



source	term_id	term_name	term_size		p_value
GO:BP	GO:0045935	positive regulation of nucleobase-containing compound metabolic process	1798		8.1e-18
GO:BP	GO:0051254	positive regulation of RNA metabolic process	1610		1.8e-17
GO:BP	GO:1903508	positive regulation of nucleic acid-templated transcription	1474		1.8e-16
GO:MF	GO:0140110	transcription regulator activity	1632		4.5e-13
REAC	REAC:R-HSA-74160	Gene expression (Transcription)	1380		3.7e-12
REAC	REAC:R-HSA-73857	RNA Polymerase II Transcription	1247		1.4e-11
GO:MF	GO:0043565	sequence-specific DNA binding	1419		2.1e-11
REAC	REAC:R-HSA-212436	Generic Transcription Pathway	1130		4.4e-11
GO:MF	GO:0000978	RNA polymerase II cis-regulatory region sequence-specific DNA binding	1002		1.4e-10
KEGG	KEGG:05168	Herpes simplex virus 1 infection	460		9.7e-08
KEGG	KEGG:00310	Lysine degradation	59		1.0e-07
GO:CC	GO:0005694	chromosome	1638		2.7e-07
GO:CC	GO:1902494	catalytic complex	1628		5.1e-07
GO:CC	GO:0016604	nuclear body	796		7.0e-07
KEGG	KEGG:04012	ErbB signaling pathway	81		1.5e-03
	GO:BP GO:BP GO:BP GO:MF REAC GO:MF REAC GO:MF KEGG KEGG GO:CC GO:CC	GO:BP GO:0045935 GO:BP GO:0051254 GO:BP GO:1903508 GO:MF GO:0140110 REAC REAC:R-HSA-74160 REAC REAC:R-HSA-73857 GO:MF GO:0043565 REAC REAC:R-HSA-212436 GO:MF GO:0000978 KEGG KEGG:05168 KEGG KEGG:05168 KEGG KEGG:00310 GO:CC GO:0005694 GO:CC GO:1902494 GO:CC GO:0016604	GO:BP GO:0045935 positive regulation of nucleobase–containing compound metabolic process GO:BP GO:0051254 positive regulation of RNA metabolic process GO:BP GO:1903508 positive regulation of nucleic acid–templated transcription GO:MF GO:0140110 transcription regulator activity REAC REAC:R–HSA–74160 Gene expression (Transcription) REAC REAC:R–HSA–73857 RNA Polymerase II Transcription GO:MF GO:0043565 sequence–specific DNA binding REAC REAC:R–HSA–212436 Generic Transcription Pathway GO:MF GO:0000978 RNA polymerase II cis–regulatory region sequence–specific DNA binding KEGG KEGG:05168 Herpes simplex virus 1 infection KEGG KEGG:00310 Lysine degradation GO:CC GO:0005694 chromosome GO:CC GO:1902494 catalytic complex GO:CC GO:0016604 nuclear body	GO:BP GO:0045935 positive regulation of nucleobase–containing compound metabolic process 1798 GO:BP GO:0051254 positive regulation of RNA metabolic process 1610 GO:BP GO:1903508 positive regulation of nucleic acid–templated transcription 1474 GO:MF GO:0140110 transcription regulator activity 1632 REAC REAC:R–HSA–74160 Gene expression (Transcription) 1380 REAC REAC:R–HSA–73857 RNA Polymerase II Transcription 1247 GO:MF GO:0043565 sequence–specific DNA binding 1419 REAC REAC:R–HSA–212436 Generic Transcription Pathway 1130 GO:MF GO:0000978 RNA polymerase II cis–regulatory region sequence–specific DNA binding 1002 KEGG KEGG:00310 Lysine degradation 59 GO:CC GO:0005694 chromosome 1638 GO:CC GO:0016604 nuclear body 796	GO:BP GO:0045935 positive regulation of nucleobase–containing compound metabolic process 1798 GO:BP GO:0051254 positive regulation of RNA metabolic process 1610 GO:BP GO:1903508 positive regulation of nucleic acid–templated transcription 1474 GO:MF GO:0140110 transcription regulator activity 1632 REAC REAC:R–HSA–74160 Gene expression (Transcription) 1380 REAC REAC:R–HSA–73857 RNA Polymerase II Transcription 1247 GO:MF GO:0043565 sequence–specific DNA binding 1419 REAC REAC:R–HSA–212436 Generic Transcription Pathway 1130 GO:MF GO:0000978 RNA polymerase II cis–regulatory region sequence–specific DNA binding 1002 KEGG KEGG:05168 Herpes simplex virus 1 infection 460 KEGG KEGG:00310 Lysine degradation 59 GO:CC GO:0005694 chromosome 1638 GO:CC GO:1902494 catalytic complex 1628 GO:CC GO:0016604 nuclear body 796

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