

1 **Table S1.** Differentially abundant protein spots under drought stress (DS).

Spot No.	Protein Name	Accession No.	Theoretical/Experimental		Pep. Count	Protein Score	Protein Score C. I. %	Coverage %	Fold change	Subcellular location	Stress response
			Mw (kDa)	pI							
Storage proteins											
6	globulin-1 S allele-like	gi 514813383	50.63/58.26	6.39/6.07	18	482	100	34.95	-2.65	vacuole	up-regulated
9	globulin-1 S allele-like	gi 514813383	50.63/38.79	6.39/5.49	26	817	100	48.79	4.41	vacuole	down-regulated
42	globulin-1 S allele, partial	gi 514819529	55.60/45.16	7.66/6.23	18	414	100	32.54	-2.99	vacuole	up-regulated
44	globulin-1 S allele, partial	gi 514819529	55.60/54.98	7.66/7.65	11	311	100	22.02	3.96	vacuole	down-regulated
48	globulin-1 S allele-like	gi 514813383	50.63/41.38	6.39/7.38	11	132	100	27.91	2.99	vacuole	up-regulated
56	globulin-1 S allele-like	gi 514813383	50.63/43.17	6.39/6.23	20	344	100	40.44	2.44	vacuole	down-regulated
57	Cupin_1	gi 944223427	61.67/59.89	6.57/6.61	15	385	100	25.09	5.2	vacuole	down-regulated
58	Cupin_1	gi 944226588	58.05/58.39	7.67/7.56	12	283	100	20.53	6.76	vacuole	down-regulated
59	globulin-1 S allele-like	gi 514813383	50.63/52.04	6.39/6.47	20	414	100	37.8	76.84	vacuole	down-regulated
73	globulin-1 S allele-like	gi 514813383	50.63/23.88	6.39/6.28	25	582	100	45.71	4.49	vacuole	down-regulated
74	globulin-1 S allele-like	gi 514813383	50.63/46.21	6.39/6.09	11	113	100	18.02	-178.63	vacuole	up-regulated
75	globulin-1 S allele-like	gi 514813383	50.63/60.27	6.39/6.08	18	460	100	38.9	18.66	vacuole	down-regulated
82	globulin-1 S allele-like	gi 514813383	50.63/51.04	6.39/6.34	20	466	100	41.32	2.66	vacuole	down-regulated
93	globulin-1 S allele, partial	gi 514819529	55.60/66.31	7.66/7.58	16	430	100	28.37	-4.01	vacuole	up-regulated
97	globulin-1 S allele-like	gi 514813383	50.63/52.04	6.39/6.42	14	421	100	35.16	5.28	vacuole	down-regulated
99	globulin-1 S allele-like	gi 514813383	50.63/39.26	6.39/6.28	26	889	100	49.67	-4	vacuole	up-regulated
101	globulin-1 S allele-like	gi 514813383	50.63/47.06	6.39/6.21	17	878	100	35.38	2.44	vacuole	down-regulated
103	globulin-1 S allele-like	gi 514813383	50.63/38.29	6.39/5.10	20	651	100	41.32	-2.29	vacuole	up-regulated
Protein folding											
3	late embryogenesis abundant protein D-34-like	gi 514764205	28.96/27.58	4.63/4.57	9	283	100	41.67	2.05	cytoplasmic	down-regulated
4	protein disulfide isomerase	gi 944229578	55.75/54.29	4.83/4.76	13	178	100	23.51	2.3	endoplasmic reticulum	down-regulated
5	protein disulfide-isomerase	gi 514808170	56.75/56.39	4.90/4.77	23	488	100	40.31	-3.95	endoplasmic reticulum	up-regulated
11	protein disulfide-isomerase	gi 514808170	56.75/57.24	4.90/4.95	34	841	100	58.51	-5.03	endoplasmic reticulum	up-regulated
12	low-temperature-induced 65 kDa protein-like	gi 836023655	56.66/57.18	4.88/4.91	23	351	100	33.45	-36.69	nucleus	up-regulated
19	protein disulfide-isomerase	gi 514808170	56.75/55.69	4.90/5.76	23	515	100	38.16	-12.86	endoplasmic reticulum	up-regulated
20	ruBisCO large subunit-binding protein subunit alpha	gi 514812327	61.67/61.09	5.31/5.28	20	659	100	34.81	-2.58	mitochondrial	up-regulated
21	heat shock 70 kDa protein	gi 514784173	71.23/70.89	5.10/4.98	23	419	100	31.33	8.61	cytoplasmic	down-regulated
23	Chaperonin 10 Kd subunit	gi 944245063	24.80/25.06	6.64/6.57	11	215	100	50.84	-2.38	mitochondrial	up-regulated
36	GroEL_like type I chaperonin	gi 944244716	62.11/63.02	5.43/5.38	31	831	100	54.4	-2.53	mitochondrial	up-regulated
37	heat shock 70 kDa protein 15-like	gi 514745327	94.57/95.01	5.10/5.17	35	575	100	40	-4.9	cytoplasmic	up-regulated
67	heat shock 70 kDa protein 8	gi 514820981	62.98/61.64	5.54/5.46	16	306	100	36.16	3.76	cytoplasmic	down-regulated
70	chaperone protein ClpC1	gi 514801078	102.31/105.07	6.23/6.29	34	329	100	34.74	2.32	mitochondrial	down-regulated
72	late embryogenesis abundant protein Lea14-A	gi 514772286	16.35/17.39	6.11/5.99	10	632	100	59.6	131.25	cytoplasmic	down-regulated
81	protein disulfide-isomerase	gi 514808170	56.75/57.26	4.90/4.28	21	441	100	39.14	-9.06	endoplasmic reticulum	up-regulated
84	heat shock 70 kDa protein	gi 514784173	71.23/70.39	5.10/4.96	24	316	100	34.88	2.53	cytoplasmic	down-regulated

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Starch and sucrose metabolism											
7	N-Acyltransferase	gi 944228140	44.75/44.06	10.93/10.34	7	87	99.985	13.09	-2.08	cytoplasmic	up-regulated
8	endochitinase A-like isoform X1	gi 514802372	29.37/32.18	5.65/5.72	5	314	100	23.36	-2.86	extracellular	up-regulated
13	1,4-alpha-glucan-branching enzyme 2	gi 514712923	90.71/76.29	5.72/5.24	23	289	100	23.84	20.7	amyloplastic	down-regulated
17	glucose-1-phosphate adenylyltransferase small subunit	gi 514728628	56.10/52.79	5.92/5.18	21	554	100	41.37	2.8	amyloplastic	down-regulated
31	glucose-1-phosphate adenylyltransferase small subunit	gi 514728628	56.10/56.67	5.92/5.73	20	577	100	43.92	-2.11	amyloplastic	up-regulated
34	UTP--glucose-1-phosphate uridylyltransferase	gi 514733064	53.14/53.03	5.20/5.13	26	840	100	62.24	-2.21	cytoplasmic	up-regulated
38	LOW QUALITY PROTEIN: pullulanase 1	gi 514800253	105.56/103.38	5.39/5.28	33	964	100	35.07	-2.18	vacuole	up-regulated
49	ADP-glucose pyrophosphorylase	gi 944249897	58.16/57.88	6.11/6.02	24	699	100	45.75	3.76	nucleus	down-regulated
62	glucose-1-phosphate adenylyltransferase	gi 944237145	52.79/53.39	5.51/4.87	16	446	100	35.7	2.44	cytoplasmic	down-regulated
63	glucose-1-phosphate adenylyltransferase	gi 944237145	52.79/52.19	5.51/5.37	14	264	100	34.03	33.28	cytoplasmic	down-regulated
65	glucose-1-phosphate adenylyltransferase	gi 944237145	52.79/53.39	5.51/5.28	24	658	100	43.84	3.56	cytoplasmic	down-regulated
71	1,4-alpha-glucan-branching enzyme 2	gi 514712923	90.71/89.03	5.72/5.76	32	264	100	31.74	4.88	amyloplastic	down-regulated
86	glucose-1-phosphate adenylyltransferase large subunit 1	gi 835968826	58.10/67.36	6.08/6.13	26	905	100	54.44	6.16	amyloplastic	down-regulated
87	glucose-1-phosphate adenylyltransferase large subunit 1	gi 835968826	58.10/69.06	6.08/6.05	18	423	100	41.51	5.4	amyloplastic	down-regulated
89	GT1_Sucrose_synthase	gi 944245085	95.34/95.73	5.88/5.84	20	113	100	19.16	-3.71	cytoplasmic	up-regulated
Glycolysis / Gluconeogenesis											
24	triosephosphate isomerase	gi 514775343	27.28/28.03	5.38/5.27	11	383	100	27.76	-4.13	cytoplasmic	up-regulated
33	enolase 1	gi 514760125	48.13/50.26	5.17/5.09	17	311	100	36.1	-3.1	cytoplasmic	up-regulated
43	triosephosphate isomerase	gi 514784219	27.44/26.82	5.34/5.29	12	464	100	41.8	-2.97	cytoplasmic	up-regulated
53	2,3-bisphosphoglycerate-independent phosphoglycerate mutase	gi 944243163	63.78/64.07	5.74/5.70	21	412	100	34.24	-2.62	cytoplasmic	up-regulated
76	fructose-1,6-bisphosphatase	gi 514749801	37.55/38.35	5.71/5.69	19	410	100	48.39	-2.74	cytoplasmic	up-regulated
77	beta-galactosidase 15 isoform X2	gi 835953566	68.60/67.95	6.21/6.32	11	141	100	16.99	9.09	cytoplasmic	down-regulated
78	Phosphoglycerate kinase	gi 944264318	42.46/43.08	5.65/5.59	16	669	100	45.52	2.4	cytoplasmic	down-regulated
79	fructose-bisphosphate aldolase cytoplasmic isozyme-like	gi 514785954	39.19/42.31	6.56/6.38	12	455	100	30.17	46.59	cytoplasmic	down-regulated
83	fructose-bisphosphate aldolase cytoplasmic isozyme-like	gi 514785954	39.19/40.86	6.56/6.43	14	574	100	37.15	29.09	cytoplasmic	down-regulated
85	fructose-bisphosphate aldolase cytoplasmic isozyme-like	gi 514785954	39.19/37.69	6.56/6.49	6	82	99.951	13.69	2.45	cytoplasmic	down-regulated
100	pyrophosphate--fructose 6-phosphate 1-phosphotransferase subunit beta-like	gi 514762846	61.59/60.34	6.18/6.09	20	372	100	34.04	3.35	mitochondrial	down-regulated
Biosynthesis of amino acids											
47	Aspartate aminotransferase	gi 944240355	43.92/43.18	5.28/5.39	10	311	100	28.17	2.53	cytoplasmic	down-regulated
51	alanine aminotransferase 2-like	gi 835938735	59.78/57.88	5.92/5.76	22	424	100	27.57	-2.03	mitochondrial	up-regulated
52	ketol-acid reductoisomerase	gi 944249953	65.45/64.83	6.12/6.08	13	271	100	27.69	-2.32	mitochondrial	up-regulated
64	3-isopropylmalate dehydratase large subunit	gi 514710509	55.69/55.21	7.08/6.94	22	616	100	38.9	2.42	cytoplasmic	down-regulated

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69	Cobalamine-independent methionine synthase	gi 944248757	84.75/83.96	5.74/5.82	12	120	100	15.42	3.1	cytoplasmic	down-regulated
80	2-isopropylmalate synthase A-like	gi 514805280	68.42/67.91	6.51/6.60	27	512	100	40.01	3.25	mitochondrial	down-regulated
98	alanine aminotransferase 2	gi 514816727	53.26/54.06	5.99/6.07	19	249	100	33.4	8.35	cytoplasmic	down-regulated
Detoxification and defense											
28	tricin synthase 1-like	gi 514797483	26.88/26.33	5.27/5.33	6	428	100	26.12	-2.11	cytoplasmic	up-regulated
39	peroxiredoxin-2C	gi 514780116	17.42/18.06	5.35/5.40	6	163	100	33.95	-2.15	cytoplasmic	up-regulated
40	probable glutathione S-transferase GSTU1	gi 514766546	25.72/26.19	5.44/5.37	10	443	100	37.78	-2.67	cytoplasmic	up-regulated
61	monodehydroascorbate reductase	gi 514727351	46.77/45.81	5.815/2.7	21	733	100	37.7	15.11	cytoplasmic	down-regulated
92	Glutathione (GSH) peroxidase	gi 944234046	27.79/28.16	9.24/9.14	11	251	100	28.35	10.26	mitochondrial	down-regulated
96	1-Cys peroxiredoxin PER1	gi 514736637	24.45/24.41	6.3/6.19	14	570	100	67.42	-21.06	cytoplasmic	up-regulated
102	Ricin-type beta-trefoil lectin domain-like	gi 944226655	39.27/40.16	6.27/6.38	25	1140	100	64.66	-2.08	cytoplasmic	up-regulated
Protein degradation											
10	trypsin inhibitor	gi 944233813	22.95/24.06	6.35/6.26	9	348	100	42.25	-4.22	cytoplasmic	up-regulated
15	proteasome subunit beta type-3-like	gi 514765484	23.15/23.68	5.17/5.25	5	250	100	15.2	-2.26	cytoplasmic	up-regulated
26	proteasome subunit alpha type-1	gi 514710216	30.54/31.10	5.21/5.17	17	713	100	57.45	-2.21	cytoplasmic	up-regulated
41	Eukaryotic aspartyl protease	gi 944250016	54.81/55.16	5.89/5.68	9	188	100	26.63	-2.66	vacuole	up-regulated
50	IAA-amino acid hydrolase ILR1-like 1	gi 514777929	47.85/48.05	5.49/5.52	13	400	100	31.91	12.65	extracellular	down-regulated
55	prolyl endopeptidase-like	gi 514768698	85.98/84.99	5.64/5.98	20	175	100	20.84	3.03	mitochondrial	down-regulated
95	trypsin inhibitor	gi 944233813	22.95/23.37	6.35/6.19	11	542	100	43.66	195.53	cytoplasmic	down-regulated
TCA cycle											
14	Pyruvate phosphate dikinase	gi 944251288	90.58/89.69	5.06/5.13	26	462	100	32	-8.82	cytoplasmic	up-regulated
27	carboxyvinyl-carboxyphosphonate phosphorylmutase	gi 514800962	33.33/34.07	5.43/5.39	16	373	100	49.52	-3.13	cytoplasmic	up-regulated
46	pyruvate dehydrogenase E1 component subunit beta-3, chloroplastic isoform X1	gi 514755118	46.30/45.79	6.83/6.68	12	281	100	21.23	-2.05	cytoplasmic	up-regulated
60	malate dehydrogenase	gi 514816242	35.80/34.96	5.76/5.57	17	476	100	54.22	-5.5	cytoplasmic	up-regulated
88	succinate dehydrogenase [ubiquinone]flavoprotein subunit	gi 514792029	68.60/68.34	6.25/6.18	27	677	100	38.45	5.81	mitochondrial	down-regulated
90	putative aconitate hydratase	gi 835993763	107.13/105.36	6.89/6.82	31	422	100	29.69	-2.17	cytoplasmic	up-regulated
91	putative aconitate hydratase	gi 835993763	107.13/106.26	6.89/6.76	27	568	100	27.97	-2.2	cytoplasmic	up-regulated
Protein synthesis											
1	Translationally controlled tumor protein	gi 944231340	23.57/22.83	7.93/6.94	7	229	100	18.52	-3.14	cytoplasmic	up-regulated
2	elongation factor 1-beta	gi 514736912	23.71/23.29	4.61/4.56	9	348	100	43.05	-11.38	nucleus	up-regulated
16	Soluble N-ethylmaleimide-sensitive factor (NSF) Attachment Protein	gi 944236969	32.57/31.08	5.04/5.11	10	214	100	36.68	-2.21	mitochondrial	up-regulated
25	eukaryotic translation initiation factor 3 subunit F	gi 514744250	31.63/30.91	5.18/5.26	12	437	100	43.36	-2.28	cytoplasmic	up-regulated
66	Superfamily II DNA and RNA helicase	gi 944249732	39.67/38.97	6.64/6.29	11	136	100	29.94	2.59	nucleus	down-regulated
68	eukaryotic translation initiation factor 3 subunit D-like	gi 514779826	65.24/62.13	5.43/5.39	27	344	100	40.99	-2.33	cytoplasmic	up-regulated
Energy metabolism											
29	Inorganic pyrophosphatase	gi 944251043	23.26/22.79	5.33/5.26	10	246	100	44.28	-2.17	nucleus	up-regulated
30	cinnamoyl-CoA reductase 1-like	gi 836027225	35.47/36.02	5.28/5.37	11	445	100	35.87	-3.27	cytoplasmic	up-regulated
32	ATP synthase F1 beta subunit	gi 944242149	66.71/67.09	5.70/5.71	17	426	100	32.16	-3.81	cytoplasmic	up-regulated
35	ATP synthase F1 beta subunit	gi 944242149	66.70/65.59	5.70/5.63	15	486	100	29.6	-3.02	cytoplasmic	up-regulated

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45	soluble inorganic pyrophosphatase	gi 514741802	24.61/24.16	5.46/5.42	11	348	100	46.76	-2.2	cytoplasmic	up-regulated
Transporter											
18	importin subunit alpha-1a	gi 514773852	58.13/58.02	5.10/5.16	10	259	100	25.81	-3.55	nucleus	up-regulated
94	outer envelope pore protein 16-2	gi 514819880	18.19/17.59	6.42/6.38	7	510	100	45.76	34.98	nucleus	up-regulated
104	protein TOC75	gi 514820490	91.86/91.37	7.64/7.49	27	392	100	34.23	-3.34	mitochondrial	up-regulated
Pentose phosphate pathway											
54	transketolase	gi 944244855	80.20/79.83	6.16/6.12	13	167	100	17.23	-2	cytoplasmic	up-regulated
Signal transduction											
22	Histidine kinase-like ATPases	gi 944238036	80.55/81.39	4.95/5.01	28	654	100	36.82	-2.17	endoplasmic reticulum	up-regulated

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