

Supplementary Table S2. Protein spots identified in the present work

Id#	Identified protein	Mascot score^a	Sequence coverage %	PMF peptides	MS/MS peptides	Theoretical/ Observed MW (kDa)	Theoretical/ Observed pI	Accession
408	sHSP	154	78	12	-	16.8/18.0	5.8/5.6	CAA69172
524	BMAI-1	93	45	7	-	16.4/15.9	5.4/5.1	P16968
536	serpin Z7	76	20	8	-	42.9 ^c /34.1	5.8 ^c /6.2	TC139354
537	1-Cys peroxiredoxin	110	47	9	-	24.2/28.0	6.3/6.2	P52572
538	serpin Zx	97	32	12	-	42.9/33.9	6.8/6.0	S29819
563	unknown function	110	51 ^b	8	-	21.8 ^c /25.3	5.5 ^c /5.8	TC109912
564	unknown function	143	51 ^b	10	-	21.8 ^c /25.2	5.5 ^c /5.8	TC109912
565	aluminium-induced protein	118	71 ^b	9	-	26.4 ^c /30.1	4.9 ^c /4.8	TC112232
566	aluminium-induced protein	96	71 ^b	6	-	26.4 ^c /30.1	4.9 ^c /4.9	TC112232
567	aluminium-induced protein	135	71 ^b	10	-	26.4 ^c /30.3	4.9 ^c /4.9	TC112232
568	short chain alcohol DH	107	65 ^b	7	-	28.0 ^c /29.1	6.2 ^c /6.5	TC110840
569	pUP13	81	58	6	-	15.3/15.7	5.4/4.8	1208404A
571	barley grain peroxidase 1	138	52	11	-	34.3/28.0	6.5/5.8	1BGP
602	serpin Z7	128	-	-	10	42.9/43.1	5.5/5.7	T06183
603	serpin	111	16	7	-	42.9/42.7	5.5/6.1	T06183
	malate dehydrogenase	94	49	12	-	35.6	5.8	Q08062
604	barley grain peroxidase 1	74	-	-	1	34.3/28.4	6.5/5.2	1BGP
605	unknown function	95	-	-	5	22.5 ^c /28.8	4.8 ^c /4.4	TC122901
606	unknown function	95	-	-	7	22.5 ^c /28.9	4.8 ^c /4.5	TC122901
607	unknown function	100	-	-	6	22.5 ^c /23.6	4.8 ^c /4.4	TC122901
608	unknown function	95	-	-	7	22.5 ^c /29.2	4.8 ^c /4.5	TC122901
609	unknown function	118	-	-	7	22.5 ^c /29.9	4.8 ^c /4.6	TC122901
610	serpin Zx	89	29	11	-	42.9/34.4	6.8/6.2	S29819

^a Mascot scores for positive identification are above the P <0.05 threshold

^b Sequence coverage applies to identified EST sequence

^c Theoretical MW and pI calculated for protein predicted from TC sequence