



id	source	term_id	term_name	term_size	p_value
1	GO:CC	GO:0016604	nuclear body	796	2.3e-48
2	GO:BP	GO:0045935	positive regulation of nucleobase-containing compound metabolic process	1798	3.0e-46
3	GO:CC	GO:1902494	catalytic complex	1628	4.6e-44
4	GO:BP	GO:0007049	cell cycle	1655	2.6e-42
5	GO:BP	GO:0051254	positive regulation of RNA metabolic process	1610	2.6e-40
6	REAC	REAC:R-HSA-74160	Gene expression (Transcription)	1380	8.6e-38
7	GO:CC	GO:0005694	chromosome	1638	1.7e-35
8	REAC	REAC:R-HSA-73857	RNA Polymerase II Transcription	1247	1.5e-34
9	GO:MF	GO:0019899	enzyme binding	1888	7.2e-34
10	GO:MF	GO:0035639	purine ribonucleoside triphosphate binding	1676	2.8e-33
11	GO:MF	GO:0032555	purine ribonucleotide binding	1739	1.7e-32
12	REAC	REAC:R-HSA-8953854	Metabolism of RNA	626	2.0e-31
13	KEGG	KEGG:03040	Spliceosome	133	1.0e-13
14	KEGG	KEGG:04144	Endocytosis	238	1.5e-12
15	KEGG	KEGG:03013	Nucleocytoplasmic transport	98	9.2e-11

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