

# a) GO Enrichment Analysis

Displaying only results with P<0.05; [click here to display all results](#)

|  | Caenorhabditis elegans (REF) | Client Text Box Input (▲ Hierarchy NEW! ?) |          |                 |     |          |
|--|------------------------------|--|----------|-----------------|-----|----------|
| PANTHER GO-Slim Biological Process   | #                            | #  | expected | Fold Enrichment | +/- | P value  |
| Unclassified   | 12877                        | 745  | 925.08   | .81             | -   | 0.00E00  |
| <a href="#">translation</a>  | 362                          | 46   | 26.01    | 1.77            | +   | 4.19E-02 |
| ↳ <a href="#">protein metabolic process</a>                                      | 1879                         | 246  | 134.99   | 1.82            | +   | 1.16E-17 |
| ↳ <a href="#">primary metabolic process</a>                                      | 4498                         | 603  | 323.14   | 1.87            | +   | 6.74E-58 |
| ↳ <a href="#">metabolic process</a>  | 5383                         | 697  | 386.71   | 1.80            | +   | 6.88E-65 |
| <a href="#">sensory perception</a>   | 454                          | 59   | 32.62    | 1.81            | +   | 3.14E-03 |
| ↳ <a href="#">neurological system process</a>                                    | 631                          | 116  | 45.33    | 2.56            | +   | 4.50E-17 |
| ↳ <a href="#">system process</a>   | 887                          | 183  | 63.72    | 2.87            | +   | 4.45E-34 |
| ↳ <a href="#">single-multicellular organism process</a>                          | 956                          | 196  | 68.68    | 2.85            | +   | 2.39E-36 |
| ↳ <a href="#">multicellular organismal process</a>                               | 956                          | 196  | 68.68    | 2.85            | +   | 2.39E-36 |
| <a href="#">cellular protein modification process</a>                            | 904                          | 123  | 64.94    | 1.89            | +   | 5.36E-09 |
| <a href="#">regulation of transcription from RNA polymerase II promoter</a>      | 695                          | 95   | 49.93    | 1.90            | +   | 8.54E-07 |
| ↳ <a href="#">transcription from RNA polymerase II promoter</a>                  | 893                          | 115  | 64.15    | 1.79            | +   | 5.34E-07 |
| ↳ <a href="#">transcription, DNA-dependent</a>                                   | 928                          | 123  | 66.67    | 1.84            | +   | 2.64E-08 |
| ↳ <a href="#">RNA metabolic process</a>  | 1258                         | 160  | 90.37    | 1.77            | +   | 8.08E-10 |
| ↳ <a href="#">nucleobase-containing compound metabolic process</a>               | 1936                         | 247  | 139.08   | 1.78            | +   | 2.25E-16 |
| ↳ <a href="#">regulation of nucleobase-containing compound metabolic process</a> | 826                          | 116  | 59.34    | 1.95            | +   | 3.13E-09 |
| ↳ <a href="#">regulation of biological process</a>                               | 1619                         | 213  | 116.31   | 1.83            | +   | 3.53E-15 |
| ↳ <a href="#">biological regulation</a>  | 2130                         | 326  | 153.02   | 2.13            | +   | 6.25E-37 |
| <a href="#">response to stress</a>   | 370                          | 53   | 26.58    | 1.99            | +   | 6.24E-04 |

# b) TEA

Drechmeria coniospora

