



id	source	term_id	term_name	term_size	p_value
1	GO:BP	GO:0045935	positive regulation of nucleobase-containing compound metabolic process	1798	3.3e-36
2	GO:BP	GO:0051254	positive regulation of RNA metabolic process	1610	1.6e-34
3	GO:BP	GO:0006325	chromatin organization	569	8.8e-31
4	GO:MF	GO:0140110	transcription regulator activity	1632	1.4e-23
5	GO:CC	GO:1902494	catalytic complex	1628	1.2e-22
6	REAC	REAC:R-HSA-4839726	Chromatin organization	244	3.7e-22
7	REAC	REAC:R-HSA-3247509	Chromatin modifying enzymes	244	3.7e-22
8	GO:MF	GO:0043565	sequence-specific DNA binding	1419	1.1e-20
9	REAC	REAC:R-HSA-74160	Gene expression (Transcription)	1380	7.1e-20
10	GO:MF	GO:0003712	transcription coregulator activity	456	1.1e-19
11	GO:CC	GO:0005694	chromosome	1638	6.9e-19
12	GO:CC	GO:0000785	chromatin	1112	5.0e-16
13	KEGG	KEGG:00310	Lysine degradation	59	5.3e-13
14	KEGG	KEGG:05168	Herpes simplex virus 1 infection	460	9.3e-05
15	KEGG	KEGG:05202	Transcriptional misregulation in cancer	158	2.4e-03

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