Table 2 – Protein identification of the spots picked from the image analysis of ProQ Diamond stained gels using MS/MS followed by database search results.

		Spot volume										
pI range of 2D-gel	Spot no.	FMV:SnRK2.8	*snrk2.8*	*P* value	Protein identification	Genome no.	Mascot score	Coverage (matched peptide)	Predicted mass, kDa	Predicted pI	Mass on gel, kDa	pI on gel
pI 3-10	339	0.236±0.106	0	0.2036	Glutamine synthetase	At5g37600	240	19%(4)	39.3	5.3	46.9	4.6
					In2-1 protein	At5g02780	192	30%(4)	28.0	4.9		
	544	0.686±0.156	0	0.0169	**OTU-like cysteine protease family protein**	At1g50670	137	10% (2)	23.6	4.9	30.8	4.4
					AALP protein	At5g60360	119	10%(3)	39.4	6.3		
					Unknown protein	At3g23600	113	15%(3)	26.1	5.2		
	484	0.306±0.038	0.073±0.021	0.0077	**glyI**	At1g11840	596	44% (8)	31.9	5.2	35.2	4.9
	350	0.164±0.036	0	0.0155	3-isopropylmalate dehydrogenase	At5g14200	479	42% (10)	44.3	5.7	47.1	4.8
					ADK1	At3g09820	343	24%(6)	38.2	5.3		
					Putative villin 2	At2g41740	241	8%(7)	106.2	5.1		
	327	0.133±0.022	0.089±0.010	0.1472	Cinnamyl-alcohol dehydrogenase	At4g34230	429	26% (6)	39.3	5.4	50.0	5.3
					Putative dTDP-glucose 4-6-dehydratase	At1g08200	393	29%(8)	44.2	5.6		

				Phosphoglycerate kinase	At1g79550	351	25% (7)	42.1	5.5		
329	0.117±0.035	0	0.0287	Unknown protein	At2g38860	519	28%(8)	43.5	5.1	54.8	4.8
				Transferase family similar to alcohol acyltransferase	At4g15390	507	21%(7)	49.1	5.1		
				Phosphoethanolamine N-methyltransferase 2	At1g48600	419	30% (9)	54.5	5.0		
				TUA4	At1g04820	389	29%(10)	50.2	4.9		
				Transaldolase	At5g13420	308	22%(8)	47.9	6.1		
222	0.584±0.132	0.157±0.090	0.0496	**Heat-shock protein 70-3**	At3g09440	454	19% (10)	71.5	4.9	75.2	4.4
				Heat-shock protein 70-1	At5g02500	447	19%(9)	71.7	5.0		
376	0.205±0.081	0	0.0476	Succinyl-CoA ligase [GDP-forming] β-chain	At2g20420	491	27%(9)	45.6	6.3	47.8	5.3
651	0.116±0.011	0.004±0.007	0.0010	Inorganic pyrophosphatase	At5g09650	220	15%(4)	33.6	5.7	35.1	5.1
				Peroxidase	At3g03670	212	15%(3)	34.9	5.0		
				Expressed protein	At3g60450	129	13%(3)	31.1	5.1		
391	0.179±0.067	0	0.0440	6-phosphogluconate dehydrogenase	At1g64190	570	28%(9)	53.7	5.3	58.9	5.3
				Cytosol aminopeptidase	At2g24200	145	7%(3)	54.7	5.7		
807	0.345±0.021	0.057±0.048	0.0092	Aconitase C-terminal domain-containing protein	At2g43100	319	42%(7)	27.4	5.7	30.8	4.4

					R5PI	At3g04790	270	28%(5)	29.4	5.7		
					Unknown protein	At3g23600	232	33%(5)	26.1	5.2		
	367	0.28±0.055	0	0.0124	DEAD BOX RNA helicase RH15	At5g11200	489	25%(8)	48.9	5.5	68.0	5.0
					Glutathione synthetase gsh2	At5g27380	298	15%(7)	60.6	6.1		
					Enolase	At2g36530	243	16%(5)	47.9	5.5		
					Transferase family protein similar to EIG-I24	At1g28680	205	14%(6)	50.1	5.5		
					S-adenosyl-L-homocysteine	At3g23810	187	8%(4)	53.8	5.5		
	446	0.062±0.020	0	0.0351	**TUA4**	At1g04820	477	36%(12)	50.2	4.9	54.8	4.85
					3-phosphoshikimate 1-carboxyvinyltransferase	At1g48860	399	19%(8)	56.3	6.4		
	472	0.058±0.024	0	0.0572	Putative lectin	At3g16470	435	19%(6)	48.5	5.1	50.6	4.88
					NADH	At5g03630	328	22%(8)	47.8	5.2		
					Carbamoyl phosphate synthetase small subunit	At3g27740	139	9%(3)	47.2	5.7		
	279	0.033±0.012	0	0.0466	Malate oxidoreductase	At5g11670	285	11%(6)	64.7	6.0	87.1	6.02
					Phosphoglucomutase	At1g23190	259	12%(6)	63.3	5.9		
					Transaldolase, putative	At5g13420	245	14%(4)	47.9	6.1		
pI; 3.9-5.1	560	0.972	0.097		**14-3-3 protein ψ**	At5g38480	148	14% (3)	28.7	4.7	26.4	4.71
					Unknown protein	At5g19230	139	21% (3)	20.8	5.8		
	436	0.74	0.269		DREPP plasma membrane	At4g20260	56	7% (2)	24.5	4.9	40.1	4.88

			polypeptide family							
503	0.473	0.009	**14-3-3-protein χ**	At4g09000	221	27% (6)	30.0	4.7		
			14-3-3 protein ψ	At5g38480	152	16%(4)	28.7	4.7	33.8	4.66
476	2.02	0.685	Cysteine protease component	At5g43060	287	13% (4)	52.7	5.9		
			G box complex protein	At1g78300	244	23% (5)	29.2	4.7	34.6	4.73
460	0.303	0.098	NAP family	At1g74560	165	17% (4)	29.4	4.2		
			14-3-3-protein χ	At4g09000	138	15% (3)	30.0	4.7	39.2	4.6
			Coatomer delta subunit	At5g05010	105	7% (3)	55.4	5.4		
			14-3-3-protein υ	At5g16050	91	7% (2)	30.3	4.7		
793	0.377	0	MD-2-related lipid recognition domain-containing	At5g23820	224	29% (5)	18.1	4.6		
748	0.367	0	Histone H2A	At1g08880	57	13% (2)	14.8	10.3	10.8	4.3
790	0.204	0.048	RPP3B	At5g57290	89	21% (2)	11.9	4.4	12.3	4.2
813	0.497	0	**RPP2A**	At2g27720	166	39% (2)	11.4	4.6		
809	0.822	0.15	Profilin 2	At4g29350	101	17% (2)	14.1	4.9	10.2	4.5
835	0.271	0	Unknown protein	At3g01670	43	1% (2)	97.4	6.2	9.1	4.7
827	0.386	0.133	COP9 signalosome subunit 5A / c-JUN coactivator	At1g71230	52	6% (3)	40.4	5.1	8.5	4.5
522	0.092	0	Heat-shock protein 81-2	At5g56030	125	5% (4)	80.3	4.9	8.5	4.7
538	0.337	0	**14-3-3 protein κ**	At5g65430	274	33% (7)	27.8	4.7	31.9	4.4

				Peroxidase	At3g03670	72	8% (2)	34.9	5.0	29.8	4.8
pI; 4.7-5.9	623	0.167	0	**R5PI**	At3g04790	316	28% (6)	29.4	5.7		
				AALP protein	At5g60360	87	10% (4)	39.4	6.3	27.5	5.0
				Eukaryotic phosphomannomutase family protein	At2g45790	138	13% (3)	27.9	5.3		
	594	0.703	0.093	Unknown protein	At5g46790	91	11% (2)	22.5	5.4		
	591	0.897	0.221	Triose phosphate isomerase, cytosolic, putative	At3g55440	49	7% (2)	27.4	5.4	28.8	5.1
				Ca^{2+}-dependent membrane-binding protein annexin	At1g35720	369	36% (9)	36.3	5.2	28.7	5.2
				Pyruvate dehydrogenase E1 component beta subunit	At5g50850	284	22% (6)	39.4	5.3		
	452	0.468	0	**ADK1**	At3g09820	226	15% (4)	38.2	5.3		
				RPP0C	At3g11250	196	15% (5)	34.4	5.1	36.9	5.2
				Serine/threonine protein phosphatase PP2A-3	At2g42500	194	13% (4)	36.4	4.9		
				Diaminopimelate epimerase family protein	At3g53580	142	9% (3)	39.4	5.4		
	312	0.128	0	RuBisCO subunit binding-protein beta subunit	At5g56500	201	9% (4)	63.4	5.7		
				S-adenosylmethionine	At3g17390	189	10% (3)	43.1	5.5	47.3	5.3

			synthetase, putative							
			Glycosyl hydrolase family 3 protein	At5g10560	177	4% (3)	88.0	5.9		
			Eukaryotic protein synthesis initiation factor 4A	At3g13920	161	11% (5)	46.9	5.5		
			Enolase (2-phospho-d-glycerate hydrolyase)	At2g36530	159	27% (7)	47.9	5.5		
			unknown protein	At1g49820	131	6% (3)	48.3	5.5		
474	0.237	0.167	2-nitropropane dioxygenase-like protein	At5g64250	116	10% (3)	36.3	5.4		
			Jacalin lectin family protein	At3g16420	111	10% (2)	32.1	5.5	35.6	5.4
			Stress-responsive protein	At3g16050	92	7% (2)	34.0	5.4		
595	0.343	0.096	Isopentenyl-diphosphate delta-isomerase II	At3g02780	304	28% (8)	32.8	6.1		
			PfkB-type carbohydrate kinase family protein	At2g31390	154	12% (3)	35.4	5.3	28.6	5.1
			Chitinase	At2g43570	132	16% (4)	30.7	5.8		
389	0.591	0.078	Glutamate-1-semialdehyde 2,1-aminomutase 1	At5g63570	340	18% (6)	50.7	6.4		
			Alcohol dehydrogenase	At1g77120	103	7% (3)	41.8	5.8	41.1	5.6
362	0.582	0.29	Oxidoreductase, 2OG-Fe(II)	At4g25310	131	9% (3)	40.0	5.4		

			oxygenase family							
			Actin 8	At1g49240	123	14% (4)	42.1	5.4	42.6	5.3
349	0.259	0.087	Glutamate-1-semialdehyde 2,1-aminomutase 1	At5g63570	362	19% (6)	50.7	6.4		
			Elongation factor Tu, putative	At4g02930	285	17% (6)	49.6	6.2	43.8	5.6
			MAPK, putative (MPK4)	At4g01370	192	17% (5)	43.3	5.7		
552	0.366	0	Glyoxalase II	At1g53580	226	22% (5)	32.2	6.5		
			Similar to auxin down-regulated protein ARG10	At3g22850	218	21% (5)	27.5	5.8	31.8	5.2
			α-soluble NSF attachment protein 2	At3g56190	211	16% (4)	33.2	5.2		
			Carbonyl reductase, putative	At1g01800	200	17% (5)	33.7	5.6		
437	0.101	0	Fructose-bisphosphate aldolase	At3g52930	676	41% (11)	38.8	6.0		
			Malate dehydrogenase, cytosolic	At1g04410	398	33% (8)	35.9	6.1	40.2	5.7
			NAD-dependent glyceraldehyde-3-phosphate dehydrogenase	At1g13440	316	24% (7)	37.0	6.7		

The score number, number of matched peptides, and percent coverage are taken directly from the Mascot Daemon report. Bold protein indicates that were used for further analysis and $P < 0.05$ indicates significantly difference between comparison.

ADK1, adenosine kinase 1; TUA4, tubulin α-2/α-4 chain; R5PI, ribose 5-phosphate isomerase; NADH, monodehydroascorbate reductase; NAP, nucleosome assembly protein; RPP3B, 60S acidic ribosomal protein P3; RPP2A, 60S acidic ribosomal protein P2; RPP0C, 60S acidic ribosomal protein P0.