

## Supplementary information

Spot no.	Protein name	Accession no.	Mr (kDa)		pI		Protein Score	Pep. count
			Theoretic	Experimental	Theoretic	Experimental		
Defense and stress response								
↑1608	Chaperonin cpn60	gi 357442729	61.5	49.5	6.27	5.51	154	3
↑5409	Monodehydroascorbate reductase (MDAR)	gi 225440936	47.5	43.2	6.32	6.7	217	7
↑7301	Cinnamyl alcohol dehydrogenase	gi 206236379	20.1	27.4	7.93	7.13	225	3
↑2311	Putative orcinol O-methyltransferase	gi 161444215	26.0	26.1	6.09	5.6	685	6
Energy metabolism								
↑7707	Phosphoenolpyruvate carboxykinase [ATP]	gi 255537864	73.8	61.28	6.57	7.31	448	13
↑5207	Malate dehydrogenase	gi 225461618	37.1	22.4	8.76	6.73	447	6
↑4802	Methionine synthase	gi 8439545	84.9	79.9	5.93	6.33	361	12
↑5701	Methionine synthase	gi 8439545	84.89	65.4	5.93	6.57	540	14
↑8608	Pyrophosphate-dependent phosphofructokinase alpha subunit	gi 3790102	68.13	55	6.71	7.85	260	12
↑4106	Predicted: triosephosphate isomerase, cytosolic-like	gi 357134081	27.2	24.9	5.24	6.43	79	6
↑6705	5-methyltetrahydropteroyltriglutamate-homocysteine methyltransferase, putative	gi 255549601	90.5	83.3	6.45	6.85	510	11
Signal transduction/ transcription								
NI0502	Vacuolar ATPase subunit B	gi 118429132	54.2	43.7	4.93	4.56	145	5
↓8112	Putative RAN2 small Ras GTP-binding nuclear protein	gi 87046111	25.3	15.2	6.65	7.54	649	11
↑9901	TUDOR-SN protein 1	gi 343172567	23.32	23.1	9.23	7.81	234	7
↑1409	Predicted: eukaryotic initiation factor 4A-11	gi 225429488	47.1	35.9	5.38	5.44	578	16

---

Protein synthesis and metabolism								
↓3407	Predicted: elongation factor Tu, chloroplastic-like	gi 356513781	52.6	33.4	6.33	6.17	398	7
↑5503	Predicted: 26S proteasome regulatory subunit 4 homolog A-like 26S	gi 356537286	49.47	43.1	5.91	6.65	348	8
↑1302	Predicted: adenosine kinase 2	gi 225449018	38.2	25.5	5.31	5.36	267	5
↑6604	Branched-chain-amino-acid aminotransferase-like protein 2-like	gi 356533600	70.9	69.7	6.96	6.93	134	8
↓3213	Esterase D, putative	gi 255565327	28.7	27.8	5.33	6.13	93	2
Photosynthesis								
↑3403	Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit	gi 33323298	45.4	34.2	8.18	6.04	127	5
Others								
↓8315	Sglf212-1o14t3	gi 359713678	35.3	34.7	8.94	7.72	120	2
↑8709	Predicted protein	gi 224071575	65.8	57.5	6.17	7.84	97	8
↑0307	No results							

---