

GO ID	Term	Annotated	Signif cant	Expected	weight01_pval
1	GO:0019344	cysteine biosynthetic process	114	16	1.98
2	GO:0010027	thylakoid membrane organization	174	17	3.03
3	GO:0015979	photosynthesis	396	51	6.89
4	GO:0009768	photosynthesis, light harvesting in phot...	15	6	0.26
5	GO:0010207	photosystem II assembly	111	12	1.93
6	GO:0018298	protein-chromophore linkage	48	8	0.84
7	GO:0019684	photosynthesis, light reaction	241	33	4.20
8	GO:0070838	divalent metal ion transport	152	16	2.65
9	GO:0045454	cell redox homeostasis	122	11	2.12
10	GO:0019288	isopentenyl diphosphate biosynthetic pro...	178	13	3.10
11	GO:0016117	carotenoid biosynthetic process	90	10	1.57
12	GO:0006012	galactose metabolic process	70	8	1.22
13	GO:0006364	rRNA processing	292	17	5.08
14	GO:0015995	chlorophyll biosynthetic process	94	9	1.64
15	GO:0006098	penicose-phosphate shunt	196	13	3.41
16	GO:0035304	regulation of protein dephosphorylation	82	8	1.43
17	GO:0006457	protein folding	275	15	4.79
18	GO:0030003	cellular cation homeostasis	139	10	2.42
19	GO:0032880	regulation of protein localization	18	4	0.31
20	GO:0071435	potassium ion export	2	0.03	0.00023
21	GO:0004590	pectin catabolic process	35	5	0.61
22	GO:0009269	response to desiccation	9	3	0.16
23	GO:0000103	sulfate assimilation	40	6	0.70
24	GO:0010411	xylophenan metabolic process	21	4	0.37
25	GO:0009773	photosynthetic electron transport in pho...	23	4	0.40
26	GO:0009416	response to light stimulus	474	26	8.25
27	GO:0006833	water transport	62	6	1.08
28	GO:0007030	Golgi organization	86	7	1.50
29	GO:0070588	calcium ion transmembrane transport	25	4	0.44
30	GO:0019685	photosynthesis, dark reaction	13	4	0.23
31	GO:0008361	regulation of cell size	26	4	0.45
32	GO:0048481	plant ovule development	67	6	1.17
33	GO:0009765	photosynthesis, light harvesting	34	10	0.59
34	GO:0006857	oligopeptide transport	30	4	0.52
35	GO:0005985	sucrose metabolic process	324	14	5.64
36	GO:0010363	regulation of plant-type hypersensitive ...	76	7	1.32
37	GO:0010103	stromal complex morphogenesis	77	6	1.34
38	GO:0019761	glucosinolate biosynthetic process	77	6	1.34
39	GO:0006662	glycerol ether metabolic process	33	4	0.57
40	GO:0045893	positive regulation of transcription, DN...	266	12	4.65
41	GO:0051603	proteolysis involved in cellular protein...	353	12	6.15
42	GO:0034599	cellular response to oxidative stress	55	5	0.96
43	GO:0009963	positive regulation of T avonoid biosynt...	17	3	0.30
44	GO:0009657	plastid organization	361	27	6.29
45	GO:0006687	glycosylating lipid metabolic process	60	5	1.04
46	GO:0003982	starch metabolic process	440	17	7.66
47	GO:0016132	brassinosteroid biosynthetic process	38	4	0.66
48	GO:0000054	ribosomal subunit export from nucleus	6	2	0.10
49	GO:0006612	protein targeting to membrane	97	7	1.69
50	GO:0009902	chlorophyll relocation	92	6	1.60
51	GO:0016126	sterol biosynthetic process	65	5	1.13
52	GO:0030154	cell differentiation	368	17	6.41
53	GO:0010105	negative regulation of ethylene-activate...	7	2	0.12
54	GO:0006782	protochlorophyll IX biosynthetic proce...	7	2	0.12
55	GO:0015996	chlorophyll catabolic process	42	4	0.73
56	GO:0009873	ethylene-activated signaling pathway	39	5	0.68
57	GO:0006027	glyoxysomal/yeast catabolic process	43	4	0.75
58	GO:0009637	response to blue light	69	5	1.20
59	GO:0061615	glycolytic process through fructose-6-ph...	8	2	0.14
60	GO:0098869	cellular oxidant detoxif cation	133	7	2.32
61	GO:0006356	unsaturated fatty acid biosynthetic proc...	48	4	0.84
62	GO:0010091	trichome branching	9	2	0.16
63	GO:0009965	leaf morphogenesis	105	6	1.83
64	GO:0006094	glucosinogenesis	245	10	4.27
65	GO:0009658	chloroplast organization	211	13	3.67
66	GO:0051114	oxidation-reduction process	2564	65	44.64
67	GO:0016226	iron-sulfur cluster assembly	108	6	1.88
68	GO:0019253	reductive penicose-phosphate cycle	10	2	0.17
69	GO:0005992	trehalose biosynthetic process	28	3	0.49
70	GO:0006412	translation	897	25	15.62
71	GO:0006081	cellular aldehyde metabolic process	418	23	7.28
72	GO:0046487	glyoxylate metabolic process	73	6	1.27
73	GO:0006749	glutathione metabolic process	82	5	1.43
74	GO:0006529	asparagine biosynthetic process	13	3	0.23
75	GO:0009690	cytokinin metabolic process	26	3	0.45
76	GO:0000463	maturation of LSU-rRNA from tritesticro...	11	2	0.19
77	GO:0016925	protein sumoylation	11	2	0.19
78	GO:0048588	developmental cell growth	109	5	1.90
79	GO:0006027	positive regulation of respiratory burst	1	1	0.02
80	GO:0090143	nucleoid organization	1	1	0.02
81	GO:0080136	priming of cellular response to stress	1	1	0.02
82	GO:0000169	activation of MAPK activity involved in ...	1	1	0.02
83	GO:0007263	nitric oxide mediated signal transductio...	1	1	0.02
84	GO:2000037	regulation of stomatal complex patternm...	1	1	0.02
85	GO:0051245	negative regulation of cellular defense ...	1	1	0.02
86	GO:0034214	protein hexamerization	1	1	0.02
87	GO:0009780	photosynthetic NADP+ reduction	1	1	0.02
88	GO:0042493	response to drug	79	2	1.38
89	GO:0006273	lagging strand elongation	12	2	0.21
90	GO:0042254	ribosome biogenesis	745	33	12.97
91	GO:0071555	cell wall organization	372	14	6.48
92	GO:0009651	response to salt stress	192	8	3.34
93	GO:0015994	chlorophyll metabolic process	196	16	3.41
94	GO:0009926	auxin polar transport	61	4	1.06
95	GO:0001731	formation of translation preinitiation c...	14	2	0.24
96	GO:0051103	DNA ligation involved in DNA repair	14	2	0.24
97	GO:0010206	photosystem II repair	15	2	0.26
98	GO:0006002	fructose 6-phosphate metabolic process	145	7	2.52
99	GO:0010015	root morphogenesis	145	7	2.52
100	GO:0042793	transcription from plastid promoter	68	4	1.18

