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GO.ID	Term	Annotated	Significant	Expected	weight01	pval branch
1	GO:0019344 cysteine biosynthetic process	114	16	1.98	1.5e-10	BP
2	GO:0010027 thylakoid membrane organization	174	17	3.03	1.2e-08	BP
3	GO:0015979 photosynthesis	396	51	6.89	5.6e-08	BP
4	GO:0009768 photosynthesis, light harvesting in phot...	15	6	0.26	1.2e-07	BP
5	GO:0010207 photosystem II assembly	111	12	1.93	5.6e-07	BP
6	GO:0018298 protein-chromophore linkage	48	8	0.84	1.6e-06	BP
7	GO:0019684 photosynthesis, light reaction	241	33	4.20	2.4e-06	BP
8	GO:0070838 divalent metal ion transport	152	16	2.65	5.6e-06	BP
9	GO:0045454 cell redox homeostasis	122	11	2.12	9.8e-06	BP
10	GO:0019288 isopentenyl diphosphate biosynthetic pro...	178	13	3.10	1.6e-05	BP
11	GO:0016117 carotenoid biosynthetic process	90	10	1.57	1.7e-05	BP
12	GO:0006012 galactose metabolic process	70	8	1.22	2.9e-05	BP
13	GO:0006364 rRNA processing	292	17	5.08	3.9e-05	BP
14	GO:0015995 chlorophyll biosynthetic process	94	9	1.64	3.9e-05	BP
15	GO:0006098 pentose-phosphate shunt	196	13	3.41	4.3e-05	BP
16	GO:0035304 regulation of protein dephosphorylation	82	8	1.43	9.2e-05	BP
17	GO:0006457 protein folding	275	15	4.79	9.6e-05	BP
18	GO:0030003 cellular cation homeostasis	139	10	2.42	0.00017	BP
19	GO:0032880 regulation of protein localization	18	4	0.31	0.00023	BP
20	GO:0071435 potassium ion export	2	2	0.03	0.00030	BP
21	GO:0045490 pectin catabolic process	35	5	0.61	0.00033	BP
22	GO:0009269 response to desiccation	9	3	0.16	0.00041	BP
23	GO:0000103 sulfate assimilation	40	6	0.70	0.00043	BP
24	GO:0010411 xyloglucan metabolic process	21	4	0.37	0.00043	BP
25	GO:0009773 photosynthetic electron transport in pho...	23	4	0.40	0.00062	BP
26	GO:0009416 response to light stimulus	474	26	8.25	0.00068	BP
27	GO:0006833 water transport	62	6	1.08	0.00073	BP
28	GO:0007030 Golgi organization	86	7	1.50	0.00076	BP
29	GO:0070588 calcium ion transmembrane transport	25	4	0.44	0.00086	BP
30	GO:0019685 photosynthesis, dark reaction	13	4	0.23	0.00089	BP
31	GO:0008361 regulation of cell size	26	4	0.45	0.00100	BP
32	GO:0048481 plant ovule development	67	6	1.17	0.00110	BP
33	GO:0009765 photosynthesis, light harvesting	34	10	0.59	0.00171	BP
34	GO:0006857 oligopeptide transport	30	4	0.52	0.00174	BP
35	GO:0005985 sucrose metabolic process	324	14	5.64	0.00177	BP
36	GO:0010363 regulation of plant-type hypersensitive ...	76	7	1.32	0.00182	BP
37	GO:0010103 stomatal complex morphogenesis	77	6	1.34	0.00225	BP
38	GO:0019761 glucosinolate biosynthetic process	77	6	1.34	0.00225	BP
39	GO:0006662 glycerol ether metabolic process	33	4	0.57	0.00249	BP
40	GO:0045893 positive regulation of transcription, DN...	266	12	4.63	0.00259	BP
41	GO:0051603 proteolysis involved in cellular protein...	353	12	6.15	0.00262	BP
42	GO:0034599 cellular response to oxidative stress	55	5	0.96	0.00266	BP
43	GO:0009963 positive regulation of flavonoid biosynt...	17	3	0.30	0.00297	BP
44	GO:0009657 plastid organization	361	27	6.29	0.00355	BP
45	GO:0006687 glycosphingolipid metabolic process	60	5	1.04	0.00389	BP
46	GO:0005982 starch metabolic process	440	17	7.66	0.00393	BP
47	GO:0016132 brassinosteroid biosynthetic process	38	4	0.66	0.00419	BP
48	GO:0000054 ribosomal subunit export from nucleus	6	2	0.10	0.00433	BP
49	GO:0006612 protein targeting to membrane	97	7	1.69	0.00486	BP
50	GO:0009902 chloroplast relocation	92	6	1.60	0.00546	BP
51	GO:0016126 sterol biosynthetic process	65	5	1.13	0.00549	BP
52	GO:0030154 cell differentiation	368	17	6.41	0.00593	BP
53	GO:0010105 negative regulation of ethylene-activate...	7	2	0.12	0.00599	BP
54	GO:0006782 protoporphyrinogen IX biosynthetic proce...	7	2	0.12	0.00599	BP
55	GO:0015996 chlorophyll catabolic process	42	4	0.73	0.00602	BP
56	GO:0009873 ethylene-activated signaling pathway	39	5	0.68	0.00625	BP
57	GO:0006027 glycosaminoglycan catabolic process	43	4	0.75	0.00655	BP
58	GO:0009637 response to blue light	69	5	1.20	0.00706	BP
59	GO:0061615 glycolytic process through fructose-6-ph...	8	2	0.14	0.00790	BP
60	GO:0098869 cellular oxidant detoxification	133	7	2.32	0.00883	BP
61	GO:0006636 unsaturated fatty acid biosynthetic proc...	48	4	0.84	0.00965	BP
62	GO:0010091 trichome branching	9	2	0.16	0.01004	BP
63	GO:0009965 leaf morphogenesis	105	6	1.83	0.01021	BP
64	GO:0006094 gluconeogenesis	245	10	4.27	0.01114	BP
65	GO:0009658 chloroplast organization	211	13	3.67	0.01150	BP
66	GO:0055114 oxidation-reduction process	2564	65	44.64	0.01160	BP
67	GO:0016226 iron-sulfur cluster assembly	108	6	1.88	0.01163	BP
68	GO:0019253 reductive pentose-phosphate cycle	10	2	0.17	0.01241	BP
69	GO:0005992 trehalose biosynthetic process	28	3	0.49	0.01244	BP
70	GO:0006412 translation	897	25	15.62	0.01403	BP
71	GO:0006081 cellular aldehyde metabolic process	418	23	7.28	0.01411	BP
72	GO:0046487 glyoxylate metabolic process	73	6	1.27	0.01428	BP
73	GO:0006749 glutathione metabolic process	82	5	1.43	0.01428	BP
74	GO:0006529 asparagine biosynthetic process	13	3	0.23	0.01493	BP
75	GO:0009690 cytokinin metabolic process	26	3	0.45	0.01495	BP