

| Category | EC Term | Count | % | P-Value | Benjamini |
|-----------------------|--|-------|------|----------|-----------|
| KEGGPathway | Metabolic pathways | 234 | 29.4 | 3.30E-10 | 3.30E-08 |
| KEGGPathway | Biosynthesis of amino acids | 59 | 7.4 | 2.00E-08 | 1.00E-06 |
| KEGGPathway | Biosynthesis of secondary metabolites | 108 | 13.6 | 7.10E-06 | 2.40E-04 |
| KEGGPathway | Biosynthesis of antibiotics | 76 | 9.5 | 3.00E-05 | 7.40E-04 |
| KEGGPathway | Lysine biosynthesis | 12 | 1.5 | 1.70E-04 | 3.30E-03 |
| KEGGPathway | 2-Oxocarboxylic acid metabolism | 15 | 1.9 | 2.20E-03 | 3.70E-02 |
| homo-sapiens Category | Term | Count | % | P-Value | Benjamini |
| KEGG_PATHWAY | Biosynthesis of antibiotics | 32 | 8 | 2.00E-12 | 3.70E-10 |
| KEGG_PATHWAY | Metabolic pathways | 83 | 20.6 | 2.90E-11 | 2.80E-09 |
| KEGG_PATHWAY | Ribosome | 23 | 5.7 | 5.50E-10 | 3.40E-08 |
| KEGG_PATHWAY | Valine, leucine and isoleucine degradation | 13 | 3.2 | 2.70E-08 | 1.30E-06 |
| KEGG_PATHWAY | Carbon metabolism | 18 | 4.5 | 1.60E-07 | 6.20E-06 |
| KEGG_PATHWAY | Oxidative phosphorylation | 19 | 4.7 | 3.60E-07 | 1.10E-05 |
| KEGG_PATHWAY | Parkinson's disease | 19 | 4.7 | 9.80E-07 | 2.60E-05 |
| KEGG_PATHWAY | Citrate cycle (TCA cycle) | 9 | 2.2 | 4.30E-06 | 1.00E-04 |
| KEGG_PATHWAY | Huntington's disease | 20 | 5 | 2.00E-05 | 4.10E-04 |
| KEGG_PATHWAY | Alzheimer's disease | 18 | 4.5 | 4.10E-05 | 7.80E-04 |
| KEGG_PATHWAY | Aminoacyl-tRNA biosynthesis | 11 | 2.7 | 5.80E-05 | 1.00E-03 |
| KEGG_PATHWAY | Butanoate metabolism | 7 | 1.7 | 2.10E-04 | 3.40E-03 |
| KEGG_PATHWAY | Proteasome | 8 | 2 | 5.70E-04 | 8.20E-03 |
| KEGG_PATHWAY | Fatty acid degradation | 7 | 1.7 | 2.50E-03 | 3.30E-02 |
| KEGG_PATHWAY | Biosynthesis of amino acids | 9 | 2.2 | 2.60E-03 | 3.30E-02 |
| KEGG_PATHWAY | Synthesis and degradation of ketone bodies | 4 | 1 | 3.70E-03 | 4.40E-02 |
| KEGG_PATHWAY | DNA replication | 6 | 1.5 | 6.50E-03 | 7.20E-02 |
| mus-musculus Category | Term | Count | % | P-Value | Benjamini |
| KEGG_PATHWAY | Metabolic pathways | 138 | 25.4 | 2.80E-28 | 6.20E-26 |
| KEGG_PATHWAY | Parkinson's disease | 31 | 5.7 | 7.60E-13 | 8.50E-11 |

| | | | | | |
|----------------------------|--|-------|------|----------|-----------|
| KEGG_PATHWAY | Oxidative phosphorylation | 29 | 5.3 | 4.60E-12 | 3.40E-10 |
| KEGG_PATHWAY | Non-alcoholic fatty liver disease (NAFLD) | 30 | 5.5 | 1.80E-11 | 1.00E-09 |
| KEGG_PATHWAY | Huntington's disease | 33 | 6.1 | 6.20E-11 | 2.80E-09 |
| KEGG_PATHWAY | Alzheimer's disease | 30 | 5.5 | 3.70E-10 | 1.40E-08 |
| KEGG_PATHWAY | Ribosome | 25 | 4.6 | 1.00E-08 | 3.30E-07 |
| KEGG_PATHWAY | Peroxisome | 18 | 3.3 | 6.30E-08 | 1.80E-06 |
| KEGG_PATHWAY | Glycine, serine and threonine metabolism | 12 | 2.2 | 6.20E-07 | 1.50E-05 |
| KEGG_PATHWAY | Pyruvate metabolism | 11 | 2 | 4.10E-06 | 9.00E-05 |
| KEGG_PATHWAY | Propanoate metabolism | 9 | 1.7 | 1.20E-05 | 2.40E-04 |
| KEGG_PATHWAY | Valine, leucine and isoleucine degradation | 11 | 2 | 1.00E-04 | 1.90E-03 |
| KEGG_PATHWAY | Glyoxylate and dicarboxylate metabolism | 8 | 1.5 | 1.80E-04 | 3.10E-03 |
| KEGG_PATHWAY | Biosynthesis of antibiotics | 22 | 4.1 | 3.50E-04 | 5.60E-03 |
| KEGG_PATHWAY | Fatty acid metabolism | 9 | 1.7 | 1.40E-03 | 2.10E-02 |
| KEGG_PATHWAY | Arginine and proline metabolism | 8 | 1.5 | 4.70E-03 | 6.50E-02 |
| KEGG_PATHWAY | Aminoacyl-tRNA biosynthesis | 9 | 1.7 | 7.20E-03 | 9.40E-02 |
| KEGG_PATHWAY | One carbon pool by folate | 5 | 0.9 | 7.90E-03 | 9.70E-02 |
| Mycobacterium tuberculosis | | | | | |
| Category | Term | Count | % | P-Value | Benjamini |
| KEGG_PATHWAY | Metabolic pathways | 170 | 30.4 | 1.00E-06 | 1.00E-04 |
| KEGG_PATHWAY | Microbial metabolism in diverse environments | 74 | 13.2 | 5.00E-06 | 2.50E-04 |
| KEGG_PATHWAY | Biosynthesis of antibiotics | 79 | 14.1 | 1.30E-05 | 4.40E-04 |
| KEGG_PATHWAY | Biosynthesis of secondary metabolites | 93 | 16.6 | 5.00E-04 | 1.00E-02 |
| KEGG_PATHWAY | Propanoate metabolism | 24 | 4.3 | 5.00E-04 | 1.00E-02 |
| KEGG_PATHWAY | Carbon metabolism | 40 | 7.2 | 1.50E-03 | 2.40E-02 |
| KEGG_PATHWAY | Valine, leucine and isoleucine degradation | 25 | 4.5 | 1.60E-03 | 2.40E-02 |

| | | | | | |
|--------------------------|---|-------|------|----------|-----------|
| KEGG_PATHWAY | Glyoxylate and dicarboxylate metabolism | 19 | 3.4 | 2.40E-03 | 3.00E-02 |
| KEGG_PATHWAY | Fatty acid metabolism | 22 | 3.9 | 3.60E-03 | 4.00E-02 |
| KEGG_PATHWAY | Biosynthesis of amino acids | 40 | 7.2 | 4.00E-03 | 4.00E-02 |
| KEGG_PATHWAY | Ribosome | 24 | 4.3 | 6.50E-03 | 6.00E-02 |
| KEGG_PATHWAY | Fatty acid degradation | 21 | 3.8 | 8.60E-03 | 7.30E-02 |
| Saccharomyces cerevisiae | | | | | |
| Category | Term | Count | % | P-Value | Benjamini |
| KEGG_PATHWAY | Metabolic pathways | 82 | 27.5 | 6.60E-07 | 5.20E-05 |
| KEGG_PATHWAY | Biosynthesis of amino acids | 25 | 8.4 | 8.10E-06 | 3.30E-04 |
| KEGG_PATHWAY | 2-Oxocarboxylic acid metabolism | 12 | 4 | 2.90E-05 | 7.90E-04 |
| KEGG_PATHWAY | Biosynthesis of antibiotics | 32 | 10.7 | 2.10E-04 | 3.50E-03 |
| KEGG_PATHWAY | Oxidative phosphorylation | 16 | 5.4 | 2.20E-04 | 3.50E-03 |
| KEGG_PATHWAY | Biosynthesis of secondary metabolites | 38 | 12.8 | 8.60E-04 | 1.10E-02 |
| KEGG_PATHWAY | Amino sugar and nucleotide sugar metabolism | 9 | 3 | 2.00E-03 | 2.30E-02 |
| KEGG_PATHWAY | Proteasome | 9 | 3 | 3.70E-03 | 3.70E-02 |
| KEGG_PATHWAY | Valine, leucine and isoleucine biosynthesis | 5 | 1.7 | 9.80E-03 | 8.70E-02 |