

A Label-Free Proteomic and Complementary Metabolomic Analysis of Leaves of the Resurrection Plant *Xerophyta schlechteri* during Dehydration

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Table S1: List of differentially expressed proteins involved early response to drying identified in *X. schlechteri* leaf samples.

Accession	Description	base Mean	log2FoldC hange	p-value	InterPro	Go-term
Xvis03_221564-PA	processed-gene-12.109- mRNA-1protein Name:"Similar to Late embryogenesis abundant protein D-34 (Gossypium hirsutum)" AED:0.11 eAED:0.19 QI:0 0 0 1 1 1 2 0 254	2.2082 56511	2.07869733	0.003377 706	IPR00701 1 (PFAM)	no GO terms
Xvis03_200886-PA	augustus-gene-6.42- mRNA-1protein Name:"Similar to PLP1 Patatin-like protein 1 (Oryza sativa subsp. japonica)" AED:0.26 eAED:0.26 QI:72 0.4 0.16 1 1 1 6 0 3 1 4	2.8898 69909	1.55299452 9	0.004367 183	IPR00264 1 (PFAM)	P:GO:000662 9
Xvis03_220002-PA	augustus-gene-50.23- mRNA-1protein Name:"Similar to Desiccation-related protein PCC3-06 (Craterostigma plantagineum)" AED:0.00 eAED:0.00 QI:100 1 1 1 1 1 2 285 21 8	8.3481 686	1.70902689 7	0.007333 848		no GO terms

Xvis03_225004-PA	processed-gene-0.29-mRNA-1 protein Name:"Similar to GLU Ferredoxin-dependent glutamate synthase, chloroplastic (Oryza sativa subsp. japonica)" AED:0.15 eAED:0.20 QI:0 0.82 0.86 0.94 1 1 36 0 1763	4.5383 97579	1.09387298 4	0.010961 575	IPR01793 2 (PFAM)	
Xvis03_211917-PA	augustus-gene-8.2- mRNA-1 protein Name:"Similar to UGT78D2 UDP-glycosyltransferase 78D2 (Arabidopsis thaliana)" AED:0.00 eAED:0.00 QI:173 1 1 1 1 1 2 210 45 4	1.6966 12041	1.92098986 8	0.011244 498	IPR00221 3 (PFAM)	F:GO:001675 8
Xvis03_202087-PA	augustus-gene-8.14-mRNA-1 protein Name:"Similar to AAE3 Oxalate--CoA ligase (Arabidopsis thaliana)" AED:0.02 eAED:0.02 QI:521 1 1 1 1 1 4 258 51 7	2.2123 68933	1.70659942 2	0.01303	IPR00087 3 (PFAM)	F:GO:000382 4
Xvis03_203578-PA	processed-gene-12.33-mRNA-1 protein Name:"Similar to Polyphenol oxidase, chloroplastic (Vitis vinifera)" AED:0.36 eAED:0.40 QI:797 0.5 0.33 1 1 1 3 0 2 73	4.5515 93209	0.95085778 2	0.016000 633	IPR00222 7	F:GO:000409 7;F:GO:0016491;P:GO:0055114
Xvis03_211325-PA	augustus-gene-1.70- mRNA-1 protein Name:"Similar to GDCSPA Glycine Dehydrogenase (decarboxylating) A, mitochondrial (Flaveria pringlei)" AED:0.11 eAED:0.11 QI:248 0.76 0.85 1 1 1 14 3 21 903	10.765 76001	0.72916386 2	0.016180 98	IPR00259 1 (PFAM);	F:GO:000382 4;F:GO:0004375;P:GO:0006546;P:GO:005514
Xvis03_221126-PA	processed-gene-11.3-mRNA-1 protein Name:"Similar to Mavicyanin (Cucurbita pepo)" AED:0.03 eAED:0.03 QI:68 1 1 1 1 1 2 217 190	0.7358 49705	1.86719922	0.016866 27	IPR00897 2	F:GO:000905

Xvis03_225456-PA	processed-gene-0.12- mRNA-1 protein Name:"Similar to Polyphenol oxidase, chloroplastic (Vitis vinifera)" AED:0.01 eAED:0.01 QI:289 1 1 1 1 2 284 597	3.9532 37343	0.91393486	0.026841 309	IPR00222 7 (PFAM)	F:GO:000409 7;F:GO:0016491;P:GO:0055114
Xvis03_222086-PA	processed-gene-4.0- mRNA-1 protein Name:"Similar to SBT3.3 Subtilisin-like protease SBT3.3 (Arabidopsis thaliana)" AED:0.15 eAED:0.15 QI:86 0.88 0.8 1 1 0.9 10 0 661	7.0814 85008	0.90675084 6	0.028952 361	IPR03704 5	no GO terms
Xvis03_215744-PA	processed-gene-5.46- mRNA-1 protein Name:"Similar to CAL1 Calmodulin (Medicago sativa)" AED:0.17 eAED:0.17 QI:127 1 1 1 1 2 496 149	0.8846 96437	1.63547264 7	0.030612 647	IPR00204 8 (PFAM)	F:GO:000550 9;P:GO:0019722
Xvis03_210936-PA	augustus-gene-1.31- mRNA-1 protein Name:"Similar to At5g61250 Heparanase-like protein 2 (Arabidopsis thaliana)" AED:0.14 eAED:0.14 QI:264 0.22 0.2 1 0.88 0.9 10 0 512	4.2412 27829	0.95413208 9	0.034425 962	IPR00519 9 (PFAM)	C:GO:00160 20;F:GO:0016798
Xvis03_225004-PA	augustus-gene-8.38- mRNA-1 protein Name:"Similar to GLU Ferredoxin-dependent glutamate synthase, chloroplastic (Oryza sativa subsp. japonica)" AED:0.12 eAED:0.12 QI:225 0.96 1 1 0.96 1 32 87 1535	4.6276 47757	0.95110059	0.036775 888	IPR03648 5	no GO terms
Xvis03_207220-PA	augustus-gene-29.99- mRNA-1 protein Name:"Similar to Bowman-Birk type trypsin	1.4674 85389	1.49031191 4	0.037523 55	IPR00087 7 (PFAM)	F:GO:000486 7;C:GO:0005576

	inhibitor (Triticum aestivum)" AED:0.14 eAED:0.14 QI:36 1 1 1 1 2 205 120					
Xvis03_225299-PA	processed-gene- 0.7- mRNA-1 protein Name:"Similar to AGT1 Serine--glyoxylate aminotransferase (Arabidopsis thaliana)" AED:0.11 eAED:0.11 QI:101 1 1 1 0.8 0.66 6 20 8 401	5.4582 4752	0.79565154 8	0.042740 279	IPR01542 1	F:GO:000382 4
Xvis03_206589-PA	processed-gene-9.106- mRNA-1 protein Name:"Similar to CYP74A2 Allene oxide synthase 2 (Oryza sativa subsp. japonica)" AED:0.00 eAED:0.00 QI:0 -1 0 1 - 1 1 1 0 486	4.1895 43295	0.85953689 8	0.042986 185	IPR00112 8 (PFAM)	F:GO:000556 ;F:GO:00165 F:GO:002003 7;P:GO:0055 114
Xvis03_221325-PA	processed-gene- 6.29- mRNA-1 protein Name:"Similar to B19.4 Late embryogenesis abundant protein B19.4 (Hordeum vulgare)" AED:0.16 eAED:0.16 QI:0 0.66 0.5 0.75 1 1 4 1 1 7 181	3.8430 70937	1.15948316 1	0.044432 356	IPR03895 6 (PFAM)	no GO terms
Xvis03_223476-PA	augustus-gene-2.101- mRNA-1 protein Name:"Similar to Pyruvate kinase, cytosolic isozyme (Glycine max)" AED:0.04 eAED:0.04 QI:138 1 1 1 1 1 3 406 53 3	3.2602 31664	0.98750497	0.047705 112	IPR00169 7	F:GO:000028 7;F:GO:0003 824;F:GO:00 04743;P:GO: 0006096;F:G O:0030955
Xvis03_223774-PA	processed-gene- 15.13- mRNA-1 protein Name:"Similar to Late embryogenesis abundant protein 76 (Brassica napus)" AED:0.02 eAED:0.02 QI:314 1 1 1 1 1 3 870 26 6	3.8306 48677	1.53385823 4	0.047990 256	IPR00486 4 (PFAM)	no GO terms
Xvis03_221252-PA	processed-gene-1.52- mRNA-1 protein Name:"Similar to SPG20 Spartin (Homo sapiens)" AED:0.03 eAED:0.03	2.6149 50623	1.38375868 6	0.049376 875	IPR00968 6	no GO terms

QI:113|1|1|1|1|1|4|834|40
1

Table S2: List of differentially expressed proteins involved mid response to drying identified in *X. schlechteri* leaf samples.

Accession	Description	base Mean	log2FoldC hange	pvalue	InterPro	Go-Terms
Xvis03_22 0002-PA	processed-gene-8.116- mRNA-1 protein Name:"Similar to Desiccation-related protein PCC3-06 (Craterostigma plantagineum)" AED:0.00 eAED:0.00 QI:334 1 1 1 1 1 2 386 231	8.3481 7	2.74168	1.13E- 05		no GO terms
Xvis03_20 2087-PA	augustus-gene-8.14-mRNA- 1 protein Name:"Similar to AAE3 Oxalate--CoA ligase (Arabidopsis thaliana)" AED:0.02 eAED:0.02 QI:521 1 1 1 1 1 4 258 517	2.2123 7	2.3688	0.00046	IPR0008 73 (PFAM)	F:GO:0003824
Xvis03_20 4003-PA	augustus-gene-27.86- mRNA-1 protein Name:"Similar to Aldose reductase (Hordeum vulgare)" AED:0.09 eAED:0.09 QI:204 1 1 1 1 1 9 270 319	3.1744 1	1.94368	0.0005	IPR0204 71	F:GO:0016491; P:GO:0055114
Xvis03_21 1917-PA	augustus-gene-8.2-mRNA-1 protein Name:"Similar to UGT78D2 UDP- glycosyltransferase 78D2 (Arabidopsis thaliana)" AED:0.00 eAED:0.00 QI:173 1 1 1 1 1 2 210 454	1.6966 1	2.56191	0.00066	IPR0022 13 (PFAM)	F:GO:0016758
Xvis03_21 5617-PA	late embryogenesis abundant protein D-29	3.298 73	2.03005	0.0009		no GO terms

Xvis03_22 1325-PA	processed-gene-6.29- mRNA-1 protein Name:"Similar to B19.4 Late embryogenesis abundant protein B19.4 (Hordeum vulgare)" AED:0.16 eAED:0.16 QI:0 0.66 0.5 0.75 1 1 4 117 181	3.843 07	1.81639	0.00126	IPR0389 56 (PFAM)	no GO terms
Xvis03_21 0802-PA	processed-gene-9.8-mRNA- 1 protein Name:"Similar to LTI65 Low-temperature- induced 65 kDa protein (Arabidopsis thaliana)" AED:0.00 eAED:0.00 QI:247 1 1 1 1 1 5 289 574	3.507 13	2.00575	0.00161		P:GO:0009737
Xvis03_21 6950-PA	augustus-gene-2.19-mRNA- 1 protein Name:"Similar to 11 kDa late embryogenesis abundant protein (Helianthus annuus)" AED:0.13 eAED:0.13 QI:0 0.5 0.33 0.66 1 1 3 337 255	5.285 24	1.65506	0.00189	IPR0055 13 (PFAM)	P:GO:0009793
Xvis03_22 1252-PA	augustus-gene-6.27-mRNA- 1 protein Name:"Similar to SPG20 Spartin (Homo sapiens)" AED:0.04 eAED:0.04 QI:93 1 1 1 0.75 0.6 5 21 403	2.614 95	2.13635	0.00196	IPR0096 86 (PFAM);	no GO terms
Xvis03_21 9751-PA	augustus-gene-2.77-mRNA- 1 protein Name:"Similar to GAPC3 Glyceraldehyde-3- phosphate dehydrogenase 3, cytosolic (Oryza sativa subsp. japonica)" AED:0.27 eAED:0.27 QI:255 0.9 1 1 1 1 1 366 28 8	12.40 61	0.86947	0.00568	IPR0208 31	F:GO:0016620; P:GO:0055114
Xvis03_21 1956-PA	embryonic protein DC-8 isoform X2	10.54 62	1.45642	0.00591		no GO terms
Xvis03_22 1252-PA	augustus-gene-6.27-mRNA- 1 protein Name:"Similar to SPG20 Spartin (Homo sapiens)" AED:0.04 eAED:0.04	1.188 63	2.13471	0.00628	IPR0096 86 (PFAM);	no GO terms

QI:93|1|1|1|0.75|0.6|5|21|403

Xvis03_20 5230-PA	processed-gene-22.97- mRNA-1 protein Name:"Similar to RAB18 Dehydrin Rab18 (Arabidopsis thaliana)" AED:0.00 eAED:0.00 QI:93 1 1 1 1 1 2 247 147	5.055 44	1.4358	0.00704	IPR0001 67 (PFAM)	P:GO:0009415
Xvis03_22 0790-PA	augustus-gene-7.89-mRNA- 1 protein Name:"Similar to SYNPCC7002_A1590 Uncharacterized protein SYNPCC7002_A1590 (Synechococcus sp. (strain ATCC 27264 / PCC 7002 / PR- 6))" AED:0.04 eAED:0.04 QI:148 1 1 1 1 1 6 744 229	1.305 24	2.0387	0.00743	IPR0189 71 (PFAM)	no GO terms
Xvis03_22 1564-PA	augustus-gene-1.8-mRNA-1 protein Name:"Similar to Late embryogenesis abundant protein D-34 (Gossypium hirsutum)" AED:0.08 eAED:0.23 QI:0 0 0.5 1 1 1 2 238 274	2.208 26	1.93331	0.0076	IPR0070 11 (PFAM)	no GO terms
Xvis03_22 3774-PA	augustus-gene-3.64-mRNA- 1 protein Name:"Similar to LEA14-A Late embryogenesis abundant protein Lea14-A (Gossypium hirsutum)" AED:0.40 eAED:0.40 QI:0 0 0 1 1 1 2 0 155	3.556 28	1.5758	0.00796	IPR0048 64 (PFAM)	no GO terms
Xvis03_20 5230-PA	processed-gene-22.97- mRNA-1 protein Name:"Similar to RAB18 Dehydrin Rab18 (Arabidopsis thaliana)" AED:0.00 eAED:0.00 QI:93 1 1 1 1 1 2 247 147	7.330 68	1.1034	0.01074	IPR0001 67 (PFAM)	P:GO:0009415

Xvis03_20 8058-PA	Processed-gene-23.43- mRNA-1 protein Name:"Similar to CML18 Probable calcium-binding protein CML18 (Oryza sativa subsp. japonica)" AED: 0.02 eAED: 0.02 QI:0 -1 0 1 - 1 1 1 0 161	0.9707	1.97236	0.01121		F:GO:0005509
Xvis03_21 8200-PA	augustus-gene-6.42-mRNA- 1 protein Name:"Similar to PLP1 Patatin-like protein 1 (Oryza sativa subsp. japonica)" AED:0.26 eAED:0.26 QI:72 0.4 0.16 1 1 1 6 0 314	2.889 87	1.4167	0.01223	IPR0026 41 (PFAM)	P:GO:0006629
Xvis03_22 0002-PA	processed-gene-8.116- mRNA-1 protein Name:"Similar to Desiccation-related protein PCC3-06 (Craterostigma plantagineum)" AED:0.00 eAED:0.00 QI:334 1 1 1 1 1 2 386 231	8.7458	1.4657	0.01353		no GO terms
Xvis03_22 1512-PA	processed-gene-2.27- mRNA-1 protein Name:"Similar to Late embryogenesis abundant protein 76 (Brassica napus)" AED:0.12 eAED:0.12 QI:0 0.33 0.5 0.75 1 1 4 219 192	1.444 62	1.87719	0.01396		no GO terms
Xvis03_20 2655-PA	processed-gene-53.13- mRNA-1 protein Name:"Similar to CCT2 Choline-phosphate cytidyltransferase 2 (Arabidopsis thaliana)" AED:0.15 eAED:0.15 QI:50 1 1 1 1 1 8 392 291	0.988 01	1.89108	0.01521	IPR0048 21 (PFAM)	F:GO:0003824; P:GO:0009058
Xvis03_22 1512-PA	processed-gene-2.27- mRNA-1 protein Name:"Similar to Late embryogenesis abundant	3.830 65	1.86211	0.01641		no GO terms

	protein 76 (Brassica napus)"					
	AED:0.12 eAED:0.12					
	QI:0 0.33 0.5 0.75 1 1 4 219 192					
Xvis03_22	processed-gene-0.13-	6.481	1.13443	0.01683	IPR0001	P:GO:0009415
5532-PA	mRNA-1 protein	03			67	
	Name:"Similar to DHN3				(PFAM);	
	Dehydrin DHN3 (Hordeum					
	vulgare)" AED:0.00					
	eAED:0.00					
	QI:270 1 1 1 1 1 2 257 183					
Xvis03_22	augustus-gene-1.8-mRNA-1	1.7858	1.70738	0.01734	IPR0070	no GO terms
1564-PA	protein Name:"Similar to				11	
	Late embryogenesis abundant				(PFAM)	
	protein D-34 (Gossypium					
	hirsutum)" AED:0.08					
	eAED:0.23					
	QI:0 0 0.5 1 1 1 1 2 238 274					
Xvis03_22	augustus-gene-8.38-mRNA-1	13.17	1.18885	0.01741		no GO terms
0240-PA	protein Name:"Similar to	91				
	LEA3 Late embryogenesis					
	abundant protein, group 3					
	(Oryza sativa subsp. indica)"					
	AED:0.00 eAED:0.00					
	QI:193 1 1 1 1 1 1 2 266 174					
Xvis03_22	processed-gene-1.22-	4.645	1.30412	0.01772	IPR0001	P:GO:0009415
0597-PA	mRNA-1 protein	28			67	
	Name:"Similar to RAB18				(PFAM	
	Dehydrin Rab18					
	(Arabidopsis thaliana)"					
	AED:0.00 eAED:0.00					
	QI:228 1 1 1 1 1 1 2 308 136					
Xvis03_22	Processed-gene-3.71-	1.654	1.62548	0.01843	IPR0020	F:GO:0003676;
3451-PA	mRNA-1 protein	54			59	F:GO:0008270
	Name:"Similar to CSP1 Cold					
	shock protein 1 (Arabidopsis					
	thaliana)" AED: 0.30 eAED:					
	0.30 QI:0 -1 0 1 -1 1 1 0 215					
Xvis03_22	augustus-gene-2.101-	3.021	1.18192	0.02167	IPR0016	F:GO:0000287;
3476-PA	mRNA-1 protein	61			97	F:GO:0003824;
	Name:"Similar to Pyruvate					F:GO:0004743;
	kinase, cytosolic isozyme					P:GO:0006096;
	(Glycine max)" AED:0.04					F:GO:0030955
	eAED:0.04					
	QI:138 1 1 1 1 1 3 406 533					

Xvis03_22 2223-PA	processed-gene-2.73- mRNA-1 protein Name:"Similar to HSP70 Heat shock cognate 70 kDa protein (Petunia hybrida)" AED:0.11 eAED:0.11 QI:205 0.5 0.33 0.66 1 1 3 0 710	18.44 19	0.60753	0.02505	IPR0131 26	no GO terms
Xvis03_21 0802-PA	processed-gene-9.8-mRNA- 1 protein Name:"Similar to LTI65 Low-temperature- induced 65 kDa protein (Arabidopsis thaliana)" AED:0.00 eAED:0.00 QI:247 1 1 1 1 1 5 289 574	18.10 56	1.16935	0.02542		P:GO:0009737
Xvis03_21 3342-PA	processed-gene-10.36- mRNA-1 protein Name:"Similar to Histone H4 (Glycine max)" AED: 0.00 eAED: 0.01 QI: 0 - 1 0 1 -1 1 1 0 103	8.218 74	0.81696	0.0291	IPR0019 51	F:GO:0003677; F:GO:0046982
Xvis03_22 3476-PA	augustus-gene-2.101- mRNA-1 protein Name:"Similar to Pyruvate kinase, cytosolic isozyme (Glycine max)" AED:0.04 eAED:0.04 QI:138 1 1 1 1 1 3 406 533	3.53294 02	1.060	0.03324	IPR0016 97	F:GO:0000287;F:GO: 0003824; F:GO:0004743; P:GO:0006096; F:GO:0030955
Xvis03_20 2976-PA	augustus-gene-30.2-mRNA- 1 protein Name:"Similar to Blue copper protein (Pisum sativum)" AED:0.02 eAED:0.02 QI:94 1 1 1 1 1 2 158 189	0.91783	1.60444	0.03689	IPR0089 72	F:GO:0009055
Xvis03_22 1126-PA	augustus-gene-1.32-mRNA- 1 protein Name:"Similar to Mavicyanin (Cucurbita pepo)" AED:0.01 eAED:0.01 QI:65 1 1 1 1 1 2 153 186	0.73585	1.63058	0.03825	IPR0089 72)	F:GO:0009055
Xvis03_22 0240-PA	augustus-gene-8.38-mRNA- 1 protein Name:"Similar to LEA3 Late embryogenesis abundant protein, group 3 (Oryza sativa subsp. indica)" AED:0.00 eAED:0.00	7.28924	1.13228	0.03889		no GO terms

QI:193|1|1|1|1|1|2|266|174

Xvis03_22	augustus-gene-6.27-mRNA-	2.68011	1.34372	0.03974	IPR0096	no GO terms
1252-PA	1 protein Name:"Similar to SPG20 Spartin (Homo sapiens)" AED:0.04 eAED:0.04 QI:93 1 1 1 0.75 0.6 5 21 403				86 (PFAM)	
Xvis03_20	processed-gene-6.86-	7.62962	0.8021	0.04235	IPR0199	F:GO:0005515
5813-PA	mRNA-1 protein Name:"Similar to RUB2 Ubiquitin-NEDD8-like protein RUB2 (Oryza sativa subsp. japonica)" AED:0.04 eAED:0.04 QI:73 1 1 1 1 1 3 301 153				56 (PRINTS)	
Xvis03_20	processed-gene-16.57-	9.19049	0.7264	0.04322	IPR0019	F:GO:0030145;
9096-PA	mRNA-1 protein Name:"Similar to ABP20 Auxin-binding protein ABP20 (Prunus persica)" AED:0.02 eAED:0.02 QI:173 1 1 1 1 1 2 671 206				29 (PRINTS)	F:GO:0045735
Xvis03_20	processed-gene-11.0-	8.90801	0.65467	0.0444		F:GO:0003983;
2124-PA	mRNA-1 protein Name:"Similar to UGPA UTP--glucose-1-phosphate uridylyltransferase (Musa acuminata)" AED:0.18 eAED:0.18 QI:271 0.88 0.89 1 1 1 19 37 2 458					P:GO:0006011; F:GO:0070569
Xvis03_20	augustus-gene-39.13-	2.41403	1.37564	0.04789	IPR0008	F:GO:0004645;
4659-PA	mRNA-1 protein Name:"Similar to PHS2 Alpha-glucan phosphorylase 2, cytosolic (Arabidopsis thaliana)" AED:0.23 eAED:0.23 QI:181 0.92 0.93 1 0.92 0.86 15 169 732				11	P:GO:0005975; F:GO:0008184; F:GO:0030170

Xvis03_22	augustus-gene-1.8-mRNA-1	0.97016	1.55308	0.04808	IPR0070	no GO terms
1564-PA	protein Name:"Similar to Late embryogenesis abundant protein D-34 (Gossypium hirsutum)" AED:0.08 eAED:0.23 QI:0 0 0.5 1 1 1 2 238 274				11 (PFAM);	
Xvis03_20	Processed-gene-16.29-	0.91371	1.54312	0.04923		F:GO:0003747;
9643-PA	mRNA-1 protein Name:"Similar to ERF1-3 Eukaryotic peptide chain release factor subunit 1-3 (Arabidopsis thaliana)" AED: 0.00 eAED: 0.00 QI:0 -1 0 1 -1 1 1 0 43					C:GO:0005737; P:GO:0006415

Table S3: List of differentially expressed proteins involved late response to drying identified in *X. schlechteri* leaf samples.

Accession	Description	base Mean	log2Fol dC hange	p- value	InterPro	Go-Terms
Xvis03_22000 2-PA	processed-gene-8.116-mRNA-1 protein Name:"Similar to Desiccation-related protein PCC3-06 (Craterostigma plantagineum)" AED:0.00 eAED:0.00 QI:334 1 1 1 1 1 2 386 231	8.745 8046 6	3.3101873 2	3.45E- 09		no GO terms
Xvis03_22059 7-PA	processed-gene-1.22-mRNA-1 protein Name:"Similar to RAB18 Dehydrin Rab18 (Arabidopsis thaliana)" AED:0.00 eAED:0.00 QI:228 1 1 1 1 1 2 308 136	5.055 4445 4	2.6869117	3.86E- 08	IPR0001 67 (PFAM	P:GO:0009415
Xvis03_21080 2-PA	processed-gene-9.8-mRNA-1 protein Name:"Similar to LTI65 Low-temperature- induced 65 kDa protein (Arabidopsis thaliana)" AED:0.00 eAED:0.00 QI:247 1 1 1 1 1 5 289 574	3.507 1254 8	3.1803771	9.73E- 08	IPR0374 91 (PANTH ER)	P:GO:0009737
Xvis03_21695 0-PA	augustus-gene-2.19-mRNA-1 protein Name:"Similar to 11 kDa late embryogenesis abundant protein (Helianthus annuus)" AED:0.13 eAED:0.13 QI:0 0.5 0.33 0.66 1 1 3 337 25 5	5.285 2439 6	2.5576639 8	3.13E- 07	IPR0055 13 (PFAM)	P:GO:0009793

Xvis03_22291 1-PA	processed-gene-1.35-mRNA-1 protein Name:"Similar to CHLI Magnesium-chelatase subunit ChII, chloroplastic (Oryza sativa subsp. japonica)" AED:0.00 eAED:0.00 QI:218 1 1 1 1 3 269 418	4.085 6321 4	2.6524454 2	3.22E- 07	IPR0005 23 (PFAM)	F:GO:0005524; P:GO:0015995; F:GO:0016851
Xvis03_22151 2-PA	processed-gene-2.27-mRNA-1 protein Name:"Similar to Late embryogenesis abundant protein 76 (Brassica napus)" AED:0.12 eAED:0.12 QI:0 0.33 0.5 0.75 1 1 4 219 19 2	3.830 6486 8	3.8618098 9	3.60E- 07		no GO terms
Xvis03_22036 3-PA	augustus-gene-1.54-mRNA-1 protein Name:"Similar to ECU03_1610 Uncharacterized protein ECU03_1610 (Encephalitozoon cuniculi (strain GB-M1))" AED:0.03 eAED:0.03 QI:89 1 1 1 1 2 303 232	3.940 1913	3.0391360 5	4.19E- 07		no GO terms
Xvis03_20076 2-PA	processed-gene-88.24-mRNA- 1 protein Name:"Similar to At4g13010 Putative quinone- oxidoreductase homolog, chloroplastic (Arabidopsis thaliana)" AED:0.26 eAED:0.26 QI:0 1 0.75 1 1 1 4 216 327	4.970 9242 5	2.4586390 7	4.22E- 07	IPR0131 54 (PFAM)	P:GO:0055114
Xvis03_21811 7-PA	augustus-gene-11.3-mRNA-1 protein Name:"Similar to Embryonic protein DC-8 (Daucus carota)" AED:0.04 eAED:0.04 QI:0 1 0.66 1 1 1 3 517 510	10.54 6181 4	2.5458122 3	5.48E- 07	PTHR33 836:SF1	P:GO:0009737
Xvis03_22125 2-PA	augustus-gene-6.27-mRNA-1 protein Name:"Similar to SPG20 Spartina (Homo sapiens)" AED:0.04 eAED:0.04 QI:93 1 1 1 0.75 0.6 5 21 403	2.614 9506 2	3.2161600 6	8.75E- 07	IPR0096 86 (PFAM)	no GO terms
Xvis03_22156 4-PA	augustus-gene-1.8-mRNA-1 protein Name:"Similar to Late embryogenesis abundant protein D-34 (Gossypium	3.298 7273 7	2.8236063 3	1.02E- 06	IPR0070 11 (PFAM)	no GO terms

hirsutum)" AED:0.08

eAED:0.23

QI:0|0|0.5|1|1|1|2|238|274

Xvis03_22291 1-PA	processed-gene-1.35-mRNA-1 protein Name:"Similar to CHLI Magnesium-chelatase subunit ChII, chloroplastic (Oryza sativa subsp. japonica)" AED:0.00 eAED:0.00 QI:218 1 1 1 1 1 3 269 418	2.711 4771 3	2.6630027 5	1.80E- 06	IPR0005 23 (PFAM);	F:GO:0005524; P:GO:0015995; F:GO:0016851
Xvis03_22132 5-PA	processed-gene-6.29-mRNA-1 protein Name:"Similar to B19.4 Late embryogenesis abundant protein B19.4 (Hordeum vulgare)" AED:0.16 eAED:0.16 QI:0 0.66 0.5 0.75 1 1 4 117 18 1	3.843 0709 4	2.5169091 9	1.85E- 06	IPR0389 56 (PFAM)	no GO terms
Xvis03_21289 4-PA	augustus-gene-2.1-mRNA-1 protein Name:"Similar to PORB Protochlorophyllide reductase B, chloroplastic (Hordeum vulgare)" AED:0.09 eAED:0.09 QI:162 1 1 1 1 1 5 457 393	3.051 4899 9	2.1124310 9	2.74E- 06	IPR0023 47 (PRINTS)	F:GO:0016630; P:GO:0055114
Xvis03_22023 9-PA	augustus-gene-8.37-mRNA-1 protein Name:"Similar to Late embryogenesis abundant protein Dc3 (Daucus carota)" AED:0.00 eAED:0.00 QI:288 1 1 1 1 1 2 197 146	3.705 5560 5	2.6248538 4	3.81E- 06		no GO terms
Xvis03_22059 7-PA	processed-gene-1.22-mRNA-1 protein Name:"Similar to RAB18 Dehydrin Rab18 (Arabidopsis thaliana)" AED:0.00 eAED:0.00 QI:228 1 1 1 1 1 2 308 136	7.330 6810 4	1.8180899 3	5.89E- 06	IPR0001 67 (PFAM)	P:GO:0009415
Xvis03_22156 4-PA	augustus-gene-1.8-mRNA-1 protein Name:"Similar to Late embryogenesis abundant protein D-34 (Gossypium hirsutum)" AED:0.08 eAED:0.23 QI:0 0 0.5 1 1 1 2 238 274	2.208 2565 1	3.0839240 5	6.38E- 06	IPR0070 11 (PFAM)	no GO terms

Xvis03_22024 0-PA	augustus-gene-8.38-mRNA-1 protein Name:"Similar to LEA3 Late embryogenesis abundant protein, group 3 (Oryza sativa subsp. indica)" AED:0.00 eAED:0.00 QI:193 1 1 1 1 2 266 174	7.289 2394 1	2.2979556 4	8.88E- 06		no GO terms
Xvis03_22079 0-PA	augustus-gene-7.89-mRNA-1 protein Name:"Similar to SYNPCC7002_A1590 Uncharacterized protein SYNPCC7002_A1590 (Synechococcus sp. (strain ATCC 27264 / PCC 7002 / PR- 6))" AED:0.04 eAED:0.04 QI:148 1 1 1 1 6 744 229	1.305 2415 1	3.2089502	9.54E- 06	IPR0189 71 (PFAM)	no GO terms
Xvis03_22125 2-PA	augustus-gene-6.27-mRNA-1 protein Name:"Similar to SPG20 Spartina (Homo sapiens)" AED:0.04 eAED:0.04 QI:93 1 1 1 0.75 0.6 5 21 403	2.680 1088 5	2.6318819 5	1.13E- 05	IPR0096 86 (PFAM)	no GO terms
Xvis03_22156 4-PA	augustus-gene-1.8-mRNA-1 protein Name:"Similar to Late embryogenesis abundant protein D-34 (Gossypium hirsutum)" AED:0.08 eAED:0.23 QI:0 0 0.5 1 1 1 2 238 274	1.785 8015 6	2.8897096 7	1.70E- 05	IPR0070 11 (PFAM)	no GO terms
Xvis03_21811 7-PA	augustus-gene-11.3-mRNA-1 protein Name:"Similar to Embryonic protein DC-8 (Daucus carota)" AED:0.04 eAED:0.04 QI:0 1 0.66 1 1 1 3 517 510	4.669 8475 7	2.5189818 7	1.74E- 05		P:GO:0009737
Xvis03_22553 2-PA	processed-gene-0.13-mRNA-1 protein Name:"Similar to DHN3 Dehydrin DHN3 (Hordeum vulgare)" AED:0.00 eAED:0.00 QI:270 1 1 1 1 2 257 183	6.481 0301 9	1.8897771 5	2.04E- 05	IPR0001 67 (PFAM)	P:GO:0009415
Xvis03_20208 7-PA	augustus-gene-8.14-mRNA-1 protein Name:"Similar to AAE3 Oxalate--CoA ligase	2.212 3689 3	2.6573145 4	5.13E- 05	IPR0008 73 (PFAM)	F:GO:0003824

(Arabidopsis thaliana)"

AED:0.02 eAED:0.02

QI:521|1|1|1|1|1|4|258|517

Xvis03_20400 3-PA	augustus-gene-27.86-mRNA-1 protein Name:"Similar to Aldose reductase (Hordeum vulgare)" AED:0.09 eAED:0.09 QI:204 1 1 1 1 1 9 270 319	3.174 4073	2.1372464 2	6.79E- 05	IPR0204 71	F:GO:0016491; P:GO:0055114
Xvis03_20359 2-PA	augustus-gene-31.41-mRNA-1 protein Name:"Similar to 1- Cys peroxiredoxin (Medicago truncatula)" AED:0.00 eAED:0.00 QI:253 1 1 1 1 1 2 509 219	9.703 8722 4	1.3351265	7.04E- 05	IPR0008 66	F:GO:0016209; F:GO:0016491; P:GO:0045454; F:GO:0051920; P:GO:0055114
Xvis03_20503 4-PA	late embryogenesis abundant protein D-34-like	1.195 8591 4	3.0903517 3	7.65E- 05	IPR0070 11 (PFAM)	no GO terms
Xvis03_22024 0-PA	augustus-gene-8.38-mRNA-1 protein Name:"Similar to LEA3 Late embryogenesis abundant protein, group 3 (Oryza sativa subsp. indica)" AED:0.00 eAED:0.00 QI:193 1 1 1 1 1 2 266 174	13.17 9127 6	1.9179068 9	7.91E- 05		no GO terms
Xvis03_22059 7-PA	processed-gene-1.22-mRNA-1 protein Name:"Similar to RAB18 Dehydrin Rab18 (Arabidopsis thaliana)" AED:0.00 eAED:0.00 QI:228 1 1 1 1 1 2 308 136	4.645 2791 6	2.0413783 3	8.67E- 05	IPR0001 67 (PFAM)	P:GO:0009415
Xvis03_22000 2-PA	processed-gene-8.116-mRNA- 1 protein Name:"Similar to Desiccation-related protein PCC3-06 (Craterostigma plantagineum)" AED:0.00 eAED:0.00 QI:334 1 1 1 1 1 2 386 231	25.90 4908 3	1.6696899 1	0.0001 35873		no GO terms
Xvis03_22172 0-PA	augustus-gene-5.43-mRNA-1 protein Name:"Similar to EIF- 5A2 Eukaryotic translation initiation factor 5A-2 (Nicotiana plumbaginifolia)" AED:0.05 eAED:0.05 QI:177 1 1 1 0.8 0.66 6 330 160	2.183 5228	2.0957290 1	0.0001 60339	IPR0201 89 (PFAM)	F:GO:0003723; F:GO:0003746; P:GO:0006452; F:GO:0043022; P:GO:0045901; P:GO:0045905

Xvis03_22345 4-PA	processed-gene-3.78-mRNA-1 protein Name:"Similar to PCKR1 Peptidyl-prolyl cis- trans isomerase (Catharanthus roseus)" AED:0.02 eAED:0.02 QI:0 -1 0 1 -1 1 1 0 173	7.480 9848 9	1.2664219 9	0.0001 63465	IPR0021 30	P:GO:0000413; F:GO:0003755
Xvis03_21191 7-PA	augustus-gene-8.2-mRNA-1 protein Name:"Similar to UGT78D2 UDP- glycosyltransferase 78D2 (Arabidopsis thaliana)" AED:0.00 eAED:0.00 QI:173 1 1 1 1 1 2 210 454	1.696 6120 4	2.7851324 4	0.0001 6923	IPR0022 13 (PFAM);	F:GO:0016758
Xvis03_22125 2-PA	augustus-gene-6.27-mRNA-1 protein Name:"Similar to SPG20 Spartina (Homo sapiens)" AED:0.04 eAED:0.04 QI:93 1 1 1 0.75 0.6 5 21 403	1.188 6259	2.8708791 4	0.0001 84897	IPR0096 86 (PFAM)	no GO terms
Xvis03_21080 2-PA	processed-gene-9.8-mRNA-1 protein Name:"Similar to LTI65 Low-temperature- induced 65 kDa protein (Arabidopsis thaliana)" AED:0.00 eAED:0.00 QI:247 1 1 1 1 1 5 289 574	18.10 5578 8	1.9090698 6	0.0002 02692	IPR0374 91 (PANTH ER)	P:GO:0009737
Xvis03_22156 4-PA	augustus-gene-1.8-mRNA-1 protein Name:"Similar to Late embryogenesis abundant protein D-34 (Gossypium hirsutum)" AED:0.08 eAED:0.23 QI:0 0 0.5 1 1 1 2 238 274	0.970 1643 4	2.8166717 7	0.0002 27483	IPR0070 11 (PFAM)	no GO terms
Xvis03_22519 9-PA	processed-gene-0.101-mRNA- 1 protein Name:"Similar to Aldose reductase (Hordeum vulgare)" AED:0.14 eAED:0.14 QI:154 0.87 0.88 1 0.62 0.55 9 25 337	6.855 5564 5	1.6145377 6	0.0002 30193	IPR0204 71	F:GO:0016491; P:GO:0055114
Xvis03_22024 0-PA	augustus-gene-8.38-mRNA-1 protein Name:"Similar to LEA3 Late embryogenesis abundant protein, group 3 (Oryza sativa subsp. indica)" AED:0.00 eAED:0.00 QI:193 1 1 1 1 1 2 266 174	10.71 7152 8	2.5468819 3	0.0002 31897		no GO terms
Xvis03_20965 3-PA	processed-gene-17.23-mRNA- 1 protein Name:"Similar to Os01g0270100 Cysteine proteinase inhibitor 12 (Oryza sativa subsp. japonica)" AED:0.07 eAED:0.07 QI:0 0 0 1 1 1 4 0 225	6.033 7838 4	1.2914246 1	0.0002 94989		F:GO:0004869

Xvis03_21437 2-PA	processed-gene-6.62-mRNA-1 protein Name:"Similar to Eukaryotic translation initiation factor 5A (Manihot esculenta)" AED:0.20 eAED:0.20 QI:188 1 1 0.8 0.66 6 353 159	2.367 6169 7	1.9349514 2	0.0003 35124	IPR0201 89 (PFAM	F:GO:0003723; F:GO:0003746; P:GO:0006452; F:GO:0043022; P:GO:0045901; P:GO:0045905
Xvis03_21763 8-PA	augustus-gene-2.63-mRNA-1 protein Name:"Similar to CCR1 Cinnamoyl-CoA reductase 1 (Arabidopsis thaliana)" AED:0.07 eAED:0.07 QI:0 0 0 1 1 1 6 0 324	1.429 2214 2	2.6004215 5	0.0003 62868	IPR0362 91 (SUPER FAMILY)	F:GO:0003824; F:GO:0050662
Xvis03_20101 5-PA	augustus-gene-109.105- mRNA-1 protein Name:"Similar to MSRB5 Peptide methionine sulfoxide reductase B5 (Oryza sativa subsp. japonica)" AED:0.11 eAED:0.11 QI:31 0.33 0.5 1 1 1 4 790 250	1.020 0315 3	2.5950097 1	0.0004 19649	IPR0025 79 (PFAM	P:GO:0006979; F:GO:0016671; P:GO:0030091; F:GO:0033743; P:GO:0055114
Xvis03_22377 4-PA	augustus-gene-3.64-mRNA-1 protein Name:"Similar to LEA14-A Late embryogenesis abundant protein Lea14-A (Gossypium hirsutum)" AED:0.40 eAED:0.40 QI:0 0 0 1 1 1 2 0 155	2.609 5367 3	2.0846299 4	0.0004 31468	IPR0048 64 (PFAM);	no GO terms
Xvis03_20964 3-PA	processed-gene-16.29-mRNA-1 protein Name:"Similar to ERF1-3 Eukaryotic peptide chain release factor subunit 1-3 (Arabidopsis thaliana)" AED:0.00 eAED:0.00 QI:0 - 1 0 1 -1 1 1 0 437	0.995 3838 5	2.6770971 3	0.0004 56625	IPR0051 42 (PFAM);	F:GO:0003747; C:GO:0005737; P:GO:0006415
Xvis03_22229 2-PA	processed-gene-3.63-mRNA-1 protein Name:"Similar to CML18 Probable calcium- binding protein CML18 (Oryza sativa subsp. japonica)" AED:0.02 eAED:0.02 QI:0 - 1 0 1 -1 1 1 0 161	0.970 7048 7	2.6432039 4	0.0005 02823	IPR0020 48 (PFAM);	F:GO:0005509
Xvis03_20620 2-PA	processed-gene-9.17-mRNA-1 protein Name:"Similar to GMPM1 18 kDa seed maturation protein (Glycine max)" AED:0.23 eAED:0.23 QI:0 -1 0 1 -1 1 1 0 132	0.775 8309 1	2.5885541 6	0.0007 67778	IPR0055 13 (PFAM)	P:GO:0009793
Xvis03_22345 1-PA	processed-gene-3.71-mRNA-1 protein Name:"Similar to CSP1 Cold shock protein 1 (Arabidopsis thaliana)" AED:0.30 eAED:0.30 QI:0 - 1 0 1 -1 1 1 0 215	1.654 539	2.1634965 3	0.0009 62503	IPR0020 59 (PFAM)	F:GO:0003676; F:GO:0008270
Xvis03_20746 6-PA	augustus-gene-21.70-mRNA-1 protein Name:"Similar to FLK Flowering locus K homology domain (Arabidopsis thaliana)" AED:0.22 eAED:0.22 QI:168 0.83 0.85 1 0.83 0.71 7 306 448	1.680 7551 6	1.9600575 6	0.0011 55202		F:GO:0003723

Xvis03_20265 5-PA	processed-gene-53.13-mRNA-1 protein Name:"Similar to CCT2 Choline-phosphate cytidyltransferase 2 (Arabidopsis thaliana)" AED:0.15 eAED:0.15 QI:50 1 1 1 1 8 392 291	0.988 0117 4	2.4340105 7	0.0014 52068	IPR0048 21 (PFAM)	F:GO:0003824; P:GO:0009058
Xvis03_20818 2-PA	processed-gene-16.15-mRNA-1 protein Name:"Similar to EIF-5A2 Eukaryotic translation initiation factor 5A- 2 (Nicotiana plumbaginifolia)" AED:0.11 eAED:0.11 QI:80 1 1 1 0.8 0.66 6 225 159	2.978 6649 2	1.4767503 2	0.0015 20635	IPR0018 84	F:GO:0003723; F:GO:0003746; P:GO:0006452; F:GO:0043022; P:GO:0045901; P:GO:0045905
Xvis03_22059 9-PA	augustus-gene-1.77-mRNA-1 protein Name:"Similar to DHN1 Dehydrin DHN1 (Hordeum vulgare)" AED:0.00 eAED:0.00 QI:161 1 1 1 1 1 2 370 123	1.288 1543 5	2.1546031 4	0.0016 07037	IPR0001 67 (PFAM)	P:GO:0009415
Xvis03_20722 0-PA	augustus-gene-29.99-mRNA-1 protein Name:"Similar to Bowman-Birk type trypsin inhibitor (Triticum aestivum)" AED:0.14 eAED:0.14 QI:36 1 1 1 1 1 2 205 120	1.355 7005 2	2.1856071 5	0.0019 60747	IPR0008 77 (PFAM)	F:GO:0004867; C:GO:0005576
Xvis03_22248 7-PA	processed-gene-2.59-mRNA-1 protein Name:"Similar to At4g22670 FAM10 family protein At4g22670 (Arabidopsis thaliana)" AED:0.11 eAED:0.11 QI:137 0.9 0.90 1 1 1 1 173 36 2	1.211 8746	2.0962292 1	0.0020 77646	IPR0346 49 (PFAM)	F:GO:0005515; F:GO:0046983
Xvis03_21811 7-PA	augustus-gene-11.3-mRNA-1 protein Name:"Similar to Embryonic protein DC-8 (Daucus carota)" AED:0.04 eAED:0.04 QI:0 1 0.66 1 1 1 3 517 510	11.15 6628 1	2.0199206	0.0021 20582		P:GO:0009737
Xvis03_22135 4-PA	augustus-gene-2.78-mRNA-1 protein Name:"Similar to RPS12 40S ribosomal protein S12 (Hordeum vulgare)" AED:0.26 eAED:0.26 QI:0 1 0.75 1 1 1 4 274 184	0.933 5730 1	2.3374963 8	0.0023 43013	IPR0040 38 (PFAM)	F:GO:0003735; C:GO:0005840; P:GO:0006412
Xvis03_20721 0-PA	augustus-gene-28.48-mRNA-1 protein Name:"Similar to CLPB3 Chaperone protein ClpB3, mitochondrial (Oryza sativa subsp. japonica)" AED:0.12 eAED:0.12 QI:139 1 1 1 1 1 10 182 968	3.191 2218 2	1.7187871 8	0.0024 14538	IPR0039 59 (PFAM)	F:GO:0005524; C:GO:0005737; P:GO:0009408; P:GO:0019538; P:GO:0042026
Xvis03_21377 2-PA	processed-gene-11.46-mRNA-1 protein Name:"Similar to MT4A Metallothionein-like protein 4A (Oryza sativa subsp.	0.667 6822	2.3806776 9	0.0024 96221	IPR0003 47 (PFAM)	F:GO:0046872

	japonica)"	AED:0.00				
	eAED:0.00					
	QI:173 1 1 1 1 1 2 379 80					
Xvis03_21556	augustus-gene-5.91-mRNA-1	12.65	1.0636296	0.0026	IPR0017	F:GO:0004089;
9-PA	protein Name:"Similar to	2092	2	88392	65	F:GO:0008270
	Carbonic anhydrase,	3			(PFAM	
	chloroplastic (Hordeum					
	vulgare)"	AED:0.12				
	eAED:0.12					
	QI:674 1 1 1 1 1 8 205 260					
Xvis03_21633	processed-gene-6.102-mRNA-	2.142	1.7195160	0.0030	IPR0021	F:GO:0003824;
0-PA	1 protein Name:"Similar to	1563	1	16808	55	F:GO:0016747
	PED1 3-ketoacyl-CoA thiolase	1				
	2, peroxisomal (Arabidopsis					
	thaliana)"	AED:0.14				
	eAED:0.14					
	QI:702 0.85 0.93 0.93 1 1 15 19					
	04 479					
Xvis03_20047	processed-gene-61.44-mRNA-	1.360	2.1990004	0.0025	IPR0119	F:GO:0005515
3-PA	1 protein Name:"Similar to	5723	6	49607	90	
	HOP3 Hsp70-Hsp90	6				
	organizing protein 3					
	(Arabidopsis thaliana)"					
	AED:0.09 eAED:0.09					
	QI:150 1 1 1 1 1 7 289 574					
Xvis03_21289	augustus-gene-2.1-mRNA-1	0.863	2.2836327	0.0026	IPR0023	F:GO:0016630;
4-PA	protein Name:"Similar to	6714	1	17543	47	P:GO:0055114
	PORB Protochlorophyllide	2				
	reductase B, chloroplastic					
	(Hordeum vulgare)"	AED:0.09				
	eAED:0.09					
	QI:162 1 1 1 1 1 5 457 393					
Xvis03_21997	processed-gene-5.16-mRNA-1	2.192	1.8584482	0.0035	IPR0055	P:GO:0009793
9-PA	protein Name:"Similar to	7572	8	30214	13	
	GMPM1 18 kDa seed	5			(PFAM)	
	maturation protein (Glycine					
	max)"	AED:0.00 eAED:0.00				
	QI:97 1 1 1 1 1 2 370 156					
Xvis03_22314	processed-gene-3.56-mRNA-1	11.93	0.8845895	0.0035	IPR0246	no GO terms
4-PA	protein Name:"Similar to	7209	1	78017	81	
	RBCS1 Ribulose biphosphate					
	carboxylase small chain,					
	chloroplastic (Musa					

	acuminata)"	AED:0.05				
	eAED:0.05					
	QI:145 1 1 1 1 1 3 356 174					
Xvis03_2212	augustus-gene-4.54-mRNA-1	2.184	1.6302500	0.0038	IPR0077	no GO terms
3 6-PA	protein Name:"Similar to PXG	4627	3	80978	36	
	Peroxygenase (Oryza sativa				(PFAM);	
	subsp. japonica)"	AED:0.38				
	eAED:0.38					
	QI:85 0.66 0.85 1 1 7 299					
	316					
Xvis03_2029	augustus-gene-28.13-mRNA-1	0.785	2.2752088	0.0038	IPR0415	F:GO:0005524;
5 4-PA	protein Name:"Similar to RPT1	8625	1	97195	69	C:GO:0005737;
	26S protease regulatory subunit	2			(PFAM)	F:GO:0016787;
	7 (Prunus persica)"	AED:0.05				P:GO:0030163
	eAED:0.05					
	QI:150 1 1 1 1 1 10 313 427					
Xvis03_2052	processed-gene-22.101-	0.748	2.2392879	0.0041	IPR0001	P:GO:0009415
3 2-PA	mRNA-1 protein	8657	2	90054	67	
	Name:"Similar to DHN1				(PFAM)	
	Dehydrin DHN1 (Hordeum					
	vulgare)"	AED:0.36				
	eAED:0.36					
	QI:115 1 1 1 1 1 2 350 132					
Xvis03_2083	desiccation-related protein	14.19	1.0339301	0.0042	PF13668	no GO terms
2 8-PA	PCC13-62-like	7445		3904	(PFAM)	
		7				
Xvis03_2246	processed-gene-1.62-mRNA-1	0.790	2.1774229	0.0046	IPR0060	F:GO:0003735;
6 0-PA	protein Name:"Similar to FEN1	0292	6	13511	84	F:GO:0004518;
	Flap endonuclease 1 (Zea	6			(PRINTS	C:GO:0005840;
	mays)"	AED:0.25)	P:GO:0006281;
	eAED:0.26					P:GO:0006412;
	QI:20 0.7 0.71 0.95 1 1 21 362					F:GO:0016788
	621					
Xvis03_2053	augustus-gene-34.43-mRNA-1	0.713	2.1407999	0.0055	IPR0003	F:GO:0046872
6 7-PA	protein Name:"Similar to MTA	2959	9	63873	47	
	Metallothionein-like protein 1	4			(PFAM);	
	(Pisum sativum)"	AED:0.00				
	eAED:0.00					
	QI:175 1 1 1 1 1 2 359 83					
Xvis03_2190	augustus-gene-7.46-mRNA-1	3.129	1.2722804	0.0062	IPR0346	F:GO:0005515;
5 5-PA	protein Name:"Similar to TDX	9734	5	35578	49	F:GO:0046983
	TPR repeat-containing	9			(PFAM)	
	thioredoxin TDX (Arabidopsis					
	thaliana)"	AED:0.04				
	eAED:0.04					

QI:262|1|1|1|1|1|1|1|486|390

Xvis03_2200 7 6-PA	augustus-gene-4.88-mRNA-1 protein Name:"Similar to GDCHS Glycine cleavage system H protein, mitochondrial (Oryza sativa subsp. japonica)" AED:0.04 eAED:0.04 QI:127 1 1 1 1 1 1 4 484 165	1.846 7886 2	1.5457459 2	0.0063 44124	IPR0174 53	C:GO:0005960; P:GO:0019464
Xvis03_2040 2 2-PA	processed-gene-29.69-mRNA- 1 protein Name:"Similar to RANBP1C Ran-binding protein 1 homolog c (Arabidopsis thaliana)" AED:0.01 eAED:0.01 QI:85 1 1 1 1 1 1 4 338 224	1.286 7017 4	1.8266814 7	0.0067 95094	IPR0001 56 (PFAM)	P:GO:0046907
Xvis03_2165 1 5-PA	augustus-gene-8.70-mRNA-1 protein Name:"Similar to SAPK7 Serine/threonine- protein kinase SAPK7 (Oryza sativa subsp. japonica)" AED:0.12 eAED:0.12 QI:115 0.83 1 1 1 1 7 226 305	1.408 9568 1	1.8659521 3	0.0070 1349	IPR0110 09	F:GO:0004672; F:GO:0005524; P:GO:0006468
Xvis03_2055 1 2-PA	processed-gene-10.28-mRNA- 1 protein Name:"Similar to Hsp83 Heat shock protein 83 (Drosophila melanogaster)" AED:0.12 eAED:0.12 QI:147 1 1 1 1 1 1 19 333 803	5.926 4619 8	1.0987413 5	0.0079 85264	IPR0205 75 (PRINTS	F:GO:0005524; P:GO:0006457; F:GO:0051082
Xvis03_2154 3 4-PA	augustus-gene-6.51-mRNA-1 protein Name:"Similar to Os01g0253300 Importin subunit alpha-1a (Oryza sativa subsp. japonica)" AED:0.21 eAED:0.21 QI:191 0.81 0.75 1 1 1 12 0 614	0.592 3643 7	2.0794711 8	0.0083 24319	IPR0119 89 (F:GO:0005515; C:GO:0005634; C:GO:0005737; P:GO:0006606; F:GO:0008565; F:GO:0061608
Xvis03_2250 4 2-PA	augustus-gene-0.56-mRNA-1 protein Name:"Similar to CSD2 Superoxide dismutase [Cu-Zn] 2, chloroplastic (Arabidopsis thaliana)" AED:0.13 eAED:0.13 QI:217 0.85 0.87 1 1 1 8 225 22 6	10.89 4930 1	0.7706707 3	0.0085 11462	IPR0014 24 (PRINTS)	P:GO:0006801; F:GO:0046872

Xvis03_2212 3 6-PA	augustus-gene-4.54-mRNA-1 protein Name:"Similar to PXG Peroxygenase (Oryza sativa subsp. japonica)" AED:0.38 eAED:0.38 QI:85 0.66 0.85 0.85 1 1 7 299 316	2.138 1232 1	1.5111337	0.0093 16845	IPR0077 36 (PFAM)	no GO terms
Xvis03_2248 8 7-PA	augustus-gene-0.36-mRNA-1 protein Name:"Similar to At4g12130 Putative transferase At4g12130, mitochondrial (Arabidopsis thaliana)" AED:0.05 eAED:0.05 QI:50 1 1 1 1 1 5 427 411	1.726 6701	1.545695	0.0102 31088	IPR0177 03	F:GO:0005515
Xvis03_2103 3 7-PA	augustus-gene-8.1-mRNA-1 protein Name:"Similar to RPS12 40S ribosomal protein S12 (Hordeum vulgare)" AED:0.38 eAED:0.38 QI:0 1 0.75 1 1 1 4 393 161	0.788 9782 9	2.0046668 6	0.0104 36181	IPR0005 30 (PRINTS	F:GO:0003735; C:GO:0005840; P:GO:0006412
Xvis03_2125 2 0-PA	augustus-gene-6.14-mRNA-1 protein Name:"Similar to TUF1B Elongation factor Tu, chloroplastic (Glycine max)" AED:0.04 eAED:0.16 QI:0 0 0.5 1 1 1 2 351 455	4.598 5812	0.9845974 2	0.0125 95747	IPR0007 95 (PRINTS)	F:GO:0003746; F:GO:0003924; F:GO:0005525; P:GO:0006414
Xvis03_2197 8 4-PA	processed-gene-6.0-mRNA-1 protein Name:"Similar to MBF1B Multiprotein-bridging factor 1b (Arabidopsis thaliana)" AED:0.06 eAED:0.06 QI:115 1 1 1 1 1 4 351 141	1.009 4991	1.8677196 4	0.0133 09481	IPR0137 29 (PFAM)	F:GO:0003677
Xvis03_2027 8 4-PA	processed-gene-9.6-mRNA-1 protein Name:"Similar to At5g12110 Elongation factor 1-beta 1 (Arabidopsis thaliana)" AED:0.07 eAED:0.07 QI:28 1 1 1 1 1 6 211 226	2.926 0132 7	1.1571813 6	0.0138 74725	IPR0147 17	F:GO:0003746; P:GO:0006414
Xvis03_2148 7 1-PA	augustus-gene-0.9-mRNA-1 protein Name:"Similar to CYS6 Cysteine proteinase inhibitor 6 (Arabidopsis thaliana)" AED:0.25 eAED:0.25	3.307 2269 5	1.0914322 6	0.0139 51824	IPR0000 10 (PFAM);	F:GO:0004869

QI:34|0.2|0.33|1|0.8|0.83|6|0|2
3 7

Xvis03_2171 9 6-PA	augustus-gene-1.26-mRNA-1 protein Name:"Similar to AKR2 Ankyrin repeat domain- containing protein 2 (Arabidopsis thaliana)" AED:0.11 eAED:0.11 QI:0 0 0 1 1 1 6 0 276	0.983 5682 7	1.7752949 7	0.0141 29423	IPR0206 83 (PFAM);	F:GO:0005515
Xvis03_2151 5 3-PA	augustus-gene-12.40-mRNA-1 protein Name:"Similar to RZ1B Glycine-rich RNA- binding protein RZ1B (Arabidopsis thaliana)" AED:0.25 eAED:0.25 QI:0 1 1 1 0.5 0.33 3 1599 326	0.738 4757 5	1.8385500 1	0.0176 2934	IPR0005 04 (PFAM);	F:GO:0003676; F:GO:0008270
Xvis03_2182 0 0-PA	augustus-gene-6.42-mRNA-1 protein Name:"Similar to PLP1 Patatin-like protein 1 (Oryza sativa subsp. japonica)" AED:0.26 eAED:0.26 QI:72 0.4 0.16 1 1 1 6 0 314	2.889 8699 1	1.3064709 9	0.0177 4307	IPR0026 41 (PFAM);	P:GO:0006629
Xvis03_2255 3 2-PA	processed-gene-0.13-mRNA-1 protein Name:"Similar to DHN3 Dehydrin DHN3 (Hordeum vulgare)" AED:0.00 eAED:0.00 QI:270 1 1 1 1 1 2 257 183	1.112 5766 4	1.5992062 4	0.0182 50186	IPR0001 67 (PFA	P:GO:0009415
Xvis03_2029 2 9-PA	augustus-gene-26.5-mRNA-1 protein Name:"Similar to RPL23A 60S ribosomal protein L23 (Arabidopsis thaliana)" AED:0.39 eAED:0.40 QI:0 0 0 0.5 1 1 1 6 0 279	2.398 3112 9	1.2000962 9	0.0182 86027	IPR0002 18 (PFAM)	F:GO:0003735; C:GO:0005840; P:GO:0006412
Xvis03_2076 2 5-PA	processed-gene-8.99-mRNA-1 protein Name:"Similar to COR47 Dehydrin COR47 (Arabidopsis thaliana)" AED:0.00 eAED:0.00 QI:100 1 1 1 1 1 2 435 268	1.896 6244 9	1.7208972 8	0.0186 44009	IPR0001 67 (PFAM)	P:GO:0009415
Xvis03_2217 5 4-PA	augustus-gene-1.62-mRNA-1 protein Name:"Similar to MORF1 Multiple organellar RNA editing factor 1, mitochondrial (Arabidopsis	0.936 6691 8	1.7289507 2	0.0187 5143	IPR0392 06 (PANTH ER);	P:GO:0016554

thaliana)" AED:0.23
 eAED:0.23
 QI:47|1|1|0.75|0.6|5|384|406

Xvis03_2052	processed-gene-22.101-	1.467	1.5839294	0.0189	IPR0001	P:GO:0009415
3 2-PA	mRNA-1 protein	1627	8	02918	67	
	Name:"Similar to DHN1	6			(PFAM)	
	Dehydrin DHN1 (Hordeum					
	vulgare)" AED:0.36					
	eAED:0.36					
	QI:115 1 1 1 1 2 350 132					
Xvis03_2181	augustus-gene-3.24-mRNA-1	2.822	1.1671811	0.0194	IPR0140	F:GO:0009055;
5 8-PA	protein Name:"Similar to	1512	2	40464	25	F:GO:0015035;
	Glutaredoxin (Ricinus	7				P:GO:0045454
	communis)" AED:0.01					
	eAED:0.01					
	QI:220 1 1 1 1 4 501 106					
Xvis03_2002	processed-gene-30.2-mRNA-1	19.81	0.5548722	0.0209	IPR0131	F:GO:0005524;
5 0-PA	protein Name:"Similar to	3914	7	00757	26	P:GO:0006457;
	HSP70 Stromal 70 kDa heat				(PRINTS	F:GO:0051082
	shock-related protein,)	
	chloroplastic (Pisum sativum)"					
	AED:0.12 eAED:0.12					
	QI:46 0.75 0.88 0.88 1 1 9 437					
	741					
Xvis03_2056	processed-gene-31.124-	13.01	0.6372995	0.0209	IPR0018	F:GO:0005524;
9 1-PA	mRNA-1 protein	9614	8	57446	44	P:GO:0042026
	Name:"Similar to RuBisCO					
	large subunit-binding protein					
	subunit beta, chloroplastic					
	(Pisum sativum)" AED:0.20					
	eAED:0.20					
	QI:97 0.8 0.81 0.87 0.93 0.87 1					
	6 0 678					
Xvis03_2064	processed-gene-30.78-mRNA- 1	4.553	0.8864205	0.0234	IPR0021	P:GO:0000413;
5 8-PA	protein Name:"Similar to	7958	6	936	30	F:GO:0003755
	PCKR1 Peptidyl-prolyl cis-	2				
	trans isomerase (Catharanthus					
	roseus)" AED:0.01 eAED:0.01					
	QI:0 -1 0 1 -1 1 1 0 173					

Xvis03_2098 7 6-PA	augustus-gene-14.5-mRNA-1 protein Name:"Similar to RPS27B 40S ribosomal protein S27-2 (Arabidopsis thaliana)" AED:0.17 eAED:0.17 QI:86 1 1 1 0.66 0.75 4 47 86	0.779 0348 2	1.7654785 2	0.0216 19681	IPR0005 92 (PFAM	F:GO:0003735; C:GO:0005840; P:GO:0006412
Xvis03_2021 0 3-PA	processed-gene-9.9-mRNA-1 protein Name:"Similar to Os02g0639900 Thioredoxin M1, chloroplastic (Oryza sativa subsp. japonica)" AED:0.00 eAED:0.00 QI:100 1 1 1 1 1 2 1208 190	1.754 2165 8	1.3518750 5	0.0216 60558	PR00421	P:GO:0006662; F:GO:0015035; P:GO:0045454
Xvis03_2212 5 2-PA	augustus-gene-6.27-mRNA-1 protein Name:"Similar to SPG20 Sparti (Homo sapiens)" AED:0.04 eAED:0.04 QI:93 1 1 1 0.75 0.6 5 21 403	4.900 4118 4	0.9144375 7	0.0235 04246	IPR0096 86 (PFAM)	no GO terms
Xvis03_2125 2 0-PA	augustus-gene-6.14-mRNA-1 protein Name:"Similar to TUF1B Elongation factor Tu, chloroplastic (Glycine max)" AED:0.04 eAED:0.16 QI:0 0 0.5 1 1 1 2 351 455	6.587 0721 9	0.7929123	0.0280 19252	IPR0007 95	F:GO:0003746; F:GO:0003924; F:GO:0005525; P:GO:0006414
Xvis03_2114 2 4-PA	augustus-gene-2.30-mRNA-1 protein Name:"Similar to GLX2-2 Hydroxyacylglutathione hydrolase cytoplasmic (Arabidopsis thaliana)" AED:0.23 eAED:0.23 QI:367 1 1 1 1 0.83 6 257 190	0.783 7434 4	1.6639410 2	0.0286 71952	IPR0322 82 (PFAM)	F:GO:0004416; P:GO:0019243
Xvis03_2218 8 3-PA	processed-gene-4.16-mRNA-1 protein Name:"Similar to HVA22A HVA22-like protein a (Arabidopsis thaliana)" AED:0.26 eAED:0.26 QI:148 0.57 0.5 0.87 0.85 0.75 8 368 228	0.456 4551 3	1.7182068 5	0.0293 54802	IPR0043 45 (PANTH ER)	no GO terms
Xvis03_2175 8 5-PA	augustus-gene-6.44-mRNA-1 protein Name:"Similar to PAB8 Polyadenylate-binding protein 8 (Arabidopsis thaliana)"	1.743 5770 4	1.2466561 2	0.0295 18147	IPR012 6 77	F:GO:0003676; F:GO:0003723

AED:0.09 eAED:0.09

QI:312|0.75|0.66|1|1|9|460|63

4

Xvis03_2095	processed-gene-8.27-mRNA-1	0.883 5437	1.6641330 9	0.0306 7983	IPR027	F:GO:0016491;
4 8-PA	protein Name:"Similar to AN3 Naringenin,2-oxoglutarate 3- dioxygenase (Fragment) (Petunia hybrida)" AED:0.02 eAED:0.02 QI:65 1 1 1 1 3 192 370	7			4 43	P:GO:0055114
Xvis03_2161	augustus-gene-2.5-mRNA-1	3.393 3298	0.9368866 8	0.0331 05684	IPR004	F:GO:0003824;
3 5-PA	protein Name:"Similar to GSA Glutamate-1-semialdehyde 2,1-aminomutase, chloroplastic (Oryza sativa subsp. japonica)" AED:0.00 eAED:0.00 QI:90 1 1 1 1 3 296 478	2			6 39	F:GO:0008483; F:GO:0030170; P:GO:0033014; F:GO:0042286
Xvis03_2025	augustus-gene-46.31-mRNA-1	2.336 4062	1.2451940 2	0.0343 20067	IPR000	P:GO:0006952
6 2-PA	protein Name:"Similar to Major pollen allergen Cor a 1 isoforms 5, 6, 11 and 16 (Corylus avellana)" AED:0.26 eAED:0.26 QI:0 1 0.5 1 1 1 2 234 182	8			9 16 (PFAM)	
Xvis03_2157	augustus-gene-6.67-mRNA-1	0.884 6234	1.6552063 4	0.0352 91239	IPR038	F:GO:0070300
5 9-PA	protein Name:"Similar to At5g39570 Uncharacterized protein At5g39570 (Arabidopsis thaliana)" AED:0.00 eAED:0.00 QI:88 1 1 1 1 1 2 401 452	4			9 43 (PANT H ER)	
Xvis03_2238	processed-gene-2.57-mRNA-1	1.202 2400	1.3756846 3	0.0373 58344	IPR024	F:GO:0003676;
6 0-PA	protein Name:"Similar to v1g171563 Eukaryotic translation initiation factor 3 subunit G (Nematostella vectensis)" AED:0.02 eAED:0.02 QI:0 1 0.5 1 1 1 2 3401 289	2			6 75 (PFAM)	F:GO:0003743; C:GO:0005737; C:GO:0005852

Xvis03_2247 5 4-PA	processed-gene-1.55-mRNA-1 protein Name:"Similar to At3g10130 Heme-binding-like protein At3g10130, chloroplastic (Arabidopsis thaliana)" AED:0.02 eAED:0.02 QI:0 - 1 0 1 - 1 1 1 0 209	0.556 5459 9	1.6212252 7	0.0397 11403	IPR006 9 17 (PFAM)	no GO terms
Xvis03_2207 1 9-PA	augustus-gene-6.9-mRNA-1 protein Name:"Similar to TSJT1 Stem-specific protein TSJT1 (Nicotiana tabacum)" AED:0.07 eAED:0.07 QI:59 0.5 0.8 0.8 1 1 5 232 256	0.527 9493 4	1.6116065 9	0.0412 78577	IPR029 0 55	no GO terms
Xvis03_2081 4 0-PA	processed-gene-11.6-mRNA-1 protein Name:"Similar to atad1a ATPase family AAA domain- containing protein 1-A (Danio rerio)" AED:0.12 eAED:0.12 QI:153 0.88 0.94 0.94 0.83 0.7 8 19 436 852	0.458 6671 1	1.5705785 9	0.0417 79846	IPR003 9 59 (PFAM)	F:GO:0005524
Xvis03_21576 4-PA	augustus-gene-6.61-mRNA-1 protein Name:"Similar to 29 kDa ribonucleoprotein B, chloroplastic (Nicotiana sylvestris)" AED:0.25 eAED:0.25 QI:94 0.75 0.6 0.8 1 1 5 0 355	3.073 1014 8	0.9518617 3	0.0427 28409	IPR0126 77	F:GO:0003676
Xvis03_20141 6-PA	processed-gene-12.20-mRNA-1 protein Name:"Similar to Phosphoglycerate kinase, chloroplastic (Nicotiana tabacum)" AED:0.04 eAED:0.04 QI:190 1 1 1 1 6 289 477	21.54 8955 5	0.4267875	0.0432 73487	IPR0015 76	F:GO:0004618; P:GO:0006096
Xvis03_22054 9-PA	processed-gene-6.81-mRNA-1 protein Name:"Similar to NFS2 Cysteine desulfurase 1, chloroplastic (Arabidopsis thaliana)" AED:0.13 eAED:0.23 QI:55 0.77 0.8 1 1 1 10 0 498	0.521 1484 4	1.5881456 9	0.0439 76028	IPR0154 21	F:GO:0003824; P:GO:0006534; F:GO:0030170; F:GO:0031071
Xvis03_20314 0-PA	processed-gene-45.24-mRNA-1 protein Name:"Similar to HSP81-1 Heat shock protein 81-1 (Oryza sativa subsp. japonica)" AED:0.48 eAED:0.48 QI:0 -1 0 1 - 1 1 1 0 114	0.541 9099 6	1.5849319	0.0443 55192	IPR0014 04 (PFAM)	F:GO:0005524; P:GO:0006457; F:GO:0051082

Xvis03_20645 3-PA	processed-gene-29.128-mRNA-1 protein Name:"Similar to CSP4 Cold shock domain-containing protein 4 (Arabidopsis thaliana)" AED:0.32 eAED:0.32 QI:0 -1 0 1 -1 1 1 0 231	1.364 6643	1.2821974 5	0.0446 71688	PR01228	F:GO:0003676; F:GO:0008270
Xvis03_21997 7-PA	augustus-gene-5.85-mRNA-1 protein Name:"Similar to Os02g0194200 Zinc finger CCH domain-containing protein 14 (Oryza sativa subsp. japonica)" AED:0.00 eAED:0.00 QI:185 1 1 1 1 3 411 290	0.560 2625 4	1.5510297 7	0.0453 28627	IPR0366 12	F:GO:0003723; F:GO:0046872
Xvis03_22277 8-PA	processed-gene-2.13-mRNA-1 protein Name:"Similar to PR1 Pathogenesis-related protein 1 (Asparagus officinalis)" AED:0.28 eAED:0.28 QI:65 1 1 1 1 1 2 141 157	1.870 5001 6	1.1787611 6	0.0462 45264	IPR0009 16 (PFAM)	P:GO:0006952
Xvis03_20559 4-PA	augustus-gene-17.68-mRNA-1 protein Name:"Similar to RPS27B 40S ribosomal protein S27-2 (Arabidopsis thaliana)" AED:0.09 eAED:0.09 QI:0 1 0.75 1 1 1 4 342 163	0.984 6833 2	1.4036832 5	0.0480 67861	IPR0005 92 (PFAM)	F:GO:0003735; C:GO:0005840; P:GO:0006412
Xvis03_20736 8-PA	processed-gene-12.44-mRNA-1 protein Name:"Similar to Polyphenol oxidase, chloroplastic (Malus domestica)" AED:0.07 eAED:0.08 QI:0 -1 0 1 -1 1 1 0 578	8.365 8069 8	0.7293521 9	0.0498 40164	IPR0022 27 (PFAM)	F:GO:0004097; F:GO:0016491; P:GO:0046148; P:GO:0055114
Xvis03_211532 - PA	est_gff_Cufflinks-gene-11.15-mRNA-1 protein Name:"Similar to Glucan endo-1,3-beta-glucosidase, acidic isoform (Zea mays)" AED:0.00 eAED:0.00 QI:59 1 1 1 1 1 2 102 335	3.1 59 9 9	-2.188	0.0038 9	IPR000490 (PFAM)	
Xvis03_2128 94- PA	augustus-gene-2.1-mRNA-1 protein Name:"Similar to PORB Protochlorophyllide reductase B, chloroplastic (Hordeum vulgare)" AED:0.09 eAED:0.09 QI:162 1 1 1 1 1 5 457 393	3.051 49	- 1.808 8	0.0068 7	IPR002 347 (PFAM)	
Xvis03_21336 3- PA	processed-gene-12.66-mRNA-1 protein Name:"Similar to Os09g0529100 Probable 6-phosphogluconolactonase 4, chloroplastic (Oryza sativa subsp. japonica)" AED:0.04	0.919 26	- 1.905 2	0.0097 4	IPR006 148 (PFAM)	F:GO:0004553; P:GO:0005975

eAED:0.04
 QI:89|1|1|1|1|3|259|276

Xvis03_22489 7- PA	augustus-gene-1.57-mRNA-1 protein Name:"Similar to HSP90 Endoplasmin homolog (Catharanthus roseus)" AED:0.10 eAED:0.10 QI:52 0.92 0.93 1 1 15 395 788	4.507 08	- 1.166 9	0.0098 7	IPR003 594 (PFAM) ;	F:GO:0016630; P:GO:0055114
Xvis03_22445 9- PA	augustus-gene-1.13-mRNA-1 protein Name:"Similar to RABA2A Ras- related protein RABA2a (Arabidopsis thaliana)" AED:0.02 eAED:0.02 QI:202 1 1 1 1 2 509 220	1.266 09	- 1.627 4	0.0140 4	IPR001 806 (PFAM)	P:GO:0005975; P:GO:0006098; F:GO:0017057
Xvis03_20731 1- PA	processed-gene-7.62-mRNA- 1 protein Name:"Similar to ADK-B Adenylate kinase 4 (Oryza sativa subsp. japonica)" AED:0.05 eAED:0.05 QI:122 1 1 1 1 6 379 246	2.075 78	- 1.441 8	0.0150 2	IPR007 862 (PFAM)	F:GO:0005524; P:GO:0006457; F:GO:0051082
Xvis03_20766 5- PA	processed-gene-12.71-mRNA-1 protein Name:"Similar to HSP90 Endoplasmin homolog (Catharanthus roseus)" AED:0.12 eAED:0.12 QI:42 1 1 1 1 15 358 812	3.284 64	- 1.220 9	0.0154 8	IPR003 594 (PFAM)	F:GO:0003924; F:GO:0005525
Xvis03_20999 2- PA	processed-gene-2.103-mRNA- 1 protein Name:"Similar to Os06g0675700 Probable alpha- glucosidase Os06g0675700 (Oryza sativa subsp. japonica)" AED:0.08 eAED:0.08 QI:226 1 1 1 1 5 499 873	2.492 02	- 1.261 4	0.0165 6	IPR025 887 (PFAM)	F:GO:0004017; F:GO:0005524; P:GO:0006139; F:GO:0016776; F:GO:0019205
Xvis03_21035 0- PA	processed-gene-9.1-mRNA-1 protein Name:"Similar to TP53I3 Quinone oxidoreductase PIG3 (Homo sapiens)" AED:0.11 eAED:0.11 QI:0 0.44 0.5 0.7 1 10 268 486	1.934 08	- 1.550 4	0.0172 1	IPR013 149 (PFAM)	F:GO:0005524; P:GO:0006457; F:GO:0051082

Xvis03_21638 7- PA	augustus-gene-11.65-mRNA-1 protein Name:"Similar to Alpha-galactosidase (Coffea arabica)" AED:0.16 eAED:0.16 QI:81 1 1 1 0.92 0.92 14 139 642	3.489 55	- 1.071 4	0.0184 5	IPR041 233 (PFAM)	F:GO:0003824; F:GO:0004553; P:GO:0005975; F:GO:0030246
Xvis03_21648 0- PA	augustus-gene-6.109-mRNA-1 protein Name:"Similar to UVR8 Ultraviolet-B receptor UVR8 (Arabidopsis thaliana)" AED:0.10 eAED:0.10 QI:223 0.9 1 1 1 1 1 1 290 403	1.254 57	- 1.567 1	0.0203 3	IPR000408	P:GO:0055114
Xvis03_20731 1- PA	processed-gene-7.62-mRNA-1 protein Name:"Similar to ADK-B Adenylate kinase 4 (Oryza sativa subsp. japonica)" AED:0.05 eAED:0.05 QI:122 1 1 1 1 1 6 379 246	2.074 74	- 1.359 7	0.0235 9	IPR007 862 (PFAM)	F:GO:0003824; F:GO:0004553; P:GO:0005975
Xvis03_20360 8- PA	processed-gene-32.69-mRNA-1 protein Name:"Similar to PNSL1 Photosynthetic NDH subunit of lumenal location 1, chloroplastic (Arabidopsis thaliana)" AED:0.12 eAED:0.08 QI:81 1 0.85 1 1 1 7 565 263	0.923 83	- 1.628 8	0.0251 9	IPR00 2683 (PFA M);	F:GO:0009881; P:GO:0010224; F:GO:0042803
Xvis03_20613 8- PA	processed-gene-3.62-mRNA-1 protein Name:"Similar to CHI4 Endochitinase PR4 (Phaseolus vulgaris)" AED:0.03 eAED:0.03 QI:30 1 1 1 1 1 2 158 277	1.246 83	- 1.702 3	0.0271 2	IPR00 1002 (PFA M)	F:GO:0004017; F:GO:0005524; P:GO:0006139; F:GO:0016776; F:GO:0019205
Xvis03_21918 5- PA	processed-gene-8.51-mRNA-1 protein Name:"Similar to tal Transaldolase (Acidothermus cellulolyticus (strain ATCC 43068 / 11B))" AED:0.03 eAED:0.03 QI:60 0.83 0.85 1 1 1 7 483 446	0.544 74	- 1.735 5	0.0277 7	IPR00 1585 (PFA M)	F:GO:0005509; C:GO:0009523; C:GO:0009654; P:GO:0015979; C:GO:0019898
Xvis03_20267 2- PA	processed-gene-54.103-mRNA-1 protein Name:"Similar to HEMC Porphobilinogen deaminase, chloroplastic (Oryza sativa	3.147 76	-1.086	0.0314	IPR02 2418 (PFA M)	F:GO:0004568; P:GO:0005975; P:GO:0006032; F:GO:0008061; P:GO:0016998

subsp. japonica)" AED:0.01

eAED:0.01

QI:117|1|1|1|1|5|327|378

Xvis03_20371	processed-gene-43.103-mRNA-1	4.416 19	- 0.894 4	0.0325 4	IPR02	F:GO:0003824;
4- PA	protein Name:"Similar to At4g26910 Dihydrolipoyllysine- residue succinyltransferase component of 2- oxoglutarate dehydrogenase complex 2, mitochondrial (Arabidopsis thaliana)" AED:0.18 eAED:0.18 QI:18 1 1 1 0.85 0.8 15 384 475				0828 (PFA M)	F:GO:0004801; C:GO:0005737; P:GO:0005975; P:GO:0006098
Xvis03_20785	augustus-gene-3.47-mRNA-1	7.893 22	-0.733	0.0328 8	IPR02	F:GO:0004418;
6- PA	protein Name:"Similar to GAPC2 Glyceraldehyde-3-phosphate dehydrogenase 2, cytosolic (Oryza sativa subsp. japonica)" AED:0.71 eAED:0.72 QI:0 0 0 0.66 1 1 6 0 224				0828 (PFA M)	P:GO:0033014
Xvis03_20041	processed-gene-51.69-mRNA-1	1.284 94	- 1.548 5	0.0377 6); IPR0109	F:GO:0004149; P:GO:0006099;
6- PA	1 protein Name:"Similar to CHLM Magnesium protoporphyrin IX methyltransferase, chloroplastic (Arabidopsis thaliana)" AED:0.34 eAED:0.34 QI:0 -1 0 1 -1 1 1 0 322				40 (PFAM	F:GO:0016620; F:GO:0016746; C:GO:0045252; P:GO:0055114
Xvis03_22011	augustus-gene-8.33-mRNA-1	3.421 34	- 0.937 8	0.0414 9	IPR03	F:GO:0016620;
2- PA	protein Name:"Similar to RPL5 50S ribosomal protein L5, chloroplastic (Arabidopsis thaliana)" AED:0.02 eAED:0.03 QI:29 0.5 0.33 1 1 1 3 0 284				1309 (PFA M)	P:GO:0055114
Xvis03_21577	augustus-gene-7.23-mRNA-1	0.901 09	- 1.542 3	0.0443 7	PTHR42	P:GO:0015995;
4- PA	protein Name:"Similar to CHLP Geranylgeranyl diphosphate reductase, chloroplastic (Nicotiana tabacum)" AED:0.00 eAED:0.00 QI:382 1 1 1 1 2 212 364				685 (PANTH ER)	F:GO:0046406

Xvis03_21360	processed-gene-14.84-mRNA-1	0.701 86	- 1.537 1	0.0450 6	IPR01	F:GO:0003735;
5- PA	protein Name:"Similar to Os08g0288200 Probable adenylate kinase 5, chloroplastic (Oryza sativa subsp. japonica)" AED:0.22 eAED:0.22 QI:25 1 0.94 1 1 1 17 0 611				8962 (PFA M)	C:GO:0005840; P:GO:0006412
Xvis03_21892	processed-gene-4.16-	2.115 55	- 1.344 3	0.0478 4	IPR00	P:GO:0015979;
7- PA	mRNA-1 protein Name:"Similar to PORB Protochlorophyllide reductase B, chloroplastic (Hordeum vulgare)" AED:0.12 eAED:0.12 QI:128 0.75 0.6 1 1 1 5 341 353				2347 (PFA M)	P:GO:0015995; F:GO:0045550; P:GO:0051188; P:GO:0055114
Xvis03_21205	augustus-gene-18.3-mRNA-1	0.879 62	- 1.475 1	0.0482 2	IPR024	F:GO:0004017;
2- PA	protein Name:"Similar to RPN8A 26S proteasome non-ATPase regulatory subunit 7 homolog A (Arabidopsis thaliana)" AED:0.29 eAED:0.29 QI:0 0.9 0.81 0.90 1 1 11 444 363				969 (PFAM)	F:GO:0005524; P:GO:0006139; F:GO:0016776; F:GO:0019205
Xvis03_21126	processed-gene-9.25-mRNA-1	0.810 8	- 1.481 1	0.0488 9	IPR001096	F:GO:0016630;
8- PA	protein Name:"Similar to Vacuolar- processing enzyme (Citrus sinensis)" AED:0.07 eAED:0.07 QI:3 1 1 1 1 1 9 417 590					P:GO:0055114
Xvis03_22309	augustus-gene-3.96-mRNA-1	1.792 06	- 1.193 4	0.0491 3	IPR005805	F:GO:0005515;
5- PA	protein Name:"Similar to petC Cytochrome b6-f complex iron- sulfur subunit, chloroplastic (Oryza sativa subsp. japonica)" AED:0.11 eAED:0.11 QI:167 0.33 0.75 1 1 1 4 287 178					C:GO:0005838
Xvis03_21211	augustus-gene-6.61-mRNA-1	3.887 92	- 2.439 4	4.44E- 05	IPR004	P:GO:0006508;
3- PA	protein Name:"Similar to GGAT1 Glutamate--glyoxylate aminotransferase 1 (Arabidopsis thaliana)" AED:0.19 eAED:0.19 QI:107 0.85 0.93 0.93 0.85 0.93 15 45 0 533				839 (PFAM) ;	F:GO:0008233

Xvis03_21985	augustus-gene-3.73-mRNA-1	18.78 78	- 1.278 3	9.28E- 05	IPR002	F:GO:0008121;
9- PA	protein Name:"Similar to PSBO Oxygen- evolving enhancer protein 1, chloroplastic (Solanum lycopersicum)" AED:0.03 eAED:0.03 QI:216 1 1 1 1 2 224 332				628 (PFAM) ; F:GO:0009496; C:GO:0009507; C:GO:0016020; F:GO:0016491; F:GO:0016679; C:GO:0042651; F:GO:0045158; F:GO:0051537; P:GO:0055114	
Xvis03_22385	processed-gene-1.15-mRNA-1	18.45 85	-1.198	0.0002 6	IPR003	F:GO:0003824;
3- PA	protein Name:"Similar to RCA2 Ribulose bisphosphate carboxylase/oxygenase activase 2, chloroplastic (Larrea tridentata)" AED:0.12 eAED:0.12 QI:111 1 1 1 0.83 0.71 7 332 438				959 (PFAM) ; P:GO:0009058; F:GO:0030170	
Xvis03_20470	processed-gene-11.1-mRNA-1	2.530 29	- 2.250 6	0.0004	IPR001	C:GO:0009654;
5- PA	protein Name:"Similar to RPS17 40S ribosomal protein S17 (Solanum lycopersicum)" AED:0.06 eAED:0.06 QI:0 -1 0 1 -1 1 1 0 143				210 (PFAM) ; P:GO:0010207; F:GO:0010242; P:GO:0042549	
Xvis03_21421	processed-gene-11.33-mRNA- 1 protein Name:"Similar to APX1 L- ascorbate peroxidase, cytosolic (Pisum sativum)" AED:0.17 eAED:0.17 QI:131 1 1 1 1 1 7 558 249	2.831 13	- 2.016 1	0.0005 2	IPR002016	F:GO:0005524
Xvis03_22307	processed-gene-1.89-mRNA-1	2.977 24	- 1.981 2	0.0005 6	IPR022	F:GO:0003735;
7- PA	protein Name:"Similar to CAB13 Chlorophyll a-b binding protein 13, chloroplastic (Solanum lycopersicum)" AED:0.07 eAED:0.07 QI:182 1 1 1 1 1 4 188 263				796 (PFAM) ; C:GO:0005840; P:GO:0006412	
Xvis03_22385	processed-gene-1.15-mRNA- 1 protein Name:"Similar to RCA2 Ribulose bisphosphate carboxylase/oxygenase activase 2, chloroplastic (Larrea tridentata)" AED:0.12 eAED:0.12 QI:111 1 1 1 0.83 0.71 7 332 4 38	8.529	- 1.415 7	0.0006 1		F:GO:0004601; P:GO:0006979; F:GO:0020037; P:GO:0055114

Xvis03_204	processed-gene-11.1-mRNA-1	2.456 9	- 2.152 5	0.0006 9	IPR001	P:GO:0009765;
705- PA	protein Name:"Similar to RPS17 40S ribosomal protein S17 (Solanum lycopersicum)" AED:0.06 eAED:0.06 QI:0 -1 0 1 -1 1 1 0 143				210 (PFAM);	C:GO:0016020
Xvis03_220	augustus-gene-8.33-mRNA-1	3.421 34	- 1.842 4	0.0009 1	IPR031	F:GO:0005524
112- PA	protein Name:"Similar to RPL5 50S ribosomal protein L5, chloroplastic (Arabidopsis thaliana)" AED:0.02 eAED:0.03 QI:29 0.5 0.33 1 1 1 3 0 284				309 (PFAM)	
Xvis03_208	augustus-gene-6.16-mRNA-1	20.07 66	- 1.030 3	0.0009 5		F:GO:0003735;
337- PA	protein Name:"Similar to PSBO Oxygen- evolving enhancer protein 1, chloroplastic (Solanum lycopersicum)" AED:0.08 eAED:0.08 QI:229 1 1 1 0.5 0.33 3 86 332					C:GO:0005840; P:GO:0006412
Xvis03_209	processed-gene-2.101-mRNA-1	8.305 61	- 1.323 2	0.0009 9	IPR002	F:GO:0003735;
988- PA	protein Name:"Similar to PSBP Oxygen-evolving enhancer protein 2, chloroplastic (Cucumis sativus)" AED:0.32 eAED:0.32 QI:142 1 1 1 1 1 4 296 262				683 (PFAM);	C:GO:0005840; P:GO:0006412
Xvis03_211	processed-gene-14.7-mRNA-1	3.490 88	- 1.591 2	0.0016 6	IPR023329	C:GO:0009654;
060- PA	protein Name:"Similar to Chlorophyll a-b binding protein, chloroplastic (Spinacia oleracea)" AED:0.01 eAED:0.01 QI:0 -1 0 1 -1 1 1 0 268					P:GO:0010207; F:GO:0010242; P:GO:0042549
Xvis03_209	processed-gene-2.103-mRNA-1	2.492 02	- 1.860 9	0.0016 8	IPR025	F:GO:0005509;
992- PA	1 protein Name:"Similar to Os06g0675700 Probable alpha- glucosidase Os06g0675700 (Oryza sativa subsp. japonica)" AED:0.08 eAED:0.08 QI:226 1 1 1 1 1 5 499 873				887 (PFAM)	C:GO:0009523; C:GO:0009654; P:GO:0015979; C:GO:0019898
Xvis03_222	augustus-gene-5.53-mRNA-1	1.934 13	- 2.149 4	0.0022 7	IPR002016	P:GO:0009765;
105- PA	protein Name:"Similar to APXT L-ascorbate peroxidase T,					C:GO:0016020

chloroplastic (Arabidopsis
thaliana)" AED:0.32 eAED:0.32
QI:0|0.5|0.45|0.72|0.9|0.81|1|1|0|364

Xvis03_219 178- PA	processed-gene-7.19-mRNA-1 protein Name:"Similar to CNX1 Calnexin homolog 1 (Arabidopsis thaliana)" AED:0.09 eAED:0.09 QI:144 1 1 1 0.83 0.71 7 378 540	5.205 08	- 1.579 1	0.0023 6	IPR001580	F:GO:0003824; F:GO:0004553; P:GO:0005975; F:GO:0030246
Xvis03_223 899- PA	processed-gene-1.98-mRNA-1 protein Name:"Similar to RCA1 Ribulose biphosphate carboxylase/oxygenase activase, chloroplastic (Zea mays)" AED:0.16 eAED:0.16 QI:463 0.90 0.91 1 0.81 0.66 12 2 25 2 80	20.31	- 0.901 6	0.0030 5	IPR003 959 (PFAM);	F:GO:0004601; P:GO:0006979; F:GO:0020037; P:GO:0055114
Xvis03_201 883- PA	augustus-gene-50.73-mRNA-1 protein Name:"Similar to APX1 L- ascorbate peroxidase, cytosolic (Pisum sativum)" AED:0.15 eAED:0.15 QI:0 0.85 0.75 1 1 0.87 8 414 307	2.256 91	- 1.834 6	0.0031 2	IPR002 207 (PRINT S);	F:GO:0005509; F:GO:0005515; C:GO:0005783; P:GO:0006457; F:GO:0051082
Xvis03_206 991- PA	augustus-gene-10.52-mRNA-1 protein Name:"Similar to CPN21 20 kDa chaperonin, chloroplastic (Arabidopsis thaliana)" AED:0.07 eAED:0.07 QI:99 1 1 1 1 1 5 439 254	5.803 16	- 1.302 9	0.0033 7	IPR020818	F:GO:0005524

Xvis03_207825-PA	processed-gene-26.31-mRNA-1 protein Name:"Similar to RPS17 40S ribosomal protein S17 (Solanum lycopersicum)" AED:0.03 eAED:0.03 QI:0 -1 0 1 -1 1 1 0 146	3.876 17	- 1.520 2	0.0035 5	IPR036401	F:GO:0004601; P:GO:0006979; F:GO:0020037; P:GO:0055114
Xvis03_213217-PA	augustus-gene-16.1-mRNA-1 protein Name:"Similar to CSP41A Chloroplast stem-loop binding protein of 41 kDa a, chloroplastic (Arabidopsis thaliana)" AED:0.01 eAED:0.01 QI:41 1 1 1 1 1 6 52 409	9.288 85	-1.198	0.0039 5		P:GO:0006457; F:GO:0046914; P:GO:1901671
Xvis03_221799-PA	processed-gene-5.86-mRNA-1 protein Name:"Similar to LHCB5 Chlorophyll a-b binding protein CP26, chloroplastic (Arabidopsis thaliana)" AED:0.06 eAED:0.06 QI:123 0.8 0.83 1 1 1 6 161 279	3.707 76	- 1.465 2	0.0043 3	IPR022796 (PFAM);	F:GO:0003735; C:GO:0005840; P:GO:0006412
Xvis03_225066-PA	processed-gene-0.82-mRNA-1 protein Name:"Similar to Chlorophyll a-b binding protein, chloroplastic (Spinacia oleracea)" AED:0.00 eAED:0.00 QI:0 -1 0 1 -1 1 1 0 268	4.243 2	- 1.304 9	0.0045 7	IPR022796 (PFAM);	F:GO:0003824; F:GO:0050662
Xvis03_203608-PA	processed-gene-32.69-mRNA-1 protein Name:"Similar to PNSL1 Photosynthetic NDH subunit of luminal location 1, chloroplastic (Arabidopsis thaliana)" AED:0.12 eAED:0.08 QI:81 1 0.85 1 1 1 7 565 263	0.923 83	- 2.058 2	0.0052	IPR002683 (PFAM);	P:GO:0009765; C:GO:0016020
Xvis03_218527-PA	augustus-gene-7.89-mRNA-1 protein Name:"Similar to FBPan1 Fructose-1,6-bisphosphatase, cytosolic (Musa acuminata)" AED:0.29 eAED:0.29 QI:151 0.63 0.75 1 0.54 0.66 12 242 350	2.849 07	- 1.559 2	0.0061 2	IPR028343	P:GO:0009765; C:GO:0016020
Xvis03_224654-PA	processed-gene-1.9-mRNA-1 protein Name:"Similar to CAB21 Chlorophyll a-b binding protein 21, chloroplastic (Nicotiana tabacum)" AED:0.11 eAED:0.11 QI:0 0 0 0.5 1 1 2 0 328	2.583 11	- 1.519 3	0.0068 4	IPR023329	F:GO:0005509; C:GO:0009523; C:GO:0009654; P:GO:0015979; C:GO:0019898
Xvis03_210597-PA	augustus-gene-8.18-mRNA-1 protein Name:"Similar to Atlg67280 Probable lactoylglutathione lyase, chloroplast (Arabidopsis thaliana)" AED:0.06 eAED:0.06 QI:224 1 1 1 1 1 9 419 372	2.837 97	-1.597	0.0070 3	IPR029068	P:GO:0005975; F:GO:0016791; F:GO:0042132
Xvis03_213652-PA	processed-gene-16.266-mRNA-1 protein Name:"Similar to RPL4 50S ribosomal protein L4, chloroplastic (Nicotiana tabacum)" AED:0.18 eAED:0.18 QI:0 -1 0 1 -1 1 1 0 272	2.157 86	- 1.756 4	0.0070 7	IPR013005	P:GO:0009765; C:GO:0016020
Xvis03_202672-PA	processed-gene-54.103-mRNA-1 protein Name:"Similar to HEMC Porphobilinogen deaminase, chloroplastic (Oryza sativa subsp. japonica)" AED:0.01 eAED:0.01 QI:117 1 1 1 1 1 5 327 378	3.145 77	- 1.466 7	0.0073 6	IPR000860	F:GO:0004462; F:GO:0046872
Xvis03_207337-PA	processed-gene-10.83-mRNA-1 protein Name:"Similar to rps5 30S ribosomal protein S5, chloroplastic (Arabidopsis thaliana)" AED:0.00 eAED:0.00 QI:186 1 1 1 1 1 2 216 309	3.171 84	- 1.462 9	0.0075 6	IPR014721	F:GO:0003735; C:GO:0005840; P:GO:0006412

Xvis03_223438-PA	augustus-gene-1.2-mRNA-1 protein Name:"Similar to APX4 Probable L-ascorbate peroxidase 4 (Oryza sativa subsp. japonica)" AED:0.10 eAED:0.10 QI:188 1 1 1 1 9 226 284	3.419 37	- 1.425 4	0.0082 8	IPR002207	F:GO:0004418; P:GO:0033014
Xvis03_225066-PA	processed-gene-0.82-mRNA-1 protein Name:"Similar to Chlorophyll a-b binding protein, chloroplastic (Spinacia oleracea)" AED:0.00 eAED:0.00 QI:0 -1 0 1 -1 1 1 0 268	2.783 97	- 1.416 4	0.0093 2	IPR0227 96 (PFAM);	F:GO:0003723; F:GO:0003735; C:GO:0005840; P:GO:0006412; C:GO:0015935
Xvis03_207668-PA	processed-gene-12.85-mRNA-1 protein Name:"Similar to PETH Ferredoxin--NADP reductase, leaf isozyme, chloroplastic (Pisum sativum)" AED:0.14 eAED:0.14 QI:231 1 1 1 1 9 392 366	9.063 96	- 0.940 5	0.0094 2	IPR001709	F:GO:0004601; P:GO:0006979; F:GO:0020037; P:GO:0055114
Xvis03_211745-PA	augustus-gene-13.21-mRNA-1 protein Name:"Similar to TPIP1 Triosephosphate isomerase, cytosolic (Petunia hybrida)" AED:0.34 eAED:0.34 QI:46 0.88 0.8 0.9 1 1 10 0 326	5.568 14	- 1.139 2	0.0097 7	IPR000652	P:GO:0009765; C:GO:0016020
Xvis03_219001-PA	processed-gene-2.79-mRNA-1 protein Name:"Similar to Transketolase, chloroplastic (Solanum tuberosum)" AED:0.04 eAED:0.04 QI:238 1 1 1 1 1 7 473 742	12.56 51	-0.754 9	0.0110 9	IPR0054 75 (PFAM)	F:GO:0016491; P:GO:0055114
Xvis03_213345-PA	augustus-gene-10.80-mRNA-1 protein Name:"Similar to PGMP Phosphoglucomutase, chloroplastic (Solanum tuberosum)" AED:0.14 eAED:0.14 QI:0 0.88 0.94 1 0.88 0.89 19 523 691	3.167 3	- 1.382 4	0.0121 9	IPR005841	F:GO:0003824; F:GO:0004807; P:GO:0006096
Xvis03_217041-PA	augustus-gene-12.20-mRNA-1 protein Name:"Similar to CPN21 20 kDa chaperonin, chloroplastic (Arabidopsis thaliana)" AED:0.12 eAED:0.12 QI:32 0.33 0.71 0.71 1 1 7 174 298	5.079 52	- 1.101 8	0.0123	IPR020818	F:GO:0003824; F:GO:0004802
Xvis03_218722-PA	augustus-gene-3.37-mRNA-1 protein Name:"Similar to ATP synthase subunit delta', mitochondrial (Ipomoea batatas)" AED:0.20 eAED:0.20 QI:67 0 0.25 0.5 0.33 0.75 4 0 208	0.935 03	- 1.859 7	0.0126 6	IPR036771	P:GO:0005975; F:GO:0016868; P:GO:0071704

Xvis03_200894-PA	augustus-gene-100.71-mRNA-1 protein Name:"Similar to CURVATURE THYLAKOID 1D, chloroplastic (Arabidopsis thaliana)" AED:0.11 eAED:0.11 QI:0 0.42 0.5 0.62 1 1 8 520 390	1.440 97	-	0.0128 5	IPR0255 64 (PFAM	P:GO:0006457
Xvis03_220998-PA	augustus-gene-7.121-mRNA-1 protein Name:"Similar to ADG2 Glucose-1-phosphate adenylyltransferase large subunit 1, chloroplastic (Arabidopsis thaliana)" AED:0.11 eAED:0.11 QI:196 0.92 0.86 1 0.85 0.86 15 136 540	4.011 3	- 1.179 7	0.0129 3	G3DSA:2.160 .1 0.10 (GENE3D);	P:GO:0015986; C:GO:0045261; F:GO:0046933
Xvis03_221570-PA	augustus-gene-2.10-mRNA-1 protein Name:"Similar to LSF1 Phosphoglucan phosphatase LSF1, chloroplastic (Arabidopsis thaliana)" AED:0.06 eAED:0.06 QI:233 0.83 0.71 1 0.5 0.42 7 831 301	4.039 39	- 1.309 6	0.0129 8	G3DSA:2.30.4 2 .10 (GENE3D);	C:GO:0009579
Xvis03_206281-PA	augustus-gene-15.74-mRNA-1 protein Name:"Similar to CYCL Cytochrome c1-1, heme protein, mitochondrial (Solanum tuberosum)" AED:0.28 eAED:0.28 QI:33 0.85 0.87 1 1 1 8 457 361	1.353 25	- 1.692 7	0.0131 7	IPR0023 26 (PRINTS);	P:GO:0009058; F:GO:0016779
Xvis03_211268-PA	processed-gene-9.25-mRNA-1 protein Name:"Similar to Vacuolar-processing enzyme (Citrus sinensis)" AED:0.07 eAED:0.07 QI:3 1 1 1 1 9 417 590	0.810 8	- 1.873 3	0.0137 3	IPR0010 96 (PRINTS);	F:GO:0005515
Xvis03_215883-PA	processed-gene-4.2-mRNA-1 protein Name:"Similar to RPL8 60S ribosomal protein L8 (Solanum lycopersicum)" AED:0.00 eAED:0.00 QI:71 1 1 1 1 1 2 167 261	2.481 07	- 1.488 8	0.0141 9	IPR014726	F:GO:0009055; F:GO:0020037
Xvis03_218222-PA	augustus-gene-8.105-mRNA-1 protein Name:"Similar to CURT1A Protein CURVATURE THYLAKOID 1A, chloroplastic (Arabidopsis thaliana)" AED:0.16 eAED:0.16 QI:215 1 1 1 0.8 0.66 6 98 167	2.179 54	- 1.573 9	0.0144 2	IPR0255 64 (PFAM);	P:GO:0006508; F:GO:0008233

Xvis03_205605-PA	processed-gene-17.119-mRNA-1 protein Name:"Similar to At1g09760 U2 small nuclear ribonucleoprotein A' (Arabidopsis thaliana)" AED:0.23 eAED:0.27 QI:0 0.83 0.71 1 1 1 7 448 347	1.146 94	-1.752	0.0145 9	PF1458 0 (PFAM);	F:GO:0003723; F:GO:0003735; C:GO:0005840; P:GO:0006412; C:GO:0015934
Xvis03_220187-PA	processed-gene-5.6-mRNA-1 protein Name:"Similar to HIR1 Hypersensitive-induced response protein 1 (Arabidopsis thaliana)" AED:0.13 eAED:0.13 QI:38 0.6 0.83 0.83 0.8 0.66 6 280 307	0.674 39	- 1.874 1	0.0145 9	G3DSA:3.30.47 9.30 (GENE3D);	C:GO:0009579
Xvis03_220863-PA	processed-gene-0.82-mRNA-1 protein Name:"Similar to RPL3 60S ribosomal protein L3 (Oryza sativa subsp. japonica)" AED:0.08 eAED:0.08 QI:54 1 1 1 1 1 6 258 389	3.214 93	- 1.416 2	0.0147 7	G3DSA:3.30.14 30.10 ();	F:GO:0005515
Xvis03_224754-PA	processed-gene-1.55-mRNA-1 protein Name:"Similar to At3g10130 Heme-binding-like protein At3g10130, chloroplastic (Arabidopsis thaliana)" AED:0.02 eAED:0.02 QI:0 -1 0 1 -1 1 1 0 209	0.969 6	- 1.844 9	0.0148 3	IPR0069 17 (PFAM);	no GO terms
Xvis03_208987-PA	augustus-gene-4.4-mRNA-1 protein Name:"Similar to BGAL9 Beta-galactosidase 9 (Arabidopsis thaliana)" AED:0.06 eAED:0.06 QI:63 1 1 1 0.94 0.94 19 309 904	4.031 6	- 1.172 1	0.0149 7	IPR0019 44 (PRINTS);	F:GO:0003735; C:GO:0005840; P:GO:0006412
Xvis03_225829-PA	augustus-gene-0.17-mRNA-1 protein Name:"Similar to LHCA1 Chlorophyll a-b binding protein 6, chloroplastic (Arabidopsis thaliana)" AED:0.45 eAED:0.45 QI:0 0.44 0.4 0.5 1 1 10 334 459	2.896 55	- 1.351 9	0.0149 9	PF0246 6 (PFAM);	no GO terms
Xvis03_207774-PA	processed-gene-21.50-mRNA-1 protein Name:"Similar to Transketolase, chloroplastic (Solanum tuberosum)" AED:0.17 eAED:0.17 QI:154 0.85 0.75 1 1 1 8 0 716	12.19 63	- 0.723 8	0.0160 5	IPR0054 75 (PFAM)	F:GO:0004553; P:GO:0005975; F:GO:0030246
Xvis03_216387-PA	augustus-gene-11.65-mRNA-1 protein Name:"Similar to Alpha-galactosidase (Coffea arabica)" AED:0.16 eAED:0.16 QI:81 1 1 1 0.92 0.92 14 139 642	3.489 55	- 1.172 2	0.0161	IPR0022 41 (PRINTS)	P:GO:0009765; C:GO:0016020

Xvis03_216480-PA	augustus-gene-6.109-mRNA-1 protein Name:"Similar to UVR8 Ultraviolet-B receptor UVR8 (Arabidopsis thaliana)" AED:0.10 eAED:0.10 QI:223 0.9 1 1 1 1 1 1 290 403	1.054 63	- 1.779 3	0.0168 1	IPR000408 (PRINTS);	F:GO:0003824
Xvis03_224225-PA	augustus-gene-0.55-mRNA-1 protein Name:"Similar to TPIP1 Triosephosphate isomerase, chloroplastic (Spinacia oleracea)" AED:0.32 eAED:0.32 QI:0 0 0 0.55 0.87 1 9 0 311	5.334 33	- 1.076 5	0.0168 7	IPR013785)	F:GO:0003824; F:GO:0004553; P:GO:0005975
Xvis03_212711-PA	processed-gene-16.130-mRNA-1 protein Name:"Similar to LHCB4.2 Chlorophyll a-b binding protein CP29.2, chloroplastic (Arabidopsis thaliana)" AED:0.05 eAED:0.05 QI:1875 1 1 1 0.5 0.33 3 204 289	5.229 23	- 1.002 2	0.0170 4	IPR022796 (PFAM	F:GO:0009881; P:GO:0010224; F:GO:0042803
Xvis03_223588-PA	processed-gene-1.56-mRNA-1 protein Name:"Similar to VIT_19s0014g02480 Probable bifunctional methylthioribulose-1- phosphate dehydratase/enolase- phosphatase E1 1 (Vitis vinifera)" AED:0.24 eAED:0.24 QI:0 0.9 0.90 0.90 1 1 1 237 411	2.125 07	- 1.450 9	0.0172 6	IPR036409	F:GO:0003824; F:GO:0004807; P:GO:0006096
Xvis03_224459-PA	augustus-gene-1.13-mRNA-1 protein Name:"Similar to RABA2A Ras- related protein RABA2a (Arabidopsis thaliana)" AED:0.02 eAED:0.02 QI:202 1 1 1 1 1 2 509 220	1.266 09	- 1.612 3	0.0172 6	PR00449 (PRINTS	P:GO:0009765; C:GO:0016020
Xvis03_213988-PA	augustus-gene-11.18-mRNA-1 protein Name:"Similar to PAB1 Proteasome subunit alpha type-2 (Oryza sativa subsp. japonica)" AED:0.05 eAED:0.05 QI:70 1 1 1 1 1 10 615 222	2.815 4	- 1.363 4	0.0177 8	IPR029055	F:GO:0000287; C:GO:0005737; F:GO:0016787; P:GO:0019509; F:GO:0043874; F:GO:0046872
Xvis03_215165-PA	augustus-gene-14.29-mRNA-1 protein Name:"Similar to EPHX2 Bifunctional epoxide hydrolase 2 (Sus scrofa)" AED:0.25 eAED:0.25 QI:33 1 1 1 0.75 0.6 5 416 321	1.403 31	- 1.622 8	0.0185 8	IPR000073 (PRINTS);	F:GO:0003924; F:GO:0005525
Xvis03_216531-PA	augustus-gene-9.118-mRNA-1 protein Name:"Similar to RPL3 60S ribosomal protein L3 (Oryza sativa	3.434 94	-1.266	0.0209 3	IPR000597 (PFAM);	F:GO:0004175; F:GO:0004298; C:GO:0005839;

	subsp. japonica)" AED:0.07					P:GO:0006511;
	eAED:0.07					C:GO:0019773;
	QI:0 1 0.83 1 1 0.83 6 237 407					P:GO:0051603
Xvis03_215806-PA	processed-gene-9.114-mRNA-1 protein Name:"Similar to ANN1 Annexin D1 (Arabidopsis thaliana)" AED:0.04 eAED:0.04 QI:119 1 1 1 1 5 186 316	2.396 82	-	0.0211 7	IPR001464 (PRINTS);	F:GO:0003824
Xvis03_224225-PA	augustus-gene-0.55-mRNA-1 protein Name:"Similar to TPIP1 Triosephosphate isomerase, chloroplastic (Spinacia oleracea)" AED:0.32 eAED:0.32 QI:0 0 0 0.55 0.87 1 9 0 311	1.629 89	-	0.0213 4	IPR013785	F:GO:0003735; C:GO:0005840; P:GO:0006412
Xvis03_201588-PA	augustus-gene-28.7-mRNA-1 protein Name:"Similar to NAD-ME1 NAD-dependent malic enzyme 1, mitochondrial (Arabidopsis thaliana)" AED:0.22 eAED:0.22 QI:0 0 0.77 0.78 0.86 0.77 0.82 23 290 790	1.195 84	-1.668	0.0213 4	IPR001891 (PRINTS);	F:GO:0005509; F:GO:0005544
Xvis03_219722-PA	augustus-gene-9.73-mRNA-1 protein Name:"Similar to CAB36 Chlorophyll a-b binding protein 36, chloroplastic (Nicotiana tabacum)" AED:0.36 eAED:0.36 QI:240 1 1 1 1 1 2 393 264	3.822 32	-	0.0223 2	IPR022796 (PFAM	F:GO:0003824; F:GO:0004807; P:GO:0006096
Xvis03_221307-PA	processed-gene-5.33-mRNA-1 protein Name:"Similar to Peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase A (Prunus dulcis)" AED:0.04 eAED:0.04 QI:0 -1 0 1 -1 1 1 0 612	1.814 13	-	0.0226	IPR021102 (PFAM)	F:GO:0004470; F:GO:0004471; F:GO:0051287; P:GO:0055114
Xvis03_205319-PA	processed-gene-30.54-mRNA-1 protein Name:"Similar to PSAH1 Photosystem I reaction center subunit VI-1, chloroplastic (Arabidopsis thaliana)" AED:0.09 eAED:0.09 QI:15 1 1 1 1 1 3 336 145	1.433 39	-	0.0230 7	IPR004928 (PFAM);	P:GO:0009765; C:GO:0016020
Xvis03_209971-PA	augustus-gene-1.88-mRNA-1 protein Name:"Similar to IMPL1 Phosphatase IMPL1, chloroplastic (Arabidopsis thaliana)" AED:0.08 eAED:0.08	0.849 49	-	0.0232 9	IPR020552 (PRINTS);	no GO terms

QI:62|1|1|1|0.9|0.81|11|343|347

Xvis03_223144-PA	processed-gene-3.56-mRNA-1 protein Name:"Similar to RBCS1 Ribulose biphosphate carboxylase small chain, chloroplastic (Musa acuminata)" AED:0.05 eAED:0.05 QI:145 1 1 1 1 1 3 356 174	11.93 72	- 0.843 6	0.025	IPR024681 (PRINTS)	C:GO:0009522; C:GO:0009538; P:GO:0015979
Xvis03_202356-PA	processed-gene-29.12-mRNA-1 protein Name:"Similar to PBG1 Proteasome subunit beta type-4 (Arabidopsis thaliana)" AED:0.13 eAED:0.13 QI:0 0.71 0.75 0.87 1 1 8 335 329	2.244 39	-1.361 9	0.0257	IPR029055	F:GO:0008934; P:GO:0046854; P:GO:0046855
Xvis03_212711-PA	processed-gene-16.130-mRNA-1 protein Name:"Similar to LHCB4.2 Chlorophyll a-b binding protein CP29.2, chloroplastic (Arabidopsis thaliana)" AED:0.05 eAED:0.05 QI:1875 1 1 1 0.5 0.33 3 204 289	4.291 18	- 1.009 8	0.0271 7	IPR022796 (PFAM)	no GO terms
Xvis03_213887-PA	remorin-like isoform X2	3.120 09	- 1.218 4	0.0272 2	IPR005516 (PFAM)	F:GO:0004298; C:GO:0005839; P:GO:0051603
Xvis03_202061-PA	processed-gene-6.69-mRNA-1 protein Name:"Similar to RPL9 50S ribosomal protein L9, chloroplastic (Arabidopsis thaliana)" AED:0.06 eAED:0.06 QI:100 1 1 1 0.83 0.71 7 568 196	1.473 36	- 1.555 7	0.0273 5	IPR020069 (PFAM)	P:GO:0009765; C:GO:0016020
Xvis03_202428-PA	augustus-gene-35.90-mRNA-1 protein Name:"Similar to CURT1A Protein CURVATURE THYLAKOID 1A, chloroplastic (Arabidopsis thaliana)" AED:0.22 eAED:0.42 QI:0 0.75 0.6 1 0.75 0.6 5 269 208	2.031 14	- 1.420 3	0.0289 7	IPR025564 (PFAM)	no GO terms
Xvis03_203635-PA	augustus-gene-35.43-mRNA-1 protein Name:"Similar to CLPP5 ATP-dependent Clp protease proteolytic subunit 5, chloroplastic (Arabidopsis thaliana)" AED:0.40 eAED:0.40 QI:0 1 0.71 1 1 1 7 484 324	1.511 63	- 1.524 8	0.0292 8	IPR001907 (PRINTS)	F:GO:0003735; C:GO:0005840; P:GO:0006412

Xvis03_208040-PA	processed-gene-21.10-mRNA-1 protein Name:"Similar to SHM4 Serine hydroxymethyltransferase 4 (Arabidopsis thaliana)" AED:0.05 eAED:0.05 QI:76 1 1 1 1 4 235 515	15.57 43	- 0.612	0.0293 1	IPR015421	C:GO:0009579
Xvis03_217729-PA	processed-gene-11.5-mRNA-1 protein Name:"Similar to PETE Plastocyanin minor isoform, chloroplastic (Arabidopsis thaliana)" AED:0.37 eAED:0.37 QI:0 0 0 0.16 1 1 6 0 366	2.785 06	- 1.268 9	0.0302 2	IPR0023 87 (PRINTS	F:GO:0004252; P:GO:0006508
Xvis03_225147-PA	augustus-gene-0.41-mRNA-1 protein Name:"Similar to CAB6A Chlorophyll a-b binding protein 6A, chloroplastic (Solanum lycopersicum)" AED:0.00 eAED:0.00 QI:106 1 1 1 1 1 3 75 204	3.862 29	- 1.046 7	0.0309 5	IPR022796 (PFAM); SSF103511 (SUPERFAMI L Y)	F:GO:0003824; F:GO:0004372; P:GO:0019264; F:GO:0030170; P:GO:0035999
Xvis03_216230-PA	Basic secretory protease	1.585 22	-1.482	0.0310 8	IPR007541 (PFAM)	F:GO:0005507; F:GO:0009055
Xvis03_217514-PA	processed-gene-7.97-mRNA-1 protein Name:"Similar to SPAC9E9.15 Uncharacterized protein C9E9.15 (Schizosaccharomyces pombe (strain 972 / ATCC 24843))" AED:0.14 eAED:0.14 QI:59 0.93 0.87 1 1 1 16 145 594	3.507 08	- 1.103 5	0.0317 2	G3DSA:2.60. 12 0.430	P:GO:0009765; C:GO:0016020
Xvis03_207968-PA	augustus-gene-15.42-mRNA-1 protein Name:"Similar to CAP10A Chlorophyll a-b binding protein CP24 10A, chloroplastic (Solanum lycopersicum)" AED:0.00 eAED:0.00 QI:218 1 1 1 1 1 2 259 254	0.648 29	-1.688	0.0319 8	IPR023329	no GO terms
Xvis03_212120-PA	augustus-gene-8.8-mRNA-1 protein Name:"Similar to CEST Protein CHLOROPLAST ENHANCING STRESS TOLERANCE, chloroplastic (Oryza sativa subsp. japonica)" AED:0.04 eAED:0.04 QI:85 1 1 1 1 1 6 455 259	1.043 13	- 1.619 3	0.0320 7	PTHR33672: SF 3 (PANTHER);	P:GO:0032981
Xvis03_223438-PA	augustus-gene-1.2-mRNA-1 protein Name:"Similar to APX4 Probable L-ascorbate peroxidase 4 (Oryza sativa subsp. japonica)" AED:0.10 eAED:0.10 QI:188 1 1 1 1 1 9 226 284	2.609 42	- 1.204 9	0.0321	IPR0022 07 (PRINTS);	P:GO:0009765; C:GO:0016020

Xvis03_211391-PA	processed-gene-20.57-mRNA-1 protein Name:"Similar to GGH2 Gamma-glutamyl hydrolase 2 (Arabidopsis thaliana)" AED:0.20 eAED:0.20 QI:39 1 0.85 1 1 1 7 0 302	2.254 12	- 1.310 1	0.0322 2	IPR0116 97 (PFAM	C:GO:0009535; P:GO:0048564; P:GO:0080183
Xvis03_224849-PA	processed-gene-1.76-mRNA-1 protein Name:"Similar to FKBP19 Peptidyl-prolyl cis-trans isomerase FKBP19, chloroplastic (Arabidopsis thaliana)" AED:0.46 eAED:0.49 QI:0 0.72 0.83 0.91 0.90 0.83 12 203 3 20	0.704 45	- 1.651 5	0.0329 7	IPR0011 79 (PFAM)	F:GO:0004601; P:GO:0006979; F:GO:0020037; P:GO:0055114
Xvis03_220733-PA	processed-gene-1.13-mRNA-1 protein Name:"Similar to CAT1 Catalase-1 (Triticum aestivum)" AED:0.19 eAED:0.19 QI:0 0 0 0.66 1 1 9 0 623	6.462 83	- 0.862 1	0.0330 2	IPR0180 28 (PRINTS)	F:GO:0008242; F:GO:0016787
Xvis03_223095-PA	augustus-gene-3.96-mRNA-1 protein Name:"Similar to petC Cytochrome b6-f complex iron- sulfur subunit, chloroplastic (Oryza sativa subsp. japonica)" AED:0.11 eAED:0.11 QI:167 0.33 0.75 1 1 1 4 287 178	1.792 06	- 1.354 2	0.0338 3	IPR0058 05 (PRINTS)	no GO terms
Xvis03_216531-PA	augustus-gene-9.118-mRNA-1 protein Name:"Similar to RPL3 60S ribosomal protein L3 (Oryza sativa subsp. japonica)" AED:0.07 eAED:0.07 QI:0 1 0.83 1 1 0.83 6 237 407	3.111 12	- 1.257 7	0.034	IPR000597 (PFAM)	F:GO:0004096; P:GO:0006979; F:GO:0020037; P:GO:0055114
Xvis03_220973-PA	augustus-gene-5.51-mRNA-1 protein Name:"Similar to RPS2C 40S ribosomal protein S2-3 (Arabidopsis thaliana)" AED:0.29 eAED:0.29 QI:54 1 1 1 0.5 0.33 3 154 274	3.119 06	- 1.164 4	0.0349 5	IPR013810 (PFAM);	F:GO:0008121; F:GO:0009496; C:GO:0009507; C:GO:0016020; F:GO:0016491; F:GO:0016679; C:GO:0042651; F:GO:0045158; F:GO:0051537; P:GO:0055114
Xvis03_213605-PA	processed-gene-14.84-mRNA-1 protein Name:"Similar to Os08g0288200 Probable adenylate kinase 5, chloroplastic (Oryza sativa subsp. japonica)" AED:0.22 eAED:0.22	0.701 86	- 1.619 5	0.0353 4	IPR000850 (PRINTS);	F:GO:0003735; C:GO:0005840; P:GO:0006412

QI:25|1|0.94|1|1|1|17|0|611

Xvis03_202672-PA	processed-gene-54.103-mRNA-1 protein Name:"Similar to HEMC Porphobilinogen deaminase, chloroplastic (Oryza sativa subsp. japonica)" AED:0.01 eAED:0.01 QI:117 1 1 1 1 1 5 327 378	4.014 03	- 1.002 4	0.0354 7	IPR000860 (PRINTS)	F:GO:0003723; F:GO:0003735; C:GO:0005840; P:GO:0006412; C:GO:0015935
Xvis03_207337-PA	processed-gene-10.83-mRNA-1 protein Name:"Similar to rps5 30S ribosomal protein S5, chloroplastic (Arabidopsis thaliana)" AED:0.00 eAED:0.00 QI:186 1 1 1 1 2 216 309	0.960 41	- 1.583 2	0.0364 9	IPR014721	F:GO:0004017; F:GO:0005524; P:GO:0006139; F:GO:0016776; F:GO:0019205
Xvis03_207968-PA	augustus-gene-15.42-mRNA-1 protein Name:"Similar to CAP10A Chlorophyll a-b binding protein CP24 10A, chloroplastic (Solanum lycopersicum)" AED:0.00 eAED:0.00 QI:218 1 1 1 1 2 259 254	0.921 33	- 1.554 2	0.0365	IPR023329	F:GO:0004418; P:GO:0033014
Xvis03_212925-PA	processed-gene-5.93-mRNA-1 protein Name:"Similar to PETH Ferredoxin--NADP reductase, leaf- type isozyme, chloroplastic (Nicotiana tabacum)" AED:0.42 eAED:0.49 QI:0 0 0 0.8 1 1 5 0 177	1.714 63	- 1.428 8	0.0365 1	IPR001433 (PFAM)	F:GO:0003723; F:GO:0003735; C:GO:0005840; P:GO:0006412; C:GO:0015935
Xvis03_211745-PA	augustus-gene-13.21-mRNA-1 protein Name:"Similar to TPIP1 Triosephosphate isomerase, cytosolic (Petunia hybrida)" AED:0.34 eAED:0.34 QI:46 0.88 0.8 0.9 1 1 10 0 326	4.984 32	- 0.934 5	0.0373 4	IPR000652	P:GO:0009765; C:GO:0016020
Xvis03_212711-PA	processed-gene-16.130-mRNA-1 protein Name:"Similar to LHCB4.2 Chlorophyll a-b binding protein CP29.2, chloroplastic (Arabidopsis thaliana)" AED:0.05 eAED:0.05 QI:1875 1 1 1 0.5 0.33 3 204 289	3.260 57	- 1.066 6	0.0381 8	IPR022796 (PFAM)	F:GO:0016491; P:GO:0055114
Xvis03_223588-PA	processed-gene-1.56-mRNA-1 protein Name:"Similar to VIT_19s0014g02480 Probable bifunctional methylthioribulose-1- phosphate dehydratase/enolase- phosphatase E1 1 (Vitis vinifera)" AED:0.24 eAED:0.24 QI:0 0.9 0.90 0.90 1 1 1 237 411	9.124 94	- 0.942 2	0.0398 1	IPR036409	F:GO:0003824; F:GO:0004807; P:GO:0006096

Xvis03_224459-PA	augustus-gene-1.13-mRNA-1 protein Name:"Similar to RABA2A Ras-related protein RABA2a (Arabidopsis thaliana)" AED:0.02 eAED:0.02 QI:202 1 1 1 1 1 2 509 220	2.841 35	-	0.0404	PR0044 9 (PRINT S)	P:GO:0009765; C:GO:0016020
Xvis03_213988-PA	augustus-gene-11.18-mRNA-1 protein Name:"Similar to PAB1 Proteasome subunit alpha type-2 (Oryza sativa subsp. japonica)" AED:0.05 eAED:0.05 QI:70 1 1 1 1 1 10 615 222	1.456 42	-	0.0439 6	IPR029055	F:GO:0000287; C:GO:0005737; F:GO:0016787; P:GO:0019509; F:GO:0043874; F:GO:0046872
Xvis03_207968-PA	augustus-gene-15.42-mRNA-1 protein Name:"Similar to CAP10A Chlorophyll a-b binding protein CP24 10A, chloroplastic (Solanum lycopersicum)" AED:0.00 eAED:0.00 QI:218 1 1 1 1 1 2 259 254	1.210 25	-	0.0444 8	IPR023329	F:GO:0003924; F:GO:0005525
Xvis03_224672-PA	processed-gene-1.89-mRNA-1 protein Name:"Similar to ALATS Alanine--tRNA ligase (Arabidopsis thaliana)" AED:0.10 eAED:0.10 QI:33 1 1 1 0.90 0.90 22 389 993	5.121 35	-	0.0458 4	IPR00231 8 (PRINTS)	F:GO:0004175; F:GO:0004298; C:GO:0005839; P:GO:0006511; C:GO:0019773; P:GO:0051603
Xvis03_208742-PA	augustus-gene-3.45-mRNA-1 protein Name:"Similar to At4g13360 3- hydroxyisobutyryl-CoA hydrolase- like protein 3, mitochondrial (Arabidopsis thaliana)" AED:0.08 eAED:0.08 QI:31 1 1 1 0.88 0.9 10 444 426	2.075 78	-1.188	0.0473 6	IPR03225 9 (PFAM)	P:GO:0009765; C:GO:0016020
Xvis03_219507-PA	augustus-gene-9.55-mRNA-1 protein Name:"Similar to POPTRDRAFT_831870 Biotin carboxylase 1, chloroplastic (Populus trichocarpa)" AED:0.11 eAED:0.11 QI:0 1 0.94 1 0.93 0.76 17 386 550	1.254 57	-	0.0487 9	IPR00548 1 (PFAM)	F:GO:0000166; F:GO:0003676; F:GO:0004812; F:GO:0004813; F:GO:0005524; C:GO:0005737; P:GO:0006419; P:GO:0043039 F:GO:0003860
Xvis03_224372-PA	processed-gene-2.16-mRNA-1 protein Name:"Similar to UAM1 UDP-arabinopyranose mutase 1 (Oryza sativa subsp. japonica)" AED:0.08 eAED:0.08 QI:87 1 1 1 1 1 4 347 359	1.291 59	-	0.0489	IPR03759 5 (PFAM)	

Xvis03_200047-PA	augustus-gene-4.43-mRNA-1 protein Name:"Similar to BGLU22 Beta-glucosidase 22 (Oryza sativa subsp. japonica)" AED:0.38 eAED:0.38 QI:56 0.9 0.81 1 1 1 1 1 40 465	0.951 13	-1.505	0.0496 3	IPR001360	F:GO:0005524; F:GO:0016874; F:GO:0046872
Xvis03_212711-PA	processed-gene-2.106-mRNA-1 protein Name:"Similar to Beta-galactosidase (Asparagus officinalis)" AED:0.13 eAED:0.13 QI:277 1 1 1 1 1 19 418 832	1.951 18	- 1.341 2	0.0498 5	IPR001944	F:GO:0016866; P:GO:0071669
		5.229 23	- 3.599 1	1.84E- 09	P:GO:000976 5; C:GO:001602 0	F:GO:0004553; P:GO:0005975
Xvis03_216014-PA	processed-gene-5.37-mRNA-1 protein Name:"Similar to PSAF Photosystem I reaction center subunit III, chloroplastic (Arabidopsis thaliana)" AED:0.24 eAED:0.24 QI:0 -1 0 1 -1 1 1 0 232	4.662 08	- 1.326 6	0.0053 4		F:GO:0004553; P:GO:0005975; F:GO:0030246
Xvis03_220507-PA	Xvis03_220507-PA processed-gene-1.26-mRNA-1 protein Name:"Similar to PAP27 Probable inactive purple acid phosphatase 27 (Arabidopsis thaliana)" AED:0.08 eAED:0.08 QI:27 1 1 1 1 1 12 227 617	0.960 41	- 2.079 6	0.0061 4		P:photosynthesis , light harvesting; C:membrane
Xvis03_219507-PA	augustus-gene-9.55-mRNA-1 protein Name:"Similar to POPTRDRAFT_831870 Biotin carboxylase 1, chloroplastic (Populus trichocarpa)" AED:0.11 eAED:0.11 QI:0 1 0.94 1 0.93 0.76 17 386 550	1.950 77	- 1.779 7	0.0062 2	F:ATP binding; F:ligase activity; F:metal ion binding	
Xvis03_208742-PA	augustus-gene-3.45-mRNA-1 protein Name:"Similar to At4g13360 3-hydroxyisobutyryl-CoA hydrolase-like protein 3, mitochondrial (Arabidopsis thaliana)" AED:0.08 eAED:0.08 QI:31 1 1 1 0.88 0.9 10 444 426	1.922 39	- 1.492 5	0.0112 6	F:3-hydroxyisobutyryl-CoA hydrolase activity	
Xvis03_224672-PA	processed-gene-1.89-mRNA-1 protein Name:"Similar to ALATS Alanine--tRNA ligase (Arabidopsis thaliana)" AED:0.10 eAED:0.10 QI:33 1 1 1 0.90 0.90 22 389 993	2.560 21	- 1.494 7	0.0116 1	F:nucleic acid binding; F:alanine tRNA ligase activity; F:ATP binding;	

C:cytoplasm;
P:alanyl
tRNAaminoacyl
ation

Xvis03_224372-PA	processed-gene-2.16-mRNA-1 protein Name:"Similar to UAM1 UDP-arabinopyranose mutase 1 (Oryza sativa subsp. japonica)" AED:0.08 eAED:0.08 QI:87 1 1 1 1 4 347 359	1.04109	-	0.01173	F:intramolecular transferase activity; P:plant-type cell wall organization or biogenesis
Xvis03_200047-PA	augustus-gene-4.43-mRNA-1 protein Name:"Similar to BGLU22 Beta-glucosidase 22 (Oryza sativa subsp. japonica)" AED:0.38 eAED:0.38 QI:56 0.9 0.81 1 1 1 11 40 465	2.0106	-	0.01191	F:hydrolase activity, hydrolyzing O-glycosyl compounds; P:carbohydrate metabolic process
Xvis03_223612-PA	augustus-gene-2.49-mRNA-1 protein Name:"Similar to CEBIP Chitin elicitor-binding protein (Oryza sativa subsp. japonica)" AED:0.27 eAED:0.27 QI:0 0.6 0.5 0.66 1 1 6 353 477	3.49938	-	0.01259	IPR036779
Xvis03_213033-PA	processed-gene-15.37-mRNA-1 protein Name:"Similar to zta1 Probable quinone oxidoreductase (Schizosaccharomyces pombe (strain 972 / ATCC 24843))" AED:0.20 eAED:0.20 QI:0 0 0 0.8 1 1 5 0 292	0.90109	-1.882	0.01455	IPR013154 (PFAM);
Xvis03_225238-PA	augustus-gene-0.18-mRNA-1 protein Name:"Similar to WAXY Granule-bound starch synthase 1, chloroplastic/amyloplastic (Antirrhinum majus)" AED:0.11 eAED:0.11 QI:73 1 1 1 0.92 0.85 14 142 611	0.87706	-	0.01633	IPR013534 (PFAM) no GO terms
Xvis03_210933-PA	augustus-gene-1.32-mRNA-1 protein Name:"Similar to PAP2 Probable inactive purple acid phosphatase 2 (Arabidopsis thaliana)" AED:0.04 eAED:0.04 QI:0 1 0.66 1 0.5 0.33 3 1759 658	3.10401	-	0.01696	IPR015914 (PFAM) P:GO:0055114

Xvis03_218675-PA	processed-gene-10.89-mRNA-1 protein Name:"Similar to AGD2 Probable LL-diaminopimelate aminotransferase, chloroplastic (Oryza sativa subsp. japonica)" AED:0.20 eAED:0.20 QI:0 0.85 0.75 1 1 1 8 209 407	0.983 22	-	0.0175 5	IPR004839 (PFAM)	F:GO:0004373
Xvis03_212280-PA	processed-gene-6.79-mRNA-1 protein Name:"Similar to THI1-2 Thiamine thiazole synthase 2, chloroplastic (Vitis vinifera)" AED:0.02 eAED:0.02 QI:212 1 1 1 1 1 2 483 354	3.044 48	-	0.0182	IPR002922	F:GO:0003993; F:GO:0016787; F:GO:0046872
Xvis03_205558-PA	augustus-gene-14.7-mRNA-1 protein Name:"Similar to CAB7 Chlorophyll a-b binding protein 7, chloroplastic (Solanum lycopersicum)" AED:0.16 eAED:0.16 QI:0 0.25 0.4 1 0.75 0.8 5 892 278	0.765 17	-	0.0240 5	IPR022796	F:GO:0003824; F:GO:0008483; P:GO:0009058; F:GO:0030170
Xvis03_205102-PA	processed-gene-9.15-mRNA-1 protein Name:"Similar to GOR Glutathione reductase, chloroplastic (Fragment) (Nicotiana tabacum)" AED:0.14 eAED:0.14 QI:0 1 0.90 1 0.9 0.81 11 639 590	2.864 2	-	0.0247 8	PR00411	P:GO:0009228
Xvis03_222506-PA	augustus-gene-4.97-mRNA-1 protein Name:"Similar to EDA2 Probable serine protease EDA2 (Arabidopsis thaliana)" AED:0.31 eAED:0.31 QI:159 0.92 0.92 1 1 1 14 279 488	1.767 9	-	0.0249 7	IPR029058	P:GO:0009765; C:GO:0016020
Xvis03_225868-PA	augustus-gene-0.5-mRNA-1 protein Name:"Similar to caa43 2- haloacrylate reductase (Burkholderia sp.)" AED:0.18 eAED:0.18 QI:0 0.25 0 0.8 0.5 0.4 5 0 313	0.847 4	-1.667	0.0274 4	IPR013149 (PFAM)	F:GO:0004362; P:GO:0006749; F:GO:0016491; P:GO:0045454; F:GO:0050660; F:GO:0050661; P:GO:0055114
Xvis03_204322-PA	processed-gene-9.15-mRNA-1 protein Name:"Similar to AFRR Monodehydroascorbate reductase (Solanum lycopersicum)" AED:0.13 eAED:0.13 QI:138 0.72 0.83 0.83 1 1 12 368 489	4.197 82	-	0.0288 8	PR00368 (P:GO:0006508; F:GO:0008236

Xvis03_211689-PA	processed-gene-6.93-mRNA-1 protein Name:"Similar to Proteasome subunit beta type-5 (Spinacia oleracea)" AED:0.07 eAED:0.07 QI:0 1 0.87 1 1 1 8 489 310	2.204 52	- 1.270 7	0.0289 9	IPR000243	P:GO:0055114
Xvis03_217074-PA	processed-gene-2.49-mRNA-1 protein Name:"Similar to PME35 Probable pectinesterase/pectinesterase inhibitor 35 (Arabidopsis thaliana)" AED:0.36 eAED:0.36 QI:662 1 1 1 1 1 3 218 442	2.798 6	- 1.409 7	0.0352 3	IPR035513	F:GO:0016491; F:GO:0050660; P:GO:0055114
Xvis03_221017-PA	processed-gene-109.26-mRNA-1 protein Name:"Similar to PPD Pyruvate, phosphate dikinase, chloroplastic (Mesembryanthemum crystallinum)" AED:0.09 eAED:0.09 QI:8 1 1 1 0.89 0.9 20 257 985	0.631 76	- 1.637 5	0.0374 8		F:GO:0004175; F:GO:0004298; C:GO:0005839; P:GO:0051603
Xvis03_221989-PA	augustus-gene-2.19-mRNA-1 protein Name:"Similar to dapb3 Dipeptidyl aminopeptidase BIII (Pseudoxanthomonas mexicana)"	0.750 18	- 1.628 1	0.0375 8	IPR011042	F:GO:0004857; F:GO:0030599; P:GO:0042545
Xvis03_200779-PA	processed-gene-89.11-mRNA-1 protein Name:"Similar to PSAL Photosystem I reaction center subunit XI, chloroplastic (Spinacia oleracea)" AED:0.06 eAED:0.06 QI:217 1 1 1 1 1 2 190 220	0.852 47	- 1.576 8			
Xvis03_217230-PA	processed-gene-4.43-mRNA-1 protein Name:"Similar to PREP1 Presequence protease 1, chloroplastic/mitochondrial (Arabidopsis thaliana)" AED:0.19 eAED:0.19 QI:1251 0.91 0.84 1 0.75 0.69 13 382 303	1.512 92	- 1.447 6	0.0389 4	IPR036592	F:GO:0003824; F:GO:0005524; P:GO:0006090; F:GO:0016301; P:GO:0016310; F:GO:0016772; F:GO:0050242
Xvis03_205724-PA	processed-gene-33.32-mRNA-1 protein Name:"Similar to IBI1 Aspartate--tRNA ligase 2, cytoplasmic (Arabidopsis thaliana)" AED:0.10 eAED:0.10 QI:60 0.77 0.8 1 1 1 10 190 552	0.943 27	- 1.558 1	0.0389 5		P:GO:0006508; F:GO:0008236
Xvis03_220977-PA	processed-gene-6.91-mRNA-1 protein Name:"Similar to CYP74B2 Lipoxygenate hydroperoxide lyase, chloroplastic (Arabidopsis thaliana)" AED:0.02 eAED:0.17 QI:0 -1 0 1 -1 1 1 0 486	2.324 82	- 1.253 7	0.0408 6	IPR002312 (PRINTS)	C:GO:0009522; C:GO:0009538; P:GO:0015979

Xvis03_210782-PA	augustus-gene-7.64-mRNA-1 protein Name:"Similar to Os08g0562700 Puro- mycin-sensitive aminopeptidase (<i>Oryza</i> <i>sativa</i> subsp. <i>japonica</i>)" AED:0.20 eAED:0.20 QI:160 0.75 0.81 0.90 0.84 0.84 33 28 4 1052	5.676 78	- 0.899 6	0.0411 1	IPR002403 (PRINTS);	F:GO:0003824; P:GO:0006508; F:GO:0046872
Xvis03_219931-PA	processed-gene-8.160-mRNA-1 protein Name:"Similar to SAG12 Senescence- specific cysteine protease SAG12 (<i>Ara-</i> <i>bidopsis thaliana</i>)" AED:0.00 eAED:0.00 QI:0 1 0.5 1 1 1 2 268 331	1.173 47	- 1.471 4	0.0416 5	IPR024601 (PFAM)	F:GO:0000166; F:GO:0003676; F:GO:0004812; F:GO:0004815; F:GO:0005524; C:GO:0005737; P:GO:0006418; P:GO:0006422
Xvis03_219642-PA	augustus-gene-3.70-mRNA-1 protein Name:"Similar to Serpin-Z1C (<i>Triti-</i> <i>cum aestivum</i>)" AED:0.04 eAED:0.04 QI:7 1 1 0.5 0.33 3 183 391	2.219 59	- 1.134 1	0.0433 5	IPR00066	F:GO:0004497; F:GO:0005506; F:GO:0016705; F:GO:0020037; P:GO:0055114
Xvis03_221434-PA	processed-gene-2.106-mRNA-1 protein Name:"Similar to Beta- galactosidase (<i>Asparagus officinalis</i>)" AED:0.13 eAED:0.13 QI:277 1 1 1 1 1 19 418 832	2.435 57	- 1.244 5	0.0459 9	IPR023796 (PFAM)	F:GO:0008237; F:GO:0008270
Xvis03_215806-PA	processed-gene-9.114-mRNA-1 pro- tein Name:"Similar to ANN1 An- nexin D1 (<i>Arabidopsis thaliana</i>)" AED:0.04 eAED:0.04 QI:119 1 1 1 1 1 5 186 316	2.396 82	- 1.230 1	0.0461 7	F:hydrolase ac- tivity, hydrolyz- ing O- glycosyl compounds; P:carbohydrate metabolic pro- cess; F:carbohydrate binding F:calcium ion binding; F:cal- cium- depend- ent phospholipid binding	F:GO:0006508; F:GO:0008234

Table S4: Upregulated proteins identified in *X. schlechteri* leaf tissue in response to dehydration at different dehydration stages. Early Response to Dehydration (ERD), Mid Response to Dehydration (MRD) and Late Response to Dehydration (LRD). The values represent the level of protein expression observed in each dehydration stage obtained from label-free quantitative proteomics data.

Protein Name	ERD	MRD	LRD	Dehydration Stage
11 kDa late embryogenesis abundant protein (Helianthus annuus)	.	1.655059944	2.557663979	MRD and LRD
1-Cys peroxiredoxin (Medicago truncatula)	.	.	1.335126495	LRD
29 kDa ribonucleoprotein B, chloroplastic (Nicotiana sylvestris)	.	.	0.951861733	LRD
AAE3 Oxalate--CoA ligase (Arabidopsis thaliana)	1.706599422	2.36880206	2.657314544	Across all dehydration stages
ABP20 Auxin-binding protein ABP20 (Prunus persica)	.	0.726395826	.	MRD
AGT1 Serine--glyoxylate aminotransferase (Arabidopsis thaliana)	0.795651548	.	.	ERD
AKR2 Ankyrin repeat domain-containing protein 2 (Arabidopsis thaliana)	.	.	1.77529497	LRD
Aldose reductase (Hordeum vulgare)	.	1.943676029	2.13724642	MRD and LRD
AN3 Naringenin,2-oxoglutarate 3-dioxygenase (Fragment) (Petunia hybrida)	.	.	1.664133089	LRD
At3g10130 Heme-binding-like protein At3g10130, chloroplastic (Arabidopsis thaliana)	.	.	1.621225267	LRD
At4g12130 Putative transferase At4g12130, mitochondrial (Arabidopsis thaliana)	.	.	1.545694996	LRD
At4g13010 Putative quinone-oxidoreductase homolog, chloroplastic (Arabidopsis thaliana)	.	.	2.458639066	LRD
At4g22670 FAM10 family protein At4g22670 (Arabidopsis thaliana)	.	.	2.096229206	LRD
At5g12110 Elongation factor 1-beta 1 (Arabidopsis thaliana)	.	.	1.157181359	LRD
At5g13200 GEM-like protein 5 (Arabidopsis thaliana)	.	.	2.050192399	LRD
At5g39570 Uncharacterized protein At5g39570 (Arabidopsis thaliana)	.	.	1.655206338	LRD
At5g61250 Heparanase-like protein 2 (Arabidopsis thaliana)	0.954132089	.	.	ERD
atad1a ATPase family AAA domain-containing protein 1-A (Danio rerio)	.	.	1.570578594	LRD
B19.4 Late embryogenesis abundant protein B19.4 (Hordeum vulgare)	1.159483161	1.816389763	2.516909095	Across all dehydration stages

Blue copper protein (<i>Pisum sativum</i>)	.	1.604443074	.	MRD
Bowman-Birk type trypsin inhibitor (<i>Triticum aestivum</i>)	1.490311914	.	2.18560715	ERD and LRD
CAISE5 Glucose and ribitol dehydrogenase (<i>Daucus carota</i>)	.	.	1.170057472	LRD
CAL1 Calmodulin (<i>Medicago sativa</i>)	1.635472647	.	.	ERD
Carbonic anhydrase, chloroplastic (<i>Hordeum vulgare</i>)	.	.	1.063629616	LRD
CCR1 Cinnamoyl-CoA reductase 1 (<i>Arabidopsis thaliana</i>)	1.561330267	1.623791745	2.600421553	Across all dehydration stages
CCT2 Choline-phosphate cytidyltransferase 2 (<i>Arabidopsis thaliana</i>)	.	1.891082235	2.434010574	MRD and LRD
CHLD Magnesium-chelatase subunit ChLD, chloroplastic (<i>Oryza sativa</i> subsp. <i>japonica</i>)	.	.	2.199000455	LRD
CHLI Magnesium-chelatase subunit ChLI, chloroplastic (<i>Oryza sativa</i> subsp. <i>japonica</i>)	.	.	2.663002746	LRD
CLPB3 Chaperone protein ClpB3, chloroplastic (<i>Arabidopsis thaliana</i>)	.	.	1.718787179	LRD
CML18 Probable calcium-binding protein CML18 (<i>Oryza sativa</i> subsp. <i>japonica</i>)	.	1.972359689	2.643203935	MRD and LRD
COR47 Dehydrin COR47 (<i>Arabidopsis thaliana</i>)	.	.	1.720897276	LRD
CSD2 Superoxide dismutase [Cu-Zn] 2, chloroplastic (<i>Arabidopsis thaliana</i>)	.	.	0.770670729	LRD
CSP1 Cold shock protein 1 (<i>Arabidopsis thaliana</i>)	.	1.625479205	2.163496526	MRD and LRD
CSP4 Cold shock domain-containing protein 4 (<i>Arabidopsis thaliana</i>)	.	.	1.282197447	LRD
CYP74A2 Allene oxide synthase 2 (<i>Oryza sativa</i> subsp. <i>japonica</i>)	0.859536898	.	.	ERD
CYS6 Cysteine proteinase inhibitor 6 (<i>Arabidopsis thaliana</i>)	.	.	1.091432261	LRD
Desiccation-related protein PCC13-62 (<i>Craterostigma plantagineum</i>)	.	1.325612786	1.66968991	MRD and LRD
Desiccation-related protein PCC3-06 (<i>Craterostigma plantagineum</i>)	1.709026897	2.741681551	3.802948804	Across all dehydration stages
DHN1 Dehydrin DHN1 (<i>Hordeum vulgare</i>)	.	.	2.239287919	LRD
DHN3 Dehydrin DHN3 (<i>Hordeum vulgare</i>)	.	1.134434404	1.889777148	MRD and LRD
ECU03_1610 Uncharacterized protein ECU03_1610 (<i>Encephalitozoon cuniculi</i> (strain GB-M1))	.	.	3.039136047	LRD
EIF-5A2 Eukaryotic translation initiation factor 5A-2 (<i>Nicotiana glauca</i>)	.	.	2.095729012	LRD

Embryonic protein DC-8 (<i>Daucus carota</i>)	.	1.456424806	2.545812228	MRD and LRD
ERF1-3 Eukaryotic peptide chain release factor subunit 1-3 (<i>Arabidopsis thaliana</i>)	.	1.543122406	2.677097134	MRD and LRD
Eukaryotic translation initiation factor 5A (<i>Manihot esculenta</i>)	.	.	1.934951423	LRD
FEN1 Flap endonuclease 1 (<i>Zea mays</i>)	.	.	2.177422956	LRD
FLK Flowering locus K homology domain (<i>Arabidopsis thaliana</i>)	.	.	1.960057559	LRD
Fructose-bisphosphate aldolase, cytoplasmic isozyme 1 (<i>Pisum sativum</i>)	.	.	0.979214196	LRD
GAPC3 Glyceraldehyde-3-phosphate dehydrogenase 3, cytosolic (<i>Oryza sativa</i> subsp. <i>japonica</i>)	.	0.869467807	.	MRD
GDCSH Glycine cleavage system H protein, mitochondrial (<i>Flaveria anomala</i>)	.	.	1.545745923	LRD
GDCSP Glycine dehydrogenase (decarboxylating), mitochondrial (<i>Solanum tuberosum</i>)	0.756563035	.	.	ERD
GDCSPA Glycine dehydrogenase (decarboxylating) A, mitochondrial (<i>Flaveria pringlei</i>)	0.870276947	.	.	ERD
GLU Ferredoxin-dependent glutamate synthase, chloroplastic (<i>Oryza sativa</i> subsp. <i>japonica</i>)	1.093872984	.	.	ERD
Glutaredoxin (<i>Ricinus communis</i>)	.	.	1.167181121	LRD
GLX2-2 Hydroxyacylglutathione hydrolase cytoplasmic (<i>Arabidopsis thaliana</i>)	.	.	1.66394102	LRD
GMPM1 18 kDa seed maturation protein (<i>Glycine max</i>)	.	.	2.588554158	LRD
GSA Glutamate-1-semialdehyde 2,1-aminomutase, chloroplastic (<i>Oryza sativa</i> subsp. <i>japonica</i>)	.	.	0.936886678	LRD
Histone H4 (<i>Glycine max</i>)	.	0.816958339	.	MRD
HOP3 Hsp70-Hsp90 organizing protein 3 (<i>Arabidopsis thaliana</i>)	.	.	2.004820501	LRD
HSP70 Heat shock cognate 70 kDa protein (<i>Petunia hybrida</i>)	.	0.607533066	.	MRD
HSP70 Stromal 70 kDa heat shock-related protein, chloroplastic (<i>Pisum sativum</i>)	.	.	0.554872272	LRD
HSP81-1 Heat shock protein 81-1 (<i>Oryza sativa</i> subsp. <i>japonica</i>)	.	.	1.584931903	LRD
Hsp83 Heat shock protein 83 (<i>Drosophila melanogaster</i>)	.	.	1.098741349	LRD
HVA22A HVA22-like protein a (<i>Arabidopsis thaliana</i>)	.	.	1.718206852	LRD
Late embryogenesis abundant protein 76 (<i>Brassica napus</i>)	1.533858234	1.877188535	3.861809893	Across all dehydration stages

Late embryogenesis abundant protein D-29 (Gossypium hirsutum)	1.5099243	2.576559174	2.865984352	Across all dehydration stages
Late embryogenesis abundant protein D-34 (Gossypium hirsutum)	2.07869733	1.933306564	3.090351727	Across all dehydration stages
Late embryogenesis abundant protein Dc3 (Daucus carota)	.	.	2.624853839	LRD
LEA14-A Late embryogenesis abundant protein Lea14-A (Gossypium hirsutum)	.	1.575799622	2.933865689	MRD and LRD
LEA3 Late embryogenesis abundant protein, group 3 (Oryza sativa subsp. indica)	.	1.310594012	2.660239854	MRD and LRD
LTI65 Low-temperature-induced 65 kDa protein (Arabidopsis thaliana)	.	2.00574943	3.1803771	MRD and LRD
Major pollen allergen Cor a 1 isoforms 5, 6, 11 and 16 (Corylus avellana)	.	.	1.245194023	LRD
Mavicyanin (Cucurbita pepo)	1.86719922	1.630580037	.	ERD and MRD
MBF1B Multiprotein-bridging factor 1b (Arabidopsis thaliana)	.	.	1.867719635	LRD
MJ1232 Uncharacterized protein MJ1232 (Methanocaldococcus jannaschii (strain ATCC 43067 / DSM 2661 / JAL-1 / JCM 10045 / NBRC 100440))	.	.	2.283632713	LRD
MORF1 Multiple organellar RNA editing factor 1, mitochondrial (Arabidopsis thaliana)	.	.	1.72895072	LRD
MSRB5 Peptide methionine sulfoxide reductase B5 (Oryza sativa subsp. japonica)	.	.	2.595009712	LRD
MT4A Metallothionein-like protein 4A (Oryza sativa subsp. japonica)	.	.	2.380677691	LRD
MTA Metallothionein-like protein 1 (Pisum sativum)	.	.	2.140799988	LRD
MTH_273 UPF0098 protein MTH_273 (Methanothermobacter thermautotrophicus (strain ATCC 29096 / DSM 1053 / JCM 10044 / NBRC 100330 / Delta H))	.	.	1.971340074	LRD
NFS2 Cysteine desulfurase 1, chloroplastic (Arabidopsis thaliana)	.	.	1.588145687	LRD
Os01g0253300 Importin subunit alpha-1a (Oryza sativa subsp. japonica)	.	.	2.079471181	LRD
Os01g0270100 Cysteine proteinase inhibitor 12 (Oryza sativa subsp. japonica)	.	.	1.291424614	LRD
Os02g0194200 Zinc finger CCCH domain-containing protein 14 (Oryza sativa subsp. japonica)	.	.	1.551029766	LRD

Os02g0639900 Thioredoxin M1, chloroplastic (Oryza sativa subsp. japonica)	.	.	1.351875046	LRD
PAB8 Polyadenylate-binding protein 8 (Arabidopsis thaliana)	.	.	1.246656116	LRD
PCKR1 Peptidyl-prolyl cis-trans isomerase (Catharanthus roseus)	.	.	1.26642199	LRD
PED1 3-ketoacyl-CoA thiolase 2, peroxisomal (Arabidopsis thaliana)	.	.	1.71951601	LRD
Peptidyl-prolyl cis-trans isomerase (Lupinus luteus)	.	.	0.90227811	LRD
Phosphoglycerate kinase, chloroplastic (Nicotiana tabacum)	.	.	0.426787502	LRD
PHS2 Alpha-glucan phosphorylase 2, cytosolic (Arabidopsis thaliana)	.	1.375643724	.	MRD
PLP1 Patatin-like protein 1 (Oryza sativa subsp. japonica)	1.552994529	1.416703369	1.306470985	Across all dehydration stages
Polyphenol oxidase, chloroplastic (Vitis vinifera)	0.950857782	.	0.729352191	ERD and LRD
PORB Protochlorophyllide reductase B, chloroplastic (Hordeum vulgare)	.	.	2.112431088	LRD
PR1 Pathogenesis-related protein 1 (Asparagus officinalis)	.	.	1.178761163	LRD
PXG Peroxygenase (Oryza sativa subsp. japonica)	.	.	1.63025003	LRD
Pyruvate kinase, cytosolic isozyme (Glycine max)	0.98750497	1.181922208	.	ERD and MRD
RAB18 Dehydrin Rab18 (Arabidopsis thaliana)	.	1.435795659	2.686911702	MRD and LRD
RANBP1C Ran-binding protein 1 homolog c (Arabidopsis thaliana)	.	.	1.826681471	LRD
RBCS1 Ribulose biphosphate carboxylase small chain, chloroplastic (Musa acuminata)	.	.	0.884589514	LRD
Remorin (Solanum tuberosum)	.	.	1.760610351	LRD
RPL23A 60S ribosomal protein L23 (Arabidopsis thaliana)	.	.	1.200096286	LRD
RPS12 40S ribosomal protein S12 (Hordeum vulgare)	.	.	2.337496384	LRD
RPS27B 40S ribosomal protein S27-2 (Arabidopsis thaliana)	.	.	1.765478524	LRD
RPT1 26S protease regulatory subunit 7 (Prunus persica)	.	.	2.275208812	LRD
RUB2 Ubiquitin-NEDD8-like protein RUB2 (Oryza sativa subsp. japonica)	.	0.80210109	.	MRD
RuBisCO large subunit-binding protein subunit beta, chloroplastic (Pisum sativum)	.	.	0.637299581	LRD

RZ1B Glycine-rich RNA-binding protein RZ1B (Arabidopsis thaliana)	.	.	1.838550014	LRD
SAPK7 Serine/threonine-protein kinase SAPK7 (Oryza sativa subsp. japonica)	.	.	1.865952133	LRD
SBT3.3 Subtilisin-like protease SBT3.3 (Arabidopsis thaliana)	0.906750846	.	.	ERD
SPG20 Spartin (Homo sapiens)	1.383758686	2.136348103	3.216160058	Across all dehydration stages
SYNPCC7002_A1590 Uncharacterized protein SYNPCC7002_A1590 (Synechococcus sp. (strain ATCC 27264 / PCC 7002 / PR-6))	.	2.038698811	3.208950202	MRD and LRD
TDX TPR repeat-containing thioredoxin TDX (Arabidopsis thaliana)	.	.	1.272280451	LRD
TMEM205 Transmembrane protein 205 (Homo sapiens)	2.770021473	2.67668267	4.380864231	Across all dehydration stages
TSJT1 Stem-specific protein TSJT1 (Nicotiana tabacum)	.	.	1.611606585	LRD
TUFB1 Elongation factor Tu, chloroplastic (Glycine max)	.	.	0.984597415	LRD
UGPA UTP--glucose-1-phosphate uridylyltransferase (Musa acuminata)	.	0.654674746	.	MRD
UGT78D2 UDP-glycosyltransferase 78D2 (Arabidopsis thaliana)	1.920989868	2.561905006	2.78513244	Across all dehydration stages
v1g171563 Eukaryotic translation initiation factor 3 subunit G (Nematostella vectensis)	.	.	1.37568463	LRD

Table S5: Down-regulated proteins identified in *X. schlechteri* leaf tissue in response to dehydration at different dehydration stages. Early Response to Dehydration (ERD), Mid Response to Dehydration (MRD) and Late Response to Dehydration (LRD). The values represent the level of protein expression observed in each dehydration stage obtained from label-free quantitative proteomics data.

Protein Name	ERD	MRD	LRD	Dehydration stage
14-3-3-like protein (<i>Pisum sativum</i>)		-1.10726		MRD
ACO2 Aconitate hydratase 2, mitochondrial (<i>Arabidopsis thaliana</i>)			-1.25587	LRD
ADG2 Glucose-1-phosphate adenylyltransferase large subunit 1, chloroplastic (<i>Arabidopsis thaliana</i>)		-1.17966	-1.16885	MRD and LRD
ADK-B Adenylate kinase 4 (<i>Oryza sativa</i> subsp. <i>japonica</i>)	-1.44179	-1.37469		ERD and MRD
AFRR Monodehydroascorbate reductase (<i>Solanum lycopersicum</i>)			-1.00416	LRD
AGD2 Probable LL-diaminopimelate aminotransferase, chloroplastic (<i>Oryza sativa</i> subsp. <i>japonica</i>)			-1.77126	LRD
ALATS Alanine--tRNA ligase (<i>Arabidopsis thaliana</i>)			-1.49467	LRD
Alpha-galactosidase (<i>Coffea arabica</i>)	-1.07142	-1.17216	-1.0592	Across all dehydration stages
Alpha-mannosidase (<i>Canavalia ensiformis</i>)		-1.36506	-1.27805	MRD and LRD
ANN1 Annexin D1 (<i>Arabidopsis thaliana</i>)		-1.51742	-1.23012	MRD and LRD
APX1 L-ascorbate peroxidase, cytosolic (<i>Pisum sativum</i>)		-2.01611	-3.26533	MRD and LRD
APX4 Probable L-ascorbate peroxidase 4 (<i>Oryza sativa</i> subsp. <i>japonica</i>)		-1.42542		MRD
APXT L-ascorbate peroxidase T, chloroplastic (<i>Arabidopsis thaliana</i>)		-2.14943		MRD
At1g09760 U2 small nuclear ribonucleoprotein A' (<i>Arabidopsis thaliana</i>)		-1.75195		MRD
At1g62810 Primary amine oxidase (<i>Arabidopsis thaliana</i>)			-2.47528	LRD
At1g67280 Probable lactoylglutathione lyase, chloroplast (<i>Arabidopsis thaliana</i>)		-1.59699		MRD
At2g04400 Indole-3-glycerol phosphate synthase, chloroplastic (<i>Arabidopsis thaliana</i>)		-1.87518		MRD
At2g21870 Probable ATP synthase 24 kDa subunit, mitochondrial (<i>Arabidopsis thaliana</i>)		-0.93448		MRD
At3g10130 Heme-binding-like protein At3g10130, chloroplastic (<i>Arabidopsis thaliana</i>)		-1.84486		MRD

At3g48420 Haloacid dehalogenase-like hydrolase domain-containing protein At3g48420 (<i>Arabidopsis thaliana</i>)		-1.65737		MRD
At3g63540 Thylakoid lumenal 19 kDa protein, chloroplastic (<i>Arabidopsis thaliana</i>)		-1.21618		MRD
At4g13360 3-hydroxyisobutyryl-CoA hydrolase-like protein 3, mitochondrial (<i>Arabidopsis thaliana</i>)			-1.4925	LRD
At4g26910 Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex 2, mitochondrial (<i>Arabidopsis thaliana</i>)	-0.89439	-1.00452		ERD and MRD
ATP synthase subunit delta', mitochondrial (<i>Ipomoea batatas</i>)		-1.85971		MRD
Basic secretory protease (Fragments) (<i>Boswellia serrata</i>)	-1.6699	-1.48199	-2.38693	Across all dehydration stages
Beta-galactosidase (<i>Asparagus officinalis</i>)		-1.86712	-1.24451	MRD and LRD
BGAL9 Beta-galactosidase 9 (<i>Arabidopsis thaliana</i>)		-1.1721		MRD
BGLU22 Beta-glucosidase 22 (<i>Oryza sativa</i> subsp. <i>japonica</i>)			-1.47715	LRD
caa43 2-haloacrylate reductase (<i>Burkholderia</i> sp.)			-1.66697	LRD
CAB13 Chlorophyll a-b binding protein 13, chloroplastic (<i>Solanum lycopersicum</i>)		-1.98118	-3.54613	MRD and LRD
CAB21 Chlorophyll a-b binding protein 21, chloroplastic (<i>Nicotiana tabacum</i>)		-1.51935	-2.68394	MRD and LRD
CAB36 Chlorophyll a-b binding protein 36, chloroplastic (<i>Nicotiana tabacum</i>)		-1.0662	-2.82067	MRD and LRD
CAB6A Chlorophyll a-b binding protein 6A, chloroplastic (<i>Solanum lycopersicum</i>)		-1.04674	-3.1886	MRD and LRD
CAB7 Chlorophyll a-b binding protein 7, chloroplastic (<i>Solanum lycopersicum</i>)			-1.71514	LRD
CAB8 Chlorophyll a-b binding protein 8, chloroplastic (<i>Solanum lycopersicum</i>)			-2.88429	LRD
CAP10A Chlorophyll a-b binding protein CP24 10A, chloroplastic (<i>Solanum lycopersicum</i>)		-1.68796	-1.89943	MRD and LRD
CAT1 Catalase-1 (<i>Triticum aestivum</i>)		-0.86209		MRD
CEBIP Chitin elicitor-binding protein (<i>Oryza sativa</i> subsp. <i>japonica</i>)			-1.27643	LRD
CEST Protein CHLOROPLAST ENHANCING STRESS TOLERANCE, chloroplastic (<i>Oryza sativa</i> subsp. <i>japonica</i>)		-1.61931		MRD
CHI4 Endochitinase PR4 (<i>Phaseolus vulgaris</i>)	-1.70233		-1.95186	ERD and LRD

CHLM Magnesium protoporphyrin IX methyltransferase, chloroplastic (Arabidopsis thaliana)	-1.54851			ERD
Chlorophyll a-b binding protein, chloroplastic (Spinacia oleracea)		-1.59118	-2.75709	MRD and LRD
CHLP Geranylgeranyl diphosphate reductase, chloroplastic (Nicotiana tabacum)	-1.54227	-1.87164	-1.88202	Across all dehydration stages
CLPP5 ATP-dependent Clp protease proteolytic subunit 5, chloroplastic (Arabidopsis thaliana)		-1.52476		MRD
CNX1 Calnexin homolog 1 (Arabidopsis thaliana)		-1.57911		MRD
CPN21 20 kDa chaperonin, chloroplastic (Arabidopsis thaliana)		-1.30291		MRD
CSP41A Chloroplast stem-loop binding protein of 41 kDa a, chloroplastic (Arabidopsis thaliana)		-1.19802		MRD
CSP41B Chloroplast stem-loop binding protein of 41 kDa b, chloroplastic (Arabidopsis thaliana)		-0.94221		MRD
CURT1A Protein CURVATURE THYLAKOID 1A, chloroplastic (Arabidopsis thaliana)		-1.5739		MRD
CURT1D Protein CURVATURE THYLAKOID 1D, chloroplastic (Arabidopsis thaliana)		-1.78231		MRD
CYCL Cytochrome c1-1, heme protein, mitochondrial (Solanum tuberosum)		-1.69274		MRD
CYP37 Peptidyl-prolyl cis-trans isomerase CYP37, chloroplastic (Arabidopsis thaliana)		-1.5542		MRD
CYP74B2 Linolenate hydroperoxide lyase, chloroplastic (Arabidopsis thaliana)			-1.25374	LRD
dapb3 Dipeptidyl aminopeptidase BIII (Pseudoxanthomonas mexicana)			-1.62806	LRD
EBM Mannosylglycoprotein endo-beta-mannosidase (Lilium longiflorum)			-1.06139	LRD
EDA2 Probable serine protease EDA2 (Arabidopsis thaliana)			-1.40294	LRD
Ephx2 Bifunctional epoxide hydrolase 2 (Mus musculus)		-1.62283		MRD
FBPban1 Fructose-1,6-bisphosphatase, cytosolic (Musa acuminata)		-1.55921		MRD
FKBP19 Peptidyl-prolyl cis-trans isomerase FKBP19, chloroplastic (Arabidopsis thaliana)		-1.65151		MRD
FKBP62 Peptidyl-prolyl cis-trans isomerase FKBP62 (Arabidopsis thaliana)		-1.4288		MRD

GAPC2 Glyceraldehyde-3-phosphate dehydrogenase 2, cytosolic (<i>Oryza sativa</i> subsp. <i>japonica</i>)	-0.73304			ERD
GGAT1 Glutamate--glyoxylate aminotransferase 1 (<i>Arabidopsis thaliana</i>)		-2.4394		MRD
GGH2 Gamma-glutamyl hydrolase 2 (<i>Arabidopsis thaliana</i>)		-1.31007		MRD
GLU Ferredoxin-dependent glutamate synthase, chloroplastic (<i>Oryza sativa</i> subsp. <i>japonica</i>)			-1.80357	LRD
Glucan endo-1,3-beta-glucosidase, acidic isoform (<i>Zea mays</i>)	-2.188			ERD
GOR Glutathione reductase, chloroplastic (Fragment) (<i>Nicotiana tabacum</i>)			-1.21042	LRD
HEMC Porphobilinogen deaminase, chloroplastic (<i>Oryza sativa</i> subsp. <i>japonica</i>)	-1.08601	-1.46669		ERD and MRD
HIR1 Hypersensitive-induced response protein 1 (<i>Arabidopsis thaliana</i>)		-1.87411		MRD
HIR1 Hypersensitive-induced response protein 1 (<i>Arabidopsis thaliana</i>)			-1.80702	LRD
HSP90 Endoplasmic homolog (<i>Catharanthus roseus</i>)	-1.16691			ERD
IBI1 Aspartate--tRNA ligase 2, cytoplasmic (<i>Arabidopsis thaliana</i>)			-1.55808	LRD
IMPL1 Phosphatase IMPL1, chloroplastic (<i>Arabidopsis thaliana</i>)		-1.75618		MRD
infC Translation initiation factor IF-3 (<i>Nostoc</i> sp. (strain PCC 7120 / UTEX 2576))		-1.50504		MRD
LHCA1 Chlorophyll a-b binding protein 6, chloroplastic (<i>Arabidopsis thaliana</i>)		-1.35192	-2.65519	MRD and LRD
LHCA4 Chlorophyll a-b binding protein 4, chloroplastic (<i>Arabidopsis thaliana</i>)		-1.45625	-2.63069	MRD and LRD
LHCB4.2 Chlorophyll a-b binding protein CP29.2, chloroplastic (<i>Arabidopsis thaliana</i>)		-1.00218	-3.71008	MRD and LRD
LHCB5 Chlorophyll a-b binding protein CP26, chloroplastic (<i>Arabidopsis thaliana</i>)		-1.46518	-3.18151	MRD and LRD
ligA DNA ligase (<i>Bradyrhizobium</i> sp. (strain ORS278))			-1.86947	LRD
LOX2.1 Linoleate 13S-lipoxygenase 2-1, chloroplastic (<i>Solanum tuberosum</i>)			-2.25474	LRD
LSF1 Phosphoglucan phosphatase LSF1, chloroplastic (<i>Arabidopsis thaliana</i>)		-1.30958		MRD
NAD-ME1 NAD-dependent malic enzyme 1, mitochondrial (<i>Arabidopsis thaliana</i>)		-1.668	-1.65009	MRD and LRD
OEP21B Outer envelope pore protein 21B, chloroplastic (<i>Arabidopsis thaliana</i>)			-1.43681	LRD

Os01g0895100 Probable membrane-associated 30 kDa protein, chloroplastic (<i>Oryza sativa</i> subsp. japonica)		-1.44434		MRD
Os02g0739600 Pyruvate dehydrogenase E1 component subunit alpha-1, mitochondrial (<i>Oryza sativa</i> subsp. japonica)			-1.4089	LRD
Os06g0675700 Probable alpha-glucosidase Os06g0675700 (<i>Oryza sativa</i> subsp. japonica)	-1.26142	-1.86095	-1.70842	Across all dehydration stages
Os08g0242700 ACT domain-containing protein DS12, chloroplastic (<i>Oryza sativa</i> subsp. japonica)		-1.61348		MRD
Os08g0288200 Probable adenylate kinase 5, chloroplastic (<i>Oryza sativa</i> subsp. japonica)	-1.53706	-1.61952	-1.57662	Across all dehydration stages
Os08g0562700 Puromycin-sensitive aminopeptidase (<i>Oryza sativa</i> subsp. japonica)			-0.89965	LRD
Os09g0529100 Probable 6-phosphogluconolactonase 4, chloroplastic (<i>Oryza sativa</i> subsp. japonica)	-1.90522			ERD
PAB1 Proteasome subunit alpha type-2 (<i>Oryza sativa</i> subsp. japonica)		-1.36335		MRD
PAP2 Probable inactive purple acid phosphatase 2 (<i>Arabidopsis thaliana</i>)			-1.20063	LRD
PAP27 Probable inactive purple acid phosphatase 27 (<i>Arabidopsis thaliana</i>)		-1.5832		MRD
PAP27 Probable inactive purple acid phosphatase 27 (<i>Arabidopsis thaliana</i>)			-2.07959	LRD
PBF1 Proteasome subunit beta type-1 (<i>Oryza sativa</i> subsp. japonica)			-1.19524	LRD
PBG1 Proteasome subunit beta type-4 (<i>Arabidopsis thaliana</i>)		-1.36101		MRD
Peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase A (<i>Prunus dulcis</i>)		-1.5359	-1.48744	MRD and LRD
petC Cytochrome b6-f complex iron-sulfur subunit, chloroplastic (<i>Oryza sativa</i> subsp. japonica)	-1.19338	-1.35424		ERD and MRD
PETE Plastocyanin minor isoform, chloroplastic (<i>Arabidopsis thaliana</i>)		-1.26885		MRD
PETH Ferredoxin--NADP reductase, leaf isozyme, chloroplastic (<i>Pisum sativum</i>)		-0.9405		MRD
PGMP Phosphoglucomutase, chloroplastic (<i>Solanum tuberosum</i>)		-1.38242		MRD

PME35 Probable pectinesterase/pectinesterase inhibitor 35 (Arabidopsis thaliana)			-1.40972	LRD
PNSL1 Photosynthetic NDH subunit of lumenal location 1, chloroplastic (Arabidopsis thaliana)	-1.62881	-2.05822		ERD and MRD
POPTRDRAFT_831870 Biotin carboxylase 1, chloroplastic (Populus trichocarpa)			-1.77974	LRD
PORB Protochlorophyllide reductase B, chloroplastic (Hordeum vulgare)	-1.80876			ERD
PPL1 PsbP-like protein 1, chloroplastic (Arabidopsis thaliana)		-1.11766		MRD
PREP1 Presequence protease 1, chloroplastic/mitochondrial (Arabidopsis thaliana)			-1.44761	LRD
Proteasome subunit beta type-5 (Spinacia oleracea)			-1.27071	LRD
psaD Photosystem I reaction center subunit II, chloroplastic (Cucumis sativus)			-1.3584	LRD
PSAD2 Photosystem I reaction center subunit II-2, chloroplastic (Arabidopsis thaliana)			-1.28325	LRD
PSAF Photosystem I reaction center subunit III, chloroplastic (Arabidopsis thaliana)			-1.32661	LRD
PSAG Photosystem I reaction center subunit V, chloroplastic (Arabidopsis thaliana)			-2.25576	LRD
PSAH1 Photosystem I reaction center subunit VI-1, chloroplastic (Arabidopsis thaliana)		-1.55564		MRD
PSAH1 Photosystem I reaction center subunit VI-1, chloroplastic (Arabidopsis thaliana)			-2.7504	LRD
PSAH2 Photosystem I reaction center subunit VI-2, chloroplastic (Arabidopsis thaliana)			-2.32278	LRD
PSAL Photosystem I reaction center subunit XI, chloroplastic (Hordeum vulgare)			-2.04454	LRD
PSAN Photosystem I reaction center subunit N, chloroplastic (Arabidopsis thaliana)			-2.69906	LRD
PSBO Oxygen-evolving enhancer protein 1, chloroplastic (Solanum lycopersicum)		-1.27835	-1.09965	MRD and LRD
PSBP Oxygen-evolving enhancer protein 2, chloroplastic (Pisum sativum)		-1.3232		MRD
PSBP Oxygen-evolving enhancer protein 2, chloroplastic (Pisum sativum)			-1.77582	LRD
PSBR Photosystem II 10 kDa polypeptide, chloroplastic (Solanum tuberosum)			-2.69774	LRD
PXG4 Probable peroxygenase 4 (Arabidopsis thaliana)		-1.81513		MRD

RABA2A Ras-related protein RABA2a (<i>Arabidopsis thaliana</i>)	-1.62736	-1.61228	-1.45266	Across all dehydration stages
RBCS1 Ribulose biphosphate carboxylase small chain, chloroplastic (<i>Musa acuminata</i>)		-0.84364		MRD
RCA1 Ribulose biphosphate carboxylase/oxygenase activase 1, chloroplastic (<i>Larrea tridentata</i>)		-0.90161		MRD
RCA2 Ribulose biphosphate carboxylase/oxygenase activase 2, chloroplastic (<i>Larrea tridentata</i>)		-1.41565		MRD
Remorin (<i>Solanum tuberosum</i>)		-1.21839		MRD
RFS Galactinol--sucrose galactosyltransferase (<i>Oryza sativa</i> subsp. <i>japonica</i>)	-1.69881	-2.55586	-2.80097	Across all dehydration stages
RPL3 60S ribosomal protein L3 (<i>Oryza sativa</i> subsp. <i>japonica</i>)		-1.41616		MRD
RPL4 50S ribosomal protein L4, chloroplastic (<i>Nicotiana tabacum</i>)		-1.75638		MRD
RPL5 50S ribosomal protein L5, chloroplastic (<i>Arabidopsis thaliana</i>)	-0.93784	-1.84237		ERD and MRD
RPL8 60S ribosomal protein L8 (<i>Solanum lycopersicum</i>)		-1.48883		MRD
RPL9 50S ribosomal protein L9, chloroplastic (<i>Arabidopsis thaliana</i>)		-1.55571		MRD
RPN8A 26S proteasome non-ATPase regulatory subunit 7 homolog A (<i>Arabidopsis thaliana</i>)	-1.47507			ERD
RPS17 40S ribosomal protein S17 (<i>Solanum lycopersicum</i>)		-2.25057		MRD
RPS2C 40S ribosomal protein S2-3 (<i>Arabidopsis thaliana</i>)		-1.16438		MRD
rps5 30S ribosomal protein S5, chloroplastic (<i>Arabidopsis thaliana</i>)		-1.46291		MRD
SAG12 Senescence-specific cysteine protease SAG12 (<i>Arabidopsis thaliana</i>)			-1.47142	LRD
Serine hydroxymethyltransferase , mitochondrial (<i>Solanum tuberosum</i>)		-0.61287		MRD
Serpin-Z1C (<i>Triticum aestivum</i>)			-1.13413	LRD
SPAC9E9.15 Uncharacterized protein C9E9.15 (<i>Schizosaccharomyces pombe</i> (strain 972 / ATCC 24843))		-1.10348	-1.52577	MRD and LRD
tal Transaldolase (<i>Shewanella loihica</i> (strain ATCC BAA-1088 / PV-4))	-1.73548			ERD

TCTP Translationally-controlled tumor protein homolog (<i>Elaeis guineensis</i> var. <i>tenera</i>)	-1.25771	-1.59903		ERD and MRD
THI1-2 Thiamine thiazole synthase 2, chloroplastic (<i>Vitis vinifera</i>)			-1.21078	LRD
TIC62 Protein TIC 62, chloroplastic (<i>Arabidopsis thaliana</i>)		-1.77576		MRD
tolB Protein TolB (<i>Geobacter metallireducens</i> (strain GS-15 / ATCC 53774 / DSM 7210))		-1.63042	-1.53492	MRD and LRD
TP53I3 Quinone oxidoreductase PIG3 (<i>Homo sapiens</i>)	-1.5504		-1.55183	ERD and LRD
TPIP1 Triosephosphate isomerase, chloroplastic (<i>Spinacia oleracea</i>)		-1.13924		MRD
Transketolase , chloroplastic (<i>Solanum tuberosum</i>)		-1.00238	-1.01196	MRD and LRD
Triosephosphate isomerase , chloroplastic (<i>Secale cereale</i>)		-1.54031		MRD
UAM1 UDP-arabinopyranose mutase 1 (<i>Oryza sativa</i> subsp. <i>japonica</i>)			-1.79507	LRD
UVR8 Ultraviolet-B receptor UVR8 (<i>Arabidopsis thaliana</i>)	-1.56712	-1.77932	-1.63009	Across all dehydration stages
Vacuolar-processing enzyme (<i>Citrus sinensis</i>)	-1.48109	-1.87333	-2.42145	Across all dehydration stages
VIT_19s0014g02480 Probable bifunctional methylthioribulose-1-phosphate dehydratase/enolase-phosphatase E1 1 (<i>Vitis vinifera</i>)		-1.45087	-1.39129	MRD and LRD
WAXY Granule-bound starch synthase 1, chloroplastic/amyloplastic (<i>Antirrhinum majus</i>)			-1.8444	LRD
zta1 Probable quinone oxidoreductase (<i>Schizosaccharomyces pombe</i> (strain 972 / ATCC 24843))			-1.81277	LRD
Keratin, type I cytoskeletal 9 - Homo sapiens (Human).	-1.58735		-2.07128	ERD and LRD
Protein of unknown function	-1.86452			ERD
Protein of unknown function	-1.59024			ERD
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	-2.02522	-1.78496	-2.07012	Across all dehydration stages

Table S6: List of *Xerophyta schlechteri* unknown proteins identified during label-free proteomics. InterPro (<https://www.ebi.ac.uk/interpro/>) was used to find GO-terms and function of the unknown protein where possible.

<i>X. schlechteri</i> ID*	Description	GO-Term	Function
Xvis03_200013-PA	processed-gene-1.89-mRNA-1 protein Name:"Protein of unknown function" AED:0.15 eAED:0.15 QI:0 -1 0 1 -1 1 1 0 178	P:GO:0009408; P:GO:0010115	P:response to heat; P:regulation of abscisic acid biosynthetic process
Xvis03_200377-PA	processed-gene-47.99-mRNA-1 protein Name:"Protein of unknown function" AED:0.68 eAED:0.68 QI:0 -1 0 1 -1 1 1 0 186	P:GO:0009408; P:GO:0010115	P:response to heat; P:regulation of abscisic acid biosynthetic process
Xvis03_200562-PA	processed-gene-71.17-mRNA-1 protein Name:"Protein of unknown function" AED:0.29 eAED:0.29 QI:199 1 1 1 1 1 5 271 381	F:GO:0005509	F:calcium ion binding
Xvis03_202413-PA	processed-gene-34.23-mRNA-1 protein Name:"Protein of unknown function" AED:0.01 eAED:0.01 QI:0 -1 0 1 -1 1 1 0 140	C:GO:0005783; P:GO:0006886; C:GO:0016021	C:endoplasmic reticulum; P:intracellular protein transport; C:integral component of membrane
Xvis03_204624-PA	augustus-gene-37.61-mRNA-1 protein Name:"Protein of unknown function" AED:0.00 eAED:0.00 QI:188 1 1 1 1 1 5 376 359	F:GO:0003723	F:RNA binding
Xvis03_205607-PA	augustus-gene-18.67-mRNA-1 protein Name:"Protein of unknown function" AED:0.34 eAED:0.34 QI:138 1 1 1 1 1 4 447 216	P:GO:0000724; F:GO:0003677	P:double-strand break repair via homologous recombination; F:DNA binding
Xvis03_206711-PA	augustus-gene-20.17-mRNA-1 protein Name:"Protein of unknown function" AED:0.00 eAED:0.00 QI:112 1 1 1 1 1 2 153 186	F:GO:0005515	F:protein binding
Xvis03_206781-PA	processed-gene-26.3-mRNA-1 protein Name:"Protein of unknown function" AED:0.19 eAED:0.19 QI:331 1 1 1 1 1 2 174 193	F:GO:0005515	F:protein binding
Xvis03_206790-PA	processed-gene-27.3-mRNA-1 protein Name:"Protein of unknown function" AED:0.52 eAED:0.52 QI:0 0.7 0.72 0.72 1 1 11 0 294	F:GO:0005515	F:protein binding
Xvis03_209030-PA	processed-gene-10.24-mRNA-1 protein Name:"Protein of unknown function"	F:GO:0003743	F:translation initiation factor activity

	AED:0.25 QI:87 0 0.5 0.5 1 1 4 0 556	eAED:0.25		
Xvis03_209250-PA	augustus-gene-6.35-mRNA-1 protein Name:"Protein of unknown function" AED:0.09 QI:9 1 1 1 0.83 1 7 549 267	eAED:0.09	F:GO:0005509; C:GO:0009654; P:GO:0015979; C:GO:0019898	F:calcium ion binding; C:photosystem II oxygen evolving complex; P:photosynthesis; C:extrinsic component of membrane
Xvis03_209551-PA	augustus-gene-8.71-mRNA-1 protein Name:"Protein of unknown function" AED:0.00 QI:115 1 1 1 1 1 3 283 52	eAED:0.00	C:GO:0000276; F:GO:0015078; P:GO:0015986	C:mitochondrial proton-transporting ATP synthase complex, coupling factor F(o); F:proton transmembrane transporter activity; P:ATP synthesis coupled proton transport
Xvis03_211981-PA	processed-gene-13.88-mRNA-1 protein Name:"Protein of unknown function" AED:0.39 QI:90 0.33 0.25 0.5 1 1 4 0 156	eAED:0.39	F:GO:0004867; C:GO:0005576	F:serine-type endopeptidase inhibitor activity; C:extracellular region
Xvis03_212079-PA	augustus-gene-19.87-mRNA-1 protein Name:"Protein of unknown function" AED:0.24 QI:126 1 0.90 1 0.6 0.45 11 424 1275	eAED:0.24	F:GO:0005515	F:protein binding
Xvis03_212518-PA	augustus-gene-6.13-mRNA-1 protein Name:"Protein of unknown function" AED:0.14 QI:93 1 0.5 1 1 1 2 0 537	eAED:0.14	F:GO:0003743	F:translation initiation factor activity
Xvis03_212553-PA	augustus-gene-10.40-mRNA-1 protein Name:"Protein of unknown function" AED:0.16 QI:74 0.92 0.92 1 0.92 0.92 14 451 363	eAED:0.16	P:GO:1900034	P:regulation of cellular response to heat
Xvis03_212807-PA	processed-gene-7.89-mRNA-1 protein Name:"Protein of unknown function" AED:0.10 QI:219 0.91 0.84 1 0.91 0.92 13 567 841	eAED:0.10	P:GO:0046373; F:GO:0046556	P:L-arabinose metabolic process; F:alpha-L-arabinofuranosidase activity
Xvis03_213271-PA	augustus-gene-4.72-mRNA-1 protein Name:"Protein of unknown function" AED:0.03 QI:529 1 1 1 1 1 5 472 382	eAED:0.03	F:GO:0005509	F:calcium ion binding

Xvis03_213561-PA	augustus-gene-11.61-mRNA-1 protein Name:"Protein of unknown function" AED:0.05 eAED:0.05 QI:138 0.5 0.6 1 1 1 5 352 338	F:GO:0003723	F:RNA binding
Xvis03_214461-PA	augustus-gene-14.50-mRNA-1 protein Name:"Protein of unknown function" AED:0.25 eAED:0.25 QI:166 1 1 1 0.88 0.9 10 542 839	F:GO:0005515	F:protein binding
Xvis03_214462-PA	augustus-gene-14.52-mRNA-1 protein Name:"Protein of unknown function" AED:0.33 eAED:0.37 QI:0 0.72 0.66 0.83 1 1 12 303 933	F:GO:0005515	F:protein binding
Xvis03_214558-PA	processed-gene-7.54-mRNA-1 protein Name:"Protein of unknown function" AED:0.02 eAED:0.02 QI:170 1 1 1 1 1 6 290 375	F:GO:0003723	F:RNA binding
Xvis03_214692-PA	processed-gene-2.8-mRNA-1 protein Name:"Protein of unknown function" AED:0.04 eAED:0.04 QI:39 1 1 1 1 1 4 584 183	P:GO:0000724; F:GO:0003677	P:double-strand break repair via homologous recombination; F:DNA binding
Xvis03_214790-PA	processed-gene-10.70-mRNA-1 protein Name:"Protein of unknown function" AED:0.08 eAED:0.08 QI:0 0 0 1 1 1 4 0 183	P:GO:0000724; F:GO:0003677	P:double-strand break repair via homologous recombination; F:DNA binding
Xvis03_214817-PA	processed-gene-12.12-mRNA-1 protein Name:"Protein of unknown function" AED:0.22 eAED:0.22 QI:0 0.5 0.55 1 1 1 9 386 285	F:GO:0005515	F:protein binding
Xvis03_215263-PA	processed-gene-5.90-mRNA-1 protein Name:"Protein of unknown function" AED:0.07 eAED:0.07 QI:25 1 1 1 1 1 3 199 124	C:GO:0009522; P:GO:0015979	C:photosystem I; P:photosynthesis
Xvis03_215636-PA	augustus-gene-11.1-mRNA-1 protein Name:"Protein of unknown function" AED:0.06 eAED:0.06 QI:45 0.87 0.88 1 0.87 0.88 9 510 884	F:GO:0005515	F:protein binding
Xvis03_216099-PA	processed-gene-0.4-mRNA-1 protein Name:"Protein of unknown function" AED:0.04 eAED:0.04 QI:300 0.5 1 1 1 1 3 3437 201	P:GO:0000724; F:GO:0003677	P:double-strand break repair via homologous recombination; F:DNA binding

Xvis03_217664-PA	augustus-gene-4.63-mRNA-1 protein Name:"Protein of unknown function" AED:0.25 eAED:0.25 QI:465 0.8 0.81 0.90 1 1 11 14 581	F:GO:0003824	F:catalytic activity
Xvis03_217665-PA	est_gff_Cufflinks-gene-4.45-mRNA-1 protein Name:"Protein of unknown function" AED:0.33 eAED:0.33 QI:81 1 1 1 0 0.5 2 546 253	P:GO:0046373; F:GO:0046556	P:L-arabinose metabolic process; F:alpha-L-arabinofuranosidase activity
Xvis03_218355-PA	augustus-gene-4.74-mRNA-1 protein Name:"Protein of unknown function" AED:0.11 eAED:0.11 QI:176 0.66 0.85 1 0.83 1 7 900 405	F:GO:0003723	F:RNA binding
Xvis03_219348-PA	augustus-gene-3.41-mRNA-1 protein Name:"Protein of unknown function" AED:0.07 eAED:0.07 QI:66 1 1 1 1 1 2 366 422	F:GO:0003743	F:translation initiation factor activity
Xvis03_219634-PA	processed-gene-3.2-mRNA-1 protein Name:"Protein of unknown function" AED:0.00 eAED:0.00 QI:123 1 1 1 1 1 3 533 203	P:GO:0010183; F:GO:0036033	P:pollen tube guidance; F:mediator complex binding
Xvis03_220523-PA	augustus-gene-3.91-mRNA-1 protein Name:"Protein of unknown function" AED:0.02 eAED:0.02 QI:101 1 1 1 0.5 0.33 3 285 67		
Xvis03_220526-PA	augustus-gene-4.0-mRNA-1 protein Name:"Protein of unknown function" AED:0.61 eAED:0.63 QI:97 0.25 0.46 0.53 0.66 0.84 13 0 505		
Xvis03_220783-PA	processed-gene-7.30-mRNA-1 protein Name:"Protein of unknown function" AED:0.03 eAED:0.03 QI:54 1 1 1 0.77 0.9 10 270 997		
Xvis03_220839-PA	augustus-gene-7.57-mRNA-1 protein Name:"Protein of unknown function" AED:0.15 eAED:0.18 QI:0 0 0 0.85 1 0.85 7 0 1206		
Xvis03_221114-PA	augustus-gene-7.153-mRNA-1 protein Name:"Protein of unknown function" AED:0.31 eAED:0.31 QI:37 0.81 0.91 0.91 0.90 0.91 12 0 389	F:GO:0005515	F:protein binding

Xvis03_221241-PA	processed-gene-5.4-mRNA-1 protein Name:"Protein of unknown function" AED:0.08 eAED:0.08 QI:245 0.2 0.66 0.66 1 1 6 196 274		
Xvis03_221245-PA	augustus-gene-5.32-mRNA-1 protein Name:"Protein of unknown function" AED:0.09 eAED:0.09 QI:132 0.75 0.8 1 0.5 0.8 5 329 209		
Xvis03_221584-PA	augustus-gene-3.67-mRNA-1 protein Name:"Protein of unknown function" AED:0.09 eAED:0.09 QI:0 1 0.88 1 1 1 9 315 844		
Xvis03_221586-PA	est_gff_Cufflinks-gene-3.18-mRNA-1 protein Name:"Protein of unknown function" AED:0.00 eAED:0.00 QI:74 1 1 1 0 0 2 161 102		
Xvis03_221803-PA	processed-gene-5.17-mRNA-1 protein Name:"Protein of unknown function" AED:0.41 eAED:0.41 QI:0 0.5 0.33 0.66 1 1 3 324 192		
Xvis03_221874-PA	processed-gene-3.62-mRNA-1 protein Name:"Protein of unknown function" AED:0.05 eAED:0.05 QI:40 1 1 1 1 1 3 57 223		
Xvis03_222141-PA	processed-gene-2.132-mRNA-1 protein Name:"Protein of unknown function" AED:0.05 eAED:0.05 QI:31 1 1 1 1 1 5 508 372		
Xvis03_222453-PA	augustus-gene-5.66-mRNA-1 protein Name:"Protein of unknown function" AED:0.10 eAED:0.10 QI:170 1 1 1 1 1 5 279 183		
Xvis03_222491-PA	augustus-gene-2.15-mRNA-1 protein Name:"Protein of unknown function" AED:0.03 eAED:0.03 QI:12 1 1 1 1 1 4 441 657		
Xvis03_222633-PA	processed-gene-2.6-mRNA-1 protein Name:"Protein of unknown function" AED:0.00 eAED:0.00 QI:74 1 1 1 1 1 2 188 155		

Xvis03_223073-PA	processed-gene-1.5-mRNA-1 protein Name:"Protein of unknown function" AED:0.19 eAED:0.19 QI:0 0.5 0.33 0.66 1 1 3 248 338		
Xvis03_223402-PA	processed-gene-3.113-mRNA-1 protein Name:"Protein of unknown function" AED:0.15 eAED:0.15 QI:0 -1 0 1 -1 1 1 0 200		
Xvis03_223551-PA	augustus-gene-0.4-mRNA-1 protein Name:"Protein of unknown function" AED:0.05 eAED:0.05 QI:85 0.66 1 1 1 1 4 290 185		
Xvis03_223700-PA	processed-gene-0.36-mRNA-1 protein Name:"Protein of unknown function" AED:0.07 eAED:0.07 QI:74 0 0.66 0.66 1 1 3 231 183		
Xvis03_223934-PA	processed-gene-3.6-mRNA-1 protein Name:"Protein of unknown function" AED:0.65 eAED:0.65 QI:0 0.28 0.12 0.5 1 1 8 0 363		
Xvis03_224176-PA	processed-gene-0.70-mRNA-1 protein Name:"Protein of unknown function" AED:0.46 eAED:0.46 QI:0 -1 0 1 -1 1 1 0 84		
Xvis03_224299-PA	processed-gene-1.45-mRNA-1 protein Name:"Protein of unknown function" AED:0.17 eAED:0.17 QI:0 -1 0 1 -1 1 1 0 442		
Xvis03_224443-PA	processed-gene-2.98-mRNA-1 protein Name:"Protein of unknown function" AED:0.37 eAED:0.42 QI:0 0 0 1 1 1 2 0 148		
Xvis03_224539-PA	processed-gene-2.15-mRNA-1 protein Name:"Protein of unknown function" AED:0.34 eAED:0.34 QI:0 1 0.8 1 1 1 5 142 253		
Xvis03_224748-PA	augustus-gene-0.35-mRNA-1 protein Name:"Protein of unknown function" AED:0.10 eAED:0.10 QI:42 0.5 1 1 0.5 0.66 3 247 139		
Xvis03_224886-PA	augustus-gene-0.35-mRNA-1 protein Name:"Protein of unknown function" AED:0.15 eAED:0.15 QI:0 1 0.83 1 1 1 6 796 313		

Xvis03_224919-PA	processed-gene-1.1-mRNA-1 protein Name:"Protein of unknown function" AED:0.11 eAED:0.11 QI:31 1 1 1 1 1 4 3638 250		
Xvis03_225115-PA	augustus-gene-0.198-mRNA-1 protein Name:"Protein of unknown function" AED:0.20 eAED:0.11 QI:39 0.71 0.75 1 1 0.87 8 1386 134		
Xvis03_225434-PA	augustus-gene-0.49-mRNA-1 protein Name:"Protein of unknown function" AED:0.01 eAED:0.01 QI:74 1 1 1 1 1 2 209 143		
Xvis03_225567-PA	processed-gene-0.22-mRNA-1 protein Name:"Protein of unknown function" AED:0.19 eAED:0.19 QI:0 0.16 0.14 0.71 1 1 7 86 485		
Xvis03_225590-PA	augustus-gene-0.1-mRNA-1 protein Name:"Protein of unknown function" AED:0.00 eAED:0.00 QI:185 1 1 1 1 1 2 42 261		
Xvis03_225702-PA	processed-gene-0.52-mRNA-1 protein Name:"Protein of unknown function" AED:0.28 eAED:0.28 QI:29 0.77 0.9 1 1 1 10 29 322		

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Table S7: Mapman BINs representing upregulated and downregulated *X. schlechteri* proteins at early response to drying.

Bin	Name	Elements	p-value
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	Upregulated proteins at ERD	(no.of proteins allocated)	
35	Not assigned	11	0.676053
9	Secondary metabolism	2	0.791296
1	Photosynthesis	1	0.140458
4	Amino acid metabolism	1	0.140458
11	Phytohormone action	1	0.259640
25	Nutrient uptake	1	0.259640
5	Lipid metabolism	1	0.435156
2	Cellular respiration	1	0.664612
Bin	Name Downregulated proteins at ERD	Elements (no.of proteins allocated)	p-value
7	Co-enzyme metabolism	5	0.785817
19	Protein homeostasis	4	0.335234
35	Not assigned	3	0.276986
3	Carbohydrate metabolism	2	0.045141
1	Photosynthesis	2	0.920212
6	Nucleotide metabolism	2	0.920212
2	Cellular respiration	1	0.127153
17	Protein biosynthesis	1	0.165518
22	Vesicle trafficking	1	0.405381
26	External stimuli response	1	0.488074
27	Multi-process regulation	1	1

Table S8: Mapman BINs representing upregulated and downregulated *X. schlechteri* proteins at Mid response to drying.

Bin	Name Upregulated proteins at MRD	Elements (no.of proteins allocated)	p-value
35	Not assigned	2	0.029297
19	Protein homeostasis	2	0.028108
3	Carbohydrate metabolism	2	0.107347
5	Lipid metabolism	2	0.941653
9	Secondary metabolism	1	0.114128
12	Chromatin organisation	1	0.202622
2	Cellular respiration	1	0.332880
17	Protein biosynthesis	1	0.798859
16	RNA processing	1	0.878482
26	External stimuli response	1	0.878482

Bin	Name Downregulated proteins at MRD	Elements (no.of proteins allocated)	p-value
1	Photosynthesis	27	2.71E-04
35	Not assigned	16	0.481927
17	Protein biosynthesis	11	0.297923
19	Protein homeostasis	6	0.855506
3	Carbohydrate metabolism	5	0.002388
2	Cellular respiration	5	0.185229
10	Redox homeostasis	5	0.210305
4	Amino acid metabolism	2	0.207697
21	Cell wall organisation	2	0.287358
18	Protein modification	2	0.575503
16	RNA processing	2	0.910829
6	Nucleotide metabolism	2	0.933061
27	Multi-process regulation	1	0.150744
26	External stimuli response	1	0.245505
22	Vesicle trafficking	1	0.442687
7	Co-enzyme metabolism	1	0.921600

Table S9: Mapman BINs representing upregulated and downregulated *X. schlechteri* proteins at late response to drying.

Bin	Name Upregulated proteins at LRD	Elements (no.of proteins allocated)	p-value
35	Not assigned	48	3.66E-04
17	Protein biosynthesis	14	0.350356
7	Co-enzyme metabolism	5	0.701357
1	Photosynthesis	4	0.004989
18	Protein modification	4	0.067196
5	Lipid metabolism	4	0.776159
16	RNA processing	4	0.845021
10	Redox homeostasis	3	0.060389
19	Protein homeostasis	3	0.213074
26	External stimuli response	3	0.775051
9	Secondary metabolism	3	0.806496
23	Protein translocation	3	0.854240
2	Cellular respiration	2	0.156297
3	Carbohydrate metabolism	1	0.086411
13	Cell cycle organisation	1	0.506139
14	DNA damage response	1	0.506139
15	RNA biosynthesis	1	0.551926

Bin	Name Downregulated proteins at LRD	Elements (no.of proteins allocated)	p-value
1	Photosynthesis	16	0.021967
35	Not assigned	14	0.335041
3	Carbohydrate metabolism	6	0.241955
19	Protein homeostasis	4	0.364960
10	Redox homeostasis	3	0.497135
21	Cell wall organisation	2	0.340023
7	Co-enzyme metabolism	2	0.896482
17	Protein biosynthesis	2	0.965407
27	Multi-process regulation	1	0.273913
26	External stimuli response	1	0.465759
4	Amino acid metabolism	1	0.584346
2	Cellular respiration	1	0.715337
22	Vesicle trafficking	1	0.761192

Table S10: List of the Bin names, id and description of the upregulated proteins at ERD

BinName	id	Description
Secondary metabolism. phenolics.flavonoid biosynthesis.flavonol glycosides.flavonol-3-O- rhamnosyltransferase'	xvis03_211917- pa	flavonol-3-O-rhamnosyltransferase (original description: augustus-gene-8.2-mRNA-1 protein Name:Similar to UGT78D2 UDP- glycosyltransferase 78D2 (Arabidopsis thaliana) AED:0.00 eAED:0.00 QI:173 1 1 1 1 1 2 210 454)'
Secondary metabolism. phenolics.flavonoid biosynthesis.aurones.aureusidin synthase'	xvis03_203578- pa	aureusidin synthase (original description: augustus-gene-30.42-mRNA-1 protein Name:Similar to Polyphenol oxidase, chloroplastic (Vitis vinifera) AED:0.01 eAED:0.01 QI:30 1 1 1 1 1 2 191 591)'

Table S11: List of the Bin names, id and description of the downregulated proteins at ERD

BinName	id	Description
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Coenzyme metabolism .tetrapyrrol biosynthesis.uroporphyrinogen III formation.porphobilinogen deaminase'	xvis03_202672-pa	porphobilinogen deaminase (original description: processed-gene-54.103- mRNA-1 protein
Coenzyme metabolism .tetrapyrrol biosynthesis.chlorophyll metabolism.chlorophyll(ide) interconversions.geranylgeranyl reductase (Chlp)'	xvis03_215774-pa	Name:Similar to HEMC geranylgeranyl reductase (Chlp) Porphobilinogen deaminase, (original description: augustus-gene- chloroplastic (Oryza sativa 7.23-mRNA-1 protein Name:Similar subsp. japonica) AED:0.01 to CHLP Geranylgeranyl diphosphate eAED:0.01 reductase, chloroplastic (Nicotiana glauca) AED:0.00 eAED:0.00 QI:117 1 1 1 1 5 327 378
Coenzyme metabolism .tetrapyrrol biosynthesis.chlorophyll metabolism.Mg- protein homeostasis .protein quality protoporphyrin IX O-methyltransferase' control.Hsp90 chaperone system.chaperone (Hsp90)'	xvis03_200416-pa xvis03_207665-pa	Mg-protoporphyrin IX O- methyltransferase (original chaperone (Hsp90) (original description: processed-gene- description: processed-gene- 51.69-mRNA-1 protein 12.71-mRNA-1 protein Name:Similar to CHLM Name:Similar to HSP90 Magnesium protoporphyrin IX Endoplasmic reticulum methyltransferase, chloroplastic (Catharanthus roseus) (Arabidopsis thaliana) AED:0.12 eAED:0.12 AED:0.34 eAED:0.34 QI:0 QI:42 1 1 1 1 15 358 812
protein homeostasis .protein quality control.Hsp90 chaperone system.chaperone Coenzyme metabolism .tetrapyrrol biosynthesis.chlorophyll metabolism.protochlorophyllide oxidoreductase (pOR) activities.light-dependent pOR'	xvis03_224897-pa xvis03_212894-pa	chaperone (Hsp90) (original description: augustus-gene- 1.57- light-dependent mRNA-1 protein Name:Similar to protochlorophyllide HSP90 Endoplasmic reticulum oxidoreductase (original (Catharanthus roseus) AED:0.10 description: augustus-gene- 2.1- eAED:0.10 mRNA-1 protein Name:Similar QI:52 0.92 0.93 1 1 15 395 788
protein homeostasis .ubiquitin-proteasome	xvis03_212052-pa	to PORB Protochlorophyllide regulatory component RPN8 of reductase B, chloroplastic (Hordeum vulgare) AED:0.09 eAED:0.09 QI:162 1 1 1 1 1 5 457 393
Coenzyme metabolism .tetrapyrrol biosynthesis.chlorophyll system.26S proteasome.19S regulatory partial.19S regulatory oxidoreductase (pOR) activities.light- dependent pOR'	xvis03_218927-pa	light-dependent protochlorophyllide 26S proteasome (original description: augustus-gene- 18.3-mRNA-1 protein Name:Similar to RPN8 of Name:Similar to RPN8 of reductase B, chloroplastic proteasome non-ATPase (Hordeum vulgare) AED:0.12 regulatory subunit 7 homolog (Arabidopsis thaliana) QI:128 0.75 0.6 1 1 1 5 341 353 AED:0.29 eAED:0.29 QI:0 0.9 0.81 0.90 1 1 1 444 3 63

protein homeostasis .proteolysis.cysteine-type peptidase activities.C13-class asparaginyl endopeptidase (Legumain)'	xvis03_211268-pa	asparaginyl endopeptidase (Legumain) (original description: processed-gene-9.25-mRNA-1 protein Name:Similar to Vacuolar-processing enzyme (Citrus sinensis) AED:0.07 eAED:0.07 QI:3 1 1 1 1 9 417 590)'
Carbohydrate metabolism .oxidative pentose phosphate pathway.oxidative phase.6-phosphogluconolactonase'	xvis03_213363-pa	6-phosphogluconolactonase (original description: processed-gene-12.66-mRNA-1 protein Name:Similar to Os09g0529100 Probable 6-
		phosphogluconolactonase 4, chloroplastic (Oryza sativa subsp. japonica) AED:0.04 eAED:0.04 QI:89 1 1 1 1 3 259 276)'
Carbohydrate metabolism .oxidative pentose phosphate pathway.non-oxidative phase.transaldolase'	xvis03_219185-pa	transaldolase (original description: processed-gene-8.51-mRNA-1 protein Name:Similar to tal Transaldolase (Acidothermus cellulolyticus (strain ATCC 43068 / 11B)) AED:0.03 eAED:0.03 QI:60 0.83 0.85 1 1 1 7 483 446)'
photosynthesis .photophosphorylation.cytochrome b6/f complex.Rieske iron-sulfur component petC'	xvis03_223095-pa	Rieske iron-sulfur component PetC of cytochrome b6/f complex (original description: augustus-gene-3.96-mRNA-1 protein Name:Similar to petC Cytochrome b6-f complex iron-sulfur subunit, chloroplastic (Oryza sativa subsp. japonica) AED:0.11 eAED:0.11 QI:167 0.33 0.75 1 1 1 4 287 178)'
photosynthesis .photophosphorylation.chlororespiration.NADH dehydrogenase-like (NDH) complex.lumen subcomplex L.component pnsL1'	xvis03_203608-pa	component PnsL1 of NDH lumen subcomplex L (original description: processed-gene-

		32.69-mRNA-1 protein Name: Similar to PNSL1 Photosynthetic NDH subunit of lumenal location 1, chloroplastic (Arabidopsis thaliana) AED:0.12 eAED:0.08 QI:81 1 0.85 1 1 1 7 565 263)'
Nucleotide metabolism.purines.phosphotransfers.adenylate kinase'	xvis03_207311-pa	adenylate kinase (original description: processed-gene- 7.62-mRNA-1 protein Name: Similar to ADK-B Adenylate kinase 4 (Oryza sativa subsp. japonica) AED:0.05 eAED:0.05 QI:122 1 1 1 1 1 6 379 246)'
Nucleotide metabolism.purines.phosphotransfers.adenylate kinase'	xvis03_213605-pa	adenylate kinase (original description: processed-gene- 14.84-mRNA-1 protein Name: Similar to Os08g0288200 Probable adenylate kinase 5, chloroplastic (Oryza sativa subsp. japonica) AED:0.22 eAED:0.22 QI:25 1 0.94 1 1 1 17 0 611)'

Table S12: List of the Bin names, id and description of the upregulated proteins at MRD

BinName	id	Description
protein homeostasis.protein quality control.cytosolic Hsp70 chaperone system.chaperone (Hsp70)'	xvis03_22222 3-pa	chaperone (Hsp70) (original description: processed-gene-2.73- mRNA-1 protein Name: Similar to HSP70 Heat shock cognate 70 kDa protein (Petunia hybrida) AED:0.11 eAED:0.11 QI:205 0.5 0.33 0.66 1 1 3 0 710)'

protein homeostasis.ubiquitin-proteasome system.ubiquitin-fold protein conjugation.RUB/NEDD8 conjugation (neddylation).ubiquitin-fold protein (RUB)'	xvis03_20581 3-pa	ubiquitin-fold protein (RUB) (original description: processed-gene-6.86-mRNA-1 protein Name: Similar to RUB2 Ubiquitin-NEDD8-like protein RUB2 (Oryza sativa subsp. japonica) AED:0.04 eAED:0.04 QI:73 1 1 1 1 1 3 301 153)'
Carbohydrate metabolism.sucrose metabolism.biosynthesis.cytosolic UDP-glucose pyrophosphorylase'	xvis03_20212 4-pa	cytosolic UDP-glucose pyrophosphorylase (original description: processed-gene-11.0-mRNA-1 protein Name: Similar to UGPA UTP--glucose-1-phosphate uridylyltransferase (Musa acuminata) AED:0.18 eAED:0.18 QI:271 0.88 0.89 1 1 1 19 372 458)'
Carbohydrate metabolism.starch metabolism.degradation.maltose metabolism.cytosolic alpha-glucan phosphorylase'	xvis03_20465 9-pa	cytosolic alpha-glucan phosphorylase (original description: augustus-gene-39.13-mRNA-1 protein Name: Similar to PHS2 Alpha-glucan phosphorylase 2, cytosolic (Arabidopsis thaliana) AED:0.23 eAED:0.23 QI:181 0.92 0.93 1 0.92 0.86 15 169 732)'
Lipid metabolism.glycerolipid biosynthesis.phosphatidylcholine.CTp:phosphorylcholine cytidylyltransferase'	xvis03_20265 5-pa	CTP:phosphorylcholine cytidylyltransferase (original description: processed-gene-53.13-mRNA-1 protein Name: Similar to CCT2 Choline-phosphate cytidylyltransferase 2 (Arabidopsis thaliana) AED:0.15 eAED:0.15 QI:50 1 1 1 1 1 8 392 291)'
Lipid metabolism.lipid degradation.phospholipase activities.phospholipase A2 activities.phospholipase A2 (ppLA2-II)'	xvis03_21820 0-pa	phospholipase A2 (pPLA2-II) (original description: augustus-gene-6.42-mRNA-1 protein Name: Similar to PLP1 Patatin-like protein 1 (Oryza sativa subsp. japonica) AED:0.26 eAED:0.26 QI:72 0.4 0.16 1 1 1 6 0 314)'

Table S13: List of the Bin names, id and description of the downregulated proteins at MRD

BinName	id	Description
photosynthesis .photophosphorylation.photosystem II.LHC-II complex.component LHCb1/2/3'	xvis03_2110 60-pa	component LHCb1/2/3 of LHC-II complex (original description: processed-gene-14.7-mRNA-1 protein Name:Similar to Chlorophyll a-b binding protein, chloroplastic (Spinacia oleracea) AED:0.01 eAED:0.01 QI:0 -1 0 1 -1 1 1 0 268)'
photosynthesis .photophosphorylation.photosystem II.LHC-II complex.component LHCb1/2/3'	xvis03_2197 22-pa	component LHCb1/2/3 of LHC-II complex (original description: augustus-gene-9.73-mRNA-1 protein Name:Similar to CAB36 Chlorophyll a-b binding protein 36, chloroplastic (Nicotiana tabacum) AED:0.36 eAED:0.36 QI:240 1 1 1 1 1 2 393 264)'
photosynthesis .photophosphorylation.photosystem II.LHC-II complex.component LHCb1/2/3'	xvis03_2230 77-pa	component LHCb1/2/3 of LHC-II complex (original description: processed-gene-1.89-mRNA-1 protein Name:Similar to CAB13 Chlorophyll a-b binding protein 13, chloroplastic (Solanum lycopersicum) AED:0.07 eAED:0.07 QI:182 1 1 1 1 1 4 188 263)'
photosynthesis .photophosphorylation.photosystem II.LHC-II complex.component LHCb1/2/3'	xvis03_2246 54-pa	component LHCb1/2/3 of LHC-II complex (original description: processed-gene-1.9-mRNA-1 protein Name:Similar to CAB21 Chlorophyll a-b binding protein 21, chloroplastic (Nicotiana tabacum) AED:0.11 eAED:0.11 QI:0 0 0 0.5 1 1 2 0 328)'
photosynthesis .photophosphorylation.photosystem II.LHC-II complex.component LHCb1/2/3'	xvis03_2250 66-pa	component LHCb1/2/3 of LHC-II complex (original description: processed-gene-0.82-mRNA-1 protein Name:Similar to Chlorophyll a-b binding protein,

		chloroplastic (Spinacia oleracea) AED:0.00 eAED:0.00 QI:0 -1 0 1 - 1 1 1 0 268)'
photosynthesis .photophosphorylation.photosystem II.LHC-II complex.component LHCb4'	xvis03_2127 11-pa	component LHCb4 of LHC-II complex (original description: processed-gene-16.130-mRNA-1 protein Name:Similar to LHCB4.2 Chlorophyll a-b binding protein CP29.2, chloroplastic (Arabidopsis thaliana) AED:0.05 eAED:0.05 QI:1875 1 1 1 0.5 0.33 3 204 289)'
photosynthesis .photophosphorylation.photosystem II.LHC-II complex.component LHCb5'	xvis03_2217 99-pa	component LHCb5 of LHC-II complex (original description: processed-gene-5.86-mRNA-1 protein Name:Similar to LHCB5 Chlorophyll a-b binding protein CP26, chloroplastic (Arabidopsis thaliana) AED:0.06 eAED:0.06 QI:123 0.8 0.83 1 1 1 6 161 279)'
photosynthesis .photophosphorylation.photosystem II.LHC-II complex.component LHCb6'	xvis03_2079 68-pa	component LHCb6 of LHC-II complex (original description: augustus-gene-15.42-mRNA-1 protein Name:Similar to CAP10A Chlorophyll a-b binding protein CP24 10A, chloroplastic (Solanum lycopersicum) AED:0.00 eAED:0.00 QI:218 1 1 1 1 1 2 259 254)'
photosynthesis .photophosphorylation.photosystem II.pS-II complex.oxygen-evolving center (OEC) extrinsic proteins.component OEC33/psbO'	xvis03_2083 37-pa	component PsbO/OEC33 of PS-II oxygen-evolving center (original description: augustus-gene-6.16-mRNA-1 protein Name:Similar to PSBO Oxygen-evolving enhancer protein 1, chloroplastic (Solanum lycopersicum) AED:0.08 eAED:0.08 QI:229 1 1 1 0.5 0.33 3 86 332)'

photosynthesis .photophosphorylation.photosystem II.pS-II complex.oxygen-evolving center (OEC) extrinsic proteins.component OEC33/psbO'	xvis03_2198 59-pa	component PsbO/OEC33 of PS-II oxygen-evolving center (original description: augustus-gene-3.73-mRNA-1 protein Name:Similar to PSBO Oxygen-evolving enhancer protein 1, chloroplastic (Solanum lycopersicum) AED:0.03 eAED:0.03 QI:216 1 1 1 1 2 224 332)'
photosynthesis .photophosphorylation.photosystem II.pS-II complex.oxygen-evolving center (OEC) extrinsic proteins.Viridiplantae-specific components.component OEC23/psbp'	xvis03_2099 88-pa	component PsbP of PS-II oxygen-evolving center (original description: processed-gene-2.101-mRNA-1 protein Name:Similar to PSBP Oxygen-evolving enhancer protein 2, chloroplastic (Cucumis sativus) AED:0.32 eAED:0.32 QI:142 1 1 1 1 1 4 296 262)'
photosynthesis .photophosphorylation.photosystem II.assembly and maintenance.assembly factor (MET1)'	xvis03_2215 70-pa	MET1 protein involved in PS-II assembly (original description: augustus-gene-2.10-mRNA-1 protein Name:Similar to LSF1 Phosphoglucan phosphatase LSF1, chloroplastic (Arabidopsis thaliana) AED:0.06 eAED:0.06 QI:233 0.83 0.71 1 0.5 0.42 7 831 301)'
photosynthesis .photophosphorylation.cytochrome b6/f complex.Rieske iron-sulfur component petC'	xvis03_2230 95-pa	Rieske iron-sulfur component PetC of cytochrome b6/f complex (original description: augustus-

		gene-3.96-mRNA-1 protein Name:Similar to petC Cytochrome b6-f complex iron-sulfur subunit, chloroplastic (Oryza sativa subsp. japonica) AED:0.11 eAED:0.11 QI:167 0.33 0.75 1 1 1 4 287 178)'
photosynthesis. photophosphorylation. Cytb6/f to pS-I electron carriers.plastocyanin'	xvis03_2177 29-pa	plastocyanin electron carrier (original description: processed-gene-11.5-mRNA-1 protein Name:Similar to PETE Plastocyanin minor isoform, chloroplastic (Arabidopsis thaliana) AED:0.37 eAED:0.37 QI:0 0 0 0.16 1 1 6 0 366)'
photosynthesis. photophosphorylation.photosystem I.LHC-I complex.component LHCA1'	xvis03_2251 47-pa	component LHCA1 of LHC-I complex (original description: augustus-gene-0.41-mRNA-1 protein Name:Similar to CAB6A Chlorophyll a-b binding protein 6A, chloroplastic (Solanum lycopersicum) AED:0.00 eAED:0.00 QI:106 1 1 1 1 1 3 75 204)'
photosynthesis. photophosphorylation.photosystem I.LHC-I complex.component LHCA1'	xvis03_2258 29-pa	component LHCA1 of LHC-I complex (original description: augustus-gene-0.17-mRNA-1 protein Name:Similar to LHCA1 Chlorophyll a-b binding protein 6, chloroplastic (Arabidopsis thaliana) AED:0.45 eAED:0.45 QI:0 0.44 0.4 0.5 1 1 10 334 459)'
photosynthesis. photophosphorylation.photosystem I.pS-I complex.component psaH'	xvis03_2053 19-pa	component PsaH of PS-I complex (original description: processed-gene-30.54-mRNA-1 protein Name:Similar to PSAH1 Photosystem I reaction center subunit VI-1, chloroplastic (Arabidopsis thaliana) AED:0.09 eAED:0.09 QI:15 1 1 1 1 1 3 336 145)'

photosynthesis .photophosphorylation.linear electron flow.ferredoxin-NADp reductase (FNR) activity.ferredoxin-NADp oxidoreductase'	xvis03_2076 68-pa	ferredoxin-NADP oxidoreductase (original description: processed-gene-12.85-mRNA-1 protein Name:Similar to PETH Ferredoxin--NADP reductase, leaf isozyme, chloroplastic (Pisum sativum) AED:0.14 eAED:0.14 QI:231 1 1 1 1 1 9 392 366)'
photosynthesis .photophosphorylation.chlororespiration.NADH dehydrogenase-like (NDH) complex.lumen subcomplex L.component pnsL1'	xvis03_2036 08-pa	component PnsL1 of NDH lumen subcomplex L (original description: processed-gene-32.69-mRNA-1 protein Name:Similar to PNSL1 Photosynthetic NDH subunit of lumenal location 1, chloroplastic (Arabidopsis thaliana)

		AED:0.12 eAED:0.08 QI:81 1 0.85 1 1 1 7 565 263)'
photosynthesis .calvin cycle.ribulose-1,5-bisphosphat carboxylase/oxygenase (RuBisCo) activity.RuBisCo heterodimer.small subunit'	xvis03_2231 44-pa	small subunit of ribulose-1,5-bisphosphat carboxylase/oxygenase heterodimer (original description: processed-gene-3.56-mRNA-1 protein Name:Similar to RBCS1 Ribulose bisphosphate carboxylase small chain, chloroplastic (Musa acuminata) AED:0.05 eAED:0.05 QI:145 1 1 1 1 1 3 356 174)'

photosynthesis.calvin cycle.ribulose-1,5-bisphosphat carboxylase/oxygenase (RuBisCo) activity.RuBisCo assembly.auxiliary co-chaperone (CpN20)'	xvis03_2069 91-pa	CPN20 auxiliary co-chaperone involved in RuBisCo assembly (original description: augustus- gene-10.52-mRNA-1 protein Name:Similar to CPN21 20 kDa chaperonin, chloroplastic (Arabidopsis thaliana) AED:0.07 eAED:0.07 QI:99 1 1 1 1 5 439 254)'
photosynthesis.calvin cycle.ribulose-1,5-bisphosphat carboxylase/oxygenase (RuBisCo) activity.RuBisCo assembly.auxiliary co-chaperone (CpN20)'	xvis03_2170 41-pa	CPN20 auxiliary co-chaperone involved in RuBisCo assembly (original description: augustus- gene-12.20-mRNA-1 protein Name:Similar to CPN21 20 kDa chaperonin, chloroplastic (Arabidopsis thaliana) AED:0.12 eAED:0.12 QI:32 0.33 0.71 0.71 1 1 7 174 298)'
photosynthesis.calvin cycle.ribulose-1,5-bisphosphat carboxylase/oxygenase (RuBisCo) activity.RuBisCo regulation.ATp-dependent activase (RCA)'	xvis03_2238 53-pa	ATP-dependent activase involved in RuBisCo regulation (original description: processed-gene-1.15- mRNA-1 protein Name:Similar to RCA2 Ribulose bisphosphate carboxylase/oxygenase activase 2, chloroplastic (Larrea tridentata) AED:0.12 eAED:0.12 QI:111 1 1 1 0.83 0.71 7 332 438)'
photosynthesis.calvin cycle.triosephosphate isomerase'	xvis03_2242 25-pa	triosephosphate isomerase (original description: augustus-gene-0.55- mRNA-1 protein Name:Similar to TPIP1 Triosephosphate isomerase, chloroplastic (Spinacia oleracea) AED:0.32 eAED:0.32 QI:0 0 0 0.55 0.87 1 9 0 311)'
photosynthesis.calvin cycle.transketolase'	xvis03_2077 74-pa	transketolase (original description: processed-gene-21.50-mRNA-1 protein Name:Similar to Transketolase, chloroplastic (Solanum tuberosum) AED:0.17 eAED:0.17 QI:154 0.85 0.75 1 1 1 8 0 716)'

photosynthesis.calvin cycle.transketolase'	xvis03_2190 01-pa	transketolase (original description: processed-gene-2.79-mRNA-1 protein Name:Similar to Transketolase, chloroplastic (Solanum tuberosum) AED:0.04 eAED:0.04 QI:238 1 1 1 1 7 473 742)'
photosynthesis.photorespiration.serine hydroxymethyltransferase (SHM)'	xvis03_2080 40-pa	serine hydroxymethyltransferase (original description: processed-gene-21.10-mRNA-1 protein Name:Similar to SHM4 Serine hydroxymethyltransferase 4 (Arabidopsis thaliana) AED:0.05 eAED:0.05 QI:76 1 1 1 1 4 235 515)'
protein biosynthesis.ribosome biogenesis.large ribosomal subunit (LSU).LSU proteome.component RpL3'	xvis03_2165 31-pa	component RPL3 of LSU proteome component (original description: augustus-gene-9.118-mRNA-1 protein Name:Similar to RPL3 60S ribosomal protein L3 (Oryza sativa subsp. japonica) AED:0.07 eAED:0.07 QI:0 1 0.83 1 1 0.83 6 237 407)'
protein biosynthesis.ribosome biogenesis.large ribosomal subunit (LSU).LSU proteome.component RpL3'	xvis03_2208 63-pa	component RPL3 of LSU proteome component (original description: processed-gene-0.82-mRNA-1 protein Name:Similar to RPL3 60S ribosomal protein L3 (Oryza sativa subsp. japonica) AED:0.08 eAED:0.08 QI:54 1 1 1 1 6 258 389)'

protein biosynthesis.ribosome biogenesis.large ribosomal subunit (LSU).LSU proteome.component RpL8'	xvis03_2158 83-pa	component RPL8 of LSU proteome component (original description: processed-gene-4.2-mRNA-1 protein Name:Similar to RPL8 60S ribosomal protein L8 (Solanum lycopersicum) AED:0.00 eAED:0.00 QI:71 1 1 1 1 2 167 261)'
protein biosynthesis.ribosome biogenesis.small ribosomal subunit (SSU).SSU proteome.component RpS2'	xvis03_2209 73-pa	component RPS2 of SSU proteome (original description: augustus-gene-5.51-mRNA-1 protein Name:Similar to RPS2C 40S ribosomal protein S2-3 (Arabidopsis thaliana) AED:0.29 eAED:0.29 QI:54 1 1 1 0.5 0.33 3 154 274)'
protein biosynthesis.ribosome biogenesis.small ribosomal subunit (SSU).SSU proteome.component RpS17'	xvis03_2047 05-pa	component RPS17 of SSU proteome (original description: processed-gene-11.1-mRNA-1 protein Name:Similar to RPS17 40S ribosomal protein S17 (Solanum lycopersicum) AED:0.06

		eAED:0.06 QI:0 -1 0 1 -1 1 1 0 143)'
protein biosynthesis.ribosome biogenesis.small ribosomal subunit (SSU).SSU proteome.component RpS17'	xvis03_2078 25-pa	component RPS17 of SSU proteome (original description: processed-gene-26.31-mRNA-1 protein Name:Similar to RPS17 40S ribosomal protein S17 (Solanum lycopersicum) AED:0.03 eAED:0.03 QI:0 -1 0 1 -

		1 1 1 0 146)'
protein biosynthesis.organelle machinery.plastidial ribosome.large ribosomal subunit proteome.component psRpL4'	xvis03_2136 52-pa	component psRPL4 of large ribosomal subunit proteome (original description: processed-gene-16.266-mRNA-1 protein Name:Similar to RPL4 50S ribosomal protein L4, chloroplastic (Nicotiana tabacum) AED:0.18 eAED:0.18 QI:0 -1 0 1 -1 1 1 0 272)'
protein biosynthesis.organelle machinery.plastidial ribosome.large ribosomal subunit proteome.component psRpL5'	xvis03_2201 12-pa	component psRPL5 of large ribosomal subunit proteome (original description: augustus-gene-8.33-mRNA-1 protein Name:Similar to RPL5 50S ribosomal protein L5, chloroplastic (Arabidopsis thaliana) AED:0.02 eAED:0.03 QI:29 0.5 0.33 1 1 1 3 0 284)'
protein biosynthesis.organelle machinery.plastidial ribosome.large ribosomal subunit proteome.component psRpL9'	xvis03_2020 61-pa	component psRPL9 of large ribosomal subunit proteome (original description: processed-gene-6.69-mRNA-1 protein Name:Similar to RPL9 50S ribosomal protein L9, chloroplastic (Arabidopsis thaliana) AED:0.06 eAED:0.06 QI:100 1 1 1 0.83 0.71 7 568 196)'
protein biosynthesis.organelle machinery.plastidial ribosome.small ribosomal subunit proteome.component psRpS5'	xvis03_2073 37-pa	component psRPS5 of small ribosomal subunit proteome (original description: processed-gene-10.83-mRNA-1 protein Name:Similar to rps5 30S ribosomal protein S5, chloroplastic (Arabidopsis thaliana) AED:0.00 eAED:0.00 QI:186 1 1 1 1 1 2 216 309)'

protein biosynthesis.organelle machinery.translation initiation.initiation factor (IF-3)'	xvis03_2242 54-pa	IF-3 translation initiation factor (original description: augustus-gene-0.0-mRNA-1 protein Name:Similar to infC Translation initiation factor IF-3 (Nostoc sp. (strain PCC 7120 / UTEX 2576)) AED:0.11 eAED:0.11 QI:31 1 1 0.55 0.5 10 360 276)'
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protein homeostasis.protein quality control.ER Quality Control (ERQC) machinery.calnexin/calreticulin chaperone system.CNX-CRT cycle.lectin chaperone (CNX)'	xvis03_2191 78-pa	lectin chaperone (CNX) (original description: processed-gene-7.19-mRNA-1 protein Name:Similar to CNX1 Calnexin homolog 1 (Arabidopsis thaliana) AED:0.09 eAED:0.09 QI:144 1 1 0.83 0.71 7 378 540)'
protein homeostasis.protein quality control.Hsp60 chaperone system.Hsp60-co-chaperone (Hsp20)'	xvis03_2069 91-pa	Hsp60-co-chaperone (Hsp20) (original description: augustus-gene-10.52-mRNA-1 protein Name:Similar to CPN21 20 kDa chaperonin, chloroplastic (Arabidopsis thaliana) AED:0.07 eAED:0.07 QI:99 1 1 1 1 5 439 254)'
protein homeostasis.protein quality control.Hsp60 chaperone system.Hsp60-co-chaperone (Hsp20)'	xvis03_2170 41-pa	Hsp60-co-chaperone (Hsp20) (original description: augustus-gene-12.20-mRNA-1 protein Name:Similar to CPN21 20 kDa chaperonin, chloroplastic (Arabidopsis thaliana) AED:0.12 eAED:0.12 QI:32 0.33 0.71 0.71 1 1 7 174 298)'

protein homeostasis.ubiquitin-proteasome system.26S proteasome.20S core particle.alpha-type components.component alpha type-2'	xvis03_2139 88-pa	component alpha type-2 of 26S proteasome (original description: augustus-gene-11.18-mRNA-1 protein Name:Similar to PAB1 Proteasome subunit alpha type-2 (Oryza sativa subsp. japonica) AED:0.05 eAED:0.05 QI:70 1 1 1 1 10 615 222)'
protein homeostasis.ubiquitin-proteasome system.26S proteasome.20S core particle.beta-type components.component beta type-7'	xvis03_2023 56-pa	component beta type-7 of 26S proteasome (original description: processed-gene-29.12-mRNA-1 protein Name:Similar to PBG1 Proteasome subunit beta type-4 (Arabidopsis thaliana) AED:0.13 eAED:0.13 QI:0 0.71 0.75 0.87 1 1 8 335 329)'
protein homeostasis.proteolysis.cysteine-type peptidase activities.C13-class asparaginyl endopeptidase (Legumain)'	xvis03_2112 68-pa	asparaginyl endopeptidase (Legumain) (original description: processed-gene-9.25-mRNA-1 protein Name:Similar to Vacuolar- processing enzyme (Citrus sinensis) AED:0.07 eAED:0.07 QI:3 1 1 1 1 1 9 417 590)'
Carbohydrate metabolism.sucrose metabolism.biosynthesis.cytosolic triose-phosphate isomerase'	xvis03_2117 45-pa	cytosolic triose-phosphate isomerase (original description: augustus-gene-13.21-mRNA-1 protein Name:Similar to TPIP1 Triosephosphate isomerase, cytosolic (Petunia hybrida) AED:0.34 eAED:0.34 QI:46 0.88 0.8 0.9 1 1 10 0 326)'

Carbohydrate metabolism. starch metabolism.biosynthesis.ADp-glucose pyrophosphorylase'	xvis03_2209 98-pa	ADP-glucose pyrophosphorylase (original description: augustus-gene-7.121-mRNA-1 protein Name:Similar to ADG2 Glucose-1-phosphate adenylyltransferase large subunit 1, chloroplastic (Arabidopsis thaliana) AED:0.11 eAED:0.11 QI:196 0.92 0.86 1 0.85 0.86 15 136 540)'
Carbohydrate metabolism. oxidative pentose phosphate pathway.non-oxidative phase.transketolase'	xvis03_2077 74-pa	transketolase (original description: processed-gene-21.50-mRNA-1 protein Name:Similar to Transketolase, chloroplastic (Solanum tuberosum) AED:0.17 eAED:0.17 QI:154 0.85 0.75 1 1 1 8 0 716)'
Carbohydrate metabolism. oxidative pentose phosphate pathway.non-oxidative phase.transketolase'	xvis03_2190 01-pa	transketolase (original description: processed-gene-2.79-mRNA-1 protein Name:Similar to Transketolase, chloroplastic (Solanum tuberosum) AED:0.04 eAED:0.04 QI:238 1 1 1 1 1 7 473 742)'
Carbohydrate metabolism. plastidial glycolysis.triosephosphate isomerase'	xvis03_2242 25-pa	triosephosphate isomerase (original description: augustus-gene-0.55-mRNA-1 protein Name:Similar to TPIP1 Triosephosphate isomerase, chloroplastic (Spinacia oleracea) AED:0.32 eAED:0.32 QI:0 0 0 0.55 0.87 1 9 0 311)'
Cellular respiration. glycolysis.cytosolic glycolysis.triosephosphate isomerase'	xvis03_2117 45-pa	triosephosphate isomerase (original description: augustus-gene-13.21-mRNA-1 protein Name:Similar to TPIP1 Triosephosphate isomerase, cytosolic (Petunia hybrida) AED:0.34 eAED:0.34 QI:46 0.88 0.8 0.9 1 1 10 0 326)'

Cellular respiration.glycolysis.methylglyoxal degradation.lactoyl-glutathione lyase (GLX1)'	xvis03_2105 97-pa	lactoyl-glutathione lyase (GLX1) (original description: augustus-gene-8.18-mRNA-1 protein Name:Similar to At1g67280 Probable lactoylglutathione lyase, chloroplast (Arabidopsis thaliana) AED:0.06 eAED:0.06 QI:224 1 1 1 1 9 419 372)'
Cellular respiration.tricarboxylic acid cycle.mitochondrial NAD-dependent malic enzyme'	xvis03_2015 88-pa	mitochondrial NAD-dependent malic enzyme (original description: augustus-gene-28.7-mRNA-1 protein Name:Similar to NAD- ME1 NAD-dependent malic enzyme 1, mitochondrial (Arabidopsis thaliana) AED:0.22 eAED:0.22

		QI:0 0.77 0.78 0.86 0.77 0.82 23 29 0 790)'
Cellular respiration.oxidative phosphorylation.cytochrome c reductase complex.component cytochrome c1'	xvis03_2062 81-pa	cytochrome c1 component of cytochrome c reductase complex (original description: augustus-gene-15.74-mRNA-1 protein Name:Similar to CYCL Cytochrome c1-1, heme protein, mitochondrial (Solanum tuberosum) AED:0.28 eAED:0.28 QI:33 0.85 0.87 1 1 1 8 457 361)'

Cellular respiration. oxidative phosphorylation.ATP synthase complex.peripheral MF1 subcomplex.subunit delta_'	xvis03_2187 22-pa	subunit delta_ of ATP synthase peripheral MF1 subcomplex (original description: augustus-gene-3.37-mRNA-1 protein Name:Similar to ATP synthase subunit delta', mitochondrial (Ipomoea batatas) AED:0.20 eAED:0.20 QI:67 0 0.25 0.5 0.33 0.75 4 0 208)'
Redox homeostasis. enzymatic reactive oxygen species scavengers.catalase'	xvis03_2207 33-pa	catalase (original description: processed-gene-1.13-mRNA-1 protein Name:Similar to CAT1 Catalase-1 (Triticum aestivum) AED:0.19 eAED:0.19 QI:0 0 0 0.66 1 1 9 0 623)'
Redox homeostasis. hydrogen peroxide removal.ascorbate-glutathione cycle.ascorbate peroxidase (ApX)'	xvis03_2018 83-pa	ascorbate peroxidase (APX) (original description: augustus-gene-50.73-mRNA-1 protein Name:Similar to APX1 L-ascorbate peroxidase, cytosolic (Pisum sativum) AED:0.15 eAED:0.15 QI:0 0.85 0.75 1 1 0.87 8 414 307)'
Redox homeostasis. hydrogen peroxide removal.ascorbate-glutathione cycle.ascorbate peroxidase (ApX)'	xvis03_2142 14-pa	ascorbate peroxidase (APX) (original description: processed-gene-11.33-mRNA-1 protein Name:Similar to APX1 L-ascorbate peroxidase, cytosolic (Pisum sativum) AED:0.17 eAED:0.17 QI:131 1 1 1 1 1 7 558 249)'
Redox homeostasis. hydrogen peroxide removal.ascorbate-glutathione cycle.ascorbate peroxidase (ApX)'	xvis03_2221 05-pa	ascorbate peroxidase (APX) (original description: augustus-gene-5.53-mRNA-1 protein Name:Similar to APXT L-ascorbate peroxidase T, chloroplastic (Arabidopsis thaliana) AED:0.32 eAED:0.32 QI:0 0.5 0.45 0.72 0.9 0.81 11 0 364)'

Redox homeostasis. hydrogen peroxide removal.ascorbate-glutathione cycle.ascorbate peroxidase (ApX)'	xvis03_2234 38-pa	ascorbate peroxidase (APX) (original description: augustus-gene-1.2-mRNA-1 protein Name:Similar to APX4 Probable L-ascorbate peroxidase 4 (Oryza sativa subsp. japonica) AED:0.10 eAED:0.10 QI:188 1 1 1 1 9 226 284)'
Amino acid metabolism. biosynthesis.aspartate family.aspartate-derived amino acids.methionine.salvage pathway.bifunctional methylthioribulose-1-phosphate dehydratase and enolase-phosphatase'	xvis03_2235 88-pa	bifunctional methylthioribulose-1-phosphate dehydratase and enolase-phosphatase (original description: processed-gene-1.56-mRNA-1 protein Name:Similar to VIT_19s0014g02480 Probable bifunctional methylthioribulose-1-phosphate dehydratase/enolase-phosphatase E1 1 (Vitis vinifera) AED:0.24 eAED:0.24 QI:0 0.9 0.90 0.90 1 1 11 237 411)'
Amino acid metabolism. biosynthesis.serine family.glycine.serine hydroxymethyltransferase	xvis03_2080 40-pa	serine hydroxymethyltransferase (original description: processed-gene-21.10-mRNA-1 protein Name:Similar to SHM4 Serine hydroxymethyltransferase 4 (Arabidopsis thaliana) AED:0.05 eAED:0.05 QI:76 1 1 1 1 4 235 515)'
Nucleotide metabolism. purines.phosphotransfers.adenylate kinase'	xvis03_2073 11-pa	adenylate kinase (original description: processed-gene-7.62-mRNA-1 protein Name:Similar to ADK-B Adenylate kinase 4 (Oryza sativa subsp. japonica) AED:0.05 eAED:0.05 QI:122 1 1 1 1 6 379 246)'

Nucleotide metabolism.purines.phosphotransfers.adenylate kinase'	xvis03_2136 05-pa	adenylate kinase (original description: processed-gene-14.84-mRNA-1 protein Name:Similar to Os08g0288200 Probable adenylate kinase 5, chloroplastic (Oryza sativa subsp. japonica) AED:0.22 eAED:0.22 QI:25 1 0.94 1 1 1 17 0 611)'
RNA processing.pre-mRNA splicing. U2-type-intron-specific major spliceosome. U2 small nuclear ribonucleoprotein particle (snRNp).protein factor (U2A)'	xvis03_2056 05-pa	protein factor U2A of U2 small nuclear ribonucleoprotein particle (snRNP) (original description: processed-gene-17.119-mRNA-1 protein Name:Similar to At1g09760 U2 small nuclear ribonucleoprotein A' (Arabidopsis thaliana) AED:0.23 eAED:0.27 QI:0 0.83 0.71 1 1 1 7 448 347)'
RNA processing.organelle machinery.ribonuclease activities.endoribonuclease (CSp41)'	xvis03_2132 17-pa	endoribonuclease (CSP41) (original description: augustus-gene-16.1-mRNA-1 protein Name:Similar to CSP41A Chloroplast stem-loop binding protein of 41 kDa a, chloroplastic (Arabidopsis thaliana) AED:0.01 eAED:0.01

protein modification.protein folding.protein folding catalyst (FKBP)'	xvis03_2086 52-pa	protein folding catalyst (FKBP) (original description: processed-gene-19.48-mRNA-1 protein Name:Similar to FKBP62 Peptidyl-prolyl cis-trans isomerase FKBP62 (Arabidopsis thaliana) AED:0.12 eAED:0.12 QI:105 0.91 0.92 1 1 1 13 323 570)'
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protein modification. protein folding.protein folding catalyst (FKBP)'	xvis03_2248 49-pa	protein folding catalyst (FKBP) (original description: processed-gene-1.76-mRNA-1 protein Name:Similar to FKBP19 Peptidyl-prolyl cis-trans isomerase FKBP19, chloroplastic (Arabidopsis thaliana) AED:0.46 eAED:0.49 QI:0 0.72 0.83 0.91 0.90 0.83 12 203 320)'
Cell wall organisation. pectin.rhamnogalacturonan I.modification and degradation.beta-galactosidase (BGAL)'	xvis03_2089 87-pa	beta-galactosidase (BGAL) (original description: augustus-gene-4.4-mRNA-1 protein Name:Similar to BGAL9 Beta-galactosidase 9 (Arabidopsis thaliana) AED:0.06 eAED:0.06 QI:63 1 1 1 0.94 0.94 19 309 904)'
Cell wall organisation. pectin.rhamnogalacturonan I.modification and degradation.beta-galactosidase (BGAL)'	xvis03_2214 34-pa	beta-galactosidase (BGAL) (original description: processed-gene-2.106-mRNA-1 protein Name:Similar to Beta-galactosidase (Asparagus officinalis) AED:0.13 eAED:0.13 QI:277 1 1 1 1 1 19 418 832)'

Table S14: List of the Bin names, id and

description of the upregulated proteins at LRD

BinName	id	Description
protein biosynthesis. ribosome biogenesis.large ribosomal subunit (LSU).LSU proteome.component RpL23'	xvis03_202929-pa	component RPL23 of LSU proteome component (original description: augustus-gene-26.5-mRNA-1 protein Name:Similar to RPL23A 60S ribosomal protein L23 (Arabidopsis thaliana) AED:0.39 eAED:0.40 QI:0 0 0 0.5 1 1 6 0 279)'
protein biosynthesis. ribosome biogenesis.small ribosomal subunit (SSU).SSU proteome.component RpS12'	xvis03_210337-pa	component RPS12 of SSU proteome (original description: augustus-gene-8.1-mRNA-1 protein Name:Similar to RPS12 40S ribosomal protein S12 (Hordeum vulgare) AED:0.38 eAED:0.38 QI:0 1 0.75 1 1 1 4 393 161)'

protein biosynthesis.ribosome biogenesis.small ribosomal subunit (SSU).SSU proteome.component RpS12'	xvis03_221354-pa	component RPS12 of SSU proteome (original description: augustus-gene-2.78-mRNA-1 protein Name:Similar to RPS12 40S ribosomal protein S12 (Hordeum vulgare) AED:0.26 eAED:0.26 QI:0 1 0.75 1 1 4 274 184)'
protein biosynthesis.ribosome biogenesis.small ribosomal subunit (SSU).SSU proteome.component RpS27'	xvis03_205594-pa	component RPS27 of SSU proteome (original description: augustus-gene-17.68-mRNA-1 protein Name:Similar to RPS27B 40S ribosomal protein S27-2 (Arabidopsis thaliana) AED:0.09 eAED:0.09 QI:0 1 0.75 1 1 4 342 163)'
protein biosynthesis.ribosome biogenesis.small ribosomal subunit (SSU).SSU proteome.component RpS27'	xvis03_209876-pa	component RPS27 of SSU proteome (original description: augustus-gene-14.5-mRNA-1 protein Name:Similar to RPS27B 40S ribosomal protein S27-2 (Arabidopsis thaliana) AED:0.17 eAED:0.17 QI:86 1 1 0.66 0.75 4 47 86)'
protein biosynthesis.mRNA quality control.NMD Nonsense-Mediated Decay.eRF1-eRF3 aberrant mRNA detection complex.component eRF1'	xvis03_209643-pa	eRF1 peptide release factor (original description: processed-gene-16.29-mRNA-1 protein Name:Similar to ERF1-3 Eukaryotic peptide chain release factor subunit 1-3 (Arabidopsis thaliana) AED:0.00 eAED:0.00 QI:0 -1 0 1 -1 1 0 437)'
protein biosynthesis.translation initiation.pre-Initiation Complex (pIC) module.eIF3 mRNA-to-pIC binding complex.component eIF3g'	xvis03_223860-pa	component eIF3g of eIF3 mRNA-to-PIC binding complex (original description: processed-gene-2.57-mRNA-1 protein Name:Similar to v1g171563 Eukaryotic translation initiation factor 3 subunit G (Nematostella vectensis) AED:0.02

		eAED:0.02 QI:0 1 0.5 1 1 2 3401 289)'
protein biosynthesis.translation initiation.mRNA loading.mRNA poly-A-tail binding factor (pABp)'	xvis03_217585-pa	mRNA poly-A-tail binding factor (PABP) (original description: augustus-gene-6.44-mRNA-1 protein Name:Similar to PAB8 Polyadenylate-binding protein 8 (Arabidopsis thaliana) AED:0.09 eAED:0.09 QI:312 0.75 0.66 1 1 1 9 460 634)'
protein biosynthesis.translation elongation.eEF1 aminoacyl-tRNA binding factor activity.eEF1B eEF1A-GDp-recycling complex.component eEF1B-beta/-delta'	xvis03_202784-pa	component eEF1B-beta/-delta of eEF1B eEF1A-GDP-recycling complex (original description: processed-gene-9.6-mRNA-1 protein Name:Similar to At5g12110 Elongation factor 1-beta 1 (Arabidopsis thaliana) AED:0.07 eAED:0.07 QI:28 1 1 1 1 1 6 211 226)'
protein biosynthesis.translation elongation.eEF5 poly-p/G elongation factor activity.poly-p/G elongation factor (eEF5/eIF5A)'	xvis03_208182-pa	poly-P/G elongation factor (eEF5/eIF5A) (original description: processed-gene-16.15-mRNA-1 protein Name:Similar to EIF-5A2 Eukaryotic translation initiation factor 5A-2 (Nicotiana glauca) AED:0.11 eAED:0.11 QI:80 1 1 1 0.8 0.66 6 225 159)'
protein biosynthesis.translation elongation.eEF5 poly-p/G elongation factor activity.poly-p/G elongation factor (eEF5/eIF5A)'	xvis03_214372-pa	poly-P/G elongation factor (eEF5/eIF5A) (original description: processed-gene-6.62-mRNA-1 protein Name:Similar to Eukaryotic translation initiation factor 5A (Manihot esculenta) AED:0.20 eAED:0.20 QI:188 1 1 1 0.8 0.66 6 353 159)'

protein biosynthesis .translation elongation.eEF5 poly-p/G elongation factor activity.poly-p/G elongation factor (eEF5/eIF5A)'	xvis03_221720-pa	poly-P/G elongation factor (eEF5/eIF5A) (original description: augustus-gene-5.43-mRNA-1 protein Name:Similar to EIF-5A2 Eukaryotic translation initiation factor 5A-2 (Nicotiana plumbaginifolia) AED:0.05 eAED:0.05 QI:177 1 1 0.8 0.66 6 330 160)'
protein biosynthesis .organelle machinery.plastidial ribosome.large ribosomal subunit proteome.component psRpL18'	xvis03_224660-pa	component psRPL18 of large ribosomal subunit proteome (original description: processed-gene-1.62-mRNA-1 protein Name:Similar to FEN1 Flap endonuclease 1 (Zea mays) AED:0.25 eAED:0.26 QI:20 0.7 0.71 0.95 1 1 21 362 621)'
protein biosynthesis .organelle machinery.translation elongation.elongation factor (EF-Tu)'	xvis03_212520-pa	EF-Tu translation elongation factor (original description: augustus-gene-6.14-mRNA-1 protein Name:Similar to TUFb1 Elongation factor Tu, chloroplastic (Glycine max) AED:0.04 eAED:0.16 QI:0 0 0.5 1 1 1 2 351 455)'
Coenzyme metabolism .iron-sulfur cluster assembly machinery.plastidial SUF system.assembly phase.SUF-SE sulfur transfer complex.cysteine desulfurase component NFS2'	xvis03_220549-pa	cysteine desulfurase component NFS2 of plastidial SUF system assembly phase (original description: processed-gene-6.81-mRNA-1 protein Name:Similar to NFS2 Cysteine desulfurase 1, chloroplastic (Arabidopsis thaliana) AED:0.13 eAED:0.23 QI:55 0.77 0.8 1 1 1 10 0 498)'
Coenzyme metabolism .iron-sulfur cluster assembly machinery.mitochondrial ISC system.transfer phase.assembly factor (IBA57)'	xvis03_224887-pa	assembly factor BA57 of mitochondrial ISC system transfer phase (original description: augustus-gene-0.36-mRNA-1 protein Name:Similar to At4g12130 Putative transferase At4g12130,

		mitochondrial (Arabidopsis thaliana) AED:0.05 eAED:0.05 QI:50 1 1 1 1 5 427 411'
Coenzyme metabolism.tetrapyrrol biosynthesis.5-aminolevulinic acid formation.glutamate-1-semialdehyde-2,1-aminomutase'	xvis03_216135-pa	glutamate-1-semialdehyde-2,1-aminomutase (original description: augustus-gene-2.5-mRNA-1 protein Name:Similar to GSA Glutamate-1-semialdehyde 2,1-aminomutase, chloroplastic (Oryza sativa subsp. japonica) AED:0.00 eAED:0.00 QI:90 1 1 1 1 3 296 478)'
Coenzyme metabolism.tetrapyrrol biosynthesis.chlorophyll metabolism.magnesium-chelatase complex.component CHL-I'	xvis03_222911-pa	component CHL-I of magnesium-chelatase complex (original description: processed-gene-1.35-mRNA-1 protein Name:Similar to CHLI Magnesium-chelatase subunit ChII, chloroplastic (Oryza sativa subsp. japonica) AED:0.00 eAED:0.00 QI:218 1 1 1 1 3 269 418)'
Coenzyme metabolism.tetrapyrrol biosynthesis.chlorophyll metabolism.protochlorophyllide oxidoreductase (pOR) activities.light-dependent pOR'	xvis03_212894-pa	light-dependent protochlorophyllide oxidoreductase (original description: augustus-gene-2.1-mRNA-1 protein Name:Similar to PORB Protochlorophyllide reductase B, chloroplastic (Hordeum vulgare) AED:0.09 eAED:0.09 QI:162 1 1 1 1 5 457 393)'
photosynthesis .photophosphorylation.chlororespiration. NADH dehydrogenase-like (NDH) complex.assembly and stabilization.Cpn60 chaperonin heterodimer.subunit beta'	xvis03_205691-pa	subunit beta of Cpn60 chaperonin complex (original description: processed-gene-31.124-mRNA-1 protein Name:Similar to RuBisCO large subunit-binding protein subunit beta, chloroplastic (Pisum sativum) AED:0.20 eAED:0.20 QI:97 0.8 0.81 0.87 0.93 0.87 16 0 678)'

photosynthesis.calvin cycle.ribulose-1,5-bisphosphat carboxylase/oxygenase (RuBisCo) activity.RuBisCo heterodimer.small subunit'	xvis03_223144-pa	small subunit of ribulose-1,5-bisphosphat carboxylase/oxygenase heterodimer (original description: processed-gene-3.56-mRNA-1 protein Name:Similar to RBCS1 Ribulose bisphosphate carboxylase small chain, chloroplastic (Musa acuminata) AED:0.05 eAED:0.05 QI:145 1 1 1 1 3 356 174)'
photosynthesis.calvin cycle.ribulose-1,5-bisphosphat carboxylase/oxygenase (RuBisCo) activity.RuBisCo assembly.CpN60 assembly chaperone complex.component CpN60b'	xvis03_205691-pa	component CPN60b of CPN60 assembly chaperone complex (original description: processed-gene-31.124-mRNA-1 protein Name:Similar to RuBisCO large subunit-binding protein subunit beta, chloroplastic (Pisum sativum) AED:0.20 eAED:0.20 QI:97 0.8 0.81 0.87 0.93 0.87 16 0 678)'
photosynthesis.calvin cycle.phosphoglycerate kinase'	xvis03_201416-pa	phosphoglycerate kinase (original description: processed-gene-12.20-mRNA-1 protein Name:Similar to Phosphoglycerate kinase, chloroplastic (Nicotiana tabacum) AED:0.04 eAED:0.04 QI:190 1 1 1 1 1 6 289 477)'
photosynthesis.photorespiration.glycine decarboxylase complex.lipoamide-containing component H-protein'	xvis03_220076-pa	lipoamide-containing component H-protein of glycine cleavage system (original description: augustus-gene-4.88-mRNA-1 protein Name:Similar to GDCSH Glycine cleavage system H protein, mitochondrial (Oryza sativa subsp. japonica) AED:0.04 eAED:0.04 QI:127 1 1 1 1 1 4 484 165)'
Cellular respiration.glycolysis.cytosolic glycolysis. Phosphoglycerate kinase'	xvis03_201416-pa	phosphoglycerate kinase (original description: processed-gene-12.20-mRNA-1 protein Name:Similar to Phosphoglycerate kinase, chloroplastic (Nicotiana tabacum)

		AED:0.04 eAED:0.04 QI:190 1 1 1 1 6 289 477)' 0.4267875
Cellular respiration.glycolysis.methylglyoxal degradation. Hydroxy-acyl-glutathione hydrolase (GLX2)'	xvis03_211424-pa	hydroxy-acyl-glutathione hydrolase (GLX2) (original description: augustus-gene-2.30-mRNA-1 protein Name:Similar to GLX2-2 Hydroxyacylglutathione hydrolase cytoplasmic (Arabidopsis thaliana) AED:0.23 eAED:0.23 QI:367 1 1 1 1 0.83 6 257 190)' 1.663941
protein modification.phosphorylation CAMK protein kinase superfamily.SNF1-related protein kinase (SnRK2)'	xvis03_216515-pa	SNF1-related protein kinase (SnRK2) (original description: augustus-gene-8.70-mRNA-1 protein Name:Similar to SAPK7 Serine/threonine-protein kinase SAPK7 (Oryza sativa subsp. japonica) AED:0.12 eAED:0.12 QI:115 0.83 1 1 1 1 7 226 305)' 1.8659521
protein modification.S-glutathionylation.glutaredoxin'	xvis03_218158-pa	glutaredoxin (original description: augustus-gene-3.24-mRNA-1 protein Name:Similar to Glutaredoxin (Ricinus communis) AED:0.01 eAED:0.01 QI:220 1 1 1 1 4 501 106)' 1.1671811
protein modification.protein folding.protein folding catalyst (Cyclophilin)'	xvis03_206458-pa	protein folding catalyst (original description: processed-gene-30.78-mRNA-1 protein Name:Similar to PCKR1 Peptidyl-prolyl cis-trans isomerase (Catharanthus roseus) AED:0.01 eAED:0.01 QI:0 -1 0 1 -1 1 0 173)' 0.88642055
protein modification.protein folding.protein folding catalyst (Cyclophilin)'	xvis03_223454-pa	protein folding catalyst (original description: processed-gene-3.78-mRNA-1 protein Name:Similar to PCKR1 Peptidyl-prolyl cis-trans

		isomerase (Catharanthus roseus) AED:0.02 eAED:0.02 QI:0 -1 0 1 -1 1 0 173)' 1.266422
protein translocation.chloroplast.outer envelope insertion system.chaperone (AKR2)	xvis03_217196-pa	chaperone (AKR2) (original description: augustus-gene-1.26-mRNA-1 protein Name:Similar to AKR2 Ankyrin repeat domain-containing protein 2 (Arabidopsis thaliana) AED:0.11 eAED:0.11 QI:0 0 0 1 1 1 6 0 276)' 1.775295
protein translocation.nucleus.nucleocytoplasmic transport.importin alpha adaptor proteins'	xvis03_215434-pa	importin alpha adaptor proteins (original description: augustus-gene-6.51-mRNA-1 protein Name:Similar to Os01g0253300 Importin subunit alpha-1a (Oryza sativa subsp. japonica) AED:0.21 eAED:0.21 QI:191 0.81 0.75 1 1 1 12 0 614)' 2.079471
protein translocation.nucleus.nucleocytoplasmic transport.GTPase activation accessory protein (RanBp1)	xvis03_204022-pa	GTPase activation accessory protein (RanBP1) (original description: processed-gene-29.69-mRNA-1 protein Name:Similar to RANBP1C Ran-binding protein 1 homolog c (Arabidopsis thaliana) AED:0.01 eAED:0.01 QI:85 1 1 1 1 1 4 338 224)' 1.8266815
RNA processing.RNA chaperone activities.RNA chaperone (CSp)'	xvis03_206453-pa	RNA chaperone (CSP) (original description: processed-gene-29.128-mRNA-1 protein Name:Similar to CSP4 Cold shock domain-containing protein 4 (Arabidopsis thaliana) AED:0.32 eAED:0.32 QI:0 -1 0 1 -1 1 1 0 231)' 1.2821975
RNA processing.RNA chaperone activities.RNA chaperone (CSp)'	xvis03_223451-pa	RNA chaperone (CSP) (original description: processed-gene-3.71-mRNA-1 protein Name:Similar to

		CSP1 Cold shock protein 1 (Arabidopsis thaliana) AED:0.30 eAED:0.30 QI:0 -1 0 1 -1 1 1 0 215)' 2.1634965
RNA processing. RNA chaperone activities.RNA chaperone (RZ1 GR-RBP)'	xvis03_215153-pa	RNA chaperone (RZ1 GR-RBP) (original description: augustus-gene-12.40-mRNA-1 protein Name:Similar to RZ1B Glycine-rich RNA-binding protein RZ1B (Arabidopsis thaliana) AED:0.25 eAED:0.25 QI:0 1 1 1 0.5 0.33 3 1599 326)' 1.83855
RNA processing. organelle machinery.RNA editing.RNA editing factor (MORF-type)'	xvis03_221754-pa	RNA editing factor (MORF) (original description: augustus-gene-1.62-mRNA-1 protein Name:Similar to MORF1 Multiple organellar RNA editing factor 1, mitochondrial (Arabidopsis thaliana) AED:0.23 eAED:0.23 QI:47 1 1 1 0.75 0.6 5 384 406)' 1.7289507
External stimuli response. Temperature. Heat response.organelle chaperone (Clp-p Clp-m)'	xvis03_207210-pa	organellar chaperone (Clp-p Clp-m) (original description: augustus-gene-28.48-mRNA-1 protein Name:Similar to CLPB3 Chaperone protein ClpB3, mitochondrial (Oryza sativa subsp. japonica) AED:0.12 eAED:0.12 QI:139 1 1 1 1 1 10 182 968)' 1.7187872
External stimuli response. temperature.cold response.mRNA chaperone (CSD)'	xvis03_206453-pa	mRNA chaperone (CSD) (original description: processed-gene-29.128-mRNA-1 protein Name:Similar to CSP4 Cold shock domain-containing protein 4 (Arabidopsis thaliana) AED:0.32 eAED:0.32 QI:0 -1 0 1 -1 1 1 0 231)' 1.2821975

External stimuli response.temperature.cold response.mRNA chaperone (CSD)'	xvis03_223451-pa	mRNA chaperone (CSD) (original description: processed-gene-3.71-mRNA-1 protein Name:Similar to CSP1 Cold shock protein 1 (Arabidopsis thaliana) AED:0.30 eAED:0.30 QI:0 -1 0 1 -1 1 0 215)' 2.1634965
Lipid metabolism.glycerolipid biosynthesis.phosphatidylcholine.CTp:phosphorylcholine cytidylyltransferase'	xvis03_202655-pa	CTP:phosphorylcholine cytidylyltransferase (original description: processed-gene-53.13-mRNA-1 protein Name:Similar to CCT2 Choline-phosphate cytidylyltransferase 2 (Arabidopsis thaliana) AED:0.15 eAED:0.15 QI:50 1 1 1 1 8 392 291)' 2.4340105
Lipid metabolism.lipid degradation.phospholipase activities.phospholipase A2 activities.phospholipase A2 (ppLA2-II)'	xvis03_218200-pa	phospholipase A2 (pPLA2-II) (original description: augustus-gene-6.42-mRNA-1 protein Name:Similar to PLP1 Patatin-like protein 1 (Oryza sativa subsp. japonica) AED:0.26 eAED:0.26 QI:72 0.4 0.16 1 1 6 0 314)' 1.306471
Lipid metabolism.lipid degradation.fatty acid degradation.core beta-oxidation.3-ketoacyl-CoA thiolase (KAT)'	xvis03_216330-pa	3-ketoacyl-CoA thiolase (KAT) (original description: processed-gene-6.102-mRNA-1 protein Name:Similar to PED1 3-ketoacyl-CoA thiolase 2, peroxisomal (Arabidopsis thaliana) AED:0.14 eAED:0.14 QI:702 0.85 0.93 0.93 1 1 15 1904 479)' 2.3141983
Lipid metabolism.lipid bodies-associated activities.caleosin lipid body surface protein (CLO/pXG)'	xvis03_2212 36-pa	caleosin (original description: augustus-gene-4.54-mRNA-1 protein Name:Similar to PXG Peroxygenase (Oryza sativa subsp. japonica) AED:0.38 eAED:0.38

		QI:85 0.66 0.85 0.85 1 1 7 299 316)' 1.63025
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Table S15: List of the Bin names, id and description of the downregulated proteins at LRD

BinName	id	Description
photosynthesis .photophosphorylation.photosystem II.LHC-II complex.component LHCb1/2/3'	xvis03_219722-pa	component LHCb1/2/3 of LHC-II complex (original description: augustus-gene-9.73-mRNA-1 protein Name:Similar to CAB36 Chlorophyll a-b binding protein 36, chloroplastic (Nicotiana tabacum) AED:0.36 eAED:0.36 QI:240 1 1 1 1 2 393 264)'
photosynthesis .photophosphorylation.photosystem II.LHC-II complex.component LHCb1/2/3'	xvis03_223077-pa	component LHCb1/2/3 of LHC-II complex (original description: processed-gene-1.89-mRNA-1 protein Name:Similar to CAB13 Chlorophyll a-b binding protein 13, chloroplastic (Solanum lycopersicum) AED:0.07 eAED:0.07 QI:182 1 1 1 1 4 188 263)'
photosynthesis .photophosphorylation.photosystem II.LHC-II complex.component LHCb1/2/3'	xvis03_224654-pa	component LHCb1/2/3 of LHC-II complex (original description: processed-gene-1.9-mRNA-1 protein Name:Similar to CAB21 Chlorophyll a-b binding protein 21, chloroplastic (Nicotiana tabacum) AED:0.11 eAED:0.11 QI:0 0 0 0.5 1 1 2 0 328)'
photosynthesis .photophosphorylation.photosystem II.LHC-II complex.component LHCb4'	xvis03_212711-pa	component LHCb4 of LHC-II complex (original description: processed-gene-16.130-mRNA-1 protein Name:Similar to LHCB4.2 Chlorophyll a-b binding protein CP29.2, chloroplastic (Arabidopsis thaliana) AED:0.05 eAED:0.05 QI:1875 1 1 1 0.5 0.33 3 204 289)'
photosynthesis .photophosphorylation.photosystem II.LHC-II complex.component LHCb5'	xvis03_202336-pa	component LHCb5 of LHC-II complex (original description: augustus-gene-27.98-mRNA-1 protein Name:Similar to LHCB5 Chlorophyll a-b binding protein CP26, chloroplastic (Arabidopsis thaliana)

		AED:0.08 eAED:0.08 QI:26 1 1 1 1 6 330 363 '
photosynthesis .photophosphorylation.photosystem II.LHC-II complex.component LHCb6'	xvis03_217301-pa	component LHCb6 of LHC-II complex (original description: augustus-gene-11.85-mRNA-1 protein Name:Similar to CAP10A Chlorophyll a-b binding protein CP24 10A, chloroplastic (Solanum lycopersicum) AED:0.00 eAED:0.00 QI:77 1 1 1 1 2 315 254 '
photosynthesis .photophosphorylation.photosystem II.pS-II complex.oxygen-evolving center (OEC) extrinsic proteins.component OEC33/psbO'	xvis03_219859-pa	component PsbO/OEC33 of PS-II oxygen-evolving center (original description: augustus-gene-3.73-mRNA-1 protein Name:Similar to PSBO Oxygen-evolving enhancer protein 1, chloroplastic (Solanum lycopersicum) AED:0.03 eAED:0.03 QI:216 1 1 1 1 2 224 332 '
photosynthesis .photophosphorylation.photosystem I.LHC-I complex.component LHCa1'	xvis03_225147-pa	component LHCa1 of LHC-I complex (original description: augustus-gene-0.41-mRNA-1 protein Name:Similar to CAB6A Chlorophyll a-b binding protein 6A, chloroplastic (Solanum lycopersicum) AED:0.00 eAED:0.00 QI:106 1 1 1 1 3 75 204 '
photosynthesis .photophosphorylation.photosystem I.LHC-I complex.component LHCa1'	xvis03_225829-pa	component LHCa1 of LHC-I complex (original description: augustus-gene-0.17-mRNA-1 protein Name:Similar to LHCA1 Chlorophyll a-b binding protein 6, chloroplastic (Arabidopsis thaliana) AED:0.45 eAED:0.45 QI:0 0.44 0.4 0.5 1 1 10 334 459 '
photosynthesis .photophosphorylation.photosystem I.LHC-I complex.component LHCa2'	xvis03_205558-pa	component LHCa2 of LHC-I complex (original description: augustus-gene-14.7-mRNA-1 protein Name:Similar to CAB7 Chlorophyll a-b binding protein 7, chloroplastic (Solanum lycopersicum) AED:0.16 eAED:0.16 QI:0 0.25 0.4 1 0.75 0.8 5 892 278 '

photosynthesis .photophosphorylation.photosystem I.pS-I complex.component psaD'	xvis03_207379-pa	component PsaD of PS-I complex (original description: processed-gene-13.65-mRNA-1 protein Name:Similar to psaD Photosystem I reaction center subunit II, chloroplastic (Cucumis sativus) AED:0.32 eAED:0.32 QI:0 -1 0 1 -1 1 1 0 274)'
photosynthesis .photophosphorylation.photosystem I.pS-I complex.component psaF'	xvis03_216014-pa	component PsaF of PS-I complex (original description: processed-gene-5.37-mRNA-1 protein Name:Similar to PSAF Photosystem I reaction center subunit III, chloroplastic (Arabidopsis thaliana) AED:0.24 eAED:0.24 QI:0 -1 0 1 -1 1 1 0 232)'
photosynthesis .photophosphorylation.photosystem I.pS-I complex.component psaH'	xvis03_205319-pa	component PsaH of PS-I complex (original description: processed-gene-30.54-mRNA-1 protein Name:Similar to PSAH1 Photosystem I reaction center subunit VI-1, chloroplastic (Arabidopsis thaliana) AED:0.09 eAED:0.09 QI:15 1 1 1 1 3 336 145)'
photosynthesis .photophosphorylation.photosystem I.pS-I complex.component psaL'	xvis03_200779-pa	component PsaL of PS-I complex (original description: processed-gene-89.11-mRNA-1 protein Name:Similar to PSAL Photosystem I reaction center subunit XI, chloroplastic (Spinacia oleracea) AED:0.06 eAED:0.06 QI:217 1 1 1 1 2 190 220)'
photosynthesis .calvin cycle.transketolase'	xvis03_207774-pa	transketolase (original description: processed-gene-21.50-mRNA-1 protein Name:Similar to Transketolase, chloroplastic (Solanum tuberosum) AED:0.17 eAED:0.17 QI:154 0.85 0.75 1 1 1 8 0 716)'
photosynthesis .calvin cycle.transketolase'	xvis03_219001-pa	transketolase (original description: processed-gene-2.79-mRNA-1 protein Name:Similar to Transketolase, chloroplastic (Solanum tuberosum) AED:0.04 eAED:0.04 QI:238 1 1 1 1 1 7 473 742)'
Carbohydrate metabolism .starch metabolism.biosynthesis.ADp-glucose pyrophosphorylase'	xvis03_220998-pa	ADP-glucose pyrophosphorylase (original description: augustus-gene-7.121-mRNA-1 protein Name:Similar to ADG2 Glucose-1-phosphate adenylyltransferase large subunit

		1, chloroplastic (<i>Arabidopsis thaliana</i>) AED:0.11 eAED:0.11 QI:196 0.92 0.86 1 0.85 0.86 15 136 540)'
Carbohydrate metabolism .starch metabolism.biosynthesis.starch synthase activities.granule-bound starch (amylose) synthase	xvis03_225238-pa	granule-bound starch (amylose) synthase (original description: augustus-gene-0.18-mRNA-1 protein Name:Similar to WAXY Granule-bound starch synthase 1, chloroplastic/amyloplastic (<i>Antirrhinum majus</i>) AED:0.11 eAED:0.11 QI:73 1 1 1 0.92 0.85 14 142 611)'
Carbohydrate metabolism .oxidative pentose phosphate pathway.non-oxidative phase.transketolase'	xvis03_207774-pa	transketolase (original description: processed-gene-21.50-mRNA-1 protein Name:Similar to Transketolase, chloroplastic (<i>Solanum tuberosum</i>) AED:0.17 eAED:0.17 QI:154 0.85 0.75 1 1 1 8 0 716)'
Carbohydrate metabolism .oxidative pentose phosphate pathway.non-oxidative phase.transketolase'	xvis03_219001-pa	transketolase (original description: processed-gene-2.79-mRNA-1 protein Name:Similar to Transketolase, chloroplastic (<i>Solanum tuberosum</i>) AED:0.04 eAED:0.04 QI:238 1 1 1 1 1 7 473 742)'
Carbohydrate metabolism .gluconeogenesis.pyruvate orthophosphate dikinase activity.pyruvate orthophosphate dikinase'	xvis03_201017-pa	pyruvate orthophosphate dikinase (original description: processed-gene-109.26-mRNA-1 protein Name:Similar to PPD Pyruvate, phosphate dikinase, chloroplastic (<i>Mesembryanthemum crystallinum</i>) AED:0.09 eAED:0.09 QI:8 1 1 1 0.89 0.9 20 257 985)'
Carbohydrate metabolism .nucleotide sugar biosynthesis.UDP-L-arabinose biosynthesis.UDP-L-arabinose mutase'	xvis03_224372-pa	UDP-L-arabinose mutase (original description: processed-gene-2.16-mRNA-1 protein Name:Similar to UAM1 UDP-arabinopyranose mutase 1 (<i>Oryza sativa</i> subsp. <i>japonica</i>) AED:0.08 eAED:0.08 QI:87 1 1 1 1 1 4 347 359)'
protein homeostasis .ubiquitin-proteasome system.26S proteasome.20S core particle.beta-type components.component beta type-5'	xvis03_211689-pa	component beta type-5 of 26S proteasome (original description: processed-gene-6.93-mRNA-1 protein Name:Similar to Proteasome subunit beta type-5 (<i>Spinacia</i>

		oleracea) AED:0.07 eAED:0.07 QI:0 1 0.87 1 1 1 8 489 310)'
protein homeostasis .proteolysis.cysteine-type peptidase activities.C13-class asparaginyl endopeptidase (Legumain)'	xvis03_211268- pa	asparaginyl endopeptidase (Legumain) (original description: processed-gene-9.25- mRNA-1 protein Name:Similar to Vacuolar- processing enzyme (Citrus sinensis) AED:0.07 eAED:0.07 QI:3 1 1 1 1 1 9 417 590)'
protein homeostasis .proteolysis.serine-type peptidase activities.S28-class serine carboxypeptidase'	xvis03_222506- pa	S28-class serine carboxypeptidase (original description: augustus-gene-4.97-mRNA-1 protein Name:Similar to EDA2 Probable serine protease EDA2 (Arabidopsis thaliana) AED:0.31 eAED:0.31 QI:159 0.92 0.92 1 1 1 14 279 488)'
Protein homeostasis .proteolysis.metallopeptidase activities.aminopeptidase activities.M1-class neutral/aromatic-hydroxyl amino acid aminopeptidase'	xvis03_210782- pa	M1 neutral/aromatic-hydroxyl amino acid aminopeptidase (original description: augustus-gene-7.64-mRNA-1 protein Name:Similar to Os08g0562700 Puromycin- sensitive aminopeptidase (Oryza sativa subsp. japonica) AED:0.20 eAED:0.20 QI:160 0.75 0.81 0.90 0.84 0.84 33 284 1052)'
Redox homeostasis .hydrogen peroxide removal.ascorbate-glutathione cycle.ascorbate peroxidase (ApX)'	xvis03_214214- pa	ascorbate peroxidase (APX) (original description: processed-gene-11.33-mRNA-1 protein Name:Similar to APX1 L-ascorbate peroxidase, cytosolic (Pisum sativum) AED:0.17 eAED:0.17 QI:131 1 1 1 1 1 7 558 249)'
Redox homeostasis .hydrogen peroxide removal.ascorbate-glutathione cycle.monodehydroascorbate reductase (MDAR)'	xvis03_204322- pa	monodehydroascorbate reductase (MDAR) (original description: processed-gene-9.15- mRNA-1 protein Name:Similar to AFRR Monodehydroascorbate reductase (Solanum lycopersicum) AED:0.13 eAED:0.13 QI:138 0.72 0.83 0.83 1 1 12 368 489)'
Redox homeostasis .hydrogen peroxide removal.ascorbate-glutathione cycle.glutathione reductase (GR)'	xvis03_205102- pa	glutathione reductase (GR) (original description: processed-gene-9.15-mRNA-1 protein Name:Similar to GOR Glutathione reductase, chloroplastic (Fragment)

		(Nicotiana tabacum) AED:0.14 eAED:0.14 QI:0 1 0.90 1 0.9 0.81 11 639 590)'
Cell organisation.pectin.homogalacturonan.modification and degradation.pectin methylesterase'	xvis03_217074- pa	pectin methylesterase (original description: processed-gene-2.49-mRNA-1 protein Name:Similar to PME35 Probable pectinesterase/pectinesterase inhibitor 35 (Arabidopsis thaliana) AED:0.36 eAED:0.36 QI:662 1 1 1 1 3 218 442)'
Cell wall organisation.pectin.rhamnogalacturonan I.modification and degradation.beta-galactosidase (BGAL)'	xvis03_221434- pa	beta-galactosidase (BGAL) (original description: processed-gene-2.106-mRNA-1 protein Name:Similar to Beta-galactosidase (Asparagus officinalis) AED:0.13 eAED:0.13 QI:277 1 1 1 1 19 418 832)'
Coenzyme metabolism .thiamine pyrophosphate biosynthesis.thiazole biosynthesis.biosynthetic protein (Thi4)'	xvis03_212280- pa	biosynthetic protein (Thi4) (original description: processed-gene-6.79-mRNA-1 protein Name:Similar to THI1-2 Thiamine thiazole synthase 2, chloroplastic (Vitis vinifera) AED:0.02 eAED:0.02 QI:212 1 1 1 1 2 483 354)'
Coenzyme metabolism .tetrapyrrol biosynthesis.chlorophyll metabolism.chlorophyll(ide) interconversions.geranylgeranyl reductase (Chlp)'	xvis03_215774- pa	geranylgeranyl reductase (Chlp) (original description: augustus-gene-7.23-mRNA-1 protein Name:Similar to CHLP Geranylgeranyl diphosphate reductase, chloroplastic (Nicotiana tabacum) AED:0.00 eAED:0.00 QI:382 1 1 1 1 2 212 364)'
protein biosynthesis .aminoacyl-tRNA synthetase activities.alanine-tRNA ligase'	xvis03_224672- pa	alanine-tRNA ligase (original description: processed-gene-1.89-mRNA-1 protein Name:Similar to ALATS Alanine--tRNA ligase (Arabidopsis thaliana) AED:0.10 eAED:0.10 QI:33 1 1 1 0.90 0.90 22 389 993)'
protein biosynthesis .aminoacyl-tRNA synthetase activities.aspartate-tRNA ligase'	xvis03_205724- pa	aspartate-tRNA ligase (original description: processed-gene-33.32-mRNA-1 protein Name:Similar to IBI1 Aspartate--tRNA ligase 2, cytoplasmic (Arabidopsis thaliana) AED:0.10 eAED:0.10 QI:60 0.77 0.8 1 1 1 10 190 552)'