Stuff stuff I say

Module	Z	N	$N_e S$	$\alpha$	$\omega$	GO Term	Description	p
bisque4	3.827	191	0.137	0.402	0.080	GO:0010207	photosystem II assembly	1.9E-09
						GO:0019252	starch biosynthetic process	6.1E-08
						GO:0005982	starch metabolic process	1.2E-07
						GO:0000023	maltose metabolic process	1.6E-07
						GO:0005984	disaccharide metabolic process	6.4E-07
black	8.104	1106	0.147	0.290	0.053	GO:1902589	single-organism organelle	4.3E-05
							organization	
						GO:0022402	cell cycle process	4.5E-05
						GO:0009630	$\operatorname{gravitropism}$	8.9E-05
						GO:0009606	tropism	8.9E-05
						GO:0009629	response to gravity	1.4E-04
blue	12.664	2066	0.134	0.230	0.035	GO:0043043	peptide biosynthetic process	1.6E-90
						GO:0006412	translation	3.8E-90
						GO:0043604	amide biosynthetic process	6.0E-87
						GO:0006518	peptide metabolic process	4.2E-86
						GO:0043603	cellular amide metabolic process	7.8E-77
brown	-1.149	2757	0.147	0.236	0.040	GO:0006914	autophagy	1.2E-09
						GO:0044248	cellular catabolic process	6.9E-07
						GO:0046700	heterocycle catabolic process	1.5E-04
						GO:0044242	cellular lipid catabolic process	1.7E-04
						GO:0019439	aromatic compound catabolic	2.2E-04
							process	
darkgrey	1.195	357	0.137	0.182	0.027	NA	NA	NA
darkorange2	4.598	982	0.144	0.196	0.031	GO:0010264	myo-inositol hexakisphosphate	2.5E-05
							biosynthetic process	
						GO:0033517	myo-inositol hexakisphosphate	2.5E-05
							metabolic process	
						GO:0032958	inositol phosphate biosynthetic	4.0E-05
							process	
						GO:0046173	polyol biosynthetic process	6.3E-05
						GO:0043647	inositol phosphate metabolic	3.4E-04
							process	

Module	Z	N	$N_e S$	$\alpha$	$\omega$	GO Term	Description	p
darkred	3.277	456	0.124	0.375	0.065	GO:0048583	regulation of response to	2.0E-05
							stimulus	
						GO:0031347	regulation of defense response	3.2E-05
						GO:0045087	innate immune response	4.5E-05
						GO:1900674	olefin biosynthetic process	5.6E-05
						GO:1900673	olefin metabolic process	5.6E-05
darkturquoise	6.152	1003	0.126	0.359	0.061	GO:1901700	response to oxygen-containing	5.4E-11
							compound	
						GO:0042221	response to chemical	5.5E-09
						GO:0050896	response to stimulus	1.5E-08
						GO:0001101	response to acid chemical	7.1E-07
						GO:0048511	rhythmic process	1.6E-06
floralwhite	5.314	249	0.108	0.376	0.057	GO:0019682	glyceraldehyde-3-phosphate	1.4E-22
							metabolic process	
						GO:0019637	organophosphate metabolic	9.5E-22
							process	
						GO:0019288	isopentenyl diphosphate	3.6E-21
							biosynthetic process	
							methylerythritol 4-phosphate	
							pathway	
						GO:0009240	isopentenyl diphosphate	4.7E-21
							biosynthetic process	
						GO:0046490	isopentenyl diphosphate	4.7E-21
							metabolic process	
green	3.104	1269	0.155	0.231	0.041	GO:0009853	photorespiration	1.2E-11
Ü						GO:0043094	cellular metabolic compound	7.8E-10
							salvage	
						GO:0080129	proteasome core complex	1.2E-06
							assembly	
						GO:0043248	proteasome assembly	1.3E-06
						GO:0051788	response to misfolded protein	1.3E-06

Module	Z	N	$N_e S$	$\alpha$	$\omega$	GO Term	Description	p
grey60	3.874	278	0.102	0.507	0.090	GO:0007169	transmembrane receptor protein	4.1E-12
							tyrosine kinase signaling	
							pathway	
						GO:0007167	enzyme linked receptor protein	4.1E-12
							signaling pathway	
						GO:0007166	cell surface receptor signaling	2.1E-11
							pathway	
						GO:0006468	protein phosphorylation	2.6E-07
						GO:0071554	cell wall organization or	3.3E-05
							biogenesis	
lightcyan	18.410	2886	0.158	0.277	0.053	GO:1901293	nucleoside phosphate	7.6E-53
							biosynthetic process	
						GO:0009165	nucleotide biosynthetic process	4.0E-52
						GO:0006221	pyrimidine nucleotide	9.8E-41
							biosynthetic process	
						GO:0006220	pyrimidine nucleotide metabolic	9.8E-41
							process	
						GO:0046390	ribose phosphate biosynthetic	2.6E-40
							process	
lightsteelblue1	-0.078	73	0.109	0.517	0.103	GO:0006897	endocytosis	6.2E-08
						GO:0048268	clathrin coat assembly	6.8E-08
						GO:0006901	vesicle coating	9.5E-08
						GO:0016050	vesicle organization	1.3E-07
						GO:0071822	protein complex subunit	3.6E-04
							organization	
magenta	0.085	807	0.146	0.166	0.025	GO:0006661	phosphatidylinositol	5.9E-06
							biosynthetic process	
						GO:0046488	phosphatidylinositol metabolic	3.7E-05
							process	
						GO:0046474	glycerophospholipid	1.0E-04
							biosynthetic process	
						GO:0006650	glycerophospholipid metabolic	4.3E-04
							process	
						GO:0045017	glycerolipid biosynthetic process	5.2E-04

Module	Z	N	$N_e S$	$\alpha$	ω	GO Term	Description	р
mediumpurple3	13.539	74	0.173	0.326	0.074	GO:0007017	microtubule-based process	1.4E-30
						GO:0000911	cytokinesis by cell plate	7.0E-30
							formation	
						GO:0032506	cytokinetic process	1.3E-29
						GO:1902410	mitotic cytokinetic process	1.3E-29
						GO:1903047	mitotic cell cycle process	8.6E-27
midnightblue	24.002	771	0.148	0.189	0.030	GO:0010200	response to chitin	4.0E-50
						GO:0010243	response to organonitrogen	4.0E-50
							compound	
						GO:1901698	response to nitrogen compound	3.2E-47
						GO:0009719	response to endogenous stimulus	5.1E-40
						GO:0010033	response to organic substance	1.7E-33
plum1	10.286	98	0.200	0.361	0.101	GO:0009620	response to fungus	3.3E-05
						GO:0009723	response to ethylene	7.6E-04
						GO:0051707	response to other organism	7.6E-04
						GO:0051704	multi-organism process	8.9E-04
royalblue	14.434	263	0.102	0.468	0.077	GO:0055085	transmembrane transport	3.2E-04
						GO:0005984	disaccharide metabolic process	4.5E-04
						GO:0009311	oligosaccharide metabolic	8.8E-04
							process	
saddlebrown	10.662	147	0.176	0.403	0.105	GO:0006260	DNA replication	1.4E-11
						GO:0006270	DNA replication initiation	1.9E-10
						GO:0040029	regulation of gene expression	3.4E-10
							epigenetic	
						GO:0061647	histone H3-K9 modification	8.3E-10
						GO:0051567	histone H3-K9 methylation	8.3E-10
sienna3	11.239	124	0.117	0.435	0.079	GO:0044710	single-organism metabolic	2.6E-07
							process	
						GO:0016109	tetraterpenoid biosynthetic	1.2E-06
							process	
						GO:0016108	tetraterpenoid metabolic	1.2E-06
							process	
						GO:0016116	carotenoid metabolic process	1.2E-06
						GO:0016117	carotenoid biosynthetic process	1.2E-06

Module	Z	N	$N_e S$	$\alpha$	$\omega$	GO Term	Description	р
skyblue3	21.610	119	0.216	-0.005	-0.001	GO:0009697	salicylic acid biosynthetic	9.3E-12
							process	
						GO:0009696	salicylic acid metabolic process	9.3E-12
						GO:0009627	systemic acquired resistance	1.0E-11
						GO:0046189	phenol-containing compound	1.3E-11
							biosynthetic process	
						GO:0018958	phenol-containing compound	1.9E-11
							metabolic process	
tan	2.090	591	0.127	0.419	0.079	GO:0045491	xylan metabolic process	9.0E-12
						GO:0010410	hemicellulose metabolic process	1.5E-11
						GO:0010413	glucuronoxylan metabolic	5.7E-11
							process	
						GO:0045492	xylan biosynthetic process	7.3E-11
						GO:0070592	cell wall polysaccharide	1.2E-10
							biosynthetic process	
turquoise	6.411	4005	0.157	0.321	0.065	GO:0006486	protein glycosylation	3.1E-14
						GO:0043413	macromolecule glycosylation	3.1E-14
						GO:0070085	glycosylation	4.2E-14
						GO:0009630	$\operatorname{gravitropism}$	1.8E-09
						GO:0009606	tropism	1.8E-09
yellowgreen	10.232	120	0.148	0.531	0.147	GO:0010200	response to chitin	1.2E-09
						GO:0010243	response to organonitrogen	1.2E-09
							compound	
						GO:1901698	response to nitrogen compound	1.4E-09
						GO:0006865	amino acid transport	3.4E-08
						GO:0002679	respiratory burst involved in	4.0E-08
							defense response	