Membrane-associated proteomics of chickpea identifies Sad1/UNC-84 protein (CaSUN1), a novel component of dehydration signaling

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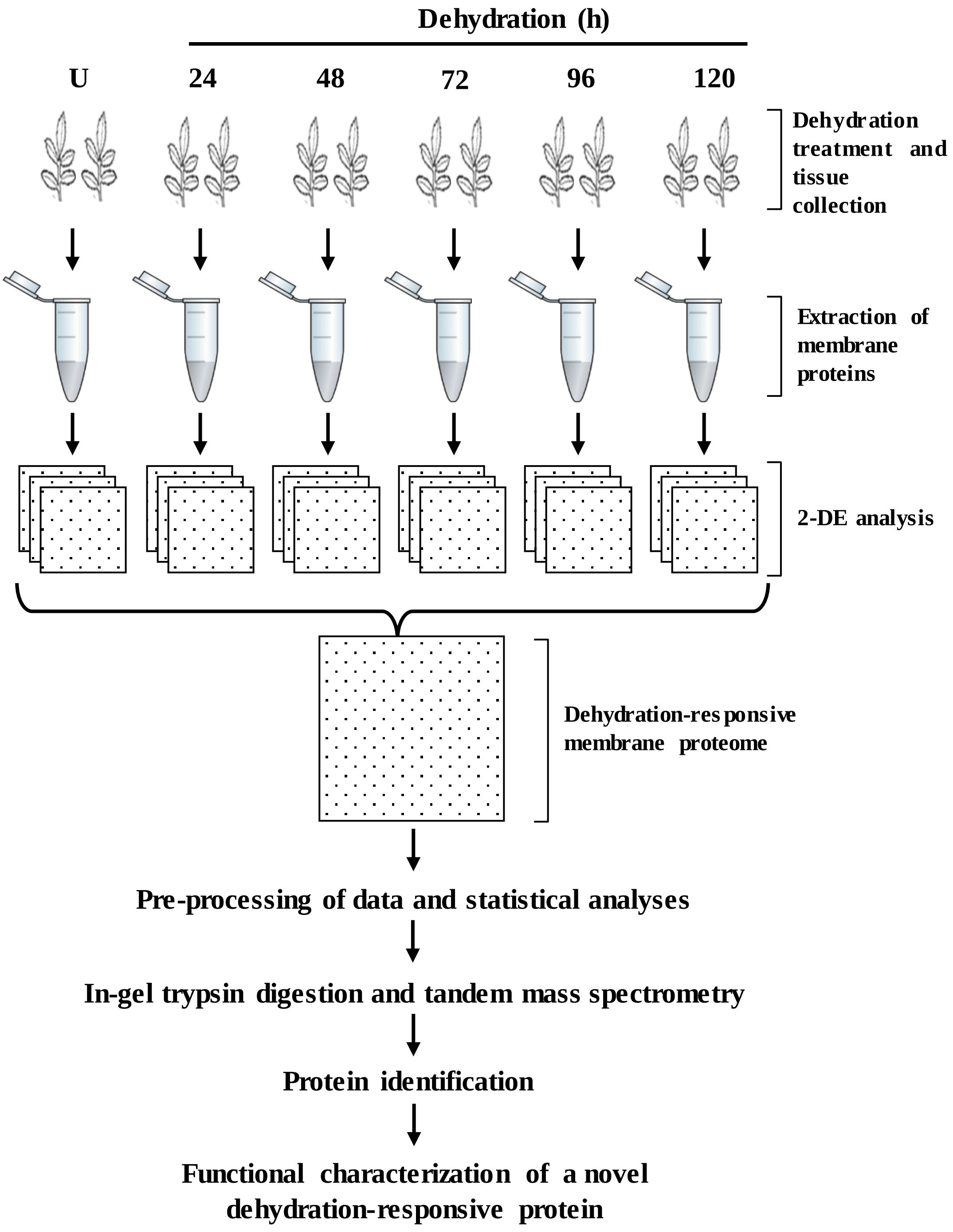
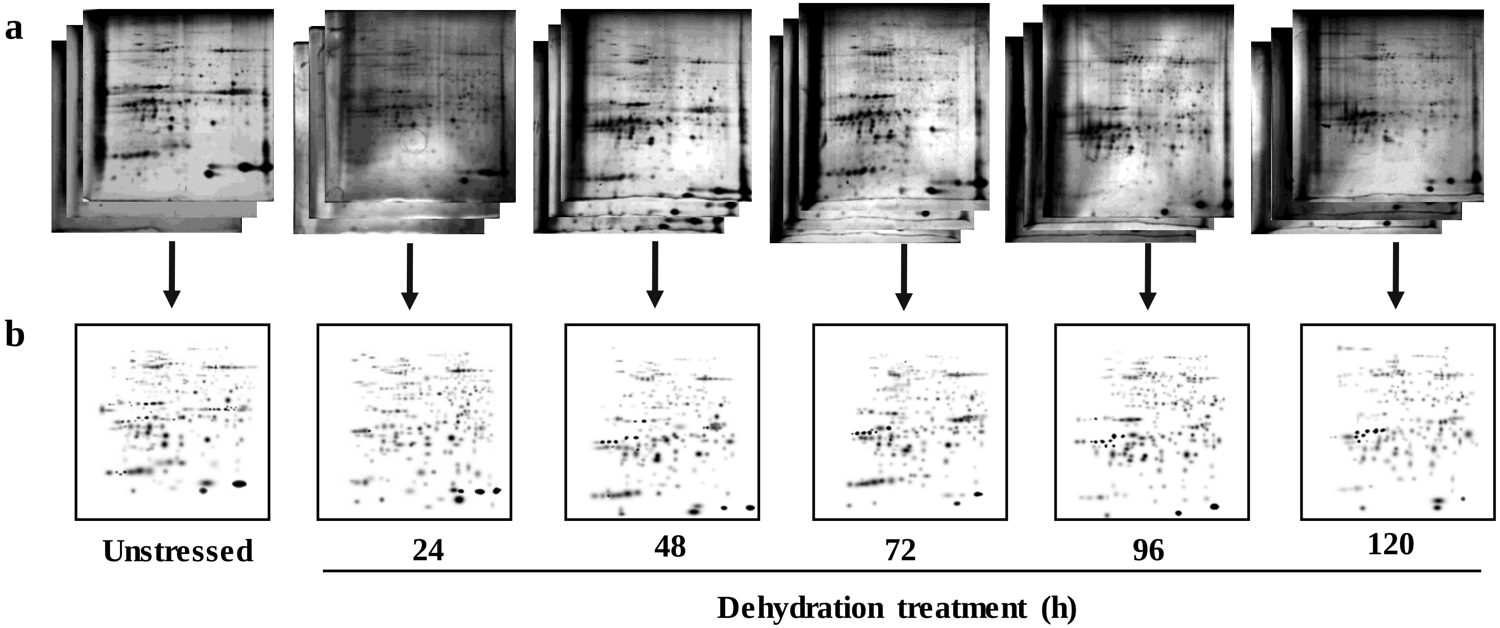
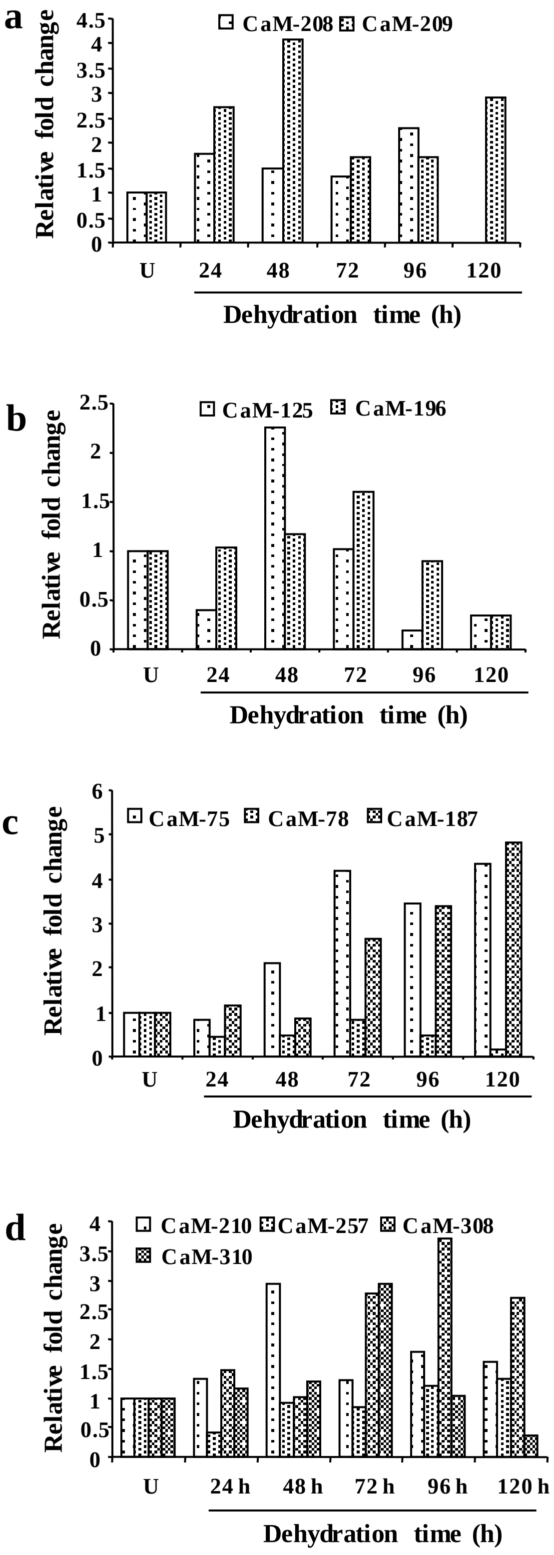


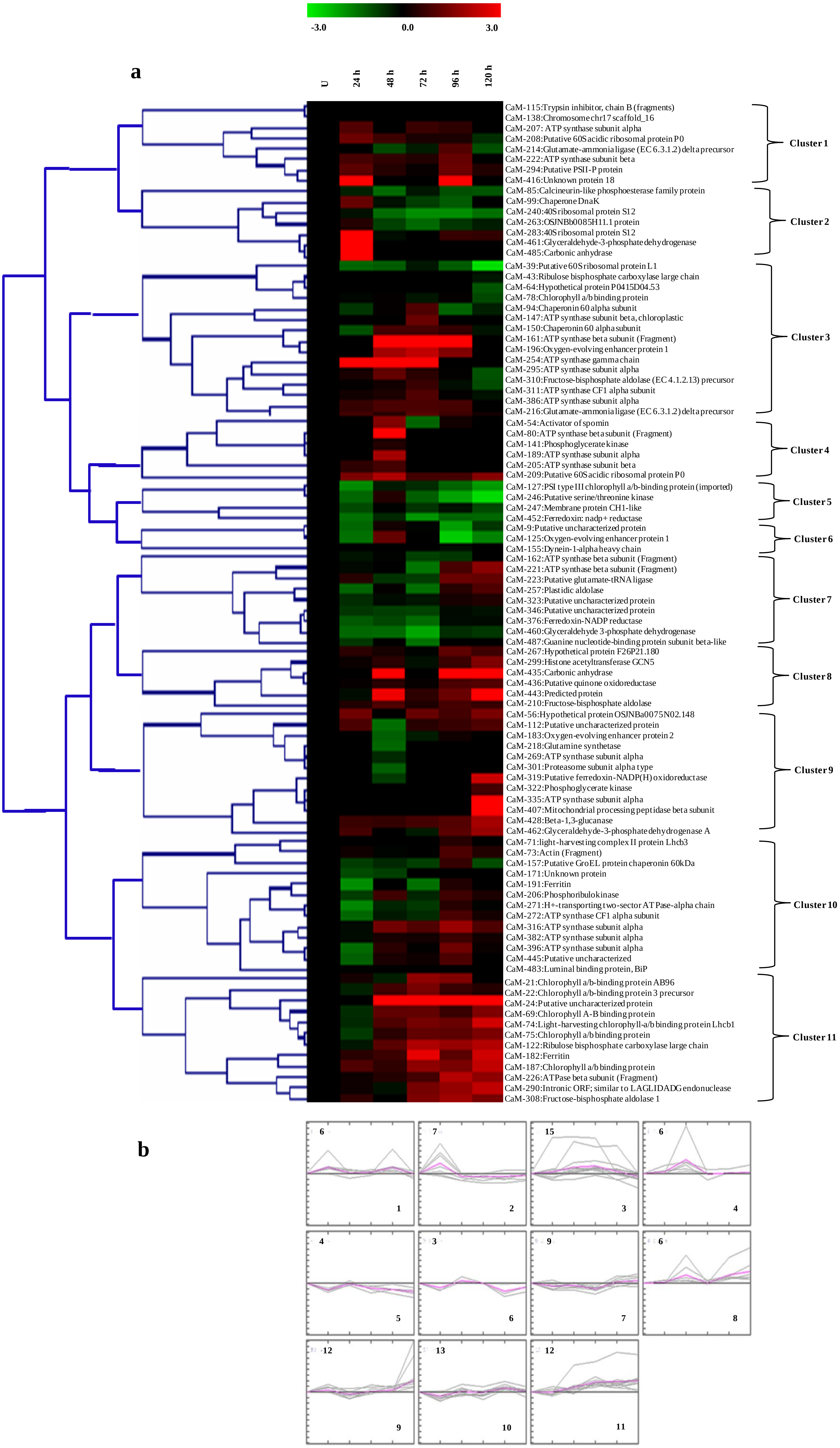
Supplementary Fig. S1. Experimental work flow used for analyzing the membrane proteome from the aerial tissue of chickpea and downstream analyses. The detailed experimental procedure is illustrated in " SI Materials methods" section. U represents the unstressed condition.



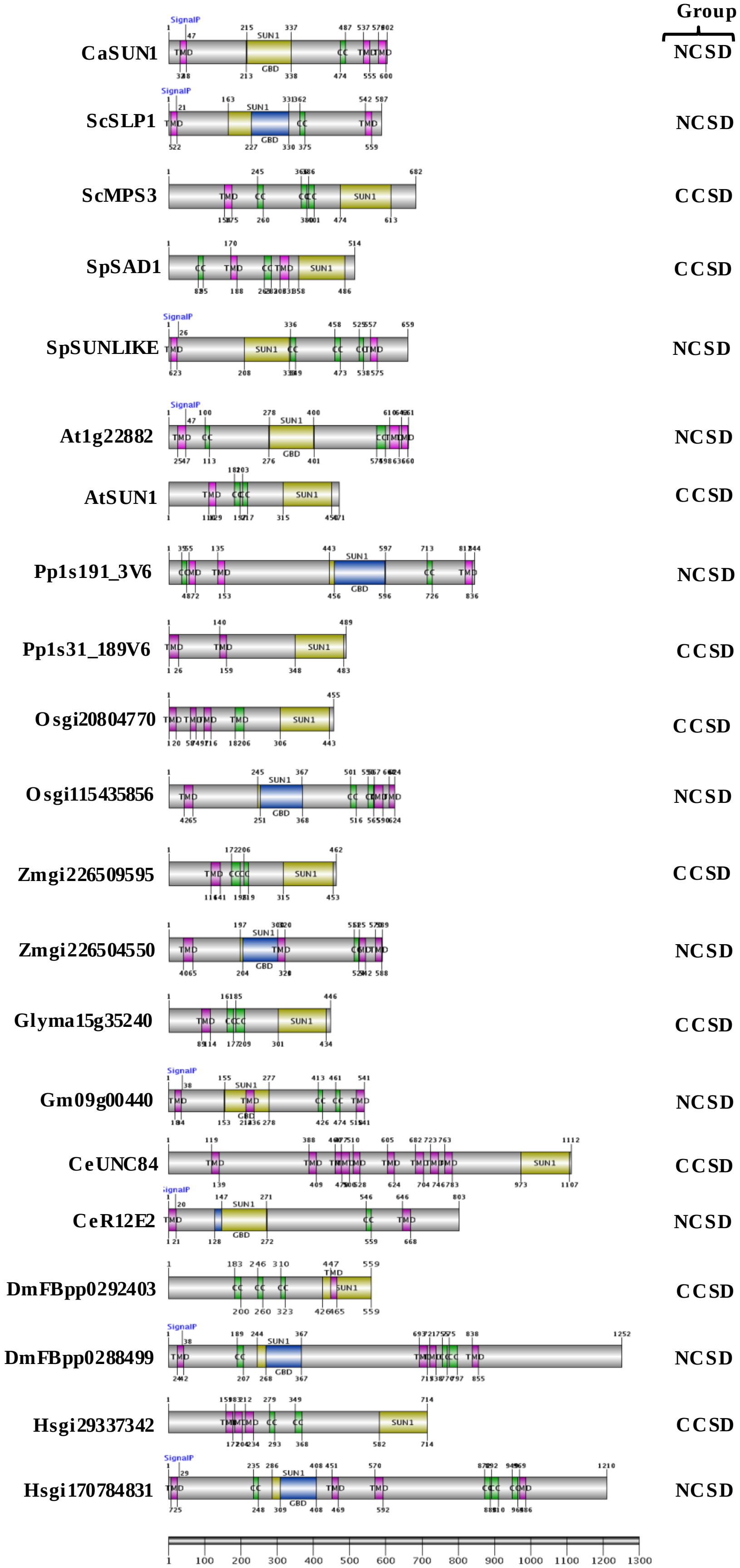
Supplementary Fig. S2. Dehydration-responsive comparative proteome of chickpea membrane and the representative 2-D gels. Three-week-old chickpea seedlings were subjected to dehydration and tissue were harvested every 24 h until 120 h. The membrane proteins were isolated from the unstressed and stressed tissue from each time point and 2-DE was performed. Three replicate gels for each time point (**a**) were computationally combined using PDQuest (version 7.2.0) software to generate the standard gels (**b**).



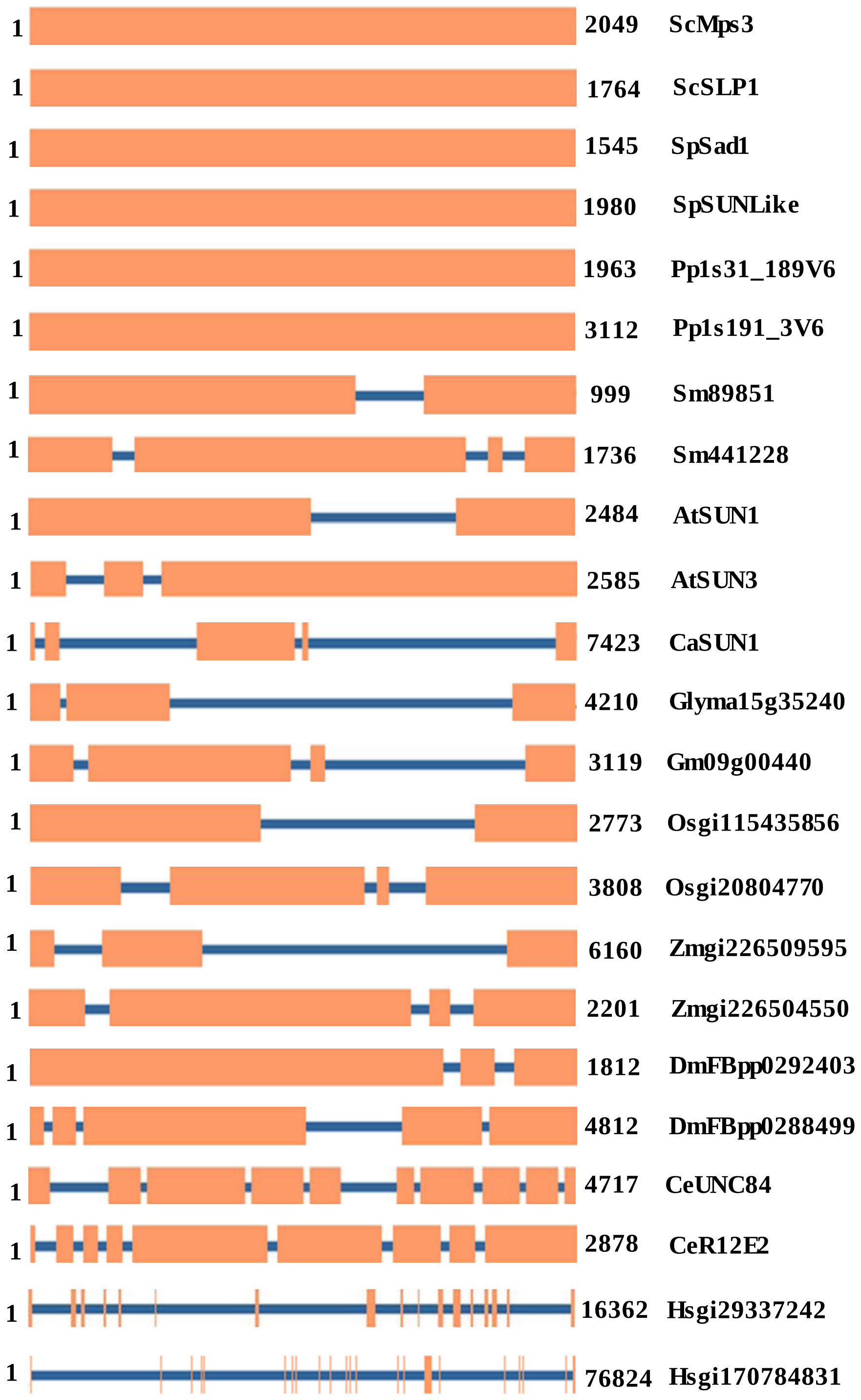
Supplementary Fig. S3. Relative abundance of few of the redundant DRPs. The expression profiles of the following proteins are represented. (**a**) Putative 60S acidic ribosomal protein P0, (**b**) Oxygen-evolving enhancer protein 1, (**c**) chlorophyll a/b binding protein type III, and (**d**) fructose-bisphosphate aldolase. The y-axis represents the fold change in expression of the protein across all the time points. The background value averaged across the replicates for a time point was used to calculate the fold changes. U represents unstressed condition.



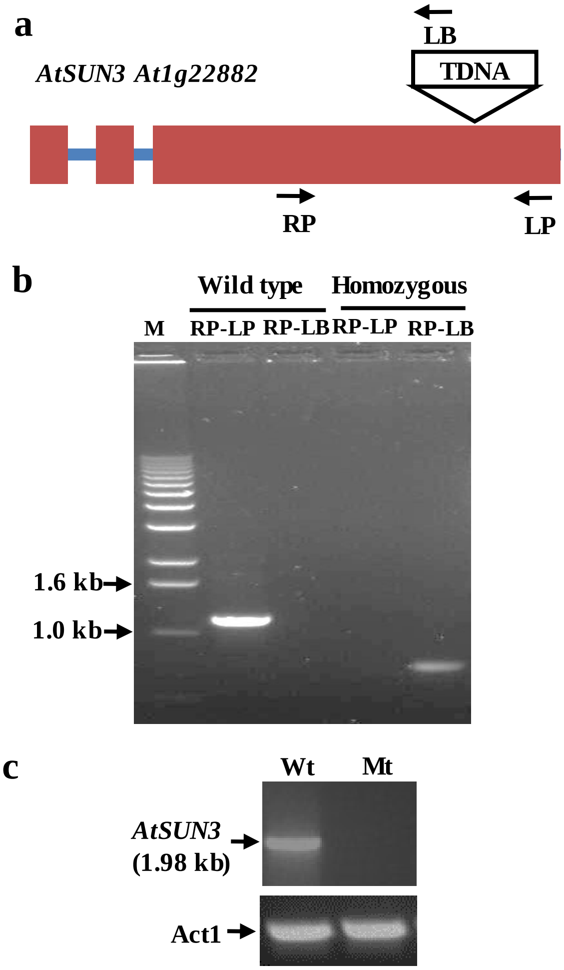
Supplementary Fig. S4. Hierarchical expression clustering of the identified DRPs in the membrane fraction of chickpea. Based on the expression profile, the DRPs were grouped into 11 clusters. The SOTA cluster tree (heat map) is shown at the top (**a**), and the expression graphs are shown below (**b**). Each DRP is represented by a single row of colored box and each time point by a single column. In the expression graph, the number of proteins in each cluster is given in the left upper corner and the cluster number is given in the right lower corner. U represents unstressed condition.



Supplementary Fig. S5. Analysis of plant and non-plant Sad1/UNC-84 (SUN) domain protein family. *In silico* analysis of putative SUN domain proteins from different organisms showing Sad1/UNC-84 (SUN) domain (InterProScan), transmembrane domain (TMPred), coiled-coil domain (Coils), galactose binding domain (InterProScan) and N-terminal signal peptide (SignalP). CCSD and NCSD denotes Canonical C-terminal SUN Domain and Non-Canonical SUN Domain, respectively.



Supplementary Fig. S6. Genomic organization of SUN protein gene family. A diagrammatic representation of the gene structures of SUN protein gene family of different taxa. The diagrams were drawn using SPIDEY program http://www.ncbi.nlm.nih. gov/spidey/ on the basis of alignments of cDNA to genomic DNA sequences. Exons are represented by filled boxes, while introns are represented by diagonal lines.



Supplementary Fig. S7. Identification of homozygous AtSUN3 T-DNA mutants. a. Schematic representation of the *AtSUN3* allele, with the T-DNA insertion shown as inverted triangle. Filled boxes indicate coding regions. **b**. Genotyping of wild type and *AtSUN3* mutant. **c**. RT-PCR analysis for the presence of full-length *AtSUN3* transcript. M: 1 kb DNA ladder, RP and LP: gene specific right primer and left primer, LB: T-DNA left border primer, Wt: wild type, Mt: *AtSUN3* mutant. Primers used in genotyping PCR and RT-PCR are listed in Supplementary Table S9.

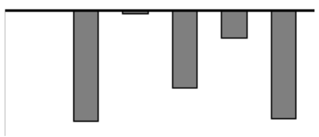
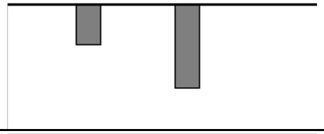
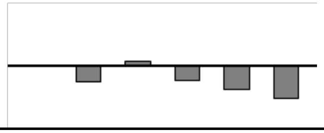
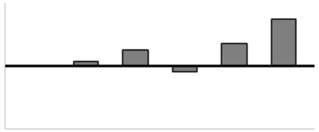
Supplementary Table S1. Reproducibility of two-dimensional gels.

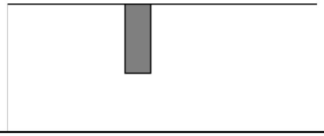
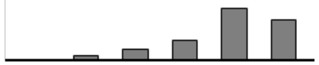
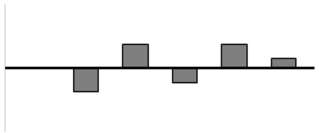
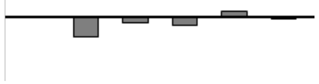
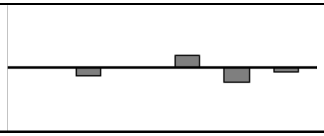
Time (h)	**Average No of spots** [a]	**High quality spots** [b]	**Reproducibility (%)**
Control	296	280	94.59
24	290	277	95.51
48	243	228	93.82
72	246	236	95.93
96	278	258	92.80
120	214	201	93.92
Total	1567	1480	94.45

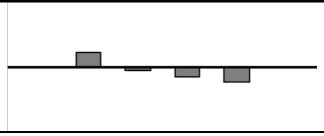
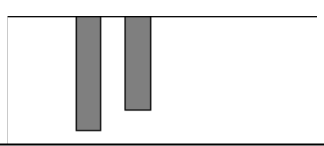
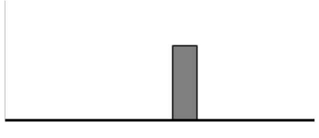
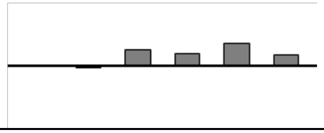
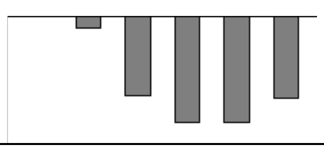
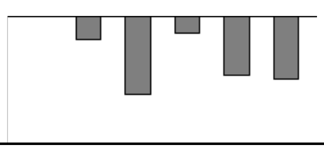
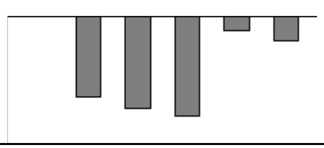
[a] Average number of spots present in three replicate gels of each time points

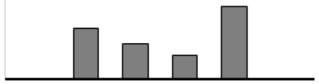
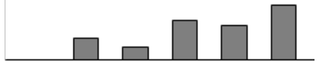
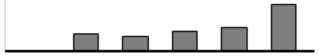
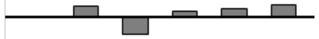
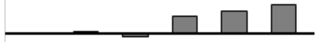
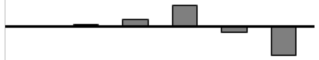
[b] Spots having a quality score more than 30 assigned by PDQuest (version 7.2.0)

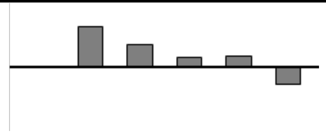
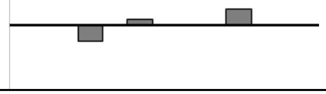
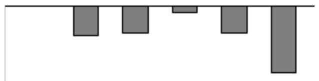
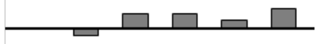
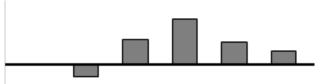
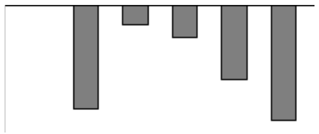
Supplementary Table S2. List of dehydration-responsive membrane proteins identified by MS/MS analysis.

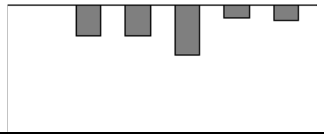
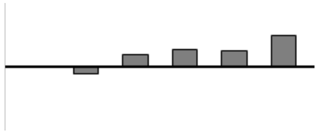
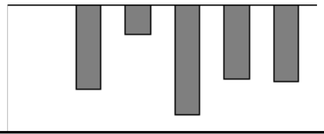
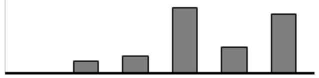
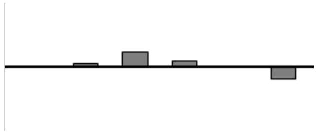
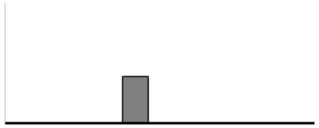
Spot No[a]	Identification	gi No[b]	Score	NP[c]	% Coverage	The MW/ pI	Exp MW/ pI	Time Kinetics[d] U 24 48 72 96 120	GO annotation
CaM-246!	Putative serine/threonine kinase	110289142	71	11	25	50.40/ 9.89	25.76/ 5.30		plastid
CaM-85!	Calcineurin-like phosphoesterase family protein	22329383	63	11	29	43.99/ 5.36	42.64/ 4.72		peroxisome, hydrolase activity
CaM-487*	Guanine nucleotide-binding protein subunit beta-like	3023847	297	7	30	31.834 /6.44	36.411 7/6.89		protein binding
CaM-247¶	Membrane protein CH1-like	115441379	41	3	2	70.30/ 4.91	30.04/ 5.45		mitochondrion, membrane
CaM-299!	Histone acetyltransferase GCN5	18410098	79	15	26	63.48/ 6.01	30.69/ 5.63		flower development, transferase activity, biosynthetic process, carbohydrate metabolic process, cellular process, secondary metabolic process, response to extracellular stimulus, cell communication, response to stress, response to endogenous stimulus, protein binding, nucleoplasm, biological_process, anatomical structure morphogenesis, multicellular organismal development, DNA binding, response to abiotic stimulus, cellular component organization, cellular protein modification process, sequence-specific DNA binding transcription factor activity

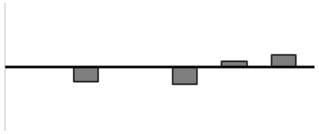
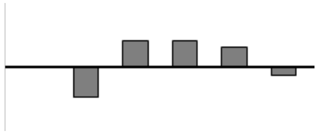
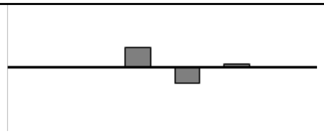
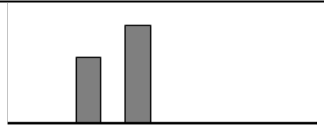
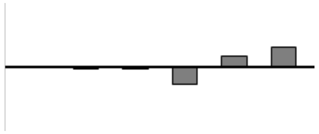
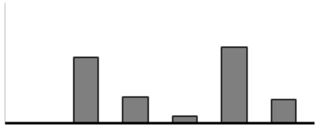
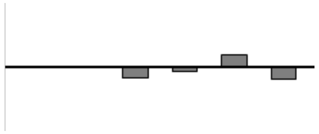
CaM-428*	Beta-1,3-glucanase	116490100	80	1	3	36.41/ 8.82	24.76/ 6.75		carbohydrate metabolic process, hydrolase activity, binding
CaM-483*	Luminal binding protein, BiP	297742397	248	7	6	73.31/ 4.96	30.25/ 6.91		nucleotide binding
CaM-182*	Ferritin	224140479	50	1	6	16.58/ 5.14	28.10/ 5.12		cellular homeostasis, catalytic activity, binding, transport, metabolic process
CaM-115!	Trypsin inhibitor, chain B (fragments)	3318877	144	7	57	19.29/ 4.79	14.86/ 5.07		enzyme regulator activity, biological_process
CaM-191*	Ferritin	255637227	129	2	9	30.23/ 5.26	30.23/ 5.23		cellular homeostasis, catalytic activity, binding, transport, metabolic process
CaM-271!	H+-transporting two-sector ATPase-alpha chain	114522	83	13	21	54.64/ 5.75	69.09/ 5.38		membrane, intracellular, transport, biosynthetic process, generation of precursor metabolites and energy, nucleobase-containing compound metabolic process, transporter activity, mitochondrion, nucleotide binding, hydrolase activity, plastid, thylakoid, cellular process
CaM-94*	Chaperonin 60 alpha subunit	217074850	764	17	28	62.00/ 5.11	72.03/ 4.7		protein metabolic process, cellular process, cytoplasm, protein binding, nucleotide binding

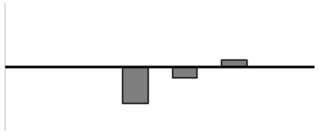
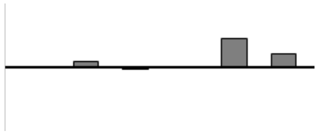
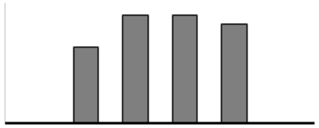
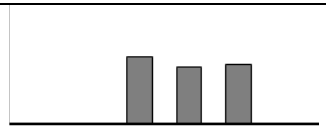
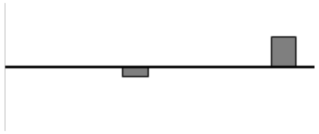
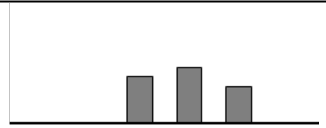
CaM-99*	Chaperone DnaK	92870233	501	11	15	75.10/5.19	83.09/4.69			protein metabolic process, cellular process, protein binding, nucleotide binding
CaM-157*	Putative GroEL protein chaperonin 60kDa	225435794	192	4	38	17.51/10.05	45.83/5.00			protein metabolic process, cellular process, cytoplasm, protein binding, nucleotide binding
CaM-150!	Chaperonin 60 alpha subunit	3790441	108	12	13	61.45/5.23	57.09/5.12			protein metabolic process, cellular process, cytoplasm, nucleotide bindin
CaM-73*	Actin (Fragment)	111610552	63	1	7	23.515/4.78	26.4341/4.75			N/F
CaM-39*	Putative 60S ribosomal protein L1	84468414	101	3	7	44.93/10.40	51.00/4.29			ribosome, structural molecule activity, translation
CaM-240*	40S ribosomal protein S12	255626071	54	2	12	15.345/5.50	19.2606/5.37			ribosome, structural molecule activity, translation
CaM-283*	40S ribosomal protein S12	255626071	162	3	23	15.345/5.50	19.0173/5.607			ribosome, structural molecule activity, translation
CaM-223!	Putative glutamate-tRNA ligase	115443869	70	14	11	63.10/6.27	74.10/5.23			ATP binding, cytoplasm, glutamate-tRNA ligase activity, glutamyl-tRNA aminoacylation

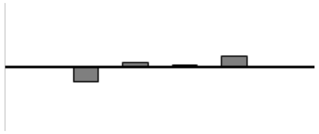
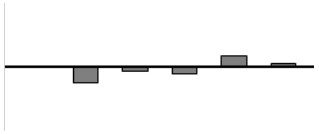
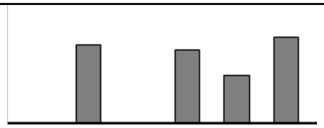
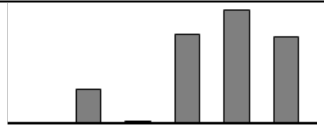
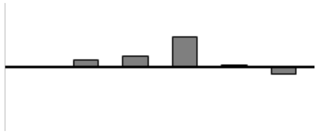
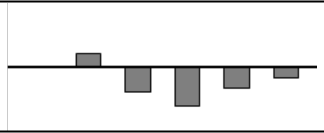
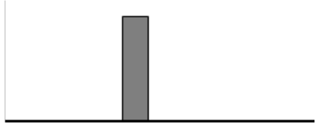
CaM-208*	Putative 60S acidic ribosomal protein P0	84468360	89	2	7	34.31/ 5.27	40.24/ 5.10		ribosome, structural molecule activity, cellular process, translation
CaM-209*	Putative 60S acidic ribosomal protein P0	84468360	82	2	7	34.31/ 5.27	40.25/ 5.21		ribosome, structural molecule activity, cellular process, translation
CaM-407!	Mitochondrial processing peptidase beta subunit	12802327	394	20	22	58.90/ 6.56	70.46/ 6.03		hydrolase activity, protein metabolic process, catabolic process, binding
CaM-301*	Proteasome subunit alpha type	224139394	199	4	21	27.38/ 5.59	31.39/ 5.81		cytoplasm, intracellular, protein metabolic process, catabolic process, cellular process, nucleus, hydrolase activity
CaM-21!	Chlorophyll a/b-binding protein AB96	115773	224	9	22	24.36/ 4.98	29.51/ 4.58		binding, generation of precursor metabolites and energy, photosynthesis, membrane, thylakoid, cellular protein modification process, plastid
CaM-187*	Chlorophyll a/b binding protein	3928140	349	11	32	28.357 /5.47	30.702 8/5.10		membrane, generation of precursor metabolites and energy, photosynthesis, plastid
CaM-75*	Chlorophyll a/b binding protein	3928140	411	12	30	28.35/ 5.47	30.58/ 4.78		membrane, generation of precursor metabolites and energy, photosynthesis, plastid
CaM-196*	Oxygen-evolving enhancer protein 1	131384	177	6	15	35.44/ 5.19	35.44/ 5.19		membrane, binding, generation of precursor metabolites and energy, photosynthesis, plastid, thylakoid

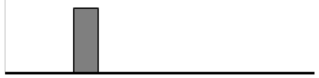
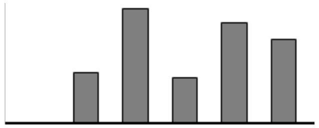
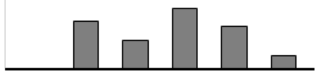
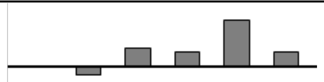
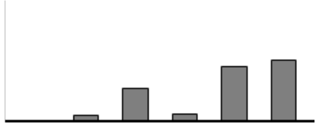
CaM-294*	Putative PSII-P protein	217072770	104	2	8	28.48/ 7.12	25.41/ 5.59		membrane, thylakoid, binding, photosynthesis
CaM-71*	light-harvesting complex II protein Lhcb3	224117282	113	3	12	24.20/ 4.77	28.14/ 4.77		membrane, generation of precursor metabolites and energy, photosynthesis, plastid
CaM-78*	Chlorophyll a/b binding protein	3928140	400	12	39	28.35/ 5.47	35.24/ 4.77		membrane, generation of precursor metabolites and energy, photosynthesis, plastid
CaM-22!	Chlorophyll a/b-binding protein 3 precursor	115800	160	7	19	27.90/ 5.46	29.38/ 4.47		binding, generation of precursor metabolites and energy, photosynthesis, membrane, thylakoid, cellular protein modification process, plastid
CaM-69!	Chlorophyll A-B binding protein	169124051	118	8	12	28.59/ 5.44	28.05/ 4.62		membrane, generation of precursor metabolites and energy, photosynthesis, plastid
CaM-127!	PSI type III chlorophyll a/b-binding protein (imported)	15219941	99	7	11	29.16/ 8.61	27.98/ 4.98		plastid, generation of precursor metabolites and energy, photosynthesis, intracellular, binding, membrane, thylakoid
CaM-125!	Oxygen-evolving enhancer protein 1	131384	111	7	14	35.10/ 6.25	27.83/ 4.87		membrane, binding, generation of precursor metabolites and energy, photosynthesis, plastid, thylakoid
CaM-183!	Oxygen-evolving enhancer protein 2	131390	89	9	14	28.20/ 8.29	25.64/ 5.16		membrane, binding, photosynthesis, plastid, thylakoid

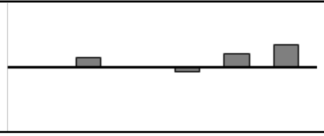
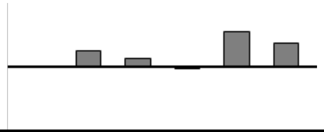
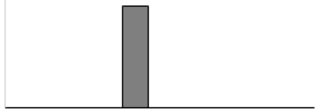
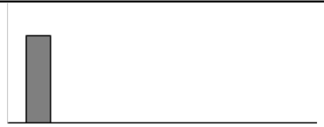
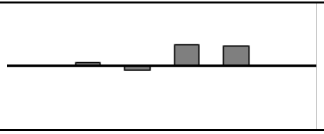
CaM-376*	Ferredoxin-NADP reductase	125553745	81	2	5	39.95/ 8.72	36.9/6. 12		plastid
CaM-74!	Light-harvesting chlorophyll-a/b binding protein Lhcb1	56809379	387	13	19	28.43/ 5.48	30.58/ 4.93		binding, generation of precursor metabolites and energy, photosynthesis, membrane, thylakoid, cellular protein modification process, plastid
CaM-319!	Putative ferredoxin-NADP(H) oxidoreductase	41052915	67	7	19	41.09/ 7.98	39.76/ 5.92		plastid
CaM-452¶	Ferredoxin: nadp+ reductase	4930119	130	3	12	34.98/ 6.54	36.58/ 6.49		nucleotide binding, protein binding, transport, plastid, catalytic activity, photosynthesis, membrane, thylakoid, generation of precursor metabolites and energy
CaM-226!	ATPase beta subunit (Fragment)	6467935	276	18	27	51.53/ 5.22	65.89/ 5.21		membrane, intracellular, transport, biosynthetic process, generation of precursor metabolites and energy, nucleobase-containing compound metabolic process, hydrolase activity, transporter activity, nucleotide binding, cellular process
CaM-147*	ATP synthase subunit beta, chloroplastic	11466372	92	2	6	51.99/ 5.10	44.87/ 4.84		membrane, intracellular, transport, biosynthetic process, generation of precursor metabolites and energy, nucleobase-containing compound metabolic process, hydrolase activity, transporter activity, nucleotide binding, plastid, thylakoid, cellular process
CaM-189*	ATP synthase subunit alpha	197294119	589	19	24	55.64/ 5.44	32.38/ 5.16		membrane, intracellular, transport, biosynthetic process, generation of precursor metabolites and energy, nucleobase-containing compound metabolic process, transporter activity, nucleotide binding, hydrolase activity, plastid, thylakoid, cellular process

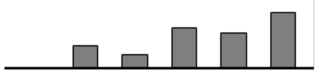
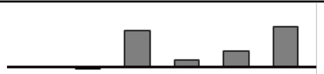
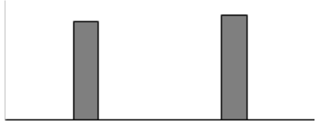
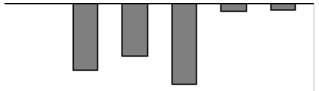
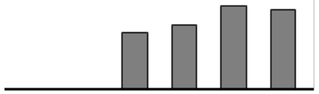
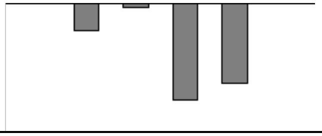
CaM-221!	ATP synthase beta subunit (Fragment)	3850926	116	13	22	52.73/ 5.15	65.80/ 5.14		membrane, intracellular, transport, biosynthetic process, generation of precursor metabolites and energy, nucleobase-containing compound metabolic process, hydrolase activity, transporter activity, nucleotide binding, plastid, thylakoid, cellular process
CaM-161!	ATP synthase beta subunit (Fragment)	7708546	918	41	51	51.18/ 5.07	65.76/ 5.04		membrane, intracellular, transport, biosynthetic process, generation of precursor metabolites and energy, nucleobase-containing compound metabolic process, hydrolase activity, transporter activity, nucleotide binding, plastid, thylakoid, cellular process
CaM-80!	ATP synthase beta subunit (Fragment)	4063542	671	19	26	49.13/ 5.06	35.75/ 4.60		membrane, intracellular, transport, biosynthetic process, generation of precursor metabolites and energy, nucleobase-containing compound metabolic process, hydrolase activity, transporter activity, nucleotide binding, plastid, thylakoid, cellular process
CaM-205*	ATP synthase subunit beta	269914683	171	4	12	59.68/ 6.18	38.234 /5.10		hydrolase activity, transporter activity, transport, cellular process, biosynthetic process, generation of precursor metabolites and energy, nucleobase-containing compound metabolic process, membrane, mitochondrion, catabolic process, nucleotide binding
CaM-162!	ATP synthase beta subunit (Fragment)	66276255	730	26	41	52.42/ 5.54	65.83/ 4.95		membrane, intracellular, transport, biosynthetic process, generation of precursor metabolites and energy, nucleobase-containing compound metabolic process, hydrolase activity, transporter activity, plastid, nucleotide binding, cellular process
CaM-207*	ATP synthase subunit alpha	197294119	196	7		55.64/ 5.44	42.15/ 5.30		membrane, intracellular, transport, biosynthetic process, generation of precursor metabolites and energy, nucleobase-containing compound metabolic process, transporter activity, nucleotide binding, hydrolase activity, plastid, thylakoid, cellular process
CaM-222*	ATP synthase subunit beta	197294097	410	19	27	52.96/ 5.16	73.99/ 5.16		membrane, intracellular, transport, biosynthetic process, generation of precursor metabolites and energy, nucleobase-containing compound metabolic process, hydrolase activity, transporter activity, nucleotide binding, plastid, thylakoid, cellular process
CaM-295*	ATP synthase subunit alpha	197294119	153	5	295	55.64/ 5.44	29.74/ 5.76		membrane, intracellular, transport, biosynthetic process, generation of precursor metabolites and energy, nucleobase-containing compound metabolic process, transporter activity, nucleotide binding, hydrolase activity, plastid, thylakoid, cellular process

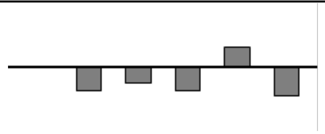
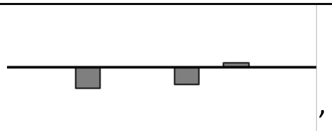
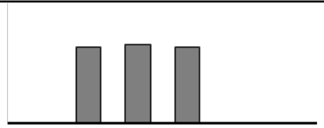
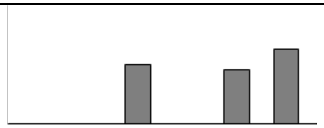
CaM-316*	ATP synthase subunit alpha	197294119	328	10	17	55.64/ 5.44	45.62/ 5.83		membrane, intracellular, transport, biosynthetic process, generation of precursor metabolites and energy, nucleobase-containing compound metabolic process, transporter activity, nucleotide binding, hydrolase activity, plastid, thylakoid, cellular process
CaM-335*	ATP synthase subunit alpha	197294119	75	2	4	55.64/ 5.44	69.22/ 5.62		membrane, intracellular, transport, biosynthetic process, generation of precursor metabolites and energy, nucleobase-containing compound metabolic process, transporter activity, nucleotide binding, hydrolase activity, plastid, thylakoid, cellular process
CaM-382*	ATP synthase subunit alpha	197294119	388	8	15	55.64/ 5.44	41.60/ 5.97		membrane, intracellular, transport, biosynthetic process, generation of precursor metabolites and energy, nucleobase-containing compound metabolic process, transporter activity, nucleotide binding, hydrolase activity, plastid, thylakoid, cellular process
CaM-386*	ATP synthase subunit alpha	197294119	424	10	22	55.64/ 5.44	44.18/ 6.18		membrane, intracellular, transport, biosynthetic process, generation of precursor metabolites and energy, nucleobase-containing compound metabolic process, transporter activity, nucleotide binding, hydrolase activity, plastid, thylakoid, cellular process
CaM-254*	ATP synthase gamma chain	217072566	207	4	13	41.18/ 8.33	34.82/ 5.48		membrane, intracellular, transporter activity, transport, biosynthetic process, generation of precursor metabolites and energy, nucleobase-containing compound metabolic process, nucleotide binding, hydrolase activity
CaM-269*	ATP synthase subunit alpha	13518443	326	8	15	55.80/ 5.22	65.19/ 5.34		membrane, intracellular, transporter activity, transport, biosynthetic process, generation of precursor metabolites and energy, nucleobase-containing compound metabolic process, nucleotide binding, hydrolase activity, plastid, thylakoid, cellular process
CaM-311*	ATP synthase CF1 alpha subunit	393396111	295	5	11	55.737 /5.21	42.490 6/5.89		ATP binding, ATP hydrolysis coupled proton transport, ATP synthesis coupled proton transport

CaM-396*	ATP synthase subunit alpha	197294119	439	10	19	55.64/ 5.44	52.90/ 5.91		membrane, intracellular, transport, biosynthetic process, generation of precursor metabolites and energy, nucleobase-containing compound metabolic process, transporter activity, nucleotide binding, hydrolase activity, plastid, thylakoid, cellular process
CaM-272!	ATP synthase CF1 alpha subunit	13518443	572	21	23	55.80/ 5.22	69.51/ 5.51		membrane, intracellular, transporter activity, transport, biosynthetic process, generation of precursor metabolites and energy, nucleobase-containing compound metabolic process, nucleotide binding, hydrolase activity, plastid, thylakoid, cellular process
CaM-218*	Glutamine synthetase	12963877	50	1	2	47.40/ 5.73	50.72/ 5.32		catalytic activity, nucleotide binding, biosynthetic process,
CaM-308*	Fructose-bisphosphate aldolase 1	399024	182	5	14	38.63/ 5.83	39.99/ 5.62		carbohydrate metabolic process, generation of precursor metabolites and energy, catabolic process, catalytic activity, plastid
CaM-310¶	Fructose-bisphosphate aldolase (EC 4.1.2.13) precursor	399024	206	6	17	38.74/ 5.83	39.89/ 5.86		carbohydrate metabolic process, generation of precursor metabolites and energy, catabolic process, catalytic activity, plastid
CaM-461*	Glyceraldehyde-3-phosphate dehydrogenase	120666	167	4		36.68/ 8.3	42.214 9/6.75		cytoplasm, nucleotide binding, carbohydrate metabolic process, generation of precursor metabolites and energy, catabolic process, catalytic activity, metabolic process
CaM-141*	Phosphoglycerate kinase	255544584	172	3		50.14/ 8.47	40.16/ 4.90		phosphoglycerate kinase activity, glycolysis
CaM-322*	Phosphoglycerate kinase	223975935	122	3	11	50.00/ 8.74	46.94/ 5.64		phosphoglycerate kinase activity, glycolysis

CaM-257¶	Plastidic aldolase	38096041	240	9	17	43.18/ 6.86	35.52/ 5.61		carbohydrate metabolic process, generation of precursor metabolites and energy, catabolic process, catalytic activity
CaM-485*	Carbonic anhydrase	270342124	227	6	21	35.04/ 8.09	27.45/ 6.95		binding, catalytic activity, metabolic process
CaM-210*	Fructose-bisphosphate aldolase	84468290	163	5	14	43.03/ 6.86	40.35/ 5.35		carbohydrate metabolic process, generation of precursor metabolites and energy, catabolic process, catalytic activity
CaM-460!	Glyceraldehyde 3-phosphate dehydrogenase	3413165	70	4	15	20.88/ 5.24	41.91/ 6.66		catalytic activity, metabolic process
CaM-216¶	Glutamate-ammonia ligase (EC 6.3.1.2) delta precursor	121344	39	1	2	47.65/ 6.18	51.86/ 5.13		catalytic activity, metabolic process, nucleotide binding, plastid, biosynthetic process, 0
CaM-214¶	Glutamate-ammonia ligase (EC 6.3.1.2) delta precursor	121344	68	1	2	47.65/ 6.18	51.14/ 5.23		catalytic activity, metabolic process, nucleotide binding, plastid, biosynthetic process, 0
CaM-206!	Phosphoribulokinase	1885326	71	6	7	39.23/ 5.41	43.82/ 5.18		carbohydrate metabolic process, kinase activity, nucleotide binding, metabolic process, cellular process
CaM-435*	Carbonic anhydrase	8954289	95	3	14	35.46/ 7.59	29.73/ 6.47		binding, catalytic activity, metabolic process

CaM-462*	Glyceraldehyde-3-phosphate dehydrogenase A	120658	200	6	12	43.31/ 8.80	44.49/ 6.81		biosynthetic process, carbohydrate metabolic process, photosynthesis, nucleotide binding, cellular process, plastid, metabolic process, catalytic activity
CaM-155!	Dynein-1-alpha heavy chain	159490411	69	63	10	525.42 /5.32	61.98/ 5.11		motor activity, cytoskeleton, cellular component organization, cellular process, intracellular, nucleobase-containing compound metabolic process, catabolic process, nucleotide binding, cell, hydrolase activity
CaM-436*	Putative quinone oxidoreductase	21068664	158	4	25	21.70/ 6.51	28.26/ 6.62		nucleotide binding, metabolic process, catalytic activity
CaM-54!	Activator of spomin	145357734	65	8	24	17.25/ 9.63	12.38/ 4.69		sequence-specific DNA binding transcription factor activity, DNA binding,
CaM-138*	Chromosome chr17 scaffold_16	225456471	149	4	4	33.35/ 5.67	37.90/ 4.97		ATP binding, protein binding, nucleoside-triphosphatase activity, protein metabolic process
CaM-43*	Ribulose bisphosphate carboxylase large chain	197294096	295	8	16	52.65/ 6.04	64.35/ 4.29		catalytic activity, plastid, photosynthesis, binding, metabolic process
CaM-122*	Ribulose bisphosphate carboxylase large chain	197294096	148	7		52.65/ 6.04	23.64/ 5.05		catalytic activity, plastid, photosynthesis, binding, metabolic process

CaM-290!	Intronic ORF; similar to LAGLIDADG endonuclease	2943730	80	11	21	29.46/ 10.01	21.47/ 6.00		DNA metabolic process, nuclease activity, DNA binding, mitochondrion
CaM-443*	Predicted protein	224119706	53	1	3	27.44/ 8.65	31.20/ 6.64		transferase activity
CaM-416*	Unknown protein 18	226493856	84	3		68.61/ 6.01	77.36/ 6.44		nucleotide binding, generation of precursor metabolites and energy, catabolic process, catalytic activity, molecular_function
CaM-263¶	OSJNBb0085H11. 1 protein	38346013	50	1	7	176.76 /9.26	53.68/ 5.61		RNA binding, RNA-directed DNA polymerase activity, RNA-dependent DNA replication, DNA integration, ribonuclease H activity
CaM-9*	Putative uncharacterized protein	217075500	82	2	10	11.323 / 4.31	14.4/4. 2		ribosome, structural molecule activity, translation
CaM-346*	Putative uncharacterized protein	118481093	108	2	2	80.69/ 6.29	85.947 7/5.75		transferase activity, metabolic process
CaM-24*	Putative uncharacterized protein	217071520	181	4	33	17.01/ 9.00	26.54/ 4.47		ribosome, structural molecule activity, translation
CaM-323*	Putative uncharacterized protein	224284512	94	2	7	40.97/ 6.04	44.21/ 5.66		nucleotide binding

CaM-112*	Putative uncharacterized protein	8894548	154	5	10	54.58/ 4.87	105/4. 72		transport, membrane
CaM-445*	Putative uncharacterized	255646048	235	4	19	29.46/ 5.79	32.89/ 6.51		transferase activity
CaM-171!	Unknown protein	15236812	67	16	8	90.90/ 5.09	74.93/ 5.11		plastid
CaM-64!	Hypothetical protein P0415D04.53	47496995	66	8	34	30.31/ 11.81	24.12/ 4.77		N/F
CaM-267!	Hypothetical protein F26P21.180	3688187	67	10	22	57.25/ 7.64	44.54/ 5.58		peptidyl-prolyl cis-trans isomerase activity, protein folding
CaM-56!	Hypothetical protein OSJNBa0075N02. 148	28972006	66	7	29	20.62/ 12.24	22.37/ 4.49		N/F

[a] Spot number as marked on 2-D gel images (**Fig. 1a**). The spot numbers were designated as CaM-X, where Ca indicates the organism (*Cicer arietinum*), M denotes the membrane fraction, and X denotes the spot number as given on 2-D gel image.

[b] Protein identification number as in GenBank.

[c] NP represent the number of peptide.

[d]Time kinetics represents the average change in spot density at various time points (Unstressed to 120 h). The data were taken in terms of fold expression with respect to the control value and were log transformed to the base two in order to level the scale of expression. The spot volume of each protein spot during the course of dehydration is given in Table S3.

Spots marked by ‘*’ were identified by Q-TRAP, ‘¶’ identified by QStar, and ‘!’ identified by MALDI analysis.

Supplementary Table S3. Average normalized spot volume, standard deviation (SD) and coefficient of variance (CV) of identified protein spots and corresponding log transformed data are given below.

Untransformed data

Dehydration (h)

Spot ID	Identification	Unstressed				24				48				72				96				120			
		Av Norm Qty		SD	CV %	Av Norm Qty		SD	CV %	Av Norm Qty		SD	CV %	Av Norm Qty		SD	CV %	Av Norm Qty		SD	CV %	Av Norm Qty		SD	CV %
CaM-9	Putative uncharacterized protein	800.7335072	±	237.4417	29.65303	344.2150004	±	61.66478	17.91461	950.9281447	±	123.3745	12.97412	772.5591554	±	153.4841	19.86697	220.5267706	±	38.36599	17.39743	511.4460741	±	16.4167	3.20986
CaM-21	Chlorophyll a/b-binding protein AB96	991.1415897	±	198.8444	20.06216	618.9333919	±	124.9067	20.18096	1410.284012	±	124.6233	8.836748	2222.80698	±	346.7256	15.59855	2119.042795	±	222.4723	10.49872	2751.962925	±	253.5388	9.213016
CaM-22	Chlorophyll a/b-binding protein 3 precursor	1029.182719	±	184.6557	17.94197	719.2843876	±	174.6066	24.27504	2284.395606	±	295.3113	12.92733	2321.580815	±	149.933	6.458227	1660.905755	±	300.3719	18.08483	2949.095664	±	678.3743	23.00279
CaM-24	Putative uncharacterized protein	0	±	0	0	0	±	0	0	106.9957406	±	23.28793	21.76529	161.7822663	±	9.527552	5.88912	514.934386	±	112.0014	21.75061	406.2080842	±	51.23652	12.61337
CaM-39	Putative 60S ribosomal protein L1	66.05713145	±	13.03683	19.73569	0	±	0	0	0	±	0	0	0	±	0	0	0	±	0	0	55.15583732	±	6.999674	12.69072
CaM-43	Ribulose bisphosphate carboxylase large chain	241.4233441	±	45.42114	18.8139	0	±	0	0	0	±	0	0	0	±	0	0	0	±	0	0	121.1134876	±	27.06799	22.34928
CaM-54	Activator of spomin	0	±	0	0	0	±	0	0	1406.839822	±	257.083	18.27379	0	±	0	0	0	±	0	0	0	±	0	0
CaM-56	Hypothetical protein OSJNBa0075N02.148	88.20980337	±	20.57835	23.32886	0	±	0	0	0	±	0	0	0	±	0	0	0	±	0	0	156.0878433	±	14.01668	8.979997
CaM-64	Hypothetical protein P0415D04.53	0	±	0	0	333.1703368	±	111.034	33.32649	372.0447538	±	70.28787	18.89231	324.293068	±	79.89235	24.63585	0	±	0	0	0	±	0	0
CaM-69	Chlorophyll A-B binding protein	700.4973267	±	219.3337	31.31114	537.8765958	±	21.50965	3.998993	1205.981431	±	208.4761	17.28685	1875.955883	±	122.3095	6.519851	1127.029965	±	216.6935	19.22695	954.5596113	±	88.10411	9.229817
CaM-71	light-harvesting complex II protein Lhcb3	665.8566257	±	110.9151	16.6575	282.3576962	±	42.74787	15.13962	940.6731595	±	91.61234	9.739019	689.271531	±	62.66822	9.09195	1643.123142	±	259.2501	15.77789	723.5203842	±	216.7145	29.95279
CaM-73	Actin (Fragment)	497.3356014	±	161.0171	32.37595	455.2059845	±	169.2435	37.17955	1263.412831	±	78.02543	6.175767	955.9093893	±	60.37319	6.315785	1742.124183	±	236.7883	13.59193	936.1911599	±	190.5594	20.35475
CaM-74	Light-harvesting chlorophyll-a/b binding protein Lhcb1	1127.892948	±	206.1494	18.27739	810.2392033	±	186.353	22.99974	2144.599597	±	420.2253	19.59458	2954.830531	±	325.6085	11.01953	2667.465339	±	181.7633	6.814085	6233.24603	±	766.9053	12.30347
CaM-75	Chlorophyll a/b binding protein	751.4159984	±	209.1888	27.83928	625.2827134	±	126.1663	20.17748	1574.70405	±	202.6045	12.86619	3134.635257	±	585.0382	18.66368	2591.648458	±	752.0811	29.01941	3256.72816	±	703.6131	21.60491
CaM-78	Chlorophyll a/b binding protein	769.9315715	±	182.222	23.66729	344.3528946	±	80.63727	23.41704	368.6046754	±	81.66259	22.15452	639.4213263	±	179.9235	28.13848	367.8027757	±	91.69916	24.93161	127.6000358	±	18.1834	14.25031
CaM-80	ATP synthase beta subunit (Fragment)	270.7012909	±	14.50287	5.357518	0	±	0	0	784.4900818	±	182.9682	23.3232	119.8634843	±	26.06627	21.74663	315.4003942	±	8.463177	2.683312	0	±	0	0
CaM-85	Calcineurin-like phosphoesterase family protein	0	±	0	0	51.17956684	±	13.83755	27.03725	0	±	0	0	0	±	0	0	0	±	0	0	0	±	0	0
CaM-94	Chaperonin 60 alpha subunit	174.0841652	±	9.66986	5.554704	113.6796404	±	15.74678	13.85189	183.1896714	±	29.83512	16.28646	333.4345357	±	85.86015	25.75023	78.70622309	±	18.88532	23.9947	135.9573183	±	11.16879	8.214921
CaM-99	Chaperone DnaK	99.57217023	±	30.27321	30.40329	228.7051359	±	64.92199	28.38677	86.11743089	±	17.49015	20.30965	60.27488451	±	16.11735	26.73974	47.12346003	±	4.891085	10.3793	0	±	0	0
CaM-112	Putative uncharacterized protein	0	±	0	0	0	±	0	0	0	±	0	0	0	±	0	0	0	±	0	0	377.3323747	±	69.43861	18.40251
CaM-115	Trypsin inhibitor, chain B (fragments)	50.82434769	±	13.00547	25.58906	0	±	0	0	0	±	0	0	0	±	0	0	0	±	0	0	0	±	0	0
CaM-122	Ribulose bisphosphate carboxylase large chain	315.0835901	±	45.16767	14.33514	374.6231751	±	54.4349	14.53057	247.3605813	±	42.32058	17.10886	1013.533567	±	300.068	29.60613	900.4561453	±	211.3709	23.47376	0	±	0	0
CaM-125	Oxygen-evolving enhancer protein 1	153.8835252	±	45.29056	29.43171	61.54537258	±	14.24627	23.14759	347.9442793	±	68.17961	19.59498	155.4561266	±	36.51646	23.48988	29.37726048	±	5.242455	17.84528	53.01742514	±	14.90821	28.11945
CaM-127	PSI type III chlorophyll	1815.295155	±	427.4387	23.54651	589.8266176	±	52.69429	8.933862	1473.517927	±	488.7744	33.17058	1274.206647	±	283.0152	22.21109	805.5078866	±	157.0596	19.49821	517.3054373	±	24.42038	4.720689

Log transformed data

Dehydration (h)

Spot ID	Identification	Unstressed				24				48				72				96				120			
		Av Norm Qty		SD	CV %	Av Norm Qty		SD	CV %	Av Norm Qty		SD	CV %	Av Norm Qty		SD	CV %	Av Norm Qty		SD	CV %	Av Norm Qty		SD	CV %
CaM-9	Putative uncharacterized protein	9.603207768	±	0.42532	4.42894	8.412229	±	0.2521	2.996831	9.885128	±	0.186656	1.888256	9.57389	±	0.293719	3.067918	7.769659	±	0.258619	3.328572	8.997939	±	0.046608	0.517981
CaM-21	Chlorophyll a/b-binding protein AB96	9.932820069	±	0.298015	3.000305	9.25478	±	0.282887	3.056657	10.45798	±	0.128467	1.228414	11.10698	±	0.217513	1.958345	11.04367	±	0.156175	1.414156	11.422	±	0.136739	1.197152
CaM-22	Chlorophyll a/b-binding protein 3 precursor	9.991259763	±	0.265601	2.658332	9.46384	±	0.333331	3.522154	11.14915	±	0.193462	1.73522	11.17884	±	0.094737	0.847468	10.68154	±	0.266912	2.498818	11.49777	±	0.358806	3.120658
CaM-24	Putative uncharacterized protein	0	±	0	0	0	±	0	0	6.719216	±	0.307808	4.581015	7.336218	±	0.085858	1.170329	8.986362	±	0.304598	3.389564	8.658089	±	0.187876	2.169953
CaM-39	Putative 60S ribosomal protein L1	6.026426103	±	0.290237	4.81607	0	±	0	0	0	±	0	0	0	±	0	0	0	±	0	0	5.777553	±	0.185619	3.212761
CaM-43	Ribulose bisphosphate carboxylase large chain	7.897615026	±	0.280701	3.55425	0	±	0	0	0	±	0	0	0	±	0	0	0	±	0	0	6.896318	±	0.321173	4.65716
CaM-54	Activator of spomin	0	±	0	0	0	±	0	0	10.44273	±	0.256813	2.459255	0	±	0	0	0	±	0	0	0	±	0	0
CaM-56	Hypothetical protein OSJNBa0075N02.148	6.435103253	±	0.351705	5.465418	0	±	0	0	0	±	0	0	0	±	0	0	0	±	0	0	7.282346	±	0.129311	1.775684
CaM-64	Hypothetical protein P0415D04.53	0	±	0	0	8.329746	±	0.459339	5.514438	8.521223	±	0.283649	3.328734	8.313427	±	0.341677	4.109943	0	±	0	0	0	±	0	0
CaM-69	Chlorophyll A-B binding protein	9.405327966	±	0.449908	4.783549	9.070351	±	0.058312	0.64289	10.22207	±	0.243424	2.381359	10.87131	±	0.095856	0.881733	10.12103	±	0.271436	2.681895	9.894431	±	0.137094	1.385571
CaM-71	light-harvesting complex II protein Lhcb3	9.365312404	±	0.245839	2.624993	8.130847	±	0.210996	2.595002	9.872794	±	0.144933	1.468005	9.425038	±	0.129063	1.369367	10.67051	±	0.22395	2.098772	9.448925	±	0.481366	5.094402
CaM-73	Actin (Fragment)	8.911433258	±	0.43961	4.933099	8.7677	±	0.512194	5.841829	10.30125	±	0.090214	0.875763	9.898762	±	0.092868	0.93818	10.75732	±	0.203063	1.88767	9.850651	±	0.294585	2.990509
CaM-74	Light-harvesting chlorophyll-a/b binding protein Lhcb1	10.12311947	±	0.266514	2.632722	9.636769	±	0.33176	3.442643	11.04891	±	0.272367	2.465106	11.52286	±	0.162316	1.408648	11.37906	±	0.097039	0.852789	12.59859	±	0.175705	1.394638
CaM-75	Chlorophyll a/b binding protein	9.516501741	±	0.399098	4.193742	9.268111	±	0.298572	3.221496	10.61251	±	0.192383	1.812796	11.59588	±	0.286348	2.469395	11.30165	±	0.398572	3.526671	11.64514	±	0.328284	2.819063
CaM-78	Chlorophyll a/b binding protein	9.561337401	±	0.344411	3.60212	8.39835	±	0.365994	4.357932	8.503532	±	0.307033	3.610657	9.276596	±	0.451636	4.868552	8.491815	±	0.369396	4.350026	6.98553	±	0.208565	2.985676
CaM-80	ATP synthase beta subunit (Fragment)	8.07918151	±	0.07713	0.954671	0	±	0	0	9.590534	±	0.325762	3.396703	6.8822	±	0.316902	4.604668	8.300693	±	0.038787	0.46728	0	±	0	0
CaM-85	Calcineurin-like phosphoesterase family protein	0	±	0	0	5.642869	±	0.385567	6.832812	0	±	0	0	0	±	0	0	0	±	0	0	0	±	0	0
CaM-94	Chaperonin 60 alpha subunit	7.442124001	±	0.081479	1.09483	6.819447	±	0.202359	2.967376	7.505081	±	0.225871	3.009571	8.347675	±	0.386183	4.626239	6.268145	±	0.369728	5.898523	7.083761	±	0.11861	1.674388
CaM-99	Chaperone DnaK	6.596698444	±	0.411617	6.23975	7.795882	±	0.43074	5.525221	6.407794	±	0.299652	4.676365	5.876815	±	0.404746	6.887174	5.553296	±	0.14748	2.655721	0	±	0	0
CaM-112	Putative uncharacterized protein	0	±	0	0	0	±	0	0	0	±	0	0	0	±	0	0	0	±	0	0	8.544313	±	0.254103	2.973942
CaM-115	Trypsin inhibitor, chain B (fragments)	5.636827104	±	0.361348	6.410485	0	±	0	0	0	±	0	0	0	±	0	0	0	±	0	0	0	±	0	0
CaM-122	Ribulose bisphosphate carboxylase large chain	8.290085054	±	0.200794	2.4221	8.538837	±	0.214333	2.510093	7.936576	±	0.244431	3.079803	9.942556	±	0.43069	4.331783	9.785783	±	0.359586	3.674572	0	±	0	0
CaM-125	Oxygen-evolving enhancer protein 1	7.216931598	±	0.476605	6.603984	5.919511	±	0.316839	5.352459	8.422452	±	0.302747	3.594518	7.250547	±	0.369267	5.092952	4.861726	±	0.252168	5.186809	5.685902	±	0.440419	7.745806
CaM-127	PSI type III chlorophyll	10.80000834	±	0.33304	3.083703	9.200338	±	0.128142	1.392801	10.4755	±	0.454651	4.340141	10.29015	±	0.335508	3.260476	9.636502	±	0.269076	2.792255	9.013781	±	0.069052	0.766075

	a/b-binding protein (imported)																																																	
CaM-138	Chromosome chr17 scaffold_16	36.40528016	±	6.381954	17.5303	0	±	0	0	0	±	0	0	0	±	0	0	0	±	0	0	0	±	0	0		5.170190649	±	0.266804	5.160428	0	±	0	0	0	±	0	0	0	±	0	0	0	±	0	0	0	±	0	0
CaM-141	Phosphoglycerate kinase	37.85786164	±	5.230238	13.81546	0	±	0	0	51.12092659	±	8.681392	16.98207	0	±	0	0	0	±	0	0	0	±	0	0		5.233607208	±	0.194937	3.724724	0	±	0	0	5.662452	±	0.238545	4.212743	0	±	0	0	0	±	0	0	0	±	0	0
CaM-147	ATP synthase subunit beta, chloroplastic	114.5677452	±	28.18687	24.6028	140.6972114	±	48.09331	34.18213	258.1128027	±	19.93688	7.724095	162.9209697	±	51.87002	31.83754	118.3816534	±	24.99765	21.11616	58.91331416	±	16.34342	27.74146		6.81248537	±	0.340437	4.997253	7.084189	±	0.46597	6.577601	8.009057	±	0.109427	1.366293	7.299478	±	0.457843	6.272268	6.864217	±	0.321782	4.687824	5.846233	±	0.377199	6.452007
CaM-150	Chaperonin 60 alpha subunit	48.41127295	±	12.36496	25.5415	0	±	0	0	0	±	0	0	114.6948351	±	28.92216	25.21662	0	±	0	0	0	±	0	0		5.562042205	±	0.401376	7.216338	0	±	0	0	0	±	0	0	6.807993	±	0.390625	5.737745	0	±	0	0	0	±	0	0
CaM-155	Dynein-1-alpha heavy chain	54.75540035	±	3.519688	6.428021	0	±	0	0	0	±	0	0	0	±	0	0	48.42000368	±	3.020575	6.238279	0	±	0	0		5.772982154	±	0.09133	1.582032	0	±	0	0	0	±	0	0	0	±	0	0	5.595622	±	0.091356	1.632626	0	±	0	0
CaM-157	Putative GroEL protein chaperonin 60kDa	90.22235079	±	21.06763	23.35079	48.68812986	±	11.24969	23.10561	54.28692971	±	8.721734	16.06599	0	±	0	0	0	±	0	0	0	±	0	0		6.468654422	±	0.342049	5.287787	5.580719	±	0.324423	5.813282	5.749898	±	0.234885	4.085021	0	±	0	0	0	±	0	0	0	±	0	0
CaM-161	ATP synthase beta subunit (Fragment)	496.0450747	±	100.6696	20.29445	260.8654688	±	67.71895	25.95934	876.5248449	±	118.113	13.47514	881.690277	±	182.664	20.71748	761.9376157	±	239.0031	31.3678	422.6798572	±	85.62186	20.25691		8.93266989	±	0.312771	3.501431	7.991192	±	0.404542	5.062352	9.766571	±	0.200155	2.049393	9.763426	±	0.299553	3.068111	9.522557	±	0.478402	5.023877	8.704225	±	0.28617	3.287716
CaM-162	ATP synthase beta subunit (Fragment)	226.2665074	±	29.15873	12.88689	210.799359	±	60.64727	28.77014	225.326332	±	35.89708	15.93115	87.67500025	±	22.37982	25.52589	403.787445	±	109.4734	27.11163	691.6554316	±	96.44676	13.94434		7.813684907	±	0.189524	2.425538	7.681608	±	0.40144	5.225987	7.804263	±	0.221216	2.834555	6.423578	±	0.360875	5.617981	8.6219	±	0.392819	4.556061	9.423975	±	0.210416	2.232768
CaM-171	Unknown protein	85.72034186	±	22.27184	25.98198	27.03065557	±	4.930122	18.239	87.58473237	±	17.10042	19.52443	34.49904696	±	3.938147	11.41523	113.090858	±	18.22585	16.11611	0	±	0	0		6.387559551	±	0.388093	6.075766	4.740202	±	0.267126	5.635319	6.432617	±	0.300305	4.668468	5.102264	±	0.163776	3.209866	6.808237	±	0.240923	3.538695	0	±	0	0
CaM-182	Ferritin	192.5626219	±	32.37781	16.81417	217.6549712	±	33.16871	15.23912	258.0313159	±	61.6936	23.90935	339.1584575	±	89.09875	26.27054	841.9076952	±	131.5988	15.63103	622.9148842	±	186.1767	29.88798		7.575404263	±	0.245033	3.234593	7.755004	±	0.215775	2.782398	7.980721	±	0.374034	4.686723	8.371748	±	0.386515	4.616891	9.706346	±	0.216997	2.235623	9.242935	±	0.407578	4.409619
CaM-183	Oxygen-evolving enhancer protein 2	252.3470803	±	61.03003	24.18496	0	±	0	0	108.1692607	±	25.89083	23.93548	0	±	0	0	0	±	0	0	0	±	0	0		7.950537083	±	0.354491	4.458704	0	±	0	0	6.729875	±	0.342634	5.091237	0	±	0	0	0	±	0	0	0	±	0	0
CaM-187	Chlorophyll a/b binding protein	690.9250072	±	187.1447	27.0861	785.5908492	±	130.4639	16.60711	602.2481424	±	87.93945	14.60186	1821.873545	±	170.0766	9.335261	2341.855699	±	639.2431	27.29643	3327.070291	±	337.2078	10.13528		9.391894401	±	0.432391	4.603873	9.603594	±	0.249946	2.60263	9.223734	±	0.214144	2.321661	10.82715	±	0.131417	1.213774	11.16025	±	0.371089	3.325096	11.69525	±	0.14282	1.221182
CaM-189	ATP synthase subunit alpha	50.71201006	±	13.7795	27.17206	0	±	0	0	192.3587548	±	46.04703	23.9381	0	±	0	0	0	±	0	0	0	±	0	0		5.631264171	±	0.370319	6.576119	0	±	0	0	7.561092	±	0.335778	4.44086	0	±	0	0	0	±	0	0	0	±	0	0
CaM-191	Ferritin	733.2627867	±	215.1226	29.33773	443.6771892	±	95.5723	21.54095	1234.591426	±	309.1218	25.03839	535.1596502	±	123.4024	23.05898	1234.284942	±	58.37271	4.729273	915.6915164	±	216.2042	23.61103		9.47718936	±	0.42013	4.433068	8.772186	±	0.298595	3.40388	10.24101	±	0.348819	3.406095	9.035951	±	0.354627	3.924623	10.2684	±	0.067502	0.657373	9.811375	±	0.345715	3.523618
CaM-196	Oxygen-evolving enhancer protein 1	763.5020689	±	192.0692	25.15634	794.3722482	±	149.7712	18.85403	892.4990401	±	206.0781	23.09001	1220.84338	±	204.8921	16.78283	685.1672949	±	191.8233	27.99657	411.1810907	±	6.544998	1.591756		9.545783221	±	0.365355	3.8274	9.617411	±	0.261794	2.722083	9.77369	±	0.355727	3.639641	10.24045	±	0.237589	2.320101	9.381851	±	0.410075	4.370938	8.683509	±	0.022911	0.263843
CaM-205	ATP synthase subunit beta	35.77270641	±	10.22507	28.58344	52.38174439	±	16.342	31.1979	62.83951916	±	8.228142	13.0939	0	±	0	0	0	±	0	0	0	±	0	0		5.118655169	±	0.434434	8.487262	5.656958	±	0.500305	8.844061	5.965249	±	0.190721	3.197209	0	±	0	0	0	±	0	0	0	±	0	0
CaM-206	Phosphoribulokinase	232.0213386	±	13.1106	5.650601	211.355778	±	31.31824	14.81778	284.6089667	±	57.40545	20.16994	273.8953421	±	60.6107	22.12914	384.5180349	±	60.18056	15.65091	271.1943856	±	48.36688	17.83477		7.856559176	±	0.082276	1.047223	7.712338	±	0.22321	2.894194	8.132971	±	0.294354	3.619266	8.071847	±	0.339951	4.211565	8.575703	±	0.217328	2.534231	8.068541	±	0.248874	3.084498
CaM-207	ATP synthase subunit alpha	64.95124803	±	14.10236	21.71222	138.1726299	±	39.63503	28.68515	88.13680708	±	15.54332	17.63545	70.2863342	±	12.13781	17.2691	155.48592	±	27.62171	17.76476	85.71563032	±	12.86475	15.00864		5.996630461	±	0.333324	5.558515	7.073139	±	0.39442	5.576303	6.446522	±	0.256909	3.985228	6.120871	±	0.248614	4.061745	7.264983	±	0.262336	3.610962	6.410048	±	0.22546	3.517295
CaM-208	Putative 60S acidic ribosomal protein P0	67.28680512	±	17.77441	26.41589	119.9400221	±	30.86665	25.73507	100.8235314	±	26.17239	25.95861	88.81349126	±	14.81022	16.67565	155.608931	±	37.76613	24.2699	0	±	0	0		6.040285775	±	0.367113	6.077744	6.872972	±	0.382983	5.572307	6.618665	±	0.413028	6.240345	6.459953	±	0.232042	3.592004	7.255331	±	0.332101	4.577342	0	±	0	0
CaM-209	Putative 60S acidic ribosomal protein P0	72.75521367	±	16.37289	22.50408	196.7398357	±	60.28763	30.64333	295.9599671	±	80.00662	27.03292	123.8026978	±	17.92141	14.47578	125.1275184	±	30.82803	24.63729	212.7154604	±	60.48727	28.43577		6.16033755	±	0.327532	5.316791	7.577725	±	0.421147	5.557701	8.169686	±	0.425697	5.210686	6.941141	±	0.2192	3.157983	6.940026	±	0.336861	4.853883	7.695522	±	0.396954	5.158243
CaM-210	Fructose-bisphosphate aldolase	133.6648646	±	6.6062	4.942361	178.3218608	±	57.44637	32.21499	258.0435917	±	18.8698	7.312639	173.5925707	±	44.90969	25.87074	237.7720859	±	6.574256	2.76494	216.6369711	±	53.3367	24.62031		7.061309766	±	0.070939	1.004614	7.431667	±	0.441126	5.935761	8.008937	±	0.104328	1.302648	7.402977	±	0.410119	5.53992	7.893064	±	0.040185	0.509115	7.730984	±	0.345837	4.473387
CaM-214	Glutamate-ammonia ligase (EC 6.3.1.2) delta precursor	113.6498881	±	21.12441	18.58727	220.1013592	±	20.05641	9.112352	0	±	0	0	183.1502494	±	43.83784	23.93545	165.8208433	±	35.5269	21.42487	0	±	0	0		6.811836617	±	0.26817	3.936828	7.77815	±	0.12848	1.651801	0	±	0	0	7.488099	±	0.356822	4.765195	7.350972	±	0.313653	4.26682	0	±	0	0
CaM-216	Glutamate-ammonia ligase (EC 6.3.1.2) delta precursor	120.7250613	±	12.20534	10.11003	208.0323825	±	17.96062	8.633568	168.9908875	±	31.24357	18.48832	244.082112	±	58.63766	24.02374	196.639634	±	30.26626	15.39174	141.614239	±	23.55728	16.63482		6.910494045	±	0.149641	2.165417	7.697177	±	0.121985	1.584804	7.384551	±	0.264422	3.580745	7.900217	±	0.376091	4.760516	7.608177	±	0.219701	2.887697	7.132965	±	0.233802	3.277773
CaM-218	Glutamine synthetase	98.57943626	±	19.05114	19.32567	244.5147696	±	47.90653	19.59249	0	±	0	0	229.977472	±	50.3153	21.87836	170.3506155	±	41.11148	24.13345	267.5550415	±	41.83113	15.63459		6.605951898	±	0.270509	4.094926	7.916162	±	0.27273	3.445233	0	±	0	0	7.820552	±	0.33356	4.265174	7.380938	±	0.378987	5.134668	8.052317	±	0.219993	2.732046
CaM-221	ATP synthase beta subunit (Fragment)	762.7289544	±	113.5038	14.88128	342.9475677	±	49.01689	14.29282	801.5072853	±	170.1117	21.22397	314.8631858	±	12.78465	4.060382	1062.689947	±	195.3628	18.3838	1458.562195	±	144.5994	9.913834		9.564594824	±	0.211359	2.20981	8.412441	±	0.199438	2.370746	9.623633	±	0.319532	3.320283	8.297797	±	0.058115	0.700372	10.03804	±	0.255359	2.543917	10.50555	±	0.144204	1.372642
CaM-222	ATP synthase subunit beta	116.2435929	±	24.77191	21.31034	118.5193104	±	14.98931	12.64714	65.54581531	±	12.04398	18.3749	93.22710503	±	8.17671	8.770744	228.1487829	±	7.056472	3.092925	61.2175754	±	10.19414	16.65231		6.838603553	±	0.313385	4.582587	6.881566	±	0.177394	2.577809	6.019061	±	0.254207	4.223364	6.539026	±	0.12531	1.916338	7.833365	±	0.045034	0.574902	5.923191	±	0.231213	3.903525
CaM-223	Putative glutamate-tRNA ligase	215.9560315	±	50.04937	23.17572	139.39921	±	20.38903	14.62636	131.2886694	±	21.66441	16.50136	125.4559922	±	34.47918	27.48309	199.3470104	±	39.19963	19.66402	188.9007868	±	41.49936	21.96887		7.729628722	±	0.325763	4.214469	7.113209	±	0.204455	2.874295	7.023967	±	0.231628	3.297683	6.930536	±	0.429745	6.200749	7.621257	±	0.275345	3.612852	7.535741	±	0.342114	4.539883
CaM-226	ATPase beta subunit (Fragment)	130.2490138	±	8.812621	6.765979	182.2657511	±	64.16402	35.20356	213.2252653	±	9.526143	4.467642	861.0704526	±	199.3425	23.15054	275.7829245	±	46.11402	16.72113	709.714617	±	154.1783	21.72399		7.02294201	±	0.097117	1.382853	7.445812	±	0.536287	7.202528	7.735261	±	0.065156	0.842324	9.725232	±	0.323847	3.329972	8.093498	±	0.247183	3.054088	9.448215	±	0.315325	3.337398

CaM-240	40S ribosomal protein S12	987.7069767	±	268.0752	27.14116	871.3950596	±	295.4913	33.91014	418.7048616	±	25.86992	6.178557	313.0595518	±	74.36789	23.75519	312.2579013	±	70.07268	22.44064	403.91059	±	36.17875	8.957119		9.914123982	±	0.377788	3.810609	9.709861	±	0.502626	5.176447	8.707968	±	0.088646	1.01799	8.264375	±	0.330836	4.003158	8.259547	±	0.351212	4.252197	8.653915	±	0.132179	1.52739
CaM-246	Putative serine/threonine kinase	1377.944007	±	255.4748	18.54029	749.5542814	±	107.1308	14.29261	1355.272892	±	231.3435	17.06989	901.5542166	±	119.0295	13.20269	1181.893661	±	130.3601	11.02977	757.9014685	±	146.2706	19.29942		10.41075801	±	0.27957	2.685392	9.539445	±	0.215782	2.262002	10.39016	±	0.248877	2.395311	9.807683	±	0.193952	1.977548	10.20124	±	0.154851	1.517964	9.548567	±	0.271153	2.839723
CaM-247	Membrane protein CH1-like	1300.527227	±	280.8634	21.59612	561.9487394	±	119.6997	21.30082	1744.187264	±	170.9282	9.799878	602.5872602	±	124.7725	20.70613	348.1276445	±	102.6666	29.49108	219.5200137	±	30.37146	13.83539		10.32369232	±	0.298256	2.889042	9.1133	±	0.298389	3.274218	10.76386	±	0.138044	1.282474	9.215666	±	0.284621	3.088444	8.401644	±	0.425444	5.063822	7.769054	±	0.198773	2.558522
CaM-254	ATP synthase gamma chain	0	±	0	0	0	±	0	0	199.0705819	±	48.07169	24.14806	110.2776753	±	15.96955	14.48122	125.2832096	±	11.74345	9.373522	0	±	0	0		0	±	0	0	0	±	0	0	7.608984	±	0.349399	4.59193	6.774239	±	0.219173	3.235397	6.964732	±	0.13743	1.97323	0	±	0	0
CaM-257	Plastidic aldolase	312.9857193	±	82.07006	26.22166	218.5006362	±	38.7164	17.71913	284.2018197	±	66.78706	23.49987	261.2836329	±	42.50557	16.26798	377.8176862	±	53.68154	14.20832	411.8996177	±	99.28867	24.10507		8.25542999	±	0.390722	4.732914	7.75537	±	0.268396	3.460772	8.120919	±	0.369519	4.550207	8.017286	±	0.227074	2.832308	8.552018	±	0.202099	2.363179	8.654601	±	0.380238	4.393475
CaM-263	OSJNBb0085H11.1 protein	99.62429324	±	15.12774	15.18479	905.1981151	±	216.8239	23.9532	89.08459307	±	6.091322	6.837683	0	±	0	0	157.2286919	±	14.59574	9.283126	148.9586991	±	7.73715	5.194158		6.626568562	±	0.230221	3.474208	9.792604	±	0.363082	3.707716	6.474798	±	0.100527	1.552592	0	±	0	0	7.292593	±	0.133525	1.830962	7.217494	±	0.073942	1.02448
CaM-267	Hypothetical protein F26P21.180	0	±	0	0	0	±	0	0	125.131373	±	21.86138	17.47074	0	±	0	0	93.95717154	±	83.67643	89.05806	308.0762108	±	278.8533	90.5144		0	±	0	0	0	±	0	0	6.951385	±	0.267582	3.849328	0	±	0	0	4.749954	±	4.118491	86.70591	5.886363	±	5.104154	86.71151
CaM-269	ATP synthase subunit alpha	71.38976393	±	18.10711	25.36373	0	±	0	0	44.59322585	±	6.294728	14.11588	0	±	0	0	0	±	0	0	368.154981	±	55.21958	14.999		6.125330751	±	0.378052	6.17194	0	±	0	0	5.469561	±	0.197302	3.607281	0	±	0	0	0	±	0	0	8.513033	±	0.221124	2.597476
CaM-271	H+-transporting two-sector ATPase-alpha chain	405.4887197	±	71.96985	17.74892	136.4659069	±	37.9864	27.83581	303.9578347	±	56.01678	18.42913	256.8052927	±	59.61912	23.21569	565.4594473	±	150.5812	26.62988	394.1985313	±	10.97133	2.783199		8.648853023	±	0.249809	2.888351	7.04957	±	0.444854	6.310372	8.231372	±	0.266143	3.233272	7.980329	±	0.317699	3.98102	9.110552	±	0.372221	4.085598	8.622403	±	0.040375	0.468263
CaM-272	ATP synthase CF1 alpha subunit	187.3827237	±	39.30421	20.97536	80.35283871	±	26.40226	32.8579	153.9713588	±	24.86762	16.15081	132.7380417	±	37.16264	27.99698	348.222826	±	51.75817	14.86352	225.9500683	±	34.65969	15.33953		7.52982039	±	0.290092	3.852579	6.278463	±	0.459052	7.311539	7.254178	±	0.230127	3.172332	7.011789	±	0.427273	6.09364	8.432578	±	0.224308	2.660017	7.807725	±	0.233063	2.985026
CaM-283	40S ribosomal protein S12	734.9789598	±	220.3164	29.97588	570.1481848	±	92.48314	16.2209	313.0553352	±	88.72583	28.3419	612.2235947	±	129.5377	21.15857	388.6666018	±	76.40449	19.65811	372.2003839	±	106.2093	28.53552		9.480481609	±	0.415844	4.386317	9.142624	±	0.232834	2.54669	8.253951	±	0.389867	4.723395	9.235079	±	0.318945	3.453621	8.582005	±	0.303645	3.538156	8.501158	±	0.408582	4.806194
CaM-290	Intronic ORF; similar to LAGLIDADG endonuclease	159.6017599	±	22.38162	14.02342	304.842141	±	65.83113	21.59515	236.5289991	±	63.83282	26.98731	516.3034927	±	172.1485	33.3425	434.9218119	±	82.93485	19.06891	778.0383992	±	245.5914	31.56546		7.30919576	±	0.197093	2.69651	8.228299	±	0.32383	3.935562	7.848063	±	0.412169	5.251852	8.954298	±	0.509768	5.692993	8.747501	±	0.270607	3.093535	9.553582	±	0.471005	4.930138
CaM-294	Putative PSII-P protein	435.1426626	±	97.57956	22.42473	1053.720162	±	174.5428	16.56444	713.5019293	±	102.5877	14.37805	544.1659433	±	150.3704	27.6332	548.8710596	±	166.5999	30.35319	300.2077469	±	77.46817	25.80485		8.74270335	±	0.307524	3.517488	10.0278	±	0.242775	2.421024	9.468259	±	0.216236	2.283804	9.052751	±	0.385479	4.258142	9.05686	±	0.431458	4.763882	8.194782	±	0.397958	4.856234
CaM-295	ATP synthase subunit alpha	367.9713898	±	43.63764	11.85898	348.1155756	±	62.81237	18.04354	385.9581669	±	86.19277	22.33215	308.5119194	±	31.89768	10.33921	386.7804766	±	73.66053	19.04453	204.888218	±	36.63627	17.8811		8.516396257	±	0.176525	2.072769	8.42756	±	0.262882	3.11931	8.568124	±	0.324128	3.782956	8.26415	±	0.146782	1.77613	8.578538	±	0.267413	3.117236	7.662104	±	0.272885	3.561489
CaM-299	Histone acetyltransferase GCN5	501.9241253	±	160.7037	32.01752	553.463453	±	47.14607	8.518371	722.6573684	±	77.36342	10.70541	441.474906	±	88.76334	20.10609	816.8477448	±	38.58331	4.72344	1428.537595	±	101.2357	7.086669		8.922279542	±	0.460035	5.156024	9.10895	±	0.120351	1.321243	9.491695	±	0.153642	1.618701	8.767904	±	0.276726	3.156124	9.67284	±	0.068629	0.709498	10.47784	±	0.104509	0.997426
CaM-301	Proteasome subunit alpha type	112.4911153	±	29.52056	26.24257	207.8970982	±	64.62029	31.08282	46.07677624	±	7.30008	15.84329	156.8899022	±	26.69462	17.01487	177.8746172	±	46.86093	26.34492	212.9129487	±	55.94538	26.27617		6.775803664	±	0.417758	6.165443	7.65532	±	0.432989	5.65606	5.514497	±	0.219842	3.986628	7.280419	±	0.235537	3.235216	7.438792	±	0.401478	5.397082	7.699846	±	0.388221	5.041928
CaM-308	Fructose-bisphosphate aldolase 1	117.393245	±	14.37543	12.24553	172.3707238	±	48.33987	28.04413	117.4644995	±	26.70737	22.73655	325.8808322	±	89.34578	27.4167	435.4156397	±	42.32943	9.721615	317.0081794	±	67.13946	21.17909		6.868197574	±	0.172882	2.517134	7.387281	±	0.437921	5.928037	6.852735	±	0.31254	4.560808	8.310296	±	0.409852	4.931854	8.761737	±	0.139506	1.592224	8.28452	±	0.329105	3.972527
CaM-310	Fructose-bisphosphate aldolase (EC 4.1.2.13) precursor	473.9764006	±	125.9747	26.57827	550.7476696	±	24.05862	4.368357	601.3152269	±	41.7425	6.941867	919.75208	±	73.36341	7.976433	494.9155719	±	62.92319	12.71392	411.1523395	±	74.0048	17.99936		8.849693978	±	0.424194	4.793315	9.10432	±	0.063535	0.697858	9.22963	±	0.101136	1.095776	9.841937	±	0.117984	1.198793	8.94322	±	0.184219	2.059871	8.668773	±	0.249105	2.873591
CaM-311	ATP synthase CF1 alpha subunit	22.34961557	±	2.695593	12.06103	0	±	0	0	86.94705594	±	14.42254	16.58773	109.0585742	±	14.18655	13.00819	64.69036924	±	12.42819	19.21181	0	±	0	0		4.475460404	±	0.168728	3.77007	0	±	0	0	6.427797	±	0.253044	3.93672	6.760693	±	0.189896	2.808821	5.996753	±	0.288436	4.809865	0	±	0	0
CaM-316	ATP synthase subunit alpha	45.37315478	±	4.455734	9.820199	0	±	0	0	0	±	0	0	0	±	0	0	62.3685241	±	15.77528	25.29366	0	±	0	0		5.499235144	±	0.139229	2.531789	0	±	0	0	0	±	0	0	0	±	0	0	5.931756	±	0.36689	6.185184	0	±	0	0
CaM-319	Putative ferredoxin-NADP(H) oxidoreductase	0	±	0	0	0	±	0	0	0	±	0	0	0	±	0	0	0	±	0	0	2345.34985	±	144.0948	6.143849		0	±	0	0	0	±	0	0	0	±	0	0	0	±	0	0	0	±	0	0	11.19377	±	0.088763	0.792966
CaM-322	Phosphoglycerate kinase	92.03106903	±	18.42314	20.01839	0	±	0	0	65.72510369	±	7.602466	11.56707	0	±	0	0	0	±	0	0	0	±	0	0		6.505646081	±	0.278802	4.28554	0	±	0	0	6.031743	±	0.170642	2.829066	0	±	0	0	0	±	0	0	0	±	0	0
CaM-323	Putative uncharacterized protein	106.3268523	±	23.50151	22.10308	91.71003081	±	24.20438	26.39229	103.5572225	±	25.80918	24.92262	63.33160573	±	9.299003	14.68304	68.88616851	±	15.30137	22.21254	0	±	0	0		6.7099829	±	0.307219	4.578531	6.485344	±	0.382167	5.892778	6.661573	±	0.384602	5.773445	5.973914	±	0.220448	3.690179	6.079723	±	0.346877	5.705482	0	±	0	0
CaM-335	ATP synthase subunit alpha	78.19729877	±	21.25928	27.18672	0	±	0	0	35.98486741	±	6.644862	18.46571	62.32824366	±	9.052298	14.52359	91.02993958	±	20.49531	22.51491	0	±	0	0		6.25206571	±	0.404054	6.46273	0	±	0	0	5.151427	±	0.28412	5.515369	5.951861	±	0.206552	3.470381	6.485398	±	0.309258	4.768521	0	±	0	0
CaM-346	Putative uncharacterized protein	101.7497065	±	16.49556	16.2119	49.59278881	±	12.70414	25.61691	57.56034035	±	14.74541	25.6173	42.54935866	±	6.325946	14.86731	93.43918406	±	29.35281	31.41381	94.22858459	±	28.05497	29.77331		6.65545499	±	0.244607	3.675291	5.599558	±	0.377833	6.747546	5.815538	±	0.368728	6.340389	5.400726	±	0.21004	3.889103	6.492108	±	0.497582	7.664419	6.513893	±	0.441368	6.7758
CaM-376	Ferredoxin-NADP reductase	412.4317184	±	104.5581	25.35162	177.6040126	±	48.36051	27.2294	174.66448	±	44.76671	25.63012	105.8574565	±	20.21901	19.10023	286.3391835	±	84.71802	29.5866	264.474037	±	53.92199	20.38839		8.656730337	±	0.369059	4.263266	7.439016	±	0.374387	5.032755	7.417759	±	0.3616	4.874781	6.708265	±	0.277557	4.137533	8.12199	±	0.407021	5.011342	8.026268	±	0.302074	3.763573
CaM-382	ATP synthase subunit alpha	88.96954338	±	21.33277	23.97761	102.1275362	±	28.16287	27.57617	85.87305001	±	15.31079	17.82957	0	±	0	0	165.3926588	±	40.05577	24.21859	118.2566175	±	22.04701	18.64337		6.444094604	±	0.377617	5.859897	6.63969	±	0.380661	5.733121	6.408611	±	0.260184	4.059912	0	±	0	0	7.340215	±	0.361646	4.926907	6.86865	±	0.273926	3.988067
CaM-386	ATP synthase subunit alpha	78.65621337	±	11.42562	14.52602	121.979841	±	8.720587	7.149204	146.1101018	±	21.29315	14.57336	146.5573015	±	19.4599	13.27802	139.2649103	±	36.3181	26.07843	0	±	0	0		6.287285733	±	0.210432	3.34694	6.928101	±	0.101229	1.46113	7.180321	±	0.216019	3.00848	7.187207	±	0.185258	2.577612	7.087711	±	0.38715	5.462266	0	±	0	0
CaM-396	ATP synthase subunit alpha	126.2813648	±	30.06988	23.81181	57.74991555	±	20.25723	35.07751	158.6402444	±	9.090456	5.730233	142.7328132	±	28.08954	19.6798	234.7983957	±	45.38721	19.33029	0	±	0	0		6.949771544	±	0.375095	5.397229	5.795692	±	0.485132	8.370559	7.308068	±	0.081389	1.113693	7.138386	±	0.285777	4.003379	7.858334	±	0.266611	3.392715	0	±	0	0
CaM	Mitochondri	63.730	±	10.48	16.44	102.98	±	36.97	35.89	97.463	±	3.821	3.921	111.62	±	25.48	22.82	126.08	±	34.45	27.32	245.74	±	53.21	21.65		5.9799	±	0.250	4.183	6.624	±	0.515	7.783	6.606	±	0.056	0.855	6.778	±	0.316	4.675	6.942	±	0.396	5.706	7.919	±	0.298	3.770

-407	al processing peptidase beta subunit	16705		002	436	5768		175	986	1973		75	224	59111		013	636	40188		244	498	26817		592	514		33731		174	564	661		62	344	047		501	293	694		914	145	098		153	536	741		623	612
CaM-416	Unknown protein 18	0	±	0	0	70.5616316	±	17.73442	25.13323	0	±	0	0	0	±	0	0	84.02396527	±	0.896625	1.067107	0	±	0	0		0	±	0	0	6.111929	±	0.348803	5.70693	0	±	0	0	0	±	0	0	6.392674	±	0.01538	0.240581	0	±	0	0
CaM-428	Beta-1,3-glucanase	438.1477228	±	106.4719	24.30046	0	±	0	0	205.203578	±	28.43722	13.85805	0	±	0	0	0	±	0	0	0	±	0	0		8.748441914	±	0.335608	3.836207	0	±	0	0	7.672071	±	0.193402	2.520857	0	±	0	0	0	±	0	0	0	±	0	0
CaM-435	Carbonic anhydrase	356.1822473	±	38.9497	10.93533	381.6660875	±	50.26738	13.17051	518.2617545	±	53.85831	10.39211	382.6089248	±	54.72737	14.30374	670.4168691	±	195.4948	29.16018	718.5139003	±	72.64008	10.10977		8.470674708	±	0.158718	1.873732	8.567342	±	0.198123	2.312537	9.012403	±	0.148623	1.649099	8.570005	±	0.204495	2.386168	9.351076	±	0.396061	4.235455	9.484123	±	0.142098	1.498267
CaM-436	Putative quinone oxidoreductase	229.4277878	±	52.1981	22.75143	327.3767682	±	28.63517	8.746855	278.4930276	±	89.6321	32.18468	221.3834424	±	21.36541	9.650861	492.7507759	±	65.13781	13.21922	380.5407977	±	34.38215	9.035077		7.818229976	±	0.315756	4.03872	8.351238	±	0.123345	1.476964	8.075468	±	0.436537	5.405717	7.786041	±	0.136483	1.752925	8.936665	±	0.184574	2.065362	8.567885	±	0.132741	1.549289
CaM-443	Predicted protein	77.88669809	±	12.20375	15.6686	71.15922172	±	21.50573	30.22198	546.9658951	±	149.0201	27.24486	113.4900892	±	12.96973	11.42807	186.2365346	±	53.35953	28.65148	694.2742047	±	85.9412	12.37857		6.271562012	±	0.225134	3.589762	6.11129	±	0.418731	6.851753	9.057238	±	0.412406	4.553327	6.819821	±	0.171089	2.508701	7.496267	±	0.453223	6.045987	9.432009	±	0.178289	1.890259
CaM-445	Putative uncharacterized	353.6638519	±	69.98482	19.78851	215.8062444	±	47.20144	21.87214	254.6946578	±	43.13467	16.93584	212.7594343	±	43.22274	20.31531	549.7833119	±	175.2759	31.8809	191.7608993	±	38.90176	20.2866		8.447662202	±	0.282507	3.344207	7.731952	±	0.301054	3.893634	7.97861	±	0.247267	3.099123	7.714299	±	0.280931	3.641686	9.052752	±	0.467627	5.165575	7.563933	±	0.286357	3.785828
CaM-452	Ferredoxin: nadp+ reductase	1079.047002	±	118.2202	10.95598	431.6249508	±	37.61836	8.715519	783.9973452	±	208.9642	26.65369	325.8860667	±	36.80407	11.29354	478.4528715	±	66.34647	13.86688	468.470566	±	113.9368	24.32103		10.06949346	±	0.163645	1.625159	8.75009	±	0.122895	1.404505	9.582907	±	0.363751	3.795834	8.341922	±	0.16625	1.992952	8.892865	±	0.202015	2.271648	8.840525	±	0.376513	4.258949
CaM-460	Glyceraldehyde 3-phosphate dehydrogenase	194.903262	±	6.192452	3.177193	269.4274053	±	14.76676	5.480793	129.6665063	±	20.97483	16.17599	118.8149542	±	4.474572	3.766001	466.1144788	±	44.00241	9.440259	441.8591759	±	88.16325	19.95279		7.606134678	±	0.045432	0.597306	8.072276	±	0.080367	0.995595	7.00597	±	0.234882	3.352602	6.891899	±	0.053804	0.78069	8.860328	±	0.134427	1.51718	8.766417	±	0.308471	3.518783
CaM-461	Glyceraldehyde-3-phosphate dehydrogenase	100.6572065	±	27.41809	27.23907	137.0510183	±	23.08058	16.84087	59.39395913	±	16.39252	27.59965	43.09398034	±	4.654117	10.79992	64.39287447	±	8.401992	13.04802	79.67463953	±	11.9758	15.03088		6.620127046	±	0.371454	5.610978	7.083841	±	0.257173	3.630418	5.851719	±	0.42912	7.333223	5.423917	±	0.153469	2.82948	6.000315	±	0.193805	3.229911	6.305323	±	0.214748	3.40582
CaM-462	Glyceraldehyde-3-phosphate dehydrogenase A	50.92275153	±	12.79008	25.11662	89.67236908	±	8.008621	8.93098	0	±	0	0	40.92019969	±	6.542041	15.98731	105.9185184	±	30.2268	28.53778	173.7523207	±	27.46277	15.8057		5.636923859	±	0.388375	6.889846	6.482829	±	0.126975	1.95864	0	±	0	0	5.342834	±	0.225147	4.214001	6.690188	±	0.390849	5.842118	7.42935	±	0.221121	2.97632
CaM-483	Luminal binding protein, BiP	90.11609163	±	17.81766	19.77189	88.02526041	±	8.930682	10.14559	0	±	0	0	0	±	0	0	0	±	0	0	0	±	0	0		6.475423223	±	0.279339	4.31384	6.454972	±	0.144666	2.24115	0	±	0	0	0	±	0	0	0	±	0	0	0	±	0	0
CaM-485	Carbonic anhydrase	0	±	0	0	163.9564766	±	32.95833	20.10188	0	±	0	0	0	±	0	0	0	±	0	0	0	±	0	0		0	±	0	0	7.338014	±	0.286865	3.909298	0	±	0	0	0	±	0	0	0	±	0	0	0	±	0	0
CaM-487	Guanine nucleotide-binding protein subunit beta-like	211.2290344	±	28.98217	13.72073	135.5103711	±	20.32426	14.99831	0	±	0	0	84.26312311	±	19.79571	23.49273	0	±	0	0	0	±	0	0		7.71305846	±	0.206839	2.68167	7.071513	±	0.215302	3.044636	0	±	0	0	6.367279	±	0.366871	5.761811	0	±	0	0	0	±	0	0

Supplementary Table S4. One-way ANOVA of the data was done using MeV (Multi Experiment Viewer) software to determine the statistically significant ($p < 0.05$) differentially regulated protein spots.

	Unstressed			24 h			48 h			72 h			96 h			120 h										
Spot ID	**Mean**		**SD**	**Mean**		**SD**	**Mean**		**SD**	**Mean**		**SD**	**Mean**		**SD**	**Mean**		**SD**	**F ratio**	**SS Group**	**SS Error**	**df(Groups)**	**df (error)**	**p value**	**Are means signif. different? (P < 0.05)**	**Identification**
CaM-9	9.603208	±	0.425321	8.412229	±	0.2521	9.885127	±	0.186657	9.57389	±	0.293719	7.769659	±	0.258619	8.997939	±	0.046608	27.550543	9.978338	0.869239	5	12	3.48922E-06	Yes	Putative uncharacterized protein
CaM-21	9.932819	±	0.298015	9.25478	±	0.282887	10.457976	±	0.128468	11.1069765	±	0.217513	11.0436735	±	0.156175	11.422005	±	0.136738	44.130737	10.14057	0.551483	5	12	2.57991E-07	Yes	Chlorophyll a/b-binding protein AB96
CaM-22	9.99126	±	0.265601	9.46384	±	0.333331	11.149154	±	0.193462	11.178841	±	0.094737	10.681541	±	0.266912	11.497771	±	0.358806	25.978151	9.266411	0.85608	5	12	4.79277E-06	Yes	Chlorophyll a/b-binding protein 3 precursor
CaM-24	0	±	0	0	±	0	6.719216	±	0.307808	7.336218	±	0.085858	8.986362	±	0.304598	8.658089	±	0.187876	1363.786	261.6141	0.46039	5	12	4.44089E-16	Yes	Putative uncharacterized protein
CaM-39	6.026426	±	0.290237	0	±	0	0	±	0	0	±	0	0	±	0	5.777553	±	0.185619	1409.6346	139.4268	0.237384	5	12	3.33067E-16	Yes	Putative 60S ribosomal protein L1
CaM-43	7.897615	±	0.280701	0	±	0	0	±	0	0	±	0	0	±	0	6.896318	±	0.321173	1453.3905	220.3644	0.36389	5	12	3.33067E-16	Yes	Ribulose bisphosphate carboxylase large chain
CaM-54	0	±	0	0	±	0	10.442727	±	0.256813	0	±	0	0	±	0	0	±	0	4960.3667	272.6264	0.131906	5	12	0	Yes	Activator of spomin
CaM-56	6.435103	±	0.351706	0	±	0	0	±	0	0	±	0	0	±	0	7.2823462	±	0.129311	1617.2704	189.2452	0.280836	5	12	1.11022E-16	Yes	Hypothetical protein OSJNBa0075N02.148
CaM-64	0	±	0	8.329746	±	0.459339	8.521224	±	0.283649	8.313427	±	0.341677	0	±	0	0	±	0	931.0425	316.7035	0.816384	5	12	4.21885E-15	Yes	Hypothetical protein P0415D04.53
CaM-69	9.405328	±	0.449908	9.070352	±	0.058313	10.222072	±	0.243425	10.871314	±	0.095856	10.121033	±	0.271435	9.894431	±	0.137094	19.862555	6.070227	0.733468	5	12	1.99029E-05	Yes	Chlorophyll A-B binding protein
CaM-71	9.365312	±	0.245839	8.130847	±	0.210996	9.872794	±	0.144933	9.425038	±	0.129063	10.6705065	±	0.223949	9.448925	±	0.481366	28.909212	10.22629	0.848972	5	12	2.6866E-06	Yes	light-harvesting complex II protein Lhcb3
CaM-73	8.911433	±	0.43961	8.767699	±	0.512194	10.301246	±	0.090214	9.898762	±	0.092868	10.757319	±	0.203063	9.850651	±	0.294584	18.102072	9.056721	1.200754	5	12	3.22008E-05	Yes	Actin (Fragment)
CaM-74	10.123119	±	0.266514	9.636769	±	0.33176	11.048905	±	0.272367	11.522855	±	0.162317	11.379059	±	0.097039	12.598586	±	0.175705	62.472404	16.75892	0.643827	5	12	3.58215E-08	Yes	Light-harvesting chlorophyll-a/b binding protein Lhcb1
CaM-75	9.516501	±	0.399097	9.268111	±	0.298572	10.612512	±	0.192383	11.595878	±	0.286348	11.301647	±	0.398572	11.645138	±	0.328284	31.256876	16.51561	1.26812	5	12	1.75379E-06	Yes	Chlorophyll a/b binding protein
CaM-78	9.561337	±	0.344411	8.398349	±	0.365994	8.503531	±	0.307033	9.276596	±	0.451636	8.4918165	±	0.369396	6.9855304	±	0.208565	19.831955	12.07713	1.461536	5	12	2.00636E-05	Yes	Chlorophyll a/b binding protein
CaM-80	8.079182	±	0.07713	0	±	0	9.590534	±	0.325762	6.8822	±	0.316902	8.3006935	±	0.038788	0	±	0	1575.1632	280.9062	0.428003	5	12	2.22045E-16	Yes	ATP synthase beta subunit (Fragment)
CaM-85	0	±	0	5.6428695	±	0.385567	0	±	0	0	±	0	0	±	0	0	±	0	642.5728	79.60492	0.297323	5	12	3.87468E-14	Yes	Calcineurin-like phosphoesterase family protein
CaM-94	7.4421234	±	0.081479	6.819447	±	0.202359	7.505081	±	0.225871	8.347675	±	0.386183	6.268145	±	0.369728	7.083761	±	0.11861	22.437126	7.451185	0.79702	5	12	1.04855E-05	Yes	Chaperonin 60 alpha subunit
CaM-99	6.5966988	±	0.411618	7.7958817	±	0.43074	6.4077945	±	0.299652	5.8768144	±	0.404746	5.5532966	±	0.14748	0	±	0	214.71172	112.7822	1.260654	5	12	2.63749E-11	Yes	Chaperone DnaK
CaM-112	0	±	0	0	±	0	0	±	0	0	±	0	0	±	0	8.5443125	±	0.254103	3392	182.5132	0.129137	5	12	0	Yes	Putative uncharacterized protein
CaM-115	5.636827	±	0.361348	0	±	0	0	±	0	0	±	0	0	±	0	0	±	0	730.02783	79.43455	0.261145	5	12	1.80966E-14	Yes	Trypsin inhibitor, chain B (fragments)
CaM-122	8.290085	±	0.200794	8.5388365	±	0.214333	7.9365754	±	0.244431	9.942555	±	0.43069	9.785783	±	0.359586	0	±	0	541.3469	207.8766	0.921597	5	12	1.07803E-13	Yes	Ribulose bisphosphate carboxylase large chain

CaM-125	7.216932	±	0.476605	5.9195113	±	0.316839	8.422452	±	0.302747	7.250547	±	0.369267	4.8617253	±	0.252168	5.6859016	±	0.440419	37.347885	25.30664	1.626222	5	12	6.56145E-07	Yes	Oxygen-evolving enhancer protein 1
CaM-127	10.800008	±	0.33304	9.200338	±	0.128142	10.475501	±	0.454651	10.290149	±	0.335508	9.636501	±	0.269075	9.013782	±	0.069052	18.129438	7.913189	1.047559	5	12	3.19513E-05	Yes	PSI type III chlorophyll a/b-binding protein (imported)
CaM-138	5.170191	±	0.266804	0	±	0	0	±	0	0	±	0	0	±	0	0	±	0	1126.5496	66.82718	0.142369	5	12	1.33227E-15	Yes	Chromosome chr17 scaffold_16
CaM-141	5.2336073	±	0.194937	0	±	0	5.6624513	±	0.238545	0	±	0	0	±	0	0	±	0	1504.6766	119	0.189808	5	12	2.22045E-16	Yes	Phosphoglycerate kinase
CaM-147	6.812485	±	0.340437	7.084189	±	0.46597	8.009057	±	0.109427	7.299478	±	0.457843	6.8642173	±	0.321782	5.846233	±	0.377199	11.237316	7.49569	1.600886	5	12	0.000340961	Yes	ATP synthase subunit beta, chloroplastic
CaM-150	5.562042	±	0.401376	0	±	0	0	±	0	6.807993	±	0.390625	0	±	0	0	±	0	594.266	155.3464	0.627381	5	12	6.17284E-14	Yes	Chaperonin 60 alpha subunit
CaM-155	5.772982	±	0.09133	0	±	0	0	±	0	0	±	0	5.5956216	±	0.091356	0	±	0	9297.633	129.2923	0.033374	5	12	0	Yes	Dynein-1-alpha heavy chain
CaM-157	6.4686546	±	0.342049	5.580719	±	0.324423	5.7498984	±	0.234885	0	±	0	0	±	0	0	±	0	690.9743	159.7407	0.554836	5	12	2.5091E-14	Yes	Putative GroEL protein chaperonin 60kDa
CaM-161	8.93267	±	0.312771	7.9911923	±	0.404543	9.76657	±	0.200155	9.763427	±	0.299553	9.522557	±	0.478401	8.704226	±	0.28617	12.696846	7.428036	1.404072	5	12	0.000190034	Yes	ATP synthase beta subunit (Fragment)
CaM-162	7.813685	±	0.189524	7.6816077	±	0.40144	7.8042636	±	0.221216	6.423578	±	0.360876	8.6219	±	0.392819	9.423976	±	0.210416	31.72158	15.19524	1.149645	5	12	1.61742E-06	Yes	ATP synthase beta subunit (Fragment)
CaM-171	6.38756	±	0.388093	4.7402024	±	0.267125	6.4326167	±	0.300305	5.1022644	±	0.163776	6.808237	±	0.240923	0	±	0	292.688	96.83617	0.794043	5	12	4.19975E-12	Yes	Unknown protein
CaM-182	7.5754046	±	0.245034	7.7550035	±	0.215775	7.9807205	±	0.374034	8.371748	±	0.386514	9.706346	±	0.216997	9.242935	±	0.407578	21.75396	11.04201	1.218207	5	12	1.23482E-05	Yes	Ferritin
CaM-183	7.950537	±	0.354491	0	±	0	6.729875	±	0.342634	0	±	0	0	±	0	0	±	0	1075.032	217.7495	0.486124	5	12	1.77636E-15	Yes	Oxygen-evolving enhancer protein 2
CaM-187	9.391894	±	0.432391	9.603595	±	0.249946	9.223733	±	0.214144	10.827149	±	0.131417	11.160247	±	0.371089	11.695248	±	0.14282	41.53925	16.29266	0.941336	5	12	3.62367E-07	Yes	Chlorophyll a/b binding protein
CaM-189	5.6312637	±	0.370319	0	±	0	7.5610924	±	0.335778	0	±	0	0	±	0	0	±	0	862.6038	179.6246	0.499765	5	12	6.66134E-15	Yes	ATP synthase subunit alpha
CaM-191	9.477189	±	0.42013	8.772186	±	0.298595	10.241011	±	0.348818	9.035951	±	0.354627	10.268399	±	0.067502	9.811376	±	0.345716	10.852541	5.762506	1.274357	5	12	0.000401719	Yes	Ferritin
CaM-196	9.545783	±	0.365355	9.617412	±	0.261794	9.77369	±	0.355727	10.240451	±	0.237589	9.381851	±	0.410075	8.683509	±	0.02291	8.516351	3.929566	1.107395	5	12	0.001211116	Yes	Oxygen-evolving enhancer protein 1
CaM-205	5.118655	±	0.434434	5.656958	±	0.500305	5.9652495	±	0.190721	0	±	0	0	±	0	0	±	0	356.48157	141.2298	0.950825	5	12	1.30029E-12	Yes	ATP synthase subunit beta
CaM-206	7.8565593	±	0.082276	7.7123375	±	0.22321	8.132972	±	0.294354	8.071847	±	0.339951	8.575703	±	0.217328	8.068541	±	0.248874	4.237996	1.299556	0.735945	5	12	0.018806586	Yes	Phosphoribulokinase
CaM-207	5.99663	±	0.333324	7.073139	±	0.394419	6.4465218	±	0.256908	6.1208706	±	0.248614	7.2649827	±	0.262336	6.410048	±	0.22546	9.141288	3.916544	1.028269	5	12	0.000883571	Yes	ATP synthase subunit alpha
CaM-208	6.0402856	±	0.367113	6.8729725	±	0.382983	6.618665	±	0.413027	6.459953	±	0.232042	7.2553315	±	0.332101	0	±	0	220.0921	113.0127	1.232349	5	12	2.278E-11	Yes	Putative 60S acidic ribosomal protein P0
CaM-209	6.1603374	±	0.327532	7.5777245	±	0.421147	8.169686	±	0.425697	6.9411416	±	0.2192	6.9400253	±	0.336861	7.695522	±	0.396954	11.605565	7.591554	1.569913	5	12	0.00029262	Yes	Putative 60S acidic ribosomal protein P0
CaM-210	7.06131	±	0.070939	7.431667	±	0.441126	8.008937	±	0.104328	7.4029765	±	0.410119	7.893064	±	0.040185	7.730984	±	0.345837	4.513447	1.880319	0.999849	5	12	0.015130141	Yes	Fructose-bisphosphate aldolase
CaM-214	6.8118367	±	0.26817	7.7781506	±	0.12848	0	±	0	7.4880986	±	0.356823	7.3509727	±	0.313653	0	±	0	832.7678	217.9928	0.628246	5	12	8.21565E-15	Yes	Glutamate-ammonia ligase (EC 6.3.1.2) delta precursor
CaM-216	6.910494	±	0.149641	7.6971774	±	0.121985	7.3845506	±	0.264422	7.9002166	±	0.376091	7.608177	±	0.219701	7.132965	±	0.233802	7.00341	2.051814	0.703137	5	12	0.002800377	Yes	Glutamate-ammonia ligase (EC 6.3.1.2) delta precursor
CaM-218	6.605952	±	0.270509	7.916162	±	0.27273	0	±	0	7.8205514	±	0.33356	7.380938	±	0.378987	8.052318	±	0.219993	390.83725	146.8398	0.901694	5	12	7.51843E-13	Yes	Glutamine synthetase
CaM-221	9.564595	±	0.21136	8.412441	±	0.199437	9.623633	±	0.319532	8.297797	±	0.058116	10.038039	±	0.25536	10.505553	±	0.144203	50.834	11.68882	0.551858	5	12	1.16062E-07	Yes	ATP synthase beta subunit (Fragment)
CaM-222	6.8386035	±	0.313385	6.8815665	±	0.177394	6.0190606	±	0.254207	6.539026	±	0.12531	7.833365	±	0.045034	5.923191	±	0.231213	32.884907	7.275508	0.53098	5	12	1.32691E-06	Yes	ATP synthase subunit beta
CaM-223	7.729629	±	0.325763	7.113209	±	0.204455	7.0239677	±	0.231628	6.9305363	±	0.429745	7.6212564	±	0.275345	7.5357413	±	0.342114	3.648903	1.760937	1.158225	5	12	0.030729257	Yes	Putative glutamate-tRNA ligase
CaM-226	7.0229416	±	0.097117	7.445812	±	0.536287	7.7352605	±	0.065156	9.725231	±	0.323848	8.093498	±	0.247183	9.4482155	±	0.315324	38.457607	18.16118	1.133373	5	12	5.57456E-07	Yes	ATPase beta subunit (Fragment)

CaM-240	9.914124	±	0.377788	9.709861	±	0.502626	8.707967	±	0.088646	8.264376	±	0.330836	8.259547	±	0.351212	8.653915	±	0.132179	14.289778	7.781838	1.306977	5	12	0.000106455	Yes	40S ribosomal protein S12
CaM-246	10.410758	±	0.27957	9.539444	±	0.215782	10.390157	±	0.248877	9.807682	±	0.193951	10.201241	±	0.154851	9.548566	±	0.271153	9.091077	2.437778	0.643561	5	12	0.000905705	Yes	Putative serine/threonine kinase
CaM-247	10.323692	±	0.298256	9.1133	±	0.298389	10.763865	±	0.138044	9.215666	±	0.284621	8.401645	±	0.425444	7.769054	±	0.198773	46.039505	19.12832	0.997143	5	12	2.0325E-07	Yes	Membrane protein CH1-like
CaM-254	0	±	0	0	±	0	7.6089835	±	0.349399	6.7742386	±	0.219173	6.9647317	±	0.13743	0	±	0	1454.0387	229.0157	0.378008	5	12	3.33067E-16	Yes	ATP synthase gamma chain
CaM-257	8.25543	±	0.390722	7.7553706	±	0.268396	8.120919	±	0.369518	8.017285	±	0.227075	8.552018	±	0.2021	8.654601	±	0.380238	3.4117472	1.700847	1.196464	5	12	0.03784779	Yes	Plastidic aldolase
CaM-263	6.6265683	±	0.230221	9.7926035	±	0.363082	6.474798	±	0.100527	0	±	0	7.292593	±	0.133525	7.2174935	±	0.073942	887.9324	161.4792	0.436463	5	12	5.55112E-15	Yes	OSJNBb0085H11.1 protein
CaM-267	0	±	0	0	±	0	6.951384	±	0.267582	0	±	0	4.749954	±	4.118491	5.8863626	±	5.104154	4.5101175	161.9356	86.17191	5	12	0.015169316	Yes	Hypothetical protein F26P21.180
CaM-269	6.1253304	±	0.378052	0	±	0	5.469561	±	0.197302	0	±	0	0	±	0	8.513032	±	0.221124	1131.4114	217.5582	0.461494	5	12	1.33227E-15	Yes	ATP synthase subunit alpha
CaM-271	8.648853	±	0.249809	7.0495706	±	0.444854	8.231373	±	0.266143	7.980329	±	0.317699	9.110553	±	0.372221	8.622403	±	0.040375	16.035912	7.647022	1.144484	5	12	5.977E-05	Yes	H+-transporting two-sector ATPase-alpha chain
CaM-272	7.529821	±	0.290092	6.278463	±	0.459052	7.2541785	±	0.230127	7.011789	±	0.427273	8.432578	±	0.224308	7.8077245	±	0.233063	15.181009	8.033733	1.270071	5	12	7.87451E-05	Yes	ATP synthase CF1 alpha subunit
CaM-283	9.480482	±	0.415844	9.142625	±	0.232834	8.253951	±	0.389867	9.235078	±	0.318945	8.582005	±	0.303645	8.501159	±	0.408582	5.734197	3.536083	1.479998	5	12	0.006252549	Yes	40S ribosomal protein S12
CaM-290	7.309196	±	0.197093	8.228299	±	0.32383	7.848063	±	0.412169	8.954298	±	0.509768	8.7475	±	0.270607	9.553581	±	0.471005	13.566553	9.819145	1.737063	5	12	0.000137545	Yes	Intronic ORF; similar to LAGLIDADG endonuclease
CaM-294	8.742703	±	0.307524	10.027801	±	0.242775	9.468259	±	0.216236	9.052751	±	0.385479	9.056861	±	0.431458	8.194781	±	0.397958	10.108934	5.841191	1.386779	5	12	0.000558801	Yes	Putative PSII-P protein
CaM-295	8.5163965	±	0.176525	8.42756	±	0.262882	8.568124	±	0.324128	8.26415	±	0.146782	8.578538	±	0.267413	7.662104	±	0.272885	5.91809	1.83879	0.745696	5	12	0.005528897	Yes	ATP synthase subunit alpha
CaM-299	8.922279	±	0.460035	9.108951	±	0.120351	9.491695	±	0.153642	8.767903	±	0.276726	9.67284	±	0.068629	10.477836	±	0.104509	20.60166	5.870297	0.683863	5	12	1.64413E-05	Yes	Histone acetyltransferase GCN5
CaM-301	6.775804	±	0.417758	7.6553197	±	0.432989	5.5144973	±	0.219843	7.280419	±	0.235537	7.4387913	±	0.401478	7.6998463	±	0.388221	15.855255	10.27566	1.55542	5	12	6.32899E-05	Yes	Proteasome subunit alpha type
CaM-308	6.868197	±	0.172882	7.387281	±	0.437921	6.852735	±	0.31254	8.310295	±	0.409852	8.761737	±	0.139507	8.28452	±	0.329105	19.532253	10.01182	1.230189	5	12	2.17205E-05	Yes	Fructose-bisphosphate aldolase 1
CaM-310	8.849694	±	0.424194	9.10432	±	0.063535	9.22963	±	0.101136	9.841937	±	0.117984	8.94322	±	0.184219	8.668774	±	0.249105	9.946508	2.520743	0.608232	5	12	0.000602046	Yes	Fructose-bisphosphate aldolase (EC 4.1.2.13) precursor
CaM-311	4.4754605	±	0.168728	0	±	0	6.427797	±	0.253044	6.7606926	±	0.189896	5.9967537	±	0.288436	0	±	0	845.0956	149.1286	0.423513	5	12	7.54952E-15	Yes	ATP synthase CF1 alpha subunit
CaM-316	5.499235	±	0.139229	0	±	0	0	±	0	0	±	0	5.9317565	±	0.36689	0	±	0	1020.4222	130.9482	0.307986	5	12	2.44249E-15	Yes	ATP synthase subunit alpha
CaM-319	0	±	0	0	±	0	0	±	0	0	±	0	0	±	0	11.1937685	±	0.088763	47710.168	313.2512	0.015758	5	12	0	Yes	Putative ferredoxin-NADP(H) oxidoreductase
CaM-322	6.5056458	±	0.278802	0	±	0	6.0317435	±	0.170642	0	±	0	0	±	0	0	±	0	1769.1051	157.523	0.213699	5	12	1.11022E-16	Yes	Phosphoglycerate kinase
CaM-323	6.7099833	±	0.307219	6.485344	±	0.382167	6.661573	±	0.384602	5.9739137	±	0.220448	6.079723	±	0.346877	0	±	0	222.20522	103.1912	1.11455	5	12	2.15268E-11	Yes	Putative uncharacterized protein
CaM-335	6.2520657	±	0.404054	0	±	0	5.151427	±	0.28412	5.9518604	±	0.206552	6.485399	±	0.309258	0	±	0	455.5965	145.141	0.764576	5	12	3.01537E-13	Yes	ATP synthase subunit alpha
CaM-346	6.655455	±	0.244607	5.5995574	±	0.377833	5.815538	±	0.368728	5.400726	±	0.21004	6.4921074	±	0.497582	6.5138936	±	0.441368	6.333008	4.354267	1.650123	5	12	0.004225173	Yes	Putative uncharacterized protein
CaM-376	8.65673	±	0.369059	7.4390163	±	0.374387	7.4177594	±	0.3616	6.7082653	±	0.277557	8.121991	±	0.407021	8.026268	±	0.302074	11.300929	6.979055	1.482155	5	12	0.000331982	Yes	Ferredoxin-NADP reductase
CaM-382	6.444095	±	0.377617	6.63969	±	0.380661	6.4086113	±	0.260184	0	±	0	7.340215	±	0.361646	6.86865	±	0.273926	246.68831	115.3302	1.122034	5	12	1.1587E-11	Yes	ATP synthase subunit alpha
CaM-	6.2872863	±	0.210432	6.928101	±	0.101229	7.1803207	±	0.216018	7.1872077	±	0.185258	7.087711	±	0.38715	0	±	0	512.56946	121.9053	0.570796	5	12	1.49325E-13	Yes	ATP synthase subunit

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CaM-396	6.9497714	±	0.375095	5.7956924	±	0.485132	7.308068	±	0.081389	7.138386	±	0.285777	7.8583336	±	0.266611	0	±	0	290.82385	129.7615	1.070846	5	12	4.36229E-12	Yes	ATP synthase subunit alpha
CaM-407	5.9799333	±	0.250174	6.624661	±	0.51562	6.606047	±	0.056501	6.778694	±	0.316914	6.942098	±	0.396153	7.919741	±	0.298623	10.695564	6.044698	1.356383	5	12	0.00043007	Yes	Mitochondrial processing peptidase beta subunit
CaM-416	0	±	0	6.1119285	±	0.348804	0	±	0	0	±	0	6.392674	±	0.015379	0	±	0	1540.4373	156.4833	0.243801	5	12	2.22045E-16	Yes	Unknown protein 18
CaM-428	8.748443	±	0.335608	0	±	0	7.672071	±	0.193402	0	±	0	0	±	0	0	±	0	2170.4297	271.3711	0.300075	5	12	0	Yes	Beta-1,3-glucanase
CaM-435	8.470675	±	0.158718	8.567342	±	0.198123	9.012403	±	0.148623	8.570005	±	0.204495	9.351075	±	0.39606	9.484123	±	0.142097	11.323921	2.881999	0.610813	5	12	0.000328804	Yes	Carbonic anhydrase
CaM-436	7.8182297	±	0.315757	8.351238	±	0.123345	8.075469	±	0.436537	7.7860413	±	0.136483	8.936665	±	0.184575	8.567885	±	0.132741	9.720878	3.044228	0.751593	5	12	0.000668755	Yes	Putative quinone oxidoreductase
CaM-443	6.271562	±	0.225134	6.11129	±	0.418731	9.057239	±	0.412406	6.8198204	±	0.171089	7.4962673	±	0.453223	9.43201	±	0.178289	54.616383	30.15594	1.325138	5	12	7.719E-08	Yes	Predicted protein
CaM-445	8.447661	±	0.282507	7.731952	±	0.301054	7.9786096	±	0.247267	7.7142997	±	0.28093	9.0527525	±	0.467627	7.5639324	±	0.286357	9.500276	4.83866	1.222363	5	12	0.000742442	Yes	Putative uncharacterized
CaM-452	10.069493	±	0.163645	8.750091	±	0.122896	9.582906	±	0.363751	8.341922	±	0.166251	8.892865	±	0.202015	8.840526	±	0.376514	18.523767	5.933938	0.76882	5	12	2.8594E-05	Yes	Ferredoxin: nadp+ reductase
CaM-460	7.606135	±	0.045432	8.072276	±	0.080367	7.00597	±	0.234882	6.8918996	±	0.053804	8.860329	±	0.134428	8.7664175	±	0.308471	72.03569	10.79411	0.359625	5	12	1.57961E-08	Yes	Glyceraldehyde 3-phosphate dehydrogenase
CaM-461	6.620127	±	0.371454	7.083841	±	0.257173	5.851719	±	0.42912	5.4239163	±	0.153469	6.000315	±	0.193805	6.305323	±	0.214748	12.576976	5.193127	0.990978	5	12	0.000198968	Yes	Glyceraldehyde-3-phosphate dehydrogenase
CaM-462	5.6369243	±	0.388375	6.4828296	±	0.126975	0	±	0	5.342834	±	0.225147	6.690188	±	0.390849	7.4293504	±	0.221121	309.6251	108.1899	0.838613	5	12	3.00637E-12	Yes	Glyceraldehyde-3-phosphate dehydrogenase A
CaM-483	6.4754233	±	0.279339	6.454972	±	0.144666	0	±	0	0	±	0	0	±	0	0	±	0	2027.4618	167.1958	0.197917	5	12	0	Yes	Luminal binding protein, BiP
CaM-485	0	±	0	7.338013	±	0.286865	0	±	0	0	±	0	0	±	0	0	±	0	1963.0132	134.6161	0.164583	5	12	0	Yes	Carbonic anhydrase
CaM-487	7.7130585	±	0.206839	7.0715127	±	0.215302	0	±	0	6.367279	±	0.366871	0	±	0	0	±	0	1214.4156	226.419	0.447463	5	12	8.88178E-16	Yes	Guanine nucleotide-binding protein subunit beta-like

Supplementary Table S5. List of identified proteins with their eMPAI (exponentially Modified Protein Abundance Index) values.

Spot No	Identification	No of identifications (peptide with ion score $p < 0.05$)	eMPAI	Summation of emPAI	mol fraction	% mol fraction
CaM-112*	Putative uncharacterized protein	Putative uncharacterized protein (Fragment) Tax_Id=3827 [Cicer arietinum]	0.22	0.35	0.628571429	62.85714286
		Chlorophyll A/B binding protein Tax_Id=114476 [Gardenia jasminoides]	0.13		0.371428571	37.14285714
CaM-121*	Ribulose bisphosphate carboxylase large chain	Ribulose bisphosphate carboxylase large chain (Fragment) Tax_Id=28975 [Hypseocharis sp. Beck s.n]	0.07	0.54	0.12962963	12.96296296
		Ribulose bisphosphate carboxylase large chain (Fragment) Tax_Id=203790 [Anarthria prolifera]	0.08		0.148148148	14.81481481
		Ribulose bisphosphate carboxylase large chain (Fragment) Tax_Id=160682 [Asterella lindenbergiana]	0.16		0.296296296	29.62962963
		Ribulose bisphosphate carboxylase large chain (Fragment) Tax_Id=124814 [Salacia undulata]	0.07		0.12962963	12.96296296
		Ribulose bisphosphate carboxylase large chain (Fragment) Tax_Id=472498 [Aspalathus shawii subsp. shawii]	0.16		0.296296296	29.62962963
CaM-122*	Ribulose bisphosphate carboxylase large chain	Ribulose bisphosphate carboxylase large chain Tax_Id=3827 [Cicer arietinum]	0.15	0.8	0.1875	18.75
		Ribulose bisphosphate carboxylase large chain (Fragment) Tax_Id=160682 [Asterella lindenbergiana]	0.34		0.425	42.5
		Ribulose bisphosphate carboxylase large chain (Fragment) Tax_Id=126692 [Osmoxylon novoguineense]	0.08		0.1	10
		Ribulose bisphosphate carboxylase large chain (Fragment) Tax_Id=221308 [Trichomanes ankersii]	0.08		0.1	10
		Ribulose bisphosphate carboxylase large chain (Fragment) Tax_Id=52857 [Stephanostema stenocarpum]	0.07		0.0875	8.75
		Ribulose bisphosphate carboxylase large chain (Fragment) Tax_Id=120586 [Dacrydium araucarioides]	0.08		0.1	10
CaM-138*	Chromosome chr17 scaffold_16	Chromosome chr17 scaffold_16, whole genome shotgun sequence Tax_Id=29760 [Vitis vinifera]	0.11	0.21	0.523809524	52.38095238
		Putative uncharacterized protein Tax_Id=39946 [Oryza sativa subsp. indica]	0.04		0.19047619	19.04761905
		ATP synthase subunit beta Tax_Id=37502 [Polytomella sp. Pringsheim 198.80]	0.06		0.285714286	28.57142857
CaM-141*	Phosphoglycerate kinase	Phosphoglycerate kinase Tax_Id=3988 [Ricinus communis	0.15	0.77	0.194805195	19.48051948

		Phosphoglycerate kinase Tax_Id=3695 [Populus trichocarpa x Populus deltoides]	0.07		0.090909091	9.090909091
		Phosphoglycerate kinase (Fragment) Tax_Id=29760 [Vitis vinifera]	0.18		0.233766234	23.37662338
		Phosphoglycerate kinase Tax_Id=3880 [Medicago truncatula]	0.3		0.38961039	38.96103896
		ATP synthase subunit beta (Fragment) Tax_Id=85203 [Eucryphia milliganii]	0.07		0.090909091	9.090909091
CaM-147*	ATP synthase subunit beta, chloroplastic	sp|Q9MUT5|ATP synthase subunit beta, chloroplastic Tax_Id=41882 [Mesostigma viride]	0.07	0.21	0.333333333	33.33333333
		ATP synthase subunit beta (Fragment) Tax_Id=227220 [Arctagrostis latifolia]	0.07		0.333333333	33.33333333
		ATP synthase subunit beta (Fragment) Tax_Id=519303 [Triodanis coloradoensis]	0.07		0.333333333	33.33333333
CaM-157*	Putative GroEL protein chaperonin 60kDa	RuBisCO large subunit-binding protein subunit beta, chloroplastic Tax_Id=3888 [Pisum sativum]	0.33	1.01	0.326732673	32.67326733
		Beta chaperonin 60 Tax_Id=4109 [Solanum commersonii]	0.19		0.188118812	18.81188119
		Putative GloEL protein:chaperonin, 60kDa (Fragment) Tax_Id=3755 [Prunus dulcis]	0.49		0.485148515	48.51485149
CaM-182*	Ferritin	Ferritin Tax_Id=3694 [Populus trichocarpa]	0.23	0.23	1	100
CaM-187*	Chlorophyll a/b binding protein	Chlorophyll a/b binding protein Tax_Id=3827 [Cicer arietinum]	1.41	5.01	0.281437126	28.14371257
		Putative uncharacterized protein Tax_Id=3847 [Glycine max]	0.88		0.175648703	17.56487026
		Putative uncharacterized protein Tax_Id=29760 [Vitis vinifera]	0.86		0.171656687	17.16566866
		Light-harvesting complex II protein Lhcb1 Tax_Id=3694 [Populus trichocarpa]	0.66		0.131736527	13.17365269
		Chlorophyll a-b binding protein, chloroplast, putative, expressed Tax_Id=39947 [Oryza sativa subsp. japonica]	1.2		0.239520958	23.95209581
CaM-189*	ATP synthase subunit alpha	ATP synthase subunit alpha Tax_Id=3827 [Cicer arietinum]	1.32	8.63	0.152954809	15.29548088
		ATP synthase subunit alpha Tax_Id=3900 [Trifolium subterraneum]	0.91		0.105446118	10.54461182
		ATP synthase subunit alpha, chloroplastic Tax_Id=3885 [Phaseolus vulgaris]	0.79		0.091541136	9.154113557
		ATP synthase subunit alpha, chloroplastic Tax_Id=34305 [Lotus japonicus	0.57		0.066048667	6.604866744

		AtpA Tax_Id=180498 [Jatropha curcas]	0.68		0.078794902	7.879490151
		ATP synthase subunit alpha, chloroplastic Tax_Id=3847 [Glycine max]	0.57		0.066048667	6.604866744
		ATP synthase subunit alpha, chloroplastic Tax_Id=4081 [Solanum lycopersicum]	0.48		0.05561993	5.561993048
		ATP synthase subunit alpha (Fragment) Tax_Id=4733 [Typha latifolia]	0.48		0.05561993	5.561993048
		ATP synthase subunit alpha, chloroplastic Tax_Id=37657 [Silene latifolia]	0.38		0.044032445	4.403244496
		ATP synthase subunit alpha, chloroplastic Tax_Id=3942 [Oenothera biennis]	0.69		0.07995365	7.995365006
		ATP synthase subunit alpha, chloroplastic Tax_Id=2711 [Citrus sinensis]	0.38		0.044032445	4.403244496
		ATP synthase subunit alpha (Fragment) Tax_Id=32095 [Lonchitis hirsuta]	0.3		0.034762457	3.476245655
		ATP synthase subunit alpha, chloroplastic Tax_Id=48387 [Anthoceros formosae]	0.38		0.044032445	4.403244496
		ATP synthase subunit alpha, chloroplastic Tax_Id=3197 [Marchantia polymorpha]	0.39		0.045191194	4.519119351
		ATP synthase subunit alpha (Fragment) Tax_Id=3311 [Ginkgo biloba]	0.14		0.01622248	1.622247972
		ATP synthase subunit alpha (Fragment) Tax_Id=28472 [Epipactis helleborine]	0.08		0.009269988	0.926998841
		ATP synthase subunit alpha (Fragment) Tax_Id=396647 [Afrothismia hydra]	0.09		0.010428737	1.042873696
CaM-191*	Ferritin	Ferritin Tax_Id=3847 [Glycine max]	0.28	0.49	0.571428571	57.14285714
		Whole genome shotgun sequence of line PN40024, scaffold_49.assembly12x (Fragment) Tax_Id=29760 [Vitis vinifera]	0.12		0.244897959	24.48979592
		Putative uncharacterized protein Tax_Id=39946 [Oryza sativa subsp. indica]	0.09		0.183673469	18.36734694
CaM-196*	Oxygen-evolving enhancer protein 1	Putative uncharacterized protein Tax_Id=3847 [Glycine max]	0.36	1.09	0.330275229	33.02752294
		Chloroplast manganese stabilizing protein-II (Fragment) Tax_Id=4113 [Solanum tuberosum]	0.25		0.229357798	22.93577982
		Putative uncharacterized protein Tax_Id=3847 [Glycine max]	0.23		0.211009174	21.10091743
		Oxygen-evolving enhancer protein 1, chloroplastic Tax_Id=3888 [Pisum sativum]	0.11		0.100917431	10.09174312

		ATP synthase subunit alpha Tax_Id=3827 [Cicer arietinum]	0.14		0.128440367	12.8440367
CaM-205*	ATP synthase subunit beta	ATP synthase subunit beta Tax_Id=128017 [Dimocarpus longan]	0.13	0.13	1	100
CaM-207*	ATP synthase subunit alpha	ATP synthase subunit alpha Tax_Id=3827 [Cicer arietinum]	0.38	0.95	0.4	40
		ATP synthase subunit alpha, chloroplastic Tax_Id=48387 [Anthoceros formosae]	0.14		0.147368421	14.73684211
		ATP synthase subunit alpha, chloroplastic Tax_Id=3197 [Marchantia polymorpha]	0.14		0.147368421	14.73684211
		ATP synthase subunit alpha (Fragment) Tax_Id=4733 [Typha latifolia]	0.22		0.231578947	23.15789474
		ATP synthase subunit alpha (Fragment) Tax_Id=32095 [Lonchitis hirsuta]	0.07		0.073684211	7.368421053
CaM-208*	Putative 60S acidic ribosomal protein P0	Putative 60S acidic ribosomal protein P0 Tax_Id=57577 [Trifolium pratense]	0.11	0.11	1	100
CaM-209*	Putative 60S acidic ribosomal protein P0	Putative 60S acidic ribosomal protein P0 Tax_Id=57577 [Trifolium pratense]	0.11	0.11	1	100
CaM-210*	Fructose-bisphosphate aldolase	Fructose-bisphosphate aldolase Tax_Id=57577 [Trifolium pratense]	0.18	0.27	0.666666667	66.66666667
		Fructose bisphosphate aldolase Tax_Id=3879 [Medicago sativa]	0.09		0.333333333	33.33333333
CaM-218*	Glutamine synthetase	Glutamine synthetase Tax_Id=161934 [Beta vulgaris]	0.08	0.08	1	100
CaM-222*	ATP synthase subunit beta	ATP synthase subunit beta Tax_Id=3827 [Cicer arietinum]	0.15	0.15	1	100
CaM-24*	Putative uncharacterized protein	Putative uncharacterized protein Tax_Id=3880 [Medicago truncatula]	0.8	1.01	0.792079208	79.20792079
		Putative uncharacterized protein Tax_Id=3880 [Medicago truncatula]	0.21		0.207920792	20.79207921
CaM-240*	40S ribosomal protein S12	40S ribosomal protein S12 Tax_Id=3847 [Glycine max]	0.57	0.57	1	100
CaM-254*	ATP synthase gamma chain	ATP synthase gamma chain Tax_Id=3880 [Medicago truncatula]	0.3	1.33	0.22556391	22.55639098
		ATP synthase gamma chain Tax_Id=3847 [Glycine max]	0.19		0.142857143	14.28571429
		ATP synthase gamma chain Tax_Id=3988 [Ricinus communis]	0.19		0.142857143	14.28571429
		Putative uncharacterized protein Tax_Id=4577 [Zea mays]	0.27		0.203007519	20.30075188
		Putative uncharacterized protein Tax_Id=3880 [Medicago truncatula]	0.38		0.285714286	28.57142857

CaM-269*	ATP synthase subunit alpha	ATP synthase subunit alpha, chloroplastic Tax_Id=34305 [Lotus japonicus]	0.38	1.6	0.2375	23.75
		ATP synthase subunit alpha Tax_Id=3827 [Cicer arietinum]	0.38		0.2375	23.75
		ATP synthase subunit beta Tax_Id=3827 [Cicer arietinum]	0.23		0.14375	14.375
		ATP synthase CF1 alpha subunit Tax_Id=157791 [Vigna radiata]	0.38		0.2375	23.75
		ATP synthase subunit beta (Fragment) Tax_Id=210340 [Bischofia javanica]	0.23		0.14375	14.375
CaM-283*	40S ribosomal protein S12	40S ribosomal protein S12 Tax_Id=3847 [Glycine max]	0.97	0.97	1	100
CaM-294*	Putative PSII-P protein	Putative PSII-P protein (Fragment) Tax_Id=57577 [Trifolium pratense]	0.13	0.13	1	100
CaM-295*	ATP synthase subunit alpha	ATP synthase subunit alpha Tax_Id=3827 [Cicer arietinum]	0.14	0.14	1	100
CaM-301*	Proteasome subunit alpha type	Proteasome subunit alpha type Tax_Id=3694 [Populus trichocarpa]	0.68	2.09	0.325358852	32.53588517
		Proteasome subunit alpha type Tax_Id=3988 [Ricinus communis]	0.47		0.224880383	22.48803828
		Proteasome subunit alpha type (Fragment) Tax_Id=3750 [Malus domestica]	0.65		0.311004785	31.10047847
		Proteasome subunit alpha type-6 Tax_Id=3847 [Glycine max]	0.29		0.138755981	13.87559809
CaM-308*	Fructose-bisphosphate aldolase	Fructose-bisphosphate aldolase 1, chloroplastic Tax_Id=3888 [Pisum sativum]	0.2	0.2	1	100
CaM-311*	ATP synthase CF1 alpha subunit	ATP synthase CF1 alpha subunit Tax_Id=157791 [Vigna radiata]	0.38	0.96	0.395833333	39.58333333
		ATP synthase subunit alpha Tax_Id=3827 [Cicer arietinum]	0.3		0.3125	31.25
		ATP synthase subunit alpha Tax_Id=326026 [Geranium palmatum]	0.14		0.145833333	14.58333333
		ATP synthase subunit alpha, chloroplastic Tax_Id=55564 [Chara vulgaris]	0.14		0.145833333	14.58333333
CaM-316*	ATP synthase subunit alpha	ATP synthase subunit alpha Tax_Id=3827 [Cicer arietinum]	0.38	0.96	0.395833333	39.58333333
		ATP synthase subunit alpha, chloroplastic Tax_Id=2711 [Citrus sinensis]	0.22		0.229166667	22.91666667
		ATP synthase subunit alpha, chloroplastic Tax_Id=48387 [Anthoceros formosae]	0.22		0.229166667	22.91666667

		ATP synthase subunit alpha Tax_Id=3369 [Cryptomeria japonica]	0.14		0.145833333	14.58333333
CaM-322*	Phosphoglycerate kinase precursor like	Phosphoglycerate kinase Tax_Id=4113 [Solanum tuberosum]	0.15	0.7	0.214285714	21.42857143
		Phosphoglycerate kinase Tax_Id=3988 [Ricinus communis]	0.16		0.228571429	22.85714286
		Putative uncharacterized protein Tax_Id=4577 [Zea mays]	0.18		0.257142857	25.71428571
		Phosphoglycerate kinase Tax_Id=3880 [Medicago truncatula]	0.14		0.2	20
		Phosphoglycerate kinase Tax_Id=29760 [Vitis vinifera]	0.07		0.1	10
CaM-323*	Putative uncharacterized protein	Putative uncharacterized protein Tax_Id=3332 [Picea sitchensis	0.19	0.36	0.527777778	52.77777778
		Putative uncharacterized protein Tax_Id=3694 [Populus trichocarpa]	0.09		0.25	25
		Ribulose bisphosphate carboxylase activase B Tax_Id=4565 [Triticum aestivum]	0.08		0.222222222	22.22222222
CaM-335*	ATP synthase subunit alpha	ATP synthase subunit alpha Tax_Id=3827 [Cicer arietinum]	0.07	0.07	1	100
CaM-346*	Putative uncharacterized protein	Putative uncharacterized protein Tax_Id=3694 [Populus trichocarpa]	0.09	0.64	0.140625	14.0625
		Transketolase (Fragment) Tax_Id=3827 [Cicer arietinum]	0.5		0.78125	78.125
		Putative uncharacterized protein Sb06g004280 Tax_Id=4558 [Sorghum bicolor]	0.05		0.078125	7.8125
CaM-376*	Ferredoxin-NADP reductase	Ferredoxin--NADP reductase Tax_Id=39946 [Oryza sativa subsp. indica]	0.09	0.16	0.5625	56.25
		ATP synthase subunit alpha, chloroplastic Tax_Id=13443 [Coffea arabica]	0.07		0.4375	43.75
CaM-382*	ATP synthase subunit alpha	ATP synthase subunit alpha Tax_Id=3827 [Cicer arietinum]	0.57	1.98	0.287878788	28.78787879
		ATP synthase subunit alpha (Fragment) Tax_Id=4733 [Typha latifolia]	0.39		0.196969697	19.6969697
		Fructose-bisphosphate aldolase, cytoplasmic isozyme 1 Tax_Id=3888 [Pisum sativum]	0.45		0.227272727	22.72727273
		ATP synthase subunit alpha Tax_Id=3369 [Cryptomeria japonica]	0.22		0.111111111	11.11111111
		Fructose-bisphosphate aldolase Tax_Id=3847 [Glycine max]	0.21		0.106060606	10.60606061
		ATP synthase subunit alpha (Fragment) Tax_Id=32095	0.14		0.070707071	7.070707071

		[Lonchitis hirsuta]				
CaM-386*	ATP synthase subunit alpha	ATP synthase subunit alpha Tax_Id=3827 [Cicer arietinum]	0.68	2.17	0.313364055	31.33640553
		ATP synthase subunit alpha (Fragment) Tax_Id=4733 [Typha latifolia]	0.39		0.179723502	17.97235023
		ATP synthase subunit alpha Tax_Id=3369 [Cryptomeria japonica]	0.3		0.138248848	13.82488479
		ATP synthase subunit alpha, chloroplastic Tax_Id=48387 [Anthoceros formosae]	0.22		0.101382488	10.13824885
		ATP synthase subunit alpha, chloroplastic Tax_Id=3197 [Marchantia polymorpha]	0.22		0.101382488	10.13824885
		ATP synthase subunit alpha (Fragment) Tax_Id=32095 [Lonchitis hirsuta]	0.14		0.064516129	6.451612903
		ATP synthase subunit alpha, chloroplastic Tax_Id=2711 [Citrus sinensis]	0.22		0.101382488	10.13824885
CaM-39*	Putative 60S ribosomal protein L1	Putative uncharacterized protein Tax_Id=3880 [Medicago truncatula]	0.08	0.08	1	100
CaM-394*	ATP synthase subunit alpha	Ribulose-1,5-bisphosphate carboxylase/oxygenase activase (Fragment) Tax_Id=74825 [Pachysandra terminalis]	0.23	0.93	0.247311828	24.7311828
		ATP synthase subunit alpha Tax_Id=3827 [Cicer arietinum]	0.14		0.150537634	15.05376344
		ATP synthase subunit alpha (Fragment) Tax_Id=4733 [Typha latifolia]	0.14		0.150537634	15.05376344
		Ribulose-1,5-bisphosphate carboxylase activase (Fragment) Tax_Id=4565 [Triticum aestivum]	0.17		0.182795699	18.27956989
		Putative uncharacterized protein Tax_Id=3694 [Populus trichocarpa]	0.09		0.096774194	9.677419355
		Putative uncharacterized protein Tax_Id=3332 [Picea sitchensis]	0.09		0.096774194	9.677419355
		ATP synthase subunit alpha (Fragment) Tax_Id=32095 [Lonchitis hirsuta]	0.07		0.075268817	7.52688172
CaM-396*	ATP synthase subunit alpha	ATP synthase subunit alpha Tax_Id=3827 [Cicer arietinum]	0.57	2.07	0.275362319	27.53623188
		ATP synthase subunit alpha (Fragment) Tax_Id=4733 [Typha latifolia]	0.48		0.231884058	23.1884058
		ATP synthase subunit alpha, chloroplastic Tax_Id=48387 [Anthoceros formosae]	0.22		0.106280193	10.62801932
		ATP synthase subunit alpha, chloroplastic Tax_Id=3197	0.22		0.106280193	10.62801932

		[Marchantia polymorpha				
		ATP synthase subunit alpha Tax_Id=3369 [Cryptomeria japonica]	0.22		0.106280193	10.62801932
		ATP synthase subunit alpha (Fragment) Tax_Id=49509 [Pilularia globulifera]	0.22		0.106280193	10.62801932
		ATP synthase subunit alpha, chloroplastic Tax_Id=3144 [Chlorokybus atmophyticus]	0.14		0.06763285	6.763285024
CaM-416*	Succinate dehydrogenase flavoprotein subunit,mitochondrial	Unknown protein 18 (Fragment) Tax_Id=3357 [Pseudotsuga menziesii]	4.22	4.32	0.976851852	97.68518519
		Putative uncharacterized protein Tax_Id=4577 [Zea mays]	0.05		0.011574074	1.157407407
		Predicted protein Tax_Id=564608 [Micromonas pusilla CCMP1545]	0.05		0.011574074	1.157407407
CaM-428*	Beta-1,3-glucanase	Beta-1,3-glucanase Tax_Id=89151 [Musa paradisiaca]	0.1	0.1	1	100
CaM-43*	Ribulose bisphosphate carboxylase large chain	Ribulose bisphosphate carboxylase large chain Tax_Id=3827 [Cicer arietinum]	0.23	3.4	0.067647059	6.764705882
		Ribulose bisphosphate carboxylase large chain (Fragment) Tax_Id=284232 [Triodanis perfoliata]	0.24		0.070588235	7.058823529
		Ribulose bisphosphate carboxylase large chain (Fragment) Tax_Id=321576 [Delonix brachycarpa]	0.23		0.067647059	6.764705882
		Ribulose bisphosphate carboxylase large chain (Fragment) Tax_Id=93819 [Orthilia secunda]	0.23		0.067647059	6.764705882
		Ribulose bisphosphate carboxylase large chain (Fragment) Tax_Id=28475 [Lasia spinosa]	0.25		0.073529412	7.352941176
		Ribulose bisphosphate carboxylase large chain (Fragment) Tax_Id=74618 [Levenhookia leptantha]	0.23		0.067647059	6.764705882
		Ribulose bisphosphate carboxylase large chain (Fragment) Tax_Id=37395 [Reboulia hemisphaerica]	0.26		0.076470588	7.647058824
		Ribulose bisphosphate carboxylase large chain (Fragment) Tax_Id=280253 [Plagiochila arbuscula]	0.25		0.073529412	7.352941176
		Ribulose bisphosphate carboxylase large chain (Fragment) Tax_Id=162704 [Caesalpinia calycina]	0.25		0.073529412	7.352941176
		Ribulose bisphosphate carboxylase large chain Tax_Id=84014 [Comarostaphylis arbutoides]	0.15		0.044117647	4.411764706
		Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (Fragment) Tax_Id=426038 [Desmidium aptogonum]	0.24		0.070588235	7.058823529
		Ribulose bisphosphate carboxylase large chain (Fragment)	0.15		0.044117647	4.411764706

		Tax_Id=43553 [Pinckneya pubens]				
		Ribulose bisphosphate carboxylase large chain (Fragment) Tax_Id=124814 [Salacia undulata]	0.23		0.067647059	6.764705882
		Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (Fragment) Tax_Id=239430 [Campanulastrum americanum]	0.16		0.047058824	4.705882353
		Ribulose bisphosphate carboxylase large chain (Fragment) Tax_Id=125047 [Pentaphylax euryoides]	0.15		0.044117647	4.411764706
		Ribulose bisphosphate carboxylase large chain (Fragment) Tax_Id=312916 [Ammannia latifolia]	0.15		0.044117647	4.411764706
CaM-435*	Carbonic anhydrase	Carbonic anhydrase Tax_Id=3916 [Phaseolus aureus]	0.11	0.22	0.5	50
		Carbonic anhydrase Tax_Id=3635 [Gossypium hirsutum]	0.11		0.5	50
CaM-436*	Putative quinone oxidoreductase	Putative quinone oxidoreductase Tax_Id=3827 [Cicer arietinum]	0.63	0.63	1	100
CaM-443*	Predicted protein	Predicted protein Tax_Id=3694 [Populus trichocarpa]	0.14	0.14	1	100
CaM-445*	Putative uncharacterized	Putative uncharacterized protein Tax_Id=3847 [Glycine max]	0.62	1.17	0.52991453	52.99145299
		Putative uncharacterized protein (Fragment) Tax_Id=3880 [Medicago truncatula]	0.55		0.47008547	47.00854701
CaM-453*	Fructose-bisphosphate aldolase	ATP synthase subunit alpha Tax_Id=3827 [Cicer arietinum]	0.3	0.81	0.37037037	37.03703704
		ATP synthase subunit alpha (Fragment) Tax_Id=4733 [Typha latifolia]	0.22		0.271604938	27.16049383
		Fructose-bisphosphate aldolase, cytoplasmic isozyme Tax_Id=3827 [Cicer arietinum]	0.1		0.12345679	12.34567901
		ATP synthase subunit alpha (Fragment) Tax_Id=32095 [Lonchitis hirsuta]	0.07		0.086419753	8.641975309
		Fructose-bisphosphate aldolase Tax_Id=3371 [Metasequoia glyptostroboides]	0.12		0.148148148	14.81481481
CaM-461*	Glyceraldehyde-3-phosphate dehydrogenase	Putative uncharacterized protein Tax_Id=3880 [Medicago truncatula]	0.61	1.29	0.472868217	47.28682171
		Glyceraldehyde 3-phosphate dehydrogenase (Fragment) Tax_Id=386278 [Scopellaria marginata]	0.29		0.224806202	22.48062016
		utative uncharacterized protein Tax_Id=4577 [Zea mays]	0.09		0.069767442	6.976744186
		Glyceraldehyde 3-phosphate dehydrogenase (Fragment) Tax_Id=386199 [Mukia maderaspatana]	0.3		0.23255814	23.25581395
CaM-462*	Glyceraldehyde-3-phosphate dehydrogenase A	Glyceraldehyde-3-phosphate dehydrogenase A, chloroplastic Tax_Id=3888 [Pisum sativum]	0.28	0.28	1	100

CaM-483*	Mitochondrial outer membrane protein porin of 34 kDa	Whole genome shotgun sequence of line PN40024, scaffold_25.assembly12x (Fragment) Tax_Id=29760 [Vitis vinifera]	0.38	0.96	0.395833333	39.58333333
		Luminal-binding protein Tax_Id=3562 [Spinacia oleracea]	0.22		0.229166667	22.91666667
		Outer plastidial membrane protein porin Tax_Id=3888 [Pisum sativum]	0.13		0.135416667	13.54166667
		Porin Tax_Id=3544 [Mesembryanthemum crystallinum]	0.13		0.135416667	13.54166667
		Luminal binding protein, BiP Tax_Id=3190 [Scherffelia dubia]	0.1		0.104166667	10.41666667
CaM-485*	Carbonic anhydrase	Carbonic anhydrase Tax_Id=3885 [Phaseolus vulgaris]	0.65	0.98	0.663265306	66.32653061
		Carbonic anhydrase Tax_Id=3635 [Gossypium hirsutum]	0.22		0.224489796	22.44897959
		Carbonic anhydrase Tax_Id=74825 [Pachysandra terminalis]	0.11		0.112244898	11.2244898
CaM-487*	Guanine nucleotide-binding protein subunit beta-like	Putative uncharacterized protein Tax_Id=3880 [Medicago truncatula]	1.19	2.9	0.410344828	41.03448276
		Putative uncharacterized protein Tax_Id=3847 [Glycine max]	0.81		0.279310345	27.93103448
		Guanine nucleotide-binding protein subunit beta-like protein Tax_Id=3879 [Medicago sativa]	0.64		0.220689655	22.06896552
		Putative uncharacterized protein Tax_Id=3332 [Picea sitchensis]	0.19		0.065517241	6.551724138
		Whole genome shotgun sequence of line PN40024, scaffold_4.assembly12x (Fragment) Tax_Id=29760 [Vitis vinifera]	0.07		0.024137931	2.413793103
CaM-71*	light-harvesting complex II protein Lhcb3	Putative uncharacterized protein Tax_Id=3695 [Populus trichocarpa x Populus deltoides]	0.16	0.41	0.390243902	39.02439024
		Putative uncharacterized protein Tax_Id=3847 [Glycine max]	0.13		0.317073171	31.70731707
		tr|Q0PWS5|Chloroplast pigment-binding protein CP26 Tax_Id=4097 [Nicotiana tabacum]	0.12		0.292682927	29.26829268
CaM-73*	Actin (Fragment)	Actin (Fragment) Tax_Id=69334 [Chara contraria]	0.16	0.26	0.615384615	61.53846154
		Actin (Fragment) Tax_Id=38836 [Pterosperma cristatum]	0.1		0.384615385	38.46153846
CaM-75*	Chlorophyll a/b binding protein	Chlorophyll a/b binding protein Tax_Id=3827 [Cicer arietinum]	1.13	3.78	0.298941799	29.89417989
		Chlorophyll a-b binding protein AB80, chloroplastic Tax_Id=3888 [Pisum sativum]	0.86		0.227513228	22.75132275
		Light-harvesting chlorophyll a/b-binding protein	0.46		0.121693122	12.16931217

		Tax_Id=3760 [Prunus persica]				
		Putative uncharacterized protein Tax_Id=29760 [Vitis vinifera]	0.64		0.169312169	16.93121693
		Chlorophyll a-b binding protein, chloroplast, putative, expressed Tax_Id=39947 [Oryza sativa subsp. japonica]	0.69		0.182539683	18.25396825
CaM-78*	Chlorophyll a/b binding protein	Chlorophyll a/b binding protein Tax_Id=3827 [Cicer arietinum]	1.41	2.92	0.482876712	48.28767123
		Putative uncharacterized protein Tax_Id=29760 [Vitis vinifera]	0.86		0.294520548	29.45205479
		Putative chloroplast chlorophyll a/b-binding protein Tax_Id=139927 [Carya cathayensis]	0.65		0.22260274	22.26027397
CaM-9*	Ribulose bisphosphate carboxylase large chain	Ribulose bisphosphate carboxylase large chain (Fragment) Tax_Id=223100 [Orobanche coerulescens]	0.16	0.51	0.31372549	31.37254902
		Putative uncharacterized protein Tax_Id=3880 [Medicago truncatula]	0.35		0.68627451	68.62745098
CaM-94*	Chaperonin 60 alpha subunit	Putative uncharacterized protein Tax_Id=3880 [Medicago truncatula]	0.9	6.84	0.131578947	13.15789474
		tr|Q2PEP1|Putative rubisco subunit binding-protein alpha subunit Tax_Id=57577 [Trifolium pratense]	0.79		0.115497076	11.5497076
		RuBisCO large subunit-binding protein subunit alpha, chloroplastic Tax_Id=3888 [Pisum sativum]	0.59		0.08625731	8.625730994
		Chaperonin 60 alpha subunit Tax_Id=28957 [Canavalia lineata]	0.7		0.102339181	10.23391813
		Predicted protein Tax_Id=3694 [Populus trichocarpa]	0.59		0.08625731	8.625730994
		Predicted protein Tax_Id=3694 [Populus trichocarpa]	0.5		0.073099415	7.30994152
		Putative rubisco subunit binding-protein alpha subunit Tax_Id=3702 [Arabidopsis thaliana]	0.42		0.061403509	6.140350877
		RuBisCO large subunit-binding protein subunit alpha, chloroplastic Tax_Id=3708 [Brassica napus]	0.55		0.080409357	8.040935673
		Putative uncharacterized protein Tax_Id=39946 [Oryza sativa subsp. indica]	0.51		0.074561404	7.456140351
		RuBisCO large subunit-binding protein subunit alpha, chloroplastic Tax_Id=4565 [Triticum aestivum]	0.29		0.042397661	4.239766082
		Putative uncharacterized protein Tax_Id=39946 [Oryza sativa subsp. indica]	0.19		0.027777778	2.777777778
		Chaperonin-60 alpha subunit Tax_Id=82927 [Avicennia marina]	0.5		0.073099415	7.30994152
		Predicted protein Tax_Id=564608 [Micromonas pusilla	0.12		0.01754386	1.754385965

		CCMP1545]				
		Plastid 60 kDa chaperonin alpha subunit (Fragment) Tax_Id=3111 [Prototheca wickerhamii]	0.19		0.027777778	2.777777778
CaM-99*	Chaperone DnaK	Chaperone DnaK Tax_Id=3880 [Medicago truncatula]	0.33	0.76	0.434210526	43.42105263
		Chloroplast heat shock protein 70-2 Tax_Id=35883 [Ipomoea nil]	0.16		0.210526316	21.05263158
		Chloroplast heat shock protein 70-1 Tax_Id=35883 [Ipomoea nil]	0.16		0.210526316	21.05263158
		Os03g0859600 protein (Fragment) Tax_Id=39947 [Oryza sativa subsp. japonica]	0.11		0.144736842	14.47368421

Supplementary Table S6. *In silico* analyses of SUN domain proteins from different organisms.

Gene/ Accession No.	Organism	Sequence length (aa)	Position of SUN domain	No. of TMD	No. of CC domain and position	Position of signal peptide
CaSUN1	*C. arietinum*	602	215 -337	N-terminus outside 3 strong transmembrane helices	1 (474 L-487 Q)	52 - 53
SLP1 (YOR154W)	*S. cerevisae*	587	204 -330	N-terminus inside 2 strong transmembrane helices	1 (362 N-375 E)	21 - 22
MPS3 (YJL019W)	*S. cerevisae*	682	474 -613	N-terminus inside 1 strong transmembrane helices	3 (245 N-260 I) (366 I-380 I) (386 N-401Q)	Non-secretory protein
SAD1 (SPBC12D12)	*S. pombe*	514	358 -486	N-terminus outside 2 strong transmembrane helices	2 (82 R-95 N) (263 L- 282 K)	Non-secretory protein
Sad1-UNC-like protein (SPBC3E7.09)	*S. pombe*	659	208 -333	N-terminus outside 2 strong transmembrane helices	3 (336 I-349 Q) (458 Y-473 K) (525 A-538 E)	25 - 26
AtSUN3 (AT1G22882)	*A. thaliana*	660	278 -400	N-terminus inside 3 strong transmembrane helices	2 (100 N-113 E) (574 R-598 V)	47 - 48
AtSUN1 (AT5G04990)	*A. thaliana*	471	315 -450	N-terminus inside 1 strong transmembrane helices	2 (181 K-197 K) (203 S-217 K)	Non-secretory protein
Hypothetical protein (Pp1s191_3V6)	*P. patens*	844	472 -595	N-terminus outside 3 strong transmembrane helices	2 (35 Q-48 K) (713 L-726 N)	Non-secretory protein
Hypothetical protein (Pp1s31_189V6)	*P. patens*	489	348 -483	N-terminus outside 2 strong transmembrane helices	0	Non-secretory protein
Hypothetical protein (gi|115435856)	*O. sativa*	455	306 -443	N-terminus outside 3 strong transmembrane helices	1 (182 L-206 D)	Non-secretory protein
Mmembrane protein CH1-like (gi20804770)	*O. sativa*	624	245 -367	N-terminus inside 3 strong transmembrane helices	2 (501 A-516 S) (550 S-565 R)	Non-secretory protein
gi 226509595	*Z. mays*	462	315 -453	N-terminus inside 1 strong transmembrane helices	2 (172 L-196 K) (206 E-219 L)	Non-secretory protein

gi226504550	*Z. mays*	589	197 -320	N-terminus outside 4 strong transmembrane helices	1 (511 E-524 E)	Non-secretory protein
Glyma15g35240	*G. max*	446	301 -434	N-terminus outside 1 strong transmembrane helices	2 (161 K-177 K) (185 L-209 E)	Non-secretory protein
Gm09g00440	*G. max*	541	155 -277	N-terminus outside 4 strong transmembrane helices	3 (413 I-426 Q) (461 E-474 N)	38 - 39
UNC-84	*C. elegans*	1111	973-1107	N-terminus inside 9 strong transmembrane helices	0	Non-secretory protein
gi:17508615	*C. elegans*	802	147-271	N-terminus inside 2 strong transmembrane helices	1 (546 K-559 Q)	20 - 21
gi221510664 |	*D. melanogaster*	1252	244 -367	N-terminus outside 4 strong transmembrane helices	3 (189 E-207 K) (755 I-770 L) (775 L-797 T)	38 - 39
DrossoFBpp0292403	*D. melanogaster*	563	426 -559	N-terminus outside 1 strong transmembrane helices	3 (183 S-200 I) (246 L-260 S) (310 L-323 N)	Non-secretory protein
gi29337242	*H. sapiens*	717	582 -714	N-terminus inside 3 strong transmembrane helices	2 (279 R-293 E) (349 R-368 Q)	Non-secretory protein
gi170784831	*H. sapiens*	1210	286 -408	N-terminus inside 4 strong transmembrane helices	3 (235 D-248 K) (872 M-888 S) (892 L-910 F) (949 V-964 S)	29 - 30

Supplementary Table S7. Genomic organization of SUN protein gene family.

Gene ID/Accession number	**Organism**	**No of introns**	**Size and position of introns**
CaSUN1	*C. arietinum*	4	1. 143 (81-222) 2. 1857(424-2279) 3. 107(3602-3707) 4. 3346(3794-7138)
SLP1	*S. cerevisae*	0	-
MPS3	*S. cerevisae*	0	-
SAD1	*S. pombe*	0	-
SUNLIKE	*S. pombe*	0	-
AT1G22882	*A. thaliana*	2	1. 181(170-349) 2. 89(536-627)
AtSUN1	*A. thaliana*	1	1. 658(1284-1940)
Pp1s191_3V6	*P. patens*	0	-
Pp1s31_189V6	*P. patens*	0	-
Selaginella_441228	*S. moellendorffii*	3	1. 70(314-382) 2. 70(1397-1465) 3. 68(1513-1579)
Selaginella_89851	*S. moellendorffii*	1	1. 124(598-720)
Osgi115435856	*O. sativa*	1	1. 1081(1167-2246)
Osgi20804770	*O. sativa*	3	1. 338(633-969) 2. 86(2316-2400) 3. 259(2487-2744)
Zmgi226509595	*Z. maize*	2	1. 537(285-820) 2. 3409(1953-5360)
Zmgi226504550	*Z. maize*	3	1. 101(230-329) 2. 76(1535-1609) 3. 95(1696-1789)
Glyma15g35240	*G. max*	2	1. 49(237-284) 2. 2641(1084-3723)
Gm09g00440	*G. max*	3	1. 87(256-341) 2. 111(1499-1608) 3. 1141(1695-2834)
DmFBpp0288499	*D. melanogaster*	4	1. 82(135-215) 2. 69(428-495) 3. 842(2436-3276) 4. 64(3977-4039)
DmFBpp0292403	*D. melanogaster*	2	1. 58(1367-1423) 64(1537-1599)
UNC-84	*C. elegans*	9	1. 495(178-691) 2. 53(973-1024) 3. 60(1854-1912) 4. 59(2356-2413) 5. 481(2678-3157) 6. 52(3314-3364) 7. 76(3823-3897)

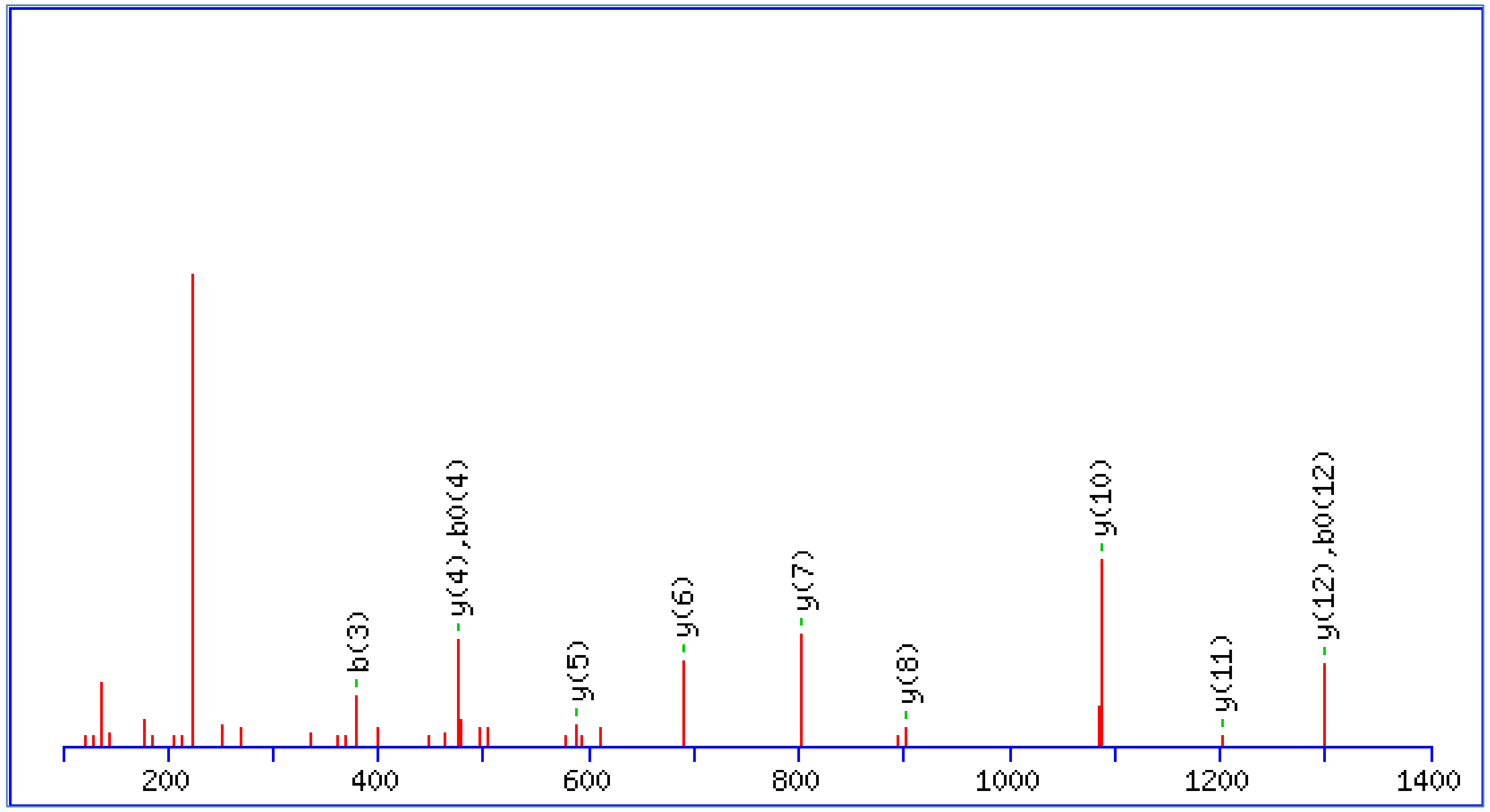
			8. 53(4219-4270) 9. 61(4544-4603)
CeR12E2	*C. elegans*	8	1. 114(30-142) 2. 53(236-287) 3. 46(368-412) 4. 53(499-550) 5. 53(1255-1306) 6. 58(1853-1909) 7. 47(2161-2206) 8. 53(2344-2395)
Hsgi29337242	*H. sapiens*	16	1. 1134(123-1255) 2. 175(1420-1593) 3. 578(1732-2308) 4. 366(2405-2769) 5. 983(2864-3845) 6. 2902(3917-6817) 7. 3129(6946-10073) 8. 730(10329-11057) 9. 444(11136-11578) 10. 575(11623-12196) 11. 324(12363-12685) 12. 296(12908-13202) 13. 354(13288-13640) 14. 119(13757-13874) 15. 322(14043-14363) 16. 1793(14457-16248)
Hsgi224514980	*H. sapiens*	21	1. 18015(63-18076) 2. 4243(18192-22433) 3. 1257(22589-23844) 4. 227(23983-24208) 5. 11225(24360-35583) 6. 905(35708-36611) 7. 492(36737-37227) 8. 3161(37296-40455) 9. 1520(40564-

			42082) 10. 2141(42189-44328) 11. 479(44386-44863) 12. 813(44955-45766) 13. 5751(45833-51582) 14. 772(51652-52422) 15. 2812(52514-55324) 16. 1058(56492-57548) 17. 8993(57637-66628) 18. 1896(66734-68628) 19. 478(68784-69260) 20. 596(69353-75311) 21. 1014(75368-76380)

Supplementary Table S8. Detail of the mass spectra of membrane proteins identified with single peptide.

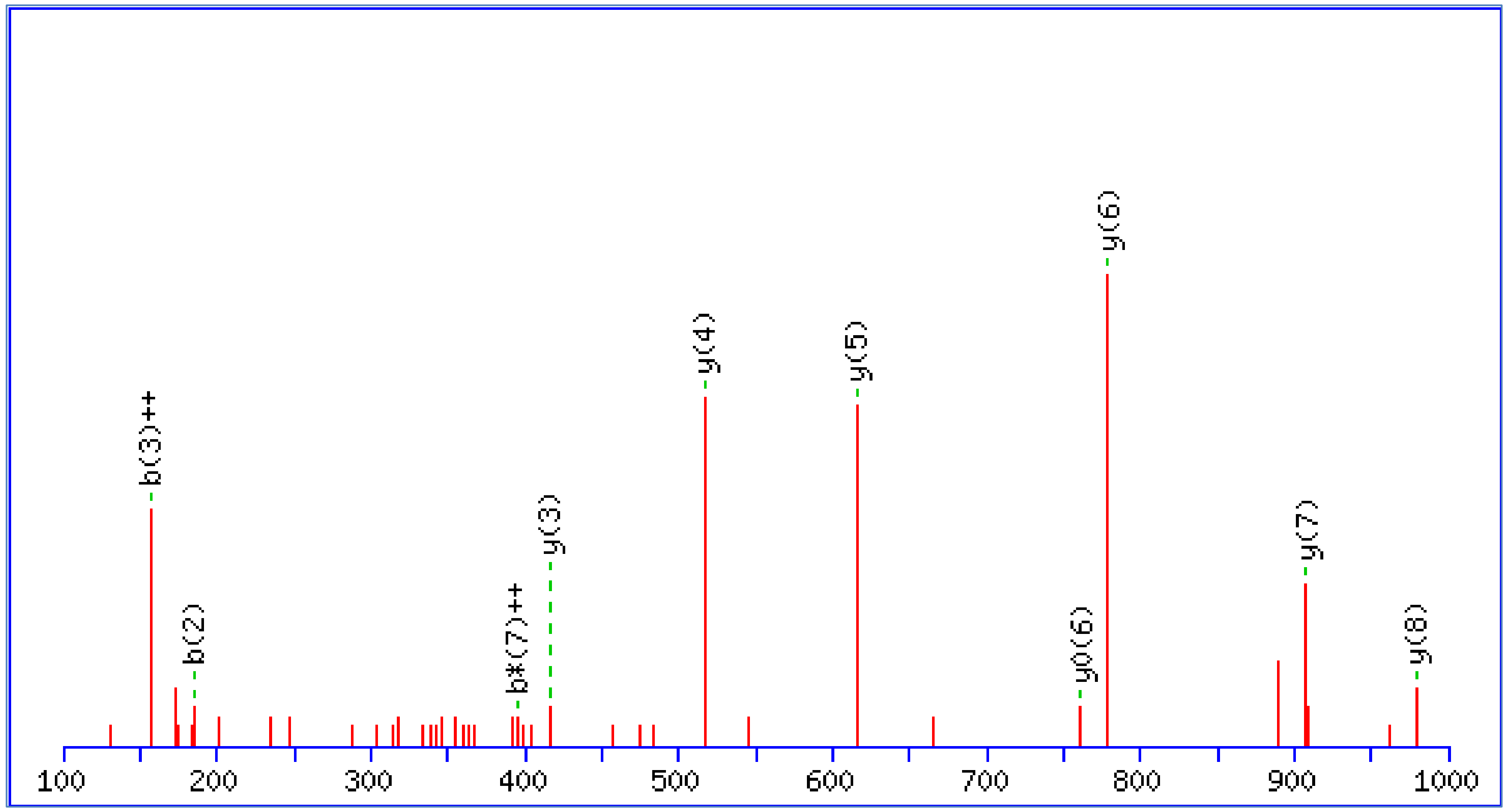
Spot No.	Identification	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide	Instrument	Taxonomy	Database	Peptide mass tolerance	Fragment mass tolerance
CaM-73	Actin (Fragment)	895.983	1789.95	1789.88	0.0666	0	63	0.0017	1	K.SYELPDGQVITIGNER.F	iTRAP	Viridiplantae	Ludwig NR	1.2 Da	0.6 Da
CaM-182	Ferritin	546.5969	1091.1792	1091.5975	-0.4183	0	50	0.027	1	K.IAEYVTQLR.M	iTRAP	Viridiplantae	Ludwig NR	1.2 Da	0.6 Da
CaM-214	Glutamate-ammonia ligase (EC 6.3.1.2) delta precursor	488.75	975.49	975.50	-0.01	0	68	7.4E-05	1	R.AAEIFSNPK.V	Qstar	Viridiplantae	MSDB	100 ppm	0.4 Da
CaM-216	Glutamate-ammonia ligase (EC 6.3.1.2) delta precursor	488.76	975.50	975.50	-0.00	0	39	0.05	1	R.AAEIFSNPK.V	Qstar	Viridiplantae	MSDB	100 ppm	0.4 Da
CaM-218	Glutamine synthetase	488.5679	975.1212	975.5025	975.5025	0	50	0.026	1	K.AAEIFSNPK.V	iTRAP	Viridiplantae	Ludwig NR	1.2 Da	0.6 Da
CaM-263	OSJNBb0085H11.1 protein	421.76	841.5	841.43	0.07	0	50	0.0076	1	K.GATVEAPR.E	Qstar	Viridiplantae	MSDB	100 ppm	0.4 Da
CaM-428	Beta-1,3-glucanase	684.39	1366.77	1366.76	0.0086	0	80	3.40E-05	1	R.NSNIQVLLDVPR.S	iTRAP	Viridiplantae	Ludwig NR	1.2 Da	0.6 Da
CaM-443	Predicted protein	522.112	1042.21	1042.6	-0.3938	0	53	0.012	1	K.LAVAINDLSK.T	iTRAP	Viridiplantae	Ludwig NR	1.2 Da	0.6 Da

CaM-73



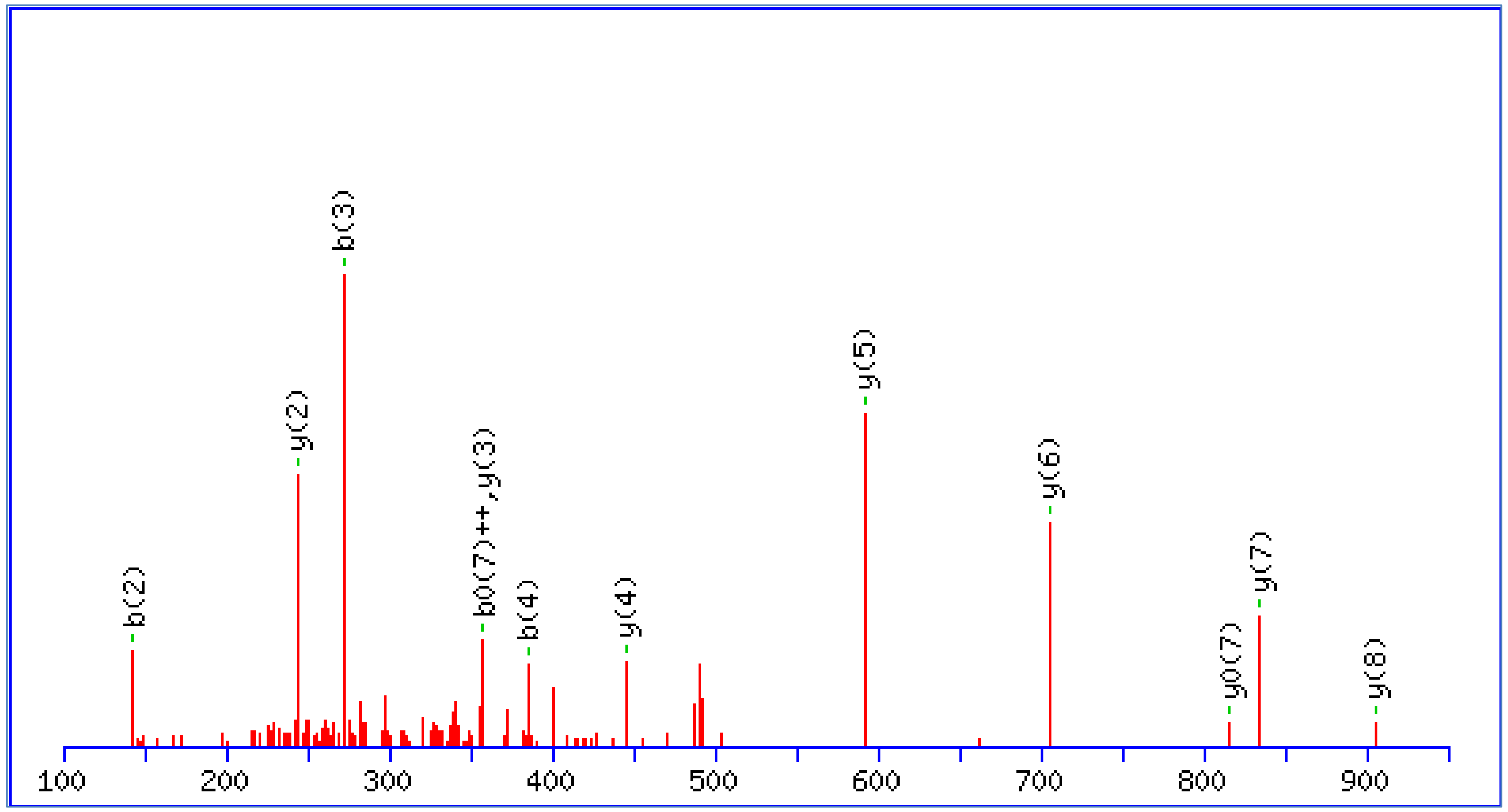
#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	88.0393	44.5233			70.0287	35.518	S							16
2	251.1026	126.055			233.0921	117.0497	Y	1703.8599	852.4336	1686.8333	843.9203	1685.849	843.4283	15
3	380.1452	190.5763			362.1347	181.571	E	1540.7966	770.9019	1523.77	762.3886	1522.786	761.8966	14
4	493.2293	247.1183			475.2187	238.113	L	1411.754	706.3806	1394.7274	697.8673	1393.743	697.3753	13
5	590.2821	295.6447			572.2715	286.6394	P	1298.6699	649.8386	1281.6434	641.3253	1280.659	640.8333	12
6	705.309	353.1581			687.2984	344.1529	D	1201.6171	601.3122	1184.5906	592.7989	1183.607	592.3069	11
7	762.3305	381.6689			744.3199	372.6636	G	1086.5902	543.7987	1069.5636	535.2855	1068.58	534.7935	10
8	890.389	445.6982	873.3625	437.1849	872.3785	436.6929	Q	1029.5687	515.288	1012.5422	506.7747	1011.558	506.2827	9
9	989.4575	495.2324	972.4309	486.7191	971.4469	486.2271	V	901.5102	451.2587	884.4836	442.7454	883.4996	442.2534	8
10	1102.542	551.7744	1085.515	543.2611	1084.531	542.7691	I	802.4417	401.7245	785.4152	393.2112	784.4312	392.7192	7
11	1203.589	602.2982	1186.563	593.785	1185.5786	593.293	T	689.3577	345.1825	672.3311	336.6692	671.3471	336.1772	6
12	1316.673	658.8403	1299.647	650.327	1298.6627	649.835	I	588.31	294.6586	571.2835	286.1454	570.2994	285.6534	5
13	1373.695	687.351	1356.668	678.8377	1355.6842	678.3457	G	475.2259	238.1166	458.1994	229.6033	457.2154	229.1113	4
14	1487.738	744.3725	1470.711	735.8592	1469.7271	735.3672	N	418.2045	209.6059	401.1779	201.0926	400.1939	200.6006	3
15	1616.78	808.8938	1599.754	800.3805	1598.7697	799.8885	E	304.1615	152.5844	287.135	144.0711	286.151	143.5791	2
16							R	175.119	88.0631	158.0924	79.5498			1

CaM-182



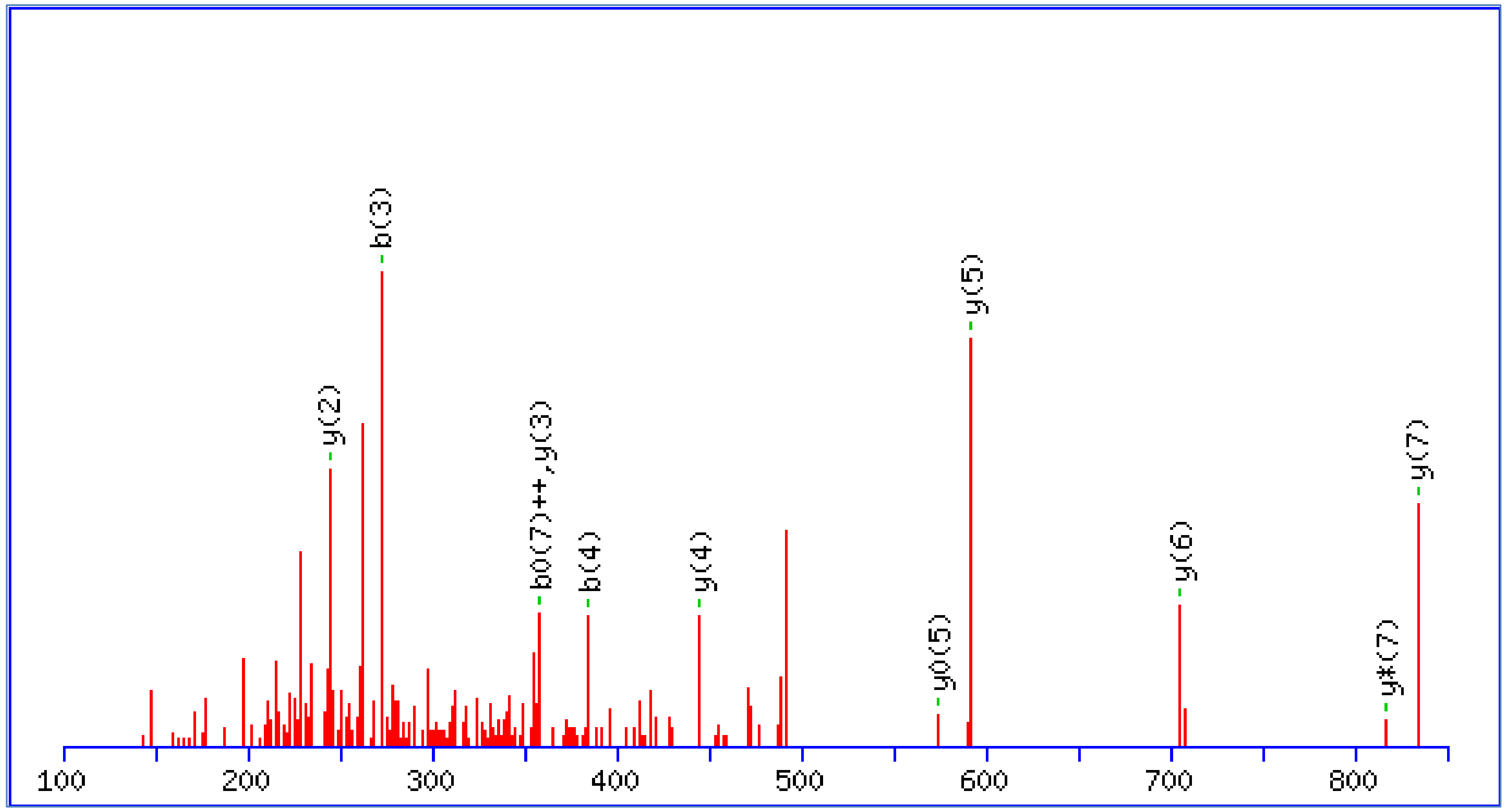
#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					I							9
2	**185.1285**	93.0679					A	**979.5207**	490.264	962.4942	481.7507	961.5102	481.2587	8
3	314.171	**157.5892**			296.1605	148.5839	E	**908.4836**	454.7454	891.4571	446.2322	890.473	445.7402	7
4	477.2344	239.1208			459.2238	230.1155	Y	**779.441**	390.2241	762.4145	381.7109	**761.4305**	381.2189	6
5	576.3028	288.655			558.2922	279.6498	V	**616.3777**	308.6925	599.3511	300.1792	598.3671	299.6872	5
6	677.3505	339.1789			659.3399	330.1736	T	**517.3093**	259.1583	500.2827	250.645	499.2987	250.153	4
7	805.409	403.2082	788.3825	**394.6949**	787.3985	394.2029	Q	**416.2616**	208.6344	399.235	200.1212			3
8	918.4931	459.7502	901.4666	451.2369	900.4825	450.7449	L	288.203	144.6051	271.1765	136.0919			2
9							R	175.119	88.0631	158.0924	79.5498			1

CaM-214



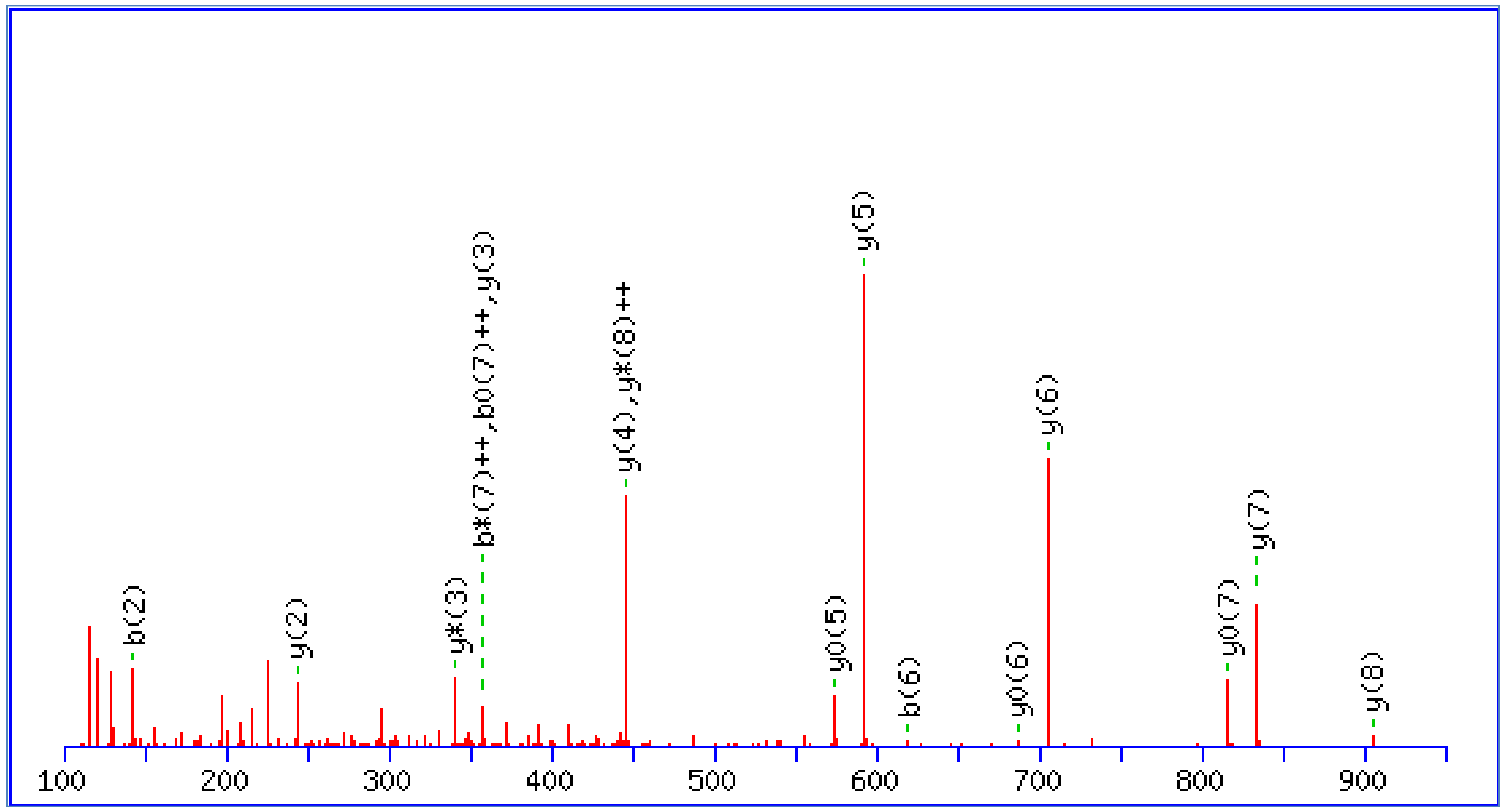
#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.04	36.53					A							9
2	**143.08**	72.04					A	**905.47**	453.24	888.45	444.73	887.46	444.23	8
3	**272.12**	136.57			254.11	127.56	E	**834.44**	417.72	817.41	409.21	**816.43**	408.72	7
4	**385.21**	193.11			367.2	184.1	I	**705.39**	353.2	688.37	344.69	687.38	344.19	6
5	532.28	266.64			514.27	257.64	F	**592.31**	296.66	575.28	288.14	574.3	287.65	5
6	619.31	310.16			601.3	301.15	S	**445.24**	223.12	428.21	214.61	427.23	214.12	4
7	733.35	367.18	716.32	358.67	715.34	**358.17**	N	**358.21**	179.61	341.18	171.09			3
8	830.4	415.71	813.38	407.19	812.39	406.7	P	**244.17**	122.59	227.14	114.07			2
9							K	147.11	74.06	130.09	65.55			1

CaM-216



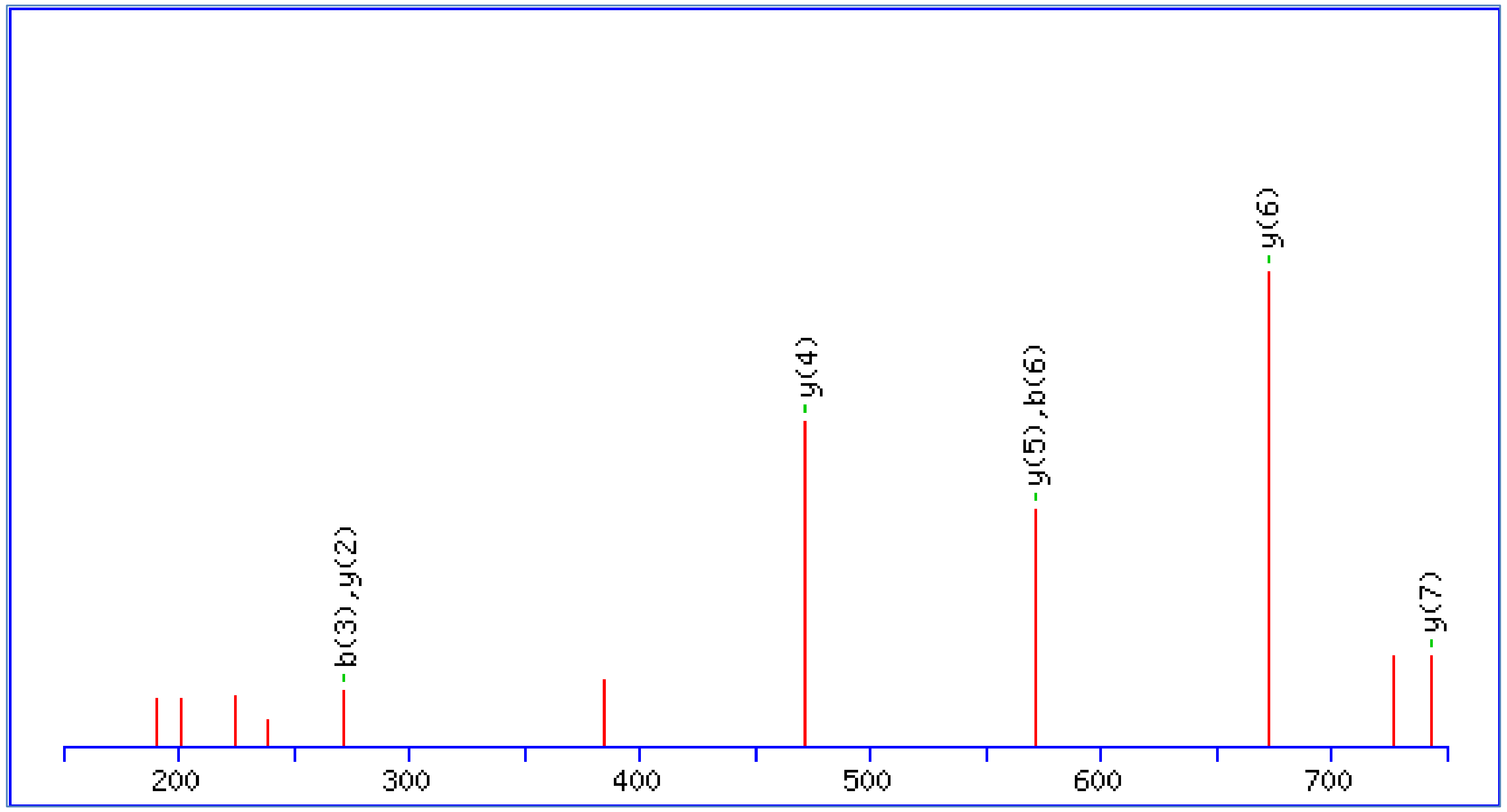
#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	72.04	36.53					A							9
2	143.08	72.04					A	905.47	453.24	888.45	444.73	887.46	444.23	8
3	272.12	136.57			254.11	127.56	E	834.44	417.72	817.41	409.21	816.43	408.72	7
4	385.21	193.11			367.2	184.1	I	705.39	353.2	688.37	344.69	687.38	344.19	6
5	532.28	266.64			514.27	257.64	F	592.31	296.66	575.28	288.14	574.3	287.65	5
6	619.31	310.16			601.3	301.15	S	445.24	223.12	428.21	214.61	427.23	214.12	4
7	733.35	367.18	716.32	358.67	715.34	358.17	N	358.21	179.61	341.18	171.09			3
8	830.4	415.71	813.38	407.19	812.39	406.7	P	244.17	122.59	227.14	114.07			2
9							K	147.11	74.06	130.09	65.55			1

CaM-218



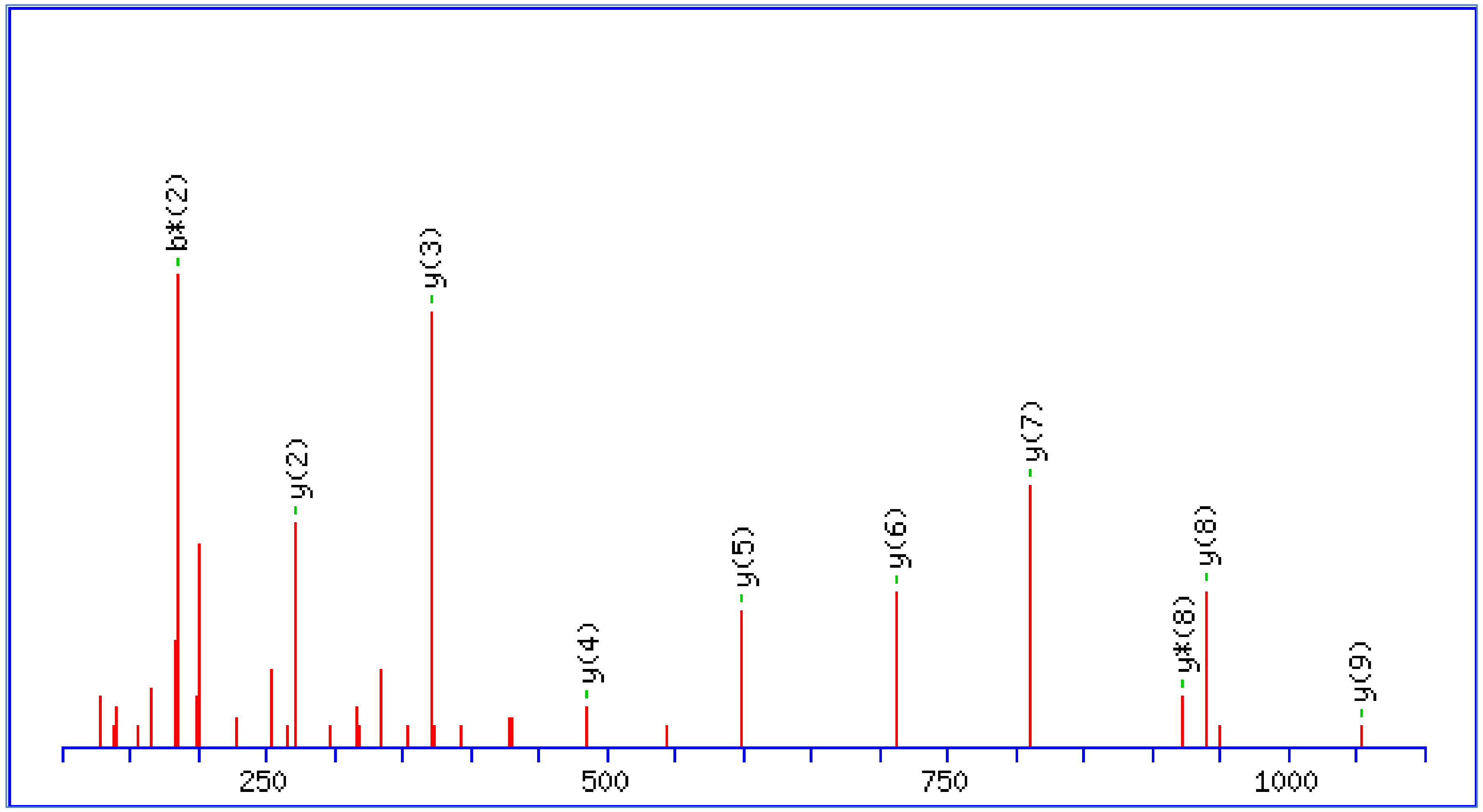
#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.0444	36.5258					A							9
2	**143.0815**	72.0444					A	**905.4727**	453.24	888.4462	**444.7267**	887.4621	444.2347	8
3	272.1241	136.5657			254.1135	127.5604	E	**834.4356**	417.7214	817.409	409.2082	**816.425**	408.7162	7
4	385.2082	193.1077			367.1976	184.1024	I	**705.393**	353.2001	688.3665	344.6869	**687.3824**	344.1949	6
5	532.2766	266.6419			514.266	257.6366	F	**592.3089**	296.6581	575.2824	288.1448	**574.2984**	287.6528	5
6	**619.3086**	310.1579			601.298	301.1527	S	**445.2405**	223.1239	428.214	214.6106	427.23	214.1186	4
7	733.3515	367.1794	716.325	**358.6661**	715.341	**358.1741**	N	**358.2085**	179.6079	**341.1819**	171.0946			3
8	830.4043	415.7058	813.3777	407.1925	812.3937	406.7005	P	**244.1656**	122.5864	227.139	114.0731			2
9							K	147.1128	74.06	130.0863	65.5468			1

CaM-263



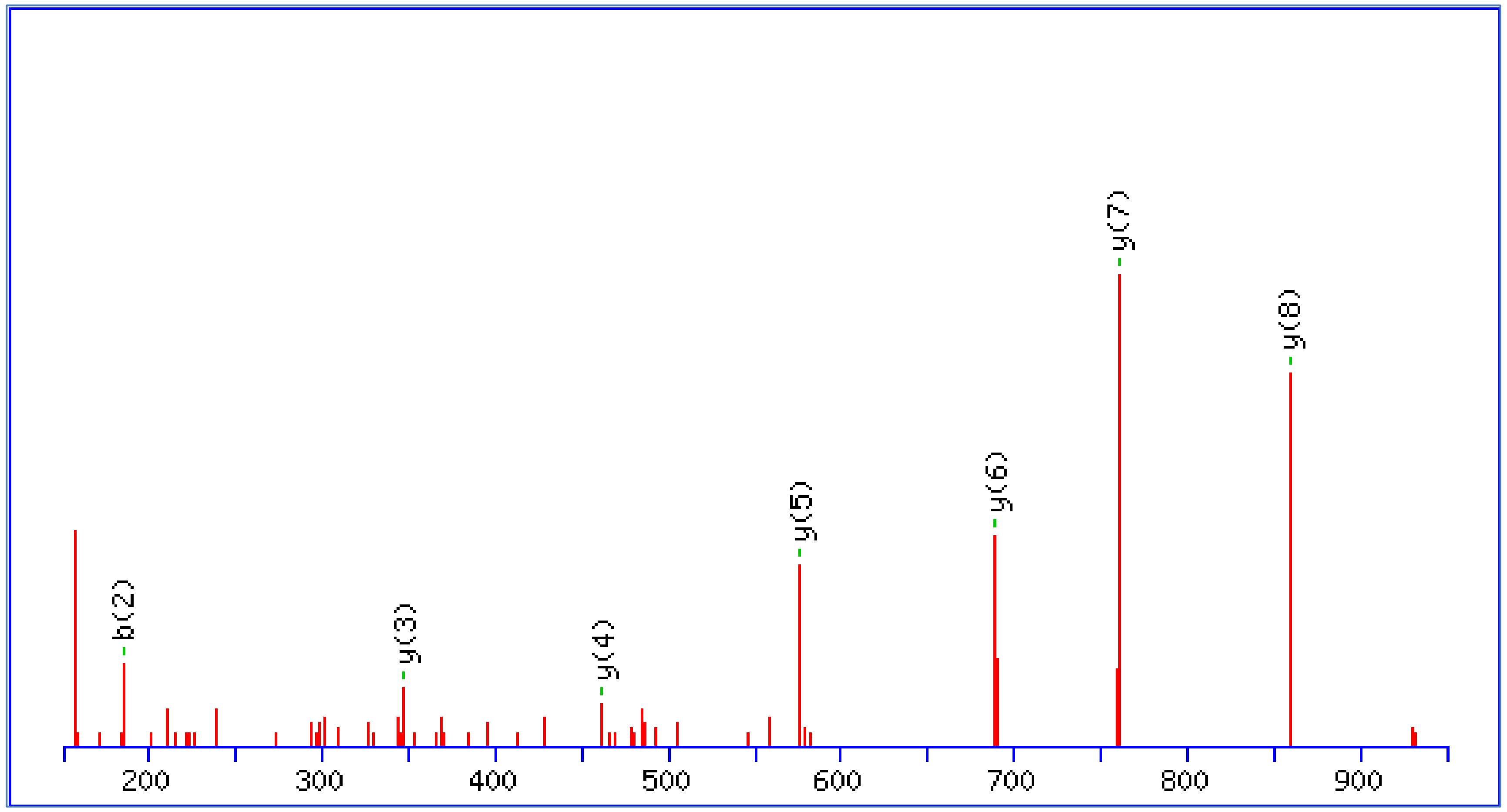
#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.04	50.52			G							8
2	171.08	86.04			A	743.4	372.21	726.38	363.69	725.39	363.2	7
3	272.12	136.57	254.11	127.56	T	672.37	336.69	655.34	328.17	654.36	327.68	6
4	371.19	186.1	353.18	177.09	V	571.32	286.16	554.29	277.65	553.31	277.16	5
5	500.24	250.62	482.22	241.62	E	472.25	236.63	455.22	228.12	454.24	227.62	4
6	571.27	286.14	553.26	277.13	A	343.21	172.11	326.18	163.59			3
7	668.32	334.67	650.31	325.66	P	272.17	136.59	255.15	128.08			2
8					R	175.12	88.06	158.09	79.55			1

CaM-428



#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	115.0502	58.0287	98.0237	49.5155			N							12
2	202.0822	101.5448	**185.0557**	93.0315	184.0717	92.5395	S	1253.7212	627.3642	1236.6947	618.851	1235.711	618.359	11
3	316.1252	158.5662	299.0986	150.0529	298.1146	149.5609	N	1166.6892	583.8482	1149.6626	575.335	1148.679	574.8429	10
4	429.2092	215.1082	412.1827	206.595	411.1987	206.103	I	**1052.6463**	526.8268	1035.6197	518.3135	1034.636	517.8215	9
5	557.2678	279.1375	540.2413	270.6243	539.2572	270.1323	Q	**939.5622**	470.2847	**922.5356**	461.7715	921.5516	461.2795	8
6	656.3362	328.6717	639.3097	320.1585	638.3256	319.6665	V	**811.5036**	406.2554	794.4771	397.7422	793.4931	397.2502	7
7	769.4203	385.2138	752.3937	376.7005	751.4097	376.2085	L	**712.4352**	356.7212	695.4087	348.208	694.4246	347.716	6
8	882.5043	441.7558	865.4778	433.2425	864.4938	432.7505	L	**599.3511**	300.1792	582.3246	291.6659	581.3406	291.1739	5
9	997.5313	499.2693	980.5047	490.756	979.5207	490.264	D	**486.2671**	243.6372	469.2405	235.1239	468.2565	234.6319	4
10	1096.6	548.8035	1079.573	540.2902	1078.5891	539.7982	V	**371.2401**	186.1237	354.2136	177.6104			3
11	1193.653	597.3299	1176.626	588.8166	1175.6419	588.3246	P	**272.1717**	136.5895	255.1452	128.0762			2
12							R	175.119	88.0631	158.0924	79.5498			1

CaM-443



#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					L							10
2	185.1285	93.0679					A	930.5255	465.7664	913.4989	457.2531	912.5149	456.7611	9
3	284.1969	142.6021					V	859.4884	430.2478	842.4618	421.7345	841.4778	421.2425	8
4	355.234	178.1206					A	760.4199	380.7136	743.3934	372.2003	742.4094	371.7083	7
5	468.318	234.6627					I	689.3828	345.1951	672.3563	336.6818	671.3723	336.1898	6
6	582.361	291.6841	565.3344	283.1709			N	576.2988	288.653	559.2722	280.1397	558.2882	279.6477	5
7	697.3879	349.1976	680.3614	340.6843	679.3774	340.1923	D	462.2558	231.6316	445.2293	223.1183	444.2453	222.6263	4
8	810.472	405.7396	793.4454	397.2264	792.4614	396.7343	L	347.2289	174.1181	330.2023	165.6048	329.2183	165.1128	3
9	897.504	449.2556	880.4775	440.7424	879.4934	440.2504	S	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	2
10							K	147.1128	74.06	130.0863	65.5468			1

Supplementary Table S9. List of oligonucleotides primers used in this study.

Primer Name	**Primer Sequences (5’- 3’)**	**Purpose**
CaMCh1-like1	GAGCCTGGTGGTGCAGAATACAATTATGCTTC	Cloning
CaMCh1-like2	GTGGATGCTGTTGAGAGAATGCTGGAGG	Cloning
CaSUN1UTRFP	ACATGGGATTCTGAACTTGCATTCCTTC	Cloning
CaSUN1IPF1	CTTGGTCTTGATGAATTCAAG	Sequencing
CaSUN1IPF2	GAGAGAATGCTGGAGGATTTG	Sequencing
CaSUN1IPF3	ATTTTCAAAGAGTACAGCAAAG	Sequencing
CaSUN1YESFP	GGATCCAAAAAAATGCAGAGATCAC	pYES2 cloning
CaSUN1YESRP	CTCGAGTAAACTTAATATGAAAATAATAATG	pYES2 cloning
CaSUN1QRTUTRFP	TTCCAGGCAGGGTAATTAATGG	qPCR
CaSUN1QRTUTRRP	ACGTGATCTCTGCATTGCACATA	qPCR
CaQRTEF1LFP	TCCACCACTTGGTCGTTTTG	qPCR
CaQRTEF1LRP	CTTAATGACACCGACAGCAACAG	qPCR
CaSUN1QRTFP	TCCCGTCCGAGGCTTTATT	qPCR
CaSUN1QRTRP	TGACTCACCAACAAAACCATTAGC	qPCR
CaSUN1GATEWFP	CACCATGCAGAGATCACGTAAAGCTC	pENTR cloning
CaSUN1GATEWRP1	CTATCATAAACTTAATATGAAAATAATAATGATA	pENTR cloning
CaSUN1GATEWRP2	TAAACTTAATATGAAAATAATAATGATACAAC	pENTR cloning
AtSUN3TDNALP	AATCACAACTGCAATAACCGC	T-DNA mutant genotyping
AtSUN3TDNARP	TCCAATTCTCGAAACAAATCG	T-DNA mutant genotyping
LBb1.3	ATTTTGCCGATTTCGGAAC	T-DNA mutant genotyping
AtSUN3FP	CACCATGCAAAGGTCGTGTAGAACTAG	PCR
AtSUN3RP	TCAAAGAGACAAAACGAACATAATGAATG	PCR
AtACT1RTFP	AGTATTGTGGGTCGTCCTCG	RT-PCR
AtACT1RTRP	GAGCTGGTTTTGGCTGTCTC	RT-PCR
ScQRTACT1FP	GAGGTTGCTGCTTTGGTTATTGA	qPCR
ScQRTACT1RP	CGTCGTCACCGGCAAAAC	qPCR
ScQRTSLP1FP	GCACGAAGCAAAGTTCAGTCAT	qPCR
ScQRTSLP1RP	TGGCAAAGTTATTCAGCAGATCTAGA	qPCR
ScQRTKAR2FP	TCCAAGGTCGCTTATCCAATTAC	qPCR
ScQRTKAR2RP	CAGCGGCACCAGAACCA	qPCR