



id	source	term_id	term_name	term_size	p_value
1	GO:BP	GO:0051254	positive regulation of RNA metabolic process	1610	3.8e-12
2	GO:BP	GO:0045935	positive regulation of nucleobase-containing compound metabolic process	1798	1.2e-11
3	GO:BP	GO:0010557	positive regulation of macromolecule biosynthetic process	1677	1.3e-09
4	GO:MF	GO:0140110	transcription regulator activity	1632	1.7e-05
5	REAC	REAC:R-HSA-3247509	Chromatin modifying enzymes	244	2.1e-04
6	REAC	REAC:R-HSA-4839726	Chromatin organization	244	2.1e-04
7	GO:CC	GO:1902494	catalytic complex	1628	2.2e-04
8	GO:MF	GO:0003682	chromatin binding	518	4.7e-04
9	REAC	REAC:R-HSA-74160	Gene expression (Transcription)	1380	6.0e-04
10	GO:CC	GO:0005694	chromosome	1638	1.3e-03
11	GO:MF	GO:0008270	zinc ion binding	707	1.8e-03
12	GO:CC	GO:0000118	histone deacetylase complex	77	1.9e-03
13	KEGG	KEGG:04360	Axon guidance	174	8.5e-03
14	KEGG	KEGG:04350	TGF-beta signaling pathway	87	2.0e-02

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