

id	source	term_id	term_name	term_size	intersection_size	p_value
1	GO:MF	GO:0008017	microtubule binding	95	69	1.2e−23
2	GO:MF	GO:0015631	tubulin binding	116	73	1.9e−19
3	GO:MF	GO:0008092	cytoskeletal protein binding	205	104	6.0e−19
4	GO:MF	GO:0003777	microtubule motor activity	56	43	2.8e−16
5	GO:MF	GO:0003774	cytoskeletal motor activity	72	46	1.5e−12
6	GO:BP	GO:0007017	microtubule-based process	136	80	1.7e−12
7	GO:BP	GO:0007018	microtubule-based movement	57	43	1.1e−11
8	GO:BP	GO:0007049	cell cycle	273	123	2.2e−09
9	GO:CC	GO:0099081	supramolecular polymer	94	54	1.0e−05
10	GO:CC	GO:0015630	microtubule cytoskeleton	106	60	1.0e−05
11	GO:CC	GO:0005874	microtubule	92	54	1.0e−05
12	GO:CC	GO:0099512	supramolecular fiber	94	54	1.0e−05
13	GO:CC	GO:0099513	polymeric cytoskeletal fiber	93	54	1.0e−05
14	GO:CC	GO:0005856	cytoskeleton	158	80	1.9e−05
15	GO:BP	GO:0000280	nuclear division	70	39	3.6e−05
16	GO:BP	GO:0007010	cytoskeleton organization	146	67	3.6e−05
17	GO:BP	GO:0022402	cell cycle process	180	79	3.6e−05
18	GO:BP	GO:0051301	cell division	143	57	8.7e−05
19	GO:CC	GO:0099080	supramolecular complex	119	61	2.3e−04
20	GO:BP	GO:0051321	meiotic cell cycle	60	33	3.3e−04
21	GO:BP	GO:0140013	meiotic nuclear division	45	27	3.3e−04
22	GO:BP	GO:1903046	meiotic cell cycle process	53	30	3.9e−04
23	GO:BP	GO:0000226	microtubule cytoskeleton organization	56	31	4.3e−04
24	GO:BP	GO:0032392	DNA geometric change	33	11	5.6e−04
25	GO:BP	GO:0032508	DNA duplex unwinding	33	11	5.6e−04
26	GO:BP	GO:0006270	DNA replication initiation	18	8	9.7e−04
27	GO:MF	GO:0043531	ADP binding	712	45	1.0e−03
28	GO:BP	GO:0000278	mitotic cell cycle	59	31	1.1e−03
29	GO:MF	GO:0003678	DNA helicase activity	29	9	1.4e−03
30	GO:BP	GO:1903047	mitotic cell cycle process	47	26	1.7e−03
31	GO:BP	GO:1902850	microtubule cytoskeleton organization involved in mitosis	8	8	1.9e−03
32	GO:BP	GO:0090224	regulation of spindle organization	8	8	1.9e−03
33	GO:BP	GO:0060236	regulation of mitotic spindle organization	8	8	1.9e−03
34	GO:BP	GO:0007052	mitotic spindle organization	8	8	1.9e−03
35	GO:BP	GO:0048285	organelle fission	91	42	2.0e−03
36	GO:MF	GO:0030527	structural constituent of chromatin	40	16	2.1e−03
37	GO:BP	GO:0000911	cytokinesis by cell plate formation	22	10	2.3e−03
38	GO:BP	GO:0000910	cytokinesis	27	11	2.9e−03
39	GO:BP	GO:0019953	sexual reproduction	81	38	2.9e−03
40	GO:BP	GO:0007051	spindle organization	20	14	3.1e−03
41	GO:BP	GO:0061640	cytoskeleton-dependent cytokinesis	7	5	3.9e−03
42	GO:BP	GO:0140527	reciprocal homologous recombination	23	15	3.9e−03
43	GO:BP	GO:0007140	male meiotic nuclear division	15	9	3.9e−03
44	GO:BP	GO:0007131	reciprocal meiotic recombination	23	15	3.9e−03
45	GO:BP	GO:0061982	meiosis I cell cycle process	32	19	4.1e−03
46	GO:BP	GO:0009834	plant-type secondary cell wall biogenesis	16	12	4.1e−03
47	GO:BP	GO:0048232	male gamete generation	19	12	6.0e−03
48	GO:BP	GO:0007127	meiosis I	28	17	6.0e−03
49	GO:BP	GO:0007059	chromosome segregation	73	34	6.0e−03
50	GO:BP	GO:0006261	DNA-templated DNA replication	46	11	6.7e−03
51	GO:BP	GO:0045492	xylan biosynthetic process	18	12	7.5e−03
52	GO:MF	GO:0043138	3'–5' DNA helicase activity	6	4	7.8e−03
53	GO:BP	GO:0070507	regulation of microtubule cytoskeleton organization	11	9	8.0e−03
54	GO:BP	GO:0022412	cellular process involved in reproduction in multicellular organism	25	14	8.0e−03
55	GO:BP	GO:0007276	gamete generation	25	14	8.0e−03
56	GO:CC	GO:0042555	MCM complex	9	5	9.6e−03
57	GO:CC	GO:0000347	THO complex	9	5	9.6e−03
58	GO:BP	GO:0071103	DNA conformation change	52	12	1.1e−02
59	GO:BP	GO:0045491	xylan metabolic process	34	18	1.1e−02
60	GO:BP	GO:0035825	homologous recombination	30	17	1.1e−02
61	GO:BP	GO:0007143	female meiotic nuclear division	6	5	1.1e−02
62	GO:BP	GO:0051513	regulation of monopolar cell growth	3	1	1.1e−02
63	GO:BP	GO:0032147	activation of protein kinase activity	6	6	1.3e−02
64	GO:BP	GO:0032886	regulation of microtubule-based process	16	11	1.6e−02
65	GO:BP	GO:0051493	regulation of cytoskeleton organization	28	16	1.6e−02
66	GO:BP	GO:0045132	meiotic chromosome segregation	23	14	1.7e−02
67	GO:MF	GO:0048040	UDP-glucuronate decarboxylase activity	6	5	1.8e−02
68	GO:BP	GO:0042814	monopolar cell growth	6	1	1.9e−02
69	GO:BP	GO:0033319	UDP-D-xylose metabolic process	6	5	2.2e−02
70	GO:BP	GO:0033320	UDP-D-xylose biosynthetic process	6	5	2.2e−02
71	GO:MF	GO:0045548	phenylalanine ammonia-lyase activity	4	4	2.3e−02
72	GO:BP	GO:0001932	regulation of protein phosphorylation	19	12	2.3e−02
73	GO:BP	GO:0009803	cinnamic acid metabolic process	4	4	2.3e−02
74	GO:BP	GO:0009800	cinnamic acid biosynthetic process	4	4	2.3e−02
75	GO:BP	GO:0045859	regulation of protein kinase activity	19	12	2.3e−02
76	GO:BP	GO:0071554	cell wall organization or biogenesis	307	62	2.4e−02
77	GO:MF	GO:0042973	glucan endo-1,3-beta-D-glucosidase activity	33	16	2.5e−02
78	GO:BP	GO:0007292	female gamete generation	7	5	2.6e−02
79	GO:BP	GO:0051510	regulation of unidimensional cell growth	10	1	2.7e−02
80	GO:BP	GO:0070192	chromosome organization involved in meiotic cell cycle	17	11	2.9e−02
81	GO:BP	GO:0098813	nuclear chromosome segregation	54	25	3.1e−02
82	GO:MF	GO:0097599	xylanase activity	18	5	3.3e−02
83	GO:BP	GO:0030261	chromosome condensation	7	6	3.7e−02
84	GO:BP	GO:0001558	regulation of cell growth	15	1	3.7e−02
85	GO:BP	GO:0005976	polysaccharide metabolic process	297	45	3.7e−02
86	GO:BP	GO:0000281	mitotic cytokinesis	5	3	3.7e−02
87	GO:MF	GO:0140575	transmembrane monodehydroascorbate reductase activity	3	3	4.3e−02
88	GO:MF	GO:0008422	beta-glucosidase activity	35	16	4.5e−02
89	GO:MF	GO:0015020	glucuronosyltransferase activity	20	11	4.5e−02
90	GO:BP	GO:0001934	positive regulation of protein phosphorylation	7	6	4.8e−02
91	GO:BP	GO:0045860	positive regulation of protein kinase activity	7	6	4.8e−02