

Table S1. Differential phosphorylated protein table of *R. chrysanthum* under UV-B stress

Protein accession	Position	Amino acid	Protein description	KEGG Gene	P value	Regulated Type
Gene.11338_CL83 5.Contig6_All	184	S	RPM1-interacting protein 4	RIN4; RPM1- interacting protein 4	0.0069796	Down
Gene.11338_CL83 5.Contig6_All	86	S	RPM1-interacting protein 4	RIN4; RPM1- interacting protein 4	0.010177	Down
Gene.13985_CL11 05.Contig1_All	109	S	"Plastid-lipid- associated protein 6, chloroplastic"		0.0023211	Down
Gene.13985_CL11 05.Contig1_All	220	S	"Plastid-lipid- associated protein 6, chloroplastic"		0.041461	Up
Gene.14291_CL11 44.Contig3_All	921	T	PREDICTED: uncharacterized protein LOC100250143 isoform X1 [Vitis vinifera]		0.028078	Down
Gene.14602_CL11 80.Contig5_All	11	S	60S ribosomal protein L6	RP-L6e; large subunit ribosomal protein L6e	0.0008157 5	Down
Gene.14686_CL11 91.Contig2_All	320	S	ABC transporter C family member 5		0.032404	Up
Gene.15319_CL12 47.Contig1_All	107	T	"Transketolase, chloroplastic"	E2.2.1.1; transketolase [EC:2.2.1.1]	0.0023804	Up
Gene.19346_CL17 03.Contig8_All	154	S	Serine/threonine- protein kinase SAPK2	SNRK2; serine/threo nine-protein kinase SRK2 [EC:2.7.11.1]	0.04842	Up
Gene.20539_CL18 24.Contig2_All	135	S	"Sec-independent protein translocase protein TATA, chloroplastic"	tatA; sec- independent protein translocase protein TatA	0.035424	Up
Gene.21159_CL19 03.Contig2_All	178	S	"ATP synthase subunit b', chloroplastic"	ATPF0B; F- type H+- transporting ATPase subunit b	0.0000627 84	Up

Gene.23080_CL21	356	T	Protein BTR1		0.0059976	Down
52.Contig1_All						
Gene.23829_CL22	60	S	CSC1-like protein		0.035557	Down
26.Contig3_All			HYP1			
Gene.24603_CL23	725	S	Nuclear pore complex protein NUP98A	NUP98; nuclear pore complex protein Nup98-Nup96	0.023098	Down
33.Contig3_All						
Gene.26206_CL25	522	S	Serine/threonine-protein kinase BLUS1		0.029463	Up
59.Contig3_All						
Gene.26206_CL25	491	S	Serine/threonine-protein kinase BLUS1		0.0137422	Up
59.Contig3_All						
Gene.26950_CL26	398	S	"Monodehydroascorbate reductase, chloroplastic/mitochondrial"	E1.6.5.4; monodehydroascorbate reductase (NADH) [EC:1.6.5.4]	0.031282	Down
40.Contig3_All						
Gene.27331_CL27	77	S	Chitin-binding lectin 1	EIF2B4; translation initiation factor eIF-2B subunit delta	0.044879	Down
04.Contig2_All						
Gene.28080_CL28	137	S	PREDICTED: uncharacterized protein LOC105120307 isoform X2 [Populus euphratica]		0.04908	Down
24.Contig6_All						
Gene.28776_CL29	91	T	Nucleoside diphosphate kinase 1	ndk; nucleoside-diphosphate kinase [EC:2.7.4.6]	0.0022381	Up
33.Contig2_All						
Gene.29020_CL29	100	S	Isocitrate dehydrogenase [NADP]	IDH1; isocitrate dehydrogenase [EC:1.1.1.42]	0.0037984	Down
93.Contig9_All						

Gene.30247_CL31	3	S	Nitrate regulatory gene2 protein		0.021555	Down
60.Contig4_All						
Gene.31339_CL33	369	T	Monosaccharide-sensing protein 2		0.0044396	Up
46.Contig6_All						
Gene.31339_CL33	419	S	Monosaccharide-sensing protein 2		0.0120847	Up
46.Contig6_All						
Gene.32668_CL35	107	T	"PGR5-like protein 1B, chloroplastic"		0.0008845	Down
93.Contig4_All						
Gene.33054_CL36	422	T	ABSCISIC ACID-INSENSITIVE 5-like protein 5	ABF; ABA responsive element binding factor	0.0020837	Up
61.Contig1_All						
Gene.34110_CL38	250	S	MAP3K epsilon protein kinase 1		0.0040816	Up
30.Contig1_All						
Gene.34124_CL38	95	T	"RuBisCO large subunit-binding protein subunit alpha, chloroplastic"		0.0046957	Up
32.Contig4_All						
Gene.34496_CL38	240	S	Auxin efflux carrier component 7		0.0054587	Up
92.Contig8_All						
Gene.34715_CL39	387	S	60S acidic ribosomal protein P0	RP-LP0; large subunit ribosomal protein LP0	0.022636	Down
46.Contig2_All						
Gene.3570_CL223	10	S	PREDICTED: conserved oligomeric Golgi complex subunit 1 [Vitis vinifera]		0.0007611	Down
.Contig5_All					7	
Gene.36597_CL43	88	S	"Phosphoglycerate kinase, chloroplastic"	PGK; phosphoglycerate kinase [EC:2.7.2.3]	0.0000835	Up
35.Contig4_All					25	
Gene.36597_CL43	86	T	"Phosphoglycerate kinase, chloroplastic"	PGK; phosphoglycerate kinase [EC:2.7.2.3]	0.0032231	Up
35.Contig4_All						
Gene.36604_CL43	409	S	Protein SRC2		0.0062008	Up
38.Contig2_All						
Gene.37414_CL44	77	S	"Ferritin-1, chloroplastic"		0.0096954	Up
89.Contig4_All						
Gene.38423_CL47	214	S	"Endo-1,3;1,4-beta-D-glucanase"		0.003559	Up
05.Contig5_All						

Gene.38510_CL47 26.Contig1_All	93	S	Tobamovirus multiplication protein 2A		0.0040639	Down
Gene.3887_CL243 .Contig4_All	439	S	"Glyceraldehyde-3- phosphate dehydrogenase B, chloroplastic"	GAPA; glyceraldehyd e-3-phosphate dehydrogenas e (NADP+) (phosphorylat ing) [EC:1.2.1.13]	0.0058047	Up
Gene.3887_CL243 .Contig4_All	144	S	"Glyceraldehyde-3- phosphate dehydrogenase B, chloroplastic"	GAPA; glyceraldehyd e-3-phosphate dehydrogenas e (NADP+) (phosphorylat ing) [EC:1.2.1.13]	0.0019579 5	Up
Gene.38972_CL48 27.Contig1_All	60	S	"Fructose- bisphosphate aldolase 2, chloroplastic"	ALDO; fructose- bisphosphate aldolase, class I [EC:4.1.2.13]	0.0003201 4	Down
Gene.38985_CL48 29.Contig2_All	221	S	"Gamma carbonic anhydrase 1, mitochondrial"		0.025757	Down
Gene.39709_CL50 12.Contig3_All	41	S	Polyadenylation and cleavage factor homolog 1	PCF11; pre- mRNA cleavage complex 2 protein Pcf11	0.004624	Down
Gene.40269_CL51 29.Contig3_All	181	T	"20 kDa chaperonin, chloroplastic"		0.010884	Up
Gene.40497_CL51 73.Contig2_All	78	S	Phosphoprotein ECPP44		0.04812	Down
Gene.4136_CL252 .Contig3_All	649	S	"Glucose-6- phosphate isomerase 1, chloroplastic"	GPI; glucose- 6-phosphate isomerase [EC:5.3.1.9]	0.0159407	Down
Gene.42653_CL56 97.Contig2_All	1408	S	Protein transport protein SEC16B homolog		0.0109043	Down

Gene.43342_CL58	146	S	"Peroxisome Q, chloroplast"		0.0003378	Up
54.Contig2_All					7	
Gene.43600_CL59	36	S	MLP-like protein		0.0000587	Down
31.Contig3_All					16	
Gene.44435_CL61	47	T	"Phosphoribulokinase, chloroplast"	PRK;	0.003202	Down
25.Contig3_All				phosphoribulokinase [EC:2.7.1.19]		
Gene.45512_CL64	519	T	Leucine-rich repeat extensin-like protein 3	ACIN1; apoptotic chromatin condensation inducer in the nucleus	0.0029379	Up
07.Contig3_All						
Gene.45512_CL64	556	S	Leucine-rich repeat extensin-like protein 3	ACIN1; apoptotic chromatin condensation inducer in the nucleus	0.0000372	Down
07.Contig3_All					21	
Gene.45512_CL64	526	S	Leucine-rich repeat extensin-like protein 3	ACIN1; apoptotic chromatin condensation inducer in the nucleus	0.0000358	Up
07.Contig3_All					16	
Gene.46142_CL65	165	S	"1,4-alpha-glucan-branching enzyme 2-2, chloroplast/amyloplastic"	GBE1; 1,4-alpha-glucan branching enzyme [EC:2.4.1.18]	0.0004442	Down
69.Contig6_All					1	
Gene.46959_CL67	168	T	RPM1-interacting protein 4	RIN4; RPM1-interacting protein 4	0.0174989	Up
76.Contig1_All						
Gene.46959_CL67	163	T	RPM1-interacting protein 4	RIN4; RPM1-interacting protein 4	0.04094	Up
76.Contig1_All						
Gene.47171_CL68	265	S	hypothetical protein Ccrd_008086 [Cynara cardunculus var. scolymus]	BABAM; BRISC and BRCA1-A complex member 1	0.0025644	Down
21.Contig2_All						

Gene.47456_CL68 76.Contig2_All	454	S	Protein phosphatase 2C and cyclic nucleotide- binding/kinase domain-containing protein	0.011857	Down
Gene.48804_CL71 47.Contig2_All	328	S	Eukaryotic translation initiation factor 4B1	0.0000201 88	Down
Gene.49846_CL73 99.Contig2_All	58	S	SUN domain- containing protein 1	0.018705	Down
Gene.49846_CL73 99.Contig2_All	48	S	SUN domain- containing protein 1	0.021356	Down
Gene.51486_CL77 52.Contig8_All	64	S	"Photosystem II 10 kDa polypeptide, chloroplastic"	psbR; photosystem II 10kDa protein	0.0044599 Down
Gene.52037_CL78 39.Contig2_All	26	S	Annexin D4	0.0082023	Down
Gene.53321_CL80 52.Contig1_All	271	T	Heat shock cognate 70 kDa protein 2	HSPA1s; heat shock 70kDa protein 1/2/6/8	0.0018776 8 Down
Gene.55228_CL82 12.Contig5_All	3	S	V-type proton ATPase catalytic subunit A	ATPeV1A; V- type H+- transporting ATPase subunit A [EC:7.1.2.2]	0.0052807 Down
Gene.56696_CL83 37.Contig10_All	392	S	"Chaperonin 60 subunit beta 2, chloroplastic"	groEL; chaperonin GroEL	0.031479 Up
Gene.57775_Unig ene284_All	96	S	Probable calcium- binding protein CML18	CALM; calmodulin	0.039236 Down
Gene.58581_Unig ene831_All	67	S	Metacaspase-4	0.0003616 6	Down
Gene.58589_Unig ene835_All	783	S	EH domain- containing protein 2	0.027299	Down
Gene.64089_Unig ene5111_All	236	S	Uncharacterized protein Atlg03900	0.0032601	Down
Gene.65018_Unig ene5787_All	524	S	GBF-interacting protein 1	0.0108382	Up

Gene.65697_Unig ene6211_All	232	S	Photosystem protein D1	II	psbA; photosystem II P680 reaction center D1 protein [EC:1.10.3.9]	0.0000245 07	Up
Gene.66649_Unig ene6892_All	237	S	"RNA pseudouridine synthase 6, chloroplastic"			0.0090224	Down
Gene.68254_Unig ene8007_All	178	S	Protein BONZAI 1			0.0006399 9	Down
Gene.6848_CL464 .Contig2_All	6	S	Probable aquaporin PIP2-8			0.0011981 8	Down
Gene.6848_CL464 .Contig2_All	282	T	Probable aquaporin PIP2-8			0.0116366	Down
Gene.69502_Unig ene8888_All	119	S	187-kDa microtubule- associated protein AIR9			0.032743	Down
Gene.70938_Unig ene9872_All	291	S	"Membrane- associated 30 kDa protein, chloroplastic"			0.0041569	Down
Gene.71075_Unig ene9967_All	51	S	"Linoleate 13S- lipoxygenase 2-1, chloroplastic"		LOX2S; lipoxygenase [EC:1.13.11.1 2]	0.0000784 86	Down
Gene.71128_Unig ene9997_All	206	S	Acyl-CoA-binding domain-containing protein 1			0.0051022	Down
Gene.71430_Unig ene10207_All	534	S	Dynamin-2B		DNM; dynamin GTPase [EC:3.6.5.5]	0.0000984 55	Down
Gene.71430_Unig ene10207_All	881	S	Dynamin-2B		DNM; dynamin GTPase [EC:3.6.5.5]	0.012035	Down
Gene.71879_Unig ene10600_All	190	S	uncharacterized protein LOC107468142 [Arachis duranensis]			0.028077	Up

Gene.72388_Unig ene11314_All	155	S	hypothetical protein [Camellia sinensis]	0.0010840 9	Down
Gene.72474_Unig ene11360_All	95	S	Mitochondrial outer membrane protein porin of 34 kDa	0.0011355 7	Down
Gene.72804_Unig ene11573_All	131	S	hypothetical protein VITISV_016468 [Vitis vinifera]	0.0049434	Down
Gene.73161_Unig ene11817_All	157	S	Methyl-CpG- binding domain- containing protein 13	0.0075173	Down
Gene.73161_Unig ene11817_All	167	S	Methyl-CpG- binding domain- containing protein 13	0.039717	Down
Gene.73460_Unig ene12021_All	60	S	"Peroxisome-2F, mitochondrial"	0.047801	Up
Gene.73584_Unig ene12104_All	149	T	Exocyst complex component EXO70B2	0.0038577	Up
Gene.73621_Unig ene12126_All	266	S	"Oxygen-dependent coproporphyrinogen -III oxidase, chloroplastic"	CPOX; coproporphyrinogen III oxidase [EC:1.3.3.3]	0.0070391 Up
Gene.73685_Unig ene12173_All	18	S	Stem-specific protein TSJT1	0.0006210 1	Up
Gene.75286_Unig ene13818_All	171	S	"50S ribosomal protein L29, chloroplastic"	RP-L29; large subunit ribosomal protein L29	0.0017037 9 Down
Gene.75292_Unig ene13824_All	56	S	Reticulon-like protein B4	0.035724	Up
Gene.7572_CL536 .Contig1_All	44	S	18.2 kDa class I heat shock protein	HSP20; HSP20 family protein	0.0051778 Down
Gene.7619_CL543 .Contig2_All	217	S	Glycine-rich protein 2	0.0016031 2	Down



Gene.76858_Unig ene15319_All	164	S	Probable ADP- ribosylation factor GTPase-activating protein AGD6	ARFGAP1; ADP- ribosylation factor GTPase- activating protein 1	0.011138	Down
Gene.77037_Unig ene15420_All	466	S	PREDICTED: putative G3BP-like protein isoform X1 [Nicotiana attenuata]		0.022538	Down
Gene.77355_Unig ene15616_All	240	S	40S ribosomal protein S6	RP-S6e; small subunit ribosomal protein S6e	0.0008411 1	Up
Gene.77538_Unig ene15752_All	257	S	Pyruvate decarboxylase 1	PDC; pyruvate decarboxylase [EC:4.1.1.1]	0.0001636 49	Down
Gene.79431_Unig ene17536_All	43	S	protein SSUH2 homolog [Manihot esculenta]		0.0151808	Up
Gene.7986_CL578 .Contig2_All	81	S	"Photosystem II 10 kDa polypeptide, chloroplastic"	psbR; photosystem II 10kDa protein	1.76886E- 05	Down
Gene.7986_CL578 .Contig2_All	73	S	"Photosystem II 10 kDa polypeptide, chloroplastic"	psbR; photosystem II 10kDa protein	0.0049196	Down
Gene.80537_Unig ene18753_All	549	S	Flowering time control protein FPA		0.033263	Down
Gene.80865_Unig ene18952_All	519	T	Kinesin-like protein KIN-14B		0.0000604 18	Up
Gene.80865_Unig ene18952_All	660	S	Kinesin-like protein KIN-14B		0.010517	Down
Gene.81168_Unig ene19137_All	29	S	PREDICTED: uncharacterized protein LOC102598108 [Solanum tuberosum]	HSPBP1; hsp70- interacting protein	0.0022984	Down

Gene.81465_Unig ene19343_All	330	S	Proline-rich receptor-like protein kinase PERK2		0.0091392	Down
Gene.81465_Unig ene19343_All	105	T	Proline-rich receptor-like protein kinase PERK2		0.002197	Down
Gene.81522_Unig ene19369_All	80	T	Leucine-rich repeat extensin-like protein 3		0.0003439 4	Down
Gene.81531_Unig ene19376_All	621	S	Eukaryotic translation initiation factor isoform 4G-2	EIF4G; translation initiation factor 4G	0.0004407 7	Down
Gene.81531_Unig ene19376_All	61	S	Eukaryotic translation initiation factor isoform 4G-2	EIF4G; translation initiation factor 4G	0.0000353 94	Down
Gene.81531_Unig ene19376_All	184	S	Eukaryotic translation initiation factor isoform 4G-2	EIF4G; translation initiation factor 4G	0.0013391 7	Down
Gene.81544_Unig ene19383_All	55	S	"Fructose- bisphosphate aldolase cytosolic"	6, ALDO; fructose- bisphosphate aldolase, class I [EC:4.1.2.13]	0.0084593	Up
Gene.82839_Unig ene20755_All	608	S	Heat shock 70 kDa protein 16		0.0002796 9	Down
Gene.83286_Unig ene21046_All	51	T	hypothetical protein TSUD_229720 [Trifolium subterraneum]		0.0008192 4	Down
Gene.83366_Unig ene21103_All	951	S	"Histidine--tRNA ligase, cytoplasmic"	HARS; histidyl-tRNA synthetase [EC:6.1.1.21]	0.0028558	Down
Gene.85388_Unig ene22921_All	159	S	2-methylene-furan- 3-one reductase		1.68112E- 05	Up
Gene.85395_Unig ene22926_All	63	S	"Protein CURVATURE THYLAKOID 1A, chloroplastic"		0.0050235	Down

Gene.85450_Unig ene22951_All	33	S	Probable serine/threonine- protein kinase SIS8	0.027439	Down
Gene.85450_Unig ene22951_All	1159	T	Probable serine/threonine- protein kinase SIS8	0.0020803	Down
Gene.85630_Unig ene23100_All	152	S	Cold shock protein 2	0.0051199	Down
Gene.86177_Unig ene24148_All	140	S	Formin-like protein 14	0.0148779	Down
Gene.87528_Unig ene32298_All	37	T	"Chlorophyll a-b binding protein CP26, chloroplastic"	LHCB5; light- harvesting complex II chlorophyll a/b binding protein 5 1	0.0004351 Down
Gene.8795_CL667 .Contig11_All	203	T	Protein NTM1-like 9	0.032002	Down
Gene.8795_CL667 .Contig11_All	510	T	Protein NTM1-like 9	0.038898	Down
Gene.8795_CL667 .Contig11_All	14	S	Protein NTM1-like 9	0.024445	Down
Gene.9131_CL681 .Contig8_All	68	S	Uncharacterized membrane protein Atlg16860	0.0103017	Down
Gene.9131_CL681 .Contig8_All	72	S	Uncharacterized membrane protein Atlg16860	KEGG Gene 6 0.0015018	Down