



| id | source | term_id | term_name | term_size | p_value |
|----|--------|-------------------|--|-----------|---------|
| 1 | REAC | REAC:R-HSA-74160 | Gene expression (Transcription) | 1380 | 1.3e-85 |
| 2 | REAC | REAC:R-HSA-73857 | RNA Polymerase II Transcription | 1247 | 3.0e-83 |
| 3 | REAC | REAC:R-HSA-212436 | Generic Transcription Pathway | 1130 | 1.3e-69 |
| 4 | KEGG | KEGG:05168 | Herpes simplex virus 1 infection | 460 | 3.0e-63 |
| 5 | GO:MF | GO:0140110 | transcription regulator activity | 1632 | 6.0e-51 |
| 6 | GO:MF | GO:0043565 | sequence-specific DNA binding | 1419 | 5.8e-47 |
| 7 | GO:MF | GO:0003690 | double-stranded DNA binding | 1415 | 9.3e-47 |
| 8 | GO:CC | GO:1902494 | catalytic complex | 1628 | 1.1e-41 |
| 9 | GO:CC | GO:0016604 | nuclear body | 796 | 1.8e-39 |
| 10 | GO:BP | GO:0007049 | cell cycle | 1655 | 1.9e-37 |
| 11 | GO:BP | GO:0044265 | cellular macromolecule catabolic process | 928 | 4.3e-34 |
| 12 | GO:BP | GO:0009057 | macromolecule catabolic process | 1239 | 1.5e-33 |
| 13 | GO:CC | GO:0140535 | intracellular protein-containing complex | 869 | 4.9e-32 |
| 14 | KEGG | KEGG:03040 | Spliceosome | 133 | 5.5e-08 |
| 15 | KEGG | KEGG:04120 | Ubiquitin mediated proteolysis | 129 | 1.2e-07 |

g:Profiler (biit.cs.ut.ee/gprofiler)