

Table S4. List of drought-responsive proteins in Maresi leaf extracts.

Spot no.	Protein name	Organism	ANOVA	MARESI control	Maresi stress	Stress/Control	Accumulation level	Method of identification	Score	% coverage	pI (theoretical)	Mw (theoretical)	Mw (experimental)	pI (experimental)	Accession number	Position on the gel	
1	2-Cys peroxidoredoxin BAS1, chloroplastic	Hordeum vulgare	0.00824781	0.0156826	0.0526933	3.359984951	INCREASED	PMF	82	40							
2	Unidentified		0.00924878	0.0151548	0.0556934	3.674967667	INCREASED				5.4	23398	11794	6.44	BAS1_HORVU	A8	
3	Delta-1-pyrroline-5-carboxylate synthetase	Vigna aconitifolia	0.017887	0.0518764	0.0252025	0.485818214	decreased	MS/MS	33	1	6.6	73531	32575	5.6	P5CS_VIGAC		
4	Cytochrome B6-F complex Fe-S subunit	Hordeum vulgare	0.00246835	0.0452852	0.117158	2.587114554	INCREASED	PMF	74	22	8.47	24124	14400	5.86	gi326518434		
5	Unidentified		0.0124549	0.0161897	0.0423942	2.618590832	INCREASED						19744	6.16			
6	Probable mannitol dehydrogenase	Maedicago sativa	0.0412959	0.0178114	0.0434522	2.439572409	INCREASED	MS/MS	30	2	7.8	39458	20351	4.67	MTDH_MEDSA		
9	Ribosomal protein L10 family	Hordeum vulgare	0.0382794	0.0696066	0.0519842	0.752733107	decreased	PMF	121	43	8.31	24197	24566	5.99	gi326507838		
10	Glutathione S-transferase	Hordeum vulgare	3.10E-04	0.0390441	0.0769928	1.971944545	INCREASED	PMF	71	37	5.67	23557	27108	6.25	gi326490728		
11	2-Cys peroxidoredoxin BAS1, chloroplastic	Hordeum vulgare	0.00135921	0.0259449	0.0712672	2.7468674	INCREASED	MS/MS	101	15	5.4	23398	26718	4.79	BAS1_HORVU		
12	Unidentified		0.0057339	0.0136764	0	decreased							28559	6.32			
13	Photosystem II oxygen-evolving complex protein 2 precursor	Triticum aestivum	0.00703619	0.0947474	0.174423	1.840926506	INCREASED	PMF	110	41	8.84	27424	30038	5.51	PSBP_WHEAT		
14	Unidentified		0.00777869	0.157115	0.105868	0.673824905	decreased						30498	5.24			
15	Signal recognition particle protein 1	Arabidopsis thaliana	0.0190491	0.0667629	0.0410989	0.615594889	decreased	MS/MS	29	1	9.7	53257	31123	5.09	SR5541_ARATH		
16	Ascorbate peroxidase	Hordeum vulgare	1.65E-05	0.0185057	0.0448493	2.423533974	INCREASED	PMF	80	34	5.85	27532	31801	6.35	gi3688398		
18	Glutathione S-transferase	Hordeum vulgare	0.00259258	0.0110753	0.0391961	3.539055375	INCREASED	PMF	112	34	8.91	33484	33709	5.56	gi326507956	A7	
19	Ubiquitin carboxyl-terminal hydrolase 19	Arabidopsis thaliana	0.00112161	0.0773346	0.0381097	0.492789773	decreased	MS/MS	28	1	4.8	77097	34750	5.15	UBP19_ARATH	A9	
20	RNA recognition motif	Hordeum vulgare	0.00440885	0.0242254	0.0786382	3.246105327	INCREASED	PMF	112	40	4.57	31872	35687	4.33	gi326493824		
21	Oxygen-evolving enhancer protein 1, chloroplastic	Solanum tuberosum	4.15E-04	0.446458	0.931164	2.085669873	INCREASED	MS/MS	330	13	5.84	35595	37164	5.06	PSBO_SOLTU		
22	Unidentified		2.05E-04	0.0239574	0	decreased							38263	5.88			
23	Oxygen-evolving enhancer protein 1, chloroplastic	Solanum tuberosum	0.0019328	0.0671474	0.0328832	0.489716653	decreased	MS/MS	164	8	5.84	35595	39195	5.27	PSBO_SOLTU		
24	Ferredoxin-NADP+ oxidoreductase	Hordeum vulgare	2.29E-05	0.171314	0.0857088	0.500302369	decreased	PMF	90	32	8.29	39971	40457	6.37	gi326492141	A10	
25	Ferredoxin-NADP+ oxidoreductase	Triticum aestivum	0.00877661	0.221392	0.159515	0.720590323	decreased	PMF	104	33	6.92	40491	39695	5.83	gi20302473		
26	Unidentified		9.99E-04	0.0540285	0.16996	3.145747152	INCREASED						41128	5.16		A14	
28	Cysteine synthase, mitochondrial	Hordeum vulgare	0.00317391	0.138881	0.078134	0.562596755	decreased	MS/MS	46	3	5.3	34207	41285	5.28	CYSK_HORVU		
29	Unidentified		0.0112754	0.0413168	0.0292089	0.706949715	decreased						42077	6.16			
30	Cysteine synthase	Triticum aestivum	1.85E-05	0.0604608	0	decreased		PMF	85	40	5.48	34207	41600	5.75	CYSK_WHEAT		
31	Ricin-type beta-trefoil (carbohydrate-binding domain)	Hordeum vulgare	2.58E-04	0.0453268	0	decreased		PMF	92	39	5.71	35765	42885	6.07	gi326517467		
33	Unidentified		2.01E-04	0.0334643	0.0768129	2.295368497	INCREASED						44041	6.06			
34	Unidentified		0.0180996	0.317756	0.586848	1.846851043	INCREASED						45318	6.18			
35	Nucleoside-diphosphate-sugar epimerase	Hordeum vulgare	0.0108349	0.362165	0.256424	0.70803087	decreased	PMF	179	42	7.06	41582	45212	6.02	gi326523629		
36	Unidentified		0.0188379	0.052239	0.022937	0.439078083	decreased						46834	5.94			
37	Dynamin-related protein 1B	Arabidopsis thaliana	0.02163	0.0732544	0.031458	0.428858881	decreased	PMF	77	39	7.64	68384	46724	5.8	T47968		
38	Ribulose biphosphate carboxylase/oxygenase activase B, chloroplastic	Triticum aestivum	3.22E-04	0.0224043	0.105816	4.72302192	INCREASED	PMF	145	41	6.92	48012	47387	5.53	gi37960277	A3	
39	Fructose-1,6-bisphosphate aldolase	Hordeum vulgare	0.00516084	0.309251	0.236565	0.764961148	decreased	PMF	198	53	6.06	38102	49901	6.37	gi326493652		
40	Unidentified		0.00517168	0.0990728	0.0588399	0.593905694	decreased						54306	6.31			
41	Glyceraldehyde-3-phosphate dehydrogenase A, chloroplastic	Arabidopsis thaliana	0.00481321	0.671513	0.38146	0.568060484	decreased	MS/MS	121	3	9.8	40507	52425	5.83	G3PB_ARATH		
42	Glutamine synthetase leaf isozyme, chloroplastic	Hordeum vulgare	1.54E-04	1.34268	0.839211	0.625026812	decreased	PMF	119	40	5.75	46902	53295	5.11	gi755762	A11	
43	ATP-sulfurylase	Hordeum vulgare	0.00290441	0.0673919	0.0431533	0.640333631	decreased	PMF	102	31	5.95	39484	58684	6.33	gi326530496		
44	Unidentified		0.042668	0.0477802	0.0234999	0.491833437	decreased						56519	5.88			
45	Elongation factor Tu, chloroplastic-like	Brachypodium distachyon	0.00381689	0.629716	0.342491	0.543881686	decreased	PMF	220	52	5.88	50638	56519	5.44	gi357149925		
46	Ribulose biphosphate carboxylase/oxygenase activase A, chloroplastic	Hordeum vulgare	0.0151096	0.363115	0.229185	0.631163681	decreased	MS/MS	441	14	8.04	51383	58822	5.23	RCAA_HORVU		
47	S-adenosylmethionine synthase 3	Hordeum vulgare	2.92E-04	0.0292473	0	decreased		PMF	122	42	5.51	43138	58409	5.70	MEAT3_HORVU		
48	Ribulose biphosphate carboxylase/oxygenase large subunit	Hordeum vulgare	0.00171349	0.360107	0.135014	0.374927452	decreased	MS/MS	346	8	6.22	53672	64014	6.72	RLT_HORVU		
49	Phosphogluconate dehydrogenase, cytosolic	Zea mays	0.00171921	0.0094449	0	decreased		PMF	93	25	5.61	52860	60790	5.77	gi357110692		
50	Enolase	Hordeum vulgare	0.00545875	0.204331	0.123793	0.605845417	decreased	PMF	132	39	5.39	48601	69384	5.57	gi326490934	A4	
51	Ribulose bisphosphate carboxylase/oxygenase large subunit-binding protein su	Secale cereale	0.016229	0.116266	0.0110193	0.094776633	decreased	MS/MS	108	3	4.88	53721	74045	5.05	RUBB_SECCCE		
52	Unidentified		1.52E-04	0.0181794	0	decreased							77196	6.25			
53	Ribulose biphosphate carboxylase/oxygenase large subunit-binding protein su	Secale cereale	5.77E-05	0.650508	0.245602	0.377554158	decreased	MS/MS	376	11	4.7	53721	76555	5.22	RUBB_SECCCE	A2	
56	Ferredoxin-nitrite reductase	Hordeum vulgare	0.0338891	0.0987507	0.0542454	0.549316612	decreased	PMF	122	20	6.33	66660	78887	6.32	gi326505210	A12	
57	Ferredoxin-nitrite reductase	Triticum aestivum	2.71E-05	0.0125165	0	decreased		PMF	118	26	6.33	66660	78624	5.95	gi326505210		
58	Unidentified		7.92E-04	0.0151719	0	decreased							78493	5.90			
59	26S proteasome non-ATPase regulatory subunit 7-like	Brachypodium distachyon	7.36E-04	0.0198593	0	decreased		PMF	77	36	6.23	34848	78624	5.70	gi357166548		
60	Unidentified		0.0170087	0.0847318	0.0548719	0.647595118	decreased						81290	5.19			
61	Unidentified		5.91E-04	0.0175965	0.00193432	0.109926406	decreased						82794	5.95			
62	Unidentified		0.00192781	0.0120464	0	decreased							84749	5.69			
63	Unidentified		0.00236225	0.023326	0.014623	0.626897025	decreased						85174	5.65			
64	Heat shock 70 kDa protein, chloroplastic	Hordeum vulgare	4.59E-04	0.144195	0.0875261	0.606998162	decreased	PMF	94	18	5.04	73955	87768	4.85	gi326492960	A6	
65	Thiamine pyrophosphate (TPP) family, transketolase subfamily	Hordeum vulgare	0.00300857	0.488119	0.20419	0.418320123	decreased	PMF	163	37	5.45	74032	86750	5.62	gi326533372		
66	Thiamine pyrophosphate (TPP) family, transketolase subfamily	Hordeum vulgare	0.0109381	0.349433	0.196495	0.562325253	decreased	PMF	124	30	5.45	74032	87185	5.54	gi326533372		
67	Methionine synthase	Hordeum vulgare	0.00456423	0.0367712	0.0190693	0.518593356	decreased	PMF	185	29	5.68	84794	87914	5.94	gi50897038		
69	Chaperone protein ClpC1, chloroplastic	Medicago truncatula	7.72E-04	0.133802	0.133802	0.327741738	decreased	PMF	145	26	6.44	102889	93507	5.63	gi357520587		
70	Chaperone protein ClpC1, chloroplastic	Oryza sativa	0.00844034	0.067875	0.0274875	0.404972376	decreased	PMF	233	30	6.14	101853	93663	5.58	CLPC1_ORYSJ		
71	Clp protease ATP binding subunit	Hordeum vulgare	0.00191313	0.0987698	0.0487688	0.493762263	decreased	PMF	133	21	6.65	102090	94763	5.77	gi326514880		
72	Clp protease ATP binding subunit	Hordeum vulgare	2.07E-04	0.0494769	0.0208708	0.421829177	decreased	PMF	127	21	6.65	102090	94921	5.71	gi326514880		
73	Unidentified		3.65E-04	0.0153261	0	decreased							98302	5.93			
74	Phosphoribulokinase	Triticum aestivum	0.00777089	1.11635	0.712787	0.638497783	decreased	PMF	201	55	5.72	45512	49203	5.15	KPPR_WHEAT		
75	Unidentified		2.81E-04	0.0586181	0	INCREASED							17868	6.53			
76	Translationally controlled tumor protein	Hordeum vulgare	0.00224604	0.0208841	0.0517688	2.478861909	INCREASED	MS/MS	118	13	4.53		18929	26718	4.61	TCTP_HORVU	
77	Unidentified		0.00129551	0.0102307	0.0787713	7.699502478	INCREASED						24213	4.99			
78	Ricin-type beta-trefoil (carbohydrate-binding domain)	Hordeum vulgare	1.51E-04	0.0312543	0.0855021	2.735690769	INCREASED	PMF	175	53	5.71	35765	43212	6.1	gi326517467		
79	Heat shock 70 kDa protein	Hordeum vulgare	0.00501415	0.0200395	0.0552657	2.578382629	INCREASED	PMF	80	19	5.11	73301	86317	5.21	gi326495158	A15	
80	Unidentified		0.00473479	0.0513186	0	INCREASED							15064	4.98			
81	Unidentified		0.0010757	0.0188894	0	INCREASED							17080	4.92			
82	Unidentified		9.40E-04	0.0245099	0	INCREASED							22070	5.52			
83	Unidentified		0.00284425	0.0438718	0	INCREASED							31241	6.7		A13	

84	Cysteine synthase	<i>Hordeum vulgare</i>	2.39E-04		0,0810459		INCREASED	PMF	85	26	6.08	41129	41024	5.1	gi326506704	
85	Fructose-1,6-bisphosphate aldolase	<i>Hordeum vulgare</i>	0.00136306	0,023501	0,0479504	2,04035573	INCREASED	PMF	114	31	6.08	39064	48742	6.78	gi226316443	A1
86	Unidentified		0.005706	0.0274107		0	decreased						37590	5.36		
87	Thiamine pyrophosphate (TPP) family, transketolase subfamily	<i>Hordeum vulgare</i>	2.64E-04	0.0100386		0	decreased	PMF	118	34	5.45	74032	89697	5.46	gi326533372	
88	Unidentified		1.05E-05	0.0233682	0.0049353	0.211197268	decreased						99788	5.37		
89	Heat shock 70 kDa protein, mitochondrial	<i>Phaseolus vulgaris</i>	0.0143218	0.0543848	0.0332916	0,612148983	decreased	MS/MS	121	3	5.95	72721	75478	5.67	HSP7M_PHAVU	A5