

Table S1. Protein identified by MALDI-TOF/TOF MS

Spot no ^a	Accession number ^b	SC ^c	Experimental ^d <i>M_r</i> /pI	Theoretical ^e <i>M_r</i> /pI	MP ^f	Kinetic trend ^g B/M/T	Protein name	Reference organism
Metabolism								
12	Q69X42	7	101/5.90	112.45/6.35	2	U/D/U	Putative glycine dehydrogenase	<i>Oryza. sativa</i>
32	Q8LL05	3	51/5.27	63.04/6.12	2	D/D/D	Granule-bound starch synthase 1b, chloroplastic/amyloplastic	<i>Hordeum vulgare</i>
44	B6T4W6	18	46/5.43	50.33/5.57	3	C/C/A	Aminoacylase-1	<i>Zea mays</i>
46	Q43772	39	43/5.36	51.79/5.2	7	A/C/B	UTP--glucose-1-phosphate uridylyltransferase	<i>H. vulgare</i>
49 ^h	Q65XK0	10	49/5.56	62.69/6.01	2	A/A/A	Ketol-acid reductoisomerase, chloroplastic	<i>O. sativa</i>
56	Q65XK0	17	49/5.78	62.69/6.01	4	C/B/D	Ketol-acid reductoisomerase, chloroplastic	<i>O. sativa</i>
57	Q65XK0	14	48/5.77	62.69/6.01	4	C/B/A	Ketol-acid reductoisomerase, chloroplastic	<i>O. sativa</i>
61	Q65XK0	11	48/5.89	62.69/6.01	2	A/B/A	Ketol-acid reductoisomerase, chloroplastic	<i>O. sativa</i>
49	Q9LIA8	20	47/5.61	53.72/5.69	2	A/A/A	Probable UDP-glucose 6-dehydrogenase 1	<i>Arabidopsis thaliana</i>
58 ^h	Q9LIA8	17	46/5.74	53.72/5.69	3	A/A/A	Probable UDP-glucose 6-dehydrogenase 1	<i>A. thaliana</i>
50	B8B7Y3	25	46/5.65	57.60/5.98	3	A/A/B	Putative uncharacterized protein	<i>O. sativa</i>
51	O64437	19	45/5.52	56.52/5.44	6	-/A/C	Inositol-3-phosphate synthase	<i>O. sativa</i>
53	C4J3S6	12	50/5.71	69.09/7	2	C/B/D	Putative uncharacterized protein	<i>Z. mays</i>
54	A2YY43	17	51/5.80	64.25/6.59	3	C/B/A	Putative uncharacterized protein	<i>O. sativa</i>
59	B6T9P0	19	46/5.81	53.51/5.71	4	A/U/A	UDP-glucose 6-dehydrogenase	<i>Z. mays</i>
62	Q9LIA8	18	46/5.97	53.72/5.69	3	A/A/U	Probable UDP-glucose 6-dehydrogenase 1	<i>A. thaliana</i>
66	Q9LIA8	17	46/6.32	53.72/5.69	3	A/A/B	Probable UDP-glucose 6-dehydrogenase 1	<i>A. thaliana</i>
67	Q6L4H5	18	44/6.1933	57.70/6.74	2	A/A/C	Putative threonine synthase	<i>O. sativa</i>
131	Q6L4H5	18	43/6.67	57.70/6.74	1	C/C/A	Putative threonine synthase	<i>O. sativa</i>
73 ^h	Q75W16	21	47/7.10	59.64/8.64	3	U/U/U	Phospho-2-dehydro-3-deoxyheptonate aldolase 2, chloroplastic	<i>O. sativa</i>
74	Q75W16	27	47/7.4	59.64/8.64	6	C/A/U	Phospho-2-dehydro-3-deoxyheptonate aldolase 2, chloroplastic	<i>O. sativa</i>
75 ^h	Q75W16	30	46/7.39	59.64/8.64	8	A/A/A	Phospho-2-dehydro-3-deoxyheptonate aldolase 2, chloroplastic	<i>O. sativa</i>
83	Q6K3Z3	5	35/6.62	41.40/6.15	2	A/D/A	putative acetyl-CoA C-acyltransferase	<i>O. sativa</i>
91 ^h	Q42942	11	40/6.59	50.08/7.71	1	C/D/D	Uridine 5'-monophosphate synthase	<i>Nicotiana tabacum</i>

Probable								
93	Q6AV34	17	36/6.58	45.11/8.61	2	A/C/A	N-acetyl-gamma-glutamyl-phosphate reductase, chloroplastic	<i>O. sativa</i>
94	O24578	14	42/5.65	52.35/6.9	2	D/A/B	Adenylosuccinate synthetase, chloroplastic	<i>Z. mays</i>
96 ⁱ	B4FZ30	17	39/5.74	49.45/6.7	4	D/D/A	Putative uncharacterized protein	<i>Z. mays</i>
98	P23902	5	39/5.86	49.51/6.86	2	A/B/A	3-oxoacyl-[acyl-carrier-protein] synthase I, chloroplastic	<i>H. vulgare</i>
99	B8BBZ7	7	39/5.88	56.27/6.1	2	D/A/A	Putative uncharacterized protein	<i>O. sativa</i>
100	A2Y053	40	37/5.58	43.66/5.74	6	A/A/U	S-adenosylmethionine synthetase 1	<i>O. sativa</i>
135	P31155	26	34/5.07	25.75/7.94	3	D/C/A	S-adenosylmethionine synthetase 1	<i>Petroselinum crispum</i>
101	Q96552	18	36/5.66	43.44/5.51	2	D/A/A	S-adenosylmethionine synthetase 2	<i>Catharanthus roseus</i>
115	Q96552	23	37/5.47	43.44/5.51	3	D/A/U	S-adenosylmethionine synthetase 2	<i>C. roseus</i>
116	Q96552	24	37/5.49	43.44/5.51	5	C/D/U	S-adenosylmethionine synthetase 2	<i>C. roseus</i>
103	P46637	17	34/5.78	37.55/6.11	4	D/D/A	Arginase	<i>A. thaliana</i>
105	Q7XPL2	32	31/5.71	44.13/6.23	1	D/B/D	Coproporphyrinogen-III oxidase, chloroplastic	<i>O. sativa</i>
107 ^h	A3AQX8	17	31/5.75	41.34/6.88	4	B/B/A	Putative uncharacterized protein	<i>O. sativa</i>
109	B4FZ29	26	41/5.51	49.45/6.7	2	D/D/C	Putative uncharacterized protein	<i>Z. mays</i>
111	Q6ZGS9	23	43/6.11	49.00/5.19	4	A/D/D	Putative silver leaf whitefly-induced protein 1	<i>O. sativa</i>
117 ^h	B6T223	15	36/5.53	44.78/6.16	1	A/A/A	Patatin T5 precursor	<i>Z. mays</i>
118 ^h	P80607	20	35/5.35	41.70/5.75	4	A/A/B	Alpha-1,4-glucan-protein synthase [UDP-forming]	<i>Z. mays</i>
119	P80607	27	35/5.46	41.70/5.75	6	A/A/A	Alpha-1,4-glucan-protein synthase [UDP-forming]	<i>Z. mays</i>
127	B6TVD6	16	37/4.99	43.15/5.62	1	D/D/D	3-isopropylmalate dehydrogenase 2	<i>Z. mays</i>
130	Q5DKU6	15	36/5.07	37.91/5.17	1	C/A/B	Adenosine kinase isoform 2T	<i>N. tabacum</i>
137	Q6Z0I4	20	30/5.19	39.28/8.81	3	C/B/D	Putative enoyl-ACP reductase	<i>O. sativa</i>
138 ^h	A2YQL4	17	31/5.07	35.90/5.02	2	C/A/U	Fructokinase-2	<i>O. sativa</i>
145	C6SZP0	19	25/5.24	26.31/5.51	2	D/C/B	Putative uncharacterized protein	<i>Glycine max</i>
170	A3BQT1	20	20/5.81	31.57/5.06	3	C/B/D	Putative uncharacterized protein	<i>O. sativa</i>
200	Q6ZIX2	19	30/5.62	38.99/5.98	3	C/B/A	Cycloartenol-C-24-methyltransferase 1	<i>O. sativa</i>
204	Q6I683	27	30/8.18	48.85/9.23	3	A/D/A	UDP-glucuronic acid decarboxylase	<i>O. sativa</i>
209	Q10NN8	23	53/5.73	65.78/6.76	1	A/A/A	Anthranilate synthase component I family protein, expressed	<i>O. sativa</i>
Energy								
9	Q8W317	18	75/5.53	82.17/5.86	2	D/A/C	NADH-ubiquinone oxidoreductase 75 kDa subunit	<i>O. sativa</i>
10	B4F8V5	22	74/5.58	81.73/6.1	2	A/C/A	NADH-ubiquinone oxidoreductase 75 kDa subunit	<i>Z. mays</i>

11	Q6YZX6	23	94/5.80	98.60/5.67	7	C/C/A	Putative aconitate hydratase, cytoplasmic	<i>O. sativa</i>
15	Q6Z8F7	15	66/9.37	71.34/9.4	3	C/-/A	26S proteasome regulatory subunit-like	<i>O. sativa</i>
23	Q5QMK7	24	52/5.65	60.98/5.42	3	A/A/A	Putative phosphoglycerate mutase	<i>O. sativa</i>
25	C5Y8Y2	8	65/5.54	82.02/5.99	2	C/D/D	Putative uncharacterized protein Sb06g030270	<i>Sorghum bicolor</i>
40	P08823	21	50/4.98	57.66/4.83	3	C/C/B	RuBisCO large subunit-binding protein subunit alpha, chloroplastic	<i>Triticum aestivum</i>
41	Q10AA5	18	49/5.03	50.48/5.01	3	B/A/B	RuBisCO subunit binding-protein alpha subunit, chloroplast, putative, expressed	<i>O. sativa</i>
43 ^h	Q43433	30	46/5.16	43.33/5.07	5	U/A/B	V-type proton ATPase subunit B 2	<i>Gossypium hirsutum</i>
45 ⁱ	Q01859	33	45/5.33	59.01/5.95	4	A/A/U	ATP synthase subunit beta, mitochondrial	<i>O. sativa</i>
60	O81237	13	42/5.86	53.31/5.92	4	D/D/D	6-phosphogluconate dehydrogenase, decarboxylating	<i>Z. mays</i>
65	Q2R480	14	42/5.98	54.50/6.09	3	A/B/D	6-phosphogluconate dehydrogenase, decarboxylating	<i>O. sativa</i>
68	Q7Y248	23	43/6.07	51.79/6.58	3	C/A/D	6-phosphogluconate dehydrogenase, decarboxylating NADP-dependent	<i>O. sativa</i>
71 ^h	Q8LK61	9	45/6.91	53.59/6.39	1	A/U/U	glyceraldehyde-3-phosphate dehydrogenase	<i>T. aestivum</i>
84	D1MY57	28	33/6.79	39.24/7.57	5	A/U/A	Fructose-bisphosphate aldolase	<i>Phyllostachys edulis</i>
85	D1MY57	43	33/6.79	39.24/7.57	4	A/A/U	Fructose-bisphosphate aldolase	<i>P. edulis</i>
86	D1MY57	56	33/6.79	39.24/7.57	7	U/U/U	Fructose-bisphosphate aldolase	<i>P. edulis</i>
87	D1MY57	59	33/6.79	39.24/7.57	7	-/C/U	Fructose-bisphosphate aldolase	<i>P. edulis</i>
89	Q75ZX4	12	40/6.28	41.71/6.2	3	C/C/A	Alcohol dehydrogenase 1	<i>O. sativa</i>
90	Q75ZX4	25	40/6.38	41.71/6.2	2	B/C/C	Alcohol dehydrogenase 1	<i>O. sativa</i>
108	B6SJN5	11	42/5.49	48.89/7.66	3	A/A/B	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex	<i>Z. mays</i>
110	P26301	28	41/5.34	48.27/5.2	4	C/A/B	Enolase 1	<i>Z. mays</i>
114	P12783	27	37/5.40	42.15/5.64	3	C/A/B	Phosphoglycerate kinase, cytosolic	<i>T. aestivum</i>
123 ^h	O81279	9	31/5.30	27.55/5.56	2	U/U/U	malate dehydrogenase	<i>G. max</i>
134 ^h	C5YSM6	41	34/5.00	46.08/5.42	4	A/D/D	Putative uncharacterized protein Sb08g004300	<i>S. bicolor</i>
136	C5Z038	23	34/5.12	35.34/5.17	1	B/A/A	Putative uncharacterized protein Sb09g003790	<i>S. bicolor</i>
143	Q6ZGJ8	27	28/5.17	31.76/5.8	2	C/D/A	Putative inorganic pyrophosphatase	<i>O. sativa</i>

144	P84989	44	27/5.20	10.66/5.36	3	U/A/C	Oxygen-evolving enhancer protein 1, chloroplastic	<i>Populus euphratica</i>
146 ^h	Q8LR75	20	25/5.39	27.49/5.58	4	C/C/D	Triosephosphate isomerase	<i>O. sativa</i>
151 ^h	C5X9U6	12	25/5.67	28.34/5.96	2	A/C/A	Putative uncharacterized protein Sb02g022080	<i>S. bicolor</i>
154	B8B5F4	7	29/5.86	68.12/6.38	2	C/C/U	Granule-bound starch synthase II	<i>O. sativa</i>
176	Q5JKQ4	42	21/4.87	22.82/4.96	4	C/A/D	Thioredoxin family Trp26-like protein	<i>O. sativa</i>
182	Q6L460	16	15/5.16	19.80/5.34	3	A/A/U	ATP synthase D chain, mitochondrial, putative	<i>Solanum demissum</i>
198 ^h	A2YIW7	9	13/5.16	13.32/5.16	1	U/U/U	Thioredoxin H-type	<i>O. sativa</i>
201	B8AC38	18	30/5.91	34.71/6.37	2	D/D/D	Aldo-keto reductase	<i>O. sativa</i>
205 ^h	Q7XKF3	22	31/8.92	41.39/9.62	5	A/A/A	Protochlorophyllide reductase A, chloroplastic	<i>O. sativa</i>
210	Q6ZDY8	8	53/5.95	69.51/6.61	1	A/B/A	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial	<i>O. sativa</i>
Cell growth/division								
8	B8ATF3	19	84/5.40	86.93/6.92	1	C/A/A	Putative uncharacterized protein	<i>O. sativa</i>
124	Q5Z6P9	19	41/4.70	43.11/4.7	2	B/B/A	Putative RAD23 protein	<i>O. sativa</i>
125	B9GXM9	6	41/4.80	38.41/4.56	2	C/C/A	Predicted protein	<i>P. trichocarpa</i>
126	B9GLR5	8	40/4.65	37.60/4.38	2	D/C/A	Predicted protein	<i>P. trichocarpa</i>
178	A2XZN0	29	17/4.41	16.49/10.6	1	C/B/B	Probable histone H2A.6	<i>O. sativa</i>
Transcription								
1	C0STZ0	23	106/4.62	114.44/5.25	1	A/D/D	Polycomb group protein	<i>Physcomitrella patens</i> subsp. <i>patens</i>
4	C5YU67	22	111/5.15	93.77/5.07	1	A/D/C	Putative uncharacterized protein Sb09g005580	<i>S. bicolor</i>
13 ^h	Q6K8D9	15	75/8.64	67.50/9.18	4	D/D/A	Putative GAMYB-binding protein	<i>O. sativa</i>
14	Q6K8D8	22	75/8.83	67.50/9.18	3	D/A/A	Os02g0759800	<i>O. sativa</i>
18	Q6YVX8	12	70/6.78	67.20/6.36	2	A/C/B	Putative Ligatin (Hepatocellular carcinoma-associated antigen 56)	<i>O. sativa</i>
24	—	17	52/5.68	52.29/5.79	4	A/B/A	Os04g0636900	<i>O. sativa</i>
26	Q6K6X2	8	54/5.53	51.89/5.56	2	A/A/D	Putative RNA recognition motif (RRM)-containing protein	<i>O. sativa</i>
38	C0PA71	11	50/4.72	42.28/4.48	2	D/B/D	Putative uncharacterized protein	<i>Z. mays</i>
47	A3AJP7	7	42/5.31	28.05/6.08	1	D/A/D	Putative uncharacterized protein	<i>O. sativa</i>
55 ^h	Q0J9Q1	4	51/5.85	52.29/5.79	3	D/B/A	Os04g0636900	<i>O. sativa</i>
63	O22607	7	46/6.01	56.25/5.81	2	C/B/D	WD-40 repeat-containing protein MSI4	<i>A. thaliana</i>
78	Q6L561	11	39/8.80	41.00/5.89	2	-/-/-	Putative nuclear RNA binding protein A	<i>O. sativa</i>
95	Q0GH11	17	40/5.68	38.88/8.42	1	D/D/A	nuclear-localized RNA binding protein	<i>Capsicum annuum</i>

102	C5XYF2	14	36/5.74	39.53/5.97	2	C/B/A	Putative uncharacterized protein Sb04g007860	<i>S. bicolor</i>
160	B8B9D0	35	27/7.73	23.91/8.59	1	A/A/A	Putative uncharacterized protein	<i>O. sativa</i>
167	Q8LNW1	28	19/6.06	17.62/6.62	2	C/C/A	Putative transcription factor	<i>O. sativa</i>
168	Q8LNW0	29	19/6.01	17.62/6.62	1	B/B/A	Os10g0483000	<i>O. sativa</i>
169 ^h	Q0IWW6	29	20/5.91	17.62/6.62	3	C/B/D	Os10g0483400	<i>O. sativa</i>
172	Q84VF8	25	21/5.48	19.20/5.26	3	C/D/A	Putative transcription factor BTF3	<i>O. sativa</i>
173 ^h	P27347	28	20/5.4	17.14/5.9	2	C/D/D	DNA-binding protein MNB1B	<i>Z. mays</i>
177	Q40436	15	22/4.38	26.66/4.83	1	D/D/A	RNA-binding glycine rich protein	<i>N. sylvestris</i>
179	A9P0L1	37	19/5.14	17.30/5.33	2	B/D/D	Putative uncharacterized protein	<i>Picea sitchensis</i>
186	B8AP37	68	14/5.15	14.09/5.17	1	D/D/D	Putative uncharacterized protein	<i>O. sativa</i>
212	Q10KN9	15	52/6.46	58.33/6.41	2	C/D/D	KH domain-containing protein, putative, expressed	<i>O. sativa</i>
213 ⁱ	Q6L561	7	39/8.52	41.00/5.89	2	C/C/D	Putative nuclear RNA binding protein A	<i>O. sativa</i>
Protein synthesis								
27	Q688X1	16	70/5.36	65.33/5.3	2	A/B/D	Putative eukaryotic translation initiation factor (EIF3d)	<i>O. sativa</i>
76	Q41803	27	46/9.55	49.55/9.19	4	D/B/C	Elongation factor 1-alpha	<i>Z. mays</i>
92 ^h	Q0D868	39	39/6.01	44.83/10.54	4	A/U/U	Os07g0180900	<i>O. sativa</i>
106	O24473	24	32/5.80	30.66/6.4	3	D/A/A	Eukaryotic translation initiation factor 2 subunit beta	<i>T. aestivum</i>
121	Q0D868	26	33/5.41	46.78/10.65	4	U/A/B	Os07g0180900	<i>O. sativa</i>
122	O24573	33	32/5.42	34.60/5.2	2	C/D/D	60S acidic ribosomal protein P0	<i>Z. mays</i>
133	A5BUU4	21	34/4.86	34.06/5.43	2	A/C/A	40S ribosomal protein SA	<i>Vitis vinifera</i>
139	P48006	18	29/4.51	25.23/4.43	2	C/A/B	Elongation factor 1-delta 1	<i>A. thaliana</i>
140	P29545	10	29/4.64	23.84/4.6	2	C/A/D	Elongation factor 1-beta	<i>O. sativa</i>
141	B6SRH8	25	25/4.35	24.32/4.39	4	D/D/D	Nascent polypeptide-associated complex alpha subunit-like protein	<i>Z. mays</i>
164	Q9M339	14	24/9.79	27.51/9.57	2	D/D/A	40S ribosomal protein S3-2	<i>A. thaliana</i>
165 ^h	Q40467	26	22/7.86	47.14/5.37	1	A/C/U	Eukaryotic initiation factor 4A-14	<i>N. tabacum</i>
174 ⁱ	Q949H0	28	21/5.33	22.12/9.77	2	A/C/U	40S ribosomal protein S7	<i>H. vulgare</i>
181	P56335	30	17/5.11	17.73/5.78	2	A/D/D	Eukaryotic translation initiation factor 5A-3	<i>S. tuberosum</i>
185 ^h	B4FGC8	18	15/5.20	15.32/5.33	1	B/C/D	40S ribosomal protein S12	<i>Z. mays</i>
189	Q9XI91	13	16/5.24	17.52/5.41	1	-/D/C	Eukaryotic translation initiation factor 5A-1	<i>A. thaliana</i>
190	Q10CJ5	25	16/5.29	17.93/5.87	2	C/D/D	Eukaryotic translation initiation factor 5A-2, putative, expressed	<i>O. sativa</i>
197	P35687	76	12/6.47	9.31/6.71	2	D/C/D	40S ribosomal protein S21	<i>O. sativa</i>
199	Q7XYB6	34	30/5.51	18.64/5.82	3	A/A/A	Elongation factor	<i>T. aestivum</i>
211	Q41803	33	53/6.17	49.55/9.19	2	D/D/D	Elongation factor 1-alpha	<i>Z. mays</i>
Protein destination and storage								
2	B8A158	10	84/4.77	52.51/5.05	2	C/C/A	Putative uncharacterized protein	<i>Z. mays</i>

3	B8A158	12	84/4.77	52.51/5.05	3	C/D/A	Putative uncharacterized protein	<i>Z. mays</i>
5	P11143	17	90/5.09	70.88/5.22	1	D/A/A	Heat shock 70 kDa protein	<i>Z. mays</i>
6	C5YP67	13	84/5.07	91.62/5.1	4	A/D/D	Putative uncharacterized protein Sb08g016560	<i>S. bicolor</i>
7	Q6ZBX8	15	88/5.36	98.61/5.42	3	A/A/U	Putative aminopeptidase N	<i>O. sativa</i>
20	B6UCD0	26	60/6.06	61.17/6.27	2	C/B/A	T-complex protein 1 subunit gamma	<i>Z. mays</i>
28	P37900	14	60/5.47	72.43/5.81	3	C/D/D	Heat shock 70 kDa protein, mitochondrial	<i>Pisum sativum</i>
29	P54411	13	54/5.40	59.58/5.39	3	D/D/B	T-complex protein 1 subunit epsilon	<i>Avena sativa</i>
30	B6TI78	22	65/5.24	61.94/5.21	3	C/D/D	Peptidyl-prolyl isomerase	<i>Z. mays</i>
31	B6UGG5	11	60/5.19	72.89/5.62	2	A/A/C	Heat shock 70 kDa protein	<i>Z. mays</i>
33	P24629	15	67/4.97	71.65/5.15	2	B/D/D	Heat shock cognate 70 kDa protein 1	<i>S. lycopersicum</i>
34	P09189	27	65/5.02	71.14/5.07	5	D/D/D	Heat shock cognate 70 kDa protein	<i>Petunia hybrida</i>
35	P52588	23	54/4.88	57.29/5.24	4	C/A/B	Protein disulfide-isomerase	<i>Z. mays</i>
36	Q93XQ7	12	55/5.00	56.88/4.96	3	D/D/C	Protein disulfide isomerase	<i>T. aestivum</i>
37	A4ZYQ0	17	69/4.79	73.14/5.23	2	D/A/A	Chloroplast heat shock protein 70	<i>Pennisetum glaucum</i>
52	A2XDW2	30	42/5.69	58.84/5.5	6	A/A/B	Putative uncharacterized protein	<i>O. sativa</i>
79	Q9SEI3	24	40/6.78	44.96/8.24	3	-/D/-	26S protease regulatory subunit 10B homolog A	<i>A. thaliana</i>
81	Q9SEI3	15	39/7.15	44.96/8.24	2	C/D/A	26S protease regulatory subunit 10B homolog A	<i>A. thaliana</i>
82	Q6F4N5	5	40/7.70	45.74/6.64	3	D/A/D	Eukaryotic aspartyl protease family protein, expressed	<i>O. sativa</i>
104	Q5EUD6	14	31/5.62	40.44/6.29	2	B/B/C	Protein disulfide isomerase	<i>Z. mays</i>
142	P0C8Z0	18	24/4.25	22.62/4.33	2	D/B/D	Uncharacterized protein OsI_027940	<i>O. sativa</i>
147	C5XTN5	29	24/5.04	26.45/7.71	4	C/D/C	Putative uncharacterized protein Sb04g035040	<i>S. bicolor</i>
149	P52428	35	28/5.48	29.90/5.37	3	C/D/D	Proteasome subunit alpha type-1	<i>O. sativa</i>
153	Q65XA1	10	29/5.95	38.46/5.81	2	A/C/A	Putative legumin	<i>O. sativa</i>
159 ^h	B6TV55	11	25/7.31	32.19/9.18	2	C/D/C	Stem 28 kDa glycoprotein	<i>Z. mays</i>
161 ^h	B6TV55	11	25/7.63	32.19/9.18	2	A/B/C	Stem 28 kDa glycoprotein	<i>Z. mays</i>
171 ^h	Q9LST9	36	21/5.57	26.37/5.47	5	A/C/C	Proteasome subunit beta type	<i>O. sativa</i>
175 ^h	B8B3P0	22	23/5.11	29.16/5.63	2	A/-/A	Putative uncharacterized protein	<i>O. sativa</i>
195	Q9SJ44	42	16/6.89	16.59/6.51	3	D/U/B	Ubiquitin-conjugating enzyme E2 variant 1C	<i>A. thaliana</i>
196	C7E3V7	16	16/7.10	18.60/8.68	3	D/B/D	Peptidyl-prolyl cis-trans isomerase	<i>Saccharum officinatum</i>
207	P0C8Z0	21	23/4.2	22.62/4.33	1	C/D/D	Uncharacterized protein OsI_027940	<i>O. sativa</i>
208 ⁱ	Q67IX6	17	63/4.74	62.45/4.76	3	C/A/A	Os02g0100100 protein	<i>O. sativa</i>
Transporters								
42	Q9SLX0	14	49/5.12	59.11/5.18	1	D/D/D	Importin subunit alpha-1b	<i>O. sativa</i>
162	B8A8P3	19	25/9.02	32.52/5.52	2	D/B/A	Putative uncharacterized protein	<i>O. sativa</i>
163	B6SS48	33	26/9.29	29.19/9.1	3	D/D/D	Outer mitochondrial membrane	<i>Z. mays</i>

protein porin

Cell structure

19	B9GND6	16	60/6.07	145.73/5.4	1	C/D/A	Predicted protein	<i>P. trichocarpa</i>
39	Q41784	24	45/4.68	50.70/4.72	1	C/B/D	Tubulin beta-7 chain	<i>Z. mays</i>
64	P37832	20	45/5.94	50.43/4.77	1	A/B/B	Tubulin beta-7 chain	<i>O. sativa</i>
77	P0C5K4	16	41/8.45	50.17/8.26	1	-/D/D	Putative formin-like protein 21a	<i>A. thaliana</i>
112	P0C539	57	37/5.25	41.89/5.31	5	C/A/B	Actin-2	<i>O. sativa</i>
113	A2XLF2	57	37/5.31	42.02/5.3	6	C/A/-	Actin-1	<i>O. sativa</i>
128	A2XLF2	31	38/5.04	42.02/5.3	1	C/B/C	Actin-1	<i>O. sativa</i>
129	P93371	14	38/5.09	37.28/5.82	1	C/A/C	Actin-93 (Fragment)	<i>N. tabacum</i>

Signal transduction

16	Q8W315	17	61/7.90	68.22/8.39	1	D/A/A	Putative GTP-binding protein	<i>O. sativa</i>
17	Q0DG31	35	58/7.46	69.05/7.66	5	A/A/U	Os05g0556100	<i>O. sativa</i>
150	Q69W96	6	25/5.60	31.13/6.07	2	A/D/A	Putative sex determination protein tasselseed 2	<i>O. sativa</i>
166	P54765	25	23/7.17	24.12/6.72	2	C/A/A	GTP-binding nuclear protein Ran1A	<i>Lotus japonicus</i>

Disease/defense

21	Q6H660	36	59/5.75	65.16/6.03	4	C/B/D	Putative stress-induced protein sti1	<i>O. sativa</i>
22	Q0DZ60	25	59/5.65	65.16/6.03	2	D/D/D	Putative stress-induced protein sti1	<i>O. sativa</i>
69	CSRZ	21	47/6.66	57.07/6.75	2	D/A/U	Catalase (EC 1.11.1.6) catA	<i>O. sativa</i>
70 ⁱ	P0C549	18	46/6.89	57.13/6.52	2	C/U/U	Catalase isozyme A	<i>O. sativa</i>
131	B4FCK0	16	35/4.66	27.36/4.88	2	C/C/A	USP family protein	<i>Z. mays</i>
132	Q5ZAV7	6	33/4.71	27.79/4.97	1	B/D/C	Universal stress protein-like	<i>O. sativa</i>
148	Q43661	8	24/5.35	30.00/7.64	2	D/B/A	Wali7 protein	<i>T. aestivum</i>
155 ⁱ	B4FT31	28	23/6.15	23.52/5.54	1	C/B/A	Putative uncharacterized protein	<i>Z. mays</i>
156 ⁱ	C5YYX3	26	23/6.02	23.57/5.56	1	C/B/A	Putative uncharacterized protein Sb09g001700	<i>S. bicolor</i>
157	Q8H8D8	28	24/6.31	25.76/6.67	2	C/U/U	Glutathione S-transferase GSTF15	<i>O. sativa</i>
158	Q10S49	27	24/6.73	25.58/6.46	2	C/U/A	Glutathione S-transferase, C-terminal domain containing protein, expressed	<i>O. sativa</i>
180	B6T2Y1	23	17/4.80	23.92/7.74	2	D/D/A	Peroxiredoxin-5	<i>Z. mays</i>
183	Q9AXN5	11	15/5.10	20.01/4.82	1	C/B/C	Dehydration stress-induced protein	<i>Brassica napus</i>
184 ⁱ	B6T9W1	19	15/4.87	20.03/5.1	1	D/A/U	Wound/stress protein	<i>Z. mays</i>
191	Q38703	28	15/5.49	13.20/7.66	3	A/A/C	Glutathione peroxidase	<i>Avena fatua</i>
193	O22668	25	15/5.62	15.36/5.45	2	C/C/C	Superoxide dismutase [Cu-Zn]	<i>Panax ginseng</i>
203 ^h	Q8RYP0	11	23/5.29	36.99/6.54	2	D/D/A	Class III peroxidase 17	<i>O. sativa</i>

Unkown

80	C5X5P4	22	39/6.73	40.76/6.62	2	C/D/C	Putative uncharacterized protein Sb02g043220	<i>S. bicolor</i>
88	A2WSA8	15	41/5.97	41.10/6.41	1	D/B/A	Putative uncharacterized protein	<i>O. sativa</i>
97	D7SLZ5	8	40/5.87	38.70/6.64	1	D/C/A	Whole genome shotgun sequence of line PN40024, scaffold_21.assembly12x	<i>V. vinifera</i>
120	C5YXT7	24	34/5.31	39.38/5.44	3	C/C/A	Putative uncharacterized protein	<i>S. bicolor</i>

Sb09g020230								
152	B9MWV9	31	23/5.74	10.34/5.82	1	D/A/A	Predicted protein	<i>P. trichocarpa</i>
187	A8HQM6	10	18/5.28	40.56/6.38	1	C/D/D	Predicted protein	<i>Chlamydomonas reinhardtii</i>
188	XP_002285837	10	17/5.55	22.24/8.89	1	C/D/D	Hypothetical protein	<i>V. vinifera</i>
192	B9FIU8	22	14/5.52	14.10/11.37	3	A/A/A	Putative uncharacterized protein	<i>O. sativa</i>
194	B9FIU8	40	15/6.62	15.66/8.05	3	B/B/C	Putative uncharacterized protein	<i>O. sativa</i>
202	Q6ZHC0	35	30/5.97	39.80/5.92	3	D/B/A	Putative GAMM1 protein	<i>O. sativa</i>
206	Q5SN58	21	23/4.89	15.81/5.27	2	A/A/A	Os01g0664500 protein	<i>O. sativa</i>

^a Spot number in 2-DE gel image as shown in Figure 7;

^b Accession number of UniPort or NCBI database;

^c Sequence coverage (%);

^d M_r (in kDa) and pI are averages of three 2-DE replicates gels;

^e M_r (in kDa) and pI were calculated with a tool available at http://www.expasy.ch/tools/pi_tool.html;

^f Number of matched peptides;

^g The kinetic trend represent the changes of protein abundance in four developmental stages (G1, G4, G7 and G9).

B, M and T represent basal, middle and terminal internode, respectively. U, D, S and - indicate increase, decrease, increased first and decreased afterwards and no signal, respectively;

^h The spots whose significant difference in abundance only appeared among different developing internodes in the same developmental stage were defined as internode-specific differential proteins;

ⁱ The spots whose significant difference in abundance appeared at both among different developmental internodes and among different developmental stages were defined as internode- and stage- dependent proteins.