

Table S1 - The protein spots identified by MALDI-TOF-MS.

Protein no.	Protein name	Accession no.	MOWSE score	NMP ^a	SC ^b	Theoretical Mr (kDa) and pI	Function ^c
1	elongation factor 2	NP_001052057	222	27	39%	94.94/5.85	8
2	elongation factor 2	NP_001046972	71	12	19%	94.99/5.85	8
3	pullulanase	ACY56106	76	17	22%	103.02/5.58	1
4	hypothetical protein OsJ_13773	EEE60487	364	35	50%	100.41/5.58	1
5	hypothetical protein OsJ_13773	EEE60487	388	43	50%	100.41/5.58	1
6	hypothetical protein OsJ_13773	EEE60487	350	32	46%	100.41/5.58	1
7	hypothetical protein OsJ_13773	EEE60487	280	32	41%	100.41/5.58	1
8	hypothetical protein OsI_19920	EEC79204	236	25	36%	94.33/5.37	5
9	hypothetical protein OsI_19920	EEC79204	170	23	33%	94.33/5.37	5
10	putative aconitate hydratase, cytoplasmic	Q6YZX6	214	23	35%	98.59/5.67	1
11	putative aconitate hydratase, cytoplasmic	Q6YZX6	272	33	47%	98.59/5.67	1
12	pyruvate orthophosphate dikinase	NP_001050430	276	30	47%	87.70/5.37	1
13	pyruvate orthophosphate dikinase	NP_001050430	116	16	23%	87.70/5.37	1
14	alcohol dehydrogenase 1	ABA92030	77	7	26%	38.14/6.19	2
15	hypothetical protein	BAD61634	65	5	36%	15.63/9.99	12
16	glycyl-tRNA synthetase	NP_001062369	95	11	22%	77.65/5.95	9
17	stress-induced-phosphoprotein 1	NP_001047563	66	7	21%	65.16/6.03	2
18	hypothetical protein OsJ_11969	EEE59627	65	4	26%	13.99/4.99	12
19	hypothetical protein	BAD20105	64	7	31%	30.32/11.81	12
20	OSJNBa0039C07.11	CAE05155	88	14	26%	75.38/5.83	3
21	phosphoglucomutase	NP_001051066	310	31	64%	63.14/5.4	4
22	heat shock cognate 70 kDa protein	ABF95267	247	28	47%	71.93/5.3	2
23	heat shock cognate 70 kDa protein	ABF95267	150	23	52%	71.93/5.3	2
24	endosperm lumenal binding protein	AAB63469	128	19	29%	73.67/5.3	3
25	endosperm lumenal binding protein	AAB63469	211	21	36%	73.67/5.3	3

26	endosperm lumenal binding protein	AAB63469	199	21	33%	73.67/5.3	3
27	hypothetical protein OsI_37938	EEC69073	184	19	37%	76.45/5.11	6
28	hypothetical protein OsI_37938	EEC69073	146	18	29%	76.45/5.11	6
29	protein disulfide-isomerase A1	NP_001045579	113	13	28%	62.44/4.76	6
30	Os10g0505900	NP_001065009	70	7	17%	45.55/4.74	2
31	Os10g0505900	NP_001065009	121	12	31%	45.55/4.74	2
32	Os10g0505900	NP_001065009	170	18	42%	45.55/4.74	2
33	Os10g0505900	NP_001065009	128	15	34%	45.55/4.74	2
34	alcohol dehydrogenase	NP_001067484	109	14	42%	41.70/6.2	1
35	succinate dehydrogenase (ubiquinone) flavoprotein subunit	NP_001058845	169	18	40%	69.49/6.61	4
36	aspartyl-tRNA synthetase	NP_001047770	165	17	35%	61.45/5.99	9
37	hypothetical protein OsJ_16432	EEE61811	166	16	40%	57.26/5.74	3
38	2-isopropylmalate synthase B	ABA91408	174	19	40%	68.86/6.46	1
39	putative β -N-acetylhexosaminidase	AAT77374	106	15	33%	59.01/5.71	1
40	2-isopropylmalate synthase	NP_001066116	151	17	35%	68.87/6.46	1
41	Os03g0214000	NP_001049368	156	15	36%	68.72/5.88	5
42	asparaginyl-tRNA synthetase	NP_001043066	199	23	40%	62.95/5.68	9
43	pyruvate decarboxylase 2	AAA90948	204	17	37%	65.34/5.9	3
44	hypothetical protein OsJ_07413	EAZ23710	70	8	19%	59.74/9.83	4
45	pyruvate decarboxylase	NP_001049811	210	17	40%	65.76/5.53	1
46	hypothetical protein OsI_04213	EEC71703	148	17	37%	60.95/5.36	5
47	heat shock 70kDa protein 1/8	NP_001044757	170	25	42%	71.31/5.1	2
48	putative globulin	AAS07324	124	14	30%	63.85/8.35	2
49	Os02g0250600	NP_001046445	64	9	22%	47.34/6.4	12
50	hypothetical protein OsI_30268	EAZ08004	118	17	34%	64.24/6.59	5
51	pyrophosphate-fructose-6-phosphate 1-phosphotransferase	NP_001057284	233	23	52%	61.91/6.01	1
52	pyrophosphate-fructose-6-phosphate 2-phosphotransferase	NP_001057284	238	24	55%	61.91/6.01	1
53	ketol-acid reductoisomerase	NP_001043738	103	10	31%	59.99/5.73	1
54	Chain A, ketol-acid reductoisomerase	3FR7_A	159	17	45%	57.57/5.46	3

55	enolase	ABB46862	79	8	26%	51.89/5.72	3
56	UTP-glucose-1-phosphate uridylyltransferase	NP_001063879	197	15	52%	51.82/5.43	1
57	Chain A, ketol-acid reductoisomerase	3FR7_A	110	12	34%	57.57/5.46	3
58	fructose-bisphosphate aldolase, class I	NP_001045130	92	9	33%	39.14/8.35	4
59	chaperonin GroEL	NP_001064784	112	13	32%	61.10/5.71	3
60	glucose-6-phosphate isomerase	NP_001063415	101	15	27%	68.84/5.71	4
61	Os06g0114000	NP_001056601	168	17	37%	64.33/5.6	3
62	60 kDa chaperonin α subunit	AAP44754	281	23	59%	61.48/5.36	3
63	60 kDa chaperonin α subunit	AAP44754	75	23	27%	61.48/5.36	3
64	protein disulfide isomerase	BAA92322	76	10	34%	33.50/4.81	6
65	protein disulfide isomerase	BAA92322	197	17	59%	33.50/4.81	6
66	granule-bound starch synthase 1	AEB52353	79	7	26%	45.35/6.14	4
67	granule-bound starch synthase 1	AEB52353	185	19	59%	45.35/6.14	4
68	UDP glucose 6-dehydrogenase	NP_00105132	184	21	57%	53.44/5.79	4
69	ATP synthase F0 subunit 1	YP_002000594	234	26	57%	55.62/5.85	10
70	hypothetical protein OsI_38072	EAY82861	80	10	35%	32.83/8.61	5
71	ATP synthase F0 subunit 1	YP_002000594	207	24	49%	55.62/5.85	10
72	putative selenium binding protein	BAB40923	139	17	51%	51.33/5.73	3
73	prolyl aminopeptidase 2	Q6K669	128	19	38%	62.18/8.29	6
74	inositol-3-phosphate synthase	ABF94421	76	9	35%	44.41/5.38	2
75	glucose-1-phosphate adenylyltransferase large chain	BAD68891	165	16	34%	57.74/5.48	1
76	hypothetical protein OsI_10505	EAY89022	104	11	29%	58.83/5.5	6
77	glucose-6-phosphate isomerase	BAD08451	196	23	43%	68.77/5.88	1
78	alanine transaminase	NP_001064504	258	28	52%	53.13/6.23	4
79	alanine transaminase	NP_001064504	217	20	46%	53.13/6.23	4
80	glutathione reductase (NADPH)	NP_001048485	118	15	41%	53.87/6.24	1
81	putative inosine monophosphate dehydrogenase	AAK09225	115	13	39%	52.85/6.03	1
82	Os03g0793700	NP_001051533	200	19	38%	52.44/6.78	2
83	alanine transaminase	NP_001064504	112	12	30%	53.13/6.23	4

84	alanine transaminase	NP_001064504	80	11	19%	53.13/6.23	4
85	aldehyde dehydrogenase (NAD ⁺)	NP_001057358	126	16	37%	59.61/6.33	1
86	glucose-1-phosphate adenylyltransferase	NP_001061603	86	9	28%	53.20/5.87	1
87	aldehyde dehydrogenase (NAD ⁺)	NP_001057358	95	14	26%	59.61/6.33	1
88	glucose-1-phosphate adenylyltransferase	NP_001061603	102	11	33%	53.20/5.87	1
89	retrotransposon protein	ABA92141	71	17	11%	218.17/8.75	3
90	wheat adenosylhomocysteinase-like protein	AAO72664	133	16	39%	53.86/5.62	3
91	hypothetical protein OsI_25188	EEC81650	261	24	56%	57.60/5.98	3
92	2-phospho-D-glycerate hydroylase	AAN04181	109	9	28%	46.20/5.16	3
93	hypothetical protein OsI_25188	EEC81650	161	18	39%	57.60/5.98	3
94	enolase	AAC49173	116	15	34%	48.30/5.42	4
95	enolase	NP_001049556	179	20	58%	48.29/5.32	4
96	2-phosphoglycerate dehydratase	Q42971	214	24	63%	48.29/5.41	4
97	UTP-glucose-1-phosphate uridylyltransferase	NP_001063879	195	19	58%	51.82/5.43	1
98	F-type H ⁺ -transporting ATPase subunit β	NP_001043900	230	20	49%	59.60/6.1	4
99	F-type H ⁺ -transporting ATPase subunit β	NP_001056261	193	17	45%	59.01/5.95	4
100	F-type H ⁺ -transporting ATPase subunit β	NP_001056261	212	18	50%	59.01/5.95	4
101	V-type H ⁺ -transporting ATPase subunit β	NP_001057902	91	9	28%	54.14/5.07	4
102	hypothetical protein OsI_17385	EEC77995	95	12	24%	54.50/6.44	1
103	Cupin family protein	ABF94466	78	14	13%	74.70/6.02	2
104	6-phosphogluconate dehydrogenase	NP_001056586	77	21	42%	52.97/5.85	1
105	argininosuccinate synthase	NP_001066459	66	11	21%	52.50/6.59	1
106	putative aminoacylase	BAD10058	64	12	30%	49.86/5.88	1
107	argininosuccinate synthase	NP_001066459	100	10	24%	52.50/6.59	1
108	argininosuccinate synthase	NP_001066459	65	14	29%	52.50/6.59	1
109	OSJNBa0052P16.16	CAD39715	64	6	20%	48.00/6.64	12
110	glucose-1-phosphate adenylyltransferase	NP_001051184	68	15	37%	55.79/7.01	1
111	Os05g0418000	NP_001055566	64	9	28%	50.07/5.44	12
112	translation initiation factor 4A	NP_001045878	80	8	25%	47.39/5.43	8

113	hypothetical protein OsI_24355	EAZ02256	123	10	38%	48.64/5.23	8
114	amidase, hydantoinase/carbamoylase family protein	ABA99240	121	8	26%	51.80/5.41	6
115	eukaryotic initiation factor 4A	BAA02152	80	12	29%	47.19/5.29	8
116	glucose-1-phosphate adenylyltransferase	NP_001062808	106	8	24%	55.10/6.23	1
117	TPA_exp: transposase	DAA02079	66	9	18%	72.82/9.31	9
118	Os10g0188500	NP_001176052	146	4	34%	21.14/4.81	12
119	hypothetical protein OsI_27570	EEC82801	64	9	10%	131.01/8.46	7
120	hypothetical protein OsI_09330	EAY87910	86	16	38%	47.04/4.94	3
121	isocitrate dehydrogenase	NP_001043749	64	8	22%	46.36/6.34	4
122	alcohol dehydrogenase 1	ABA92030	64	10	22%	38.14/6.19	2
123	hypothetical protein OsI_18007	EEC78293	94	10	23%	59.89/5.58	5
124	L-idoitol 2-dehydrogenase	NP_001062412	70	9	33%	39.99/6.03	4
125	alcohol dehydrogenase 1	ABA92030	65	6	14%	38.14/6.19	2
126	L-idoitol 2-dehydrogenase	NP_001062412	98	16	55%	39.99/6.03	1
127	L-idoitol 3-dehydrogenase	NP_001062412	68	11	30%	39.99/6.03	1
128	L-idoitol 4-dehydrogenase	NP_001062412	113	17	55%	39.99/6.03	1
129	hypothetical protein OsJ_06802	EEE57026	90	5	25%	34.307/8.1	3
130	hypothetical protein OsI_05369	EAY77382	95	6	18%	45.69/5.74	3
131	tryptophanyl-tRNA synthetase	NP_001066951	83	13	37%	46.53/5.62	9
132	guanine nucleotide-exchange protein GEP2	AAM00191	105	13	7%	199.20/5.49	7
133	Os02g0158900	NP_001045960	70	10	31%	44.69/5.47	12
134	Os04g0429200	NP_001173940	85	5	31%	15.49/6.89	12
135	hypothetical protein OsJ_11020	EAZ27089	66	4	60%	7.64/9.76	12
136	OSJNBb0050003.16	CAE01726	64	5	25%	36.58/5.37	3
137	monodehydroascorbate reductase	BAA77282	66	12	50%	43.04/5.36	2
138	actin	NP_001065830	68	13	45%	41.82/5.31	3
139	actin	NP_001054419	86	12	40%	41.90/5.23	3
140	retrotransposon protein	ABA95357	87	11	4%	319.63/8.44	1
141	3-isopropylmalate dehydrogenase	NP_001050807	85	10	29%	41.37/5.3	1

142	hypothetical protein OsI_13391	EAY91751	64	5	30%	14.96/9.58	12
143	glyceraldehyde 3-phosphate dehydrogenase	NP_001053139	65	14	48%	36.92/6.34	4
144	phosphoglycerate kinase	NP_001058317	64	9	31%	42.31/6.19	5
145	glyceraldehyde 3-phosphate dehydrogenase	NP_001053139	129	11	39%	36.92/6.34	1
146	Os04g0338000	NP_001052494	80	11	33%	38.50/6.03	1
147	RGP2 protein	CAA09470	99	9	26%	39.53/8.08	3
148	aspartate aminotransferase	NP_001048397	76	14	35%	50.55/8.16	1
149	L-idoitol 2-dehydrogenase	NP_001062412	93	11	29%	39.99/6.03	1
150	OrysaZxa	Q75H81	219	19	54%	42.11/5.75	12
151	L-idoitol 2-dehydrogenase	NP_001062412	66	18	59%	39.99/6.03	1
152	elongation factor Tu	NP_001051912	83	18	44%	48.56/6.04	8
153	aspartate-semialdehyde dehydrogenase	NP_001051347	111	8	32%	40.44/6.73	1
154	Os06g0215100	NP_001057134	70	7	29%	43.7/9.51	12
155	IAA-amino acid hydrolase	NP_001043347	138	13	41%	47.28/5.66	1
156	phosphoglycerate kinase	NP_001046020	69	14	47%	42.20/5.64	5
157	Os07g0120900	NP_001058784	66	8	20%	58.43/8	12
158	Os04g0386600	NP_001052622	72	14	47%	41.64/5.66	1
159	reversibly glycosylated polypeptide	CAA77235	82	11	37%	41.86/5.82	3
160	succinyl-CoA synthetase β subunit	NP_001047463	119	8	21%	45.41/5.98	4
161	glucose-6-phosphate 1-epimerase	NP_001054126	177	11	51%	38.10/5.1	1
162	Os03g0843300	NP_001051862	66	7	28%	34.78/4.9	12
163	hypothetical protein OsI_32784	EAY77740	91	7	26%	36.60/5.27	1
164	Os03g0161100	NP_001049041	69	18	7%	317.24/4.96	7
165	glucose and ribitol dehydrogenase homolog	Q75KH3	64	11	31%	32.48/5.76	1
166	enoyl-[acyl-carrier protein] reductase I	NP_001061557	64	10	36%	39.28/8.81	1
167	malate dehydrogenase	NP_001064860	65	7	26%	35.89/5.75	4
168	malate dehydrogenase	NP_001064860	105	11	44%	35.89/5.75	4
169	Os05g0116000	NP_001054469	71	7	31%	38.46/5.81	12
170	Os02g0821001	NP_001173211	67	4	72%	8.81/10.25	12

171	guanine nucleotide-binding protein subunit β -2-like 1 protein	NP_001043910	77	6	27%	36.67/5.97	7
172	acyl-[acyl-carrier-protein] desaturase 2, chloroplastic	Q8S059	66	14	39%	45.08/6.39	1
173	malate dehydrogenase	NP_001064860	65	8	33%	35.89/5.75	4
174	Os03g0793700	NP_001051533	67	13	31%	52.44/6.78	2
175	guanine nucleotide-binding protein subunit β -2-like 1 protein	NP_001043910	65	6	31%	36.67/5.97	7
176	hypothetical protein OsJ_12925	EAZ28885	110	9	23%	49.98/7.74	2
177	hypothetical protein OsJ_12925	EAZ28885	76	7	21%	49.98/7.74	2
178	globulin-like protein	AAM33459	64	9	18%	52.38/6.78	2
179	Os03g0793700	NP_001051533	64	15	35%	52.44/6.78	2
180	hypothetical protein OsJ_12925	EAZ28885	66	10	26%	49.98/7.74	2
181	Os03g0327600	NP_001049995	64	10	39%	39.25/6.3	12
182	globulin-like protein	AAM33459	66	7	23%	52.38/6.78	2
183	Os03g0327600	NP_001049995	72	10	39%	39.25/6.3	12
184	hypothetical protein OsJ_06082	EEE56662	66	8	15%	53.83/9.14	6
185	Os01g0762500	NP_001044328	66	7	24%	56.78/9.09	6
186	Os03g0793700	NP_001051533	88	9	28%	52.47/6.78	2
187	Os11g0701100	NP_001068520	76	9	29%	31.86/6.12	1
188	translation initiation factor 3 subunit I	NP_001061508	121	8	26%	36.53/5.94	8
189	metal-dependent hydrolase-like protein	BAD15421	71	8	30%	29.60/6.19	1
190	receptor protein kinase-like	BAD73679	86	7	16%	70.30/7.1	5
191	hypothetical protein OsI_07904	EEC73520	69	10	16%	81.34/9.36	12
192	Os03g0663800	NP_001173574	96	10	35%	45.51/6.07	2
193	Os03g0663800	NP_001173574	66	10	35%	45.51/6.07	2
194	Os03g0663800	NP_001173574	161	9	30%	45.51/6.07	2
195	unknown protein	AAN05517	107	7	41%	35.44/5.57	12
196	Os03g0663800	NP_001173574	67	10	35%	45.51/6.07	2
197	Os03g0663800	NP_001173574	72	10	35%	45.51/6.07	2
198	lactoylglutathione lyase	NP_001061172	64	9	39%	32.88/5.51	1
199	Os03g0663800	NP_001173574	103	8	31%	45.51/6.07	2

200	enoyl-[acyl-carrier protein] reductase I	NP_001061557	73	9	34%	39.28/8.81	1
201	unnamed protein product	BAH00330	65	5	44%	20.73/6.18	1
202	hypothetical protein OsJ_13801	EAZ29742	67	12	37%	54.48/9.06	2
203	putative glucanase	BAB85436	181	12	42%	34.23/5.35	4
204	lactoylglutathione lyase	NP_001061172	83	12	46%	32.88/5.51	1
205	hypothetical protein	AAT44171	182	6	52%	16.21/10.35	12
206	hypothetical protein OsI_11164	EEC75053	134	5	33%	31.78/5.11	1
207	hypothetical protein OsI_11164	EEC75053	81	9	31%	31.78/5.11	1
208	α -soluble NSF attachment protein	NP_001061446	64	5	20%	32.75/5.04	3
209	Os06g0341300	NP_001057565	64	10	48%	27.91/4.19	12
210	Os12g0626500	NP_001067326	156	8	41%	19.89/4.57	12
211	Os03g0663800	NP_001173574	120	9	33%	45.51/6.07	2
212	Os02g0580300	NP_001047234	68	14	54%	29.85/4.71	3
213	14-3-3-like protein gf14-6	ABR25721	87	5	58%	16.42/4.57	3
214	Os04g0462500	NP_001053003	64	8	37%	29.96/4.76	3
215	Os08g0430500	NP_001061856	118	5	30%	28.98/4.78	3
216	Os11g0546900	NP_001068067	109	13	56%	29.36/4.83	3
217	Os08g0480800	NP_001062060	68	13	48%	29.10/4.85	3
218	Os04g0404400	NP_001052704	219	12	48%	31.33/4.9	12
219	hypothetical protein	BAD16983	161	4	72%	10.94/8.53	12
220	OSJNBb0014D23.1	CAE05267	154	6	12%	74.92/5.76	12
221	Os03g0663800	NP_001173574	75	9	33%	45.51/6.07	2
222	hydroxyacylglutathione hydrolase	NP_001050016	71	9	46%	29.00/5.43	1
223	inorganic pyrophosphatase	NP_001054331	150	10	50%	24.29/5.59	1
224	Os07g0170200	NP_001058990	75	6	21%	31.09/9.6	7
225	Os05g0569500	NP_001056364	124	10	35%	26.74/5.58	12
226	Cupin family protein, expressed	ABF95817	103	13	26%	61.74/7.18	2
227	hypothetical protein OsJ_12925	EAZ28885	68	7	19%	49.98/7.74	2
228	globulin-like protein	AAM33459	120	9	21%	52.38/6.78	2

229	hypothetical protein OsJ_25289	EEE67666	80	10	7%	213.77/4.93	12
230	hypothetical protein OsJ_19146	EEE64309	65	7	21%	30.55/6.66	1
231	Cupin family protein	ABF95817	87	15	30%	61.74/7.18	2
232	hypothetical protein	BAD81742	99	5	46%	18.85/9.00	12
233	thioredoxin peroxidase A	P0C5C8	89	6	31%	24.23/5.97	1
234	hypothetical protein OsI_26825	EAZ04671	67	5	40%	23.72/5.78	2
235	protein of unknown function DUF1264 family protein	NP_001044131	66	13	60%	27.72/5.98	3
236	retrotransposon protein, putative, Ty3-gypsy subclass	ABB47110	103	10	10%	151.89/7.91	7
237	Os03g0277500	NP_001049720	65	8	66%	15.05/5.54	12
238	thioredoxin 1	NP_001051587	119	7	52%	14.90/5.67	3
239	20S proteasome subunit β 6	NP_001063603	141	8	39%	24.61/6.43	3
240	Os03g0822200	NP_001051733	82	11	52%	27.95/6.34	1
241	Os11g0701100	NP_001068520	73	8	30%	31.86/6.12	1
242	Cupin family protein	ABF95817	70	10	21%	61.74/7.18	2
243	Os03g0659300	NP_001050818	94	5	50%	15.17/5.48	1
244	Os05g0116100	NP_001054470	67	7	46%	23.73/5.81	3
245	Os05g0542500	NP_001056195	66	10	36%	20.50/5.89	3
246	unnamed protein product	AAA72362	66	10	36%	20.26/6.6	12
247	unnamed protein product	AAA72362	65	10	35%	20.26/6.6	12
248	unnamed protein product	AAA72362	109	12	38%	20.26/6.6	12
249	Os09g0467200	NP_001063423	128	10	39%	25.34/5.5	3
250	triosephosphate isomerase (TIM)	NP_001042016	116	8	62%	27.27/5.38	4
251	20S proteasome subunit α 2	NP_001047516	112	10	48%	25.83/5.39	3
252	unnamed protein product	AAA72362	75	9	28%	20.26/6.6	12
253	hypothetical protein	BAD62040	92	4	46%	8.49/4.75	12
254	triosephosphate isomerase (TIM)	NP_001042016	66	7	35%	27.27/5.38	4
256	triosephosphate isomerase (TIM)	NP_001042016	105	8	44%	27.27/5.38	4
255	unknown protein	BAD53921	67	11	17%	70.92/8.08	12
257	triosephosphate isomerase (TIM)	NP_001063777	118	13	43%	32.715/6.96	4

258	putative chaperonin 21 precursor	BAD35232	64	13	69%	23.20/5.72	3
259	hypothetical protein	BAD19892	102	3	76%	7.02/9.4	12
260	glutathione S-transferase	NP_001059595	82	9	42%	26.04/5.01	1
261	Os03g0197300	NP_001049271	106	7	21%	68.53/5.52	2
262	Os03g0197300	NP_001049271	146	8	21%	68.53/5.52	2
263	Os03g0197300	NP_001049271	86	8	19%	68.53/5.52	2
264	Os03g0197300	NP_001049271	67	8	18%	68.53/5.52	2
265	Os01g0210500	NP_001042368	116	5	34%	23.75/4.73	3
266	hypothetical protein	BAD87149	111	4	47%	12.71/11.12	12
267	Os03g0197300	NP_001049271	175	6	18%	68.53/5.52	2
268	Os03g0197300	NP_001049271	67	6	18%	68.53/5.52	2
269	hypothetical protein OsI_19379	EEC78937	94	7	21%	53.68/5.55	1
270	hypothetical protein OsI_28286	EAZ06044	89	11	20%	38.65/5.85	3
271	Os05g0468800	NP_001055802	103	8	47%	18.23/5.71	1
272	Os10g0437500	NP_001064677	98	5	25%	19.16/5.61	12
273	Os08g0129200	NP_001060914	64	5	47%	19.02/6.28	3
274	Os03g0305600	NP_001049884	97	9	54%	18.42/6.42	2
275	Os07g0191700	NP_001059096	64	8	8%	129.06/8.84	12
276	α -amylase inhibitor	ACV41264	65	5	35%	15.89/6.51	2
277	hypothetical protein OsI_09038	EEC74046	147	6	21%	42.96/8.85	9
278	hypothetical protein OsI_01558	EEC70487	124	5	36%	17.91/6.41	12
279	hypothetical protein OsI_08519	EEC73809	79	6	22%	44.51/4.94	12
280	hypothetical protein OsJ_05706	EEE56482	80	11	15%	90.63/8.69	12
281	hypothetical protein OsI_11558	EEC75250	104	8	19%	55.96/5.48	1
282	hypothetical protein OsJ_33343	EEE51843	92	8	19%	61.38/6.98	5
283	regulator of ribonuclease activity	ABR25651	65	8	64%	18.28/5.61	9
284	Os01g0184100	NP_001042231	81	6	40%	18.13/5.61	2
285	Os01g0722800	NP_001044103	69	5	36%	18.34/5.35	12
286	Os05g0157200	NP_001054704	69	8	45%	18.16/5.22	2

287	hypothetical protein OsI_35528	EAY80356	64	5	56%	19.19/6.36	12
288	Os01g0225600	NP_001042461	88	6	52%	16.29/5	2
289	Os06g0363701	NP_001174783	64	10	11%	152.05/5.3	12
290	hypothetical protein OsI_19752	EEC79115	64	4	41%	17.41/6.49	1
291	hypothetical protein OsJ_13801	EAZ29742	70	7	20%	54.48/9.06	2
292	retrotransposon protein	ABA95630	68	6	27%	36.39/6.27	9
293	hypothetical protein OsI_21855	EEC80108	67	4	13%	15.02/5.85	1
294	hypothetical protein OsJ_09934	EEE58599	66	4	58%	11.23/10.32	12
295	hypothetical protein OsJ_30719	EEE50570	65	4	38%	15.26/5.08	1
296	OSJNBa0009K15.7	CAE05087	90	11	8%	195.33/8.62	11
297	hypothetical protein	AAL84309	64	7	22%	35.02/6.51	11
298	hypothetical protein	BAD05367	64	4	34%	12.67/7.85	12
299	Os06g0221300	NP_001057177	65	6	32%	18.45/6.18	3
300	transposon protein	AAK52138	68	7	35%	23.00/11.05	9
301	putative gypsy-type retrotransposon	AAL58269	74	8	7%	165.47/9.53	7
302	cofilin	NP_001051721	64	6	56%	16.05/5.72	3

^a Number of matched peptides.

^b Sequence coverage.

^c Functional categories of the proteins. The numbers indicate the protein function category: 1 - Metabolism, 2 - Disease/defense, 3 - Cell structure, 4 - Energy, 5 - Signal transduction, 6 - Protein destination and storage, 7 - Cell growth/division, 8 - Protein synthesis, 9 - Transcription, 10 - Transporters, 11 - Intracellular traffic and 12 - Unknown protein.