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Table S1

Spot	Experimental molecular weight (kDa)/pI	Wheat protein/peptide database			NCBInr green plant protein database			
		Homologous protein	Theoretical molecular weight (kDa)/pI	Coverage (%) (number of matched peptides)	Homologous protein	Taxon	Calculated molecular weight (kDa)/pI	Coverage (%) (number of matched peptides)
1	16.6/4.7	pathogenesis-related protein	17.1/4.7	67% (8)	hypothetical protein LOC100383551	*Zea mays*	32.6/8.1	34% (8)
2	19.0/5.5	pleckstrin homology domain-containing protein 1	18.5/5.7	45% (6)	hypothetical protein	*Oryza sativa*	13.8/9.0	39% (6)
3	23.4/5.5	UMP/CMP kinase a	23.2/5.4	70% (10)	conserved hypothetical protein	*Ricinus communis*	7.7/10.3	67% (4)
4	24.3/5.8	proteasome subunit beta type 1	24.3/5.9	66% (15)	predicted protein	*Physcomitrella patens*	66.5/5.9	30% (16)
5	24.4/6.1	proteasome subunit beta type 1	24.3/6.0	62% (12)	Chain A, Solution Structure Of The Cnmp-Binding Domain From Arabidopsis Thaliana Cyclic Nucleotide-Regulated Ion Channel	*Arabidopsis Thaliana*	15.2/5.3	51% (7)
6	31.8/5.8	glyoxalase I	32.3/5.6	38% (16)	glycolate dehydrogenase	*Chlamydomonas reinhardtii*	120.4/8.0	24% (17)
7	32.5/6.3	isoflavone reductase IRL	32.9/5.5	47% (12)	hypothetical protein VOLCADRAFT_60049	*Volvox carteri f. nagariensis*	35.9/11.0	17% (7)
8	34.7/6.6	deoxymugineic acid synthase1	35.2/6.5	26% (7)	valacyclovir hydrolase, putative	*Ricinus communis*	27.7/9.9	25% (5)
9	35.2/5.9	putative NADPH-dependent mannose 6-phosphate reductase	35.4/5.9	38% (12)	NADP-dependent D-sorbitol-6-phosphate dehydrogenase1_3	*Hordeum vulgare*	41.5/6.5	26% (9)
10	35.3/6.4	annexin 2	35.7/6.2	55% (17)	Similar to NBS-LRR disease resistance protein homologue	*Oryza sativa*	59.8/6.2	29% (9)
11	36.1/5.8	Fructokinase-2	35.9/5.1	30% (13)	unknown protein	*Arabidopsis thaliana*	78.3/9.2	29% (20)
12	36.2/4.8	Fructokinase-2	35.9/5.1	58% (13)	hypothetical protein OsJ_14606	*Oryza sativa*	70.4/10.4	35% (16)

13	36.4/8.1	putative peroxidase	36.1/8.0	56% (21)	remorin family protein	*Arabidopsis thaliana*	34.3/5.9	23% (11)
14	36.5/4.6	adenosine kinase-like protein	36.5/5.2	52% (13)	Phosphoribulokinase, chloroplastic	*Triticum aestivum*	45.5/5.7	28% (10)
15	41.3/5.2	reversibly glycosylated polypeptide	41.5/5.8	38% (8)	hypothetical protein CHLREDRAFT_164198	*Chlamydomonas reinhardtii*	31.3/5.7	26% (6)
16	42.9/6.0	chloroplast fructose-bisphosphate aldolase	42.0/5.9	55% (16)	Similar to shaggy related protein kinase. Belongs to the CDC2/CDKX subfamily	*Arabidopsis thaliana*	51.5/8.8	43% (16)
17	44.2/5.1	aspartyl protease family protein	44.5/4.7	59% (9)	casein kinase, putative	*Brachypodium sylvaticum*	72.4/9.0	34% (16)
18	47.3/8.6	photolyase/blue-light receptor PHR2, putative, expressed	48.7/8.4	46% (10)	Oxygen-evolving enhancer protein 3, chloroplast precursor	*Ricinus communis*	25.1/9.5	34% (7)
19	53.9/6.6	Fumarate hydratase 1, mitochondrial precursor, putative, expressed	53.7/6.9	33% (16)	ribulose-1,5-bisphosphate carboxylase/ oxygenase large subunit	*Anisopogon avenaceus*	49.9/6.2	31% (13)
20	63.2/5.2	trehalase 1	63.1/5.5	55% (5)	hypothetical protein	*Medicago truncatula*	7.9/9.5	72% (3)
21	66.9/8.5	phage head-tail adaptor family protein	66.8/8.2	76% (8)	chloroplast ribulose-1,5-bisphosphate carboxylase/ oxygenase small subunit	*Musa AAAB Group*	18.6/9.1	47% (7)
22	68.7/8.3	CER1 protein, putative, expressed	68.1/8.2	26% (5)	hypothetical protein	*Zea mays*	4.4/10.4	100% (2)
23	71.0/5.0	Heat shock cognate 70 kDa protein, putative, expressed	71.3/5.1	53% (7)	heat shock protein, putative	*Ricinus communis*	71.3/5.1	19% (9)
24	25.5/6.9	cytosolic malate dehydrogenase	24.6/6.6	56% (16)	cytosolic malate dehydrogenase	*Triticum aestivum*	24.6/6.6	56% (16)
25	37.3/7.3	glyceraldehyde-3-phosphate dehydrogenase	36.9/7.1	50% (14)	glyceraldehyde-3-phosphate dehydrogenase	*Triticum aestivum*	36.9/7.1	46% (13)
26	39.2/5.4	caffeic acid 3-O-methyltransferase	39.0/5.5	47% (18)	caffeic acid 3-O-methyltransferase	*Triticum aestivum*	39.0/5.5	44% (16)
27	39.3/8.8	ferredoxin-NADP(H) oxidoreductase	39.2/8.3	37% (16)	ferredoxin-NADP(H) oxidoreductase	*Triticum aestivum*	39.2/8.3	37% (16)
28	43.0/6.3	chloroplast fructose-bisphosphate aldolase	42.2/5.9	47% (15)	chloroplast fructose-bisphosphate aldolase	*Triticum aestivum*	42.2/5.9	44% (14)
29	57.1/6.3	catalase	57.0/6.5	40% (21)	Catalase-1	*Triticum aestivum*	57.0/6.5	40% (21)
30	64.4/6.3	Beta-glucosidase	64.9/6.5	31% (20)	Beta-glucosidase	*Triticum aestivum*	64.9/6.5	31% (20)
31	26.7/5.5	ascorbate peroxidase	27.5/5.8	58% (11)	ascorbate peroxidase	*Hordeum vulgare*	27.5/5.8	45% (9)
32	27.8/4.9	ascorbate peroxidase	27.9/5.1	59% (12)	ascorbate peroxidase	*Hordeum vulgare*	27.9/5.1	53% (11)
33	36.1/6.1	chloroplast oxygen-evolving	34.7/5.8	51% (11)	chloroplast oxygen-evolving	*Hordeum vulgare*	34.7/5.8	41% (11)

		enhancer protein 1			enhancer protein 1			
34	38.3/7.2	UDP-D-glucuronate decarboxylase	39.0/7.4	79% (32)	UDP-D-glucuronate decarboxylase	*Hordeum vulgare*	39.1/7.1	72% (30)
35	44.0/5.3	S-adenosylmethionine synthase 3	43.1/5.5	46% (10)	S-adenosylmethionine synthase 3	*Hordeum vulgare*	43.1/5.5	38% (10)
36	49.9/8.5	putative aminotransferase AGD2	49.9/8.3	45% (13)	putative aminotransferase AGD2	*Hordeum vulgare*	50.2/8.3	27% (10)
37	84.3/5.6	methionine synthase 2 enzyme	84.8/5.7	35% (26)	methionine synthase	*Hordeum vulgare*	84.8/5.7	31% (20)
38	35.3/4.5	Fructokinase-2	35.9/5.1	68% (15)	Fructokinase-2	*Oryza sativa*	35.9/5.1	43% (13)
39	40.8/6.9	Putative r40c1 protein	41.7/6.3	34% (7)	Putative r40c1 protein	*Oryza sativa*	39.1/6.3	22% (5)
40	44.6/8.3	phosphoserine aminotransferase	45.3/8.5	41% (16)	Putative phosphoserine aminotransferase	*Oryza sativa*	45.3/8.5	23% (9)
41	53.5/5.0	Enolase, putative, expressed	48.3/5.4	48% (22)	enolase	*Oryza sativa*	48.3/5.4	37% (15)
42	54.2/5.1	Enolase, putative, expressed	48.3/5.4	57% (21)	enolase	*Oryza sativa*	48.3/5.4	41% (16)
43	54.1/5.3	Enolase, putative, expressed	48.3/5.4	54% (19)	enolase	*Oryza sativa*	48.3/5.4	36% (14)
44	79.4/8.3	phenylalanine ammonia-lyase	76.3/8.5	37% (9)	phenylalanine ammonia-lyase	*Oryza sativa*	76.3/8.5	9% (6)
45	37.6/4.8	adenosine kinase-like protein	36.5/5.2	57% (16)	adenosine kinase	*Zea mays*	36.5/5.2	24% (9)
46	62.6/5.9	Pyrophosphate fructose 6-phosphate, 1-phosphotransferase beta-subunit	61.2/6.2	27% (14)	Pyrophosphate fructose 6-phosphate, 1-phosphotransferase beta-subunit	*Zea mays*	61.2/6.2	18% (9)
47	82.6/6.0	NADH-ubiquinone oxidoreductase, 75 kDa subunit	81.7/6.1	32% (11)	NADH-ubiquinone oxidoreductase, 75 kDa subunit	*Zea mays*	81.7/6.1	13% (8)
48	48.2/6.4	26S proteasome regulatory subunit	47.7/6.0	38% (19)	26S protease regulatory subunit 7	*Populus trichocarpa*	48.1/6.0	32% (16)