



id	source	term_id	term_name	term_size	p_value
1	GO:BP	GO:0045935	positive regulation of nucleobase-containing compound metabolic process	1798	1.1e-26
2	GO:BP	GO:0051254	positive regulation of RNA metabolic process	1610	8.7e-26
3	GO:BP	GO:0031328	positive regulation of cellular biosynthetic process	1760	1.9e-25
4	GO:CC	GO:1902494	catalytic complex	1628	1.5e-16
5	GO:MF	GO:0140110	transcription regulator activity	1632	2.3e-15
6	REAC	REAC:R-HSA-3247509	Chromatin modifying enzymes	244	5.4e-15
7	REAC	REAC:R-HSA-4839726	Chromatin organization	244	5.4e-15
8	GO:MF	GO:0003712	transcription coregulator activity	456	1.9e-13
9	GO:MF	GO:0042054	histone methyltransferase activity	58	5.1e-12
10	GO:CC	GO:0140513	nuclear protein-containing complex	1523	5.5e-12
11	REAC	REAC:R-HSA-74160	Gene expression (Transcription)	1380	1.6e-11
12	KEGG	KEGG:00310	Lysine degradation	59	8.5e-11
13	GO:CC	GO:0000118	histone deacetylase complex	77	2.0e-10
14	KEGG	KEGG:04330	Notch signaling pathway	55	3.1e-03
15	KEGG	KEGG:03250	Viral life cycle – HIV–1	60	3.5e-03

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