Table S2. Enriched GO functional categories of interacting proteins within the ABA signaling network.

GO	Term	Category	FDR	P value	No. of test genes in category	Percent in test	No. of reference genes in category	Percent in reference	Fold
GO functional analysis of proteins by compared to those in AraPPINet.									
GO:0051716	cellular response to stimulus	P	1.17E-210	2.27E-212	667	37.28	826	7.67	4.86
GO:0050794	regulation of cellular process	P	1.17E-210	2.27E-212	667	37.28	826	7.67	4.86
GO:0007165	signal transduction	P	1.17E-210	2.27E-212	667	37.28	826	7.67	4.86
GO:0023052	signaling	P	6.16E-207	1.79E-208	678	37.90	879	8.16	4.64
GO:0044700	single organism signaling	P	6.16E-207	1.79E-208	678	37.90	879	8.16	4.64
GO:0050789	regulation of biological process	P	9.34E-197	3.17E-198	736	41.14	1126	10.46	3.93
GO:0050896	response to stimulus	P	4.04E-187	1.76E-188	1247	69.70	3542	32.90	2.12
GO:0007154	cell communication	P	1.18E-185	5.71E-187	718	40.13	1129	10.49	3.83
GO:0065007	biological regulation	P	2.50E-181	1.34E-182	768	42.93	1338	12.43	3.45
GO:0009719	response to endogenous stimulus	P	1.79E-174	1.04E-175	579	32.36	736	6.84	4.73
GO:0044763	single-organism cellular process	P	2.20E-137	1.39E-138	1100	61.49	3254	30.22	2.03
GO:0044260	cellular macromolecule metabolic process	P	8.68E-113	6.32E-114	1058	59.14	3319	30.83	1.92
GO:0044699	single-organism process	P	9.71E-111	7.54E-112	1352	75.57	5116	47.52	1.59
GO:0043170	macromolecule metabolic process	P	3.90E-107	3.21E-108	1168	65.29	4017	37.31	1.75
GO:0006950	response to stress	P	1.65E-102	1.44E-103	847	47.34	2366	21.97	2.15
GO:0009628	response to abiotic stimulus	P	7.15E-93	6.59E-94	658	36.78	1611	14.96	2.46
GO:0090304	nucleic acid metabolic process	P	8.27E-87	8.03E-88	673	37.62	1740	16.16	2.33
GO:0044271	cellular nitrogen compound biosynthetic process	P	2.07E-80	2.81E-81	572	31.97	1375	12.77	2.50
GO:0019438	aromatic compound biosynthetic process	P	2.07E-80	2.81E-81	572	31.97	1375	12.77	2.50
GO:0006350	transcription, DNA-templated	P	2.07E-80	2.81E-81	572	31.97	1375	12.77	2.50
GO:0032774	RNA biosynthetic process	P	2.07E-80	2.81E-81	572	31.97	1375	12.77	2.50
GO:1901362	organic cyclic compound biosynthetic process	P	2.07E-80	2.81E-81	572	31.97	1375	12.77	2.50
GO:0016070	RNA metabolic process	P	2.07E-80	2.81E-81	572	31.97	1375	12.77	2.50
GO:0034654	nucleobase-containing compound biosynthetic process	P	2.07E-80	2.81E-81	572	31.97	1375	12.77	2.50
GO:0018130	heterocycle biosynthetic process	P	2.07E-80	2.81E-81	572	31.97	1375	12.77	2.50
GO:0036211	protein modification process	P	9.48E-74	1.52E-74	592	33.09	1532	14.23	2.33
GO:0043412	macromolecule modification	P	9.48E-74	1.52E-74	592	33.09	1532	14.23	2.33
GO:0006464	cellular protein modification process	P	9.48E-74	1.52E-74	592	33.09	1532	14.23	2.33
GO:0044237	cellular metabolic process	P	5.03E-71	8.29E-72	1243	69.48	5044	46.85	1.48
GO:0009791	post-embryonic development	P	2.05E-64	3.48E-65	517	28.90	1317	12.23	2.36
GO:0032502	developmental process	P	3.60E-63	6.30E-64	763	42.65	2471	22.95	1.86
GO:0009987	cellular process	P	3.68E-63	6.61E-64	1681	93.96	8478	78.74	1.19
GO:0007275	multicellular organismal development	P	5.34E-63	9.86E-64	735	41.08	2335	21.69	1.89
GO:0044707	single-multicellular organism process	P	6.05E-63	1.15E-63	746	41.70	2391	22.21	1.88
GO:0044767	single-organism developmental process	P	2.77E-62	5.38E-63	739	41.31	2366	21.97	1.88
GO:0032501	multicellular organismal process	P	7.49E-62	1.49E-62	749	41.87	2421	22.49	1.86
GO:0009607	response to biotic stimulus	P	2.51E-55	5.12E-56	424	23.70	1033	9.59	2.47
GO:0010467	gene expression	P	4.87E-55	1.02E-55	621	34.71	1902	17.67	1.97
GO:0071704	organic substance metabolic process	P	2.00E-54	4.28E-55	1434	80.16	6651	61.77	1.30
GO:1901576	organic substance biosynthetic process	P	6.55E-54	1.53E-54	593	33.15	1788	16.61	2.00
GO:0044249	cellular biosynthetic process	P	6.55E-54	1.53E-54	593	33.15	1788	16.61	2.00
GO:0009059	macromolecule biosynthetic process	P	6.55E-54	1.53E-54	593	33.15	1788	16.61	2.00
GO:0034645	cellular macromolecule biosynthetic process	P	6.55E-54	1.53E-54	593	33.15	1788	16.61	2.00
GO:0044238	primary metabolic process	P	7.47E-54	1.78E-54	1431	79.99	6642	61.69	1.30
GO:0016265	death	P	1.00E-51	2.48E-52	191	10.68	247	2.29	4.65
GO:0008219	cell death	P	1.00E-51	2.48E-52	191	10.68	247	2.29	4.65
GO:1901360	organic cyclic compound metabolic process	P	7.71E-47	2.09E-47	791	44.21	2892	26.86	1.65
GO:0046483	heterocycle metabolic process	P	7.71E-47	2.09E-47	791	44.21	2892	26.86	1.65
GO:0006139	nucleobase-containing compound metabolic process	P	7.71E-47	2.09E-47	791	44.21	2892	26.86	1.65
GO:0006725	cellular aromatic compound metabolic process	P	7.71E-47	2.09E-47	791	44.21	2892	26.86	1.65
GO:0034641	cellular nitrogen compound metabolic process	P	7.71E-47	2.09E-47	791	44.21	2892	26.86	1.65
GO:0044267	cellular protein metabolic process	P	8.59E-45	2.38E-45	603	33.71	1977	18.36	1.84
GO:0019538	protein metabolic process	P	7.85E-44	2.21E-44	740	41.36	2682	24.91	1.66
GO:0009058	biosynthetic process	P	7.85E-42	2.25E-42	1068	59.70	4557	42.32	1.41
GO:0008152	metabolic process	P	3.86E-40	1.20E-40	1514	84.63	7546	70.08	1.21
GO:0048856	anatomical structure development	P	9.45E-39	3.03E-39	509	28.45	1627	15.11	1.88
GO:0006807	nitrogen compound metabolic process	P	6.85E-37	2.23E-37	880	49.19	3583	33.28	1.48
GO:0009605	response to external stimulus	P	1.88E-36	6.20E-37	274	15.32	645	5.99	2.56
GO:0009908	flower development	P	3.14E-31	1.11E-31	238	13.30	562	5.22	2.55
GO:0090567	reproductive shoot system development	P	3.14E-31	1.11E-31	238	13.30	562	5.22	2.55
GO:0048367	shoot system development	P	3.14E-31	1.11E-31	238	13.30	562	5.22	2.55
GO:0061458	reproductive system development	P	4.55E-31	1.72E-31	238	13.30	565	5.25	2.54
GO:0044702	single organism reproductive process	P	4.55E-31	1.72E-31	238	13.30	565	5.25	2.54
GO:0048608	reproductive structure development	P	4.55E-31	1.72E-31	238	13.30	565	5.25	2.54
GO:0003006	developmental process involved in reproduction	P	4.55E-31	1.72E-31	238	13.30	565	5.25	2.54
GO:0048731	system development	P	4.55E-31	1.72E-31	238	13.30	565	5.25	2.54
GO:0000003	reproduction	P	1.56E-29	5.98E-30	430	24.04	1415	13.14	1.83
GO:0007049	cell cycle	P	1.22E-28	4.75E-29	214	11.96	498	4.63	2.59
GO:0009653	anatomical structure morphogenesis	P	2.32E-28	9.13E-29	364	20.35	1132	10.51	1.94

GO:0022414	reproductive process	P	1.58E-23	6.30E-24	270	15.09	793	7.37	2.05
GO:0016043	cellular component organization	P	8.76E-20	3.87E-20	561	31.36	2283	21.20	1.48
GO:0071840	cellular component organization or biogenesis	P	8.76E-20	3.87E-20	561	31.36	2283	21.20	1.48
GO:0040007	growth	P	2.34E-15	1.06E-15	197	11.01	606	5.63	1.96
GO:0030154	cell differentiation	P	2.55E-15	1.17E-15	226	12.63	734	6.82	1.85
GO:0048869	cellular developmental process	P	2.55E-15	1.17E-15	226	12.63	734	6.82	1.85
GO:0006259	DNA metabolic process	P	9.08E-11	4.58E-11	160	8.94	524	4.87	1.84
GO:0016049	cell growth	P	9.57E-11	4.88E-11	147	8.22	467	4.34	1.89
GO:0009790	embryo development	P	1.73E-10	8.91E-11	127	7.10	383	3.56	2.00
GO:0010468	regulation of gene expression	P	2.27E-05	1.34E-05	90	5.03	317	2.94	1.71
GO:0019222	regulation of metabolic process	P	2.27E-05	1.34E-05	90	5.03	317	2.94	1.71
GO:0040029	regulation of gene expression, epigenetic	P	2.27E-05	1.34E-05	90	5.03	317	2.94	1.71
GO:0060255	regulation of macromolecule metabolic process	P	2.27E-05	1.34E-05	90	5.03	317	2.94	1.71
GO:0009838	abscission	P	6.47E-05	3.93E-05	16	0.89	23	0.21	4.19
GO:0009606	tropism	P	7.73E-05	4.73E-05	40	2.24	109	1.01	2.21
GO:0009056	catabolic process	P	1.79E-04	1.13E-04	358	20.01	1751	16.26	1.23
GO:0006810	transport	P	2.76E-04	1.78E-04	459	25.66	2329	21.63	1.19
GO:0051234	establishment of localization	P	2.76E-04	1.78E-04	459	25.66	2329	21.63	1.19
GO:0051179	localization	P	2.76E-04	1.78E-04	459	25.66	2329	21.63	1.19
GO:0019748	secondary metabolic process	P	5.16E-04	3.38E-04	196	10.96	895	8.31	1.32
GO:0009991	response to extracellular stimulus	P	8.73E-04	5.77E-04	67	3.75	248	2.30	1.63
GO:0006091	generation of precursor metabolites and energy	P	1.36E-02	1.04E-02	99	5.53	449	4.17	1.33
GO:0007267	cell-cell signaling	P	4.60E-02	3.55E-02	18	1.01	61	0.57	1.78
GO:0005515	protein binding	F	0	0	1123	62.77	1289	11.97	5.24
GO:0005488	binding	F	2.30E-191	8.93E-193	1572	87.87	5701	52.95	1.66
GO:0003700	sequence-specific DNA binding transcription factor activity	F	3.62E-78	5.28E-79	426	23.81	826	7.67	3.10
GO:0001071	nucleic acid binding transcription factor activity	F	3.62E-78	5.28E-79	426	23.81	826	7.67	3.10
GO:0003677	DNA binding	F	7.88E-39	2.49E-39	383	21.41	1061	9.85	2.17
GO:0016301	kinase activity	F	6.85E-35	2.33E-35	297	16.60	753	6.99	2.37
GO:0016772	transferase activity, transferring phosphorus-containing groups	F	6.85E-35	2.33E-35	297	16.60	753	6.99	2.37
GO:0004871	signal transducer activity	F	3.51E-21	1.48E-21	72	4.02	86	0.80	5.04
GO:0060089	molecular transducer activity	F	3.51E-21	1.48E-21	72	4.02	86	0.80	5.04
GO:0097159	organic cyclic compound binding	F	6.92E-21	2.99E-21	802	44.83	3569	33.15	1.35
GO:1901363	heterocyclic compound binding	F	6.92E-21	2.99E-21	802	44.83	3569	33.15	1.35
GO:0003676	nucleic acid binding	F	3.21E-13	1.51E-13	431	24.09	1791	16.63	1.45
GO:0030234	enzyme regulator activity	F	2.83E-12	1.39E-12	82	4.58	181	1.68	2.73
GO:0030528	transcription regulator activity	F	1.14E-11	5.64E-12	37	2.07	43	0.40	5.18
GO:0004872	receptor activity	F	1.18E-11	5.91E-12	40	2.24	51	0.47	4.72
GO:0005102	receptor binding	F	4.68E-05	2.81E-05	18	1.01	28	0.26	3.87
GO:0016740	transferase activity	F	3.43E-04	2.23E-04	363	20.29	1795	16.67	1.22
GO:0008289	lipid binding	F	5.99E-03	4.19E-03	41	2.29	146	1.36	1.69
GO functional analysis of proteins by compared to those in Arabidopsis genome									
GO:0051716	cellular response to stimulus	P	0	0	667	37.28	1227	4.66	8.00
GO:0050794	regulation of cellular process	P	0	0	667	37.28	1227	4.66	8.00
GO:0007165	signal transduction	P	0	0	667	37.28	1227	4.66	8.00
GO:0023052	signaling	P	0	0	678	37.90	1307	4.96	7.63
GO:0044700	single organism signaling	P	0	0	678	37.90	1307	4.96	7.63
GO:0050789	regulation of biological process	P	0	0	736	41.14	1619	6.15	6.69
GO:0050896	response to stimulus	P	0	0	1247	69.70	4926	18.71	3.73
GO:0044699	single-organism process	P	0	0	1352	75.57	6974	26.49	2.85
GO:0007154	cell communication	P	0	0	718	40.13	1656	6.29	6.38
GO:0065007	biological regulation	P	0	0	768	42.93	1876	7.13	6.02
GO:0044763	single-organism cellular process	P	0	0	1100	61.49	4268	16.21	3.79
GO:0009987	cellular process	P	0	0	1681	93.96	12722	48.32	1.94
GO:0009719	response to endogenous stimulus	P	1.76E-300	1.28E-301	579	32.36	1034	3.93	8.24
GO:0043170	macromolecule metabolic process	P	6.71E-269	5.21E-270	1168	65.29	6420	24.38	2.68
GO:0044238	primary metabolic process	P	3.95E-263	3.26E-264	1431	79.99	10135	38.49	2.08
GO:0071704	organic substance metabolic process	P	1.79E-262	1.57E-263	1434	80.16	10199	38.74	2.07
GO:0006950	response to stress	P	3.22E-262	2.97E-263	847	47.34	3231	12.27	3.86
GO:0044260	cellular macromolecule metabolic process	P	2.24E-258	2.17E-259	1058	59.14	5341	20.29	2.92
GO:0044237	cellular metabolic process	P	1.37E-255	1.40E-256	1243	69.48	7592	28.84	2.41
GO:0008152	metabolic process	P	7.13E-245	7.62E-246	1514	84.63	11932	45.32	1.87
GO:0009628	response to abiotic stimulus	P	2.71E-240	3.02E-241	658	36.78	1975	7.50	4.90
GO:0090304	nucleic acid metabolic process	P	2.47E-207	2.87E-208	673	37.62	2435	9.25	4.07
GO:0032502	developmental process	P	9.05E-207	1.10E-207	763	42.65	3200	12.15	3.51
GO:0044707	single-multicellular organism process	P	1.50E-202	1.89E-203	746	41.70	3107	11.80	3.53
GO:0032501	multicellular organismal process	P	1.73E-201	2.26E-202	749	41.87	3148	11.96	3.50
GO:0007275	multicellular organismal development	P	1.52E-200	2.07E-201	735	41.08	3038	11.54	3.56
GO:0044767	single-organism developmental process	P	4.90E-200	6.90E-201	739	41.31	3080	11.70	3.53
GO:0009058	biosynthetic process	P	8.50E-187	1.24E-187	1068	59.70	6751	25.64	2.33
GO:0006807	nitrogen compound metabolic process	P	5.94E-179	8.94E-180	880	49.19	4774	18.13	2.71
GO:0044271	cellular nitrogen compound biosynthetic process	P	7.52E-179	1.42E-179	572	31.97	1979	7.52	4.25
GO:0019438	aromatic compound biosynthetic process	P	7.52E-179	1.42E-179	572	31.97	1979	7.52	4.25
GO:0006350	transcription, DNA-templated	P	7.52E-179	1.42E-179	572	31.97	1979	7.52	4.25
GO:0032774	RNA biosynthetic process	P	7.52E-179	1.42E-179	572	31.97	1979	7.52	4.25
GO:1901362	organic cyclic compound biosynthetic process	P	7.52E-179	1.42E-179	572	31.97	1979	7.52	4.25
GO:0016070	RNA metabolic process	P	7.52E-179	1.42E-179	572	31.97	1979	7.52	4.25

GO:0034654	nucleobase-containing compound biosynthetic process	P	7.52E-179	1.42E-179	572	31.97	1979	7.52	4.25
GO:0018130	heterocycle biosynthetic process	P	7.52E-179	1.42E-179	572	31.97	1979	7.52	4.25
GO:1901360	organic cyclic compound metabolic process	P	1.14E-175	2.43E-176	791	44.21	3929	14.92	2.96
GO:0046483	heterocycle metabolic process	P	1.14E-175	2.43E-176	791	44.21	3929	14.92	2.96
GO:0006139	nucleobase-containing compound metabolic process	P	1.14E-175	2.43E-176	791	44.21	3929	14.92	2.96
GO:0006725	cellular aromatic compound metabolic process	P	1.14E-175	2.43E-176	791	44.21	3929	14.92	2.96
GO:0034641	cellular nitrogen compound metabolic process	P	1.14E-175	2.43E-176	791	44.21	3929	14.92	2.96
GO:0036211	protein modification process	P	4.53E-175	1.03E-175	592	33.09	2178	8.27	4.00
GO:0043412	macromolecule modification	P	4.53E-175	1.03E-175	592	33.09	2178	8.27	4.00
GO:0006464	cellular protein modification process	P	4.53E-175	1.03E-175	592	33.09	2178	8.27	4.00
GO:0009791	post-embryonic development	P	5.34E-170	1.24E-170	517	28.90	1671	6.35	4.55
GO:0009607	response to biotic stimulus	P	5.76E-148	1.45E-148	424	23.70	1250	4.75	4.99
GO:0048856	anatomical structure development	P	8.48E-131	2.18E-131	509	28.45	2081	7.90	3.60
GO:0019538	protein metabolic process	P	2.71E-123	7.10E-124	740	41.36	4382	16.64	2.49
GO:0010467	gene expression	P	4.29E-117	1.15E-117	621	34.71	3304	12.55	2.77
GO:0016043	cellular component organization	P	5.64E-116	1.56E-116	561	31.36	2760	10.48	2.99
GO:0071840	cellular component organization or biogenesis	P	5.64E-116	1.56E-116	561	31.36	2760	10.48	2.99
GO:1901576	organic substance biosynthetic process	P	1.57E-112	4.65E-113	593	33.15	3121	11.85	2.80
GO:0044249	cellular biosynthetic process	P	1.57E-112	4.65E-113	593	33.15	3121	11.85	2.80
GO:0009059	macromolecule biosynthetic process	P	1.57E-112	4.65E-113	593	33.15	3121	11.85	2.80
GO:0034645	cellular macromolecule biosynthetic process	P	1.57E-112	4.65E-113	593	33.15	3121	11.85	2.80
GO:0044267	cellular protein metabolic process	P	1.76E-105	5.31E-106	603	33.71	3354	12.74	2.65
GO:0000003	reproduction	P	3.28E-102	1.02E-102	430	24.04	1842	7.00	3.44
GO:0016265	death	P	5.74E-98	1.87E-98	191	10.68	309	1.17	9.10
GO:0008219	cell death	P	5.74E-98	1.87E-98	191	10.68	309	1.17	9.10
GO:0009653	anatomical structure morphogenesis	P	1.73E-94	5.70E-95	364	20.35	1425	5.41	3.76
GO:0009605	response to external stimulus	P	3.69E-92	1.25E-92	274	15.32	812	3.08	4.97
GO:0009908	flower development	P	3.94E-79	1.59E-79	238	13.30	710	2.70	4.93
GO:0090567	reproductive shoot system development	P	3.94E-79	1.59E-79	238	13.30	710	2.70	4.93
GO:0048367	shoot system development	P	3.94E-79	1.59E-79	238	13.30	710	2.70	4.93
GO:0061458	reproductive system development	P	7.41E-79	3.16E-79	238	13.30	713	2.71	4.91
GO:0044702	single organism reproductive process	P	7.41E-79	3.16E-79	238	13.30	713	2.71	4.91
GO:0048608	reproductive structure development	P	7.41E-79	3.16E-79	238	13.30	713	2.71	4.91
GO:0003006	developmental process involved in reproduction	P	7.41E-79	3.16E-79	238	13.30	713	2.71	4.91
GO:0048731	system development	P	7.41E-79	3.16E-79	238	13.30	713	2.71	4.91
GO:0007049	cell cycle	P	3.59E-76	1.55E-76	214	11.96	588	2.23	5.36
GO:0022414	reproductive process	P	8.60E-71	3.76E-71	270	15.09	1029	3.91	3.86
GO:0030154	cell differentiation	P	6.94E-56	3.10E-56	226	12.63	901	3.42	3.69
GO:0048869	cellular developmental process	P	6.94E-56	3.10E-56	226	12.63	901	3.42	3.69
GO:0006810	transport	P	7.18E-54	3.31E-54	459	25.66	3093	11.75	2.18
GO:0051234	establishment of localization	P	7.18E-54	3.31E-54	459	25.66	3093	11.75	2.18
GO:0051179	localization	P	7.18E-54	3.31E-54	459	25.66	3093	11.75	2.18
GO:0040007	growth	P	4.01E-51	1.87E-51	197	11.01	750	2.85	3.87
GO:0009056	catabolic process	P	3.07E-48	1.44E-48	358	20.01	2212	8.40	2.38
GO:0006259	DNA metabolic process	P	5.08E-40	2.42E-40	160	8.94	628	2.39	3.75
GO:0016049	cell growth	P	1.45E-37	6.97E-38	147	8.22	566	2.15	3.82
GO:0044710	single-organism metabolic process	P	1.24E-36	6.00E-37	387	21.63	2842	10.79	2.00
GO:0019748	secondary metabolic process	P	1.34E-32	7.10E-33	196	10.96	1048	3.98	2.75
GO:0009790	embryo development	P	5.86E-31	3.13E-31	127	7.10	511	1.94	3.66
GO:0005975	carbohydrate metabolic process	P	3.86E-24	2.19E-24	267	14.92	1978	7.51	1.99
GO:0006629	lipid metabolic process	P	1.13E-19	6.78E-20	213	11.91	1559	5.92	2.01
GO:0010468	regulation of gene expression	P	9.42E-19	5.85E-19	90	5.03	417	1.58	3.18
GO:0019222	regulation of metabolic process	P	9.42E-19	5.85E-19	90	5.03	417	1.58	3.18
GO:0040029	regulation of gene expression, epigenetic	P	9.42E-19	5.85E-19	90	5.03	417	1.58	3.18
GO:0060255	regulation of macromolecule metabolic process	P	9.42E-19	5.85E-19	90	5.03	417	1.58	3.18
GO:0044281	small molecule metabolic process	P	3.06E-18	1.99E-18	169	9.45	1153	4.38	2.16
GO:0043436	oxoacid metabolic process	P	3.06E-18	1.99E-18	169	9.45	1153	4.38	2.16
GO:1901564	organonitrogen compound metabolic process	P	3.06E-18	1.99E-18	169	9.45	1153	4.38	2.16
GO:0006082	organic acid metabolic process	P	3.06E-18	1.99E-18	169	9.45	1153	4.38	2.16
GO:0006519	cellular amino acid metabolic process	P	3.06E-18	1.99E-18	169	9.45	1153	4.38	2.16
GO:0019752	carboxylic acid metabolic process	P	3.06E-18	1.99E-18	169	9.45	1153	4.38	2.16
GO:0006091	generation of precursor metabolites and energy	P	1.21E-16	8.21E-17	99	5.53	530	2.01	2.75
GO:0009606	tropism	P	2.26E-13	1.60E-13	40	2.24	126	0.48	4.67
GO:0009991	response to extracellular stimulus	P	8.30E-13	5.92E-13	67	3.75	338	1.28	2.92
GO:0015979	photosynthesis	P	8.63E-11	6.24E-11	58	3.24	302	1.15	2.83
GO:0065008	regulation of biological quality	P	8.56E-08	6.56E-08	48	2.68	279	1.06	2.53
GO:0019725	cellular homeostasis	P	8.56E-08	6.56E-08	48	2.68	279	1.06	2.53
GO:0042592	homeostatic process	P	8.56E-08	6.56E-08	48	2.68	279	1.06	2.53
GO:0009838	abscission	P	1.82E-07	1.41E-07	16	0.89	38	0.14	6.20
GO:0007267	cell-cell signaling	P	1.51E-04	1.20E-04	18	1.01	88	0.33	3.01
GO:0044706	multi-multicellular organism process	P	6.36E-03	5.31E-03	38	2.12	338	1.28	1.65
GO:0044703	multi-organism reproductive process	P	6.36E-03	5.31E-03	38	2.12	338	1.28	1.65
GO:0051704	multi-organism process	P	6.36E-03	5.31E-03	38	2.12	338	1.28	1.65
GO:0009856	pollination	P	6.36E-03	5.31E-03	38	2.12	338	1.28	1.65
GO:0005515	protein binding	F	0	0	1123	62.77	1574	5.98	10.50
GO:0005488	binding	F	0	0	1572	87.87	9375	35.61	2.47
GO:0003700	sequence-specific DNA binding transcription factor activity	F	1.02E-148	2.53E-149	426	23.81	1256	4.77	4.99
GO:0001071	nucleic acid binding transcription factor activity	F	1.02E-148	2.53E-149	426	23.81	1256	4.77	4.99

GO:0003677	DNA binding	F	3.94E-94	1.32E-94	383	21.41	1579	6.00	3.57
GO:0097159	organic cyclic compound binding	F	4.56E-92	1.59E-92	802	44.83	5839	22.18	2.02
GO:1901363	heterocyclic compound binding	F	4.56E-92	1.59E-92	802	44.83	5839	22.18	2.02
GO:0016301	kinase activity	F	5.24E-84	1.88E-84	297	16.60	1059	4.02	4.13
GO:0016772	transferase activity, transferring phosphorus-containing groups	F	5.24E-84	1.88E-84	297	16.60	1059	4.02	4.13
GO:0003676	nucleic acid binding	F	8.01E-36	3.93E-36	431	24.09	3357	12.75	1.89
GO:0016740	transferase activity	F	6.11E-35	3.10E-35	363	20.29	2640	10.03	2.02
GO:0004871	signal transducer activity	F	6.11E-35	3.12E-35	72	4.02	129	0.49	8.21
GO:0060089	molecular transducer activity	F	6.11E-35	3.12E-35	72	4.02	129	0.49	8.21
GO:0036094	small molecule binding	F	2.70E-33	1.41E-33	394	22.02	3035	11.53	1.91
GO:1901265	nucleoside phosphate binding	F	2.70E-33	1.41E-33	394	22.02	3035	11.53	1.91
GO:0000166	nucleotide binding	F	2.70E-33	1.41E-33	394	22.02	3035	11.53	1.91
GO:0030234	enzyme regulator activity	F	5.69E-23	3.31E-23	82	4.58	294	1.12	4.10
GO:0004872	receptor activity	F	5.04E-22	2.96E-22	40	2.24	60	0.23	9.81
GO:0030528	transcription regulator activity	F	5.25E-22	3.11E-22	37	2.07	48	0.18	11.34
GO:0003824	catalytic activity	F	2.28E-21	1.36E-21	741	41.42	7993	30.36	1.36
GO:0008289	lipid binding	F	2.02E-07	1.57E-07	41	2.29	225	0.85	2.68
GO:0005102	receptor binding	F	2.60E-07	2.04E-07	18	1.01	51	0.19	5.19
GO:0016787	hydrolase activity	F	2.80E-02	2.35E-02	226	12.63	2865	10.88	1.16