id	source	term_id	term_name	term_size	intersection_size	p_value
1		GO:1903508	positive regulation of nucleic acid–templated transcription	76	2	2.8e-01
3		GO:0010817 GO:0010941	regulation of hormone levels regulation of cell death	8	1	2.8e-01 2.8e-01
4		GO:0010941 GO:0051225	spindle assembly	8	1	2.8e-01 2.8e-01
5	GO:BP	GO:1902680	positive regulation of RNA biosynthetic process	76	2	2.8e-01
6	GO:BP	GO:0051173 GO:0051028	positive regulation of nitrogen compound metabolic process	101	2	2.8e-01
7 8	GO:BP GO:BP	GO:0051028 GO:0050658	mRNA transport RNA transport	11	1	2.8e-01 2.8e-01
9	GO:BP	GO:0090306	meiotic spindle assembly	1	1	2.8e-01
10		GO:0019359	nicotinamide nucleotide biosynthetic process	7	1	2.8e-01
11 12	GO:BP GO:BP	GO:0140694 GO:0072525	non-membrane-bounded organelle assembly pyridine-containing compound biosynthetic process	17	1	2.8e-01 2.8e-01
13		GO:0072323 GO:0045893	positive regulation of DNA-templated transcription	76	2	2.8e-01
14	GO:BP	GO:0019363	pyridine nucleotide biosynthetic process	9	1	2.8e-01
15	GO:BP	GO:0019674	NAD metabolic process	7	1	2.8e-01
16 17	GO:BP GO:BP	GO:0010604 GO:0046496	positive regulation of macromolecule metabolic process nicotinamide nucleotide metabolic process	104	1	2.8e-01 2.8e-01
18	GO:BP	GO:0031325	positive regulation of cellular metabolic process	92	2	2.8e-01
19		GO:0031328	positive regulation of cellular biosynthetic process	79	2	2.8e-01
20 21	GO:BP GO:BP	GO:0045935 GO:0048759	positive regulation of nucleobase–containing compound metabolic process xylem vessel member cell differentiation	3	1	2.8e-01 2.8e-01
22		GO:0034728	nucleosome organization	12	1	2.8e-01
23	GO:BP	GO:0042181	ketone biosynthetic process	13	1	2.8e-01
24		GO:0044283	small molecule biosynthetic process	240	3	2.8e-01
25 26	GO:BP GO:BP	GO:0045132 GO:0050657	nucleic acid transport	13 16	1	2.8e-01 2.8e-01
27		GO:0010557	positive regulation of macromolecule biosynthetic process	78	2	2.8e-01
28		GO:0051236	establishment of RNA localization	16	1	2.8e-01
29 30		GO:0051254 GO:0006744	positive regulation of RNA metabolic process ubiquinone biosynthetic process	81	1	2.8e-01 2.8e-01
31	GO:BP	GO:0006744 GO:0060918	auxin transport	16	1	2.8e-01
32	GO:BP	GO:0006743	ubiquinone metabolic process	8	1	2.8e-01
33		GO:0008152	· · · · · · · · · · · · · · · · · · ·	5473	26	2.8e-01
34 35		GO:0006547 GO:0006526	histidine metabolic process arginine biosynthetic process	8	1	2.8e-01 2.8e-01
36	GO:BP	GO:0006525	arginine metabolic process	10	1	2.8e-01
37		GO:1905177	tracheary element differentiation	3	1	2.8e-01
38 39	GO:BP GO:BP	GO:0006403 GO:0006334	RNA localization nucleosome assembly	16 12	1	2.8e-01 2.8e-01
40	GO:BP	GO:0000212	meiotic spindle organization	3	1	2.8e-01
41	GO:BP	GO:0000184	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	9	1	2.8e-01
42 43	GO:BP GO:BP	GO:0007051 GO:0000105	spindle organization histidine biosynthetic process	15 7	1	2.8e-01 2.8e-01
44		GO:0008652	amino acid biosynthetic process	102	2	2.8e-01
45	GO:BP	GO:0009057	macromolecule catabolic process	212	3	2.8e-01
46 47		GO:0009435	NAD biosynthetic process	3	1	2.8e-01
47 48		GO:0009850 GO:0009891	auxin metabolic process positive regulation of biosynthetic process	5 81	2	2.8e-01 2.8e-01
49		GO:0009914	hormone transport	16	1	2.8e-01
50		GO:1901661	quinone metabolic process	12	1	2.8e-01
51 52	GO:BP GO:BP	GO:0009926 GO:1901663	auxin polar transport quinone biosynthetic process	10	1	2.8e-01 2.8e-01
53		GO:1901663 GO:0010089	xylem development	4	1	2.8e-01 2.8e-01
54		GO:0060548	negative regulation of cell death	3	1	2.8e-01
55 56	GO:BP	GO:0065008	regulation of biological quality	71	2	2.8e-01
56 57	GO:BP GO:BP	GO:0009084 GO:0009893	glutamine family amino acid biosynthetic process positive regulation of metabolic process	18	2	2.9e-01 2.9e-01
58		GO:0048366	leaf development	18	1	2.9e-01
59		GO:0048522	positive regulation of cellular process	112	2	2.9e-01
60 61		GO:0019362 GO:1901575	pyridine nucleotide metabolic process organic substance catabolic process	19 418	4	2.9e-01 3.0e-01
62		GO:1901575 GO:0051603	proteolysis involved in protein catabolic process	120	2	3.1e-01
63	GO:BP	GO:0000956	nuclear-transcribed mRNA catabolic process	22	1	3.1e-01
64 65	GO:BP	GO:0030163	protein catabolic process	134	2	3.1e-01
65 66		GO:0065004 GO:0140013	protein–DNA complex assembly meiotic nuclear division	25 23	1	3.1e-01 3.1e-01
67	GO:BP	GO:0072524	pyridine-containing compound metabolic process	24	1	3.1e-01
68		GO:0042180	cellular ketone metabolic process	26	1	3.1e-01
69 70		GO:0009056 GO:0070925	catabolic process organelle assembly	442 25	1	3.1e-01 3.1e-01
70		GO:0070925 GO:0001522	pseudouridine synthesis	25	1	3.1e-01 3.1e-01
72		GO:0010087	phloem or xylem histogenesis	25	1	3.1e-01
73 74		GO:0009408 GO:0071824	response to heat	25 25	1	3.1e-01
74 75		GO:0071824 GO:0008219	protein–DNA complex subunit organization cell death	25 26	1	3.1e-01 3.1e-01
76		GO:0071704	organic substance metabolic process	5200	24	3.1e-01
77 70		GO:0046148	pigment biosynthetic process	27	1	3.1e-01
78 79	GO:BP GO:BP	GO:0042445 GO:0031347	regulation of defense response	28	1	3.1e-01 3.1e-01
80	GO:BP	GO:0031347 GO:1903046	meiotic cell cycle process	28	1	3.1e-01
81		GO:0098813	nuclear chromosome segregation	28	1	3.1e-01
82 83		GO:0009064 GO:0051321	glutamine family amino acid metabolic process meiotic cell cycle	30	1	3.3e-01 3.3e-01
84		GO:0051321 GO:0006402	mRNA catabolic process	32	1	3.3e-01 3.3e-01
85		GO:0016579	protein deubiquitination	32	1	3.3e-01
86		GO:0048518	positive regulation of biological process	152	2	3.3e-01
87 88	GO:BP GO:BP	GO:0048827 GO:1901564	phyllome development organonitrogen compound metabolic process	33 2473	13	3.4e-01 3.4e-01
89		GO:0070646	protein modification by small protein removal	34	1	3.4e-01
90	GO:BP	GO:0006401	RNA catabolic process	35	1	3.4e-01
91		GO:0022414	reproductive process	160	2	3.4e-01
92 93		GO:0000003 GO:0042440	reproduction pigment metabolic process	166 37	1	3.5e-01 3.5e-01
93 94		GO:0007059	chromosome segregation	39	1	3.6e-01
95		GO:0000280	nuclear division	39	1	3.6e-01
96 97		GO:0044238	• • •	4847	22	3.6e-01
97 98		GO:0015931 GO:0048316	nucleobase–containing compound transport seed development	42	1	3.8e-01 3.8e-01
99		GO:0010154	fruit development	45	1	3.8e-01
	GO:BP	GO:0006338	chromatin remodeling	46	1	3.8e-01
00				g:Pr	ofiler (biit.cs.ut.ee/gpr	oniel)
00					(31	