



id	source	term_id	term name	term_size	p_value
1	GO:BP	GO:0045935	positive regulation of nucleobase–containing compound metabolic process	1798	2.7e-10
2	GO:BP	GO:0006325	chromatin organization	569	7.7e-10
3	REAC	REAC:R-HSA-3247509	Chromatin modifying enzymes	244	6.5e-09
4	REAC	REAC:R-HSA-4839726	Chromatin organization	244	6.5e-09
5	GO:BP	GO:0051254	positive regulation of RNA metabolic process	1610	1.4e-08
6	GO:CC	GO:1902494	catalytic complex	1628	2.1e-08
7	GO:MF	GO:0003682	chromatin binding	518	2.2e-08
8	GO:CC	GO:1990234	transferase complex	798	3.0e-08
9	GO:MF	GO:0042393	histone binding	220	9.1e-08
10	REAC	REAC:R-HSA-74160	Gene expression (Transcription)	1380	1.5e-07
11	GO:MF	GO:0016279	protein-lysine N-methyltransferase activity	58	3.0e-07
12	GO:CC	GO:0016604	nuclear body	796	1.8e-06
13	KEGG	KEGG:00310	Lysine degradation	59	3.0e-06
14	KEGG	KEGG:03013	Nucleocytoplasmic transport	98	4.8e-04
15	KEGG	KEGG:03015	mRNA surveillance pathway	85	1.5e-03
	g:Profiler (biit.cs.ut.ee/gpro				

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