



id	source	term_id	term_name	term_size	p_value
1	GO:BP	GO:0032989	cellular component morphogenesis	713	1.1e-08
2	GO:BP	GO:0048812	neuron projection morphogenesis	588	5.2e-08
3	GO:BP	GO:0120039	plasma membrane bounded cell projection morphogenesis	604	8.4e-08
4	GO:MF	GO:0140110	transcription regulator activity	1632	7.0e-06
5	GO:CC	GO:0030054	cell junction	1916	7.5e-06
6	GO:CC	GO:0036477	somatodendritic compartment	794	1.2e-05
7	GO:MF	GO:0003700	DNA-binding transcription factor activity	1177	5.2e-05
8	GO:CC	GO:0045202	synapse	1219	1.0e-04
9	GO:MF	GO:0000978	RNA polymerase II cis-regulatory region sequence-specific DNA binding	1002	1.5e-04
10	REAC	REAC:R-HSA-73980	RNA Polymerase III Transcription Termination	23	3.4e-03
11	REAC	REAC:R-HSA-111957	Cam-PDE 1 activation	4	4.8e-03
12	REAC	REAC:R-HSA-74158	RNA Polymerase III Transcription	41	1.1e-02
13	KEGG	KEGG:04924	Renin secretion	58	1.3e-02
14	KEGG	KEGG:04540	Gap junction	82	3.3e-02

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