

Supplemental Table 1. Identification of Soybean Plasma Membrane Proteins using 2-DE MS/Sequencer Based Proteomics

Spot No.	Exp. Mr (kDa) / pI	N-terminal amino acid sequences	Protein name	Accession No.	Identity	Score (MP) %Cov	Theo. Mr (Da) / pI	Class	GRAVY value	Number of TM helices
1	99.1/ 4.70	n-blocked (MS)	two-component sensor histidine kinase	Q17YU_HELAC	-	78 (7) 10%	50146 / 5.3	Sgnl		
3	96.5/ 5.30	AVFXVDL	phosphate import ATP-binding protein pstB	Q21E72	100	-	-	Trpotr	-0.161	0
4	96.3/ 6.53	n-blocked (MS)	plasma membrane proton ATPase	gil5669151	-	66 (4) 6%	105132 / 6.48	Trpotr	0.115	8
10	85.5/ 8.50	n-blocked (MS)	F1-ATPase alpha subunit	gil34539397	-	65 (2) 7%	44921 / 8.26	Engy	-0.003	0
12	80.9/ 4.4	EGDTDXLVD	hypothetical protein F28F9.4	T29205	87.5	-	-	Unclass	0.767	6
14	80.6/ 5.6	n-blocked (MS)	patellin 1	gil15218382	-	62 (2) 10%	64007 / 4.82	Trpotr	-0.535	0
15	80.4/ 5.2	DFVVEDNXLT	ATP synthase epsilon chain	P33255	85.7	-	-	Engy	-0.191	0
16	80.3 5.4	n-blocked (MS)	patellin 1	gil15218382	-	62 (2) 10%	64007 / 4.82	Trpotr	-0.535	0
17	80.2/ 6.0	n-blocked (MS)	glycerophosphoryl diester phosphodiesterase	gil83281191	-	77 (2) 2%	81954 / 5.34	CelStr	0.009	0
19	75.9/ 4.6	n-blocked (MS)	Not-hit							

20	75.9/ 5.2	KEEATKLGTV	luminal-binding protein precursor	P49118	100	-	-	PrDsSt	-0.45	0
21	75.8/ 4.50	n-blocked (MS)	diguanilate cyclase	gil114321799	-	45 (2) 2%	61604 / 6.30	Sgnl	-0.528	0
22	75.0/ 5.30	n-blocked (MS)	hsc70-cognate binding protein precursor	AAB86942	-	106 (5) 10%	71587 / 5.08	PrDsSt	-0.434	1
23	65.7/ 4.70	n-blocked (MS)	heat shock cognate 70 kDa protein, expressed	Gm0063x00346.1 (ABA95501)	-	315 (12) 21%	67940 / 4.51	PrDsSt	-0.369	0
25	65.0/ 5.30	n-blocked (MS)	protein disulfide-isomerase precursor	Gm0065x00031.3 (P29828)	-	320 (21) 39%	58963 / 4.95	PrDsSt	-0.357	1
26	64.5/ 4.40	KVFFEERFDD	calreticulin	P30806	90	-	-	PrDsSt	-1.53	0
27	64.5/ 4.70	n-blocked (MS)	protein disulfide-isomerase precursor	Gm0021x00405.1 (P29828)	-	901 (42) 52%	54292 / 5.46	PrDsSt	-0.357	1
29	64.4/ 8.1	GVAENIPD	urease subunit gamma	Q8XXS8	88	-	-	PriMtb	0.09	0
30	55.0/ 8.0	n-blocked (MS)	Not-hit							
31	55.0/ 4.70	KVAENIPDME (MS)	vacuolar H ⁺ -ATPase B subunit	A6Y950 Gm0021x00405.1 (A6Y950)	100	1958 (69) 74%	54292 / 4.93	Trpotr	-0.249	0
32	58.9/ 5.71	n-blocked (MS)	chaperonin GroEL	gil13474837	-	390 (8) 27%	57715 / 5.18	PrDsSt	-0.047	0
34	57.7/ 5.90	n-blocked (MS)	maturation polypeptide	AAA33985	-	1689 (28) 56%	47800 / 6.33	PrDsSt	-1.229	0
37	57.2/ 5.90	n-blocked (MS)	glycoside hydrolase	gil124360054	-	45	53583	PriMtb	0.128	0

	6.00					(2)	/ 6.8				
						2%					
40	54.9/ 5.20	n-blocked (MS)	51 kDa seed maturation protein	gil414977	-	103	50951	PrDsSt	-1.227	1	
						(2)	/ 5.9				
						3%					
41	55.0/ 8.0	n-blocked (MS)	beta-tubulin	gil56112435	-	128	46856	CelStr	-0.283	0	
						(3)	/ 9.2				
						10%					
42	54.9/ 5.81	n-blocked (MS)	protein kinase	gil140069565	-	187	72133	Sgnl	-0.076	1	
						(3)	/ 6.75				
						5%					
43	54.4/ 5.90	n-blocked (MS)	BiP	gil62433284	-	653	73549	PrDsSt	-0.415	1	
						(14)	/ 5.06				
						27%					
44	55.9/ 6.0	n-blocked (MS)	beta-D-glucan exohydrolase	gil3582436	-	148	68401	DsDf	-0.066	0	
						(3)	/ 9.03				
						4%					
45	55.9/ 5.3	n-blocked (MS)	copper ion binding, SKU5	gil15234551	-	98	65596	CelGrw	-0.236	0	
						(2)	/ 9.16				
						2%					
46	49.8/ 5.0	n-blocked (MS)	heat shock protein 70	gil75271998	-	99	49242	PrDsSt	-0.18	0	
						(2)	/ 5.5				
						2%					
52	51.4/ 5.70	n-blocked (MS)	matrix metalloproteinase, MMP2	Gm066x00014 (AAL27029.1)	-	72	40165	DsDf	-0.161	3	
						(7)	/ 5.36				
						15%					
54	47.8/ 6.52	n-blocked (MS)	ATPase F1 alpha subunit	gil27461619	-	65	44865	Engy	-0.03	0	
						(2)	/ 6.55				
						7%					
65	45.0/ 5.36	DDVVVMXE	protein disulfide isomerase	P38661	75	-	-	PrDsSt	-0.335	1	
66	27.0/ 5.61	n-blocked (MS)	stem 31 kDa glycoprotein	Gm0113x00272.1 (P10743)	-	54	29433	ProDsS t	-0.341	1	
						(3)	/ 6.72				
						12%					

72	25.8/ 5.67	n-blocked (MS)	stem 31 kDa glycoprotein	Gm0113x00272.1 (P10743)	-	44 (2) 8%	29433 / 6.72	PrDsSt	-0.341	1
74	23.4/ 5.04	SDXEDSVF	Not hit	-	-	-	-	Not hit		
77	24.7/ 5.09	n-blocked (MS)	putative uncharacterized protein	Gm0076x00259 (ABD32399)	-	186 (13) 25%	22324 / 4.87	Unclass	0.058	1
79	45.2/ 5.81	SDKEDSVFKG	ribosome biogenesis protein BOP1	P97452	70	-	-	ProSyn	-0.485	0
80	26.8/ 8.50	n-blocked (MS)	unknown	Gm0203x00030 (ABK92585.1)	-	276 (22) 59%	21698 / 8.43	Unclass	-0.727	0
81	27.3/ 5.98	SDKEDSVFKG	proteasome subunit beta type 2	P91477	88.9	-	-	PrDsSt	-0.285	0
82	21.0/ 5.04	n-blocked (MS)	plasma membrane intrinsic polypeptide	Gm0086x00171 (CAB1742)		97 (10) 30%	23118 / 4.95	Unclr		
92	41.2/ 5.72	n-blocked (MS)	Unknown protein	ABK92585		215 (11) 35%	41290 / 9.13	Unclr	-0.727	0
100	38.1/ 5.07	n-blocked (MS)	Unknown protein	ABK93565	-	226 (13) 66%	33111 / 4.99	Unclass	-0.448	0
101	38.2/ 5.43	ADXEVGDTTT	GTP-binding protein lepA	Q9CGI8	70	-	-	Sgnl	-0.109	0
102	40.1/ 4.8	n-blocked (MS)	band 7 family protein	Gm0196x00029.1 (CAA45777.1)	-	264 (14) 40%	31815 / 5.11	Unclr	-0.161	1
103	39.2/ 5.3	ADHEVGDT	T-complex protein 1, beta subunit	P47207	100	-	-	PrDsSt	-0.048	0
110	31.5/ 6.42	n-blocked (MS)	stem 31 kDa glycoprotein	Gm0113x00272.1 (P10743)		735 (16)	29433 / 5.85	PrDsSt	-0.341	1

116	35.0/ 4.8	n-blocked (MS)	14-3-3 protein	Gm0026x00182.1 BAB47119		418 (24)	29226 / 4.66	Sgnl	-0.545	0
124	31.5/ 8.0	n-blocked (MS)	acid phosphatase	Gm0146x00211.2 (CAA11075)	-	100 (-)	28997 / 8.50	Sgnl	-0.385	0
128	29.7/ 7.0	KVNDFXVAD (MS)	Not hit	-	-	-	-	Not hit		
131	29.0/ 6.9	KXFVIDPTE	ferredoxin-like protein in nif region	P12712	71.4	-	-	Engy	-0.055	0
139	21.5/ 4.50	DFVLDNEGPN (MS)	trypsin inhibitor (Kunitz-type inhibitor)	P01071 Gm0119x00246 (P01071)	100	112 (5)	24346 / 4.99	DsDf	-0.241	0
140	21.5/ 5.30	VKAVAVLGS	superoxide dismutase	Q7M1R5	100	-	-	DsDf	-0.172	0
146	21.0/ 4.55	GVFTFVVXKS	transmembrane protein 141	Q96I45	100	-	-	Unclr	0.097	2

Identity: amino acid sequence identity from protein sequencer; MP: number of matched peptides from MS data; Cov.: coverage (%) from MS data; GRAVY: grand average of hydropathy; TM: transmembrane.

PiMtb: Primary metabolism; Engy: Energy; CelGrw: Cell growth/division; Trcrpt: Transcription; ProSyn: Protein synthesis; PrDsSt: Protein destination/storage; Trpotr: Transporters; ICTrf: Intracellular traffic; CelStr: Cell structure; Sgnl: Signal transduction; DsDf:

Disease/defense; ScdMtb: Secondary metabolism; Unclr: Unclear classification; Unclass: Unclassified.

The following protein spots that had hits were not identified by database search, although for the following protein spots, MS peaks were obtained: spots 2, 5, 6, 8, 9, 13, 18, 33, 35, 36, 51, 53, 56, 57, 58, 59, 61, 63, 64, 67, 69, 70, 71, 73, 75, 83, 84, 85, 86, 88, 89, 90, 93, 96, 99, 105, 107, 108, 109, 112, 113, 114, 115, 117, 118, 119, 120, 121, 122, 125, 126, 127, 132, 135, 136, 137, 138, 141, 142, 143, 144, 147 and 150.

Supplemental Table 2. Identification of Soybean Plasma Membrane Proteins using nanoLC MS/MS-Based Proteomics in NCBI Database

No.	Accession No.	Protein name	Score	MP	Cov. (%)	Theoretical		Class	GRAVY value	Number of TM helices
						Mr	pI			
1	gil311698	lea protein [Glycine max]	166	6	12	49484	7.08	ProDsSt	-1.223	1
2	gil159162564	chainA, solution structure of leginsulin, a plant hormone	143	5	86	4265	6.73	ProDsSt	0.265	0
3	gil145203152	heat shock protein 70 [Cyclamen persicum]	107	5	8	71488	5.13	ProDsSt	-0.4	0
4	gil115456247	Os03g0821100 [Oryza sativa] (heat shock cognate protein)	105	8	12	71666	5.1	ProDsSt	-0.424	0
5	gil147853956	hypothetical protein [Vitis vinifera]	104	8	13	71589	5.17	Unclass	-0.404	0
6	gil21604	ubiquitin [Solanum tuberosum]	104	8	66	6255	5.17	ProDsSt	-0.461	0
7	gil45331285	70 kDa heat shock cognate protein 3 [Vigna radiata]	104	6	8	71870	5.07	ProDsSt	-0.415	0
8	gil60592632	vacuolar H ⁺ -ATPase catalytic subunit [Pyrus communis]	103	9	18	68999	5.43	Trpotr	-0.189	0
9	gil1710521	60S ribosomal protein L24	102	2	8	18559	10.65	ProSyn	-1.053	0
10	gil195616644	unknown [Zea mays]	99	5	8	71493	5.06	Unclass	-0.455	0
11	gil2493127	V-type proton ATPase subunit B 1	99	3	7	54798	5.24	Trpotr	-0.244	0
12	gil166627	nucleotide-binding subunit of vacuolar ATPase [Arabidopsis]	99	3	10	54819	4.98	Trpotr	-0.227	0
13	gil26985221	non-cell-autonomous heat shock cognate protein 70	98	6	10	71790	5.1	ProDsSt	-0.434	0
14	gil134145	stem 28 kDa glycoprotein precursor	97	6	17	29218	8.75	ProDsSt	-0.384	1
15	gil533692	protease inhibitor [Glycine max]	95	3	30	9279	9.06	DsDf	0.028	1
16	gil18772	trypsin inhibitor subtype B [Glycine max]	93	4	22	24293	4.98	DsDf	-0.129	1
17	gil1173642	lipxygenase	88	4	7	96517	5.99	PriMtb	-0.324	0
18	gil40287540	ly200 protein [Capsicum annuum] (Ribosomal L32)	84	2	18	15704	10.65	ProSyn	-0.714	0
19	gil118483741	unknown [Populus trichocarpa]	84	2	13	17675	9.04	Unclass	-0.205	0

20	gil32401377	ribosomal protein L19 [Triticum aestivum]	79	3	13	24686	11.05	ProSyn	-1.079	0
21	gil47026900	ribosomal protein L19 [Hyacinthus orientalis]	79	3	14	23905	11.23	ProSyn	-1.068	0
22	gil114522	ATP synthase subunit alpha	79	3	9	54649	5.75	Trpotr	-0.044	0
23	gil115444549	Os02g0175400 [Oryza sativa] (Vacuolar proton-ATPase)	77	7	14	68833	5.37	Trpotr	-0.201	0
24	gil82568440	Polyubiquitin [Raphidiophrys contractilis]	76	8	21	19268	5.81	ProDsSt	-0.442	0
25	gil9651843	vacuolar ATP synthase subunit B [Emericella nidulans]	74	2	8	43702	5.53	Trpotr	-0.319	0
26	gil169858607	hypothetical protein CC1G_12318	74	2	5	58015	5.36	Unclass	-0.303	0
27	gil22742	pseudo-atpA [Glycine max]	73	4	14	34899	5.62	Trpotr	0.095	2
28	gil218228	ras-related GTP binding protein [Oryza sativa]	73	2	18	24080	5.37	Sgnl	-0.351	0
29	gil110669124	V-type ATP synthase subunit B	67	2	5	52697	4.14	Trpotr	-0.405	0
30	gil189380223	heat shock protein 70 [Camellia sinensis]	67	6	10	75582	5.54	ProDsSt	-0.272	0
31	gil414977	51 kDa seed maturation protein (Lea protein)	67	4	5	51065	6.65	ProDsSt	-1.227	1
32	gil13016808	P-type H ⁺ -ATPase [Vicia faba]	67	5	4	105142	6.62	Trpotr	0.039	8
33	gil2605911	plasma membrane H ⁺ -ATPase [Kosteletzkya virginica]	67	4	14	26667	7.23	Trpotr	-0.344	0
34	gil5669151	plasma membrane proton ATPase [Nicotiana plumbaginifolia]	66	4	6	105132	6.48	Trpotr	0.115	8
35	gil66132297	plasma membrane H ⁺ ATPase [Lupinus albus]	65	6	7	105083	6.54	Trpotr	0.058	10
36	gil33440146	P-type H ⁺ -ATPase [Vicia faba]	65	5	23	26838	7.14	Trpotr	-0.348	0
37	gil34539397	F1-ATPase alpha subunit [Pandanus copelandii]	65	2	7	44921	8.26	Trpotr	-0.003	0
38	gil27461619	ATPase F1 alpha subunit [Xyris bicephala]	65	2	7	44865	6.55	Trpotr	-0.03	0
39	gil115464309	Os05g0460000 [Oryza sativa] (heat shock protein)	64	5	8	71190	5.1	ProDsSt	-0.42	0

40	gil123593	heat shock 70 kDa protein	64	4	11	70901	5.22	ProDsSt	-0.419	0
41	gil18071348	putative GTP-binding protein [Oryza sativa]	63	2	5	68217	8.39	Sgnl	-0.355	0
42	gil475600	BiP isoform B	60	6	11	73674	5.11	ProDsSt	-0.428	1
43	gil56554972	heat shock protein 70 [Medicago sativa]	57	4	8	71351	5.08	ProDsSt	-0.423	0
44	gil3023068	heat shock 70kD protein [Mesembryanthemum crystallinum]	57	2	29	15216	5.36	ProDsSt	-0.114	0
45	gil115583757	heat shock protein 70 [Cryptosporidium baileyi]	57	2	8	70179	5.4	ProDsSt	-0.439	0
46	gil39944360	hypothetical protein MGG_04191 [Magnaporthe grisea 70-15]	57	2	5	72561	5.89	Unclass	-0.403	0
47	gil758250	H ⁺ -transporting ATPase [Phaseolus vulgaris]	56	6	5	104776	6.77	Trpotr	0.075	10
48	gil114332	Plasma membrane ATPase 1	56	5	6	105379	6.41	Trpotr	0.14	8
49	gil7378773	H ⁺ -ATPase [Medicago truncatula]	56	4	18	29436	8.49	Trpotr	-0.39	0
50	gil12697490	p-type H ⁺ -ATPase [Sesbania rostrata]	56	4	20	27087	6.64	Trpotr	-0.324	0
51	gil49257109	protein disulfide isomerase-like protein [Glycine max]	56	4	7	58963	5.06	ProDsSt	-0.431	1
52	gil31580855	plasma membrane H ⁺ -ATPase [Sesbania rostrata]	55	7	9	105806	5.93	Trpotr	0.143	8
53	gil27371880	plasma membrane H+ ATPase [Populus alba]	53	5	26	25717	8.94	Trpotr	-0.253	0
54	gil62433284	BiP [Glycine max]	53	5	11	73834	5.06	ProDsSt	-0.415	1
55	gil157356338	unnamed protein product [Vitis vinifera]	53	5	6	102625	6.27	Unclass	0.14	8
56	gil3023194	14-3-3-like protein A (SGF14A)	52	3	12	29145	4.72	Sgnl	-0.432	0
57	gil147773781	hypothetical protein [Vitis vinifera]	51	4	5	98683	6.08	Unclass	0.201	10
58	gil157327742	unnamed protein[Vitis vinifera]	51	3	5	68034	5.62	Unclass	0.052	2
59	gil12230460	ATPase 7, plasma membrane-type (Proton pump 7)	51	3	6	105909	6.38	Trpotr	0.056	7
60	gil44662864	ribosomal protein S6 [Glycine max]	50	2	11	28323	10.71	ProSyn	-0.77	0
61	gil87240515	ribosomal protein S6 [Medicago truncatula]	50	2	11	28430	10.76	ProSyn	-0.842	0

62	gil6911549	heat shock protein 70 [Cucumis sativus]	49	3	7	73599	5.08	ProDsSt	-0.482	1
63	gil7592732	plasma membrane H ⁺ -ATPase [Nepenthes alata]	48	2	10	22039	8.92	Trpotr	-0.302	0
64	gil134146	stem 31 kDa glycoprotein precursor	48	2	13	29433	6.72	ProDsSt	-0.341	1
65	gil157345594	unnamed protein [Vitis vinifera]	48	4	5	105269	6.45	Unclass	0.159	9
66	gil16223	calmodulin [Arabidopsis thaliana]	48	2	10	16882	4.18	Sgnl	-0.626	0
67	gil2654122	ribosomal protein L23 [Arabidopsis thaliana]	47	4	25	17462	10.2	ProSyn	-0.778	0
68	gil29838374	proton pump protein [Citrus limon]	46	3	11	26883	6.6	Trpotr	-0.204	0
69	gil147845490	hypothetical protein [Vitis vinifera]	46	4	15	23826	10.84	Unclass	-0.827	0
70	gil147800127	hypothetical protein [Vitis vinifera]	45	4	6	105610	6.56	Unclass	0.079	9
71	gil5762251	Csf-1 [Cucumis sativus]	44	3	23	15989	10.13	ProSyn	-0.459	0
72	gil118485504	unknown [Populus trichocarpa]	44	2	16	18438	10.23	Unclass	-0.451	0
73	gil134598	superoxide dismutase [Cu-Zn] 4AP	43	2	6	15175	5.64	DsDf	-0.182	0
74	gil38327504	ribosomal protein L3 [Lycopersicon esculentum]	41	5	11	44836	10.1	ProSyn	-0.583	0

Score greater than 40 was significant (P<0.05).

Cov.: coverage from MS data; MP: number of matched peptides from MS data; GRAVY: grand average of hydropathy; TM: transmembrane.

Matched peptide number less than 2 and coverage less than 5% were excluded.

PiMtb: Primary metabolism; Engy: Energy; CelGrw: Cell growth/division; Trcrpt: Transcription; ProSyn: Protein synthesis; ProDsSt:

Protein destination/storage; Trpotr: Transporters; ICTrf: Intracellular traffic; CelStr: Cell structure; Sgnl: Signal transduction; DsDf:

Disease/defense; ScdMtb: Secondary metabolism; Unclr: Unclear classification; Unclass: Unclassified.

Supplemental Table 3. Identification of Soybean Plasma Membrane Proteins using nanoLC MS/MS-Based Proteomics and Soybean Genome Sequence Database

No.	Accession No.	Protein name	Score (*)	MP	Cov. (%)	Theoretical		Class	GRAVY value	Number of TM helices
						Mr	pI			
1	Gm0090x00044 (BAE71278)	fasciclin-like arabinogalactan protein FLA2	211 (492)	6	26	43764	6.41	CelStr	-0.032	1
2	Gm0063x00346.1 (ABA95501)	heat shock cognate 70 kDa protein	206 (1066)	9	16	67939	4.98	ProDsSt	-0.369	0
3	Gm0025x00312 (CAA80491)	lea protein	194 (730)	6	12	49484	7.08	ProDsSt	-1.223	1
4	Gm0253x00028 (AAS57913)	70 kDa heat shock cognate protein 2	168 (360)	6	32	20335	5.89	ProDsSt	-0.45	0
5	Gm0078x00166 (AAR08912)	plant defensin precursor	155 (74.3)	15	44	8877	9.49	DsDf	0.116	0
6	Gm0098x00335 (ABA54143)	glycine-rich protein	151 (139)	4	18	19150	6.28	Trcrpt	-0.721	0
7	Gm0146x00211.2 (CAA11075)	acid phosphatase	150 (304)	6	32	28997	6.34	Sgnl	-0.385	0
8	Gm0041x00080.1 (Q9FUL4)	60S ribosomal protein L24	142 (197)	4	24	17912	10.16	ProSyn	-0.799	0
9	Gm0030x00447 (ABK94713)	unknown	142 (242)	8	29	34559	5.03	Unclass	-0.924	0
10	Gm0021x00168 (ABV27484)	fasciclin-like arabinogalactan protein 13	139 (395)	7	23	39046	6.08	CelStr	0.098	1
11	Gm0070x00278 (ABK94713)	unknown	138 (260)	8	21	35334	5.08	Unclass	-0.924	0
12	Gm0112x00186 (AAS57912)	70 kDa heat shock cognate protein 1	134 (1140)	6	10	71442	5.10	ProDsSt	-0.426	0
13	Gm0107x00278.2 (P15490)	stem 28 kDa glycoprotein	128 (528)	6	17	29218	8.75	ProDsSt	-0.384	1
14	Gm0136x00056	peroxidase precursor	127	2	10	36410	9.84	DsDf	-0.302	1

	(AAR31108)		(431)								
15	Gm0215x00082 (P13548)	V-type proton ATPase catalytic subunit A	125 (1194)	13	27	69021	5.35	Trpotr	-0.189	0	
16	Gm0001x00072.1 (NP_189215)	dihydrolipoyllysine- residue acetyltransferase	121 (538)	6	16	49051	8.78	PriMtb	0.045	0	
17	Gm0021x00405.1 (ABO61030)	vacuolar H ⁺ -ATPase B subunit	120 (944)	4	12	54292	4.95	Trpotr	-0.249	0	
18	Gm0026x00399 (CAC29436)	P-type H ⁺ -ATPase	117 (1675)	9	10	104829	6.61	Trpotr	0.039	8	
19	Gm0041x00128 (AAZ20285)	ubiquitin fusion protein	117 (259)	8	28	14892	9.94	ProSyn	-0.638	0	
20	Gm0015x00799 (AAM67267)	dihydrolipoamide succinyltransferase	114 (543)	5	13	50522	9.25	Engy	-0.255	0	
21	Gm0086x00087 (BAC77531)	plasma membrane H ⁺ -ATPase	112 (1581)	6	9	97394	6.83	Trpotr	0.076	10	
22	Gm0026x00621 (ABK93997)	Unknown	107 (256)	2	11	28488	9.87	Unclass	-0.28	1	
23	Gm0088x00167.1 (ABX60411)	lipoxygease-like protein	104 (1583)	3	6	94454	6.13	PriMtb	-0.338	0	
24	Gm0134x00170 (AAC49159)	lipxygenase	104 (635)	5	13	60222	5.69	PriMtb	-0.324	0	
25	Gm0099x00162 (CAN66258)	hypothetical protein	103 (317)	2	13	17923	9.05	Unclass	-0.328	0	
26	Gm0025x00841 (CAB69824)	plasma membrane H ⁺ ATPase	102 (1584)	9	11	105418	6.28	Trpotr	0.111	8	
27	Gm0158x00064 (CAB69824)	plasma membrane H ⁺ ATPase	102 (1554)	11	14	105506	6.39	Trpotr	0.111	8	
28	Gm0076x00486 (CAO40052)	unnamed protein product	101 (334)	4	23	24652	11.45	Unclass	-1.119	0	
29	Gm0262x00016 (YP_538770)	ATP synthase CF1 alpha subunit	96 (900)	4	11	55760	5.15	Engy	-0.045	0	
30	Gm0061x00070 (AAC97524)	protease inhibitor	95 (106)	4	31	9266	9.16	DsDf	0.028	1	
31	Gm0088x00166	lipxygenase-B	94	3	5	96752	5.78	PriMtb	-0.383	0	

	(2IUJ_A)		(1588)								
32	Gm0035x00128 (CAO70326)	unnamed protein product	91 (209)	2	10	31102	5.93	Unclass	-0.234	0	
33	Gm0026x00182.3 (BAB47119)	14-3-3 protein	90 (306)	5	31	20099	5.41	Sgnl	-0.545	0	
34	Gm0014x00048 (CAA59799)	H ⁺ -transporting ATPase	85 (1580)	6	8	97432	7.64	Trpotr	0.075	10	
35	Gm0007x00137 (ABK93702)	Unknown	84 (227)	2	22	15676	10.70	Unclass	-0.791	0	
36	Gm0070x00240.1 (AAS47511)	ribosomal protein S6	80 (390)	3	18	28512	10.71	ProSyn	-0.77	0	
37	Gm0078x00363 (Q39821)	dynamamin-related protein 12A	80 (1163)	3	6	68667	8.04	ICTrf	-0.297	0	
38	Gm0078x00382 (AAB86942)	HSC70-cognate binding protein precursor	79 (1186)	7	11	73822	5.08	ProDsSt	-0.434	1	
39	Gm0085x00010 (ABA40467)	glycoprotein-like protein	78 (229)	5	34	15391	10.42	Unclr	-0.231	0	
40	Gm0191x00013 (CAN72815)	hypothetical protein	78 (199)	7	24	20247	9.46	Unclass	-1.127	0	
41	Gm0176x00072 (CAO18150)	unnamed protein product	78 (112)	2	21	12244	6.15	Unclass	-0.672	0	
42	Gm0025x00326 (XP_001950434)	Polyubiquitin	76 (273)	4	16	17124	5.10	ProDsSt	-0.481	0	
43	Gm0022x01040 (NP_172936)	GTP binding /GTPase	75 (1031)	4	9	69308	7.72	ICTrf	-0.36	0	
44	Gm0003x00249 (ABK93702)	Unknown	74 (232)	3	23	15722	10.72	Unclass	-0.791	0	
45	Gm0144x00053 (AAN03472)	GTP-binding protein	73 (422)	5	24	24163	5.87	Sgnl	-0.252	0	
46	Gm0015x00457 (CAO69125)	unnamed protein product	73 (374)	2	12	24179	6.43	Unclass	-0.192	0	
47	Gm0092x00134 (BAD95470)	BiP	70 (1160)	6	8	100036	5.36	ProDsSt	-0.415	1	
48	Gm0126x00173	ribosomal protein S6	70	3	18	28480	10.71	ProSyn	-0.77	0	

	(AAS47511)		(389)							
49	Gm0047x00212 (CAB69824)	plasma membrane H+ ATPase	70 (1096)	5	11	73051	7.22	Trpotr	0.111	8
50	Gm0107x00224 (CAO69559)	unnamed protein product	65 (387)	3	19	28392	9.99	Unclass	-0.558	0
51	Gm0003x00462 (BAE71282)	putative receptor-like GPI-anchored protein 2	65 (405)	2	7	41166	6.99	Sgnl	-0.089	0
52	Gm0002x00082 (CAN83920)	hypothetical protein	63 (264)	2	15	15940	10.18	Unclass	-0.431	0
53	Gm0192x00030 (NP_192979)	copper ion binding protein	61 (397)	4	10	29052	9.71	CelGrDv	-0.236	0
54	Gm0065x00031.3 (BAD24712)	protein disulfide isomerase-like protein	60 (1029)	4	7	58963	5.06	ProDsSt	-0.431	1
55	Gm0030x00211 (ABK92614)	Unknown	58 (355)	4	23	21381	10.44	Unclass	-0.783	0
56	Gm0016x00130 (AAC49690)	Prohibitin	58 (402)	2	10	30373	7.93	Unclass	-0.011	0
57	Gm0044x00036 (ABN08356)	heat shock protein Hsp70	57 (695)	2	5	55602	6.25	ProDsSt	-0.278	0
58	Gm0061x00021.1 (CAO64572)	unnamed protein product	56 (262)	4	20	19207	11.61	Unclass	-0.802	0
59	Gm0002x00478 (P17928)	calmodulin	56 (297)	2	10	16908	4.12	Sgnl	-0.619	0
60	Gm0018x00067.1 (O49884)	60S ribosomal protein L30	55 (226)	3	27	12565	9.61	ProSyn	-0.252	0
61	Gm0021x00744 (O22644)	60S ribosomal protein L23A	54 (226)	4	25	17517	10.27	ProSyn	-0.649	0
62	Gm0107x00278.1 (P15490)	Stem 28 kDa glycoprotein precursor	54 (405)	4	10	28727	9.15	ProDsSt	-0.384	1
63	Gm0021x00860 (Q96450)	14-3-3-like protein A	53 (459)	3	12	29160	4.72	Sgnl	-0.432	0
64	Gm0049x00188.1 (ABK92923)	Unknown	53 (317)	2	13	21407;	5.87	Unclass	-0.152	1
65	Gm0022x00132	unnamed protein	52	3	13	25745;	10.20	Unclass	-0.601	0

	(CAO15090)		(318)								
66	Gm0054x00033 (ABK93076)	Unknown	52 (308)	3	16	25915	10.15	Unclass	-0.645	0	
67	Gm0203x00030 (ABK92585)	Unknown	51 (166)	4	22	21698	8.43	Unclass	-0.727	0	
68	Gm0119x00226 (AAS47511)	ribosomal protein S6	50 (363)	2	11	28380	10.71	ProSyn	-0.77	0	
69	Gm0006x00174 (AAL17949)	type IIB calcium ATPase	50 (1636)	5	5	114629	5.82	Trpotr	0.123	8	
70	Gm0053x00331 (NP_195336)	60S ribosomal protein L8 (RPL8C)	49 (481)	4	16	28430	10.81	ProSyn	-0.454	0	
71	Gm0157x00003 (CAD12839)	putative metallophosphatase	49 (1092)	3	6	71090	5.80	PriMtb	-0.452	1	
72	Gm0113x00272.1 (P10743)	stem 31 kDa glycoprotein	48 (500)	2	13	29433	6.72	ProDsSt	-0.341	1	
73	Gm0131x00027 (CAN63848)	hypothetical protein	47 (724)	7	15	44642	10.17	Unclass	-0.64	0	
74	Gm0138x00202.1 (NP_190470)	breast basic conserved 1	46 (353)	5	22	23806	11.02	ProSyn	-0.924	0	
75	Gm0096x00299.1 (P30707)	60S ribosomal protein L9	43 (341)	2	15	21786	9.45	ProSyn	-0.268	0	
76	Gm0041x00574.1 (Q7M1R5)	superoxide dismutase [Cu-Zn]	43 (284)	2	6	15298	5.27	DsDf	-0.172	0	
77	Gm0176x00036 (BAE71215)	60S ribosomal protein L1	43 (677)	4	12	44691	10.48	ProSyn	-0.438	0	
78	Gm0073x00126 (CAO70517)	unnamed protein product	42 (123)	2	12	19329	5.14	Unclass	0.141	0	
79	Gm0022x00644.2 (Q6E2Z6)	1-Cys peroxiredoxin	42 (398)	2	15	24542	6.44	DsDf	-0.489	0	
80	Gm0098x00338 (AAF06346)	SCUTL1	42 (384)	2	13	24877	8.11	Unclr	0.121	0	
81	Gm0112x00189 (Q41350)	osmotin-like protein	41 (387)	2	12	27212	8.13	DsDf	-0.063	0	
82	Gm0052x00582	unnamed protein product	40	3	14	51100	4.72	Unclass	-0.378	0	

	(CAO15467)		(849)								
83	Gm0053x00107 (AAA74208)	protein localized in the nucleoli of pea nuclei	40 (295)	3	10	56047	4.96	Unclr	-1.191	0	
84	Gm0025x00865 (CAO14950)	unnamed protein product	40 (348)	4	19	23109	10.37	Unclass	-0.722	0	
85	Gm0013x00154 (NP_195272)	leucine-rich repeat family protein	39 (475)	2	6	36490	5.94	Unclr	-0.265	0	
86	Gm0006x00098 (AAF31643)	Actin	39 (749)	3	9	41865	5.31	CelStr	-0.17	0	
87	Gm0072x00108 (CAB85495)	H ⁺ -ATPase	38 (1499)	4	5	103995	6.52	Trpotr	0.093	8	
88	Gm0052x00090 (CAA90082)	small GTP-binding protein	37 (356)	3	19	24059	7.66	Sgnl	-0.318	0	
89	Gm0041x00538 (Q8RVH5)	basic 7S globulin 2	37 (720)	2	5	40682	8.45	ProDsSt	-0.078	0	
90	Gm0030x00460 (ACF74333)	putative L24 ribosomal protein	37 (218)	2	8	16688	10.92	ProSyn	-0.819	0	
91	Gm0047x00072 (ABK06440)	activated protein kinase	37 (539)	2	5	40160	6.84	Sgnl	-0.34	0	
92	Gm0068x00141 (BAE71239)	calcium dependent protein kinase	37 (874)	3	10	59083	5.82	Sgnl	-0.476	0	
93	Gm0025x00102 (BAE71239)	calcium dependent protein kinase	37 (870)	3	10	60123	5.80	Sgnl	-0.476	0	
94	Gm0070x00480 (NP_172964)	ubiquinol-cytochrome C reductase complex	37 (138)	2	33	8394	7.57	Engy	-0.632	0	
95	Gm0026x00589 (CAO43886)	unnamed protein product	37 (301)	2	19	24729	6.28	Unclass	-0.011	0	
96	Gm0022x00946 (NP_564528)	RKL1 (Receptor-like kinase 1)	37 (687)	3	7	70731	6.06	Sgnl	-0.19	2	
97	Gm0075x00380 (BAG09368)	peroxisomal voltage- dependent anion-selective channel protein	37 (543)	2	8	29738	8.57	Trpotr	-0.19	0	
98	Gm0088x00170.1 (ABX60408)	lipoxygenase L-3	36 (1484)	4	7	84657	5.84	PriMtb	-0.346	0	

99	Gm0146x00090 (ABX60408)	lipoxygenase L-3	36 (1287)	3	7	97082	6.7	PriMtb	-0.346	0
100	Gm0013x00528 (ABX57816)	alpha tubulin	36 (831)	2	6	50295	4.92	CelStr	-0.188	0
101	Gm0026x00412 (NP_194843)	glycosyl hydrolase family 17 protein	35 (665)	2	5	51143	5.98	PriMtb	0.061	1
102	Gm0023x00035.1 (P25698)	elongation factor 1-alpha	35 (895)	2		49667	9.14	ProSyn	-0.35	0
103	Gm0107x00187 (NP_191432)	vacuolar ATP synthase subunit D	34 (387)	2	9	28975	9.62	Trpotr	-0.243	0
104	Gm0077x00288 (AAX86048)	tubulin B4	33 (844)	3	11	51198	4.70	CelStr	-0.364	0
105	Gm0107x00302 (ABK93022)	Unknown	32 (254)	2	18	16878	10.70	Unclass	-0.675	0
106	Gm0109x00094 (ABK95474)	Unknown	31 (261)	2	12	34839	6.65	Unclass	-1.208	0
107	Gm0076x00259 (ABD32399)	hypothetical protein	31 (245)	2	5	22324	4.99	Unclass	0.058	1
108	Gm0021x00433 (CAA66481)	Trcrpt factor	30 (207)	2	8	34866	6.84	Trcrpt	-1.259	0
109	Gm0119x00135 (ABK93590)	Unknown	30 (384)	3	11	23952	10.26	Unclass	-0.373	0
110	Gm0053x00130 (AAL51087)	Cyclophilin	28 (321)	2	16	18441	8.70	ProDsSt	-0.241	0
111	Gm0164x00142 (CAN59843)	hypothetical protein	28 (424)	3	19	27182	9.18	Unclass	-0.101	0
112	Gm0152x10033 (NP_565484)	protein binding / protein Trpotrstructural molecule	28 (199)	2	5	35501	5.78	ICTrf	-1.298	0
113	Gm0082x00051 (CAO69802)	unnamed protein product	28 (219)	2	10	26630	8.56	Unclass	0.055	0
114	Gm0042x00145 (ABK92614)	Unknown	27 (159)	2	33	10060	10.26	Unclass	-0.783	0
115	Gm0038x00256.1 (BAG09380)	peroxisomal 3-ketoacyl-CoA thiolase precursor	27 (591)	2	14	36688	7.52	PriMtb	-0.027	0

116	Gm0098x00268 (AAX94775)	Cyclophilin	26 (310)	2	18	18343	7.68	ProDsSt	-0.191	0
117	Gm0013x00874 (ABK94712)	Unknown	26 (234)	2	9	21942	4.61	Unclass	0.038	1
118	Gm0004x00484 (AAQ87021)	VDAC1.3	24 (510)	2	11	29771	7.07	Trpotr	-0.151	0
119	Gm0010x00270 (AAO49473)	serine/threonine kinase	23 (274)	2	15	16544	4.73	Sgnl	-0.413	0
120	Gm0041x00006 (Q9M5Z9)	40S ribosomal protein S23	22 (286)	3	29	15834	10.37	ProSyn	-0.563	0
121	Gm0037x00027 (ABS50097)	ribosomal protein S6	22 (363)	2	9	28243	10.71	ProSyn	-0.821	0
122	Gm0052x00448 (ABQ63097)	photosystem I subunit PsaD	22 (366)	2	5	23046	9.63	Engy	-0.441	0
123	Gm0013x00492 (ACF74333)	L24 ribosomal protein	22 (223)	2	8	16720	11.02	ProSyn	-0.819	0
124	Gm0168x00069 (NP_182229)	serine/threonine protein kinase	21 (537)	2	7	36600	5.94	Sgnl	-0.338	0

Score greater than 20 was significant ($P < 0.05$).

(*): Score in parenthesis indicates the protein score in BLAST search.

Cov.: coverage from MS data; MP: number of matched peptides from MS data; GRAVY: grand average of hydropathy; TM: transmembrane.

Matched peptide number less than 2 and coverage less than 5% were excluded.

PiMtb: Primary metabolism; Engy: Energy; CelGrw: Cell growth/division; Trcrpt: Transcription; ProSyn: Protein synthesis; ProDsSt:

Protein destination/storage; Trpotr: Transporters; ICTrf: Intracellular traffic; CelStr: Cell structure; Sgnl: Signal transduction; DsDf:

Disease/defense; ScdMtb: Secondary metabolism; Unclr: Unclear classification; Unclass: Unclassified.