

Supplementary data

Supplementary Table 1. List of proteins identified from leaf and stem of 7-day-old sprouts in common buckwheat under light or dark

Spot #	Accession #	Protein Identity	Protein Source	Sample Source	Molecular function	Subcellular localization	Matched peptides	pI ¹	Mr (Da) ²	Seq. cov. (%) ³
A1	Q0D831	Os07g0187900 protein	<i>Oryza sativa</i>	Leaf, Light	Unknown	Unknown	7	12.37	25,931	28
A2	A2Z0C0	Probable protein arginine N-methyltransferase 1	<i>Oryza sativa</i>	Leaf, Light	Metabolism	Nucleus	8	5.26	42,986	20
A3	Q39199	DNA repair protein recA homolog 1, chloroplastic	<i>Arabidopsis thaliana</i>	Leaf, Light	Recombination	Plastid	8	6.00	47,703	23
A4	B9SIU1	Alpha-1,4-glucan-protein synthase [UDP-forming]	<i>Ricinus communis</i>	Leaf, Light	Metabolism	Cell Wall	4	5.83	29,440	22
A5	Q19HM0	Disease resistance protein	<i>Arabidopsis thaliana</i>	Leaf, Light	Defense	Cytoplasm	3	9.85	23,743	18
A6	Q9XIX4	Putative uncharacterized protein P0681F10.28	<i>Oryza sativa</i>	Leaf, Light	Unknown	Unknown	3	11.57	7,805	32
A7	Q9LRS0	Probable peroxisomal (S)-2-hydroxy-acid oxidase 1	<i>Arabidopsis thaliana</i>	Leaf, Light	Metabolism	Plastid	8	8.99	40,281	26
A8	Q942D6	Heat stress transcription factor C-1b	<i>Oryza sativa</i>	Leaf, Light	Stress Response, Transcription	Nucleus	7	8.93	27,202	21
A9	NP_973524*	nucleic acid binding / zinc ion binding	<i>Arabidopsis thaliana</i>	Leaf, Light	Transcription	Nucleus	10	9.07	41,569	38
A10	Q9LPC4	Pentatricopeptide repeat-containing protein At1g01970	<i>Arabidopsis thaliana</i>	Leaf, Light	Unknown	Unknown	11	6.58	46,048	40
A11	Q9C7Z8	En/Spm-like transposon protein, 5' partial; 97242-96760	<i>Arabidopsis thaliana</i>	Leaf, Light	Recombination	Nucleus	5	8.87	12,330	40
A12	Q39845	small GTP-binding protein	<i>Glycine max</i>	Leaf, Light	Signal Transduction	Cytoplasm	3	5.12	22,410	16
A13	Q9XIR8	Probable 26S proteasome complex subunit sem1-1	<i>Arabidopsis thaliana</i>	Leaf, Light	Cellular Process	Cytoplasm	6	3.91	8,854	24
A14	Q9M9L6	Transcription factor bHLH150	<i>Arabidopsis thaliana</i>	Leaf, Light	Transcription	Nucleus	7	11.82	23,171	19
A15	P43401	EC protein homolog	<i>Zea mays</i>	Leaf, Light	Defense	Cytoplasm	8	7.37	7,700	55
A16	B2XWR0	50S ribosomal protein L14, chloroplastic	<i>Fagopyrum esculentum</i>	Leaf, Light	Translation	Plastid	4	9.91	13,702	23
A18	Q9T098	forever young gene (FEY)	<i>Arabidopsis thaliana</i>	Leaf, Light	Metabolism	Cytoplasm	3	6.07	25,315	24
A19	P42791	60S ribosomal protein L18-2	<i>Arabidopsis thaliana</i>	Leaf, Light	Translation	Cytoplasm	3	10.97	20,913	15
A20	Q0DHD4	Os05g0474500 protein	<i>Oryza sativa</i>	Leaf, Light	Unknown	Unknown	3	10.04	10,013	46
A21	P12811	Heat shock 22 kDa protein, chloroplastic	<i>Chlamydomonas reinhardtii</i>	Leaf, Light	Stress Response	Plastid	4	6.08	16,693	21

A22	O04132	Cold stress protein SRC1	<i>Glycine max</i>	Leaf, Light	Stress Response	Cytoplasm	5	7.10	11,549	21
A23 B23	O82204	60S ribosomal protein L28	<i>Arabidopsis thaliana</i>	Leaf, Light/Dark	Translation	Cytoplasm	9	10.58	15,886	22
A24	Q8H8D3	Putative ATP phosphoribosyl transferase	<i>Oryza sativa</i>	Leaf, Light	Transport	Cytoplasm	6	6.32	18,676	23
A25	Q6XW87	Resistance candidate RPP8-like protein	<i>Arabidopsis thaliana</i>	Leaf, Light	Defense	Cytoplasm	4	9.10	56,744	15
B1	Q8L NK6	Monothiol glutaredoxin-S15	<i>Arabidopsis thaliana</i>	Leaf, Dark	Transport	Cytoplasm	5	5.92	18,722	48
B2	Q9M1R6	Putative uncharacterized protein T17J13.40	<i>Arabidopsis thaliana</i>	Leaf, Dark	Transport	Unknown	4	5.02	47,464	16
B3	Q8LJU4	F1 beta subunit of ATP synthase	<i>Glycine max</i>	Leaf, Dark	Energy	Plasma Membrane	8	8.42	9,553	17
B4	B2XWL4	Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta	<i>Fagopyrum esculentum</i>	Leaf, Dark	Metabolism	Plastid	4	4.92	52,827	9
B5 B6	B2XWJ7	NAD(P)H-quinone oxidoreductase subunit H, chloroplastic	<i>Fagopyrum esculentum</i>	Leaf, Dark	Transport	Plasma Membrane	3	5.30	45,447	11
B7	Q9LDH3	Putative F-box protein At3g28330	<i>Arabidopsis thaliana</i>	Leaf, Dark	Transcription	Unknown	3	6.50	48,686	11
B8	P54233	Inducible nitrate reductase [NADH] 1	<i>Glycine max</i>	Leaf, Dark	Metabolism	Cytoplasm	4	6.33	99,735	9
B9	A6N046	Chloroplast ATP synthase delta chain precursor	<i>Oryza sativa</i>	Leaf, Dark	Transport	Plasma Membrane	6	4.01	4,899	59
B10	Q2L394	Cyclin dependent protein kinase	<i>Triticum aestivum</i>	Leaf, Dark	Signal Transduction	Cytoplasm	4	8.84	25,363	28
B11	P92918	Major allergen Api g 2	<i>Apium graveolens</i>	Leaf, Dark	Defense	Cytoplasm	5	4.62	17,079	19
B12	Q8L7G7	Defensin-like protein 96	<i>Arabidopsis thaliana</i>	Leaf, Dark	Defense	Extracellular	4	5.30	9,817	39
B13	O22487	Ribulose-bisphosphate carboxylase, small chain	<i>Oryza sativa</i>	Leaf, Dark	Photosynthesis	Plastid	4	9.40	19,562	45
B14	Q9AXJ5	Phytochrome B	<i>Pisum sativum</i>	Leaf, Dark	Signal Transduction	Cytoplasm	3	11.53	4,511	42
B15	P51431	40S ribosomal protein S27a	<i>Oryza sativa</i>	Leaf, Dark	Translation	Cytoplasm	3	10.06	9,170	31
B16	Q9AVF3	NADPH-protochlorophyllide oxidoreductase 1	<i>Amaranthus tricolor</i>	Leaf, Dark	Transport	Cytoplasm	13	8.86	24,882	49
B17	Q5Q114	Mucin-like protein	<i>Oryza sativa</i>	Leaf, Dark	Cellular Process	Cytoplasm	7	5.33	22,794	49
B18	P46251	Actin-depolymerizing factor 1	<i>Zea mays</i>	Leaf, Dark	Cytoskeleton	Cytoplasm	6	5.58	16,158	42
B19	P82722	Putative defensin-like protein 139	<i>Arabidopsis thaliana</i>	Leaf, Dark	Defense	Extracellular	8	8.56	8,519	51
B20	Q9FK25	Quercetin 3-O-methyltransferase	<i>Arabidopsis thaliana</i>	Leaf, Dark	Metabolism	Cytoplasm	7	5.62	39,592	28
B21	Q0E0Y3	RNA pseudourine synthase 7	<i>Oryza sativa</i>	Leaf, Dark	Metabolism	Cytoplasm	3	9.35	19,505	24
B22 D18	A2Y1D7	Metallothionein-like protein 3B	<i>Oryza sativa</i>	Leaf, Dark	Cellular Process	Cytoplasm	3	5.19	6,875	44
B23 A23	O82204	60S ribosomal protein L28	<i>Arabidopsis thaliana</i>	Leaf, Light/Dark	Translation	Cytoplasm	9	10.58	15,886	22
B24	O64960	Heat shock 22 kDa protein	<i>Zea mays</i>	Leaf, Dark	Stress Response	Cytoplasm	5	6.47	23,801	11
B25	Q9XFM4	13S globulin seed storage protein 3	<i>Fagopyrum</i>	Leaf/Stem,	Seed Storage	Cytoplasm	3	6.00	61,127	12

B26
B27
D27
D28
F10

esculentum

Dark

E1	P31093	Photosystem I reaction center subunit N, chloroplastic	<i>Hordeum vulgare</i>	Stem, Light	Photosynthesis	Plastid	5	9.54	15,490	25
E2 E3	Q40459	Oxygen-evolving enhancer protein 1, chloroplastic	<i>Nicotiana tabacum</i>	Stem, Light	Photosynthesis	Plastid	6	5.89	35,206	33
E4	Q42450	Ribulose biphosphate carboxylase/oxygenase activase B, chloroplastic	<i>Hordeum vulgare</i>	Stem, Light	Energy	Plastid	9	7.59	47,198	24
E5	Q8L844	Pentatricopeptide repeat-containing protein At5g42310, mitochondrial	<i>Arabidopsis thaliana</i>	Stem, Light	Unknown	Mitochondria	9	6.68	79,951	26
E6	P0C8Q3	Pentatricopeptide repeat-containing protein At4g19895	<i>Arabidopsis thaliana</i>	Stem, Light	Unknown	Unknown	12	8.47	78,932	27
E7	O49139	Putative DNA (cytosine-5)-methyltransferase CMT1	<i>Arabidopsis thaliana</i>	Stem, Light	Transcription	Nucleus	6	5.99	89,162	18
E8	Q84NP7	Probable AMP deaminase	<i>Oryza sativa</i>	Stem, Light	Energy	Mitochondria	11	6.25	93,796	15
E9	Q8GUH8	Putative uncharacterized protein At5g54130	<i>Arabidopsis thaliana</i>	Stem, Light	Signal Transduction	Cytoplasm	10	7.64	50,503	29
E10	Q56Y85	Methionine aminopeptidase 2B	<i>Arabidopsis thaliana</i>	Stem, Light	Cellular Process	Cytoplasm	8	5.51	49,029	24
E11 C8	P19124	NAD(P)H-quinone oxidoreductase subunit J, chloroplastic	<i>Zea mays</i>	Stem, Light	Transport	Plasma Membrane	5	6.04	18,657	42
E12	Q08480	Adenylate kinase B	<i>Oryza sativa</i>	Stem, Light	Signal Transduction	Cytoplasm	6	7.64	26,658	35
E13 D14	P56805	30S ribosomal protein S15, chloroplastic	<i>Arabidopsis thaliana</i>	Stem, Light	Translation	Plastid	4	10.81	10,712	46
E14	B6TRD1	retrotransposon protein	<i>Zea mays</i>	Stem, Light	Cellular Process	Cytoplasm	8	6.84	22,241	36
E15	O22212	U4/U6 small nuclear ribonucleoprotein PRP4-like protein	<i>Arabidopsis thaliana</i>	Stem, Light	Cellular Process	Nucleus	7	5.45	61,803	14
E16	Q5FR44	Phosphoethanolamine N-methyltransferase 1	<i>Arabidopsis thaliana</i>	Stem, Light	Metabolism	Cytoplasm	9	5.39	56,067	16
E17	Q940A6	Pentatricopeptide repeat-containing protein At4g19440, chloroplastic	<i>Arabidopsis thaliana</i>	Stem, Light	Unknown	Plastid	11	8.58	94,555	20
E18	P22177	Proliferating cell nuclear antigen	<i>Glycine max</i>	Stem, Light	Replication	Nucleus	6	4.65	26,118	38
E19 G2	P12468	Ribulose biphosphate carboxylase small chain 4, chloroplastic	<i>Glycine max</i>	Stem, Light	Photosynthesis	Plastid	7	8.87	20,004	53
E20	Q6EU14	Protein argonaute 1A	<i>Oryza sativa</i>	Stem, Light	Transcription	Nucleus	9	9.46	120,373	11
E21 G6	O23373	Formin-like protein 3	<i>Arabidopsis thaliana</i>	Stem, Light	Cytoskeleton	Plasma Membrane	10	8.25	85,991	14
E22	Q08000	Em protein H2	<i>Triticum aestivum</i>	Stem, Light	Stress Response	Cytoplasm	4	5.50	9,981	55

E23	Q9SN90	Structural maintenance of chromosomes protein 2-2	<i>Arabidopsis thaliana</i>	Stem, Light	Cellular Process	Nucleus	10	6.59	132,233	9
E24	B4FAF3	UPF0737 protein 1	<i>Zea mays</i>	Stem, Light	Unknown	Nucleus	9	8.99	41,493	27
E25	Q9MUM9	Photosystem I iron-sulfur center	<i>Mesostigma viride</i>	Stem, Light	Photosynthesis	Plastid	10	6.51	8,778	91
E26	Q70XX1	50S ribosomal protein L22, chloroplastic	<i>Amborella trichopoda</i>	Stem, Light	Translation	Plastid	6	10.02	14,007	55
E27	Q10JI3	UPF0737 protein Os03g0419100	<i>Oryza sativa</i>	Stem, Light	Unknown	Nucleus	5	9.60	32,419	23
F1	P42777	G-box-binding factor 4	<i>Arabidopsis thaliana</i>	Stem, Dark	Transcription	Nucleus	7	5.68	30,567	19
F2	Q9SR43	Phytochromobilin:ferredoxin oxidoreductase, chloroplastic Bifunctional	<i>Arabidopsis thaliana</i>	Stem, Dark	Metabolism	Plastid	6	8.23	38,105	16
F3	P49080	aspartokinase/homoserine dehydrogenase 2, chloroplast	<i>Zea mays</i>	Stem, Dark	Metabolism	Plastid	9	6.37	99,520	13
F4	P15280	Glucose-1-phosphate adenylyltransferase small subunit, amyloplast	<i>Oryza sativa</i>	Stem, Dark	Metabolism	Plastid, Amyloplast	7	6.58	56,069	18
F5	Q9C5P6	Calcineurin B-like protein 6	<i>Arabidopsis thaliana</i>	Stem, Dark	Signal Transduction	Cytoplasm	6	5.55	26,012	38
F6	Q05046	Chaperonin CPN60-2, mitochondrial	<i>Cucurbita maxima</i>	Stem, Dark	Stress Response	Mitochondria	8	6.28	61,092	22
F7	Q06429	1-aminocyclopropane-1-carboxylate synthase-like protein 1	<i>Arabidopsis thaliana</i>	Stem, Dark	Metabolism	Cytoplasm	7	7.18	54,967	19
F8	Q9LRZ6	Myrcene/ocimene synthase 2, chloroplastic	<i>Arabidopsis thaliana</i>	Stem, Dark	Metabolism	Plastid	9	5.80	69,767	18
F9	Q8H2T0	Probable protein phosphatase 2C	<i>Oryza sativa</i>	Stem, Dark	Signal Transduction	Cytoplasm	7	5.06	41,595	21
F10 B25 B26 B27 D27 D28	Q9XFM4	13S globulin seed storage protein 3	<i>Fagopyrum esculentum</i>	Leaf/Stem, Dark	Seed Storage	Cytoplasm	3	6.00	61,127	12
F11	Q8GYM4	B3 domain-containing protein REM14	<i>Arabidopsis thaliana</i>	Stem, Dark	Transcription	Nucleus	7	9.46	55,494	25

^{1,2} *pI* and *Mr* were theoretically determined using UniProt database (<http://www.uniprot.org>).

³ Seq. Cov. (%) indicates the percentage of the protein's sequence covered by identified peptide fragments.

* NCBI reference sequence

Supplementary Table 2 List of proteins identified from leaf and stem of 7-day-old sprouts in tatary buckwheat under light or dark

Spot #	Accession #	Protein Identity	Protein Source	Sample Source	Molecular function	Subcellular localization	Matched peptides	pI1	Mr (Da) 2	Seq. cov. (%)3
C1	Q6UU68	Putative DNA-binding protein	<i>Oryza sativa</i>	Leaf, Light	Transcription	Cytoplasm	7	8.94	59,225	12
C2	P92985	RNA-binding protein 1 homolog c	<i>Arabidopsis thaliana</i>	Leaf, Light	Transport	Nucleus	5	4.71	24,707	29
C3	B7ZWR6	At5g21990	<i>Arabidopsis thaliana</i>	Leaf, Light	Unknown	Unknown	11	5.66	60,718	28
C4	Q9M2C8	Pentatricopeptide repeat-containing protein At3g61360	<i>Arabidopsis thaliana</i>	Leaf, Light	Unknown	Unknown	11	8.84	56,943	25
C5 G4 G21	Q9S818	Naringenin,2-oxoglutarate 3-dioxygenase	<i>Arabidopsis thaliana</i>	Leaf/Stem, Light	Metabolism	Cytoplasm	8	4.92	27,759	40
C6	A6MZU0	tubulin alpha-1 chain	<i>Oryza sativa</i>	Leaf, Light	Cytoskeleton	Cytoplasm	7	4.70	28,598	40
C7	Q9SFD8	Nuclear transcription factor Y subunit B-9	<i>Arabidopsis thaliana</i>	Leaf, Light	Transcription	Nucleus	4	5.57	22,665	38
C8 E11	P19124	NAD(P)H-quinone oxidoreductase subunit J, chloroplastic	<i>Zea mays</i>	Leaf, Light	Transport	Plasma Membrane	5	6.04	18,657	42
C9	Q157M4	Nitric oxide synthase	<i>Oryza sativa</i>	Leaf, Light	Metabolism	Cytoplasm	3	9.38	17,398	24
C10	Q41266	Alternative oxidase 2, mitochondrial	<i>Glycine max</i>	Leaf, Light	Transport	Mitochondria	8	9.40	4,696	35
C11	B2XWN9	DNA-directed RNA polymerase subunit beta	<i>Fagopyrum esculentum</i>	Leaf, Light	Transcription	Plastid	3	9.59	154,803	4
C12	P83171	Ginkbilobin (GNL)	<i>Ginko biloba</i>	Leaf, Light	Defense	Cytoplasm	6	11.7 2	4,211	47
C13	Q9XHY7	Probable histone acetyltransferase HAC-like 3	<i>Oryza sativa</i>	Leaf, Light	Transcription	Nucleus	3	8.93	15,882	31
C14	Q9SD80	Mitochondrial import receptor subunit TOM5 homolog	<i>Arabidopsis thaliana</i>	Leaf, Light	Transport	Mitochondria	9	8.82	6,087	51
C15	B2XWM6	50S ribosomal protein L33, chloroplastic.	<i>Fagopyrum esculentum</i>	Leaf, Light	Translation	Plastid	7	10.1 7	7,736	22
C16	Q5XLE0	Bet v I allergen	<i>Zea mays</i>	Leaf, Light	Defense	Cytoplasm	3	4.68	17,075	24
C17	Q56ZG8	Putative acyl-CoA synthetase	<i>Arabidopsis thaliana</i>	Leaf, Light	Metabolism	Cytoplasm	4	9.69	5,427	46
C18	Q6QJL3	Glucosyl-transferase	<i>Fagopyrum esculentum</i>	Leaf, Light	Metabolism	Cytoplasm	3	8.04	27,020	13
C19	Q6K8M3	Cytokinin inducible protein-like	<i>Oryza sativa</i>	Leaf, Light	Signal Transduction	Cytoplasm	4	8.96	37,734	17
C20	P00232	Ferredoxin-2	<i>Phytolacca esculenta</i>	Leaf, Light	Transport	Plastid	5	4.04	10,258	20
C21	Q9FML6	40S ribosomal protein S15-6	<i>Arabidopsis thaliana</i>	Leaf, Light	Translation	Cytoplasm	3	10.5 9	18,564	26
C22	Q8S3D2	Transcription factor bHLH87	<i>Arabidopsis thaliana</i>	Leaf, Light	Transcription	Nucleus	3	6.23	41,295	14
C23	B6TNH4	kelch motif family protein	<i>Zea mays</i>	Leaf, Light	Transcription	Unknown	9	7.03	45,235	33
D1	Q9FJP3	50S ribosomal protein L29, chloroplastic	<i>Arabidopsis</i>	Leaf, Dark	Translation	Plastid	9	10.5	19,365	23

			<i>thaliana</i>					1		
D3	Q2ARA6	retrotransposon protein, putative, Ty3-gypsy subclass	<i>Oryza sativa</i>	Leaf, Dark	Recombination	Nucleus	6	6.07	5,566	30
D4	Q7Y0W5	Two-component response regulator EHD1	<i>Oryza sativa</i>	Leaf, Dark	Transcription	Nucleus	3	5.61	38,838	12
D6	P92567	Uncharacterized mitochondrial protein AtMg01410	<i>Arabidopsis thaliana</i>	Leaf, Dark	Unknown	Mitochondria	7	9.58	22,800	18
D7	P20158	Defensin-like protein 1	<i>Triticum aestivum</i>	Leaf, Dark	Defense	Cytoplasm	4	9.49	5,235	25
D8	Q7XPL2	proporphyrinogen-III oxidase, chloroplastic	<i>Oryza sativa</i>	Leaf, Dark	Metabolism	Plastid	3	6.23	43,844	14
D9	Q9XFI1	Thioredoxin-like 3, chloroplastic	<i>Arabidopsis thaliana</i>	Leaf, Dark	Transport	Plastid	7	7.60	26,872	62
D10	Q8LMR4	Putative peroxidase	<i>Oryza sativa</i>	Leaf, Dark	Signal Transduction	Unknown	8	5.41	33,625	47
D11	Q9TJU8	Ribosomal protein S4	<i>Taxus baccata</i>	Leaf, Dark	Translation	Plastid	4	10.95	23,777	23
D12	B2XWP0	DNA-directed RNA polymerase subunit beta'	<i>Fagopyrum esculentum</i>	Leaf, Dark	Transcription	Plastid	3	8.88	78,090	7
D13	Q9LJI5	V-type proton ATPase subunit d1	<i>Arabidopsis thaliana</i>	Leaf, Dark	Transport	Plasma Membrane	6	5.04	40,765	27
D14 E13	P56805	30S ribosomal protein S15, chloroplastic	<i>Arabidopsis thaliana</i>	Leaf, Dark	Translation	Plastid	4	10.81	10,712	46
D15	B9RZR9	Major allergen Pru ar, putative	<i>Ricinus communis</i>	Leaf, Dark	Defense	Cytoplasm	4	5.17	17,122	17
D16	Q8LAC6	Glycine rich protein-like	<i>Arabidopsis thaliana</i>	Leaf, Dark	Unknown	Unknown	7	9.95	14,328	31
D17	O82255	Glutaredoxin-C13	<i>Arabidopsis thaliana</i>	Leaf, Dark	Transport	Cytoplasm	9	7.63	11,268	30
D18 B22	A2Y1D7	Metallothionein-like protein 3B	<i>Oryza sativa</i>	Leaf, Dark	Cellular Process	Cytoplasm	3	5.19	6,875	44
D19	Q1W7A3	Mitochondrial ATP synthesis coupled proton transport protein	<i>Solanum habrochaites</i>	Leaf, Dark	Energy	Mitochondria	3	8.73	14,113	31
D20	Q30C58	Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit	<i>Ascocentrum ampullaceum</i>	Leaf, Dark	Photosynthesis	Plastid	3	5.91	1,764	87
D21	Q9LVK3	Autophagy-related protein 12b	<i>Arabidopsis thaliana</i>	Leaf, Dark	Transport	Cytoplasm	8	7.88	10,351	29
D22	Q66GP4	Pentatricopeptide repeat-containing protein At5g13770, chloroplastic	<i>Arabidopsis thaliana</i>	Leaf, Dark	Unknown	Plastid	15	9.07	69,464	27
D23	C6EMY9	putative Sm ribonucleoprotein-related protein	<i>Arabidopsis thaliana</i>	Leaf, Dark	Transcription	Unknown	9	7.16	23,577	35
D24	Q6R4S2	DNA binding protein	<i>Brassica napus</i>	Leaf, Dark	Transcription	Nucleus	3	9.51	11,105	50
D25	Q9AY76	Actin-depolymerizing factor 2	<i>Oryza sativa</i>	Leaf, Dark	Cytoskeleton	Cytoplasm	3	5.65	16,783	25
D26 G28	Q8RWG8	RNA-binding protein 1 homolog b	<i>Arabidopsis thaliana</i>	Leaf, Dark Stem, Light	Transport	Nucleus	3	5.65	16783	25

D27 D28 F10 B25 B26 B27	Q9XFM4	13S globulin seed storage protein 3	<i>Fagopyrum esculentum</i>	Leaf/Stem, Dark	Seed Storage	Vacuolar	8	6	61127	21
G1	Q3HRP2	Calcineurin B-like protein 5	<i>Oryza sativa</i>	Stem, Light	Signal Transduction	Cytoplasm	6	4.79	25,073	25
G2 E19 G3	P12468	Ribulose biphosphate carboxylase small chain 4, chloroplastic	<i>Glycine max</i>	Stem, Light	Photosynthesis	Plastid	7	8.87	20,004	53
G8 G9 G4	Q5SMK6	Probable protein phosphatase 2C 54	<i>Oryza sativa</i>	Stem, Light	Signal Transduction	Cytoplasm	6	5.18	39,327	24
G21 C5	Q9S818	Naringenin,2-oxoglutarate 3-dioxygenase	<i>Arabidopsis thaliana</i>	Leaf/Stem, Light	Metabolism	Cytoplasm	8	4.92	27,759	40
G5	O24408	Auxin-responsive protein IAA18	<i>Arabidopsis thaliana</i>	Stem, Light	Transcription	Nucleus	7	9.26	29,879	32
G6 E21	O23373	Formin-like protein 3	<i>Arabidopsis thaliana</i>	Stem, Light	Cytoskeleton	Plasma Membrane	10	8.25	85,991	14
G7	O82256	Zinc finger protein CONSTANS-LIKE 13	<i>Arabidopsis thaliana</i>	Stem, Light	Transcription	Nucleus	9	9.26	29,879	32
G10	Q9C9E3	Protein TIFY 11B	<i>Arabidopsis thaliana</i>	Stem, Light	Defense, Transcription	Nucleus	6	9.21	29,831	24
G11	Q94HW3	Probable disease resistance protein RDL6/RF9	<i>Arabidopsis thaliana</i>	Stem, Light	Defense	Cytoplasm	15	6.85	120,968	16
G12	O23878	13S globulin seed storage protein 1	<i>Fagopyrum esculentum</i>	Stem, Light	Seed Storage	Cytoplasm	9	5.68	64,479	21
G13	A2WYS7	Esterase PIR7B	<i>Oryza sativa</i>	Stem, Light	Metabolism	Cytoplasm	7	5.86	28,816	32
G14	Q9FGB0	Transcription factor bHLH145	<i>Arabidopsis thaliana</i>	Stem, Light	Transcription	Nucleus	8	5.08	34,692	31
G15 H1	Q9LRR9	Probable peroxisomal (S)-2-hydroxy-acid oxidase 2	<i>Arabidopsis thaliana</i>	Stem, Light/Dark	Photosynthesis	Peroxisome	10	9.16	40,316	32
G16	O80933	Scarecrow-like protein 9	<i>Arabidopsis thaliana</i>	Stem, Light	Transcription	Nucleus	9	5.99	80,864	18
G17	Q9ZNT3	Actin-depolymerizing factor 5	<i>Arabidopsis thaliana</i>	Stem, Light	Cytoskeleton	Cytoplasm	4	6.82	16,457	37
G18	Q9LIG6	NifU-like protein 4, mitochondrial	<i>Arabidopsis thaliana</i>	Stem, Light	Cellular Process	Mitochondria	7	4.90	30,485	24
G19	P39871	Nitrate reductase [NAD(P)H]	<i>Zea mays</i>	Stem, Light	Metabolism	Cytoplasm	6	6.16	26,237	39
G20	Q8LEM7	Calcineurin B-like protein 3	<i>Arabidopsis thaliana</i>	Stem, Light	Signal Transduction	Plasma Membrane	6	4.80	26,015	26
G21 G4 C5	Q9S818	Naringenin,2-oxoglutarate 3-dioxygenase	<i>Arabidopsis thaliana</i>	Leaf/Stem, Light	Metabolism	Cytoplasm	8	4.92	27,759	40

G22	Q8RV83	B3 domain-containing protein At2g31720	<i>Arabidopsis thaliana</i>	Stem, Light	Transcription	Nucleus	6	6.92	53,821	26
G23	Q9LGU6	S-adenosylmethionine synthetase 3	<i>Oryza sativa</i>	Stem, Light	Metabolism	Cytoplasm	6	5.22	43,283	23
G24	Q94A97	Ubiquitin carrier protein E2 35	<i>Arabidopsis thaliana</i>	Stem, Light	Cellular Process	Cytoplasm	4	6.74	17,181	41
G25 G26	Q7PC70	Probable xyloglucan glycosyltransferase 2	<i>Oryza sativa</i>	Stem, Light	Metabolism	Golgi	10	9.09	79,323	20
G27	A2YXJ7	Retinoblastoma-related protein 1	<i>Oryza sativa</i>	Stem, Light	Transcription	Nucleus	10	8.84	111,439	17
G28 D26	Q8RWG8	RNA-binding protein 1 homolog b	<i>Arabidopsis thaliana</i>	Leaf, Dark Stem, Light	Transport	Nucleus	5	4.83	24,374	30
G29	Q9LW27	Cytochrome P450 71B15	<i>Arabidopsis thaliana</i>	Stem, Light	Metabolism	Endoplasmic reticulum	9	8.45	56,025	21
H1 G15	Q9LRR9	Probable peroxisomal (S)-2-hydroxy-acid oxidase 2	<i>Arabidopsis thaliana</i>	Stem, Light/Dark	Photosynthesis	Peroxisome	10	9.16	40,316	32
H2	Q9ZQR6	Serpin-Z2	<i>Arabidopsis thaliana</i>	Stem, Dark	DNA Repair	Nucleus	7	5.67	45,858	26
H3	O82261	Protease Do-like 2, chloroplastic	<i>Arabidopsis thaliana</i>	Stem, Dark	Photosynthesis	Plastid	8	5.70	66,760	16
H4	Q0JNL7	Calmodulin-3	<i>Oryza sativa</i>	Stem, Dark	Signal Transduction	Cytoplasm	5	4.11	16,821	33
H5	Q9SVR0	60S ribosomal protein L13a-3	<i>Arabidopsis thaliana</i>	Stem, Dark	Translation	Plastid	6	10.39	23,614	38
H6	Q9LVQ5	Pentatricopeptide repeat-containing protein At5g55840	<i>Arabidopsis thaliana</i>	Stem, Dark	Unknown	Unknown	13	8.84	122,417	21
H7	Q5QM99	60S ribosomal protein L37a	<i>Oryza sativa</i>	Stem, Dark	Translation	Cytoplasm	4	10.31	10,236	52
H8	Q9M1U2	GATA transcription factor 8	<i>Arabidopsis thaliana</i>	Stem, Dark	Transcription	Nucleus	6	9.48	23,161	35
H9	Q9LNF6	F-box protein At1g48060	<i>Arabidopsis thaliana</i>	Stem, Dark	Transcription	Unknown	9	9.62	28,313	39
H10	Q05736	Pathogenesis-related protein 1	<i>Asparagus officinalis</i>	Stem, Dark	Defense	Cytoplasm	7	6.51	16,911	45
H11	O81037	Transcription factor bHLH70	<i>Arabidopsis thaliana</i>	Stem, Dark	Transcription	Nucleus	7	6.85	42,974	21
H12	Q8H6B1	FACT complex subunit SPT16	<i>Zea mays</i>	Stem, Dark	Replication	Nucleus	10	5.57	118,431	16
H13	Q9LTM4	Cytochrome P450 71B19	<i>Arabidopsis thaliana</i>	Stem, Dark	Metabolism	Endoplasmic reticulum	8	7.28	57,482	22
H14	Q5G1S8	Pentatricopeptide repeat-containing protein At3g18110, chloroplastic	<i>Arabidopsis thaliana</i>	Stem, Dark	Cellular Process	Plastid	16	7.04	160,925	18
H15	Q08891	Fatty acyl-CoA reductase 2	<i>Arabidopsis thaliana</i>	Stem, Dark	Metabolism	Cytoplasm	9	8.54	68,372	20

^{1,2} pI and Mr were theoretically determined using UniProt database (<http://www.uniprot.org>).

³ Seq Cov (%) indicates the percentage of the protein's sequence covered by identified peptide fragments.