

Supplemental Table I - Summary of identified tissue specific *Medicago truncatula* proteins with supporting analytical rigor

Tissue	Spot #	PMFQ	% Relative Abundance	Gel MW (kD)	Gel pI	Identification/Comment	Accession Number	Databases	LC/MS/MS score	# Peptides Matched	m/z Accuracy ± SD (ppm)	% Protein Coverage	Theoret MW (kD)	Theoret pI	Organism Matched	Function
lvs	35	5	0.095	92	5.5	er ATPase (CDC48-like protein) ^b	NP190891	N		11	19±34	17	90	5.0	Arabidopsis thaliana	Energy
lvs	39	5	0.170	91	5.6	DNA mismatch repair protein ^b	O66652	S		8	35±40	15	98	5.9	Aquifex aeolicus	Cell growth/division
lvs	47	4	0.306	78	6.5	rubisco	BE420942	E/Hv, (E)		7	47±50	18	50	6.8	Centropodia glauca	Energy
lvs	52	3	0.098	75	6.6	rubisco	BE420942	E/Hv		5	20±23	16	50	6.8	Centropodia glauca	Energy
lvs	51	5	0.110	75	6.2	F23N19.10, TPR repeat protein	AW694998	E/Mt, (E)	513	4	12±10	13	64	5.8	Arabidopsis thaliana	Protein destination/storage
lvs	63	4	0.145	62	4.6	cell division prt. FTSK homolog ^b	P45264	S, N		8	5±6	10	59	5.4	Haemophilus influenza	Cell growth/division
lvs	78	5	1.462	57	4.8	rubisco	BAA20039	N, S, E/Hv		11	38±14	24	48	6.4	Chrysosplenium album	Energy
lvs	82	4	9.495	57	5.2	rubisco	AAF97663	N, S, E/Hv		9	28±30	24	50	6.3	Narcissus elegans	Energy
lvs	84	5	4.487	57	6.6	rubisco	AAF15326	N, S, E/Hv		9	39±33	21	50	6.5	Teramnus labialis	Energy
lvs	92	3	2.080	56	4.2	rubisco	X69528	N	389				53	6.1	Casuarina cunninghamiana	Energy
lvs	98	4	0.252	55	7.3	transcription factor ^b	BF004459	(E)		5	3±4 ^c	15	40	6.7	Vicia faba	Transcription
lvs	105	3	0.208	53	6.1	s-adenosylmethionine synthetase	BG581653	E/Mt, N, S		12	39±47	44	43	5.7	Elaeagnus embellata	Metabolism
lvs	108	5	0.250	52	6.4	s-adenosylmethionine synthetase	P50303	S		8	36±44	29	40	6.2	Actinidia chrysantha	Metabolism
lvs	111	5	0.625	49	5.2	rubisco activase	AF251264	N	372				48	6.9	Triticum aestivum	Energy
lvs	113 ^a	5	0.639	49	5.1	ATP synthase beta chain	NP077960	N		8	41±58	29	51	5.4	Ureaplasma urealyticum	Energy
lvs	113 ^a	5	0.639	49	5.1	rubisco activase	Q42450	S, E/Sb		6	21±33	22	47	7.6	Sorghum bicolor	Energy
lvs	124	5	2.018	48	5.6	rubisco activase	AAG61120	N, S		9	38±15	24	48	5.5	Gossypium hirsutum	Energy
lvs	126	5	1.499	48	5.7	rubisco activase	AAG61120	N, S		8	19±12	20	48	5.5	Gossypium hirsutum	Energy
lvs	123	5	0.206	48	8.3	aminomethyl transferase, mito. Precursor ^b	BF521422	E/Mt, (E)		12	33±23	38	44	8.8	Pisum sativum	Metabolism
lvs	128	5	0.199	48	8.9	aminomethyl transferase, (T protein) ^b	P49364	N, S, E/M.t,		11	17±29	29	44	8.8	Pisum sativum	Metabolism
lvs	136	4	0.142	46	6.9	fructose biphosphate aldolase	BI309468	(E), N, S, E/Mt		9	6±8 ^c	45	38	6.9	Pisum sativum	Energy
lvs	138	5	0.386	46	6.6	spermine synthase	BE204391	E/Mt		5	22±34	12	38	5.3	Arabidopsis thaliana	Metabolism
lvs	139	3	0.089	46	4.7	putative Arabidopsis thaliana protein ^b	AW685607	E/Mt		5	45±22	23	25	4.5	Arabidopsis thaliana	Unclear
lvs	141	4	0.177	45	4.2	ankyrin repeat protein	AL388433	E/Mt		5	60±55	30	37	4.2	Nicotiana tabaccum	Protein destination/storage
lvs	144 ^a	4	0.148	44	7.3	glyceraldehyde-3-phosphate dehydrogenase	BF003409	E/Mt, (E)		10	39±44	37	37	6.7	Pisum sativum	Energy
lvs	144 ^a	4	0.148	44	7.3	possible tartrate dehydrogenase	P70792	S, N		6	41±53	17	39	5.3	Arabidopsis thaliana	Energy
lvs	149 ^a	5	0.081	43	7.0	glyceraldehyde-3-phosphate dehydrogenase	BG453922	(E)		7	5±8 ^c	36	37	7.1	Pisum sativum	Energy
lvs	149 ^a	5	0.081	43	7.0	tartrate dehydrogenase	P70792	N, S		6	40±45	16	39	5.3	Rhizobium vitis	Energy
lvs	155	5	0.092	42	4.1	Leu2 (3-isopropyl malate dehydrogenase) ^b	P18120	N, S		7	42±54	27	43	5.7	Yarrowia lipolytica	Energy
lvs	158	5	0.219	41	6.6	malate dehydrogenase	T09286	N, E/Mt, (E)		14	5±6	71	36	8.8	Medicago sativa	Energy

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Mt=M. truncatula, Hv=H. vulgare, Sb=S. bicolor, Le=L. esculentum

PMQ=peptide mass fingerprint quality

a=multiple ids/spot

b=unique ids/tissue, c=Intellical

Supplemental Table I is a summary of the proteins identified from specific tissues of *Medicago truncatula* and the supporting data composing the analytical rigor of the identifications. These data are separated according to tissue and include an assigned protein spot number (see Figure 1), an arbitrary peptide mass fingerprint data quality (PMFQ, see Materials and Methods) score of 1 to 5 with 5 being best, percent relative abundance of each protein, experimental M_r and pI, database accession number of the best match and databases that yielded concurrent identifications, LC/MS/MS data for select proteins, number of peptides matched, mass/charge (m/z) accuracy and standard deviation of peptides matched, percent protein coverage, theoretical M_r and pI, the organism to which the matching protein was identified through similarity, and protein function.

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lvs	196 ^a	5	0.195	36	6.6	ascorbate peroxidase	BG587041	(E)		5	4±6 ^c	44	46	8.5	Spinacia oleracea	Disease/defense
lvs	187	5	0.465	36	5.3	oxygen evolving enhancer protein	P14226	S, N, E/Mt, (E)		7	23±7	36	35	6.2	Pisum sativum	Energy
lvs	191	4	1.852	36	5.4	oxygen evolving enhancer protein	P14226	S, N, E/Mt, (E)		9	12±17	36	35	6.3	Pisum sativum	Energy
lvs	188	5	0.138	36	8.5	remorin ²	BG588209	(E)		7	2±2 ^c	38	22	5.7	Lycopersicon esculentum	Signal transduction
lvs	189	5	0.062	36	8.5	remorin ²	BG588209	(E)		8	7±8 ^c	52	22	5.7	Lycopersicon esculentum	Signal transduction
lvs	196 ^a	5	0.195	35	6.6	rubisco	AAC35045	N, S		8	13±17	21	49	6.3	Cleistes sp. chase O-430	Energy
lvs	206 ^a	5	0.115	34	7.1	mitotic cyclin B1-1 ^b	AAC24244	N		8	49±34	39	49	7.6	Lupinus luteus	Cell growth/division
lvs	206 ^a	5	0.115	34	7.1	ATP synthase ^b	BG582863	(E)		9	8±10 ^c	31	27	7.0	Gossypium hirsutum	Energy
lvs	205	3	0.336	34	5.3	oxygen evolving enhancer protein 1	BG449793	(E)		5	2±2 ^c	25	35	6.6	Pisum sativum	Energy
lvs	219	4	0.238	33	6.6	cystathione-B-lyase ^b	P53780	S		6	27±38	13	50	6.9	Arabidopsis thaliana	Metabolism
lvs	222	5	0.093	32	7.0	chloro mem assoc 30 kD protein/transit pept ^b	AW776774	E/Mt, (E)		9	24±9	29	36	9.5	Pisum sativum	Protein destination/storage
lvs	223	5	0.480	32	4.4	RNA-binding protein	BF641320	E/Mt, (E)		8	4±3	24	32	4.8	Mesembryanthemum cryst.	Transcription
lvs	238	5	0.184	31	5.9	L-ascorbate peroxidase	P48534	N, S, E/Mt, (E)		6	10±16	30	27	5.5	Pisum sativum	Disease/defense
lvs	241	5	0.439	31	6.1	ascorbate peroxidase	AAL15164	N, S, (E)		6	11±12	40	20	5.3	Medicago sativa	Disease/defense
lvs	237	4	0.375	31	6.7	acid phosphatase	BG588612	(E)		8	8±8 ^c	38	30	7.4	Glycine max	Signal transduction
lvs	239	4	0.167	31	6.4	acid phosphatase	BG588612	(E)		11	6±7 ^c	46	30	7.4	Glycine max	Signal transduction
lvs	251	4	0.126	30	6.3	triose phosphate isomerase, cytosolic	BF642390	E/Mt, (E)		10	16±16	50	28	5.7	Coptis japonica	Energy
lvs	250	4	0.094	30	7.2	ABC transporter ^b	NP488322	N		7	41±46	25	30	9.0	Nostoc sp. PCC 7120	Transporters
lvs	258 ^a	5	0.133	29	6.4	pyrimidine-nucleoside phosphorylase ^b	P39N9	S		8	30±30	24	46	5.1	Bacillus subtilus	Metabolism
lvs	263	5	0.294	29	6.0	chaperonin 21 precursor ^b	AW775755	E/Mt		6	44±57	28	27	7.4	Lycopersicon esculentum	Protein destination/storage
lvs	265	5	0.350	29	6.2	chaperonin 21 precursor ^b	AW776607	E/Mt, (E)		5	3±4	44	26	7.4	Arabidopsis thaliana	Protein destination/storage
lvs	261	4	0.489	29	7.6	patatin-like protein ^b	AAF98369	N		5	53±68	24	45	7.7	Nicotiana tabacum	Protein destination/storage
lvs	258 ^a	5	0.133	29	6.4	transcription factor VSE-1 ^b	CAA05898	N		6	36±21	27	48	9.0	Lycopersicon esculentum	Transcription
lvs	270	5	0.208	28	5.4	oxygen evolving enhancer protein	P16059	S, E/Mt, (E)		7	6±7	50	28	8.3	Pisum sativum	Energy
lvs	280	5	2.155	27	5.7	oxygen evolving enhancer protein	BF521386	E/Mt, S, (E)		12	36±21	53	28	8.2	Pisum sativum	Energy
lvs	281	5	0.262	27	8.8	plastid specific ribosomal protein ^b	BE318731	(E)		4	6±6 ^c	23	28	8.3	Spinacia oleracea	Protein synthesis
lvs	287	4	0.213	26	6.7	glycine rich cell wall structural protein 2 ^b	AL366848	E/Mt, (E)		8	75±17	43	20	5.9	Nicotiana glauca	Cell structure
lvs	284	5	0.557	26	5.4	oxygen evolving enhancer protein	P16059	S, E/Mt (E)		5	43±56	36	28	8.3	Pisum sativum	Energy
lvs	338	5	0.245	19	4.0	hypothetical protein ^b	NP180029	N		5	58±61	19	28	5.6	Arabidopsis thaliana	Unclear
lvs	363	3	1.989	17	4.5	aspartate 1-decarboxylase precursor ^b	P52999	S		4	15±6	31	14	5.7	Bacillus subtilus	Metabolism
lvs	388	4	0.642	15	6.5	rubisco small subunit	BF520627	E/Mt, (E)		9	32±31	55	20	8.6	Medicago sativa	Energy
lvs	387	5	3.076	15	6.9	rubisco small subunit	BF519126	E/Mt		5	55±67	46	20	8.6	Medicago sativa	Energy

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lvs	397	3	1.244	14	4.1	plastocyanine precursor	AW776926	E/M. t., (E)		7	73 \pm 6	40	10	4.1	Pisum sativum	Energy
lvs	422	4	0.649	8	6.8	photosystem I iron-sulfur protein ^b	NP039445	N, S		8	57 \pm 14	85	9	6.5	Oryza sativa	Energy
stm	5	5	0.375	90	5.3	cell division (valosin containing) protein	P54774	N, S		8	44 \pm 42	10	90	5.2	Glycine max	Cell growth/division
stm	7	4	0.464	70	4.8	heat shock protein 70	1909352A	N, S		10	81 \pm 14	13	75	5.2	Pisum sativum	Protein destination/storage
stm	10	5	0.196	66	6.2	TPR repeat protein	AW694998	(E), E/Mt		7	4 \pm 7 ^c	15	65	6.2	Arabidopsis thaliana	Protein destination/storage
stm	9	4	0.144	66	5.7	heat shock protein 70	P37900	N, S, E/Mt		8	83 \pm 8	13	72	5.8	Pisum sativum	Protein destination/storage
stm	17	4	1.091	57	4.3	rubisco	CAA93074	N, S		8	38 \pm 37	16	52	6.1	Rutidea orientalis	Energy
stm	16	4	0.619	57	3.9	rubisco	P28400	N, S		7	50 \pm 52	16	52	6.1	Dillenia indica	Energy
stm	18 ^a	5	0.578	55	6.9	ATP synthase ^b	CAB85681	N		7	31 \pm 27	25	53	6.3	Thesium humile	Energy
stm	18 ^a	5	0.578	55	6.9	rubisco	P30401	S, N		7	22 \pm 13	19	55	6.2	Cuscuta reflexa	Energy
stm	19	4	0.338	54	8.2	rubisco	P04991	S, N, E/Mt		13	28 \pm 19	34	53	6.1	Medicago sativa	Energy
stm	20	4	3.390	53	6.5	rubisco	AAF97641	N, S, E/Mt		6	46 \pm 33	12	49	6.4	Caliphurria korsakoffii	Energy
stm	22	4	0.228	51	5.4	tubulin alpha chain	Q43473	N, S, E/Mt		13	87 \pm 10	23	50	4.9	Hordeum vulgare	Cell structure
stm	23	5	0.439	51	3.9	26S proteasome AAA-ATPase subunit ^b	BE325937	E/Mt		5	56 \pm 28	14	47	8.9	Arabidopsis thaliana	Protein destination/storage
stm	24	5	0.222	51	5.2	26S proteasome (TAT binding) ^b	NP187204	N, S, E/Mt		7	73 \pm 7	19	47	4.9	Arabidopsis thaliana	Protein destination/storage
stm	26	4	0.858	49	5.9	SAM synthetase	P46611	N, S, E/Mt		7	80 \pm 9	19	43	5.7	Oryza sativa	Metabolism
stm	29	3	0.614	47	5.5	actin	Q96483	N, S, E/Mt		7	28 \pm 18	33	37	5.3	Lycopersicon esculentum	Cell structure
stm	36	5	0.235	43	4.8	ATPase or P loop kinase ^b	NP347611	N		9	44 \pm 52	19	67	7.1	Clostridium acetobutylicum	Energy
stm	37	4	0.804	42	6.9	fructose 1,6 biphosphate aldolase	O65735	N, S, E/Mt		8	53 \pm 17	26	38	6.2	Pisum sativum	Energy
stm	39	4	0.381	41	5.1	adenosine kinase ^b	BF004017	(E)		10	3 \pm 5 ^c	34	38	5.3	Arabidopsis thaliana	Metabolism
stm	40	4	0.375	40	6.5	malate dehydrogenase	BI310064	(E)		6	2 \pm 2 ^c	37	36	6.9	Medicago sativa	Energy
stm	42	4	0.293	39	5.7	annexin ²	T09552	N, E/Mt		6	48 \pm 58	17	35	5.4	Medicago sativa	Cell structure
stm	43	4	0.165	39	5.3	fructokinase	AW584645	E/Mt, (E)		7	21 \pm 28	27	35	5.6	Beta vulgaris	Energy
stm	44	4	0.183	36	8.3	ribose-phosphate pyrophosphokinase ^b	P47304	S		7	39 \pm 53	38	34	7	Mycoplasma aenitalium	Metabolism
stm	45	2	0.388	36	6.7	IFR-like oxidoreductase	BF644624	E/Mt, (E)		5	10 \pm 7	21	34	7	Medicago sativa	Secondary metabolism
stm	48	4	0.390	35	4.6	atran bp1a (Ran binding protein 1 domain) ^b	AW686211	(E)		7	2 \pm 2 ^c	29	26	5	Arabidopsis thaliana	Intracellular traffic
stm	46	3	0.479	35	5.9	cinnamoyl-CoA reductase ^b	BF635045	(E)		7	4 \pm 7 ^c	34	36	5.9	Arabidopsis thaliana	Secondary metabolism
stm	49	3	0.172	35	7.6	G protein beta subunit ^b	Q39836	N, S, E/Mt, (E)	265	4	39 \pm 13	21	36	7.6	Glycine max	Signal transduction
stm	51	4	1.012	33	5.3	oxygen evolving enhancer protein I	P14226	S, N		10	10 \pm 13	34	35	6.2	Pisum sativum	Energy
stm	52	3	0.157	33	6.9	RNA-binding protein-like	NP196048	N		6	28 \pm 36	18	33	9.1	Arabidopsis thaliana	Transcription

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stm	57	4	0.532	31	3.8	ascorbate peroxidase	BG648814	(E)		4	7±9 ^c	30	27	5.8	Pisum sativum	Disease/defense
stm	58	3	0.157	31	7.6	proteasome subunit alpha type 7 (20S)	Q9SXU1	S, N, E/Mt, (E)		5	33±41	20	27	6.9	Pisum sativum	Protein destination/storage
stm	55	5	0.287	31	5.6	SAM:trans-caffeoyl CoA 3-O methyl transf. ^b	T09399	N, E/Mt		10	7±5	37	28	5.6	Medicago sativa	Secondary metabolism
stm	54	4	0.682	31	4.3	RNA-binding protein-like	BF641320	E/Mt,		5	84±10	15	32	4.8	Arabidopsis thaliana	Transcription
stm	60	4	0.822	30	5.9	ascorbate peroxidase	BG648814	(E), E/Mt		5	1±1 ^c	34	27	5.8	Pisum sativum	Disease/defense
stm	61	3	1.265	30	6.6	acid phosphatase	BG588612	(E), E/Mt		6	4±5 ^c	28	30	7.4	Glycine max	Signal transduction
stm	62	4	0.382	29	6.1	triosphosphate isomerase	BF642390	E/Mt, (E)		10	17±20	34	27	5.7	Coptis japonica	Energy
stm	64	3	0.222	29	4.5	expressed protein ^b	AI774799	E/Le		5	40±50	14	28	6.8	Arabidopsis thaliana	Unclear
stm	66	4	0.395	28	5.8	uridylate monophosphate kinase	AW981222	E/Mt, (E)		8	18±30	43	22	6	Arabidopsis thaliana	Metabolism
stm	70	3	0.499	25	5.5	23 kD O ₂ evolving pht. sys. II precursor ^b	P16059	N, S, E/Mt, (E)		7	46±15	26	28	8.3	Pisum sativum	Energy
stm	72	4	0.196	24	4.8	ATP synthase, delta chain ^b	Q41000	S		4	22±33	18	21	6.7	Pisum sativum	Energy
stm	81	3	0.474	20	9.6	vcCYP	AW775250	E/Mt, (E), N		8	36±4	53	18	8.2	Vicia faba	Protein destination/storage
stm	85	3	0.331	18	5.8	40S ribosomal protein S12 ^b	AL375805	E/Mt		4	27±27	45	15	5.5	Hordeum vulgare	Protein synthesis
stm	86	4	0.203	18	5.6	glycine rich RNA binding protein	AL379229	E/Mt, (E)		4	23±6	43	11	4.7	Medicago sativa	Transcription
stm	88	4	0.484	17	4.3	60S ribosomal protein	AW776748	E/Mt, (E)		4	5±5	32	12	4.3	Parthenium argentatum	Protein synthesis
stm	90	3	0.508	16	6.6	nucleoside diphosphate kinase I	P47922	S		5	13±6	28	16	5.9	Pisum sativum	Metabolism
stm	89	4	0.523	16	5.4	glycine rich RNA binding protein	AA660717	E/Mt, (E), N		9	23±5	78	11	4.7	Medicago sativa	Transcription
stm	95	3	0.278	11	7.1	hypothetical ^b	NP174644	N		6	35±17	20	21	7.1	Arabidopsis thaliana	Unclear
Tissue	Spot #	PMFQ	% Relative Abundance	Gel MW (kD)	Gel pI	Identification/Comment	Accession Number	Databases	LC/MS/MS score	# Peptides Matched	m/z Accuracy ± SD (ppm)	% Protein Coverage	Theoret MW (kD)	Theoret pI	Organism Matched	Function
rts	2	4	0.109	81	5.2	heat shock 70	Q02028	N, S, E/Mt		22	52±12	32	75	5.2	Pisum sativum	Protein destination/storage
rts	5	3	0.150	66	6.0	phosphoglyceromutase	BG585916	(E)		5	2±3 ^c	12	61	5.5	Apium graveolens	Energy
rts	6	4	0.161	66	5.4	protein disulfide isomerase	BI309490	E/Mt, (E), N, S		10	42±13	23	57	5.1	Medicago sativa	Energy
rts	9	2	0.115	63	4.9	putative methyl binding domain	AL378817	E/Mt		4	26±4	15	43	4.5	Arabidopsis thaliana	Unclear
rts	12	5	0.436	59	5.7	ATPase beta subunit	CAA75477	N, S, E/Mt, (E)		13	4±7	37	49	5.2	Sorghum bicolor	Energy
rts	19	3	0.322	49	5.7	actin isoform B	T51183	N, S, E/Mt, (E)		13	9±7	41	41	5.3	Mimosa pudica	Cell structure
rts	20	5	0.113	47	8.4	peroxidase precursor	AL369822	(E), E/Mt		8	3±3 ^c	27	38	8.1	Glycine max	Disease/defense
rts	22	4	0.247	46	4.9	ankyrin repeat protein HBP1	BI311773	(E), E/Mt		12	4±5 ^c	28	37	4.5	Nicotiana tabacum	Protein destination/storage
rts	28	3	0.395	42	7.4	glyceraldehyde-3-phosphate dehydrogenase	BG453922	(E), S		10	3±5 ^c	37	36	7.1	Pisum sativum	Energy
rts	32	5	0.280	41	4.8	cationic peroxidase precursor	BG584470	(E)		7	6±6 ^c	41	33	7.8	Arachis hypogea	Disease/defense
rts	33	4	0.491	40	5.9	isoflavone reductase	BG645198	(E)		13	3±3 ^c	39	35	5.6	Medicago truncatula	Secondary metabolism
rts	36	3	0.303	39	6.1	isoflavone reductase homolog	BI312226	E/Mt, (E)		5	4±6	24	34	6.1	Glycine max	Secondary metabolism

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rts	39	2	0.276	36	8.4	acidic glucanase ^b	BF650084	(E), E/Mt, N		4	2±3 ^c	16	40	7.0	Medicago sativa	Metabolism
rts	40	4	0.497	36	4.9	cytochrome c oxidase subunit 6b-1	BI310278	(E), E/Mt		8	3±4 ^c	35	21	4.3	Oryza sativa	Energy
rts	41	3	0.248	35	7.6	gluco endo-1,3-beta-d-glucosidase	BE239884	E/Mt		4	2±4	19	35	5.7	Cicer arietinum	Metabolism
rts	42	3	0.634	32	5.9	hydroxyacyl glutathione hydrolase ^b	BG584417	(E)		8	3±4 ^c	29	28	6.4	Arabidopsis thaliana	Metabolism
rts	43	5	0.467	32	7.3	chitinase ^b	CAA71402	N, S, E/Mt, (E)		9	12±12	49	35	6.8	Medicago truncatula	Disease/defense
rts	44	4	0.089	32	8.3	chitinase ^b	CAA71402	N, S, E/Mt, (E)		12	16±30	66	35	6.8	Medicago truncatula	Disease/defense
rts	45	4	0.188	31	7.8	chitinase ^b	CAA71402	N, S, E/Mt, (E)		10	12±27	60	35	6.8	Medicago truncatula	Disease/defense
rts	46	3	0.417	31	5.3	cystein proteinase	BI269594	(E), E/Mt		4	2±4 ^c	17	38	6.7	Pisum sativum	Protein destination/storage
rts	47	4	0.421	31	4.9	cystein proteinase precursor	BG645760	(E), E/Mt		6	4±6 ^c	20	51	6.4	Phaseous vulgaris	Protein destination/storage
rts	48	3	0.107	31	4.7	ascorbate peroxidase	BG648814	(E)		4	4±6 ^c	30	27	5.8	Pisum sativum	Disease/defense
rts	51	2	0.587	30	6.1	ascorbate peroxidase	P48534	S, N, E/Mt, (E)		4	3±3	21	27	5.5	Pisum sativum	Disease/defense
rts	52	5	0.532	29	6.3	triose phosphate isomerase	BG584164	(E), E/Mt		11	4±5 ^c	45	27	5.7	Coptis japonica	Energy
rts	53	4	0.265	29	5.8	in2-1protein ^b	BF635446	E/Mt, (E)		7	23±6	38	27	5.4	Glycine max	Disease/defense
rts	54	5	0.378	28	5.9	uridylate kinase (UDP kinase)	AW981222	E/Mt, (E)		4	9±11	34	22	6.0	Arabidopsis thaliana	Metabolism
rts	56	2	0.319	27	5.7	chalcone-flavone isomerase	AW559891	(E), E/Mt, N, S		6	3±6 ^c	46	23	5.3	Medicago sativa	Secondary metabolism
rts	60	3	0.481	26	6.4	unknown protein ^b	AW686250	(E), E/Mt		9	9±7 ^c	51	21	6.2	Prunus armeniaca	Unclear
rts	61	4	0.516	25	5.3	alpha fucosidase ^b	BE942130	(E)		6	3±3 ^c	38	23	5.1	Cicer arietinum	Metabolism
rts	63	3	0.303	25	5.8	putative protein T25B15.70 ^b	BF520168	E/Mt, (E)		8	10±15	51	20	5.2	Arabidopsis thaliana	Unclear
rts	65	2	0.849	22	5.4	seed protein precursor	AL371551	E/Mt, (E)		4	10±7	23	24	6.1	Theobromo cacao	Protein destination/storage
rts	66	2	0.190	22	6.3	Vc Cyp (peptidyl isomerase)	BE316900	(E), E/Mt		4	2±3 ^c	23	18	8.2	Vicia faba	Protein destination/storage
rts	69	2	0.063	21	7.7	profucosidase ^b	AW126318	(E)		5	6±9 ^c	22	23	6.5	Pisum sativum	Metabolism
rts	75	2	0.262	19	7.2	putative protein ^b	BF005271	(E), E/Mt		8	5±5 ^c	45	22	9.0	Arabidopsis thaliana	Unclear
rts	77	4	0.191	18	9.0	glyceraldehyde-3-phosphate dehydrogenase	BF635050	E/Mt, (E), N		9	15±10	27	36	7.1	Pisum sativum	Energy
rts	79	3	0.881	17	6.0	Cu/Zn superoxide dismutase ^b	AL387737	E/Mt		4	13±14	48	15	6.0	Pisum sativum	Disease/defense
rts	80	4	3.311	17	5.4	aba responsive protein ABR17	BF648027	E/Mt, (E)		8	9±5	51	17	5.2	Pisum sativum	Disease/defense
rts	81	4	0.2157	17	6.7	unknown protein ^b	AL365549	E/Mt, (E)		6	9±6	48	20	7.8	Arabidopsis thaliana	Unclear
rts	82	4	0.469	16	5.8	putative ripening related protein ^b	BE943167	E/Mt, (E)		4	13±4	26	17	5.2	Vitis vinifera	Unclear
rts	92	4	0.317	10	6.1	thioredoxin	BE997543	(E), E/Mt		4	2±2 ^c	38	13	5.8	Ricinus communis	Energy
Tissue	Spot #	PMFQ	% Relative	Gel MW	Gel pI	Identification/Comment	Accession	Databases	LC/MS/MS	# Peptides	m/z Accuracy	% Protein	Theoret	Theoret	Organism Matched	Function
			Abundance	(kD)			Number		score	Matched	± SD (ppm)	Coverage	MW (kD)	pI		
flw	3	3	0.165	90	5.6	valosin containing cell division protein	P54774	S, N		16	53±11	21	89	5.2	Glycine max	Cell growth/division
flw	6	4	0.200	76	6.9	NADH ubiquinone oxidoreductase	AW587332	E/Mt, (E)		6	4±5	9	79	6.0	Solanum tuberosum	Energy

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flw	7	4	0.388	73	5.1	heat shock 70	Q02028	N, S		10	77±3	20	75	5.2	Pisum sativum	Protein destination/storage
flw	8	3	0.130	70	8.5	polyA binding protein ^b	BG584083	(E)		5	6±9 ^c	9	71	7.4	Daucus carota	Transcription
flw	11	4	0.118	63	6.0	phosphoglyceromutase	BG585916	(E), E/Mt, N, S		10	5±7 ^c	20	60	5.5	Apium graveolens	Energy
flw	13	3	0.217	60	4.8	putative methyl binding domain	AL378817	(E), E/Mt		5	75±12 ^c	48	43	4.5	Zea mays	Unclear
flw	14	5	0.952	58	4.4	calreticulin	AW773889	E/Mt	348	4	34±14	15	48	4.5	Beta vulgaris	Transporters
flw	17	4	0.443	56	5.8	ATPase beta subunit	CAA75477	N, S, E/Mt, (E)		8	12±8	26	49	5.2	Sorghum bicolor	Energy
flw	18	4	0.422	54	6.1	enolase	CAB75428	N, S, E/Mt, (E)		7	74±13	25	47	5.1	Lupinus lutetuim	Energy
flw	21	4	0.326	51	6.2	s-adenosyl methionine synthetase	AAL16064	N, S, E/Mt, (E)		8	83±12	31	43	5.4	Dendrobium crumentum	Metabolism
flw	23	5	0.162	50	5.6	rubisco activase	AAK25798	N, S, E/Mt, (E)		9	85±17	18	47	5.3	Zantedeschia aethiopia	Energy
flw	27	5	0.141	45	4.4	ankyrin repeat protein HBP1	BI311773	(E)		9	5±6 ^c	25	37	4.5	Nicotiana tabacum	Protein destination/storage
flw	26	5	0.701	44	7.2	fructose-1,6-biphosphate aldolase	O65735	N, S, E/Mt, (E)		7	79±15	23	38	6.2	Cicer arietinum	Energy
flw	28	4	0.194	44	7.8	aspartate aminotransferase	P46643	S, N, E/Mt	115	4	52±30	11	47	8.4	Arabidopsis thaliana	Metabolism
flw	31	3	0.320	41	5.7	1-aminocyclopro. carboxylic acid oxidase ^b	AY062251	N, (E)		6	21±5	16	35	5.2	Medicago truncatula	Energy
flw	32	3	0.217	41	5.9	pyruvate dehydrogenase beta unit ^b	BF645846	(E), E/Mt		6	19±4 ^c	20	38	5.9	Pisum sativum	Energy
flw	30	3	0.615	41	7.6	glyceraldehyde-3-phosphate dehydrogenase	P34922	N, S, E/Mt, (E)		8	10±6	31	36	6.6	Pisum sativum	Energy
flw	33	4	0.352	41	7.0	malate dehydrogenase	O48905	S, N		4	22±6	18	35	6.4	Medicago sativa	Energy
flw	34	4	0.607	40	6.8	malate dehydrogenase	O48905	N, S, (E)		8	87±8	40	35	6.4	Medicago sativa	Energy
flw	35	3	0.212	40	6.0	ripening induced protein ^b	BI308422	(E)		8	4±4 ^c	44	35	6.7	Fragaria vesca	Cell growth/division
flw	39	5	0.445	35	4.4	cytochrome c oxidase subunit 6b	BI310278	(E), E/Mt		5	10±13 ^c	35	21	4.3	Arabidopsis thaliana	Energy
flw	40	5	0.334	34	6.5	stromal ascorbate peroxidase	Z67113	(E), E/Mt		7	3±7 ^c	21	40	8.0	Mesembryanthemum cryst.	Disease/defense
flw	50	3	0.377	30	6.6	acid phosphatase	BG588612	(E), E/Mt		7	79±9 ^c	30	29	6.9	Glycine max	Signal transduction
flw	51	3	0.583	30	6.9	acid phosphatase	BF004054	(E), E/Mt		6	89±5 ^c	30	29	6.9	Glycine max	Signal transduction
flw	53	3	0.345	29	6.5	triose phosphate isomerase	BG584164	(E)		11	2±3 ^c	45	27	5.7	Coptis japonica	Energy
flw	55	4	0.466	29	8.1	osmotin like protein	BI270608	(E)		8	3±3 ^c	34	27	7.9	Lycopersicon esculentum	Disease/defense
flw	56	5	0.393	28	6.6	chalcone isomerase	BI310352	(E), E/Mt		6	6±8 ^c	39	25	5.3	Vitis vinifera	Secondary metabolism
flw	57	5	0.294	27	5.1	ascorbate peroxidase	AAL15164	N, S, E/Mt, (E)		5	89±6	35	20	5.3	Medicago sativa	Disease/defense
flw	60	5	0.522	25	5.9	oxygen evolving enhancer protein 2	BF636854	E/Mt, (E)		5	81±15	13	28	8.2	Pisum sativum	Energy
flw	71	2	0.312	20	8.6	peptidyl prolyl isomerase	BE999037	(E), E/Mt		5	7±8 ^c	29	18	8.7	Vicia faba	Protein destination/storage
flw	73	3	0.203	20	6.5	acid phosphatase	AW584917	(E), E/Mt	131	4	35±8 ^c	19	30	7.4	Glycine max	Signal transduction
flw	74	3	0.377	20	9.2	peptidyl prolyl isomerase	BE997455	(E), E/Mt		6	4±3 ^c	42	18	8.7	Vicia faba	Protein destination/storage
flw	75	3	0.513	20	5.6	glycine rich RNA binding protein	BF637655	E/Mt		4	5±3	41	16	5.6	Pelargonium hortorum	Transcription
flw	77	3	0.253	20	6.3	peroxiredoxin (peroxidase)	AW585033	(E), E/Mt		12	12±11 ^c	83	17	6.5	Arabidopsis thaliana	Disease/defense

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flw	78	3	0.250	18	5.3	ubiquitin like SMT3 protein	AL376595	(E), E/Mt, S		8	13±7 ^c	53	11	5.6	Arabidopsis thaliana	Protein destination/storage
flw	79	3	0.508	18	6.2	ubiquitin like SMT3 protein	P55852	S, N, E/Mt mt		7	15±10	26	11	5.3	Arabidopsis thaliana	Protein destination/storage
flw	81	3	0.496	18	3.9	60S acidic ribosomal protein p3	BF003585	(E), E/Mt	123	4	59±9 ^c	16	12	4.5	Arabidopsis thaliana	Protein synthesis
flw	82	2	0.496	17	4.6	glycine cleavage system h precursor ^b	BF518986	(E), E/Mt		5	7±8 ^c	29	17	5.3	Pisum sativum	Metabolism
flw	88	3	0.268	16	4.5	acid ribosomal protein P2a2	AW329482	(E)		5	7±9 ^c	74	11	4.6	Zea mays	Protein synthesis
flw	91	3	0.124	15	9.0	immunophilin	AW574158	(E), E/Mt		6	75±3 ^c	55	12	8.0	Vicia faba	Protein destination/storage
flw	92	3	0.864	13	7.2	rubisco small chain	BI268542	(E), E/Mt		5	2±3 ^c	48	12	6.5	Medicago sativa	Energy
flw	94	3	0.494	13	5.1	profilin 1 ^b	AL373653	(E)		9	6±7 ^c	44	14	5.2	Phaseolus vulgaris	Cell structure
flw	96	3	0.313	6	7.1	NADH plastoquinone oxidoreductase 4 ^b	BF631701	(E)		6	2±3 ^c	64	9	6.9	Nicotiana tabacum	Energy
Tissue	Spot #	PMFQ	% Relative Abundance	Gel MW (kD)	Gel pI	Identification/Comment	Accession Number	Databases	LC/MS/MS score	# Peptides Matched	m/z Accuracy ± SD (ppm)	% Protein Coverage	Theoret MW (kD)	Theoret pI	Organism Matched	Function
pds	5	4	0.372	70	6.4	convicilin ^b	BI312063	(E)		5	5±6 ^c	15	49	5.5	Pisum sativum	Protein destination/storage
pds	6	5	0.366	68	5.9	convicilin ^b	BI310979	E/Mt		10	3±4	21	49	5.5	Pisum sativum	Protein destination/storage
pds	7	4	0.328	65	5.3	heat shock 70	Q02028	N, S		9	21±13	26	75	5.2	Pisum sativum	Protein destination/storage
pds	8	5	0.353	59	7.0	legumin a2 precursor ^b	BI312252	E/Mt		9	5±8	18	56	6.6	Pisum sativum	Protein destination/storage
pds	9	5	0.690	58	5.5	protein disulfide iosmerase	P29828	N, S, (E), E/Mt		7	42±31	17	57	5.0	Medicago sativa	Energy
pds	10	4	0.611	58	6.7	glycinin ^b	BI308459	(E)		7	5±6 ^c	19	56	5.9	Pisum sativum	Protein destination/storage
pds	13	4	0.566	55	6.5	legumin a2 precursor ^b	BI311943	(E)		9	11±8 ^c	18	58	6.6	Pisum sativum	Protein destination/storage
pds	12 ^a	5	0.683	55	4.6	rubisco	AAK70985	N, S		8	45±55	20	51	6.1	Mascagania bracteosa	Energy
pds	12 ^a	5	0.683	55	4.6	NAp1p (plasma membrane intrinsic protein) ^b	AW774263	E/Mt, (E)		10	19±20	28	41	4.5	Pisum sativum	Transporters
pds	14	5	0.224	52	3.4	vicilin 47kD precursor ^b	BI310576	(E)		9	2±3 ^c	25	52	5.7	Pisum sativum	Protein destination/storage
pds	15	4	0.452	52	4.0	provicilin precursor ^b	BI312400	(E)		6	9±10 ^c	14	49	5.6	Pisum sativum	Protein destination/storage
pds	16	5	0.641	50	4.7	vicilin 47kD precursor ^b	BI311712	(E)		4	8±7 ^c	16	49	5.6	Pisum sativum	Protein destination/storage
pds	19	5	0.084	50	10.2	vicilin 47kD precursor ^b	BI311712	(E)		7	4±5 ^c	24	49	5.6	Pisum sativum	Protein destination/storage
pds	22	4	0.096	46	10.2	glycinin ^b	BI311592	(E)		13	3±4 ^c	26	56	5.9	Glycine max	Protein destination/storage
pds	20	4	0.455	46	6.2	glycinin ^b	BI311729	(E)		4	11±13 ^c	13	56	5.9	Glycine max	Protein destination/storage
pds	21	5	1.210	45	5.3	glycinin ^b	BI308883	(E)		12	3±4 ^c	20	56	5.9	Glycine max	Protein destination/storage
pds	23	4	1.526	45	6.7	glycinin ^b	BI308883	(E)		6	2±3 ^c	19	56	5.9	Glycine max	Protein destination/storage
pds	24	4	0.165	43	3.4	legumin a2 precursor ^b	BI309500	(E)		11	8±9 ^c	18	58	6.6	Pisum sativum	Protein destination/storage
pds	28	4	0.117	41	10.2	legumin a2 precursor ^b	BI311943	(E)		14	4±6 ^c	24	58	6.6	Pisum sativum	Protein destination/storage
pds	27	4	0.089	41	9.2	legumin a2 precursor ^b	BI311943	(E)		11	5±7 ^c	20	58	6.6	Pisum sativum	Protein destination/storage
pds	31	5	0.411	41	7.2	fructose 1,6-biphosphate aldolase	O65735	N, S, (E), E/Mt		7	4±5	25	38	6.2	Cicer arietinum	Energy

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pds	30	5	5.187	41	6.4	legumin a2 precursor ^b	BI311943	(E)		11	3±3 ^c	18	58	6.6	Pisum sativum	Protein destination/storage
pds	29	5	0.914	40	5.2	legumin a2 precursor ^b	BI311943	(E)		8	5±6 ^c	17	58	6.6	Pisum sativum	Protein destination/storage
pds	32	5	0.446	40	7.4	legumin a2 ^b	BI307938	(E)		5	6±7 ^c	11	58	6.6	Pisum sativum	Protein destination/storage
pds	34	4	0.214	38	6.8	cytosolic malate dehydrogenase	BG583001	(E, N, S)		6	3±4 ^c	29	35	6.9	Cicer arietinum	Energy
pds	38	5	0.240	36	6.9	malate dehydrogenase precursor	AW688679	E/Mt, N		7	31±62	36	35	8.7	Medicago sativa	Energy
pds	37	4	1.932	36	6.0	glycinin ^b	BI311164	(E)		10	9±11 ^c	32	56	5.9	Pisum sativum	Protein destination/storage
pds	39	4	0.261	35	7.0	IFR like NADH dependent oxidoreductase	BE325778	E/Mt		7	29±31	36	34	7.0	Medicago sativa	Secondary metabolism
pds	41	4	0.220	33	6.9	peroxidase 2	CAC38106	N, E/Mt		16	28±30	54	35	9.2	Medicago sativa	Disease/defense
pds	43 ^a	5	0.156	31	5.2	rubisco	CAA62888	N, S		10	33±32	25	51	6.0	Thevetia peruviana	Energy
pds	43 ^a	5	0.156	31	5.2	enolase	BG362941	E/Gm		7	14±23	36	50	6.3	Glycine max	Energy
pds	44	5	0.334	31	3.9	vicilin 47kD precursor ^b	BI310576	(E)		9	4±5 ^c	25	52	5.7	Pisum sativum	Protein destination/storage
pds	47	4	0.307	29	6.6	acid phosphatase	BF004054	E/Mt		5	40±32	17	30	7.4	Glycine max	Signal transduction
pds	46	5	0.230	29	6.4	acid phosphatase	BF004054	E/Mt		7	37±41	31	30	7.4	Glycine max	Signal transduction
pds	51	4	0.276	28	6.9	acid phosphatase	BG588612	(E)		9	4±6 ^c	33	30	7.4	Glycine max	Signal transduction
pds	52	3	0.195	27	5.1	proteosome 20S subunit	BE922062	E/St		7	16±19	39	26	4.8	Glycine max	Protein destination/storage
pds	53	5	0.151	27	5.6	ascorbate peroxidase	BG648703	(E), E/Mt		10	5±7 ^c	46	27	5.8	Pisum sativum	Disease/defense
pds	54	5	0.211	27	8.0	osmotin like protein precursor	BG582096	(E), E/Mt		8	1±2 ^c	41	27	7.9	Lycopersicon esculentum	Disease/defense
pds	55	4	0.226	26	6.4	put. GSH dpnd. dehydroascorbate reductase ^b	BF636747	E/Mt, (E)		6	8±10	42	23	5.9	Arabidopsis thaliana	Unclear
pds	56	4	0.377	26	6.5	legumin a2 precursor ^b	BI307938	(E)		7	7±7 ^c	17	58	6.6	Pisum sativum	Protein destination/storage
pds	57	5	0.523	25	5.7	legumin a2 precursor ^b	BI309895	(E)		6	6±9 ^c	20	58	6.6	Pisum sativum	Protein destination/storage
pds	58	5	0.592	25	6.0	oxygen evolving enhancer protein 2	AW775879	E/Mt, (E), S		12	19±18	45	28	8.2	Pisum sativum	Energy
pds	59	5	0.152	25	10.3	legumin a2 precursor ^b	BI309155	(E)		9	11±12 ^c	20	58	6.6	Pisum sativum	Protein destination/storage
pds	62	4	0.167	23	3.3	legumin b (minor small) ^b	BI311720	(E)		9	3±5 ^c	26	56	6.0	Pisum sativum	Protein destination/storage
pds	65	3	0.624	23	9.8	legumin b (minor small) ^b	BI311720	(E)		12	6±6 ^c	29	56	6.0	Pisum sativum	Protein destination/storage
pds	66	4	0.793	22	6.0	legumin b (minor small) ²	BI311437	(E)		6	3±5 ^c	21	54	6.0	Pisum sativum	Protein destination/storage
pds	68	5	0.148	22	4.9	legumin related high MW polypeptide ^b	BI310430	(E)		8	2±3 ^c	21	64	5.6	Vicia faba	Protein destination/storage
pds	70	3	0.118	20	7.1	hypothetical protein ^b	AW685677	E/Mt, (E)		9	12±22	55	18	6.0	Arabidopsis thaliana	Unclear
pds	71	3	0.053	20	6.8	vicilin 47kD precursor ^b	BI312335	(E)		10	6±7 ^c	32	50	5.6	Pisum sativum	Protein destination/storage
pds	75	3	0.303	19	8.9	LEA protein ^b	BG454568	(E)		4	9±8 ^c	36	16	9.0	Cicer arietinum	Cell growth/division
pds	73	3	0.176	19	6.5	legumin a2 precursor ^b	BI309500	(E)		4	1±1 ^c	15	36	5.4	Vicia faba	Protein destination/storage
pds	72	5	0.215	19	4.2	eukaryotic initiation factor 5a ^b	AL389124	E/Mt		4	15±18	47	18	5.8	Medicago sativa	Protein synthesis
pds	77	4	0.188	18	8.5	VcCyP peptidylprolyl isomerase	BE997455	E/Mt, (E)		10	15±12	59	18	8.2	Vicia faba	Protein destination/storage

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pds	78	3	0.344	18	9.1	VcCyP peptidylprolyl isomerase	BE997455	E/Mt, (E)		13	53±57	78	18	8.2	Vicia faba	Protein destination/storage
pds	80	4	0.229	17	5.2	ubiquitin like protein	AL376595	E/Mt		5	25±14	47	11	5.1	Arabidopsis thaliana	Protein destination/storage
pds	82	3	0.254	16	5.5	aba responsive protein abr 17	BF648027	(E)		5	3±4 ^c	36	16	5.2	Pisum sativum	Disease/defense
pds	84	5	0.404	15	5.9	glycine rich RNA binding protein	BI309824	(E), E/Mt		11	4±6 ^c	94	10	4.7	Medicago sativa	Transcription
pds	85	5	0.177	15	4.7	acidic ribosomal protein	AL383563	E/Mt		5	42±49	68	11	4.3	Zea mays	Protein destination/storage
pds	91	4	0.288	14	9.8	legumin (minor small) ^b	BI311437	(E)		7	6±8 ^c	22	54	6.4	Pisum sativum	Protein destination/storage
pds	95	4	1.135	11	7.1	rubisco small subunit	BF519894	E/Mt		8	43±38	46	20	8.6	Medicago sativa	Energy
pds	94	3	0.374	11	4.4	plastocyanin precursor	BF005687	E/Mt		6	40±44	40	17	5.2	Pisum sativum	Energy
Tissue	Spot #	PMFQ	% Relative Abundance	Gel MW (kD)	Gel pI	Identification/Comment	Accession Number	Databases	LC/MS/MS score	# Peptides Matched	m/z Accuracy ± SD (ppm)	% Protein Coverage	Theoret MW (kD)	Theoret pI	Organism Matched	Function
cls	2	5	0.214	91	5.7	cell division cyle prt 48 (valosin contain. prt)	P54774	S		10	10±11	13	90	5.2	Glycine max	Cell growth/division
cls	5	5	0.123	74	5.1	heat shock protein 70 kD (Bip A)	T06598	E/Hv, N, S		10	32±18	20	73	5.1	Glycine max	Protein destination/storage
cls	6	4	0.260	73	5.5	luminal binding protein	CAC14168	N, S, E/Hv		8	44±51	15	74	5.0	Corylus avellana	Protein destination/storage
cls	7	4	0.402	72	5.2	Psst 70	Q02028	N, S, E/Hv		9	6±7	20	76	5.2	Pisum sativum	Protein destination/storage
cls	8	4	0.455	71	5.6	putative luminal binding protein	CAC14168	N, S, (E)		9	38±33	21	71	5.0	Corylus avellana	Protein destination/storage
cls	10	3	0.565	68	6.4	leucyl aminopeptidase ^b	S57811	N, S		4	20±26	16	55	5.2	Lycopersicon esculentum	Protein destination/storage
cls	9	4	0.344	68	5.8	70 kD heat shock protein	Q01899	N, S, E/Mt, (E)		8	19±24	17	73	5.9	Phaseolus vulgaris	Protein destination/storage
cls	20	4	0.312	57	7.6	catalase ^b	P49315	N, S, (E)		6	24±37	18	56	6.8	Nicotiana tabacum	Disease/defense
cls	15	4	0.258	57	6.2	selenium binding protein ^b	CAC67501	N, (E)		12	20±23	40	54	5.7	Medicago sativa	Disease/defense
cls	16	5	0.181	57	6.9	selenium binding protein ^b	CAC67501	N, (E)		7	30±12	28	54	5.7	Medicago sativa	Disease/defense
cls	14 ^a	4	0.847	57	4.6	calreticulin	Q40401	N, E/Mt	135	4	42±62	16	47	4.4	Nicotiana tabacum	Transporters
cls	14 ^a	4	0.847	57	4.6	nucleosome assembly protein 1 ^b	S60893	E/Mt	208				42	4.4	Glycine max	Transcription
cls	18	5	0.242	56	5.8	ATP synthase beta subunit	CAA75478	N, S, E/Mt, (E)		6	46±40	20	49	5.4	Sorghum bicolor	Energy
cls	19	3	0.215	56	6.4	inosine-5'-monophosphate dehydrogenase ^b	AAL18815	N, E/Mt, (E)		5	18±18	15	42	6.7	Glycine max	Metabolism
cls	21	4	0.180	56	7.4	hydroxymethyltransferase ^b	AW980652	E/Mt, (E)		4	4±5	10	52	7.2	Arabidopsis thaliana	Metabolism
cls	22	3	0.379	55	6.1	enolase	CAB75428	N, E/Mt		6	29±35	22	48	5.1	Lupinus luteus	Energy
cls	23	3	0.495	51	6.4	SAM synthetase	AAG17666	N, E/Mt, (E)		5	13±17	23	43	5.4	Brassica juncea	Metabolism
cls	24 ^a	3	0.541	50	6.3	glucose-6-phosphate 1 dehydrogenase	Q42919	S		5	31±30	15	59	5.8	Medicago sativa	Energy
cls	24 ^a	3	0.541	50	6.3	SAM synthetase 2	Q96552	N, E/Mt, E/Gm		5	54±68	27	43	5.5	Catharanthus roseus	Metabolism
cls	28	4	0.557	48	9.1	aspartate aminotransferase	P28011	N, S, E/Mt		17	33±42	49	46	8.9	Medicago sativa	Metabolism
cls	29	4	0.447	48	6.7	putative heat shock protein	AAK63929	N		5	48±61	14	57	7.9	Oryza sativa	Unclear
cls	30	4	0.074	47	6.2	12-oxophytodienoic acid 10,11-reductase ^b	BG648922	E/Mt, (E)		6	11±11	17	41	6.2	Pisum sativum	Metabolism

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cls	31	5	0.052	47	6.3	12-oxophytodienoate reductase (OPR2) ^b	AW776305	E/Mt		6	22±22	23	42	7.5	Arabidopsis thaliana	Metabolism
cls	27	3	0.209	47	4.8	RAD23 (ubiquitin like protein) ^b	AW586882	(E)		4	9±11 ^c	11	42	4.8	Lycopersicon esculentum	Protein destination/storage
cls	33	3	0.486	45	6.3	probable mannitol dehydrogenase	AW981164	(E)		6	9±10 ^c	28	39	6.9	Fragaria x ananassa	Energy
cls	32	4	0.392	45	6.6	alcohol dehydrogenase ^b	P12886	S, (E)		5	19±14	12	41	6.1	Pisum sativum	Energy
cls	35 ^a	4	1.518	44	7.0	catalase ^b	P45739	S		5	48±55	15	57	6.6	Helianthus	Disease/defense
cls	35 ^a	4	1.518	44	7.0	fructose-1,6-biphosphate aldolase	P46257	N, S, E/Mt		5	30±38	16	38	6.8	Pisum sativum	Energy
cls	37	5	0.256	41	6.2	2-nitropropane dioxygenase like protein ^b	BF518520	E/Mt, (E)		7	13±9	34	32	5.9	Arabidopsis thaliana	Metabolism
cls	39	4	0.465	39	5.6	fructokinase	AW584645	E/Mt, N, S		8	48±47	37	35	5.6	Beta vulgaris	Energy
cls	46	2	0.335	36	8.9	beta-1,3-glucanase	BF650622	E/Mt	378	4	31±41	19	39	9.0	Phaseolus vulgaris	Metabolism
cls	49	3	0.268	35	6.4	stromal L-ascorbate peroxidase precursor	BE941206	E/Mt, (E)		5	6±8	24	41	8.0	Mesembryanthemum cryst.	Disease/defense
cls	53	3	0.157	33	7.2	cytochrome b5 reductase ^b	NP 568391	E/Mt	406				36	8.7	Arabidopsis thaliana	Energy
cls	60	4	0.561	31	6.2	glyceraldehyde-3-phosphate dehydrogenase	P54270	N, S		5	59±43	20	36	5.9	Gracilaria gracilis	Energy
cls	62	3	0.454	29	6.1	rubisco, small subunit	PS6577	S		4	28±13	33	20	7.6	Solanum tuberosum	Energy
cls	64	4	0.489	29	5.0	proteosome subunit α type 5 (20S subunit)	Q9M4T8	E/Mt, N, S	449				26	4.8	Glycine max	Protein destination/storage
cls	67	3	1.378	26	6.7	NADH ubiquinone oxidoreductase	BG448277	(E)		4	1±1 ^c	10	26	5.6	Solanum tuberosum	Energy
cls	74	4	0.995	21	8.8	vcCyp (peptidylprolyl isomerase)	AW775250	E/Mt		9	34±39	56	18	8.7	Vicia faba	Protein destination/storage
cls	78	4	0.129	20	6.2	peroxiredoxin TPx1 (thioredoxin peroxidase)	AW559683	(E), E/Mt		11	9±11 ^c	70	17	6.5	Capsicum annuum	Disease/defense
cls	81	3	0.294	20	7.3	peptidylprolyl isomerase (immunophilin)	BF635887	E/Mt, (E)		5	13±24	48	16	7.3	Vicia faba	Protein destination/storage
cls	83	4	0.572	18	5.1	disease resistance response protein ^b	BE942549	E/Mt, S		9	31±29	74	17	5.1	Pisum sativum	Disease/defense
cls	82 ^a	4	3.762	18	5.4	aba responsive protein	BF648027	E/Mt, (E)		10	31±37	75	17	5.2	Pisum sativum	Disease/defense
cls	82 ^a	4	3.762	18	5.4	leghemoglobin 2 (Pprg2) ^b	P27993	S	680	4	64±24	41	16	6.3	Medicago truncatula	Metabolism
cls	87	3	1.695	17	4.8	class 10 PR protein ^b	Q43560	N, S, E/Mt		5	37±45	42	17	4.6	Medicago sativa	Disease/defense
cls	85	5	0.299	17	6.2	cytochrome C-555 ^b	P00124	S		5	66±53	65	11	6.8	Prosthecochloris aestuarii	Energy
cls	88	3	0.728	17	6.7	nucleoside diphosphate kinase	P47922	S		7	18±16	36	16	5.9	Pisum sativum	Metabolism
cls	86	4	0.514	17	5.8	glycine rich RNA binding protein	AAF06329	E/Mt, N		9	55±42	78	11	4.7	Medicago sativa	Transcription
cls	90	5	0.221	16	8.5	immunophilin	AL377066	E/Mt		4	12±13	51	12	8.0	Vicia faba	Protein destination/storage
cls	92	4	0.601	15	4.5	acidic ribosomal protein (60S)	AL378424	E/Mt		5	27±34	59	11	4.7	Arabidopsis thaliana	Protein synthesis
cls	96	4	0.333	10	8.7	10 kD chaperonin ^b	AL377948	E/Mt	121	4	32±50	44	11	7.4	Brassica napus	Protein destination/storage

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