

| 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   | -          | -     | -        | -          |
| 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   |

