



id	source	term_id	term_name	term_size	p_value
1	GO:MF	GO:0003712	transcription coregulator activity	456	6.0e-15
2	GO:BP	GO:0016570	histone modification	434	1.7e-14
3	GO:BP	GO:0045935	positive regulation of nucleobase-containing compound metabolic process	1798	3.6e-14
4	GO:BP	GO:0051254	positive regulation of RNA metabolic process	1610	1.9e-13
5	REAC	REAC:R-HSA-3247509	Chromatin modifying enzymes	244	6.4e-12
6	REAC	REAC:R-HSA-4839726	Chromatin organization	244	6.4e-12
7	GO:MF	GO:0140110	transcription regulator activity	1632	2.1e-11
8	GO:MF	GO:0003682	chromatin binding	518	1.6e-10
9	GO:CC	GO:0035097	histone methyltransferase complex	67	1.1e-08
10	GO:CC	GO:0005694	chromosome	1638	2.7e-08
11	GO:CC	GO:0000785	chromatin	1112	3.1e-08
12	KEGG	KEGG:00310	Lysine degradation	59	5.4e-08
13	REAC	REAC:R-HSA-3214841	PKMTs methylate histone lysines	64	4.1e-07
14	KEGG	KEGG:04330	Notch signaling pathway	55	2.5e-03
15	KEGG	KEGG:04152	AMPK signaling pathway	109	1.2e-02