0059 | 3 | 0.0153 | 0.0796470 | E |
| <input type="radio"/> | GO:0007165 | 4 | signal transduction | 209 | 0.0323 | 9 | 0.0459 | 0.0806186 | E |
| <input type="radio"/> | GO:0048519 | 4 | negative regulation of biological process | 242 | 0.0374 | 10 | 0.0510 | 0.0817010 | E |
| <input type="radio"/> | GO:0045934 | 7,6 | negative regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process | 179 | 0.0276 | 8 | 0.0408 | 0.0821680 | E |
| <input type="radio"/> | GO:0006333 | 8 | chromatin assembly or disassembly | 119 | 0.0184 | 6 | 0.0306 | 0.0827455 | E |
| <input type="radio"/> | GO:0043285 | 5 | biopolymer catabolic process | 277 | 0.0428 | 11 | 0.0561 | 0.0837714 | E |
| <input type="radio"/> | GO:0016584 | 6,10 | nucleosome positioning | 3 | 0.0005 | 1 | 0.0051 | 0.0854099 | E |
| <input type="radio"/> | GO:0030543 | 5 | 2-micrometer plasmid partitioning | 3 | 0.0005 | 1 | 0.0051 | 0.0854099 | E |
| <input type="radio"/> | GO:0000917 | 6,4 | barrier septum formation | 3 | 0.0005 | 1 | 0.0051 | 0.0854099 | E |
| <input type="radio"/> | GO:0006114 | 7,6 | glycerol biosynthetic process | 3 | 0.0005 | 1 | 0.0051 | 0.0854099 | E |
| <input type="radio"/> | GO:0009303 | 8,7 | rRNA transcription | 3 | 0.0005 | 1 | 0.0051 | 0.0854099 | E |
| <input type="radio"/> | GO:0046173 | 6 | polyol biosynthetic process | 3 | 0.0005 | 1 | 0.0051 | 0.0854099 | E |
| <input type="radio"/> | GO:0045821 | 7,11,12,6 | positive regulation of glycolysis | 3 | 0.0005 | 1 | 0.0051 | 0.0854099 | E |
| <input type="radio"/> | GO:0030541 | 4 | plasmid partitioning | 3 | 0.0005 | 1 | 0.0051 | 0.0854099 | E |
| <input type="radio"/> | GO:0006370 | 8 | mRNA capping | 3 | 0.0005 | 1 | 0.0051 | 0.0854099 | E |
| <input type="radio"/> | GO:0051054 | 8,7 | positive regulation of DNA metabolic process | 3 | 0.0005 | 1 | 0.0051 | 0.0854099 | E |
| <input type="radio"/> | GO:0030242 | 4,6 | peroxisome degradation | 3 | 0.0005 | 1 | 0.0051 | 0.0854099 | E |
| <input type="radio"/> | GO:0000183 | 11,7,8,12,10 | chromatin silencing at rDNA | 18 | 0.0028 | 2 | 0.0102 | 0.0856599 | E |
| <input type="radio"/> | GO:0006273 | 9,8 | lagging strand elongation | 18 | 0.0028 | 2 | 0.0102 | 0.0856599 | E |
| <input type="radio"/> | GO:0007584 | 6,4 | response to nutrient | 18 | 0.0028 | 2 | 0.0102 | 0.0856599 | E |
| <input type="radio"/> | GO:0022414 | 3,2 | reproductive process | 183 | 0.0283 | 8 | 0.0408 | 0.0871660 | E |

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|-----------------------|------------|----------------|------------------------------------------------------------------------------------------|-----|--------|----|--------|-----------|---|
| <input type="radio"/> | GO:0030467 | 7,4,8 | establishment and/or maintenance of cell polarity (sensu Fungi) | 66 | 0.0102 | 4 | 0.0204 | 0.0899077 | E |
| <input type="radio"/> | GO:0030468 | 8,5,9 | establishment of cell polarity (sensu Fungi) | 66 | 0.0102 | 4 | 0.0204 | 0.0899077 | E |
| <input type="radio"/> | GO:0007105 | 6,4 | cytokinesis, site selection | 66 | 0.0102 | 4 | 0.0204 | 0.0899077 | E |
| <input type="radio"/> | GO:0000282 | 7,9,5,6,10 | cellular bud site selection | 66 | 0.0102 | 4 | 0.0204 | 0.0899077 | E |
| <input type="radio"/> | GO:0045893 | 9,8 | positive regulation of transcription, DNA-dependent | 95 | 0.0147 | 5 | 0.0255 | 0.0926317 | E |
| <input type="radio"/> | GO:0016044 | 4 | membrane organization and biogenesis | 188 | 0.0290 | 8 | 0.0408 | 0.0933117 | E |
| <input type="radio"/> | GO:0042244 | 5,6 | spore wall assembly | 42 | 0.0065 | 3 | 0.0153 | 0.0959596 | E |
| <input type="radio"/> | GO:0030476 | 8,6,7 | spore wall assembly (sensu Fungi) | 42 | 0.0065 | 3 | 0.0153 | 0.0959596 | E |
| <input type="radio"/> | GO:0006812 | 5,6 | cation transport | 97 | 0.0150 | 5 | 0.0255 | 0.0969561 | E |
| <input type="radio"/> | GO:0006261 | 7 | DNA-dependent DNA replication | 97 | 0.0150 | 5 | 0.0255 | 0.0969561 | E |
| <input type="radio"/> | GO:0007097 | 7,8,5,6 | nuclear migration | 20 | 0.0031 | 2 | 0.0102 | 0.1000795 | E |
| <input type="radio"/> | GO:0051647 | 6,5 | nucleus localization | 20 | 0.0031 | 2 | 0.0102 | 0.1000795 | E |
| <input type="radio"/> | GO:0040023 | 6,7,4,5 | establishment of nucleus localization | 20 | 0.0031 | 2 | 0.0102 | 0.1000795 | E |
| <input type="radio"/> | GO:0007052 | 5,4,9 | mitotic spindle organization and biogenesis | 44 | 0.0068 | 3 | 0.0153 | 0.1041621 | E |
| <input type="radio"/> | GO:0006367 | 8,9,7 | transcription initiation from RNA polymerase II promoter | 44 | 0.0068 | 3 | 0.0153 | 0.1041621 | E |
| <input type="radio"/> | GO:0031505 | 6 | chitin- and beta-glucan-containing cell wall organization and biogenesis | 44 | 0.0068 | 3 | 0.0153 | 0.1041621 | E |
| <input type="radio"/> | GO:0031324 | 6,5 | negative regulation of cellular metabolic process | 198 | 0.0306 | 8 | 0.0408 | 0.1050573 | E |
| <input type="radio"/> | GO:0006974 | 4 | response to DNA damage stimulus | 234 | 0.0361 | 9 | 0.0459 | 0.1063459 | E |
| <input type="radio"/> | GO:0009057 | 4 | macromolecule catabolic process | 345 | 0.0533 | 12 | 0.0612 | 0.1064037 | E |
| <input type="radio"/> | GO:0051246 | 5,4 | regulation of protein metabolic process | 72 | 0.0111 | 4 | 0.0204 | 0.1069257 | E |
| <input type="radio"/> | GO:0045324 | 8,6,7 | late endosome to vacuole transport | 21 | 0.0032 | 2 | 0.0102 | 0.1072903 | E |
| <input type="radio"/> | GO:0006312 | 7 | mitotic recombination | 45 | 0.0069 | 3 | 0.0153 | 0.1082535 | E |
| <input type="radio"/> | GO:0032200 | 7 | telomere organization and biogenesis | 274 | 0.0423 | 10 | 0.0510 | 0.1094519 | E |
| <input type="radio"/> | GO:0000723 | 8 | telomere maintenance | 274 | 0.0423 | 10 | 0.0510 | 0.1094519 | E |
| <input type="radio"/> | GO:0000731 | 7,6 | DNA synthesis during DNA repair | 4 | 0.0006 | 1 | 0.0051 | 0.1104492 | E |
| <input type="radio"/> | GO:0000350 | 8,7,10,12 | generation of catalytic spliceosome for second transesterification step | 4 | 0.0006 | 1 | 0.0051 | 0.1104492 | E |
| <input type="radio"/> | GO:0009452 | 7 | RNA capping | 4 | 0.0006 | 1 | 0.0051 | 0.1104492 | E |
| <input type="radio"/> | GO:0030071 | 8,10,6,9,7,5 | regulation of mitotic metaphase/anaphase transition | 4 | 0.0006 | 1 | 0.0051 | 0.1104492 | E |
| <input type="radio"/> | GO:0000349 | 8,7,10,12 | generation of catalytic spliceosome for first transesterification step | 4 | 0.0006 | 1 | 0.0051 | 0.1104492 | E |
| <input type="radio"/> | GO:0031578 | 9,11,10,8 | mitotic cell cycle spindle orientation checkpoint | 4 | 0.0006 | 1 | 0.0051 | 0.1104492 | E |
| <input type="radio"/> | GO:0045722 | 7,9,8,10,6,11 | positive regulation of gluconeogenesis | 4 | 0.0006 | 1 | 0.0051 | 0.1104492 | E |
| <input type="radio"/> | GO:0000735 | 7,9,8 | removal of nonhomologous ends | 4 | 0.0006 | 1 | 0.0051 | 0.1104492 | E |
| <input type="radio"/> | GO:0015793 | 5,6 | glycerol transport | 4 | 0.0006 | 1 | 0.0051 | 0.1104492 | E |
| <input type="radio"/> | GO:0009719 | 3 | response to endogenous stimulus | 243 | 0.0375 | 9 | 0.0459 | 0.1142366 | E |
| <input type="radio"/> | GO:0007064 | 10,8,5,6,9,7,4 | mitotic sister chromatid cohesion | 22 | 0.0034 | 2 | 0.0102 | 0.1144723 | E |
| <input type="radio"/> | GO:0006311 | 10,8,7,5,9,6,4 | meiotic gene conversion | 22 | 0.0034 | 2 | 0.0102 | 0.1144723 | E |
| <input type="radio"/> | GO:0040020 | 7,9,8,6 | regulation of meiosis | 22 | 0.0034 | 2 | 0.0102 | 0.1144723 | E |
| <input type="radio"/> | GO:0030472 | 6,5,10 | mitotic spindle organization and biogenesis in nucleus | 22 | 0.0034 | 2 | 0.0102 | 0.1144723 | E |
| <input type="radio"/> | GO:0007051 | 8 | spindle organization and biogenesis | 47 | 0.0073 | 3 | 0.0153 | 0.1163880 | E |
| <input type="radio"/> | GO:0045944 | 10,9 | positive regulation of transcription from RNA polymerase II promoter | 76 | 0.0117 | 4 | 0.0204 | 0.1180542 | E |
| <input type="radio"/> | GO:0042221 | 3 | response to chemical stimulus | 382 | 0.0590 | 12 | 0.0612 | 0.1188527 | E |

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|-----------------------|------------|-------------------|---------------------------------------------------------------------------------------|-----|--------|----|--------|-----------|---|
| <input type="radio"/> | GO:0042158 | 7,5 | lipoprotein biosynthetic process | 48 | 0.0074 | 3 | 0.0153 | 0.1204203 | E |
| <input type="radio"/> | GO:0042157 | 6 | lipoprotein metabolic process | 48 | 0.0074 | 3 | 0.0153 | 0.1204203 | E |
| <input type="radio"/> | GO:0006497 | 8,7,6 | protein amino acid lipidation | 48 | 0.0074 | 3 | 0.0153 | 0.1204203 | E |
| <input type="radio"/> | GO:0007534 | 6,8,7 | gene conversion at mating-type locus | 23 | 0.0036 | 2 | 0.0102 | 0.1216058 | E |
| <input type="radio"/> | GO:0007020 | 8 | microtubule nucleation | 23 | 0.0036 | 2 | 0.0102 | 0.1216058 | E |
| <input type="radio"/> | GO:0007005 | 5 | mitochondrion organization and biogenesis | 110 | 0.0170 | 5 | 0.0255 | 0.1239756 | E |
| <input type="radio"/> | GO:0016197 | 7,5,6 | endosome transport | 49 | 0.0076 | 3 | 0.0153 | 0.1244224 | E |
| <input type="radio"/> | GO:0006896 | 9,8,7,6 | Golgi to vacuole transport | 24 | 0.0037 | 2 | 0.0102 | 0.1286726 | E |
| <input type="radio"/> | GO:0031577 | 8,7 | spindle checkpoint | 24 | 0.0037 | 2 | 0.0102 | 0.1286726 | E |
| <input type="radio"/> | GO:0044265 | 5 | cellular macromolecule catabolic process | 314 | 0.0485 | 10 | 0.0510 | 0.1287207 | E |
| <input type="radio"/> | GO:0065003 | 5,4 | macromolecular complex assembly | 328 | 0.0506 | 10 | 0.0510 | 0.1303902 | E |
| <input type="radio"/> | GO:0048610 | 3,4 | reproductive cellular process | 149 | 0.0230 | 6 | 0.0306 | 0.1314168 | E |
| <input type="radio"/> | GO:0022413 | 5,4 | reproductive process in single-celled organism | 149 | 0.0230 | 6 | 0.0306 | 0.1314168 | E |
| <input type="radio"/> | GO:0000226 | 7 | microtubule cytoskeleton organization and biogenesis | 81 | 0.0125 | 4 | 0.0204 | 0.1314578 | E |
| <input type="radio"/> | GO:0006811 | 4,5 | ion transport | 115 | 0.0178 | 5 | 0.0255 | 0.1334923 | E |
| <input type="radio"/> | GO:0051083 | 8 | cotranslational protein folding | 5 | 0.0008 | 1 | 0.0051 | 0.1339017 | E |
| <input type="radio"/> | GO:0000707 | 11,9,8,5,6,10,7,4 | meiotic DNA recombinase assembly | 5 | 0.0008 | 1 | 0.0051 | 0.1339017 | E |
| <input type="radio"/> | GO:0007026 | 8,7,11,9,6 | negative regulation of microtubule depolymerization | 5 | 0.0008 | 1 | 0.0051 | 0.1339017 | E |
| <input type="radio"/> | GO:0042176 | 6,7,5 | regulation of protein catabolic process | 5 | 0.0008 | 1 | 0.0051 | 0.1339017 | E |
| <input type="radio"/> | GO:0051247 | 6,5 | positive regulation of protein metabolic process | 5 | 0.0008 | 1 | 0.0051 | 0.1339017 | E |
| <input type="radio"/> | GO:0000730 | 7,9,10,8,6 | DNA recombinase assembly | 5 | 0.0008 | 1 | 0.0051 | 0.1339017 | E |
| <input type="radio"/> | GO:0031111 | 7,10,6 | negative regulation of microtubule polymerization or depolymerization | 5 | 0.0008 | 1 | 0.0051 | 0.1339017 | E |
| <input type="radio"/> | GO:0045991 | 10,8,9,6 | positive regulation of transcription by carbon catabolites | 5 | 0.0008 | 1 | 0.0051 | 0.1339017 | E |
| <input type="radio"/> | GO:0031114 | 7,10,6,8 | regulation of microtubule depolymerization | 5 | 0.0008 | 1 | 0.0051 | 0.1339017 | E |
| <input type="radio"/> | GO:0000411 | 11,9,10,7 | positive regulation of transcription by galactose | 5 | 0.0008 | 1 | 0.0051 | 0.1339017 | E |
| <input type="radio"/> | GO:0000409 | 10,8,9,6 | regulation of transcription by galactose | 5 | 0.0008 | 1 | 0.0051 | 0.1339017 | E |
| <input type="radio"/> | GO:0042710 | 3 | biofilm formation | 5 | 0.0008 | 1 | 0.0051 | 0.1339017 | E |
| <input type="radio"/> | GO:0000082 | 8,5,6,7,4 | G1/S transition of mitotic cell cycle | 52 | 0.0080 | 3 | 0.0153 | 0.1361996 | E |
| <input type="radio"/> | GO:0006281 | 6,5 | DNA repair | 193 | 0.0298 | 7 | 0.0357 | 0.1377232 | E |
| <input type="radio"/> | GO:0019953 | 3 | sexual reproduction | 118 | 0.0182 | 5 | 0.0255 | 0.1388787 | E |
| <input type="radio"/> | GO:0000747 | 4 | conjugation with cellular fusion | 118 | 0.0182 | 5 | 0.0255 | 0.1388787 | E |
| <input type="radio"/> | GO:0000746 | 3 | conjugation | 118 | 0.0182 | 5 | 0.0255 | 0.1388787 | E |
| <input type="radio"/> | GO:0019954 | 3 | asexual reproduction | 85 | 0.0131 | 4 | 0.0204 | 0.1416159 | E |
| <input type="radio"/> | GO:0007114 | 5,4 | cell budding | 85 | 0.0131 | 4 | 0.0204 | 0.1416159 | E |
| <input type="radio"/> | GO:0019318 | 6,7 | hexose metabolic process | 85 | 0.0131 | 4 | 0.0204 | 0.1416159 | E |
| <input type="radio"/> | GO:0006506 | 10,9,8,7,11 | GPI anchor biosynthetic process | 26 | 0.0040 | 2 | 0.0102 | 0.1425413 | E |
| <input type="radio"/> | GO:0006897 | 6,5 | endocytosis | 86 | 0.0133 | 4 | 0.0204 | 0.1440620 | E |
| <input type="radio"/> | GO:0006352 | 7,8,6 | transcription initiation | 55 | 0.0085 | 3 | 0.0153 | 0.1475418 | E |
| <input type="radio"/> | GO:0007088 | 7,9,8,6 | regulation of mitosis | 55 | 0.0085 | 3 | 0.0153 | 0.1475418 | E |
| <input type="radio"/> | GO:0006066 | 4 | alcohol metabolic process | 163 | 0.0252 | 6 | 0.0306 | 0.1482270 | E |
| <input type="radio"/> | GO:0051646 | 6,5 | mitochondrion localization | 27 | 0.0042 | 2 | 0.0102 | 0.1493144 | E |
| <input type="radio"/> | GO:0006505 | 9,10 | GPI anchor metabolic process | 27 | 0.0042 | 2 | 0.0102 | 0.1493144 | E |
| <input type="radio"/> | GO:0007093 | 8,10,9,7 | mitotic cell cycle checkpoint | 27 | 0.0042 | 2 | 0.0102 | 0.1493144 | E |

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| <input type="checkbox"/> | GO:0007019 | 9,7 | microtubule depolymerization | 6 | 0.0009 | 1 | 0.0051 | 0.1558400 | E |
| <input type="checkbox"/> | GO:0015791 | 4,5 | polyol transport | 6 | 0.0009 | 1 | 0.0051 | 0.1558400 | E |
| <input type="checkbox"/> | GO:0031930 | 6 | mitochondrial signaling pathway | 6 | 0.0009 | 1 | 0.0051 | 0.1558400 | E |
| <input type="checkbox"/> | GO:0045996 | 10,9,6 | negative regulation of transcription by pheromones | 6 | 0.0009 | 1 | 0.0051 | 0.1558400 | E |
| <input type="checkbox"/> | GO:0006110 | 6,10,11,5 | regulation of glycolysis | 6 | 0.0009 | 1 | 0.0051 | 0.1558400 | E |
| <input type="checkbox"/> | GO:0046020 | 11,10,7 | negative regulation of transcription from RNA polymerase II promoter by pheromones | 6 | 0.0009 | 1 | 0.0051 | 0.1558400 | E |
| <input type="checkbox"/> | GO:0006906 | 6,5 | vesicle fusion | 28 | 0.0043 | 2 | 0.0102 | 0.1559629 | E |
| <input type="checkbox"/> | GO:0042144 | 6 | vacuole fusion, non-autophagic | 28 | 0.0043 | 2 | 0.0102 | 0.1559629 | E |
| <input type="checkbox"/> | GO:0046489 | 9,8,10 | phosphoinositide biosynthetic process | 28 | 0.0043 | 2 | 0.0102 | 0.1559629 | E |
| <input type="checkbox"/> | GO:0005996 | 5,6 | monosaccharide metabolic process | 92 | 0.0142 | 4 | 0.0204 | 0.1578371 | E |
| <input type="checkbox"/> | GO:0006944 | 5 | membrane fusion | 59 | 0.0091 | 3 | 0.0153 | 0.1618113 | E |
| <input type="checkbox"/> | GO:0019236 | 4 | response to pheromone | 94 | 0.0145 | 4 | 0.0204 | 0.1620546 | E |
| <input type="checkbox"/> | GO:0006885 | 7 | regulation of pH | 29 | 0.0045 | 2 | 0.0102 | 0.1624757 | E |
| <input type="checkbox"/> | GO:0051656 | 6,3,5,4 | establishment of organelle localization | 29 | 0.0045 | 2 | 0.0102 | 0.1624757 | E |
| <input type="checkbox"/> | GO:0006470 | 8,7 | protein amino acid dephosphorylation | 29 | 0.0045 | 2 | 0.0102 | 0.1624757 | E |
| <input type="checkbox"/> | GO:0007533 | 5,7,6 | mating type switching | 29 | 0.0045 | 2 | 0.0102 | 0.1624757 | E |
| <input type="checkbox"/> | GO:0006109 | 5,4 | regulation of carbohydrate metabolic process | 29 | 0.0045 | 2 | 0.0102 | 0.1624757 | E |
| <input type="checkbox"/> | GO:0010324 | 5 | membrane invagination | 96 | 0.0148 | 4 | 0.0204 | 0.1660706 | E |
| <input type="checkbox"/> | GO:0006644 | 6,7 | phospholipid metabolic process | 97 | 0.0150 | 4 | 0.0204 | 0.1680007 | E |
| <input type="checkbox"/> | GO:0007015 | 8 | actin filament organization | 61 | 0.0094 | 3 | 0.0153 | 0.1685233 | E |
| <input type="checkbox"/> | GO:0030466 | 11,7,8,12,10 | chromatin silencing at silent mating-type cassette | 30 | 0.0046 | 2 | 0.0102 | 0.1688427 | E |
| <input type="checkbox"/> | GO:0000122 | 10,9 | negative regulation of transcription from RNA polymerase II promoter | 63 | 0.0097 | 3 | 0.0153 | 0.1749257 | E |
| <input type="checkbox"/> | GO:0043161 | 10,9,11 | proteasomal ubiquitin-dependent protein catabolic process | 63 | 0.0097 | 3 | 0.0153 | 0.1749257 | E |
| <input type="checkbox"/> | GO:0043330 | 5,6 | response to exogenous dsRNA | 7 | 0.0011 | 1 | 0.0051 | 0.1763337 | E |
| <input type="checkbox"/> | GO:0000433 | 12,10,11,8 | negative regulation of transcription from RNA polymerase II promoter by glucose | 7 | 0.0011 | 1 | 0.0051 | 0.1763337 | E |
| <input type="checkbox"/> | GO:0043331 | 4 | response to dsRNA | 7 | 0.0011 | 1 | 0.0051 | 0.1763337 | E |
| <input type="checkbox"/> | GO:0045014 | 11,9,10,7 | negative regulation of transcription by glucose | 7 | 0.0011 | 1 | 0.0051 | 0.1763337 | E |
| <input type="checkbox"/> | GO:0000430 | 11,9,10,7 | regulation of transcription from RNA polymerase II promoter by glucose | 7 | 0.0011 | 1 | 0.0051 | 0.1763337 | E |
| <input type="checkbox"/> | GO:0000372 | 10 | Group I intron splicing | 7 | 0.0011 | 1 | 0.0051 | 0.1763337 | E |
| <input type="checkbox"/> | GO:0019722 | 7 | calcium-mediated signaling | 7 | 0.0011 | 1 | 0.0051 | 0.1763337 | E |
| <input type="checkbox"/> | GO:0051707 | 3,4 | response to other organism | 7 | 0.0011 | 1 | 0.0051 | 0.1763337 | E |
| <input type="checkbox"/> | GO:0009102 | 6,7,8 | biotin biosynthetic process | 7 | 0.0011 | 1 | 0.0051 | 0.1763337 | E |
| <input type="checkbox"/> | GO:0000429 | 10,8,9,6 | regulation of transcription from RNA polymerase II promoter by carbon catabolites | 7 | 0.0011 | 1 | 0.0051 | 0.1763337 | E |
| <input type="checkbox"/> | GO:0000376 | 9 | RNA splicing, via transesterification reactions with guanosine as nucleophile | 7 | 0.0011 | 1 | 0.0051 | 0.1763337 | E |
| <input type="checkbox"/> | GO:0000710 | 11,9,8,6,5,10,7,4 | meiotic mismatch repair | 7 | 0.0011 | 1 | 0.0051 | 0.1763337 | E |
| <input type="checkbox"/> | GO:0009615 | 4,5 | response to virus | 7 | 0.0011 | 1 | 0.0051 | 0.1763337 | E |
| <input type="checkbox"/> | GO:0006768 | 5,7,6 | biotin metabolic process | 7 | 0.0011 | 1 | 0.0051 | 0.1763337 | E |
| <input type="checkbox"/> | GO:0000437 | 11,9,10,7 | negative regulation of transcription from RNA polymerase II promoter by carbon catabolites | 7 | 0.0011 | 1 | 0.0051 | 0.1763337 | E |
| <input type="checkbox"/> | GO:0051129 | 6,5 | negative regulation of cell organization and biogenesis | 7 | 0.0011 | 1 | 0.0051 | 0.1763337 | E |

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| <input type="checkbox"/> | GO:0051168 | 9,7,8 | nuclear export | 102 | 0.0158 | 4 | 0.0204 | 0.1768438 | E |
| <input type="checkbox"/> | GO:0030010 | 7,4,8 | establishment of cell polarity | 103 | 0.0159 | 4 | 0.0204 | 0.1784468 | E |
| <input type="checkbox"/> | GO:0007121 | 8,6,10,7,11,5 | bipolar cellular bud site selection | 32 | 0.0049 | 2 | 0.0102 | 0.1811048 | E |
| <input type="checkbox"/> | GO:0019932 | 6 | second-messenger-mediated signaling | 32 | 0.0049 | 2 | 0.0102 | 0.1811048 | E |
| <input type="checkbox"/> | GO:0051028 | 5,7,6,8 | mRNA transport | 66 | 0.0102 | 3 | 0.0153 | 0.1839119 | E |
| <input type="checkbox"/> | GO:0006406 | 11,9,6,8,10,7 | mRNA export from nucleus | 66 | 0.0102 | 3 | 0.0153 | 0.1839119 | E |
| <input type="checkbox"/> | GO:0031326 | 6,5 | regulation of cellular biosynthetic process | 67 | 0.0103 | 3 | 0.0153 | 0.1867358 | E |
| <input type="checkbox"/> | GO:0009889 | 5,4 | regulation of biosynthetic process | 69 | 0.0107 | 3 | 0.0153 | 0.1921178 | E |
| <input type="checkbox"/> | GO:0006892 | 8,6,5,7 | post-Golgi vesicle-mediated transport | 69 | 0.0107 | 3 | 0.0153 | 0.1921178 | E |
| <input type="checkbox"/> | GO:0007034 | 7,5,6 | vacuolar transport | 114 | 0.0176 | 4 | 0.0204 | 0.1923184 | E |
| <input type="checkbox"/> | GO:0007163 | 6,3,7 | establishment and/or maintenance of cell polarity | 115 | 0.0178 | 4 | 0.0204 | 0.1932356 | E |
| <input type="checkbox"/> | GO:0018318 | 10,9,8 | protein amino acid palmitoylation | 8 | 0.0012 | 1 | 0.0051 | 0.1954495 | E |
| <input type="checkbox"/> | GO:0000751 | 8,9,7,6 | cell cycle arrest in response to pheromone | 8 | 0.0012 | 1 | 0.0051 | 0.1954495 | E |
| <input type="checkbox"/> | GO:0045013 | 10,8,9,6 | negative regulation of transcription by carbon catabolites | 8 | 0.0012 | 1 | 0.0051 | 0.1954495 | E |
| <input type="checkbox"/> | GO:0018345 | 9,8,7 | protein palmitoylation | 8 | 0.0012 | 1 | 0.0051 | 0.1954495 | E |
| <input type="checkbox"/> | GO:0031146 | 11,10,12 | SCF-dependent proteasomal ubiquitin-dependent protein catabolic process | 8 | 0.0012 | 1 | 0.0051 | 0.1954495 | E |
| <input type="checkbox"/> | GO:0008614 | 7 | pyridoxine metabolic process | 8 | 0.0012 | 1 | 0.0051 | 0.1954495 | E |
| <input type="checkbox"/> | GO:0046015 | 10,8,9,6 | regulation of transcription by glucose | 8 | 0.0012 | 1 | 0.0051 | 0.1954495 | E |
| <input type="checkbox"/> | GO:0015677 | 9,10 | copper ion import | 8 | 0.0012 | 1 | 0.0051 | 0.1954495 | E |
| <input type="checkbox"/> | GO:0042816 | 6 | vitamin B6 metabolic process | 8 | 0.0012 | 1 | 0.0051 | 0.1954495 | E |
| <input type="checkbox"/> | GO:0000019 | 9,8 | regulation of mitotic recombination | 8 | 0.0012 | 1 | 0.0051 | 0.1954495 | E |
| <input type="checkbox"/> | GO:0045039 | 10,9,7,8 | protein import into mitochondrial inner membrane | 8 | 0.0012 | 1 | 0.0051 | 0.1954495 | E |
| <input type="checkbox"/> | GO:0006979 | 4 | response to oxidative stress | 71 | 0.0110 | 3 | 0.0153 | 0.1971384 | E |
| <input type="checkbox"/> | GO:0003006 | 3,4 | reproductive developmental process | 35 | 0.0054 | 2 | 0.0102 | 0.1982131 | E |
| <input type="checkbox"/> | GO:0046165 | 5 | alcohol biosynthetic process | 35 | 0.0054 | 2 | 0.0102 | 0.1982131 | E |
| <input type="checkbox"/> | GO:0007531 | 4,6,5 | mating type determination | 35 | 0.0054 | 2 | 0.0102 | 0.1982131 | E |
| <input type="checkbox"/> | GO:0007530 | 4,5 | sex determination | 35 | 0.0054 | 2 | 0.0102 | 0.1982131 | E |
| <input type="checkbox"/> | GO:0006643 | 5,6 | membrane lipid metabolic process | 125 | 0.0193 | 4 | 0.0204 | 0.1993346 | E |
| <input type="checkbox"/> | GO:0051169 | 7,5,6 | nuclear transport | 129 | 0.0199 | 4 | 0.0204 | 0.2002717 | E |
| <input type="checkbox"/> | GO:0006913 | 8,6,7 | nucleocytoplasmic transport | 129 | 0.0199 | 4 | 0.0204 | 0.2002717 | E |
| <input type="checkbox"/> | GO:0016051 | 5 | carbohydrate biosynthetic process | 77 | 0.0119 | 3 | 0.0153 | 0.2099779 | E |
| <input type="checkbox"/> | GO:0006283 | 8,7 | transcription-coupled nucleotide-excision repair | 9 | 0.0014 | 1 | 0.0051 | 0.2132516 | E |
| <input type="checkbox"/> | GO:0030847 | 10,9 | transcription termination from Pol II promoter, RNA polymerase(A)-independent | 9 | 0.0014 | 1 | 0.0051 | 0.2132516 | E |
| <input type="checkbox"/> | GO:0019935 | 7 | cyclic-nucleotide-mediated signaling | 9 | 0.0014 | 1 | 0.0051 | 0.2132516 | E |
| <input type="checkbox"/> | GO:0000921 | 8,7 | septin ring assembly | 9 | 0.0014 | 1 | 0.0051 | 0.2132516 | E |
| <input type="checkbox"/> | GO:0006071 | 6 | glycerol metabolic process | 9 | 0.0014 | 1 | 0.0051 | 0.2132516 | E |
| <input type="checkbox"/> | GO:0046685 | 5 | response to arsenic | 9 | 0.0014 | 1 | 0.0051 | 0.2132516 | E |
| <input type="checkbox"/> | GO:0000128 | 3 | flocculation | 9 | 0.0014 | 1 | 0.0051 | 0.2132516 | E |
| <input type="checkbox"/> | GO:0007076 | 10,8,5,6,9,7,4 | mitotic chromosome condensation | 9 | 0.0014 | 1 | 0.0051 | 0.2132516 | E |
| <input type="checkbox"/> | GO:0032185 | 6 | septin cytoskeleton organization and biogenesis | 9 | 0.0014 | 1 | 0.0051 | 0.2132516 | E |
| <input type="checkbox"/> | GO:0019751 | 5 | polyol metabolic process | 9 | 0.0014 | 1 | 0.0051 | 0.2132516 | E |
| <input type="checkbox"/> | GO:0019933 | 8 | cAMP-mediated signaling | 9 | 0.0014 | 1 | 0.0051 | 0.2132516 | E |
| <input type="checkbox"/> | GO:0031106 | 7 | septin ring organization | 9 | 0.0014 | 1 | 0.0051 | 0.2132516 | E |

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|--------------------------|------------|----------------|--------------------------------------------------------------------------------------------|----|--------|---|--------|-----------|---|
| <input type="checkbox"/> | GO:0000501 | 4 | flocculation via cell wall protein-carbohydrate interaction | 9 | 0.0014 | 1 | 0.0051 | 0.2132516 | E |
| <input type="checkbox"/> | GO:0006405 | 10,8,5,7,9,6 | RNA export from nucleus | 79 | 0.0122 | 3 | 0.0153 | 0.2135098 | E |
| <input type="checkbox"/> | GO:0016485 | 8 | protein processing | 38 | 0.0059 | 2 | 0.0102 | 0.2136580 | E |
| <input type="checkbox"/> | GO:0050657 | 5,6 | nucleic acid transport | 80 | 0.0124 | 3 | 0.0153 | 0.2151357 | E |
| <input type="checkbox"/> | GO:0050658 | 4,6,5,7 | RNA transport | 80 | 0.0124 | 3 | 0.0153 | 0.2151357 | E |
| <input type="checkbox"/> | GO:0051236 | 3,4,5 | establishment of RNA localization | 80 | 0.0124 | 3 | 0.0153 | 0.2151357 | E |
| <input type="checkbox"/> | GO:0006888 | 8,6,5,7 | ER to Golgi vesicle-mediated transport | 81 | 0.0125 | 3 | 0.0153 | 0.2166687 | E |
| <input type="checkbox"/> | GO:0046474 | 8,7,9 | glycerophospholipid biosynthetic process | 39 | 0.0060 | 2 | 0.0102 | 0.2184208 | E |
| <input type="checkbox"/> | GO:0048308 | 5 | organelle inheritance | 40 | 0.0062 | 2 | 0.0102 | 0.2229873 | E |
| <input type="checkbox"/> | GO:0006512 | 8 | ubiquitin cycle | 88 | 0.0136 | 3 | 0.0153 | 0.2248477 | E |
| <input type="checkbox"/> | GO:0006766 | 4 | vitamin metabolic process | 89 | 0.0137 | 3 | 0.0153 | 0.2256610 | E |
| <input type="checkbox"/> | GO:0006767 | 5 | water-soluble vitamin metabolic process | 89 | 0.0137 | 3 | 0.0153 | 0.2256610 | E |
| <input type="checkbox"/> | GO:0015931 | 4,5 | nucleobase, nucleoside, nucleotide and nucleic acid transport | 90 | 0.0139 | 3 | 0.0153 | 0.2263883 | E |
| <input type="checkbox"/> | GO:0006403 | 4 | RNA localization | 90 | 0.0139 | 3 | 0.0153 | 0.2263883 | E |
| <input type="checkbox"/> | GO:0016311 | 6 | dephosphorylation | 41 | 0.0063 | 2 | 0.0102 | 0.2273564 | E |
| <input type="checkbox"/> | GO:0000271 | 6,7 | polysaccharide biosynthetic process | 41 | 0.0063 | 2 | 0.0102 | 0.2273564 | E |
| <input type="checkbox"/> | GO:0051052 | 7,6 | regulation of DNA metabolic process | 41 | 0.0063 | 2 | 0.0102 | 0.2273564 | E |
| <input type="checkbox"/> | GO:0030447 | 3 | filamentous growth | 94 | 0.0145 | 3 | 0.0153 | 0.2284617 | E |
| <input type="checkbox"/> | GO:0051261 | 6 | protein depolymerization | 10 | 0.0015 | 1 | 0.0051 | 0.2298016 | E |
| <input type="checkbox"/> | GO:0046019 | 10,9,6 | regulation of transcription from RNA polymerase II promoter by pheromones | 10 | 0.0015 | 1 | 0.0051 | 0.2298016 | E |
| <input type="checkbox"/> | GO:0006616 | 9,12,11,7,10,8 | SRP-dependent cotranslational protein targeting to membrane, translocation | 10 | 0.0015 | 1 | 0.0051 | 0.2298016 | E |
| <input type="checkbox"/> | GO:0006882 | 10,8 | cellular zinc ion homeostasis | 10 | 0.0015 | 1 | 0.0051 | 0.2298016 | E |
| <input type="checkbox"/> | GO:0051181 | 4,5 | cofactor transport | 10 | 0.0015 | 1 | 0.0051 | 0.2298016 | E |
| <input type="checkbox"/> | GO:0009373 | 9,8,5 | regulation of transcription by pheromones | 10 | 0.0015 | 1 | 0.0051 | 0.2298016 | E |
| <input type="checkbox"/> | GO:0051336 | 5 | regulation of hydrolase activity | 10 | 0.0015 | 1 | 0.0051 | 0.2298016 | E |
| <input type="checkbox"/> | GO:0030846 | 10,9 | transcription termination from Pol II promoter, RNA polymerase(A) coupled | 10 | 0.0015 | 1 | 0.0051 | 0.2298016 | E |
| <input type="checkbox"/> | GO:0055069 | 9 | zinc ion homeostasis | 10 | 0.0015 | 1 | 0.0051 | 0.2298016 | E |
| <input type="checkbox"/> | GO:0001403 | 6,4,8,9 | invasive growth (sensu Saccharomyces) | 42 | 0.0065 | 2 | 0.0102 | 0.2315272 | E |
| <input type="checkbox"/> | GO:0030384 | 8,9 | phosphoinositide metabolic process | 43 | 0.0066 | 2 | 0.0102 | 0.2354996 | E |
| <input type="checkbox"/> | GO:0006887 | 8,6,5,7 | exocytosis | 44 | 0.0068 | 2 | 0.0102 | 0.2392737 | E |
| <input type="checkbox"/> | GO:0050790 | 4 | regulation of catalytic activity | 45 | 0.0069 | 2 | 0.0102 | 0.2428502 | E |
| <input type="checkbox"/> | GO:0007109 | 7,6,5,4 | cytokinesis, completion of separation | 11 | 0.0017 | 1 | 0.0051 | 0.2451584 | E |
| <input type="checkbox"/> | GO:0006276 | 3 | plasmid maintenance | 11 | 0.0017 | 1 | 0.0051 | 0.2451584 | E |
| <input type="checkbox"/> | GO:0030261 | 6 | chromosome condensation | 11 | 0.0017 | 1 | 0.0051 | 0.2451584 | E |
| <input type="checkbox"/> | GO:0007039 | 7,8 | vacuolar protein catabolic process | 11 | 0.0017 | 1 | 0.0051 | 0.2451584 | E |
| <input type="checkbox"/> | GO:0016226 | 6 | iron-sulfur cluster assembly | 11 | 0.0017 | 1 | 0.0051 | 0.2451584 | E |
| <input type="checkbox"/> | GO:0031163 | 5 | metallo-sulfur cluster assembly | 11 | 0.0017 | 1 | 0.0051 | 0.2451584 | E |
| <input type="checkbox"/> | GO:0065002 | 8,6,7 | intracellular protein transport across a membrane | 11 | 0.0017 | 1 | 0.0051 | 0.2451584 | E |
| <input type="checkbox"/> | GO:0007050 | 7,8,6 | cell cycle arrest | 11 | 0.0017 | 1 | 0.0051 | 0.2451584 | E |
| <input type="checkbox"/> | GO:0065009 | 3 | regulation of a molecular function | 46 | 0.0071 | 2 | 0.0102 | 0.2462299 | E |
| <input type="checkbox"/> | GO:0042364 | 6 | water-soluble vitamin biosynthetic process | 46 | 0.0071 | 2 | 0.0102 | 0.2462299 | E |
| <input type="checkbox"/> | GO:0009110 | 5 | vitamin biosynthetic process | 46 | 0.0071 | 2 | 0.0102 | 0.2462299 | E |
| <input type="checkbox"/> | GO:0006417 | 7,6,5 | regulation of translation | 47 | 0.0073 | 2 | 0.0102 | 0.2494143 | E |
| <input type="checkbox"/> | GO:0007007 | 6,7 | inner mitochondrial membrane | 12 | 0.0018 | 1 | 0.0051 | 0.2502787 | E |

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| <input type="radio"/> | GO:0007007 | 9,7 | organization and biogenesis | 12 | 0.0019 | 1 | 0.0051 | 0.2593787 | E |
| <input type="radio"/> | GO:0006904 | 9,5,7,6,8 | vesicle docking during exocytosis | 12 | 0.0019 | 1 | 0.0051 | 0.2593787 | E |
| <input type="radio"/> | GO:0048468 | 3,5 | cell development | 52 | 0.0080 | 2 | 0.0102 | 0.2624722 | E |
| <input type="radio"/> | GO:0006400 | 7,8 | tRNA modification | 52 | 0.0080 | 2 | 0.0102 | 0.2624722 | E |
| <input type="radio"/> | GO:0006368 | 9,7,8 | RNA elongation from RNA polymerase II promoter | 53 | 0.0082 | 2 | 0.0102 | 0.2645279 | E |
| <input type="radio"/> | GO:0000075 | 7,6 | cell cycle checkpoint | 53 | 0.0082 | 2 | 0.0102 | 0.2645279 | E |
| <input type="radio"/> | GO:0006302 | 7,6 | double-strand break repair | 57 | 0.0088 | 2 | 0.0102 | 0.2709968 | E |
| <input type="radio"/> | GO:0006997 | 5 | nuclear organization and biogenesis | 57 | 0.0088 | 2 | 0.0102 | 0.2709968 | E |
| <input type="radio"/> | GO:0000749 | 5 | response to pheromone during conjugation with cellular fusion | 57 | 0.0088 | 2 | 0.0102 | 0.2709968 | E |
| <input type="radio"/> | GO:0008654 | 7,6,8 | phospholipid biosynthetic process | 58 | 0.0090 | 2 | 0.0102 | 0.2721924 | E |
| <input type="radio"/> | GO:0045786 | 6,7,5 | negative regulation of progression through cell cycle | 13 | 0.0020 | 1 | 0.0051 | 0.2725169 | E |
| <input type="radio"/> | GO:0000920 | 6,4 | cell separation during cytokinesis | 13 | 0.0020 | 1 | 0.0051 | 0.2725169 | E |
| <input type="radio"/> | GO:0006111 | 8,7,9,10,6 | regulation of gluconeogenesis | 13 | 0.0020 | 1 | 0.0051 | 0.2725169 | E |
| <input type="radio"/> | GO:0006334 | 6,7,10 | nucleosome assembly | 13 | 0.0020 | 1 | 0.0051 | 0.2725169 | E |
| <input type="radio"/> | GO:0006354 | 8,6,7 | RNA elongation | 59 | 0.0091 | 2 | 0.0102 | 0.2732267 | E |
| <input type="radio"/> | GO:0006650 | 7,8 | glycerophospholipid metabolic process | 60 | 0.0093 | 2 | 0.0102 | 0.2741032 | E |
| <input type="radio"/> | GO:0007124 | 6,4,8,9 | pseudohyphal growth | 61 | 0.0094 | 2 | 0.0102 | 0.2748258 | E |
| <input type="radio"/> | GO:0007264 | 6 | small GTPase mediated signal transduction | 61 | 0.0094 | 2 | 0.0102 | 0.2748258 | E |
| <input type="radio"/> | GO:0043543 | 7 | protein amino acid acylation | 62 | 0.0096 | 2 | 0.0102 | 0.2753985 | E |
| <input type="radio"/> | GO:0006006 | 7,8 | glucose metabolic process | 65 | 0.0100 | 2 | 0.0102 | 0.2762557 | E |
| <input type="radio"/> | GO:0044264 | 5,6 | cellular polysaccharide metabolic process | 65 | 0.0100 | 2 | 0.0102 | 0.2762557 | E |
| <input type="radio"/> | GO:0005976 | 5 | polysaccharide metabolic process | 65 | 0.0100 | 2 | 0.0102 | 0.2762557 | E |
| <input type="radio"/> | GO:0016567 | 9 | protein ubiquitination | 66 | 0.0102 | 2 | 0.0102 | 0.2762679 | E |
| <input type="radio"/> | GO:0048278 | 4,5,6 | vesicle docking | 14 | 0.0022 | 1 | 0.0051 | 0.2846249 | E |
| <input type="radio"/> | GO:0022406 | 3 | membrane docking | 14 | 0.0022 | 1 | 0.0051 | 0.2846249 | E |
| <input type="radio"/> | GO:0042787 | 10,9,11 | protein ubiquitination during ubiquitin-dependent protein catabolic process | 14 | 0.0022 | 1 | 0.0051 | 0.2846249 | E |
| <input type="radio"/> | GO:0000011 | 6 | vacuole inheritance | 14 | 0.0022 | 1 | 0.0051 | 0.2846249 | E |
| <input type="radio"/> | GO:0007018 | 8,7,6 | microtubule-based movement | 15 | 0.0023 | 1 | 0.0051 | 0.2957528 | E |
| <input type="radio"/> | GO:0000114 | 10,8,9,5,7,4 | G1-specific transcription in mitotic cell cycle | 15 | 0.0023 | 1 | 0.0051 | 0.2957528 | E |
| <input type="radio"/> | GO:0005978 | 8,7,9 | glycogen biosynthetic process | 15 | 0.0023 | 1 | 0.0051 | 0.2957528 | E |
| <input type="radio"/> | GO:0007091 | 9,7,5,8,6,4 | mitotic metaphase/anaphase transition | 15 | 0.0023 | 1 | 0.0051 | 0.2957528 | E |
| <input type="radio"/> | GO:0030473 | 8,9,6,7 | nuclear migration, microtubule-mediated | 15 | 0.0023 | 1 | 0.0051 | 0.2957528 | E |
| <input type="radio"/> | GO:0000737 | 6,7 | DNA catabolic process, endonucleolytic | 15 | 0.0023 | 1 | 0.0051 | 0.2957528 | E |
| <input type="radio"/> | GO:0006031 | 9,7,8,10 | chitin biosynthetic process | 15 | 0.0023 | 1 | 0.0051 | 0.2957528 | E |
| <input type="radio"/> | GO:0000079 | 8,7,6 | regulation of cyclin-dependent protein kinase activity | 15 | 0.0023 | 1 | 0.0051 | 0.2957528 | E |
| <input type="radio"/> | GO:0031145 | 11,10,12 | anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process | 15 | 0.0023 | 1 | 0.0051 | 0.2957528 | E |
| <input type="radio"/> | GO:0016050 | 5 | vesicle organization and biogenesis | 16 | 0.0025 | 1 | 0.0051 | 0.3059485 | E |
| <input type="radio"/> | GO:0045003 | 9,8 | double-strand break repair via synthesis-dependent strand annealing | 17 | 0.0026 | 1 | 0.0051 | 0.3152577 | E |
| <input type="radio"/> | GO:0046349 | 6,7 | amino sugar biosynthetic process | 17 | 0.0026 | 1 | 0.0051 | 0.3152577 | E |
| <input type="radio"/> | GO:0000741 | 6 | karyogamy | 17 | 0.0026 | 1 | 0.0051 | 0.3152577 | E |
| <input type="radio"/> | GO:0000742 | 7,5 | karyogamy during conjugation with cellular fusion | 17 | 0.0026 | 1 | 0.0051 | 0.3152577 | E |
| <input type="radio"/> | GO:0045132 | 9,7,8,6,4 | meiotic chromosome segregation | 17 | 0.0026 | 1 | 0.0051 | 0.3152577 | E |

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| <input type="radio"/> | GO:0030705 | 7,5,6 | cytoskeleton-dependent intracellular transport | 17 | 0.0026 | 1 | 0.0051 | 0.3152577 | E |
| <input type="radio"/> | GO:0007004 | 9 | telomere maintenance via telomerase | 17 | 0.0026 | 1 | 0.0051 | 0.3152577 | E |
| <input type="radio"/> | GO:0006042 | 7,8 | glucosamine biosynthetic process | 17 | 0.0026 | 1 | 0.0051 | 0.3152577 | E |
| <input type="radio"/> | GO:0006030 | 8,6,7,9 | chitin metabolic process | 17 | 0.0026 | 1 | 0.0051 | 0.3152577 | E |
| <input type="radio"/> | GO:0006045 | 8,9 | N-acetylglucosamine biosynthetic process | 17 | 0.0026 | 1 | 0.0051 | 0.3152577 | E |
| <input type="radio"/> | GO:0042147 | 8,6,7 | retrograde transport, endosome to Golgi | 17 | 0.0026 | 1 | 0.0051 | 0.3152577 | E |
| <input type="radio"/> | GO:0006113 | 5 | fermentation | 17 | 0.0026 | 1 | 0.0051 | 0.3152577 | E |
| <input type="radio"/> | GO:0051248 | 6,5 | negative regulation of protein metabolic process | 18 | 0.0028 | 1 | 0.0051 | 0.3237247 | E |
| <input type="radio"/> | GO:0000084 | 8,7,6 | S phase of mitotic cell cycle | 18 | 0.0028 | 1 | 0.0051 | 0.3237247 | E |
| <input type="radio"/> | GO:0006369 | 9,8 | transcription termination from RNA polymerase II promoter | 18 | 0.0028 | 1 | 0.0051 | 0.3237247 | E |
| <input type="radio"/> | GO:0000018 | 8,7 | regulation of DNA recombination | 18 | 0.0028 | 1 | 0.0051 | 0.3237247 | E |
| <input type="radio"/> | GO:0031668 | 5,4 | cellular response to extracellular stimulus | 19 | 0.0029 | 1 | 0.0051 | 0.3313914 | E |
| <input type="radio"/> | GO:0009228 | 7,8 | thiamin biosynthetic process | 19 | 0.0029 | 1 | 0.0051 | 0.3313914 | E |
| <input type="radio"/> | GO:0009267 | 7,6,5 | cellular response to starvation | 19 | 0.0029 | 1 | 0.0051 | 0.3313914 | E |
| <input type="radio"/> | GO:0000245 | 7,6,9,11 | spliceosome assembly | 19 | 0.0029 | 1 | 0.0051 | 0.3313914 | E |
| <input type="radio"/> | GO:0031669 | 6,5 | cellular response to nutrient levels | 19 | 0.0029 | 1 | 0.0051 | 0.3313914 | E |
| <input type="radio"/> | GO:0006041 | 6,7 | glucosamine metabolic process | 19 | 0.0029 | 1 | 0.0051 | 0.3313914 | E |
| <input type="radio"/> | GO:0043255 | 7,6,5 | regulation of carbohydrate biosynthetic process | 19 | 0.0029 | 1 | 0.0051 | 0.3313914 | E |
| <input type="radio"/> | GO:0006044 | 7,8 | N-acetylglucosamine metabolic process | 19 | 0.0029 | 1 | 0.0051 | 0.3313914 | E |
| <input type="radio"/> | GO:0042594 | 6,4 | response to starvation | 19 | 0.0029 | 1 | 0.0051 | 0.3313914 | E |
| <input type="radio"/> | GO:0006040 | 5,6 | amino sugar metabolic process | 19 | 0.0029 | 1 | 0.0051 | 0.3313914 | E |
| <input type="radio"/> | GO:0045053 | 7,6,5,4 | protein retention in Golgi | 20 | 0.0031 | 1 | 0.0051 | 0.3382984 | E |
| <input type="radio"/> | GO:0006772 | 7 | thiamin metabolic process | 20 | 0.0031 | 1 | 0.0051 | 0.3382984 | E |
| <input type="radio"/> | GO:0006614 | 11,10,9,8,7 | SRP-dependent cotranslational protein targeting to membrane | 20 | 0.0031 | 1 | 0.0051 | 0.3382984 | E |
| <input type="radio"/> | GO:0006754 | 7,9,6,8,10 | ATP biosynthetic process | 20 | 0.0031 | 1 | 0.0051 | 0.3382984 | E |
| <input type="radio"/> | GO:0015986 | 8,10,7,9,11,5 | ATP synthesis coupled proton transport | 20 | 0.0031 | 1 | 0.0051 | 0.3382984 | E |
| <input type="radio"/> | GO:0016579 | 9 | protein deubiquitination | 20 | 0.0031 | 1 | 0.0051 | 0.3382984 | E |
| <input type="radio"/> | GO:0015985 | 6,8,7,9 | energy coupled proton transport, down electrochemical gradient | 20 | 0.0031 | 1 | 0.0051 | 0.3382984 | E |
| <input type="radio"/> | GO:0007094 | 9,11,10,8 | mitotic cell cycle spindle assembly checkpoint | 20 | 0.0031 | 1 | 0.0051 | 0.3382984 | E |
| <input type="radio"/> | GO:0042724 | 7 | thiamin and derivative biosynthetic process | 20 | 0.0031 | 1 | 0.0051 | 0.3382984 | E |
| <input type="radio"/> | GO:0006308 | 5,6 | DNA catabolic process | 20 | 0.0031 | 1 | 0.0051 | 0.3382984 | E |
| <input type="radio"/> | GO:0051320 | 7,6,5 | S phase | 20 | 0.0031 | 1 | 0.0051 | 0.3382984 | E |
| <input type="radio"/> | GO:0006353 | 8,7 | transcription termination | 20 | 0.0031 | 1 | 0.0051 | 0.3382984 | E |
| <input type="radio"/> | GO:0006753 | 7 | nucleoside phosphate metabolic process | 20 | 0.0031 | 1 | 0.0051 | 0.3382984 | E |
| <input type="radio"/> | GO:0000209 | 10 | protein polyubiquitination | 20 | 0.0031 | 1 | 0.0051 | 0.3382984 | E |
| <input type="radio"/> | GO:0046034 | 5,9 | ATP metabolic process | 21 | 0.0032 | 1 | 0.0051 | 0.3444843 | E |
| <input type="radio"/> | GO:0051716 | 3 | cellular response to stimulus | 21 | 0.0032 | 1 | 0.0051 | 0.3444843 | E |
| <input type="radio"/> | GO:0033554 | 4 | cellular response to stress | 21 | 0.0032 | 1 | 0.0051 | 0.3444843 | E |
| <input type="radio"/> | GO:0019674 | 9,8 | NAD metabolic process | 21 | 0.0032 | 1 | 0.0051 | 0.3444843 | E |
| <input type="radio"/> | GO:0030150 | 10,9,8,7 | protein import into mitochondrial matrix | 22 | 0.0034 | 1 | 0.0051 | 0.3499862 | E |
| <input type="radio"/> | GO:0009145 | 7,8 | purine nucleoside triphosphate biosynthetic process | 22 | 0.0034 | 1 | 0.0051 | 0.3499862 | E |
| <input type="radio"/> | GO:0009206 | 8,9 | purine ribonucleoside triphosphate biosynthetic process | 22 | 0.0034 | 1 | 0.0051 | 0.3499862 | E |

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| <input type="radio"/> | GO:0042723 | 6 | thiamin and derivative metabolic process | 22 | 0.0034 | 1 | 0.0051 | 0.3499862 | E |
| <input type="radio"/> | GO:0048284 | 5 | organelle fusion | 22 | 0.0034 | 1 | 0.0051 | 0.3499862 | E |
| <input type="radio"/> | GO:0007120 | 8,6,10,7,11,5 | axial cellular bud site selection | 22 | 0.0034 | 1 | 0.0051 | 0.3499862 | E |
| <input type="radio"/> | GO:0044272 | 5 | sulfur compound biosynthetic process | 22 | 0.0034 | 1 | 0.0051 | 0.3499862 | E |
| <input type="radio"/> | GO:0009144 | 7 | purine nucleoside triphosphate metabolic process | 23 | 0.0036 | 1 | 0.0051 | 0.3548396 | E |
| <input type="radio"/> | GO:0009205 | 8 | purine ribonucleoside triphosphate metabolic process | 23 | 0.0036 | 1 | 0.0051 | 0.3548396 | E |
| <input type="radio"/> | GO:0009408 | 5,4 | response to heat | 23 | 0.0036 | 1 | 0.0051 | 0.3548396 | E |
| <input type="radio"/> | GO:0006613 | 10,9,8,7,6 | cotranslational protein targeting to membrane | 23 | 0.0036 | 1 | 0.0051 | 0.3548396 | E |
| <input type="radio"/> | GO:0015992 | 5,7,6,8 | proton transport | 24 | 0.0037 | 1 | 0.0051 | 0.3590785 | E |
| <input type="radio"/> | GO:0000288 | 10,8,9 | mRNA catabolic process, deadenylation-dependent decay | 24 | 0.0037 | 1 | 0.0051 | 0.3590785 | E |
| <input type="radio"/> | GO:0007096 | 8,10,9,7 | regulation of exit from mitosis | 24 | 0.0037 | 1 | 0.0051 | 0.3590785 | E |
| <input type="radio"/> | GO:0006818 | 4,5 | hydrogen transport | 24 | 0.0037 | 1 | 0.0051 | 0.3590785 | E |
| <input type="radio"/> | GO:0006096 | 9,10 | glycolysis | 24 | 0.0037 | 1 | 0.0051 | 0.3590785 | E |
| <input type="radio"/> | GO:0010035 | 4 | response to inorganic substance | 24 | 0.0037 | 1 | 0.0051 | 0.3590785 | E |
| <input type="radio"/> | GO:0051452 | 12,9,10 | cellular pH reduction | 24 | 0.0037 | 1 | 0.0051 | 0.3590785 | E |
| <input type="radio"/> | GO:0006890 | 8,6,5,7 | retrograde vesicle-mediated transport, Golgi to ER | 24 | 0.0037 | 1 | 0.0051 | 0.3590785 | E |
| <input type="radio"/> | GO:0007006 | 5,6 | mitochondrial membrane organization and biogenesis | 24 | 0.0037 | 1 | 0.0051 | 0.3590785 | E |
| <input type="radio"/> | GO:0007035 | 13,10,6,11 | vacuolar acidification | 24 | 0.0037 | 1 | 0.0051 | 0.3590785 | E |
| <input type="radio"/> | GO:0045851 | 8 | pH reduction | 24 | 0.0037 | 1 | 0.0051 | 0.3590785 | E |
| <input type="radio"/> | GO:0009201 | 7,8 | ribonucleoside triphosphate biosynthetic process | 24 | 0.0037 | 1 | 0.0051 | 0.3590785 | E |
| <input type="radio"/> | GO:0009199 | 7 | ribonucleoside triphosphate metabolic process | 25 | 0.0039 | 1 | 0.0051 | 0.3627354 | E |
| <input type="radio"/> | GO:0009607 | 3 | response to biotic stimulus | 25 | 0.0039 | 1 | 0.0051 | 0.3627354 | E |
| <input type="radio"/> | GO:0043549 | 6 | regulation of kinase activity | 25 | 0.0039 | 1 | 0.0051 | 0.3627354 | E |
| <input type="radio"/> | GO:0051453 | 11,8,9 | regulation of cellular pH | 25 | 0.0039 | 1 | 0.0051 | 0.3627354 | E |
| <input type="radio"/> | GO:0009250 | 7,8 | glucan biosynthetic process | 25 | 0.0039 | 1 | 0.0051 | 0.3627354 | E |
| <input type="radio"/> | GO:0045859 | 7 | regulation of protein kinase activity | 25 | 0.0039 | 1 | 0.0051 | 0.3627354 | E |
| <input type="radio"/> | GO:0006298 | 7,9,6 | mismatch repair | 25 | 0.0039 | 1 | 0.0051 | 0.3627354 | E |
| <input type="radio"/> | GO:0045005 | 8,6 | maintenance of fidelity during DNA-dependent DNA replication | 25 | 0.0039 | 1 | 0.0051 | 0.3627354 | E |
| <input type="radio"/> | GO:0000724 | 8,7 | double-strand break repair via homologous recombination | 25 | 0.0039 | 1 | 0.0051 | 0.3627354 | E |
| <input type="radio"/> | GO:0030641 | 10,8 | cellular hydrogen ion homeostasis | 25 | 0.0039 | 1 | 0.0051 | 0.3627354 | E |
| <input type="radio"/> | GO:0048311 | 7,6 | mitochondrion distribution | 26 | 0.0040 | 1 | 0.0051 | 0.3658415 | E |
| <input type="radio"/> | GO:0051338 | 5 | regulation of transferase activity | 26 | 0.0040 | 1 | 0.0051 | 0.3658415 | E |
| <input type="radio"/> | GO:0042274 | 6,5 | ribosomal small subunit biogenesis and assembly | 26 | 0.0040 | 1 | 0.0051 | 0.3658415 | E |
| <input type="radio"/> | GO:0006379 | 8 | mRNA cleavage | 26 | 0.0040 | 1 | 0.0051 | 0.3658415 | E |
| <input type="radio"/> | GO:0000001 | 8,7,6 | mitochondrion inheritance | 26 | 0.0040 | 1 | 0.0051 | 0.3658415 | E |
| <input type="radio"/> | GO:0051318 | 6,7,5 | G1 phase | 27 | 0.0042 | 1 | 0.0051 | 0.3684266 | E |
| <input type="radio"/> | GO:0009142 | 6,7 | nucleoside triphosphate biosynthetic process | 27 | 0.0042 | 1 | 0.0051 | 0.3684266 | E |
| <input type="radio"/> | GO:0000080 | 7,8,6 | G1 phase of mitotic cell cycle | 27 | 0.0042 | 1 | 0.0051 | 0.3684266 | E |
| <input type="radio"/> | GO:0006094 | 8,9 | gluconeogenesis | 28 | 0.0043 | 1 | 0.0051 | 0.3705192 | E |
| <input type="radio"/> | GO:0000750 | 8,7,6 | pheromone-dependent signal transduction during conjugation with cellular fusion | 28 | 0.0043 | 1 | 0.0051 | 0.3705192 | E |
| <input type="radio"/> | GO:0009636 | 4 | response to toxin | 28 | 0.0043 | 1 | 0.0051 | 0.3705192 | E |

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| <input type="radio"/> | GO:0009266 | 4 | response to temperature stimulus | 28 | 0.0043 | 1 | 0.0051 | 0.3705192 | E |
| <input type="radio"/> | GO:0043624 | 7,6 | cellular protein complex disassembly | 28 | 0.0043 | 1 | 0.0051 | 0.3705192 | E |
| <input type="radio"/> | GO:0043241 | 6,5 | protein complex disassembly | 28 | 0.0043 | 1 | 0.0051 | 0.3705192 | E |
| <input type="radio"/> | GO:0032005 | 7,6 | signal transduction during conjugation with cellular fusion | 28 | 0.0043 | 1 | 0.0051 | 0.3705192 | E |
| <input type="radio"/> | GO:0000054 | 10,11,6,8,9 | ribosome export from nucleus | 28 | 0.0043 | 1 | 0.0051 | 0.3705192 | E |
| <input type="radio"/> | GO:0000725 | 7,6 | recombinational repair | 29 | 0.0045 | 1 | 0.0051 | 0.3721466 | E |
| <input type="radio"/> | GO:0006999 | 6 | nuclear pore organization and biogenesis | 29 | 0.0045 | 1 | 0.0051 | 0.3721466 | E |
| <input type="radio"/> | GO:0051651 | 5,4,3 | maintenance of cellular localization | 29 | 0.0045 | 1 | 0.0051 | 0.3721466 | E |
| <input type="radio"/> | GO:0032507 | 6,5,4 | maintenance of cellular protein localization | 29 | 0.0045 | 1 | 0.0051 | 0.3721466 | E |
| <input type="radio"/> | GO:0031137 | 6,5 | regulation of conjugation with cellular fusion | 30 | 0.0046 | 1 | 0.0051 | 0.3733350 | E |
| <input type="radio"/> | GO:0009141 | 6 | nucleoside triphosphate metabolic process | 30 | 0.0046 | 1 | 0.0051 | 0.3733350 | E |
| <input type="radio"/> | GO:0046999 | 5,4 | regulation of conjugation | 30 | 0.0046 | 1 | 0.0051 | 0.3733350 | E |
| <input type="radio"/> | GO:0019319 | 7,8 | hexose biosynthetic process | 30 | 0.0046 | 1 | 0.0051 | 0.3733350 | E |
| <input type="radio"/> | GO:0006893 | 9,7,6,8 | Golgi to plasma membrane transport | 30 | 0.0046 | 1 | 0.0051 | 0.3733350 | E |
| <input type="radio"/> | GO:0045185 | 5,4,3 | maintenance of protein localization | 30 | 0.0046 | 1 | 0.0051 | 0.3733350 | E |
| <input type="radio"/> | GO:0046364 | 6,7 | monosaccharide biosynthetic process | 30 | 0.0046 | 1 | 0.0051 | 0.3733350 | E |
| <input type="radio"/> | GO:0000002 | 6 | mitochondrial genome maintenance | 31 | 0.0048 | 1 | 0.0051 | 0.3741091 | E |
| <input type="radio"/> | GO:0015672 | 6,7 | monovalent inorganic cation transport | 32 | 0.0049 | 1 | 0.0051 | 0.3744930 | E |
| <input type="radio"/> | GO:0006418 | 8,7,9,6 | tRNA aminoacylation for protein translation | 32 | 0.0049 | 1 | 0.0051 | 0.3744930 | E |
| <input type="radio"/> | GO:0006694 | 6,5,7 | steroid biosynthetic process | 32 | 0.0049 | 1 | 0.0051 | 0.3744930 | E |
| <input type="radio"/> | GO:0005977 | 7,6,8 | glycogen metabolic process | 32 | 0.0049 | 1 | 0.0051 | 0.3744930 | E |
| <input type="radio"/> | GO:0032984 | 5 | macromolecular complex disassembly | 32 | 0.0049 | 1 | 0.0051 | 0.3744930 | E |
| <input type="radio"/> | GO:0043038 | 6,7 | amino acid activation | 32 | 0.0049 | 1 | 0.0051 | 0.3744930 | E |
| <input type="radio"/> | GO:0016126 | 6,7,8 | sterol biosynthetic process | 32 | 0.0049 | 1 | 0.0051 | 0.3744930 | E |
| <input type="radio"/> | GO:0043039 | 7,8 | tRNA aminoacylation | 32 | 0.0049 | 1 | 0.0051 | 0.3744930 | E |
| <input type="radio"/> | GO:0045047 | 9,8,7,6,5 | protein targeting to ER | 33 | 0.0051 | 1 | 0.0051 | 0.3745093 | E |
| <input type="radio"/> | GO:0051235 | 3,2 | maintenance of localization | 33 | 0.0051 | 1 | 0.0051 | 0.3745093 | E |
| <input type="radio"/> | GO:0009272 | 7 | chitin- and beta-glucan-containing cell wall biogenesis | 33 | 0.0051 | 1 | 0.0051 | 0.3745093 | E |
| <input type="radio"/> | GO:0000096 | 6,7,5 | sulfur amino acid metabolic process | 33 | 0.0051 | 1 | 0.0051 | 0.3745093 | E |
| <input type="radio"/> | GO:0006270 | 8,6 | DNA replication initiation | 33 | 0.0051 | 1 | 0.0051 | 0.3745093 | E |
| <input type="radio"/> | GO:0042546 | 6 | cell wall biogenesis | 33 | 0.0051 | 1 | 0.0051 | 0.3745093 | E |
| <input type="radio"/> | GO:0008150 | 1 | biological process | 6476 | 1.0000 | 196 | 1.0000 | 1.0000000 | D |
| <input type="radio"/> | GO:0006007 | 8,9 | glucose catabolic process | 34 | 0.0053 | 1 | 0.0051 | 0.3741799 | D |
| <input type="radio"/> | GO:0030004 | 9,7 | cellular monovalent inorganic cation homeostasis | 34 | 0.0053 | 1 | 0.0051 | 0.3741799 | D |
| <input type="radio"/> | GO:0006360 | 8,7 | transcription from RNA polymerase I promoter | 34 | 0.0053 | 1 | 0.0051 | 0.3741799 | D |
| <input type="radio"/> | GO:0007186 | 6 | G-protein coupled receptor protein signaling pathway | 34 | 0.0053 | 1 | 0.0051 | 0.3741799 | D |
| <input type="radio"/> | GO:0055067 | 8 | monovalent inorganic cation homeostasis | 34 | 0.0053 | 1 | 0.0051 | 0.3741799 | D |
| <input type="radio"/> | GO:0030433 | 9,11,10,12 | ER-associated protein catabolic process | 35 | 0.0054 | 1 | 0.0051 | 0.3735256 | D |
| <input type="radio"/> | GO:0022411 | 4 | cellular component disassembly | 36 | 0.0056 | 1 | 0.0051 | 0.3725663 | D |
| <input type="radio"/> | GO:0006090 | 7 | pyruvate metabolic process | 38 | 0.0059 | 1 | 0.0051 | 0.3698075 | D |
| <input type="radio"/> | GO:0006515 | 8,9 | misfolded or incompletely synthesized protein catabolic process | 38 | 0.0059 | 1 | 0.0051 | 0.3698075 | D |
| <input type="radio"/> | GO:0009152 | 7,8 | purine ribonucleotide biosynthetic process | 38 | 0.0059 | 1 | 0.0051 | 0.3698075 | D |
| <input type="radio"/> | GO:0019320 | 7,8 | hexose catabolic process | 39 | 0.0060 | 1 | 0.0051 | 0.3680434 | D |

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| <input type="checkbox"/> | GO:0006612 | 9,7,8 | protein targeting to membrane | 39 | 0.0060 | 1 | 0.0051 | 0.3680434 | D |
| <input type="checkbox"/> | GO:0006865 | 5,6,7 | amino acid transport | 39 | 0.0060 | 1 | 0.0051 | 0.3680434 | D |
| <input type="checkbox"/> | GO:0007265 | 7 | Ras protein signal transduction | 39 | 0.0060 | 1 | 0.0051 | 0.3680434 | D |
| <input type="checkbox"/> | GO:0006112 | 5 | energy reserve metabolic process | 39 | 0.0060 | 1 | 0.0051 | 0.3680434 | D |
| <input type="checkbox"/> | GO:0001302 | 5 | replicative cell aging | 39 | 0.0060 | 1 | 0.0051 | 0.3680434 | D |
| <input type="checkbox"/> | GO:0043681 | 6,7,8 | protein import into mitochondrion | 40 | 0.0062 | 1 | 0.0051 | 0.3660452 | D |
| <input type="checkbox"/> | GO:0009260 | 6,7 | ribonucleotide biosynthetic process | 40 | 0.0062 | 1 | 0.0051 | 0.3660452 | D |
| <input type="checkbox"/> | GO:0016573 | 11,9 | histone acetylation | 40 | 0.0062 | 1 | 0.0051 | 0.3660452 | D |
| <input type="checkbox"/> | GO:0007031 | 5 | peroxisome organization and biogenesis | 40 | 0.0062 | 1 | 0.0051 | 0.3660452 | D |
| <input type="checkbox"/> | GO:0009150 | 7 | purine ribonucleotide metabolic process | 41 | 0.0063 | 1 | 0.0051 | 0.3638285 | D |
| <input type="checkbox"/> | GO:0006164 | 6,7 | purine nucleotide biosynthetic process | 41 | 0.0063 | 1 | 0.0051 | 0.3638285 | D |
| <input type="checkbox"/> | GO:0016125 | 5,6,7 | sterol metabolic process | 42 | 0.0065 | 1 | 0.0051 | 0.3614083 | D |
| <input type="checkbox"/> | GO:0006769 | 8,7 | nicotinamide metabolic process | 42 | 0.0065 | 1 | 0.0051 | 0.3614083 | D |
| <input type="checkbox"/> | GO:0008202 | 5,6 | steroid metabolic process | 43 | 0.0066 | 1 | 0.0051 | 0.3587990 | D |
| <input type="checkbox"/> | GO:0009259 | 6 | ribonucleotide metabolic process | 43 | 0.0066 | 1 | 0.0051 | 0.3587990 | D |
| <input type="checkbox"/> | GO:0006752 | 6 | group transfer coenzyme metabolic process | 44 | 0.0068 | 1 | 0.0051 | 0.3560142 | D |
| <input type="checkbox"/> | GO:0006289 | 7,6 | nucleotide-excision repair | 44 | 0.0068 | 1 | 0.0051 | 0.3560142 | D |
| <input type="checkbox"/> | GO:0046365 | 6,7 | monosaccharide catabolic process | 44 | 0.0068 | 1 | 0.0051 | 0.3560142 | D |
| <input type="checkbox"/> | GO:0006914 | 3 | autophagy | 45 | 0.0069 | 1 | 0.0051 | 0.3530668 | D |
| <input type="checkbox"/> | GO:0019362 | 7,6 | pyridine nucleotide metabolic process | 45 | 0.0069 | 1 | 0.0051 | 0.3530668 | D |
| <input type="checkbox"/> | GO:0006119 | 7,4 | oxidative phosphorylation | 46 | 0.0071 | 1 | 0.0051 | 0.3499692 | D |
| <input type="checkbox"/> | GO:0006073 | 6,7 | glucan metabolic process | 46 | 0.0071 | 1 | 0.0051 | 0.3499692 | D |
| <input type="checkbox"/> | GO:0046164 | 5 | alcohol catabolic process | 47 | 0.0073 | 1 | 0.0051 | 0.3467331 | D |
| <input type="checkbox"/> | GO:0006163 | 6 | purine nucleotide metabolic process | 47 | 0.0073 | 1 | 0.0051 | 0.3467331 | D |
| <input type="checkbox"/> | GO:0006473 | 8 | protein amino acid acetylation | 48 | 0.0074 | 1 | 0.0051 | 0.3433698 | D |
| <input type="checkbox"/> | GO:0007568 | 3 | aging | 49 | 0.0076 | 1 | 0.0051 | 0.3398898 | D |
| <input type="checkbox"/> | GO:0007569 | 4 | cell aging | 49 | 0.0076 | 1 | 0.0051 | 0.3398898 | D |
| <input type="checkbox"/> | GO:0006606 | 9,10,7,8,6 | protein import into nucleus | 50 | 0.0077 | 1 | 0.0051 | 0.3363034 | D |
| <input type="checkbox"/> | GO:0015837 | 4,5 | amine transport | 50 | 0.0077 | 1 | 0.0051 | 0.3363034 | D |
| <input type="checkbox"/> | GO:0051170 | 9,7,8 | nuclear import | 50 | 0.0077 | 1 | 0.0051 | 0.3363034 | D |
| <input type="checkbox"/> | GO:0006626 | 9,8,7,6 | protein targeting to mitochondrion | 52 | 0.0080 | 1 | 0.0051 | 0.3288490 | D |
| <input type="checkbox"/> | GO:0007166 | 5 | cell surface receptor linked signal transduction | 52 | 0.0080 | 1 | 0.0051 | 0.3288490 | D |
| <input type="checkbox"/> | GO:0046942 | 5,6 | carboxylic acid transport | 54 | 0.0083 | 1 | 0.0051 | 0.3210779 | D |
| <input type="checkbox"/> | GO:0015849 | 4,5 | organic acid transport | 55 | 0.0085 | 1 | 0.0051 | 0.3170939 | D |
| <input type="checkbox"/> | GO:0006611 | 9,10,7,8 | protein export from nucleus | 56 | 0.0086 | 1 | 0.0051 | 0.3130543 | D |
| <input type="checkbox"/> | GO:0006733 | 6 | oxidoreduction coenzyme metabolic process | 56 | 0.0086 | 1 | 0.0051 | 0.3130543 | D |
| <input type="checkbox"/> | GO:0009165 | 5,6 | nucleotide biosynthetic process | 59 | 0.0091 | 1 | 0.0051 | 0.3006701 | D |
| <input type="checkbox"/> | GO:0031509 | 7,11 | telomeric heterochromatin formation | 60 | 0.0093 | 1 | 0.0051 | 0.2964746 | D |
| <input type="checkbox"/> | GO:0006348 | 11,7,8,12,10 | chromatin silencing at telomere | 60 | 0.0093 | 1 | 0.0051 | 0.2964746 | D |
| <input type="checkbox"/> | GO:0042273 | 6,5 | ribosomal large subunit biogenesis and assembly | 64 | 0.0099 | 1 | 0.0051 | 0.2795032 | D |
| <input type="checkbox"/> | GO:0006790 | 4 | sulfur metabolic process | 67 | 0.0103 | 2 | 0.0102 | 0.2761498 | D |
| <input type="checkbox"/> | GO:0043623 | 7,6 | cellular protein complex assembly | 69 | 0.0107 | 2 | 0.0102 | 0.2755394 | D |
| <input type="checkbox"/> | GO:0006839 | 7,5,6 | mitochondrial transport | 65 | 0.0100 | 1 | 0.0051 | 0.2752375 | D |
| <input type="checkbox"/> | GO:0009108 | 6 | coenzyme biosynthetic process | 66 | 0.0102 | 1 | 0.0051 | 0.2709714 | D |

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|-----------------------|------------|---------|----------------------------------------------------------------------------|-----|--------|---|--------|-----------|---|
| <input type="radio"/> | GO:0046467 | 6,5,7 | membrane lipid biosynthetic process | 78 | 0.0120 | 2 | 0.0102 | 0.2673957 | D |
| <input type="radio"/> | GO:0006623 | 9,8,7,6 | protein targeting to vacuole | 67 | 0.0103 | 1 | 0.0051 | 0.2667088 | D |
| <input type="radio"/> | GO:0008033 | 7 | tRNA processing | 84 | 0.0130 | 2 | 0.0102 | 0.2580239 | D |
| <input type="radio"/> | GO:0032446 | 8 | protein modification by small protein conjugation | 84 | 0.0130 | 2 | 0.0102 | 0.2580239 | D |
| <input type="radio"/> | GO:0045333 | 5 | cellular respiration | 89 | 0.0137 | 2 | 0.0102 | 0.2484437 | D |
| <input type="radio"/> | GO:0006970 | 4 | response to osmotic stress | 89 | 0.0137 | 2 | 0.0102 | 0.2484437 | D |
| <input type="radio"/> | GO:0043413 | 6 | biopolymer glycosylation | 73 | 0.0113 | 1 | 0.0051 | 0.2414012 | D |
| <input type="radio"/> | GO:0006486 | 8,7,6 | protein amino acid glycosylation | 73 | 0.0113 | 1 | 0.0051 | 0.2414012 | D |
| <input type="radio"/> | GO:0046483 | 4 | heterocycle metabolic process | 76 | 0.0117 | 1 | 0.0051 | 0.2290490 | D |
| <input type="radio"/> | GO:0009117 | 5 | nucleotide metabolic process | 111 | 0.0171 | 3 | 0.0153 | 0.2241560 | D |
| <input type="radio"/> | GO:0006468 | 8,7 | protein amino acid phosphorylation | 101 | 0.0156 | 2 | 0.0102 | 0.2212004 | D |
| <input type="radio"/> | GO:0009101 | 7,5 | glycoprotein biosynthetic process | 78 | 0.0120 | 1 | 0.0051 | 0.2209687 | D |
| <input type="radio"/> | GO:0006461 | 6,5 | protein complex assembly | 116 | 0.0179 | 3 | 0.0153 | 0.2195761 | D |
| <input type="radio"/> | GO:0009628 | 3 | response to abiotic stimulus | 117 | 0.0181 | 3 | 0.0153 | 0.2185159 | D |
| <input type="radio"/> | GO:0051188 | 5 | cofactor biosynthetic process | 79 | 0.0122 | 1 | 0.0051 | 0.2169806 | D |
| <input type="radio"/> | GO:0009100 | 6 | glycoprotein metabolic process | 79 | 0.0122 | 1 | 0.0051 | 0.2169806 | D |
| <input type="radio"/> | GO:0006399 | 6 | tRNA metabolic process | 121 | 0.0187 | 3 | 0.0153 | 0.2138459 | D |
| <input type="radio"/> | GO:0044275 | 6 | cellular carbohydrate catabolic process | 80 | 0.0124 | 1 | 0.0051 | 0.2130292 | D |
| <input type="radio"/> | GO:0016052 | 5 | carbohydrate catabolic process | 80 | 0.0124 | 1 | 0.0051 | 0.2130292 | D |
| <input type="radio"/> | GO:0008610 | 5,4,6 | lipid biosynthetic process | 129 | 0.0199 | 3 | 0.0153 | 0.2027588 | D |
| <input type="radio"/> | GO:0017038 | 5,6,7 | protein import | 109 | 0.0168 | 2 | 0.0102 | 0.2013183 | D |
| <input type="radio"/> | GO:0009060 | 6 | aerobic respiration | 84 | 0.0130 | 1 | 0.0051 | 0.1976190 | D |
| <input type="radio"/> | GO:0015980 | 4 | energy derivation by oxidation of organic compounds | 145 | 0.0224 | 4 | 0.0204 | 0.1964703 | D |
| <input type="radio"/> | GO:0044257 | 6,7 | cellular protein catabolic process | 160 | 0.0247 | 4 | 0.0204 | 0.1841493 | D |
| <input type="radio"/> | GO:0051186 | 4 | cofactor metabolic process | 170 | 0.0263 | 5 | 0.0255 | 0.1800255 | D |
| <input type="radio"/> | GO:0030163 | 6,5 | protein catabolic process | 173 | 0.0267 | 5 | 0.0255 | 0.1793460 | D |
| <input type="radio"/> | GO:0022618 | 6,5 | protein-RNA complex assembly | 144 | 0.0222 | 3 | 0.0153 | 0.1778167 | D |
| <input type="radio"/> | GO:0006091 | 3 | generation of precursor metabolites and energy | 183 | 0.0283 | 5 | 0.0255 | 0.1751360 | D |
| <input type="radio"/> | GO:0019941 | 8,7,9 | modification-dependent protein catabolic process | 148 | 0.0229 | 3 | 0.0153 | 0.1706599 | D |
| <input type="radio"/> | GO:0006511 | 9,8,10 | ubiquitin-dependent protein catabolic process | 148 | 0.0229 | 3 | 0.0153 | 0.1706599 | D |
| <input type="radio"/> | GO:0051603 | 7,8 | proteolysis involved in cellular protein catabolic process | 151 | 0.0233 | 3 | 0.0153 | 0.1652311 | D |
| <input type="radio"/> | GO:0044262 | 5 | cellular carbohydrate metabolic process | 213 | 0.0329 | 6 | 0.0306 | 0.1627219 | D |
| <input type="radio"/> | GO:0006508 | 6 | proteolysis | 178 | 0.0275 | 4 | 0.0204 | 0.1623248 | D |
| <input type="radio"/> | GO:0032787 | 6 | monocarboxylic acid metabolic process | 126 | 0.0195 | 2 | 0.0102 | 0.1590618 | D |
| <input type="radio"/> | GO:0043632 | 6 | modification-dependent macromolecule catabolic process | 155 | 0.0239 | 3 | 0.0153 | 0.1579555 | D |
| <input type="radio"/> | GO:0016310 | 6 | phosphorylation | 155 | 0.0239 | 3 | 0.0153 | 0.1579555 | D |
| <input type="radio"/> | GO:0005975 | 4 | carbohydrate metabolic process | 233 | 0.0360 | 6 | 0.0306 | 0.1513483 | D |
| <input type="radio"/> | GO:0006796 | 5 | phosphate metabolic process | 212 | 0.0327 | 5 | 0.0255 | 0.1503267 | D |
| <input type="radio"/> | GO:0006793 | 4 | phosphorus metabolic process | 212 | 0.0327 | 5 | 0.0255 | 0.1503267 | D |
| <input type="radio"/> | GO:0006886 | 7,5,6 | intracellular protein transport | 274 | 0.0423 | 7 | 0.0357 | 0.1371395 | D |
| <input type="radio"/> | GO:0006732 | 5 | coenzyme metabolic process | 136 | 0.0210 | 2 | 0.0102 | 0.1359282 | D |
| <input type="radio"/> | GO:0015031 | 4,5,6 | protein transport | 280 | 0.0432 | 7 | 0.0357 | 0.1327587 | D |
| <input type="radio"/> | GO:0044255 | 4,5 | cellular lipid metabolic process | 229 | 0.0354 | 5 | 0.0255 | 0.1309649 | D |

| | | | | | | | | | |
|--------------------------|------------|-------|-------------------------------------------------------------------|------|--------|----|--------|-----------|---|
| <input type="checkbox"/> | GO:0008104 | 4 | protein localization | 330 | 0.0510 | 9 | 0.0459 | 0.1294875 | D |
| <input type="checkbox"/> | GO:0009451 | 6 | RNA modification | 139 | 0.0215 | 2 | 0.0102 | 0.1293702 | D |
| <input type="checkbox"/> | GO:0033036 | 3 | macromolecule localization | 382 | 0.0590 | 11 | 0.0561 | 0.1228096 | D |
| <input type="checkbox"/> | GO:0045184 | 3,4,5 | establishment of protein localization | 296 | 0.0457 | 7 | 0.0357 | 0.1197460 | D |
| <input type="checkbox"/> | GO:0006629 | 4 | lipid metabolic process | 242 | 0.0374 | 5 | 0.0255 | 0.1155053 | D |
| <input type="checkbox"/> | GO:0009056 | 3 | catabolic process | 438 | 0.0676 | 12 | 0.0612 | 0.1118509 | D |
| <input type="checkbox"/> | GO:0044248 | 4 | cellular catabolic process | 425 | 0.0656 | 11 | 0.0561 | 0.1065428 | D |
| <input type="checkbox"/> | GO:0006605 | 8,6,7 | protein targeting | 258 | 0.0398 | 5 | 0.0255 | 0.0968853 | D |
| <input type="checkbox"/> | GO:0042493 | 4 | response to drug | 121 | 0.0187 | 1 | 0.0051 | 0.0901697 | D |
| <input type="checkbox"/> | GO:0006364 | 6,7 | rRNA processing | 249 | 0.0384 | 4 | 0.0204 | 0.0688080 | D |
| <input type="checkbox"/> | GO:0016072 | 6 | rRNA metabolic process | 256 | 0.0395 | 4 | 0.0204 | 0.0617778 | D |
| <input type="checkbox"/> | GO:0044249 | 4 | cellular biosynthetic process | 366 | 0.0565 | 7 | 0.0357 | 0.0602452 | D |
| <input type="checkbox"/> | GO:0019538 | 4 | protein metabolic process | 1547 | 0.2389 | 43 | 0.2194 | 0.0562190 | D |
| <input type="checkbox"/> | GO:0044260 | 4 | cellular macromolecule metabolic process | 1552 | 0.2397 | 43 | 0.2194 | 0.0552682 | D |
| <input type="checkbox"/> | GO:0044267 | 5 | cellular protein metabolic process | 1498 | 0.2313 | 41 | 0.2092 | 0.0533462 | D |
| <input type="checkbox"/> | GO:0006520 | 5,6 | amino acid metabolic process | 187 | 0.0289 | 2 | 0.0102 | 0.0524430 | D |
| <input type="checkbox"/> | GO:0009308 | 4 | amine metabolic process | 228 | 0.0352 | 3 | 0.0153 | 0.0519081 | D |
| <input type="checkbox"/> | GO:0006519 | 4 | amino acid and derivative metabolic process | 202 | 0.0312 | 2 | 0.0102 | 0.0382412 | D |
| <input type="checkbox"/> | GO:0006807 | 3 | nitrogen compound metabolic process | 251 | 0.0388 | 3 | 0.0153 | 0.0336511 | D |
| <input type="checkbox"/> | GO:0006082 | 4 | organic acid metabolic process | 314 | 0.0485 | 4 | 0.0204 | 0.0225940 | D |
| <input type="checkbox"/> | GO:0019752 | 5 | carboxylic acid metabolic process | 314 | 0.0485 | 4 | 0.0204 | 0.0225940 | D |
| <input type="checkbox"/> | GO:0022613 | 4 | ribonucleoprotein complex biogenesis and assembly | 483 | 0.0746 | 8 | 0.0408 | 0.0201495 | D |
| <input type="checkbox"/> | GO:0009059 | 4 | macromolecule biosynthetic process | 886 | 0.1368 | 18 | 0.0918 | 0.0145807 | D |
| <input type="checkbox"/> | GO:0043284 | 5 | biopolymer biosynthetic process | 354 | 0.0547 | 4 | 0.0204 | 0.0102698 | D |
| <input type="checkbox"/> | GO:0042254 | 5 | ribosome biogenesis and assembly | 410 | 0.0633 | 5 | 0.0255 | 0.0081851 | D |
| <input type="checkbox"/> | GO:0006412 | 6,5 | translation | 688 | 0.1062 | 11 | 0.0561 | 0.0052913 | D |
| <input type="checkbox"/> | GO:0006414 | 7,6 | translational elongation | 313 | 0.0483 | 2 | 0.0102 | 0.0027283 | D |
| <input type="checkbox"/> | GO:0009058 | 3 | biosynthetic process | 1249 | 0.1929 | 23 | 0.1173 | 0.0013953 | D |