



id	source	term_id	term_name	term_size	p_value
1	GO:MF	GO:0019899	enzyme binding	1888	3.9e-42
2	GO:BP	GO:0033554	cellular response to stress	1790	1.1e-41
3	GO:BP	GO:0045935	positive regulation of nucleobase-containing compound metabolic process	1798	2.5e-39
4	REAC	REAC:R-HSA-74160	Gene expression (Transcription)	1380	1.6e-38
5	GO:CC	GO:1902494	catalytic complex	1628	7.9e-38
6	GO:BP	GO:0031328	positive regulation of cellular biosynthetic process	1760	8.6e-38
7	GO:MF	GO:0000166	nucleotide binding	1973	3.9e-34
8	GO:MF	GO:1901265	nucleoside phosphate binding	1974	4.2e-34
9	REAC	REAC:R-HSA-73857	RNA Polymerase II Transcription	1247	5.5e-33
0	GO:CC	GO:0030054	cell junction	1916	9.3e-32
1	GO:CC	GO:0043005	neuron projection	1254	2.9e-27
2	REAC	REAC:R-HSA-392499	Metabolism of proteins	1729	7.5e-26
3	KEGG	KEGG:04144	Endocytosis	238	4.5e-12
4	KEGG	KEGG:04142	Lysosome	122	4.6e-08
15	KEGG	KEGG:01100	Metabolic pathways	1334	3.2e-07