

	category	ID	term	count	genes
1	BP	GO:0019344	cysteine biosynthetic process	16	COMP10448_C0.SE
17	BP	GO:0010027	thylakoid membrane organization	17	COMP10974_C0.SE
34	BP	GO:0015979	photosynthesis	51	COMP104278_C0.S
144	BP	GO:0070838	divalent metal ion transport	16	COMP1798_C0.SE
173	BP	GO:0016117	carotenoid biosynthetic process	10	COMP12906_C0.SE
183	BP	GO:0006012	galactose metabolic process	8	COMP1080_C0.SE
240	BP	GO:0032880	regulation of protein localization	4	COMP15715_C0.SE
246	BP	GO:0045490	pectin catabolic process	5	COMP11391_C0.SE
254	BP	GO:0000103	sulfate assimilation	6	COMP15214_C0.SE
260	BP	GO:0010411	xyloglucan metabolic process	4	COMP1272_C0.SE
268	BP	GO:0009416	response to light stimulus	26	COMP10270_C0.SE
294	BP	GO:0006833	water transport	6	COMP139_C0.SEQ
335	BP	GO:0006857	oligopeptide transport	4	COMP10631_C0.SE
339	BP	GO:0005985	sucrose metabolic process	14	COMP11151_C0.SE
353	BP	GO:0010363	regulation of plant-type hypersensitive ...	7	COMP12524_C0.SE
366	BP	GO:0019761	glucosinolate biosynthetic process	6	COMP15214_C0.SE
388	BP	GO:0051603	proteolysis involved in cellular protein...	12	COMP10208_C0.SE
461	BP	GO:0000054	ribosomal subunit export from nucleus	2	COMP5339_C0.SE
481	BP	GO:0030154	cell differentiation	17	COMP10270_C0.SE
498	BP	GO:0010105	negative regulation of ethylene-activate...	2	COMP4820_C0.SE
500	BP	GO:0006782	protoporphyrinogen IX biosynthetic proce...	2	COMP12222_C0.SE
502	BP	GO:0015996	chlorophyll catabolic process	4	COMP12715_C0.SE
506	BP	GO:0009873	ethylene-activated signaling pathway	5	COMP2553_C0.SE
522	BP	GO:0098869	cellular oxidant detoxification	7	COMP159_C0.SEQ
541	BP	GO:0006094	gluconeogenesis	10	COMP1082_C0.SE
564	BP	GO:0055114	oxidation-reduction process	65	COMP104278_C0.S
640	BP	GO:0006412	translation	25	COMP1059_C0.SE
699	BP	GO:0006529	asparagine biosynthetic process	3	COMP13352_C0.SE
702	BP	GO:0009690	cytokinin metabolic process	3	COMP13696_C0.SE
707	BP	GO:0016925	protein sumoylation	2	COMP3483_C0.SE
714	BP	GO:0060267	positive regulation of respiratory burst	1	COMP4737_C0.SE
715	BP	GO:0090143	nucleoid organization	1	COMP4968_C0.SE
720	BP	GO:0051245	negative regulation of cellular defense ...	1	COMP8919_C0.SE
727	BP	GO:0042254	ribosome biogenesis	33	COMP11085_C0.SE
760	BP	GO:0071555	cell wall organization	14	COMP10270_C0.SE
782	BP	GO:0015994	chlorophyll metabolic process	16	COMP12222_C0.SE

	category	ID	term	count	genes	logFC	a
1403	CC	GO:0048046	apoplast	18	COMP10372_C0_SEQ1	-1.08	
1494	CC	GO:0009507	chloroplast	96	COMP104278_C0_SEQ1	0.58	
1650	CC	GO:0000795	synaptonemal complex	3	COMP32314_C0_SEQ1	-0.95	
1658	CC	GO:0005622	intracellular	308	COMP10017_C0_SEQ1	-1.26	
2876	CC	GO:0009325	nitrate reductase complex	1	COMP78387_C0_SEQ1	-1.87	

	category	ID	term	count	genes
1061	MF	GO:0052624	2-phytyl-1,4-naphthoquinone methyltransf...	1	COMP15713_C0_S
1066	MF	GO:0050178	phenylpyruvate tautomerase activity	1	COMP16664_C0_S
1288	MF	GO:0004674	protein serine/threonine kinase activity	16	COMP10172_C0_S
1304	MF	GO:0008987	quinolinate synthetase A activity	1	COMP30135_C0_S