

	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
76	GO:0000463	maturation of LSU-rRNA from tricistronic...	11	2	0.19	0.01499	BP
77	GO:0016925	protein sumoylation	11	2	0.19	0.01499	BP
78	GO:0048588	developmental cell growth	109	5	1.90	0.01733	BP
79	GO:0060267	positive regulation of respiratory burst	1	1	0.02	0.01741	BP
80	GO:0090143	nucleoid organization	1	1	0.02	0.01741	BP
81	GO:0080136	priming of cellular response to stress	1	1	0.02	0.01741	BP
82	GO:0000169	activation of MAPK activity involved in ...	1	1	0.02	0.01741	BP
83	GO:0007263	nitric oxide mediated signal transductio...	1	1	0.02	0.01741	BP
84	GO:2000037	regulation of stomatal complex patternin...	1	1	0.02	0.01741	BP
85	GO:0051245	negative regulation of cellular defense ...	1	1	0.02	0.01741	BP
86	GO:0034214	protein hexamerization	1	1	0.02	0.01741	BP
87	GO:0009780	photosynthetic NADP+ reduction	1	1	0.02	0.01741	BP
88	GO:0042493	response to drug	79	2	1.38	0.01743	BP
89	GO:0006273	lagging strand elongation	12	2	0.21	0.01779	BP
90	GO:0042254	ribosome biogenesis	745	33	12.97	0.01869	BP
91	GO:0071555	cell wall organization	372	14	6.48	0.01954	BP
92	GO:0009651	response to salt stress	192	8	3.34	0.01968	BP
93	GO:0015994	chlorophyll metabolic process	196	16	3.41	0.02022	BP
94	GO:0009926	auxin polar transport	61	4	1.06	0.02171	BP
95	GO:0001731	formation of translation preinitiation c...	14	2	0.24	0.02397	BP
96	GO:0051103	DNA ligation involved in DNA repair	14	2	0.24	0.02397	BP
97	GO:0010206	photosystem II repair	15	2	0.26	0.02734	BP
98	GO:0006002	fructose 6-phosphate metabolic process	15	2	0.26	0.02734	BP
99	GO:0010015	root morphogenesis	145	7	2.52	0.02980	BP
100	GO:0042793	transcription from plastid promoter	68	4	1.18	0.03085	BP
101	GO:0016168	chlorophyll binding	40	10	0.66	7.7e-10	MF
102	GO:0031409	pigment binding	14	5	0.23	2.2e-06	MF
103	GO:0030570	pectate lyase activity	9	4	0.15	8.8e-06	MF
104	GO:0005515	protein binding	3192	88	52.91	2.3e-05	MF
105	GO:0016762	xyloglucan:xyloglucosyl transferase acti...	16	4	0.27	0.00012	MF
106	GO:0015035	protein disulfide oxidoreductase activit...	77	7	1.28	0.00029	MF
107	GO:0042803	protein homodimerization activity	62	6	1.03	0.00056	MF
108	GO:0004565	beta-galactosidase activity	24	4	0.40	0.00061	MF
109	GO:0003825	alpha, alpha-trehalose-phosphate synthase...	11	3	0.18	0.00068	MF
110	GO:0051740	ethylene binding	3	2	0.05	0.00081	MF
111	GO:0016630	protochlorophyllide reductase activity	3	2	0.05	0.00081	MF
112	GO:0004066	asparagine synthase (glutamine-hydrolyzi...	13	3	0.22	0.00114	MF
113	GO:0016874	ligase activity	726	23	12.03	0.00135	MF
114	GO:0016671	oxidoreductase activity, acting on a sul...	54	6	0.90	0.00152	MF
115	GO:0003950	NAD+ ADP-ribosyltransferase activity	32	4	0.53	0.00186	MF
116	GO:0003735	structural constituent of ribosome	432	16	7.16	0.00252	MF
117	GO:0008177	succinate dehydrogenase (ubiquinone) act...	5	2	0.08	0.00265	MF
118	GO:0005509	calcium ion binding	320	13	5.30	0.00285	MF
119	GO:0051082	unfolded protein binding	91	6	1.51	0.00409	MF
120	GO:0004364	glutathione transferase activity	40	4	0.66	0.00425	MF
121	GO:0004805	trehalose-phosphatase activity	21	3	0.35	0.00482	MF
122	GO:0004497	monooxygenase activity	216	10	3.58	0.00632	MF
123	GO:0046556	alpha-L-arabinofuranosidase activity	8	2	0.13	0.00719	MF
124	GO:0010277	chlorophyllide a oxygenase [overall] act...	8	2	0.13	0.00719	MF
125	GO:0003872	6-phosphofructokinase activity	10	2	0.17	0.01130	MF
126	GO:0016705	oxidoreductase activity, acting on paire...	287	10	4.76	0.01267	MF
127	GO:0030246	carbohydrate binding	192	8	3.18	0.01514	MF
128	GO:0001055	RNA polymerase II activity	12	2	0.20	0.01621	MF
129	GO:0032441	pheophorbide a oxygenase activity	1	1	0.02	0.01658	MF
130	GO:0033947	mannosylglycoprotein endo-beta-mannosida...	1	1	0.02	0.01658	MF
131	GO:0080124	pheophytinase activity	1	1	0.02	0.01658	MF
132	GO:0052624	2-phytyl-1,4-naphthoquinone methyltransf...	1	1	0.02	0.01658	MF
133	GO:0048529	magnesium-protoporphyrin IX monomethyl e...	1	1	0.02	0.01658	MF
134	GO:0004558	alpha-1,4-glucosidase activity	1	1	0.02	0.01658	MF
135	GO:0005222	intracellular cAMP activated cation chan...	1	1	0.02	0.01658	MF

136	GO:0043864	indoleacetamide hydrolase activity	1	1	0.02	0.01658	MF
137	GO:0050178	phenylpyruvate tautomerase activity	1	1	0.02	0.01658	MF
138	GO:0038199	ethylene receptor activity	1	1	0.02	0.01658	MF
139	GO:0045435	lycopene epsilon cyclase activity	1	1	0.02	0.01658	MF
140	GO:0004038	allantoinase activity	1	1	0.02	0.01658	MF
141	GO:0052893	N1-acetylspermine:oxygen oxidoreductase ...	1	1	0.02	0.01658	MF
142	GO:0052896	spermidine oxidase (propane-1,3-diamine-...	1	1	0.02	0.01658	MF
143	GO:0052897	N8-acetylspermidine:oxygen oxidoreductas...	1	1	0.02	0.01658	MF
144	GO:0032450	maltose alpha-glucosidase activity	1	1	0.02	0.01658	MF
145	GO:0052898	N1-acetylspermidine:oxygen oxidoreductas...	1	1	0.02	0.01658	MF
146	GO:0052900	spermine oxidase (propane-1,3-diamine-fo...	1	1	0.02	0.01658	MF
147	GO:0005524	ATP binding	3193	68	52.93	0.01825	MF
148	GO:0016984	ribulose-bisphosphate carboxylase activi...	14	2	0.23	0.02187	MF
149	GO:0015254	glycerol channel activity	16	2	0.27	0.02822	MF
150	GO:0046872	metal ion binding	5795	94	96.06	0.02980	MF
151	GO:0015250	water channel activity	17	2	0.28	0.03164	MF
152	GO:0045174	glutathione dehydrogenase (ascorbate) ac...	2	1	0.03	0.03288	MF
153	GO:0080123	jasmonate-amino synthetase activity	2	1	0.03	0.03288	MF
154	GO:0050203	oxalate-CoA ligase activity	2	1	0.03	0.03288	MF
155	GO:0019148	D-cysteine desulfhydrase activity	2	1	0.03	0.03288	MF
156	GO:0008660	1-aminocyclopropane-1-carboxylate deamin...	2	1	0.03	0.03288	MF
157	GO:0080048	GDP-D-glucose phosphorylase activity	2	1	0.03	0.03288	MF
158	GO:0047995	hydroxyphenylpyruvate reductase activity	2	1	0.03	0.03288	MF
159	GO:0004818	glutamate-tRNA ligase activity	2	1	0.03	0.03288	MF
160	GO:0009916	alternative oxidase activity	2	1	0.03	0.03288	MF
161	GO:0003954	NADH dehydrogenase activity	100	3	1.66	0.03526	MF
162	GO:0003910	DNA ligase (ATP) activity	20	2	0.33	0.04279	MF
163	GO:0050897	cobalt ion binding	47	3	0.78	0.04289	MF
164	GO:0020037	heme binding	328	10	5.44	0.04805	MF
165	GO:0004604	phosphoadenylyl-sulfate reductase (thior...	3	1	0.05	0.04891	MF
166	GO:0004758	serine C-palmitoyltransferase activity	3	1	0.05	0.04891	MF
167	GO:0042286	glutamate-1-semialdehyde 2,1-aminomutase...	3	1	0.05	0.04891	MF
168	GO:0004335	galactokinase activity	3	1	0.05	0.04891	MF
169	GO:0051538	3 iron, 4 sulfur cluster binding	3	1	0.05	0.04891	MF
170	GO:0008878	glucose-1-phosphate adenylyltransferase ...	3	1	0.05	0.04891	MF
171	GO:0048027	mRNA 5'-UTR binding	3	1	0.05	0.04891	MF
172	GO:0005242	inward rectifier potassium channel activ...	3	1	0.05	0.04891	MF
173	GO:0001053	plastid sigma factor activity	3	1	0.05	0.04891	MF
174	GO:0004853	uroporphyrinogen decarboxylase activity	3	1	0.05	0.04891	MF
175	GO:0004418	hydroxymethylbilane synthase activity	3	1	0.05	0.04891	MF
176	GO:0004816	asparagine-tRNA ligase activity	3	1	0.05	0.04891	MF
177	GO:0004615	phosphomannomutase activity	3	1	0.05	0.04891	MF
178	GO:0008124	4-alpha-hydroxytetrahydrobiopterin dehyd...	3	1	0.05	0.04891	MF
179	GO:0051537	2 iron, 2 sulfur cluster binding	51	3	0.85	0.05252	MF
180	GO:0004674	protein serine/threonine kinase activity	607	16	10.06	0.05407	MF
181	GO:0008987	quinolinate synthetase A activity	4	1	0.07	0.06468	MF
182	GO:0004742	dihydrolipoylysine-residue acetyltransf...	4	1	0.07	0.06468	MF
183	GO:0005262	calcium channel activity	4	1	0.07	0.06468	MF
184	GO:0003852	2-isopropylmalate synthase activity	4	1	0.07	0.06468	MF
185	GO:0004047	aminomethyltransferase activity	4	1	0.07	0.06468	MF
186	GO:0004435	phosphatidylinositol phospholipase C act...	4	1	0.07	0.06468	MF
187	GO:0003959	NADPH dehydrogenase activity	4	1	0.07	0.06468	MF
188	GO:0004197	cysteine-type endopeptidase activity	32	3	0.53	0.06838	MF
189	GO:0005544	calcium-dependent phospholipid binding	27	2	0.45	0.07332	MF
190	GO:0005506	iron ion binding	310	9	5.14	0.07469	MF
191	GO:0004185	serine-type carboxypeptidase activity	60	3	0.99	0.07756	MF
192	GO:0046906	tetrapyrrole binding	373	21	6.18	0.07777	MF
193	GO:0032442	phenylcoumaran benzylic ether reductase ...	5	1	0.08	0.08019	MF
194	GO:0031386	protein tag	5	1	0.08	0.08019	MF
195	GO:0050236	pyridoxine:NADP 4-dehydrogenase activity	5	1	0.08	0.08019	MF
196	GO:0019789	SUMO transferase activity	5	1	0.08	0.08019	MF
197	GO:0003999	adenine phosphoribosyltransferase activi...	5	1	0.08	0.08019	MF
198	GO:0032440	2-alkenal reductase [NAD(P)] activity	63	3	1.04	0.08688	MF
199	GO:0003713	transcription coactivator activity	30	2	0.50	0.08801	MF
200	GO:0008289	lipid binding	174	7	2.88	0.09127	MF
201	GO:0009535	chloroplast thylakoid membrane	227	30	4.70	9.4e-14	CC
202	GO:0010287	plastoglobule	24	8	0.50	1.7e-08	CC
203	GO:0009941	chloroplast envelope	425	29	8.80	2.0e-08	CC

204	GO:0048046	apoplast	174	18	3.60	2.3e-08	CC
205	GO:0009522	photosystem I	54	15	1.12	3.1e-07	CC
206	GO:0009538	photosystem I reaction center	5	4	0.10	8.9e-07	CC
207	GO:0009534	chloroplast thylakoid	310	40	6.42	4.5e-06	CC
208	GO:0005618	cell wall	295	18	6.11	1.6e-05	CC
209	GO:0009507	chloroplast	1878	96	38.87	0.00015	CC
210	GO:0031977	thylakoid lumen	45	6	0.93	0.00031	CC
211	GO:0009523	photosystem II	129	14	2.67	0.00055	CC
212	GO:0009570	chloroplast stroma	491	31	10.16	0.00094	CC
213	GO:0009341	beta-galactosidase complex	23	4	0.48	0.00117	CC
214	GO:0030076	light-harvesting complex	6	3	0.12	0.00126	CC
215	GO:0030093	chloroplast photosystem I	3	2	0.06	0.00126	CC
216	GO:0000795	synaptonemal complex	14	3	0.29	0.00270	CC
217	GO:0009654	photosystem II oxygen evolving complex	50	5	1.04	0.00365	CC
218	GO:0005622	intracellular	12244	308	253.45	0.00407	CC
219	GO:0019898	extrinsic component of membrane	96	7	1.99	0.00702	CC
220	GO:0009573	chloroplast ribulose biphosphate carbox...	7	2	0.14	0.00838	CC
221	GO:0005763	mitochondrial small ribosomal subunit	9	2	0.19	0.01398	CC
222	GO:0031410	cytoplasmic vesicle	802	26	16.60	0.01644	CC
223	GO:0017177	glucosidase II complex	10	2	0.21	0.01723	CC
224	GO:0005945	6-phosphofructokinase complex	10	2	0.21	0.01723	CC
225	GO:0005794	Golgi apparatus	526	14	10.89	0.01986	CC
226	GO:0005623	cell	13500	325	279.45	0.02183	CC
227	GO:0009506	plasmodesma	338	13	7.00	0.02442	CC
228	GO:0016282	eukaryotic 43S preinitiation complex	13	2	0.27	0.02867	CC
229	GO:0005852	eukaryotic translation initiation factor...	14	2	0.29	0.03300	CC
230	GO:0005737	cytoplasm	8378	236	173.43	0.03650	CC
231	GO:0033290	eukaryotic 48S preinitiation complex	15	2	0.31	0.03757	CC
232	GO:0034357	photosynthetic membrane	347	40	7.18	0.03764	CC
233	GO:0009783	photosystem II antenna complex	2	1	0.04	0.04097	CC
234	GO:0009332	glutamate-tRNA ligase complex	2	1	0.04	0.04097	CC
235	GO:0080085	signal recognition particle, chloroplast...	2	1	0.04	0.04097	CC
236	GO:0005764	lysosome	17	2	0.35	0.04736	CC
237	GO:0005840	ribosome	636	23	13.17	0.04811	CC
238	GO:0005665	DNA-directed RNA polymerase II, core com...	18	2	0.37	0.05257	CC
239	GO:0045281	succinate dehydrogenase complex	8	2	0.17	0.06069	CC
240	GO:0000311	plastid large ribosomal subunit	3	1	0.06	0.06083	CC
241	GO:0070545	PeBoW complex	3	1	0.06	0.06083	CC
242	GO:0017059	serine C-palmitoyltransferase complex	3	1	0.06	0.06083	CC
243	GO:0031519	PcG protein complex	3	1	0.06	0.06083	CC
244	GO:0017071	intracellular cyclic nucleotide activate...	3	1	0.06	0.06083	CC
245	GO:0009517	PSII associated light-harvesting complex...	3	1	0.06	0.06083	CC
246	GO:0009579	thylakoid	490	53	10.14	0.07150	CC
247	GO:0042765	GPI-anchor transamidase complex	4	1	0.08	0.08027	CC
248	GO:0022626	cytosolic ribosome	158	6	3.27	0.09337	CC
249	GO:0044434	chloroplast part	970	63	20.08	0.09916	CC
250	GO:0030688	preribosome, small subunit precursor	5	1	0.10	0.09931	CC
251	GO:0010007	magnesium chelatase complex	5	1	0.10	0.09931	CC
252	GO:0005749	mitochondrial respiratory chain complex ...	5	1	0.10	0.09931	CC
253	GO:0043073	germ cell nucleus	5	1	0.10	0.09931	CC
254	GO:0005948	acetolactate synthase complex	5	1	0.10	0.09931	CC
255	GO:0031201	SNARE complex	28	2	0.58	0.11367	CC
256	GO:0005787	signal peptidase complex	6	1	0.12	0.11796	CC
257	GO:0005829	cytosol	1091	31	22.58	0.12385	CC
258	GO:0042651	thylakoid membrane	276	35	5.71	0.12685	CC
259	GO:0009325	nitrate reductase complex	7	1	0.14	0.13623	CC
260	GO:0042644	chloroplast nucleoid	7	1	0.14	0.13623	CC
261	GO:0005744	mitochondrial inner membrane presequence...	7	1	0.14	0.13623	CC
262	GO:0009539	photosystem II reaction center	7	1	0.14	0.13623	CC
263	GO:0031012	extracellular matrix	7	1	0.14	0.13623	CC
264	GO:0005615	extracellular space	33	2	0.68	0.14868	CC
265	GO:0005742	mitochondrial outer membrane translocase...	8	1	0.17	0.15411	CC
266	GO:0045254	pyruvate dehydrogenase complex	8	1	0.17	0.15411	CC
267	GO:0010598	NAD(P)H dehydrogenase complex (plastoqui...	8	1	0.17	0.15411	CC
268	GO:0019773	proteasome core complex, alpha-subunit c...	8	1	0.17	0.15411	CC
269	GO:0070847	core mediator complex	9	1	0.19	0.17163	CC
270	GO:0030687	preribosome, large subunit precursor	9	1	0.19	0.17163	CC
271	GO:0005773	vacuole	522	16	10.81	0.17497	CC

272	GO:0022627	cytosolic small ribosomal subunit	37	2	0.77	0.17803	CC
273	GO:0009508	plastid chromosome	10	1	0.21	0.18879	CC
274	GO:0016272	prefoldin complex	10	1	0.21	0.18879	CC
275	GO:0031969	chloroplast membrane	75	3	1.55	0.20300	CC
276	GO:0016529	sarcoplasmic reticulum	11	1	0.23	0.20559	CC
277	GO:0005886	plasma membrane	1336	27	27.66	0.20911	CC
278	GO:0030176	integral component of endoplasmic reticu...	16	2	0.33	0.22158	CC
279	GO:0005736	DNA-directed RNA polymerase I complex	13	1	0.27	0.23816	CC
280	GO:0005834	heterotrimeric G-protein complex	13	1	0.27	0.23816	CC
281	GO:0005743	mitochondrial inner membrane	178	6	3.68	0.24538	CC
282	GO:0042720	mitochondrial inner membrane peptidase c...	14	1	0.29	0.25394	CC
283	GO:0000123	histone acetyltransferase complex	49	2	1.01	0.26954	CC
284	GO:0031248	protein acetyltransferase complex	65	3	1.35	0.28392	CC
285	GO:0016592	mediator complex	54	2	1.12	0.30798	CC
286	GO:0005654	nucleoplasm	257	7	5.32	0.31316	CC
287	GO:0019013	viral nucleocapsid	55	2	1.14	0.31562	CC
288	GO:0009505	plant-type cell wall	97	3	2.01	0.32547	CC
289	GO:0070469	respiratory chain	123	3	2.55	0.32819	CC
290	GO:0005666	DNA-directed RNA polymerase III complex	21	1	0.43	0.35564	CC
291	GO:0005667	transcription factor complex	785	18	16.25	0.35835	CC
292	GO:0009536	plastid	2777	113	57.48	0.37357	CC
293	GO:0005774	vacuolar membrane	239	6	4.95	0.37461	CC
294	GO:0031224	intrinsic component of membrane	6538	121	135.34	0.38567	CC
295	GO:0045261	proton-transporting ATP synthase complex...	24	1	0.50	0.39488	CC
296	GO:0000775	chromosome, centromeric region	25	1	0.52	0.40742	CC
297	GO:0010319	stromule	25	1	0.52	0.40742	CC
298	GO:0005762	mitochondrial large ribosomal subunit	29	1	0.60	0.45505	CC
299	GO:0000136	alpha-1,6-mannosyltransferase complex	31	1	0.64	0.47741	CC
300	GO:0005856	cytoskeleton	269	4	5.57	0.47910	CC

	GO.ID	Term	Annotated	Significant	Expected	weight01_pval	branch
1	GO:0019288	isopentenyl diphosphate biosynthetic pro...	178	109	22.72	< 1e-30	BP
2	GO:0006098	pentose-phosphate shunt	196	103	25.02	< 1e-30	BP
3	GO:0042254	ribosome biogenesis	745	270	95.09	< 1e-30	BP
4	GO:0006412	translation	897	285	114.50	< 1e-30	BP
5	GO:0010027	thylakoid membrane organization	174	84	22.21	2.9e-30	BP
6	GO:0010207	photosystem II assembly	111	62	14.17	3.2e-27	BP
7	GO:0006364	rRNA processing	292	106	37.27	6.2e-27	BP
8	GO:0016117	carotenoid biosynthetic process	90	56	11.49	1.1e-25	BP
9	GO:0019252	starch biosynthetic process	122	63	15.57	9.6e-25	BP
10	GO:0000023	maltose metabolic process	105	55	13.40	8.9e-22	BP
11	GO:0015995	chlorophyll biosynthetic process	94	50	12.00	1.0e-21	BP
12	GO:0043085	positive regulation of catalytic activit...	253	72	32.29	3.1e-21	BP
13	GO:0019344	cysteine biosynthetic process	114	53	14.55	5.5e-20	BP
14	GO:0009902	chloroplast relocation	92	50	11.74	1.8e-19	BP
15	GO:0051788	response to misfolded protein	80	43	10.21	1.9e-18	BP
16	GO:0006457	protein folding	275	98	35.10	4.2e-17	BP
17	GO:0006096	glycolytic process	228	80	29.10	6.2e-17	BP
18	GO:0035304	regulation of protein dephosphorylation	82	39	10.47	1.7e-16	BP
19	GO:0009637	response to blue light	69	38	8.81	3.8e-16	BP
20	GO:0080129	proteasome core complex assembly	60	34	7.66	8.0e-16	BP
21	GO:0006636	unsaturated fatty acid biosynthetic proc...	48	30	6.13	9.4e-16	BP
22	GO:0006094	gluconeogenesis	245	79	31.27	1.4e-15	BP
23	GO:0010114	response to red light	43	28	5.49	1.8e-15	BP
24	GO:0006511	ubiquitin-dependent protein catabolic pr...	262	102	33.44	2.4e-15	BP
25	GO:0009853	photorespiration	74	38	9.45	5.4e-15	BP
26	GO:0010155	regulation of proton transport	34	24	4.34	1.2e-14	BP
27	GO:0043161	proteasome-mediated ubiquitin-dependent ...	109	46	13.91	1.6e-14	BP
28	GO:0045893	positive regulation of transcription, DN...	266	81	33.95	2.0e-13	BP
29	GO:0015976	carbon utilization	102	44	13.02	2.0e-13	BP
30	GO:0007264	small GTPase mediated signal transductio...	112	40	14.30	9.6e-13	BP
31	GO:0009651	response to salt stress	192	62	24.51	1.3e-12	BP
32	GO:0009773	photosynthetic electron transport in pho...	23	18	2.94	1.4e-12	BP
33	GO:0019761	glucosinolate biosynthetic process	77	35	9.83	1.8e-12	BP
34	GO:0019684	photosynthesis, light reaction	241	130	30.76	2.0e-12	BP
35	GO:0010218	response to far red light	47	26	6.00	4.3e-12	BP
36	GO:0006446	regulation of translational initiation	91	38	11.62	5.1e-12	BP

37	GO:0015979	photosynthesis	396	184	50.55	2.9e-11	BP
38	GO:0006119	oxidative phosphorylation	203	71	25.91	5.7e-11	BP
39	GO:0030154	cell differentiation	368	87	46.97	5.9e-11	BP
40	GO:0007030	Golgi organization	86	35	10.98	8.3e-11	BP
41	GO:0042793	transcription from plastid promoter	68	31	8.68	1.1e-10	BP
42	GO:0009407	toxin catabolic process	61	28	7.79	2.2e-10	BP
43	GO:0009657	plastid organization	361	162	46.08	5.1e-10	BP
44	GO:0002181	cytoplasmic translation	31	20	3.96	6.5e-10	BP
45	GO:0006833	water transport	62	27	7.91	2.0e-09	BP
46	GO:0000398	mRNA splicing, via spliceosome	138	58	17.61	2.0e-09	BP
47	GO:0042742	defense response to bacterium	113	40	14.42	5.8e-09	BP
48	GO:0046686	response to cadmium ion	103	36	13.15	6.3e-09	BP
49	GO:0006972	hyperosmotic response	62	24	7.91	6.8e-09	BP
50	GO:0000413	protein peptidyl-prolyl isomerization	61	26	7.79	6.8e-09	BP
51	GO:0006623	protein targeting to vacuole	65	27	8.30	6.9e-09	BP
52	GO:0006886	intracellular protein transport	596	197	76.08	1.0e-08	BP
53	GO:0030003	cellular cation homeostasis	139	39	17.74	1.5e-08	BP
54	GO:0018298	protein-chromophore linkage	48	22	6.13	1.9e-08	BP
55	GO:0010264	myo-inositol hexakisphosphate biosynthet...	35	18	4.47	4.0e-08	BP
56	GO:0009644	response to high light intensity	77	31	9.83	4.4e-08	BP
57	GO:0010103	stomatal complex morphogenesis	77	27	9.83	4.8e-08	BP
58	GO:0009073	aromatic amino acid family biosynthetic ...	136	39	17.36	5.0e-08	BP
59	GO:0006766	vitamin metabolic process	319	62	40.72	5.9e-08	BP
60	GO:0045036	protein targeting to chloroplast	45	25	5.74	6.1e-08	BP
61	GO:0009658	chloroplast organization	211	89	26.93	6.6e-08	BP
62	GO:0006655	phosphatidylglycerol biosynthetic proces...	55	23	7.02	7.7e-08	BP
63	GO:0006546	glycine catabolic process	31	16	3.96	7.8e-08	BP
64	GO:0009768	photosynthesis, light harvesting in phot...	15	11	1.91	1.2e-07	BP
65	GO:0009106	lipate metabolic process	25	14	3.19	3.4e-07	BP
66	GO:0015996	chlorophyll catabolic process	42	19	5.36	5.3e-07	BP
67	GO:0009266	response to temperature stimulus	298	85	38.04	5.6e-07	BP
68	GO:0006120	mitochondrial electron transport, NADH t...	69	25	8.81	5.8e-07	BP
69	GO:0070838	divalent metal ion transport	152	44	19.40	6.0e-07	BP
70	GO:0006470	protein dephosphorylation	238	80	30.38	6.2e-07	BP
71	GO:0031408	oxylipin biosynthetic process	23	13	2.94	7.6e-07	BP
72	GO:0032880	regulation of protein localization	18	12	2.30	8.5e-07	BP
73	GO:0007033	vacuole organization	55	23	7.02	1.1e-06	BP
74	GO:0009416	response to light stimulus	474	146	60.50	1.2e-06	BP
75	GO:0048481	plant ovule development	67	24	8.55	1.2e-06	BP
76	GO:0034660	ncRNA metabolic process	687	159	87.69	2.1e-06	BP
77	GO:0016226	iron-sulfur cluster assembly	108	33	13.79	2.3e-06	BP
78	GO:0000245	spliceosomal complex assembly	24	14	3.06	2.5e-06	BP
79	GO:0032544	plastid translation	10	8	1.28	2.5e-06	BP
80	GO:0000165	MAPK cascade	80	24	10.21	2.6e-06	BP
81	GO:0055114	oxidation-reduction process	2564	483	327.28	3.2e-06	BP
82	GO:0052541	plant-type cell wall cellulose metabolic...	8	7	1.02	3.9e-06	BP
83	GO:0010304	PSII associated light-harvesting complex...	19	11	2.43	4.1e-06	BP
84	GO:0016192	vesicle-mediated transport	416	112	53.10	4.2e-06	BP
85	GO:0070534	protein K63-linked ubiquitination	6	6	0.77	4.3e-06	BP
86	GO:0006448	regulation of translational elongation	71	23	9.06	4.3e-06	BP
87	GO:0006744	ubiquinone biosynthetic process	113	33	14.42	4.4e-06	BP
88	GO:0010200	response to chitin	58	21	7.40	4.6e-06	BP
89	GO:0009793	embryo development ending in seed dorman...	239	54	30.51	5.2e-06	BP
90	GO:0015986	ATP synthesis coupled proton transport	46	18	5.87	6.2e-06	BP
91	GO:0010310	regulation of hydrogen peroxide metaboli...	34	15	4.34	6.4e-06	BP
92	GO:0006007	glucose catabolic process	42	17	5.36	6.5e-06	BP
93	GO:0009744	response to sucrose	70	24	8.94	8.2e-06	BP
94	GO:0006397	mRNA processing	210	81	26.81	9.2e-06	BP
95	GO:0015991	ATP hydrolysis coupled proton transport	43	17	5.49	9.5e-06	BP
96	GO:0009408	response to heat	104	31	13.27	9.9e-06	BP
97	GO:0006012	galactose metabolic process	70	23	8.94	1.1e-05	BP
98	GO:0009697	salicylic acid biosynthetic process	44	17	5.62	1.4e-05	BP
99	GO:0000387	spliceosomal snRNP assembly	14	10	1.79	1.6e-05	BP
100	GO:0006913	nucleocytoplasmic transport	180	55	22.98	1.6e-05	BP
101	GO:0003735	structural constituent of ribosome	432	171	52.01	< 1e-30	MF
102	GO:0005515	protein binding	3192	639	384.32	1.8e-22	MF
103	GO:0005525	GTP binding	287	93	34.56	6.1e-20	MF
104	GO:0051082	unfolded protein binding	91	44	10.96	1.6e-17	MF

105	GO:0016168	chlorophyll binding	40	24	4.82	7.2e-13	MF
106	GO:0003924	GTPase activity	176	57	21.19	9.0e-13	MF
107	GO:0003743	translation initiation factor activity	105	40	12.64	7.2e-12	MF
108	GO:0000166	nucleotide binding	4725	723	568.90	2.9e-10	MF
109	GO:0061630	ubiquitin protein ligase activity	72	29	8.67	1.2e-09	MF
110	GO:0003723	RNA binding	1026	258	123.53	1.3e-09	MF
111	GO:0005509	calcium ion binding	320	77	38.53	1.6e-09	MF
112	GO:0003755	peptidyl-prolyl cis-trans isomerase acti...	61	26	7.34	2.0e-09	MF
113	GO:0031625	ubiquitin protein ligase binding	38	19	4.58	1.2e-08	MF
114	GO:0019904	protein domain specific binding	15	11	1.81	6.5e-08	MF
115	GO:0031072	heat shock protein binding	36	18	4.33	1.2e-07	MF
116	GO:0016157	sucrose synthase activity	16	11	1.93	1.9e-07	MF
117	GO:0008137	NADH dehydrogenase (ubiquinone) activity	75	26	9.03	3.0e-07	MF
118	GO:0003746	translation elongation factor activity	54	21	6.50	4.5e-07	MF
119	GO:0004298	threonine-type endopeptidase activity	18	11	2.17	1.1e-06	MF
120	GO:0005528	FK506 binding	19	11	2.29	2.3e-06	MF
121	GO:0031409	pigment binding	14	10	1.69	2.4e-06	MF
122	GO:0004722	protein serine/threonine phosphatase act...	83	25	9.99	7.1e-06	MF
123	GO:0046524	sucrose-phosphate synthase activity	9	7	1.08	1.1e-05	MF
124	GO:0008139	nuclear localization sequence binding	18	10	2.17	1.1e-05	MF
125	GO:0043130	ubiquitin binding	12	8	1.44	1.4e-05	MF
126	GO:0051537	2 iron, 2 sulfur cluster binding	51	18	6.14	1.5e-05	MF
127	GO:0046961	proton-transporting ATPase activity, rot...	34	14	4.09	1.7e-05	MF
128	GO:0005198	structural molecule activity	530	200	63.81	2.0e-05	MF
129	GO:0019843	rRNA binding	91	32	10.96	4.7e-05	MF
130	GO:0004176	ATP-dependent peptidase activity	29	12	3.49	6.5e-05	MF
131	GO:0046872	metal ion binding	5795	662	697.73	9.2e-05	MF
132	GO:0032440	2-alkenal reductase [NAD(P)] activity	63	19	7.59	0.00010	MF
133	GO:0001055	RNA polymerase II activity	12	7	1.44	0.00017	MF
134	GO:0045548	phenylalanine ammonia-lyase activity	9	6	1.08	0.00018	MF
135	GO:0008565	protein transporter activity	104	33	12.52	0.00020	MF
136	GO:0015078	hydrogen ion transmembrane transporter a...	211	56	25.40	0.00022	MF
137	GO:0042803	protein homodimerization activity	62	18	7.46	0.00026	MF
138	GO:0016874	ligase activity	726	107	87.41	0.00028	MF
139	GO:0043022	ribosome binding	33	12	3.97	0.00028	MF
140	GO:0004004	ATP-dependent RNA helicase activity	96	24	11.56	0.00035	MF
141	GO:0030955	potassium ion binding	17	8	2.05	0.00039	MF
142	GO:0004743	pyruvate kinase activity	17	8	2.05	0.00039	MF
143	GO:0004784	superoxide dismutase activity	10	6	1.20	0.00041	MF
144	GO:0042802	identical protein binding	132	37	15.89	0.00044	MF
145	GO:0004842	ubiquitin-protein transferase activity	226	62	27.21	0.00060	MF
146	GO:0045156	electron transporter, transferring elect...	18	8	2.17	0.00063	MF
147	GO:0017025	TBP-class protein binding	11	6	1.32	0.00082	MF
148	GO:0008553	hydrogen-exporting ATPase activity, phos...	23	9	2.77	0.00088	MF
149	GO:0004721	phosphoprotein phosphatase activity	155	41	18.66	0.00090	MF
150	GO:0016671	oxidoreductase activity, acting on a sul...	54	17	6.50	0.00092	MF
151	GO:0005200	structural constituent of cytoskeleton	37	12	4.45	0.00092	MF
152	GO:0003729	mRNA binding	45	14	5.42	0.00094	MF
153	GO:0004427	inorganic diphosphatase activity	8	5	0.96	0.00103	MF
154	GO:0016688	L-ascorbate peroxidase activity	8	5	0.96	0.00103	MF
155	GO:0070181	small ribosomal subunit rRNA binding	8	5	0.96	0.00103	MF
156	GO:0046933	proton-transporting ATP synthase activit...	33	11	3.97	0.00116	MF
157	GO:0004222	metalloendopeptidase activity	81	20	9.75	0.00123	MF
158	GO:0008047	enzyme activator activity	66	20	7.95	0.00145	MF
159	GO:0043424	protein histidine kinase binding	12	6	1.44	0.00147	MF
160	GO:0005524	ATP binding	3193	437	384.44	0.00149	MF
161	GO:0015035	protein disulfide oxidoreductase activit...	77	19	9.27	0.00162	MF
162	GO:0035798	2-alkenal reductase (NADP+) activity	3	3	0.36	0.00174	MF
163	GO:0035671	enone reductase activity	3	3	0.36	0.00174	MF
164	GO:0005506	iron ion binding	310	56	37.32	0.00195	MF
165	GO:0000822	inositol hexakisphosphate binding	9	5	1.08	0.00209	MF
166	GO:0004707	MAP kinase activity	17	7	2.05	0.00236	MF
167	GO:0042132	fructose 1,6-bisphosphate 1-phosphatase ...	6	4	0.72	0.00257	MF
168	GO:0050897	cobalt ion binding	47	13	5.66	0.00292	MF
169	GO:0008536	Ran GTPase binding	32	10	3.85	0.00331	MF
170	GO:0015450	P-P-bond-hydrolysis-driven protein trans...	13	7	1.57	0.00376	MF
171	GO:0009882	blue light photoreceptor activity	10	5	1.20	0.00376	MF
172	GO:0000287	magnesium ion binding	192	36	23.12	0.00455	MF

173	GO:0035091	phosphatidylinositol binding	33	12	3.97	0.00489	MF
174	GO:0004602	glutathione peroxidase activity	7	4	0.84	0.00543	MF
175	GO:0080130	L-phenylalanine:2-oxoglutarate aminotran...	7	4	0.84	0.00543	MF
176	GO:0004739	pyruvate dehydrogenase (acetyl-transferr...	7	4	0.84	0.00543	MF
177	GO:0030060	L-malate dehydrogenase activity	7	4	0.84	0.00543	MF
178	GO:0015266	protein channel activity	11	5	1.32	0.00622	MF
179	GO:0019888	protein phosphatase regulator activity	23	6	2.77	0.00622	MF
180	GO:0043021	ribonucleoprotein complex binding	45	19	5.42	0.00628	MF
181	GO:0000386	second spliceosomal transesterification ...	4	3	0.48	0.00635	MF
182	GO:0008266	poly(U) RNA binding	4	3	0.48	0.00635	MF
183	GO:0004128	cytochrome-b5 reductase activity, acting...	4	3	0.48	0.00635	MF
184	GO:0016710	trans-cinnamate 4-monooxygenase activity	4	3	0.48	0.00635	MF
185	GO:0009055	electron carrier activity	265	57	31.91	0.00651	MF
186	GO:0051087	chaperone binding	25	8	3.01	0.00714	MF
187	GO:0005507	copper ion binding	157	31	18.90	0.00718	MF
188	GO:0009931	calcium-dependent protein serine/threoni...	52	13	6.26	0.00744	MF
189	GO:0030276	clathrin binding	14	6	1.69	0.00961	MF
190	GO:0004747	ribokinase activity	12	5	1.44	0.00962	MF
191	GO:0004069	L-aspartate:2-oxoglutarate aminotransfer...	8	4	0.96	0.00983	MF
192	GO:0036402	proteasome-activating ATPase activity	8	4	0.96	0.00983	MF
193	GO:0004843	thiol-dependent ubiquitin-specific prote...	8	4	0.96	0.00983	MF
194	GO:0046910	pectinesterase inhibitor activity	22	7	2.65	0.01204	MF
195	GO:2001070	starch binding	13	5	1.57	0.01410	MF
196	GO:0005388	calcium-transporting ATPase activity	13	5	1.57	0.01410	MF
197	GO:0019903	protein phosphatase binding	9	4	1.08	0.01444	MF
198	GO:0004449	isocitrate dehydrogenase (NAD+) activity	5	3	0.60	0.01444	MF
199	GO:0070180	large ribosomal subunit rRNA binding	5	3	0.60	0.01444	MF
200	GO:0004775	succinate-CoA ligase (ADP-forming) activ...	5	3	0.60	0.01444	MF
201	GO:0009941	chloroplast envelope	425	193	66.13	< 1e-30	CC
202	GO:0009535	chloroplast thylakoid membrane	227	130	35.32	< 1e-30	CC
203	GO:0009570	chloroplast stroma	491	213	76.40	< 1e-30	CC
204	GO:0005829	cytosol	1091	381	169.75	< 1e-30	CC
205	GO:0009507	chloroplast	1878	660	292.20	1.0e-25	CC
206	GO:0009534	chloroplast thylakoid	310	182	48.23	3.1e-24	CC
207	GO:0005840	ribosome	636	252	98.96	5.6e-23	CC
208	GO:0022625	cytosolic large ribosomal subunit	96	56	14.94	9.1e-22	CC
209	GO:0005737	cytoplasm	8378	1920	1303.55	8.6e-21	CC
210	GO:0048046	apoplast	174	70	27.07	3.1e-15	CC
211	GO:0005622	intracellular	12244	2408	1905.06	9.1e-14	CC
212	GO:0022627	cytosolic small ribosomal subunit	37	24	5.76	1.7e-11	CC
213	GO:0010287	plastoglobule	24	18	3.73	1.4e-10	CC
214	GO:0031977	thylakoid lumen	45	25	7.00	1.8e-10	CC
215	GO:0010319	stromule	25	18	3.89	4.3e-10	CC
216	GO:0009579	thylakoid	490	234	76.24	2.3e-09	CC
217	GO:0005774	vacuolar membrane	239	73	37.19	7.7e-09	CC
218	GO:0005794	Golgi apparatus	526	122	81.84	9.6e-09	CC
219	GO:0005747	mitochondrial respiratory chain complex ...	37	20	5.76	7.0e-08	CC
220	GO:0005886	plasma membrane	1336	270	207.87	6.6e-07	CC
221	GO:0005783	endoplasmic reticulum	404	114	62.86	9.3e-07	CC
222	GO:0009506	plasmodesma	338	86	52.59	1.5e-06	CC
223	GO:0005773	vacuole	522	143	81.22	6.0e-06	CC
224	GO:0071013	catalytic step 2 spliceosome	37	17	5.76	1.2e-05	CC
225	GO:0005686	U2 snRNP	18	11	2.80	1.4e-05	CC
226	GO:0009840	chloroplastic endopeptidase Clp complex	6	6	0.93	1.4e-05	CC
227	GO:0010598	NAD(P)H dehydrogenase complex (plastoqui...	8	7	1.24	1.5e-05	CC
228	GO:0009522	photosystem I	54	26	8.40	1.6e-05	CC
229	GO:0030126	COPI vesicle coat	11	8	1.71	3.6e-05	CC
230	GO:0005682	U5 snRNP	12	8	1.87	9.3e-05	CC
231	GO:0071011	precatalytic spliceosome	21	11	3.27	9.8e-05	CC
232	GO:0033290	eukaryotic 48S preinitiation complex	15	9	2.33	0.00011	CC
233	GO:0030529	intracellular ribonucleoprotein complex	918	341	142.83	0.00013	CC
234	GO:0070469	respiratory chain	123	49	19.14	0.00018	CC
235	GO:0019013	viral nucleocapsid	55	19	8.56	0.00041	CC
236	GO:0005689	U12-type spliceosomal complex	14	8	2.18	0.00042	CC
237	GO:0008287	protein serine/threonine phosphatase com...	91	28	14.16	0.00060	CC
238	GO:0009523	photosystem II	129	41	20.07	0.00064	CC
239	GO:0005665	DNA-directed RNA polymerase II, core com...	18	9	2.80	0.00067	CC
240	GO:0071004	U2-type prespliceosome	19	9	2.96	0.00110	CC

241	GO:0046540	U4/U6 x U5 tri-snRNP complex	16	8	2.49	0.00135	CC
242	GO:0016282	eukaryotic 43S preinitiation complex	13	7	2.02	0.00158	CC
243	GO:0005839	proteasome core complex	18	11	2.80	0.00167	CC
244	GO:0005685	U1 snRNP	20	9	3.11	0.00172	CC
245	GO:0097526	spliceosomal tri-snRNP complex	21	12	3.27	0.00254	CC
246	GO:0009538	photosystem I reaction center	5	4	0.78	0.00256	CC
247	GO:0005853	eukaryotic translation elongation factor...	5	4	0.78	0.00256	CC
248	GO:0005681	spliceosomal complex	88	35	13.69	0.00271	CC
249	GO:0005852	eukaryotic translation initiation factor...	14	7	2.18	0.00273	CC
250	GO:0000325	plant-type vacuole	57	12	8.87	0.00274	CC
251	GO:0009654	photosystem II oxygen evolving complex	50	16	7.78	0.00282	CC
252	GO:0005623	cell	13500	2557	2100.49	0.00288	CC
253	GO:0005762	mitochondrial large ribosomal subunit	29	11	4.51	0.00288	CC
254	GO:0000243	commitment complex	11	6	1.71	0.00321	CC
255	GO:0019773	proteasome core complex, alpha-subunit c...	8	5	1.24	0.00337	CC
256	GO:0045254	pyruvate dehydrogenase complex	8	5	1.24	0.00337	CC
257	GO:0005654	nucleoplasm	257	52	39.99	0.00338	CC
258	GO:0005789	endoplasmic reticulum membrane	163	43	25.36	0.00358	CC
259	GO:0031361	integral component of thylakoid membrane	3	3	0.47	0.00376	CC
260	GO:0000311	plastid large ribosomal subunit	3	3	0.47	0.00376	CC
261	GO:0034715	pICln-Sm protein complex	3	3	0.47	0.00376	CC
262	GO:0005730	nucleolus	254	61	39.52	0.00498	CC
263	GO:0030687	preribosome, large subunit precursor	9	5	1.40	0.00660	CC
264	GO:0015030	Cajal body	6	4	0.93	0.00673	CC
265	GO:0031305	integral component of mitochondrial inne...	6	4	0.93	0.00673	CC
266	GO:0010494	cytoplasmic stress granule	6	4	0.93	0.00673	CC
267	GO:0009706	chloroplast inner membrane	30	11	4.67	0.00953	CC
268	GO:0009508	plastid chromosome	10	5	1.56	0.01153	CC
269	GO:0005618	cell wall	295	58	45.90	0.01308	CC
270	GO:0000276	mitochondrial proton-transporting ATP sy...	4	3	0.62	0.01330	CC
271	GO:0005771	multivesicular body	4	3	0.62	0.01330	CC
272	GO:0009512	cytochrome b6f complex	4	3	0.62	0.01330	CC
273	GO:0008540	proteasome regulatory particle, base sub...	14	6	2.18	0.01372	CC
274	GO:0005751	mitochondrial respiratory chain complex ...	7	4	1.09	0.01378	CC
275	GO:0000220	vacuolar proton-transporting V-type ATPa...	7	4	1.09	0.01378	CC
276	GO:0000974	Prp19 complex	7	4	1.09	0.01378	CC
277	GO:0009573	chloroplast ribulose biphosphate carbox...	7	4	1.09	0.01378	CC
278	GO:0009504	cell plate	7	4	1.09	0.01378	CC
279	GO:0005795	Golgi stack	49	6	7.62	0.01386	CC
280	GO:0031965	nuclear membrane	22	8	3.42	0.01407	CC
281	GO:0016529	sarcoplasmic reticulum	11	5	1.71	0.01846	CC
282	GO:0000502	proteasome complex	54	26	8.40	0.01924	CC
283	GO:0009332	glutamate-tRNA ligase complex	2	2	0.31	0.02420	CC
284	GO:0031372	UBC13-MMS2 complex	2	2	0.31	0.02420	CC
285	GO:0043614	multi-eIF complex	2	2	0.31	0.02420	CC
286	GO:0080085	signal recognition particle, chloroplast...	2	2	0.31	0.02420	CC
287	GO:0005850	eukaryotic translation initiation factor...	2	2	0.31	0.02420	CC
288	GO:0016607	nuclear speck	8	4	1.24	0.02420	CC
289	GO:0031595	nuclear proteasome complex	8	4	1.24	0.02420	CC
290	GO:0005929	cilium	24	5	3.73	0.02425	CC
291	GO:0019898	extrinsic component of membrane	96	22	14.94	0.02445	CC
292	GO:0034399	nuclear periphery	21	8	3.27	0.02630	CC
293	GO:0022626	cytosolic ribosome	158	88	24.58	0.02775	CC
294	GO:0071010	prespliceosome	24	12	3.73	0.02924	CC
295	GO:0005753	mitochondrial proton-transporting ATP sy...	14	9	2.18	0.02928	CC
296	GO:0045275	respiratory chain complex III	12	6	1.87	0.02935	CC
297	GO:0005845	mRNA cap binding complex	5	3	0.78	0.02940	CC
298	GO:0042709	succinate-CoA ligase complex	5	3	0.78	0.02940	CC
299	GO:0005948	acetolactate synthase complex	5	3	0.78	0.02940	CC
300	GO:0000275	mitochondrial proton-transporting ATP sy...	5	3	0.78	0.02940	CC