

| Module | | | Enriched Subset | | | | |
|--------|------------|--|---|------------|-------|----------|------------|
| ID | Gene Count | | Top Ontology | Gene Count | % | PValue | Bonferroni |
| 20 | 76 | | BP transport | 14 | 21.88 | 1.30E-02 | 1.00E+00 |
| | | | CC NONE | - | - | - | - |
| | | | MF Ras GTPase activator activity | 3 | 4.69 | 2.87E-02 | 9.96E-01 |
| 3 | 49 | | BP translational elongation | 42 | 85.71 | 7.82E-90 | 3.09E-87 |
| | | | CC ribosome | 42 | 85.71 | 5.28E-75 | 2.74E-73 |
| | | | MF structural constituent of ribosome | 40 | 81.63 | 5.20E-73 | 3.22E-71 |
| 12 | 42 | | BP NONE | - | - | - | - |
| | | | CC NONE | - | - | - | - |
| | | | MF NONE | - | - | - | - |
| 13 | 26 | | BP cellular component biogenesis | 5 | 21.74 | 5.54E-03 | 9.05E-01 |
| | | | CC NONE | - | - | - | - |
| | | | MF NONE | - | - | - | - |
| 15 | 26 | | BP nuclear division | 15 | 57.69 | 1.25E-19 | 4.99E-17 |
| | | | CC spindle | 11 | 42.31 | 1.07E-15 | 1.01E-13 |
| | | | MF ATP binding | 11 | 42.31 | 6.26E-05 | 6.43E-03 |
| 10 | 14 | | BP glycolysis | 3 | 23.08 | 4.80E-04 | 2.08E-01 |
| | | | CC extracellular region part | 5 | 38.46 | 4.41E-03 | 3.04E-01 |
| | | | MF protein binding | 10 | 76.92 | 1.96E-02 | 8.62E-01 |
| 7 | 13 | | BP nervous system development | 6 | 50.00 | 4.89E-04 | 2.64E-01 |
| | | | CC cell fraction | 4 | 33.33 | 3.44E-02 | 8.90E-01 |
| | | | MF transporter activity | 6 | 50.00 | 8.66E-04 | 1.14E-01 |
| 11 | 12 | | BP regulation of Ras protein signal transduction | 2 | 20.00 | 5.82E-02 | 1.00E+00 |
| | | | CC NONE | - | - | - | - |
| | | | MF ATPase activity, coupled to transmembrane movement of substances | 2 | 20.00 | 2.85E-02 | 9.12E-01 |
| 1 | 11 | | BP oxidative phosphorylation | 4 | 36.36 | 3.76E-05 | 7.56E-03 |
| | | | CC mitochondrial inner membrane | 6 | 54.55 | 5.94E-07 | 3.92E-05 |
| | | | MF hydrogen ion transmembrane transporter activity | 4 | 36.36 | 1.66E-05 | 8.80E-04 |
| 2 | 11 | | BP glycolysis | 4 | 36.36 | 1.91E-06 | 4.36E-04 |
| | | | CC NONE | - | - | - | - |
| | | | MF NONE | - | - | - | - |

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|--------|------------|--|---|------------|-------|----------|------------|
| ID | Gene Count | | Top Ontology | Gene Count | % | PValue | Bonferroni |
| 5 | 11 | | BP response to DNA damage stimulus | 3 | 27.27 | 1.34E-02 | 9.65E-01 |
| | | | CC nuclear lumen | 5 | 45.45 | 5.95E-03 | 2.45E-01 |
| | | | MF NONE | - | - | - | - |
| 6 | 11 | | BP anti-apoptosis | 3 | 27.27 | 7.13E-03 | 8.78E-01 |
| | | | CC extracellular region | 6 | 54.55 | 2.60E-03 | 1.77E-01 |
| | | | MF protein binding | 9 | 81.82 | 3.31E-02 | 7.73E-01 |
| 9 | 11 | | BP nervous system development | 4 | 36.36 | 2.70E-02 | 9.99E-01 |
| | | | CC microtubule | 3 | 27.27 | 1.21E-02 | 5.31E-01 |
| | | | MF protein binding | 7 | 63.64 | 9.18E-02 | 9.96E-01 |
| 16 | 10 | | BP translational elongation | 5 | 55.56 | 1.69E-07 | 4.56E-05 |
| | | | CC cytosolic ribosome | 5 | 55.56 | 4.30E-08 | 2.71E-06 |
| | | | MF structural constituent of ribosome | 5 | 55.56 | 9.88E-07 | 5.34E-05 |
| 4 | 9 | | BP protein folding | 4 | 50.00 | 6.54E-05 | 1.53E-02 |
| | | | CC endoplasmic reticulum lumen | 6 | 75.00 | 5.90E-11 | 4.19E-09 |
| | | | MF unfolded protein binding | 4 | 50.00 | 1.46E-05 | 1.11E-03 |
| 8 | 8 | | BP response to organic substance | 6 | 75.00 | 6.61E-06 | 1.63E-03 |
| | | | CC synaptosome | 2 | 25.00 | 2.64E-02 | 6.29E-01 |
| | | | MF protein dimerization activity | 3 | 37.50 | 2.38E-02 | 7.21E-01 |
| 19 | 8 | | BP DNA replication | 4 | 50.00 | 8.07E-05 | 1.30E-02 |
| | | | CC nucleoplasm | 4 | 50.00 | 2.99E-03 | 1.44E-01 |
| | | | MF ATP binding | 4 | 50.00 | 2.40E-02 | 8.64E-01 |
| 21 | 8 | | BP response to inorganic substance | 3 | 37.50 | 2.04E-03 | 2.06E-01 |
| | | | CC cytoplasm | 4 | 50.00 | 9.74E-02 | 9.83E-01 |
| | | | MF copper ion binding | 4 | 50.00 | 3.13E-06 | 1.34E-04 |
| 14 | 7 | | BP cellular amino acid metabolic process | 2 | 33.33 | 3.18E-02 | 9.02E-01 |
| | | | CC NONE | - | - | - | - |
| | | | MF NONE | - | - | - | - |
| 17 | 7 | | BP anatomical structure development | 4 | 57.14 | 7.48E-02 | 1.00E+00 |
| | | | CC cell fraction | 3 | 42.86 | 4.03E-02 | 8.82E-01 |
| | | | MF NONE | - | - | - | - |
| 18 | 7 | | BP antigen processing and presentation of peptide antigen | 3 | 50.00 | 3.78E-05 | 9.07E-03 |
| | | | CC MHC class I protein complex | 2 | 33.33 | 8.77E-03 | 3.39E-01 |
| | | | MF MHC class I receptor activity | 2 | 33.33 | 5.60E-03 | 1.78E-01 |