

Table S1. GO Terms in biological process significantly enriched in each module found by TopGO analysis according to different tests.

The column Annotated and Expected represent number of annotated genes and those of significant genes.

The column Expected represents the expected number of interesting genes mapped to the GO term if the interesting genes were randomly distributed over all GO terms (Alexa et al. 2006).

The columns, "classicFisher", "classicKS", "elimKS" and "wight" represent the p-values on the GO terms returned by each test statistics used in the TopGO package.

Module ID	P_value(classicFisher) <1e-5	GOID	GO Term	Annotate d	Significan t	Expected	Rank in classic	classicFisher	classicKS	elimKS	weight
module_113	6.00E-06	GO:0006413	translational initiation	44	3	0.04	1	6.00E-06	0.007	0.00033	6.00E-06
module_118	5.70E-08	GO:0042550	photosystem I stabilization	3	2	0	1	5.70E-08	1	5.70E-08	5.70E-08
module_118	1.10E-07	GO:0019375	galactolipid biosynthetic process	4	2	0	2	1.10E-07	1	1.10E-07	1.10E-07
module_118	7.70E-06	GO:0006643	membrane lipid metabolic process	29	2	0.01	10	7.70E-06	0.77504	1	1
module_118	1.00E-06	GO:0006664	glycolipid metabolic process	11	2	0	5	1.00E-06	1	1	1
module_118	6.80E-07	GO:0009247	glycolipid biosynthetic process	9	2	0	4	6.80E-07	0.92575	1	1
module_118	2.60E-06	GO:0010109	regulation of photosynthesis	17	2	0	8	2.60E-06	0.99932	1	1
module_118	1.10E-07	GO:0019374	galactolipid metabolic process	4	2	0	3	1.10E-07	1	1	1
module_118	1.30E-06	GO:0042548	regulation of photosynthesis, light reac...	12	2	0	6	1.30E-06	1	1	1
module_118	1.30E-06	GO:0043467	regulation of generation of precursor me...	12	2	0	7	1.30E-06	1	1	1
module_118	2.60E-06	GO:0046467	membrane lipid biosynthetic process	17	2	0	9	2.60E-06	0.94877	1	1
module_12	1.10E-07	GO:0006556	S-adenosylmethionine biosynthetic proces...	4	2	0	1	1.10E-07	0.28511	1.10E-07	1.10E-07
module_12	9.40E-06	GO:0000097	sulfur amino acid biosynthetic process	32	2	0.01	6	9.40E-06	0.86312	1	1
module_12	7.20E-06	GO:0009119	ribonucleoside metabolic process	28	2	0.01	5	7.20E-06	0.18336	1	1
module_12	4.00E-06	GO:0042278	purine nucleoside metabolic process	21	2	0	3	4.00E-06	0.06187	1	1
module_12	4.00E-06	GO:0046128	purine ribonucleoside metabolic process	21	2	0	4	4.00E-06	0.06187	1	1
module_12	1.90E-07	GO:0046500	S-adenosylmethionine metabolic process	5	2	0	2	1.90E-07	0.41626	1	1
module_125	4.20E-10	GO:0009853	photorespiration	26	5	0.04	1	4.20E-10	1	4.20E-10	4.20E-10
module_125	6.80E-09	GO:0043094	cellular metabolic compound salvage	44	5	0.07	2	6.80E-09	0.96117	1	1
module_128	5.40E-07	GO:0006878	cellular copper ion homeostasis	10	3	0.02	1	5.40E-07	0.88344	5.40E-07	5.40E-07
module_128	5.90E-06	GO:0030005	cellular di-, tri-valent inorganic catio...	21	3	0.04	3	5.90E-06	0.45763	1	1
module_128	7.40E-07	GO:0055070	copper ion homeostasis	11	3	0.02	2	7.40E-07	0.96133	1	1
module_141	7.30E-06	GO:0006468	protein amino acid phosphorylation	609	6	0.59	1	7.30E-06	0.47199	7.30E-06	7.30E-06
module_142	1.10E-10	GO:0006656	phosphatidylcholine biosynthetic process	6	3	0	1	1.10E-10	0.74643	1.10E-10	1.10E-10
module_142	2.10E-07	GO:0006576	cellular biogenic amine metabolic proces...	62	3	0.02	9	2.10E-07	0.64382	1	1
module_142	3.30E-07	GO:0006644	phospholipid metabolic process	72	3	0.02	10	3.30E-07	0.27062	1	1
module_142	4.00E-08	GO:0006650	glycerophospholipid metabolic process	36	3	0.01	6	4.00E-08	0.62325	1	1
module_142	7.90E-08	GO:0008654	phospholipid biosynthetic process	45	3	0.01	8	7.90E-08	0.22598	1	1
module_142	4.90E-07	GO:0019637	organophosphate metabolic process	82	3	0.02	11	4.90E-07	0.13516	1	1
module_142	2.50E-09	GO:0042439	ethanolamine and derivative metabolic pr...	15	3	0	3	2.50E-09	0.78653	1	1
module_142	7.40E-09	GO:0045017	glycerolipid biosynthetic process	21	3	0.01	5	7.40E-09	0.63406	1	1
module_142	9.20E-10	GO:0046470	phosphatidylcholine metabolic process	11	3	0	2	9.20E-10	0.46535	1	1
module_142	2.50E-09	GO:0046474	glycerophospholipid biosynthetic process	15	3	0	4	2.50E-09	0.90877	1	1
module_142	6.80E-08	GO:0046486	glycerolipid metabolic process	43	3	0.01	7	6.80E-08	0.31831	1	1
module_167	6.50E-14	GO:0006334	nucleosome assembly	81	8	0.12	1	6.50E-14	0.24956	6.50E-14	6.50E-14
module_167	7.90E-14	GO:0006323	DNA packaging	83	8	0.12	4	7.90E-14	0.22698	1	1
module_167	9.60E-12	GO:0006325	chromatin organization	149	8	0.22	8	9.60E-12	0.28623	1	1
module_167	5.10E-13	GO:0006333	chromatin assembly or disassembly	104	8	0.15	7	5.10E-13	0.098	1	1
module_167	4.30E-08	GO:0006996	organelle organization	428	8	0.63	15	4.30E-08	0.20531	1	1
module_167	2.20E-07	GO:0016043	cellular component organization	762	9	1.11	17	2.20E-07	0.14767	0.384	1
module_167	2.60E-09	GO:0022607	cellular component assembly	300	8	0.44	14	2.60E-09	0.17592	1	1
module_167	7.20E-14	GO:0031497	chromatin assembly	82	8	0.12	3	7.20E-14	0.28547	1	1
module_167	1.40E-10	GO:0034621	cellular macromolecular complex subunit ...	207	8	0.3	11	1.40E-10	0.41022	1	1
module_167	7.80E-11	GO:0034622	cellular macromolecular complex assembly	193	8	0.28	10	7.80E-11	0.25527	1	1
module_167	6.50E-14	GO:0034728	nucleosome organization	81	8	0.12	2	6.50E-14	0.24956	1	1
module_167	1.90E-09	GO:0043933	macromolecular complex subunit organizat...	289	8	0.42	13	1.90E-09	0.27	1	1
module_167	1.30E-07	GO:0044085	cellular component biogenesis	496	8	0.72	16	1.30E-07	0.46086	1	1
module_167	2.70E-11	GO:0051276	chromosome organization	169	8	0.25	9	2.70E-11	0.30852	1	1
module_167	1.30E-09	GO:0065003	macromolecular complex assembly	275	8	0.4	12	1.30E-09	0.15484	1	1
module_167	7.90E-14	GO:0065004	protein-DNA complex assembly	83	8	0.12	5	7.90E-14	0.32381	1	1
module_167	3.70E-13	GO:0071103	DNA conformation change	100	8	0.15	6	3.70E-13	0.17799	1	1
module_168	9.60E-06	GO:0007049	cell cycle	105	4	0.14	1	9.60E-06	0.69464	0.09637	1
module_170	1.50E-08	GO:0019253	reductive pentose-phosphate cycle	7	4	0.03	1	1.50E-08	0.95879	1.50E-08	1.50E-08
module_170	1.30E-06	GO:0015979	photosynthesis	175	8	0.82	5	1.30E-06	0.63278	0.00566	0.09569
module_170	9.60E-07	GO:0015977	carbon fixation	17	4	0.08	3	9.60E-07	0.99999	1	1
module_170	5.20E-08	GO:0019685	photosynthesis, dark reaction	9	4	0.04	2	5.20E-08	0.99046	1	1
module_170	9.60E-07	GO:0071704	organic substance metabolic process	17	4	0.08	4	9.60E-07	0.99999	1	1
module_180	1.00E-07	GO:0006084	acetyl-CoA metabolic process	32	4	0.05	1	1.00E-07	0.83085	1	1
module_180	6.70E-06	GO:0015980	energy derivation by oxidation of organi...	89	4	0.13	3	6.70E-06	0.7401	0.07032	1
module_180	2.10E-06	GO:0045333	cellular respiration	67	4	0.1	2	2.10E-06	0.8114	0.04591	1
module_202	3.40E-07	GO:0033014	tetrapyrrole biosynthetic process	46	4	0.06	1	3.40E-07	0.16705	0.00029	3.40E-07
module_202	8.80E-07	GO:0033013	tetrapyrrole metabolic process	58	4	0.08	2	8.80E-07	0.55222	1	1
module_222	5.10E-09	GO:0006364	rRNA processing	35	5	0.07	2	5.10E-09	0.99999	2.20E-07	2.20E-07
module_222	1.60E-09	GO:0006396	RNA processing	197	8	0.38	1	1.60E-09	0.99261	1	1
module_222	5.10E-09	GO:0016072	rRNA metabolic process	35	5	0.07	3	5.10E-09	0.99999	1	1
module_222	9.50E-06	GO:0022613	ribonucleoprotein complex biogenesis	155	5	0.3	7	9.50E-06	0.99995	1	1
module_222	2.10E-07	GO:0034470	ncRNA processing	72	5	0.14	4	2.10E-07	0.96828	1	1
module_222	5.60E-06	GO:0034660	ncRNA metabolic process	139	5	0.27	5	5.60E-06	0.8343	1	1
module_222	9.20E-06	GO:0042254	ribosome biogenesis	154	5	0.3	6	9.20E-06	0.99995	1	1
module_236	3.20E-06	GO:0009411	response to UV	69	4	0.11	9	3.20E-06	0.99662	0.02764	3.20E-06
module_236	1.50E-09	GO:0009698	phenylpropanoid metabolic process	153	7	0.24	1	1.50E-09	0.97213	0.00385	4.70E-06
module_236	8.70E-06	GO:0006519	cellular amino acid and derivative metab...	546	7	0.85	11	8.70E-06	0.77454	1	1
module_236	5.10E-08	GO:0006575	cellular amino acid derivative metabolic...	255	7	0.4	4	5.10E-08	0.61246	1	1
module_236	3.50E-09	GO:0006725	cellular aromatic compound metabolic pro...	286	8	0.45	2	3.50E-09	0.97548	1	1
module_236	1.10E-06	GO:0009699	phenylpropanoid biosynthetic process	128	5	0.2	7	1.10E-06	0.8877	0.0782	1
module_236	3.60E-08	GO:0009812	flavonoid metabolic process	65	5	0.1	3	3.60E-08	0.97765	0.00703	1
module_236	1.70E-06	GO:0009813	flavonoid biosynthetic process	59	4	0.09	8	1.70E-06	0.9653	0.00196	1
module_236	2.90E-07	GO:0019438	aromatic compound biosynthetic process	194	6	0.3	6	2.90E-07	0.99665	0.13349	1
module_236	6.00E-08	GO:0019748	secondary metabolic process	261	7	0.41	5	6.00E-08	0.82491	1	1
module_236	8.00E-06	GO:0042398	cellular amino acid derivative biosynthe...	192	5	0.3	10	8.00E-06	0.66457	0.14569	1
module_237	1.70E-09	GO:0006412	translation	576	7	0.39	1	1.70E-09	0.19391	1.70E-09	1.70E-09
module_237	2.30E-06	GO:0009059	macromolecule biosynthetic process	1610	7	1.1	4	2.30E-06	0.14067	1	1
module_237	1.40E-06	GO:0010467	gene expression	1498	7	1.02	2	1.40E-06	0.31593	1	1
module_237	2.30E-06	GO:0034645	cellular macromolecule biosynthetic proc...	1605	7	1.09	3	2.30E-06	0.15373	1	1
module_249	1.10E-08	GO:0006558	L-phenylalanine metabolic process	19	4	0.03	2	1.10E-08	1	1	1.10E-08
module_249	1.80E-06	GO:0009698	phenylpropanoid metabolic process	153	5	0.22	7	1.80E-06	0.99428	3.90E-05	3.90E-05
module_249	1.80E-07	GO:0019438	aromatic compound biosynthetic process	194	6	0.28	4	1.80E-07	0.99665	0.00113	6.90E-05
module_249	2.80E-07	GO:0006519	cellular amino acid and derivative metab...	546	8	0.8	5	2.80E-07	0.78633	0.266	1
module_249	1.80E-09	GO:0006725	cellular aromatic compound metabolic pro...	286	8	0.42	1	1.80E-09	0.97548	1	1
module_249	2.90E-08	GO:0009072	aromatic amino acid family metabolic pro...	67	5	0.1	3	2.90E-08	0.98401	0.05036	1
module_249	3.00E-06	GO:0043648	dicarboxylic acid metabolic process	73	4	0.11	8	3.00E-06	0.88944	0.00313	1
module_249	1.40E-06	GO:0044281	small molecule metabolic process	1277	10	1.87	6	1.40E-06	0.91529	1	1
module_259	3.90E-12	GO:0006511	ubiquitin-dependent protein catabolic pr...	182	8	0.21	1	3.90E-12	0.4383	3.90E-12	3.90E-12
module_259	1.90E-08	GO:0006508	proteolysis	527	8	0.62	10	1.90E-08	0.49625	1	1
module_259	1.20E-07	GO:0009056	catabolic process	664	8	0.78	11	1.20E-07	0.95544	1	1
module_259	7.30E-11	GO:0009057	macromolecule catabolic process	262	8	0.31	8	7.30E-11	0.75168	1	1
module_259	4.10E-12	GO:0019941	modification-dependent protein catabolic...	183	8	0.21	2	4.10E-12	0.49042	1	1
module_259	9.10E-12	GO:0030163	protein catabolic process	202	8	0.24	6	9.10E-12	0.34961	1	1
module_259	4.10E-12	GO:0043632	modification-dependent macromolecule cat...	183	8	0.21	3	4.10E-12	0.49042	1	1
module_259	5.50E-09	GO:0044									

module_259	9.40E-12	GO:0044265	cellular macromolecule catabolic process	203	8	0.24	7	9.40E-12	0.49969	1	1
module_259	4.30E-12	GO:0051603	proteolysis involved in cellular protein...	184	8	0.22	4	4.30E-12	0.4565	1	1
module_261	6.00E-06	GO:0046865	terpenoid transport	6	2	0	1	6.00E-06	0.81549	6.00E-06	6.00E-06
module_261	6.00E-06	GO:0046864	isoprenoid transport	6	2	0	2	6.00E-06	0.81549	1	1
module_263	2.60E-06	GO:0048700	acquisition of desiccation tolerance	3	2	0	1	2.60E-06	1	2.60E-06	2.60E-06
module_265	3.00E-08	GO:0006633	fatty acid biosynthetic process	92	4	0.04	1	3.00E-08	0.57779	3.00E-08	3.00E-08
module_265	2.10E-07	GO:0006631	fatty acid metabolic process	148	4	0.07	2	2.10E-07	0.16502	1	1
module_265	1.20E-06	GO:0008610	lipid biosynthetic process	229	4	0.11	3	1.20E-06	0.35523	1	1
module_265	2.60E-06	GO:0016053	organic acid biosynthetic process	279	4	0.14	5	2.60E-06	0.93746	1	1
module_265	2.20E-06	GO:0032787	monocarboxylic acid metabolic process	267	4	0.13	4	2.20E-06	0.94051	1	1
module_265	4.00E-06	GO:0044255	cellular lipid metabolic process	311	4	0.15	7	4.00E-06	0.20016	1	1
module_265	2.60E-06	GO:0046394	carboxylic acid biosynthetic process	279	4	0.14	6	2.60E-06	0.93746	1	1
module_266	8.00E-06	GO:0006355	regulation of transcription, DNA-depende...	369	4	0.18	1	8.00E-06	0.89439	8.00E-06	8.00E-06
module_266	8.60E-06	GO:0051252	regulation of RNA metabolic process	376	4	0.18	2	8.60E-06	0.92283	1	1
module_271	6.00E-06	GO:0018401	peptidyl-proline hydroxylation to 4-hydr...	7	2	0	1	6.00E-06	1	6.00E-06	6.00E-06
module_271	6.00E-06	GO:0018208	peptidyl-proline modification	7	2	0	2	6.00E-06	1	1	1
module_271	6.00E-06	GO:0019471	4-hydroxyproline metabolic process	7	2	0	3	6.00E-06	1	1	1
module_271	6.00E-06	GO:0019511	peptidyl-proline hydroxylation	7	2	0	4	6.00E-06	1	1	1
module_272	9.00E-06	GO:0006096	glycolysis	80	3	0.05	1	9.00E-06	0.82105	9.00E-06	9.00E-06
module_277	1.10E-14	GO:0009408	response to heat	107	7	0.07	1	1.10E-14	0.84791	1.10E-14	1.10E-14
module_277	1.40E-06	GO:0042542	response to hydrogen peroxide	36	3	0.02	5	1.40E-06	0.99734	1.40E-06	1.40E-06
module_277	1.90E-06	GO:0009644	response to high light intensity	40	3	0.03	6	1.90E-06	0.95189	1.90E-06	1.90E-06
module_277	5.50E-06	GO:0006457	protein folding	208	4	0.14	8	5.50E-06	0.96837	5.50E-06	5.50E-06
module_277	5.60E-06	GO:0000302	response to reactive oxygen species	57	3	0.04	9	5.60E-06	0.84566	1	1
module_277	1.00E-06	GO:0006950	response to stress	1432	7	0.98	4	1.00E-06	0.46267	1	1
module_277	3.70E-11	GO:0009266	response to temperature stimulus	335	7	0.23	2	3.70E-11	0.64964	1	1
module_277	3.90E-08	GO:0009628	response to abiotic stimulus	899	7	0.61	3	3.90E-08	0.84806	1	1
module_277	8.30E-06	GO:0009642	response to light intensity	65	3	0.04	10	8.30E-06	0.92282	1	1
module_277	3.00E-06	GO:0010035	response to inorganic substance	448	5	0.31	7	3.00E-06	0.83165	1	1
module_285	1.30E-08	GO:0006412	translation	576	7	0.45	1	1.30E-08	0.25234	1.30E-08	1.30E-08
module_285	9.70E-06	GO:0010467	gene expression	1498	7	1.17	2	9.70E-06	0.38433	1	1
module_286	1.50E-22	GO:0006334	nucleosome assembly	81	12	0.13	1	1.50E-22	0.4731	1.50E-22	1.50E-22
module_286	2.00E-22	GO:0006323	DNA packaging	83	12	0.14	4	2.00E-22	0.43804	1	1
module_286	3.20E-19	GO:0006325	chromatin organization	149	12	0.25	8	3.20E-19	0.45415	1	1
module_286	3.60E-21	GO:0006333	chromatin assembly or disassembly	104	12	0.17	7	3.60E-21	0.2106	1	1
module_286	1.20E-13	GO:0006996	organelle organization	428	12	0.71	15	1.20E-13	0.32683	1	1
module_286	3.40E-12	GO:0016043	cellular component organization	762	13	1.26	17	3.40E-12	0.3399	0.2925	1
module_286	1.70E-15	GO:0022607	cellular component assembly	300	12	0.5	14	1.70E-15	0.48637	1	1
module_286	1.70E-22	GO:0031497	chromatin assembly	82	12	0.14	3	1.70E-22	0.52009	1	1
module_286	1.90E-17	GO:0034621	cellular macromolecular complex subunit ...	207	12	0.34	11	1.90E-17	0.68078	1	1
module_286	7.90E-18	GO:0034622	cellular macromolecular complex assembly	193	12	0.32	10	7.90E-18	0.58741	1	1
module_286	1.50E-22	GO:0034728	nucleosome organization	81	12	0.13	2	1.50E-22	0.4731	1	1
module_286	1.10E-15	GO:0043933	macromolecular complex subunit organizat...	289	12	0.48	13	1.10E-15	0.57566	1	1
module_286	7.00E-13	GO:0044085	cellular component biogenesis	496	12	0.82	16	7.00E-13	0.75816	1	1
module_286	1.50E-18	GO:0051276	chromosome organization	169	12	0.28	9	1.50E-18	0.47649	1	1
module_286	5.90E-16	GO:0065003	macromolecular complex assembly	275	12	0.46	12	5.90E-16	0.49443	1	1
module_286	2.00E-22	GO:0065004	protein-DNA complex assembly	83	12	0.14	5	2.00E-22	0.56749	1	1
module_286	2.20E-21	GO:0071103	DNA conformation change	100	12	0.17	6	2.20E-21	0.34448	1	1
module_290	< 1e-30	GO:0006412	translation	576	53	3.59	1	< 1e-30	0.95546	< 1e-30	< 1e-30
module_290	1.90E-14	GO:0042254	ribosome biogenesis	154	15	0.96	11	1.90E-14	0.99995	1.90E-14	1.90E-14
module_290	< 1e-30	GO:0034645	cellular macromolecule biosynthetic proc...	1605	55	10	3	< 1e-30	0.61303	0.329	0.5183
module_290	< 1e-30	GO:0010467	gene expression	1498	55	9.34	2	< 1e-30	0.86828	0.2819	0.5937
module_290	< 1e-30	GO:0009059	macromolecule biosynthetic process	1610	55	10.04	4	< 1e-30	0.58445	0.3312	0.6435
module_290	2.30E-06	GO:0006414	translational elongation	35	5	0.22	17	2.30E-06	0.99962	2.30E-06	1
module_290	4.70E-06	GO:0008152	metabolic process	6134	55	38.24	18	4.70E-06	0.6545	0.9987	1
module_290	1.20E-24	GO:0009058	biosynthetic process	2570	55	16.02	7	1.20E-24	0.76134	0.6947	1
module_290	4.40E-07	GO:0009987	cellular process	6016	56	37.5	16	4.40E-07	0.63214	0.9875	1
module_290	1.80E-24	GO:0019538	protein metabolic process	2320	53	14.46	8	1.80E-24	0.75974	1	1
module_290	2.10E-14	GO:0022613	ribonucleoprotein complex biogenesis	155	15	0.97	12	2.10E-14	0.99995	1	1
module_290	2.00E-17	GO:0043170	macromolecule metabolic process	3543	55	22.09	10	2.00E-17	0.9834	0.8951	1
module_290	2.60E-07	GO:0044085	cellular component biogenesis	496	15	3.09	15	2.60E-07	0.64819	1	1
module_290	6.10E-11	GO:0044237	cellular metabolic process	4791	55	29.87	13	6.10E-11	0.73795	0.9823	1
module_290	1.90E-10	GO:0044238	primary metabolic process	4907	55	30.59	14	1.90E-10	0.78822	0.9854	1
module_290	1.40E-25	GO:0044249	cellular biosynthetic process	2467	55	15.38	6	1.40E-25	0.67123	0.6634	1
module_290	5.50E-20	GO:0044260	cellular macromolecule metabolic process	3156	55	19.67	9	5.50E-20	0.9747	0.8344	1
module_290	7.70E-28	GO:0044267	cellular protein metabolic process	1991	53	12.41	5	7.70E-28	0.8444	1	1
module_293	1.20E-08	GO:0006418	tRNA aminoacylation for protein translat...	73	4	0.04	1	1.20E-08	0.71782	1	1.20E-08
module_293	6.30E-08	GO:0048481	ovule development	20	3	0.01	5	6.30E-08	0.9993	6.30E-08	6.30E-08
module_293	4.90E-08	GO:0006399	tRNA metabolic process	104	4	0.05	4	4.90E-08	0.74577	1	1
module_293	1.90E-06	GO:0006431	methionyl-tRNA aminoacylation	5	2	0	11	1.90E-06	1	1.90E-06	1
module_293	6.20E-06	GO:0006520	cellular amino acid metabolic process	346	4	0.17	12	6.20E-06	0.51051	1	1
module_293	1.60E-07	GO:0034660	ncRNA metabolic process	139	4	0.07	8	1.60E-07	0.83546	1	1
module_293	1.20E-08	GO:0043038	amino acid activation	73	4	0.04	2	1.20E-08	0.71782	1	1
module_293	1.20E-08	GO:0043039	tRNA aminoacylation	73	4	0.04	3	1.20E-08	0.71782	1	1
module_293	9.40E-06	GO:0044106	cellular amine metabolic process	384	4	0.19	14	9.40E-06	0.48329	1	1
module_293	1.40E-06	GO:0048437	floral organ development	54	3	0.03	10	1.40E-06	0.99641	1	1
module_293	6.80E-07	GO:0048438	floral whorl development	43	3	0.02	9	6.80E-07	0.99357	1	1
module_293	8.50E-08	GO:0048440	carpel development	22	3	0.01	6	8.50E-08	1	1	1
module_293	8.50E-08	GO:0048467	gynoecium development	22	3	0.01	7	8.50E-08	1	1	1
module_293	8.30E-06	GO:0048569	post-embryonic organ development	98	3	0.05	13	8.30E-06	0.81071	1	1
module_296	8.00E-06	GO:0006552	leucine catabolic process	8	2	0	1	8.00E-06	0.93515	8.00E-06	8.00E-06
module_303	8.90E-21	GO:0009765	photosynthesis, light harvesting	58	12	0.16	3	8.90E-21	0.99918	8.40E-12	8.90E-21
module_303	< 1e-30	GO:0015979	photosynthesis	175	23	0.48	1	< 1e-30	0.88284	6.80E-14	3.70E-15
module_303	6.30E-16	GO:0006091	generation of precursor metabolites and ...	326	15	0.89	4	6.30E-16	0.89169	1	1
module_303	1.30E-11	GO:0009768	photosynthesis, light harvesting in phot...	9	5	0.02	5	1.30E-11	0.98069	1.30E-11	1
module_303	7.10E-23	GO:0019684	photosynthesis, light reaction	115	15	0.31	2	7.10E-23	0.66004	1	1
module_313	2.20E-18	GO:0006412	translation	576	15	0.9	1	2.20E-18	0.32844	2.20E-18	2.20E-18
module_313	3.80E-12	GO:0044267	cellular protein metabolic process	1991	16	3.1	3	3.80E-12	0.35996	0.146	0.146
module_313	1.10E-08	GO:0009058	biosynthetic process	2570	15	4.01	9	1.10E-08	0.45087	1	1
module_313	1.10E-11	GO:0009059	macromolecule biosynthetic process	1610	15	2.51	5	1.10E-11	0.19577	1	1
module_313	3.80E-12	GO:0010467	gene expression	1498	15	2.33	2	3.80E-12	0.4101	1	1
module_313	4.40E-11	GO:0019538	protein metabolic process	2320	16	3.62	6	4.40E-11	0.33173	0.18	1
module_313	1.10E-11	GO:0034645	cellular macromolecule biosynthetic proc...	1605	15	2.5	4	1.10E-11	0.21239	1	1
module_313	4.00E-08	GO:0043170	macromolecule metabolic process	3543	16	5.52	10	4.00E-08	0.81158	0.3062	1
module_313	5.00E-06	GO:0044237	cellular metabolic process	4791	16	7.47	11	5.00E-06	0.48733	0.4349	1
module_313	7.30E-06	GO:0044238	primary metabolic process	4907	16	7.65	12	7.30E-06	0.50049	0.4469	1
module_313	6.20E-09	GO:0044249	cellular biosynthetic process	2467	15	3.84	7	6.20E-09	0.35704	1	1
module_313	6.20E-09	GO:0044260	cellular macromolecule metabolic process	3156	16	4.92	8	6.20E-09	0.79175	0.2662	1
module_315	1.90E-07	GO:0010025	wax biosynthetic process	14	4	0.05	1	1.90E-07	0.76043	1.90E-07	1.90E-07
module_315	1.90E-07	GO:0010166	wax metabolic process	14	4	0.05	2	1.90E-07	0.76043	1	1
module_316	5.10E-06	GO:0016068	type I hypersensitivity	4	2	0	1	5.10E-06	0.9408	5.10E-06	5.10E-06
module_316	5.10E-06	GO									

module_316		5.10E-06	GO:0016064	immunoglobulin mediated immune response	4	2	0	10	5.10E-06	0.9408	1	1
module_316		5.10E-06	GO:0019724	B cell mediated immunity	4	2	0	11	5.10E-06	0.9408	1	1
module_317	< 1e-30		GO:0009769	photosynthesis, light harvesting in phot...	18	13	0.04	1	< 1e-30	1	< 1e-30	< 1e-30
module_317		3.60E-07	GO:0010114	response to red light	29	4	0.06	6	3.60E-07	0.92568	3.60E-07	3.60E-07
module_317		5.50E-07	GO:0010218	response to far red light	32	4	0.07	7	5.50E-07	0.96941	5.50E-07	5.50E-07
module_317		7.90E-07	GO:0009637	response to blue light	35	4	0.07	8	7.90E-07	0.82683	7.90E-07	7.90E-07
module_317	< 1e-30		GO:0009765	photosynthesis, light harvesting	58	16	0.12	2	< 1e-30	0.99086	4.60E-06	4.60E-06
module_317		4.70E-20	GO:0006091	generation of precursor metabolites and ...	326	16	0.7	5	4.70E-20	0.89169	1	1
module_317		1.70E-24	GO:0015979	photosynthesis	175	16	0.37	4	1.70E-24	0.72673	1	1
module_317		1.50E-27	GO:0019684	photosynthesis, light reaction	115	16	0.25	3	1.50E-27	0.77179	1	1
module_319		3.00E-08	GO:0006979	response to oxidative stress	254	8	0.54	1	3.00E-08	0.55943	3.00E-08	3.00E-08
module_323		1.60E-07	GO:0009767	photosynthetic electron transport chain	33	4	0.05	2	1.60E-07	0.86031	1.00E-05	1.60E-07
module_323		3.70E-09	GO:0015979	photosynthesis	175	7	0.27	1	3.70E-09	0.63435	0.00052	0.00052
module_323		2.70E-07	GO:0006091	generation of precursor metabolites and ...	326	7	0.51	3	2.70E-07	0.89169	0.02953	0.02995
module_323		6.40E-07	GO:0019684	photosynthesis, light reaction	115	5	0.18	4	6.40E-07	0.76899	0.09207	1
module_323		1.70E-06	GO:0022900	electron transport chain	59	4	0.09	5	1.70E-06	0.87414	1	1
module_333		8.50E-06	GO:0009870	defense response signaling pathway, resi...	10	2	0	1	8.50E-06	0.708	8.50E-06	8.50E-06
module_342		3.20E-06	GO:0015700	arsenite transport	4	2	0	1	3.20E-06	1	3.20E-06	3.20E-06
module_343		1.40E-08	GO:0009408	response to heat	107	5	0.09	1	1.40E-08	0.84692	1.40E-08	1.40E-08
module_343		1.10E-06	GO:0006950	response to stress	1432	8	1.26	3	1.10E-06	0.48647	0.00782	0.00766
module_343		8.90E-08	GO:0009266	response to temperature stimulus	335	6	0.29	2	8.90E-08	0.64527	0.0868	0.0868
module_343		1.20E-06	GO:0009628	response to abiotic stimulus	899	7	0.79	4	1.20E-06	0.84507	1	1
module_355		3.40E-07	GO:0010289	homogalacturonan biosynthetic process	4	2	0	1	3.40E-07	1	3.40E-07	3.40E-07
module_355		4.40E-07	GO:0000271	polysaccharide biosynthetic process	79	3	0.02	3	4.40E-07	0.90439	1	1
module_355		2.70E-06	GO:0005976	polysaccharide metabolic process	144	3	0.04	6	2.70E-06	0.9694	1	1
module_355		5.60E-06	GO:0016051	carbohydrate biosynthetic process	183	3	0.05	9	5.60E-06	0.89274	1	1
module_355		4.10E-07	GO:0033692	cellular polysaccharide biosynthetic pro...	77	3	0.02	2	4.10E-07	0.9806	1	1
module_355		2.70E-06	GO:0034637	cellular carbohydrate biosynthetic proce...	144	3	0.04	7	2.70E-06	0.9354	1	1
module_355		1.10E-06	GO:0044264	cellular polysaccharide metabolic proces...	106	3	0.03	4	1.10E-06	0.95604	1	1
module_355		3.10E-06	GO:0045488	pectin metabolic process	11	2	0	8	3.10E-06	0.66776	1	1
module_355		1.60E-06	GO:0045489	pectin biosynthetic process	8	2	0	5	1.60E-06	0.93018	1	1
module_356		1.30E-08	GO:0009652	thigmotropism	6	3	0.01	1	1.30E-08	1	1.30E-08	1.30E-08
module_356		3.60E-06	GO:0009606	tropism	33	3	0.03	3	3.60E-06	0.47255	1	1
module_356		2.40E-07	GO:0009612	response to mechanical stimulus	14	3	0.01	2	2.40E-07	0.53646	1	1
module_357		2.10E-08	GO:0055062	phosphate ion homeostasis	4	3	0.01	1	2.10E-08	1	0.0033	2.10E-08
module_357		3.20E-06	GO:0030002	cellular anion homeostasis	2	2	0	4	3.20E-06	1	1	1
module_357		3.20E-06	GO:0030319	cellular di-, tri-valent inorganic anion...	2	2	0	5	3.20E-06	1	1	1
module_357		3.20E-06	GO:0030643	cellular phosphate ion homeostasis	2	2	0	6	3.20E-06	1	3.20E-06	1
module_357		2.10E-08	GO:0055061	di-, tri-valent inorganic anion homeosta...	4	3	0.01	2	2.10E-08	1	1	1
module_357		1.10E-07	GO:0055081	anion homeostasis	6	3	0.01	3	1.10E-07	1	1	1
module_358		1.10E-07	GO:0019751	polyol metabolic process	32	3	0.01	1	1.10E-07	0.28065	1	1
module_361		1.00E-06	GO:0010477	response to sulfur dioxide	2	2	0	1	1.00E-06	1	1.00E-06	1.00E-06
module_371		4.90E-06	GO:0016070	RNA metabolic process	725	7	0.85	1	4.90E-06	0.992	0.0171	1
module_375		3.40E-07	GO:0015712	hexose phosphate transport	3	2	0	1	3.40E-07	0.71994	3.40E-07	3.40E-07
module_375		3.40E-07	GO:0008645	hexose transport	3	2	0	2	3.40E-07	0.71994	1	1
module_375		3.40E-07	GO:0015749	monosaccharide transport	3	2	0	3	3.40E-07	0.71994	1	1
module_378		3.80E-08	GO:0015977	carbon fixation	17	3	0.01	1	3.80E-08	0.99618	3.80E-08	3.80E-08
module_378		3.80E-08	GO:0071704	organic substance metabolic process	17	3	0.01	2	3.80E-08	0.99618	1	1
module_380		7.40E-14	GO:0006412	translation	576	14	1.12	1	7.40E-14	0.21129	9.00E-13	1.00E-11
module_380		2.90E-08	GO:0009058	biosynthetic process	2570	17	5.01	6	2.90E-08	0.41265	0.2744	1
module_380		5.70E-09	GO:0009059	macromolecule biosynthetic process	1610	15	3.14	4	5.70E-09	0.16259	0.4919	1
module_380		2.00E-09	GO:0010467	gene expression	1498	15	2.92	2	2.00E-09	0.35518	0.4512	1
module_380		9.40E-07	GO:0019538	protein metabolic process	2320	15	4.52	8	9.40E-07	0.28911	0.696	1
module_380		5.40E-09	GO:0034645	cellular macromolecule biosynthetic proc...	1605	15	3.13	3	5.40E-09	0.17715	0.4902	1
module_380		1.50E-08	GO:0044249	cellular biosynthetic process	2467	17	4.81	5	1.50E-08	0.32346	0.2526	1
module_380		7.70E-06	GO:0044260	cellular macromolecule metabolic process	3156	16	6.15	9	7.70E-06	0.75678	0.5042	1
module_380		1.10E-07	GO:0044267	cellular protein metabolic process	1991	15	3.88	7	1.10E-07	0.31588	0.6122	1
module_391		5.90E-06	GO:0006468	protein amino acid phosphorylation	609	7	0.83	1	5.90E-06	0.38005	5.90E-06	5.90E-06
module_400		4.10E-11	GO:0006334	nucleosome assembly	81	6	0.08	1	4.10E-11	0.1673	4.10E-11	4.10E-11
module_400		4.80E-11	GO:0006323	DNA packaging	83	6	0.08	4	4.80E-11	0.15103	1	1
module_400		1.70E-09	GO:0006325	chromatin organization	149	6	0.15	8	1.70E-09	0.21657	1	1
module_400		1.90E-10	GO:0006333	chromatin assembly or disassembly	104	6	0.1	7	1.90E-10	0.06255	1	1
module_400		9.20E-07	GO:0006996	organelle organization	428	6	0.42	15	9.20E-07	0.20232	1	1
module_400		1.10E-07	GO:0022607	cellular component assembly	300	6	0.29	14	1.10E-07	0.17257	1	1
module_400		4.40E-11	GO:0031497	chromatin assembly	82	6	0.08	3	4.40E-11	0.19544	1	1
module_400		1.20E-08	GO:0034621	cellular macromolecular complex subunit ...	207	6	0.2	11	1.20E-08	0.40558	1	1
module_400		8.10E-09	GO:0034622	cellular macromolecular complex assembly	193	6	0.19	10	8.10E-09	0.25183	1	1
module_400		4.10E-11	GO:0034728	nucleosome organization	81	6	0.08	2	4.10E-11	0.1673	1	1
module_400		9.00E-08	GO:0043933	macromolecular complex subunit organizat...	289	6	0.28	13	9.00E-08	0.27763	1	1
module_400		2.20E-06	GO:0044085	cellular component biogenesis	496	6	0.48	16	2.20E-06	0.5041	1	1
module_400		3.60E-09	GO:0051276	chromosome organization	169	6	0.16	9	3.60E-09	0.24367	1	1
module_400		6.70E-08	GO:0065003	macromolecular complex assembly	275	6	0.27	12	6.70E-08	0.1711	1	1
module_400		4.80E-11	GO:0065004	protein-DNA complex assembly	83	6	0.08	5	4.80E-11	0.22628	1	1
module_400		1.50E-10	GO:0071103	DNA conformation change	100	6	0.1	6	1.50E-10	0.11959	1	1
module_403		1.50E-06	GO:0010201	response to continuous far red light sti...	2	2	0	1	1.50E-06	1	1.50E-06	1.50E-06
module_403		1.50E-06	GO:0010203	response to very low fluence red light s...	2	2	0	2	1.50E-06	1	1.50E-06	1.50E-06
module_403		8.90E-06	GO:0007600	sensory perception	4	2	0.01	4	8.90E-06	0.99189	8.90E-06	8.90E-06
module_403		8.90E-06	GO:0010161	red light signaling pathway	4	2	0.01	5	8.90E-06	0.7377	8.90E-06	8.90E-06
module_403		8.90E-06	GO:0017006	protein-tetrapyrrole linkage	4	2	0.01	6	8.90E-06	0.99189	8.90E-06	8.90E-06
module_403		8.90E-06	GO:0018298	protein-chromophore linkage	4	2	0.01	7	8.90E-06	0.99189	8.90E-06	8.90E-06
module_403		8.90E-06	GO:0003008	system process	4	2	0.01	8	8.90E-06	0.99189	1	1
module_403		8.90E-06	GO:0050877	neurological system process	4	2	0.01	9	8.90E-06	0.99189	1	1
module_403		1.50E-06	GO:0055122	response to very low light intensity sti...	2	2	0	3	1.50E-06	1	1	1
module_403		8.90E-06	GO:0071491	cellular response to red light	4	2	0.01	10	8.90E-06	0.7377	1	1
module_404		2.50E-09	GO:0006468	protein amino acid phosphorylation	609	7	0.42	1	2.50E-09	0.43286	2.50E-09	2.50E-09
module_404		1.50E-07	GO:0006464	protein modification process	1086	7	0.74	6	1.50E-07	0.26963	1	1
module_404		1.40E-08	GO:0006793	phosphorus metabolic process	775	7	0.53	4	1.40E-08	0.22624	1	1
module_404		1.30E-08	GO:0006796	phosphate metabolic process	774	7	0.53	3	1.30E-08	0.23398	1	1
module_404		6.20E-09	GO:0016310	phosphorylation	693	7	0.47	2	6.20E-09	0.43395	1	1
module_404		2.10E-07	GO:0043412	macromolecule modification	1141	7	0.78	7	2.10E-07	0.31187	1	1
module_404		2.50E-08	GO:0043687	post-translational protein modification	847	7	0.58	5	2.50E-08	0.26777	1	1
module_406		6.60E-14	GO:0009961	response to 1-aminocyclopropane-1-carbox...	7	5	0.01	1	6.60E-14	1	6.60E-14	6.60E-14
module_406		3.60E-11	GO:0009631	cold acclimation	19	5	0.03	2	3.60E-11	1	3.60E-11	3.60E-11
module_406		5.20E-08	GO:0009414	response to water deprivation	157	6	0.23	3	5.20E-08	1	5.20E-08	5.20E-08
module_406		8.60E-07	GO:0009790	embryo development	252	6	0.37	5	8.60E-07	0.15193	0.00087	8.60E-07
module_406		6.30E-06	GO:0009737	response to abscisic acid stimulus	197	5	0.29	6	6.30E-06	0.99996	6.30E-06	6.30E-06
module_406		8.30E-08	GO:0009415	response to water	170	6	0.25	4	8.30E-08	1	1	1
module_408		1.10E-11	GO:0007018	microtubule-based movement	37	6	0.06	2	1.10E-11	0.81338	1.10E-11	1.10E-11
module_408		6.80E-06	GO:0051225									

module_41	3.30E-07	GO:0043170	macromolecule metabolic process	3543	14	4.83	10	3.30E-07	0.79715	1	1
module_41	2.10E-09	GO:0044249	cellular biosynthetic process	2467	14	3.36	7	2.10E-09	0.31192	1	1
module_41	6.60E-08	GO:0044260	cellular macromolecule metabolic process	3156	14	4.3	9	6.60E-08	0.74743	1	1
module_41	1.00E-10	GO:0044267	cellular protein metabolic process	1991	14	2.71	5	1.00E-10	0.31981	1	1
module_410	9.20E-21	GO:0006412	translation	576	19	1.29	1	9.20E-21	0.26418	9.20E-21	9.20E-21
module_410	3.00E-08	GO:0042254	ribosome biogenesis	154	7	0.34	11	3.00E-08	0.99381	3.00E-08	3.00E-08
module_410	6.90E-10	GO:0009058	biosynthetic process	2570	20	5.76	7	6.90E-10	0.41265	1	1
module_410	2.20E-12	GO:0009059	macromolecule biosynthetic process	1610	19	3.61	4	2.20E-12	0.18005	1	1
module_410	5.80E-13	GO:0010467	gene expression	1498	19	3.36	2	5.80E-13	0.38433	1	1
module_410	1.70E-09	GO:0019538	protein metabolic process	2320	19	5.2	8	1.70E-09	0.37674	1	1
module_410	3.10E-08	GO:0022613	ribonucleoprotein complex biogenesis	155	7	0.35	12	3.10E-08	0.99711	1	1
module_410	2.10E-12	GO:0034645	cellular macromolecule biosynthetic proc...	1605	19	3.6	3	2.10E-12	0.19571	1	1
module_410	2.20E-08	GO:0043170	macromolecule metabolic process	3543	21	7.94	10	2.20E-08	0.82688	0.359	1
module_410	6.50E-07	GO:0044237	cellular metabolic process	4791	22	10.73	13	6.50E-07	0.56269	0.403	1
module_410	1.10E-06	GO:0044238	primary metabolic process	4907	22	10.99	14	1.10E-06	0.56207	0.42	1
module_410	3.20E-10	GO:0044249	cellular biosynthetic process	2467	20	5.53	6	3.20E-10	0.32346	1	1
module_410	2.10E-09	GO:0044260	cellular macromolecule metabolic process	3156	21	7.07	9	2.10E-09	0.78063	0.289	1
module_410	1.10E-10	GO:0044267	cellular protein metabolic process	1991	19	4.46	5	1.10E-10	0.41866	1	1
module_413	1.90E-07	GO:0005998	xylulose catabolic process	2	2	0	3	1.90E-07	1	1.90E-07	1.90E-07
module_413	4.00E-06	GO:0006573	valine metabolic process	7	2	0	11	4.00E-06	1	4.00E-06	4.00E-06
module_413	4.10E-07	GO:0005996	monosaccharide metabolic process	176	4	0.09	5	4.10E-07	0.89757	1	1
module_413	5.70E-07	GO:0005997	xylulose metabolic process	3	2	0	7	5.70E-07	1	1	1
module_413	1.50E-06	GO:0006066	alcohol metabolic process	244	4	0.12	9	1.50E-06	0.89312	1	1
module_413	5.00E-07	GO:0016052	carbohydrate catabolic process	185	4	0.09	6	5.00E-07	0.75488	1	1
module_413	1.10E-06	GO:0019323	pentose catabolic process	4	2	0	8	1.10E-06	0.81127	1	1
module_413	2.20E-07	GO:0044275	cellular carbohydrate catabolic process	151	4	0.07	4	2.20E-07	0.69897	1	1
module_413	1.50E-06	GO:0044282	small molecule catabolic process	244	4	0.12	10	1.50E-06	0.89312	1	1
module_413	7.10E-08	GO:0046164	alcohol catabolic process	114	4	0.06	2	7.10E-08	0.81672	1	1
module_413	5.30E-08	GO:0046365	monosaccharide catabolic process	106	4	0.05	1	5.30E-08	0.8674	1	1
module_414	9.80E-06	GO:0006412	translation	576	4	0.22	1	9.80E-06	0.22174	9.80E-06	9.80E-06
module_419	7.50E-06	GO:0051555	flavonol biosynthetic process	12	2	0	1	7.50E-06	0.85007	7.50E-06	7.50E-06
module_419	7.50E-06	GO:0051552	flavone metabolic process	12	2	0	2	7.50E-06	0.85007	1	1
module_419	7.50E-06	GO:0051553	flavone biosynthetic process	12	2	0	3	7.50E-06	0.85007	1	1
module_419	7.50E-06	GO:0051554	flavonol metabolic process	12	2	0	4	7.50E-06	0.85007	1	1
module_421	6.40E-06	GO:0006796	phosphate metabolic process	774	10	1.88	1	6.40E-06	0.36447	0.0163	0.2449
module_421	6.50E-06	GO:0006793	phosphorus metabolic process	775	10	1.89	2	6.50E-06	0.35423	0.0166	1
module_429	6.80E-07	GO:0009765	photosynthesis, light harvesting	58	3	0.02	1	6.80E-07	0.95703	6.70E-05	6.80E-07
module_429	5.40E-06	GO:0019684	photosynthesis, light reaction	115	3	0.04	2	5.40E-06	0.55294	1	1
module_433	1.70E-06	GO:0016119	carotene metabolic process	10	3	0.03	1	1.70E-06	0.19307	1	1.70E-06
module_433	5.10E-06	GO:0042440	pigment metabolic process	103	5	0.26	2	5.10E-06	0.2751	1	1
module_443	4.20E-08	GO:0006412	translation	576	9	0.9	1	4.20E-08	0.21623	4.20E-08	4.20E-08
module_447	2.30E-06	GO:0015074	DNA integration	16	2	0	1	2.30E-06	0.23164	2.30E-06	2.30E-06
module_448	1.70E-06	GO:0001666	response to hypoxia	15	3	0.02	1	1.70E-06	0.51008	1.70E-06	1.70E-06
module_448	1.70E-06	GO:0070482	response to oxygen levels	15	3	0.02	2	1.70E-06	0.51008	1	1
module_456	2.60E-06	GO:0045337	farnesyl diphosphate biosynthetic proces...	3	2	0	1	2.60E-06	0.87986	2.60E-06	2.60E-06
module_456	5.10E-06	GO:0016090	prenol metabolic process	4	2	0	4	5.10E-06	0.96903	1	1
module_456	2.60E-06	GO:0016091	prenol biosynthetic process	3	2	0	2	2.60E-06	0.87986	1	1
module_456	5.10E-06	GO:0016093	polyprenol metabolic process	4	2	0	5	5.10E-06	0.96903	1	1
module_456	2.60E-06	GO:0016094	polyprenol biosynthetic process	3	2	0	3	2.60E-06	0.87986	1	1
module_456	5.10E-06	GO:0045338	farnesyl diphosphate metabolic process	4	2	0	6	5.10E-06	0.96903	1	1
module_467	7.80E-09	GO:0006457	protein folding	208	10	0.85	1	7.80E-09	0.96696	7.80E-09	8.20E-08
module_467	6.80E-07	GO:0006779	porphyrin biosynthetic process	42	5	0.17	2	6.80E-07	0.39304	4.30E-05	6.80E-07
module_467	9.80E-07	GO:0044237	cellular metabolic process	4791	35	19.6	3	9.80E-07	0.57226	0.0098	0.5486
module_467	2.90E-06	GO:0006778	porphyrin metabolic process	56	5	0.23	5	2.90E-06	0.85856	1	1
module_467	3.50E-06	GO:0033013	tetrapyrrole metabolic process	58	5	0.24	6	3.50E-06	0.95083	1	1
module_467	1.10E-06	GO:0033014	tetrapyrrole biosynthetic process	46	5	0.19	4	1.10E-06	0.59297	1	1
module_467	7.80E-06	GO:0044267	cellular protein metabolic process	1991	21	8.14	7	7.80E-06	0.37317	0.1179	1
module_471	8.70E-07	GO:0043086	negative regulation of catalytic activit...	31	3	0.02	1	8.70E-07	0.8741	8.70E-07	8.70E-07
module_471	1.40E-06	GO:0007186	G-protein coupled receptor protein signa...	36	3	0.02	2	1.40E-06	0.9961	1.40E-06	1.40E-06
module_471	1.40E-06	GO:0044092	negative regulation of molecular functio...	36	3	0.02	3	1.40E-06	0.76524	1	1
module_473	4.40E-06	GO:0006396	RNA processing	197	4	0.13	1	4.40E-06	0.6695	0.05965	0.05928
module_476	1.70E-06	GO:0010143	cutin biosynthetic process	4	2	0	1	1.70E-06	0.8266	1.70E-06	1.70E-06
module_480	6.40E-16	GO:0006412	translation	576	13	0.79	1	6.40E-16	0.19391	6.40E-16	6.40E-16
module_480	1.60E-07	GO:0009058	biosynthetic process	2570	13	3.5	8	1.60E-07	0.38194	1	1
module_480	4.00E-10	GO:0009059	macromolecule biosynthetic process	1610	13	2.2	4	4.00E-10	0.14067	1	1
module_480	1.60E-10	GO:0010467	gene expression	1498	13	2.04	2	1.60E-10	0.31593	1	1
module_480	4.30E-08	GO:0019538	protein metabolic process	2320	13	3.16	6	4.30E-08	0.24431	1	1
module_480	3.80E-10	GO:0034645	cellular macromolecule biosynthetic proc...	1605	13	2.19	3	3.80E-10	0.15373	1	1
module_480	9.20E-06	GO:0043170	macromolecule metabolic process	3543	13	4.83	10	9.20E-06	0.71234	1	1
module_480	9.50E-08	GO:0044249	cellular biosynthetic process	2467	13	3.36	7	9.50E-08	0.2941	1	1
module_480	2.20E-06	GO:0044260	cellular macromolecule metabolic process	3156	13	4.3	9	2.20E-06	0.71313	1	1
module_480	6.10E-09	GO:0044267	cellular protein metabolic process	1991	13	2.71	5	6.10E-09	0.26408	1	1
module_482	3.10E-06	GO:0006412	translation	576	5	0.34	1	3.10E-06	0.16523	3.10E-06	3.10E-06
module_485	5.60E-07	GO:0007005	mitochondrion organization	27	3	0.02	1	5.60E-07	0.93307	5.60E-07	5.60E-07
module_491	6.80E-06	GO:0006418	tRNA aminoacylation for protein translat...	73	3	0.04	1	6.80E-06	0.71782	0.0255	6.80E-06
module_491	6.80E-06	GO:0043038	amino acid activation	73	3	0.04	2	6.80E-06	0.71782	0.0255	1
module_491	6.80E-06	GO:0043039	tRNA aminoacylation	73	3	0.04	3	6.80E-06	0.71782	0.0255	1
module_502	8.90E-06	GO:0046274	lignin catabolic process	13	2	0.01	1	8.90E-06	1	8.90E-06	8.90E-06
module_502	8.90E-06	GO:0046271	phenylpropanoid catabolic process	13	2	0.01	2	8.90E-06	1	1	1
module_521	1.70E-07	GO:0010253	UDP-rhamnose biosynthetic process	3	2	0	1	1.70E-07	1	1.70E-07	1.70E-07
module_521	1.20E-06	GO:0009226	nucleotide-sugar biosynthetic process	7	2	0	5	1.20E-06	0.73186	1	1
module_521	3.40E-07	GO:0019299	rhamnose metabolic process	4	2	0	3	3.40E-07	1	1	1
module_521	3.40E-07	GO:0019300	rhamnose biosynthetic process	4	2	0	4	3.40E-07	1	1	1
module_521	9.70E-06	GO:0019319	hexose biosynthetic process	19	2	0.01	6	9.70E-06	1	1	1
module_521	1.70E-07	GO:0033478	UDP-rhamnose metabolic process	3	2	0	2	1.70E-07	1	1	1
module_529	1.80E-16	GO:0006412	translation	576	21	2.24	1	1.80E-16	0.28574	1.70E-15	1.80E-16
module_529	1.70E-09	GO:0019538	protein metabolic process	2320	27	9.04	3	1.70E-09	0.42113	0.72521	0.71872
module_529	2.80E-06	GO:0009058	biosynthetic process	2570	24	10.01	8	2.80E-06	0.4189	0.98009	1
module_529	7.20E-08	GO:0009059	macromolecule biosynthetic process	1610	21	6.27	6	7.20E-08	0.17444	1	1
module_529	2.00E-08	GO:0010467	gene expression	1498	21	5.84	4	2.00E-08	0.37571	1	1
module_529	6.80E-08	GO:0034645	cellular macromolecule biosynthetic proc...	1605	21	6.25	5	6.80E-08	0.18977	1	1
module_529	1.30E-06	GO:0044249	cellular biosynthetic process	2467	24	9.61	7	1.30E-06	0.32831	0.97503	1
module_529	8.00E-06	GO:0044260	cellular macromolecule metabolic process	3156	26	12.3	9	8.00E-06	0.76604	0.98674	1
module_529	3.50E-10	GO:0044267	cellular protein metabolic process	1991	26	7.76	2	3.50E-10	0.4435	0.87066	1
module_530	8.80E-06	GO:0009644	response to high light intensity	40	3	0.04	3	8.80E-06	0.99999	8.80E-06	8.80E-06
module_530	3.00E-07	GO:0009416	response to light stimulus	311	6	0.33	1	3.00E-07	0.77763	0.00093	0.00093
module_530	3.30E-07	GO:0009314	response to radiation	316	6	0.34	2	3.30E-07	0.82781	1	1
module_538	2.80E-07	GO:0051453	regulation of intracellular pH	2	2	0	1	2.80E-07	1	2.80E-07	2.80E-07
module_538	4.30E-06	GO:0015743	malate transport	6	2	0	4	4.30E-06	1	4.30E-06	4.30E-06
module_538	4.30E-06	GO:0006835	dicarboxylic acid transport	6	2	0	5	4.30E-06	1	1	1
module_538	4.30E-06	GO:0015740	C4-dicarboxylate transport	6	2	0	6	4.30E-06	1	1	1
module_538	1.70E-06	GO:0030004	cellular monovalent inorganic cation hom...	4	2	0</					

module_548	3.90E-06	GO:0030244	cellulose biosynthetic process	34	3	0.03	2	3.90E-06	0.99792	3.90E-06	3.90E-06
module_548	7.00E-06	GO:0009832	plant-type cell wall biogenesis	41	3	0.04	4	7.00E-06	0.99998	1	1
module_548	4.70E-06	GO:0030243	cellulose metabolic process	36	3	0.04	3	4.70E-06	0.87439	1	1
module_548	9.90E-06	GO:0042546	cell wall biogenesis	46	3	0.04	5	9.90E-06	0.98974	1	1
module_553	1.10E-15	GO:0006268	DNA unwinding involved in replication	11	7	0.04	3	1.10E-15	0.99999	1.10E-15	1.10E-15
module_553	5.90E-15	GO:0006270	DNA-dependent DNA replication initiation	13	7	0.05	6	5.90E-15	0.85824	5.90E-15	5.90E-15
module_553	4.10E-11	GO:0008283	cell proliferation	38	7	0.13	9	4.10E-11	0.67536	4.10E-11	4.10E-11
module_553	1.70E-17	GO:0006259	DNA metabolic process	235	16	0.82	2	1.70E-17	0.84413	0.1104	8.90E-07
module_553	1.20E-09	GO:0006139	nucleobase, nucleoside, nucleotide and n...	1478	21	5.18	10	1.20E-09	0.77671	0.1045	1
module_553	8.40E-18	GO:0006260	DNA replication	74	12	0.26	1	8.40E-18	0.97428	1.60E-05	1
module_553	9.80E-14	GO:0006261	DNA-dependent DNA replication	32	8	0.11	7	9.80E-14	0.91186	1	1
module_553	1.90E-07	GO:0006807	nitrogen compound metabolic process	1949	21	6.83	13	1.90E-07	0.82725	0.2657	1
module_553	1.60E-06	GO:0009059	macromolecule biosynthetic process	1610	18	5.65	15	1.60E-06	0.16895	0.2586	1
module_553	2.70E-15	GO:0032392	DNA geometric change	12	7	0.04	4	2.70E-15	0.89835	1	1
module_553	2.70E-15	GO:0032508	DNA duplex unwinding	12	7	0.04	5	2.70E-15	0.89835	1	1
module_553	1.00E-07	GO:0034641	cellular nitrogen compound metabolic pro...	1883	21	6.6	12	1.00E-07	0.89048	0.2396	1
module_553	1.50E-06	GO:0034645	cellular macromolecule biosynthetic proc...	1605	18	5.63	14	1.50E-06	0.18395	0.2563	1
module_553	4.20E-06	GO:0043170	macromolecule metabolic process	3543	26	12.42	17	4.20E-06	0.83982	0.0918	1
module_553	1.90E-06	GO:0044260	cellular macromolecule metabolic process	3156	25	11.07	16	1.90E-06	0.77521	0.1036	1
module_553	4.50E-08	GO:0071103	DNA conformation change	100	7	0.35	11	4.50E-08	0.17034	1	1
module_553	3.00E-11	GO:0090304	nucleic acid metabolic process	1220	21	4.28	8	3.00E-11	0.80536	0.0481	1
module_554	3.00E-07	GO:0006260	DNA replication	74	4	0.06	1	3.00E-07	0.80891	1.20E-05	7.20E-06
module_557	5.10E-06	GO:0030418	nicotianamine biosynthetic process	4	2	0	1	5.10E-06	1	5.10E-06	5.10E-06
module_557	5.10E-06	GO:0030417	nicotianamine metabolic process	4	2	0	2	5.10E-06	1	1	1
module_56	1.10E-23	GO:0006334	nucleosome assembly	81	12	0.12	1	1.10E-23	0.94388	1.10E-23	1.10E-23
module_56	1.50E-23	GO:0006323	DNA packaging	83	12	0.12	4	1.50E-23	0.91859	1	1
module_56	2.40E-20	GO:0006325	chromatin organization	149	12	0.22	8	2.40E-20	0.83113	1	1
module_56	2.70E-22	GO:0006333	chromatin assembly or disassembly	104	12	0.15	7	2.70E-22	0.61464	1	1
module_56	9.60E-15	GO:0006996	organelle organization	428	12	0.63	15	9.60E-15	0.4766	1	1
module_56	9.50E-12	GO:0016043	cellular component organization	762	12	1.11	17	9.50E-12	0.33492	1	1
module_56	1.30E-16	GO:0022607	cellular component assembly	300	12	0.44	14	1.30E-16	0.56129	1	1
module_56	1.30E-23	GO:0031497	chromatin assembly	82	12	0.12	3	1.30E-23	0.96542	1	1
module_56	1.40E-18	GO:0034621	cellular macromolecular complex subunit ...	207	12	0.3	11	1.40E-18	0.93125	1	1
module_56	6.00E-19	GO:0034622	cellular macromolecular complex assembly	193	12	0.28	10	6.00E-19	0.80441	1	1
module_56	1.10E-23	GO:0034728	nucleosome organization	81	12	0.12	2	1.10E-23	0.94388	1	1
module_56	8.30E-17	GO:0043933	macromolecular complex subunit organizat...	289	12	0.42	13	8.30E-17	0.71852	1	1
module_56	5.70E-14	GO:0044085	cellular component biogenesis	496	12	0.72	16	5.70E-14	0.81462	1	1
module_56	1.20E-19	GO:0051276	chromosome organization	169	12	0.25	9	1.20E-19	0.81188	1	1
module_56	4.60E-17	GO:0065003	macromolecular complex assembly	275	12	0.4	12	4.60E-17	0.54295	1	1
module_56	1.50E-23	GO:0065004	protein-DNA complex assembly	83	12	0.12	5	1.50E-23	0.9818	1	1
module_56	1.60E-22	GO:0071103	DNA conformation change	100	12	0.15	6	1.60E-22	0.8012	1	1
module_563	3.90E-06	GO:0030244	cellulose biosynthetic process	34	3	0.03	4	3.90E-06	1	3.90E-06	3.90E-06
module_563	7.00E-06	GO:0009832	plant-type cell wall biogenesis	41	3	0.04	6	7.00E-06	1	1	7.00E-06
module_563	6.60E-07	GO:0000271	polysaccharide biosynthetic process	79	4	0.08	2	6.60E-07	0.98999	1	1
module_563	7.30E-06	GO:0005976	polysaccharide metabolic process	144	4	0.14	7	7.30E-06	0.9694	1	1
module_563	4.70E-06	GO:0030243	cellulose metabolic process	36	3	0.04	5	4.70E-06	0.9734	1	1
module_563	5.90E-07	GO:0033692	cellular polysaccharide biosynthetic pro...	77	4	0.07	1	5.90E-07	0.9806	1	1
module_563	7.30E-06	GO:0034637	cellular carbohydrate biosynthetic proce...	144	4	0.14	8	7.30E-06	0.97784	1	1
module_563	9.90E-06	GO:0042546	cell wall biogenesis	46	3	0.04	9	9.90E-06	1	1	1
module_563	2.10E-06	GO:0044264	cellular polysaccharide metabolic proces...	106	4	0.1	3	2.10E-06	0.95604	1	1
module_567	1.70E-10	GO:0043687	post-translational protein modification	847	9	0.74	1	1.70E-10	0.36184	0.0246	1.70E-10
module_567	1.60E-09	GO:0006464	protein modification process	1086	9	0.95	3	1.60E-09	0.35107	0.0494	1
module_567	1.30E-09	GO:0006468	protein amino acid phosphorylation	609	8	0.53	2	1.30E-09	0.56823	1.30E-09	1
module_567	8.60E-09	GO:0006793	phosphorus metabolic process	775	8	0.68	7	8.60E-09	0.31382	1	1
module_567	8.50E-09	GO:0006796	phosphate metabolic process	774	8	0.68	6	8.50E-09	0.32335	1	1
module_567	3.50E-09	GO:0016310	phosphorylation	693	8	0.61	5	3.50E-09	0.5597	1	1
module_567	1.50E-06	GO:0019538	protein metabolic process	2320	9	2.03	9	1.50E-06	0.2802	0.1304	1
module_567	2.50E-09	GO:0043412	macromolecule modification	1141	9	1	4	2.50E-09	0.39711	0.0551	1
module_567	3.80E-07	GO:0044267	cellular protein metabolic process	1991	9	1.75	8	3.80E-07	0.30071	0.1431	1
module_569	1.80E-11	GO:0006412	translation	576	11	0.84	1	1.80E-11	0.28768	1.80E-11	1.80E-11
module_569	1.00E-06	GO:0009059	macromolecule biosynthetic process	1610	11	2.35	6	1.00E-06	0.18005	1	1
module_569	4.80E-07	GO:0010467	gene expression	1498	11	2.19	3	4.80E-07	0.38433	1	1
module_569	2.60E-07	GO:0019538	protein metabolic process	2320	13	3.39	2	2.60E-07	0.3039	0.151	1
module_569	9.80E-07	GO:0034645	cellular macromolecule biosynthetic proc...	1605	11	2.34	5	9.80E-07	0.19571	1	1
module_569	3.40E-06	GO:0043170	macromolecule metabolic process	3543	14	5.18	7	3.40E-06	0.75931	0.088	1
module_569	7.00E-07	GO:0044267	cellular protein metabolic process	1991	12	2.91	4	7.00E-07	0.30595	0.468	1
module_581	6.50E-07	GO:0006468	protein amino acid phosphorylation	609	8	0.89	1	6.50E-07	0.5503	6.50E-07	6.50E-07
module_581	4.10E-06	GO:0006793	phosphorus metabolic process	775	8	1.13	4	4.10E-06	0.29789	1	1
module_581	4.00E-06	GO:0006796	phosphate metabolic process	774	8	1.13	3	4.00E-06	0.30715	1	1
module_581	1.70E-06	GO:0016310	phosphorylation	693	8	1.01	2	1.70E-06	0.54054	1	1
module_581	7.90E-06	GO:0043687	post-translational protein modification	847	8	1.24	5	7.90E-06	0.34376	1	1
module_589	7.70E-08	GO:0019252	starch biosynthetic process	11	3	0.01	1	7.70E-08	0.5158	0.0041	7.70E-08
module_589	6.80E-07	GO:0010444	guard mother cell differentiation	2	2	0	2	6.80E-07	1	6.80E-07	6.80E-07
module_589	9.30E-07	GO:0005982	starch metabolic process	24	3	0.02	3	9.30E-07	0.80409	1	1
module_589	6.80E-06	GO:0010021	amylopectin biosynthetic process	5	2	0	5	6.80E-06	0.90361	6.80E-06	1
module_589	4.10E-06	GO:0010440	stomatal lineage progression	4	2	0	4	4.10E-06	0.37844	1	1
module_592	4.30E-08	GO:0006468	protein amino acid phosphorylation	609	6	0.36	1	4.30E-08	0.34884	4.30E-08	4.30E-08
module_592	1.40E-06	GO:0006464	protein modification process	1086	6	0.63	6	1.40E-06	0.22243	1	1
module_592	1.80E-07	GO:0006793	phosphorus metabolic process	775	6	0.45	4	1.80E-07	0.20036	1	1
module_592	1.80E-07	GO:0006796	phosphate metabolic process	774	6	0.45	3	1.80E-07	0.20748	1	1
module_592	9.30E-08	GO:0016310	phosphorylation	693	6	0.4	2	9.30E-08	0.39364	1	1
module_592	1.90E-06	GO:0043412	macromolecule modification	1141	6	0.67	7	1.90E-06	0.26137	1	1
module_592	3.10E-07	GO:0043687	post-translational protein modification	847	6	0.49	5	3.10E-07	0.21438	1	1
module_598	2.00E-13	GO:0006334	nucleosome assembly	81	6	0.05	1	2.00E-13	0.35303	2.00E-13	2.00E-13
module_598	2.30E-13	GO:0006323	DNA packaging	83	6	0.05	4	2.30E-13	0.32381	1	1
module_598	8.40E-12	GO:0006325	chromatin organization	149	6	0.09	8	8.40E-12	0.36659	1	1
module_598	9.30E-13	GO:0006333	chromatin assembly or disassembly	104	6	0.06	7	9.30E-13	0.147	1	1
module_598	5.10E-09	GO:0006996	organelle organization	428	6	0.25	15	5.10E-09	0.24356	1	1
module_598	1.60E-07	GO:0016043	cellular component organization	762	6	0.45	17	1.60E-07	0.17062	1	1
module_598	5.90E-10	GO:0022607	cellular component assembly	300	6	0.18	14	5.90E-10	0.21738	1	1
module_598	2.20E-13	GO:0031497	chromatin assembly	82	6	0.05	3	2.20E-13	0.39571	1	1
module_598	6.30E-11	GO:0034621	cellular macromolecular complex subunit ...	207	6	0.12	11	6.30E-11	0.48995	1	1
module_598	4.10E-11	GO:0034622	cellular macromolecular complex assembly	193	6	0.11	10	4.10E-11	0.32116	1	1
module_598	2.00E-13	GO:0034728	nucleosome organization	81	6	0.05	2	2.00E-13	0.35303	1	1
module_598	4.70E-10	GO:0043933	macromolecular complex subunit organizat...	289	6	0.17	13	4.70E-10	0.32519	1	1
module_598	1.20E-08	GO:0044085	cellular component biogenesis	496	6	0.29	16	1.20E-08	0.51463	1	1
module_598	1.80E-11	GO:0051276	chromosome organization	169	6	0.1	9	1.80E-11	0.3712	1	1
module_598	3.50E-10	GO:0065003	macromolecular complex assembly	275	6	0.16	12	3.50E-10	0.19462	1	1
module_598	2.30E-13	GO:0065004	protein-DNA complex assembly	83	6	0.05	5	2.30E-13	0.44005	1	1
module_598	7.30E-13	GO:0071103	DNA conformation change	100	6	0.06	6	7.30E-13	0.25339	1	1
module_603	1.20E-06	GO:0030244	cellulose biosynthetic process	34	3	0.02	1	1.20E-06	0.99189	1.20E-06	1.20E-06
module_603	6.50E-06	GO:0009250	glucan biosynthetic process	60	3	0.04	3	6.50E-06	0.84311	1	1
module_603	1.40E-06										

module_72	2.90E-07	GO:0005975	carbohydrate metabolic process	645	11	1.7	1	2.90E-07	0.93111	2.90E-07	5.90E-06
module_72	1.10E-06	GO:0009739	response to gibberellin stimulus	31	4	0.08	2	1.10E-06	0.96192	5.60E-05	3.60E-05
module_82	4.10E-07	GO:0019915	lipid storage	8	3	0.02	1	4.10E-07	0.09963	4.10E-07	4.10E-07
module_86	3.80E-07	GO:0006119	oxidative phosphorylation	56	4	0.07	1	3.80E-07	0.96229	1	0.00069
module_94	2.50E-09	GO:0005986	sucrose biosynthetic process	15	3	0	1	2.50E-09	0.39479	2.50E-09	2.50E-09
module_94	1.60E-07	GO:0005984	disaccharide metabolic process	57	3	0.02	6	1.60E-07	0.76379	1	1
module_94	5.10E-08	GO:0005985	sucrose metabolic process	39	3	0.01	5	5.10E-08	0.77869	1	1
module_94	2.10E-07	GO:0009311	oligosaccharide metabolic process	62	3	0.02	8	2.10E-07	0.61302	1	1
module_94	1.60E-08	GO:0009312	oligosaccharide biosynthetic process	27	3	0.01	2	1.60E-08	0.71085	1	1
module_94	5.60E-06	GO:0016051	carbohydrate biosynthetic process	183	3	0.05	10	5.60E-06	0.8978	1	1
module_94	2.00E-07	GO:0016137	glycoside metabolic process	61	3	0.02	7	2.00E-07	0.68744	1	1
module_94	4.00E-08	GO:0016138	glycoside biosynthetic process	36	3	0.01	4	4.00E-08	0.66059	1	1
module_94	2.70E-06	GO:0034637	cellular carbohydrate biosynthetic proce...	144	3	0.04	9	2.70E-06	0.9354	1	1
module_94	1.60E-08	GO:0046351	disaccharide biosynthetic process	27	3	0.01	3	1.60E-08	0.71085	1	1