

id	source	term_id	term_name	term_size	intersection_size	p_value
1	GO:CC	GO:0009536	plastid	547	221	5.0e-56
2	GO:CC	GO:0009579	thylakoid	130	96	6.8e-54
3	GO:CC	GO:0009507	chloroplast	505	206	3.2e-53
4	GO:BP	GO:0015979	photosynthesis	117	89	3.7e-49
5	GO:CC	GO:0034357	photosynthetic membrane	103	78	3.2e-45
6	GO:CC	GO:0042651	thylakoid membrane	87	66	2.7e-38
7	GO:CC	GO:0031976	plastid thylakoid	89	65	4.8e-36
8	GO:CC	GO:0009534	chloroplast thylakoid	88	64	2.3e-35
9	GO:CC	GO:0055035	plastid thylakoid membrane	75	57	2.9e-33
10	GO:CC	GO:0009535	chloroplast thylakoid membrane	73	56	4.2e-33
11	GO:CC	GO:0009521	photosystem	60	50	8.4e-33
12	GO:CC	GO:0009523	photosystem II	48	40	3.2e-26
13	GO:CC	GO:0009526	plastid envelope	176	81	9.6e-25
14	GO:CC	GO:0042170	plastid membrane	156	75	2.0e-24
15	GO:CC	GO:0031968	organelle outer membrane	115	60	6.2e-22
16	GO:CC	GO:0019867	outer membrane	115	60	6.2e-22
17	GO:BP	GO:0019684	photosynthesis, light reaction	54	39	3.1e-19
18	GO:CC	GO:0009654	photosystem II oxygen evolving complex	18	18	3.3e-15
19	GO:CC	GO:0009522	photosystem I	32	25	3.3e-15
20	GO:BP	GO:0009657	plastid organization	97	45	7.9e-12
21	GO:BP	GO:0006468	protein phosphorylation	1264	268	4.5e-11
22	GO:BP	GO:0016310	phosphorylation	1421	294	4.6e-11
23	GO:CC	GO:0009532	plastid stroma	81	36	1.4e-10
24	GO:MF	GO:0004672	protein kinase activity	1289	268	1.6e-10
25	GO:MF	GO:0016773	phosphotransferase activity, alcohol group as acceptor	1403	287	1.6e-10
26	GO:MF	GO:0016491	oxidoreductase activity	1821	356	1.6e-10
27	GO:MF	GO:0016301	kinase activity	1480	298	2.9e-10
28	GO:CC	GO:0009570	chloroplast stroma	68	32	2.9e-10
29	GO:MF	GO:0004674	protein serine/threonine kinase activity	540	133	1.2e-09
30	GO:CC	GO:0016020	membrane	6248	952	7.1e-09
31	GO:BP	GO:0009765	photosynthesis, light harvesting	25	18	2.2e-08
32	GO:BP	GO:0009416	response to light stimulus	145	51	2.5e-08
33	GO:BP	GO:0009658	chloroplast organization	79	34	6.5e-08
34	GO:BP	GO:0009314	response to radiation	150	51	7.9e-08
35	GO:BP	GO:0006091	generation of precursor metabolites and energy	213	64	1.6e-07
36	GO:MF	GO:0016772	transferase activity, transferring phosphorus-containing groups	1647	310	2.2e-07
37	GO:BP	GO:0006796	phosphate-containing compound metabolic process	1805	336	3.4e-07
38	GO:MF	GO:0016168	chlorophyll binding	22	15	1.1e-06
39	GO:BP	GO:0006793	phosphorus metabolic process	1837	338	1.1e-06
40	GO:BP	GO:0009767	photosynthetic electron transport chain	15	12	2.4e-06
41	GO:BP	GO:0009773	photosynthetic electron transport in photosystem I	9	9	2.8e-06
42	GO:CC	GO:0031975	envelope	386	87	7.2e-06
43	GO:CC	GO:0031967	organelle envelope	386	87	7.2e-06
44	GO:MF	GO:0003824	catalytic activity	8918	1347	1.1e-05
45	GO:BP	GO:0009605	response to external stimulus	1268	241	1.3e-05
46	GO:MF	GO:0043168	anion binding	3675	604	1.6e-05
47	GO:BP	GO:0046148	pigment biosynthetic process	64	26	1.7e-05
48	GO:BP	GO:0015994	chlorophyll metabolic process	32	17	2.1e-05
49	GO:BP	GO:0044237	cellular metabolic process	6149	961	2.1e-05
50	GO:MF	GO:0036094	small molecule binding	3768	615	3.0e-05
51	GO:BP	GO:0009620	response to fungus	589	126	3.4e-05
52	GO:BP	GO:0042440	pigment metabolic process	79	29	3.5e-05
53	GO:MF	GO:0043167	ion binding	6224	966	4.1e-05
54	GO:BP	GO:0015995	chlorophyll biosynthetic process	21	13	4.7e-05
55	GO:MF	GO:0030246	carbohydrate binding	180	50	4.8e-05
56	GO:MF	GO:0038023	signaling receptor activity	118	37	5.3e-05
57	GO:MF	GO:1901265	nucleoside phosphate binding	3593	585	6.4e-05
58	GO:MF	GO:0000166	nucleotide binding	3593	585	6.4e-05
59	GO:CC	GO:0010598	NAD(P)H dehydrogenase complex (plastoquinone)	6	6	7.1e-05
60	GO:MF	GO:0140096	catalytic activity, acting on a protein	2446	414	7.8e-05
61	GO:BP	GO:0050896	response to stimulus	3233	535	8.5e-05
62	GO:MF	GO:0032559	adenyl ribonucleotide binding	3041	502	9.0e-05
63	GO:CC	GO:0019898	extrinsic component of membrane	41	17	1.0e-04
64	GO:MF	GO:0060089	molecular transducer activity	124	37	1.4e-04
65	GO:BP	GO:0009607	response to biotic stimulus	1200	223	1.6e-04
66	GO:BP	GO:0043207	response to external biotic stimulus	1165	217	1.7e-04
67	GO:BP	GO:0051707	response to other organism	1165	217	1.7e-04
68	GO:CC	GO:1990204	oxidoreductase complex	51	19	1.9e-04
69	GO:BP	GO:0044419	biological process involved in interspecies interaction between organisms	1170	217	2.1e-04
70	GO:BP	GO:0009644	response to high light intensity	12	9	2.1e-04
71	GO:BP	GO:0050832	defense response to fungus	456	99	2.2e-04
72	GO:MF	GO:0030554	adenyl nucleotide binding	3157	515	2.3e-04
73	GO:MF	GO:0032553	ribonucleotide binding	3328	540	2.3e-04
74	GO:BP	GO:0006778	porphyrin-containing compound metabolic process	57	22	2.3e-04
75	GO:MF	GO:0032555	purine ribonucleotide binding	3293	534	2.8e-04
76	GO:MF	GO:0016987	sigma factor activity	6	6	3.0e-04
77	GO:MF	GO:0097367	carbohydrate derivative binding	3361	543	3.1e-04
78	GO:MF	GO:0005524	ATP binding	2320	389	3.1e-04
79	GO:MF	GO:0051536	iron-sulfur cluster binding	120	35	3.1e-04
80	GO:MF	GO:0051540	metal cluster binding	120	35	3.1e-04
81	GO:MF	GO:0030247	polysaccharide binding	56	21	3.1e-04
82	GO:BP	GO:0033013	tetrapyrrole metabolic process	58	22	3.2e-04
83	GO:BP	GO:0006952	defense response	1567	277	4.2e-04
84	GO:BP	GO:0006779	porphyrin-containing compound biosynthetic process	43	18	4.3e-04
85	GO:CC	GO:0009538	photosystem I reaction center	5	5	4.7e-04
86	GO:BP	GO:0009637	response to blue light	22	12	5.2e-04
87	GO:MF	GO:0017076	purine nucleotide binding	3409	547	5.5e-04
88	GO:BP	GO:0016108	tetraterpenoid metabolic process	19	11	5.5e-04
89	GO:BP	GO:0016116	carotenoid metabolic process	19	11	5.5e-04
90	GO:BP	GO:0033014	tetrapyrrole biosynthetic process	45	18	8.1e-04
91	GO:MF	GO:0015291	secondary active transmembrane transporter activity	168	43	1.1e-03
92	GO:MF	GO:0035639	purine ribonucleoside triphosphate binding	2572	421	1.1e-03
93	GO:BP	GO:0071482	cellular response to light stimulus	27	13	1.1e-03
94	GO:MF	GO:0016701	oxidoreductase activity, acting on single donors with incorporation of molecular oxygen	44	17	1.2e-03
95	GO:MF	GO:0046906	tetrapyrrole binding	610	119	1.3e-03
96	GO:MF	GO:0016703	oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of one atom of oxygen (internal monooxygenases or internal mixed function oxidases)	5	5	1.4e-03
97	GO:MF	GO:0097159	organic cyclic compound binding	6736	1015	1.6e-03
98	GO:MF	GO:1901363	heterocyclic compound binding	6735	1015	1.6e-03
99	GO:BP	GO:0048544	recognition of pollen	73	24	1.6e-03
00	GO:MF	GO:0106310	protein serine kinase activity	63	21	1.7e-03
001	GO:BP	GO:0071478	cellular response to radiation	28	13	1.8e-03
002	GO:BP	GO:0009628	response to abiotic stimulus	389	83	1.8e-03
003	GO:BP	GO:0008037	cell recognition	74	24	1.9e-03
004	GO:BP	GO:0009668	plastid membrane organization	15	9	2.0e-03
005	GO:BP	GO:0010027	thylakoid membrane organization	15	9	2.0e-03
006	GO:BP	GO:0010207	photosystem II assembly	5	5	2.3e-03
007	GO:BP	GO:0009642	response to light intensity	29	13	2.4e-03
008	GO:CC	GO:0098796	membrane protein complex	263	56	2.9e-03
009	GO:BP	GO:0098542	defense response to other organism	667	128	3.3e-03
010	GO:BP	GO:0071214	cellular response to abiotic stimulus	42	16	3.6e-03
011	GO:BP	GO:0104004	cellular response to environmental stimulus	42	16	3.6e-03
012	GO:MF	GO:0004888	transmembrane signaling receptor activity	76	23	4.1e-03
013	GO:MF	GO:0008066	glutamate receptor activity	21	10	4.2e-03
014	GO:MF	GO:0004970	ionotropic glutamate receptor activity	21	10	4.2e-03
015	GO:MF	GO:0005506	iron ion binding	537	104	4.2e-03
016	GO:MF	GO:0005230	extracellular ligand-gated monoatomic ion channel activity	21	10	4.2e-03
017	GO:MF	GO:0015276	ligand-gated monoatomic ion channel activity	21	10	4.2e-03
018	GO:MF	GO:0022834	ligand-gated channel activity	21	10	4.2e-03
019	GO:MF	GO:0022835	transmitter-gated channel activity	21	10	4.2e-03
020	GO:MF	GO:0022824	transmitter-gated monoatomic ion channel activity	21	10	4.2e-03
021	GO:MF	GO:0030594	neurotransmitter receptor activity	21	10	4.2e-03
022	GO:BP	GO:0006950	response to stress	2241	369	5.3e-03
023	GO:MF	GO:0015145	monosaccharide transmembrane transporter activity	15	8	6.7e-03
024	GO:MF	GO:0022839	monoatomic ion gated channel activity	70	21	6.7e-03
025	GO:MF	GO:0022836	gated channel activity	70	21	6.7e-03
026	GO:MF	GO:0010277	chlorophyllide a oxygenase [overall] activity	4	4	6.7e-03
027	GO:MF	GO:0005216	monoatomic ion channel activity	105	28	6.7e-03
028	GO:CC	GO:0098588	bounding membrane of organelle	388	75	6.8e-03
029	GO:MF	GO:0051537	2 iron, 2 sulfur cluster binding	43	15	7.3e-03
030	GO:BP	GO:0072598	protein localization to chloroplast	14	8	7.6e-03
031	GO:MF	GO:0048038	quinone binding	19	9	8.0e-03
032	GO:BP	GO:0022900	electron transport chain	111	30	8.0e-03
033	GO:MF	GO:0051119	sugar transmembrane transporter activity	27	11	8.9e-03
034	GO:MF	GO:0071949	FAD binding	72	21	8.9e-03
035	GO:MF	GO:0015293	symporter activity	31	12	8.9e-03
036	GO:BP	GO:0017038	protein import	6	5	1.0e-02
037	GO:BP	GO:0010275	NAD(P)H dehydrogenase complex assembly	6	5	1.0e-02
038	GO:MF	GO:0003700	DNA-binding transcription factor activity	638	117	1.1e-02
039	GO:MF	GO:0051213	dioxygenase activity	208	46	1.1e-02
040	GO:MF	GO:0016730	oxidoreductase activity, acting on iron-sulfur proteins as donors	7	5	1.3e-02
041	GO:BP	GO:0042362	fat-soluble vitamin biosynthetic process	4	4	1.3e-02
042	GO:BP	GO:0006775	fat-soluble vitamin metabolic process	4	4	1.3e-02
043	GO:BP	GO:0010258	NADH dehydrogenase complex (plastoquinone) assembly	4	4	1.3e-02
044	GO:BP	GO:2000142	regulation of DNA-templated transcription initiation	9	6	1.4e-02
045	GO:BP	GO:0034219	carbohydrate transmembrane transport	43	15	1.5e-02
046	GO:MF	GO:0004176	ATP-dependent peptidase activity	33	12	1.6e-02
047	GO:CC	GO:0031977	thylakoid lumen	8	5	1.6e-02
048	GO:BP	GO:1901564	organonitrogen compound metabolic process	4179	645	1.9e-02
049	GO:MF	GO:0003729	mRNA binding	202	44	1.9e-02
050	GO:MF	GO:0016859	cis-trans isomerase activity	57	17	2.0e-02
051	GO:CC	GO:0005777	peroxisome	61	17	2.0e-02
052	GO:CC	GO:0042579	microbody	61	17	2.0e-02
053	GO:MF	GO:0016705	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	695	124	2.0e-02
054	GO:CC	GO:0098807	chloroplast thylakoid membrane protein complex	3	3	2.1e-02
055	GO:BP	GO:0015749	monosaccharide transmembrane transport	16	8	2.1e-02
056	GO:MF	GO:0015144	carbohydrate transmembrane transporter activity	48	15	2.2e-02
057	GO:MF	GO:0102756	very-long-chain 3-ketoacyl-CoA synthase activity	22	9	2.4e-02
058	GO:BP	GO:0072596	establishment of protein localization to chloroplast	13	7	2.6e-02
059	GO:BP	GO:0045036	protein targeting to chloroplast	13	7	2.6e-02
060	GO:BP	GO:0051644	plastid localization	7	5	2.6e-02
061	GO:BP	GO:0019750	chloroplast localization	7	5	2.6e-02
062	GO:BP	GO:0009638	phototropism	7	5	2.6e-02
063	GO:BP	GO:0036211	protein modification process	2006	326	2.7e-02
064	GO:BP	GO:0071483	cellular response to blue light	10	6	2.7e-02
065	GO:BP	GO:0010109	regulation of photosynthesis	10	6	2.7e-02
066	GO:MF	GO:0016702	oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen	31	11	2.9e-02
067	GO:CC	GO:0005886	plasma membrane	613	106	3.0e-02
068	GO:MF	GO:0022804	active transmembrane transporter activity	394	75	3.0e-02
069	GO:MF	GO:0005315	inorganic phosphate transmembrane transporter activity	15	7	3.1e-02
070	GO:CC	GO:0031978	plastid thylakoid lumen	6	4	3.1e-02
071	GO:CC	GO:0009543	chloroplast thylakoid lumen	6	4	3.1e-02
072	GO:CC	GO:0009941	chloroplast envelope	91	22	3.1e-02
073	GO:MF	GO:0003755	peptidyl-prolyl cis-trans isomerase activity	55	16	3.3e-02
074	GO:MF	GO:0016851	magnesium chelatase activity	3	3	