

Supplemental Table 1. Primer sequences of genes selected for qRT-PCR

protein ID ^a	Name	Sequence of primers
Os04t0501600-01	AT hook_ DNA_binding_ conserved site domain containing protein.	F: 5'-ACTCCACCCGATGAAGACAC-3' R: 5'-GGCCACCACACTTTGATTCT-3'
Os11t0303500-01	Nucleotide_binding_ alpha_beta plait domain containing protein.	F: 5'-TTGAAACAGTTGGTGCAAGC-3' R: 5'-AGCTCTACGCCCCACCTTAT-3'
Os02t0161200-01	Zinc finger_ CCCH_type domain containing protein.	F: 5'-TGAAGAAGCGAAAGCTGTGA-3' R: 5'-ACGGGAGAACCTTTGACCTT-3'
Os07t0557500-01	WRC domain containing protein.	F: 5'-GAGAAGCTGCCCAAGATGTC-3' R: 5'-GTCGCCACAACCACCTAACT-3'
Os01t0924900-01	GTP_binding signal recognition particle SRP54_ G_domain containing protein.	F: 5'-GAAAGGCAGACGAGAACCTG-3' R: 5'-TCCTTCTTTGTGGCTGCTCT-3'
Os01t0582400-01	Similar to Multidomain cyclophilin type peptidyl_prolyl cis_trans isomerase.	F: 5'-GGGTGATATCGAGGGGAAAT-3' R: 5'-TTGTCCTCTTGCTCCTTGGT-3'
Os01t0104800-01	Sas10/Utp3 family protein.	F: 5'-AGGCATCCAACCATCAAGTC-3' R: 5'-TCCAAAGGCTGCATTTTACC-3'
Os02t0728700-01	Ribosomal RNA_processing protein 7 domain containing protein.	F: 5'-TGCATGGGAATCAAGATGAA-3' R: 5'-TTGCTGCTTTTCCCTGATTT-3'
Os03t0733400-01	Zinc finger_ BED_type predicted domain containing protein	F: 5'- TGGTGGATGATGCTGTTCAT -3' R: 5'- GATTTTGTTGGCTGGCTTGT -3'

^aProtein ID is according to The Rice Annotation Project Database

Supplemental Table 2. Total proteins identified in rice embryos after 24 h of imbibition

No.	Protein ID ^a	Mass(Da)	M.P. ^b	Mol (%) ^c	Description	WoLFPSORT ^d	NucPre ^d	Function ^f
1	Os01t0147900-01	27274	89	1.95	Triosephosphate isomerase, cytosolic (EC 5.3.1.1)	cyto	0.03	PS
2	Os01t0905800-01	39141	236	1.36	Aldolase C-1.	cyto	0.05	PS
3	Os05t0140800-01	39249	114	1.28	Similar to Dormancy related protein (Fragment).	mito	0.3	misc
4	Os07t0638300-01	24198	99	1.26	Similar to 1-Cys peroxiredoxin.	cyto /nucl	0.03	redox
5	Os02t0268100-01	57229	222	1.25	Similar to Glutelin (Fragment).	vacu	0.39	development
6	Os04t0508300-01	11938	23	1.25	Glutaredoxin.	chlo	0.03	redox
7	Os02t0121300-01	18634	80	1.22	Cyclophilin 2.	cyto	0.01	cell
8	Os05t0445500-01	14419	23	1.20	Similar to Acidic ribosomal protein (Fragment).	chlo	0	protein
9	Os01t0762500-00	56782	308	1.10	Glutelin subunit mRNA.	chlo	0.44	development
10	Os10t0400200-01	56841	282	1.06	Glutelin type II precursor.	vacu	0.4	development
11	Os01t0675100-01	17337	21	1.00	Similar to peroxiredoxin.	cyto	0.01	redox
12	Os01t0276300-01	24470	21	0.96	Similar to Group 3 late embryogenesis abundant protein (Fragment).	mito	0.44	not assigned
13	Os03t0159600-01	27174	30	0.94	Similar to Rab28 protein.	cyto	0.02	not assigned
14	Os10t0563700-01	16769	23	0.91	Similar to Nucleoside diphosphate kinase I (EC 2.7.4.6)	cyto	0.02	nucleotide metabolism
15	Os06t0668200-01	42310	86	0.91	Similar to Phosphoglycerate kinase, cytosolic (EC 2.7.2.3).	chlo	0.01	PS
16	Os07t0214300-01	18423	25	0.89	Seed allergenic protein RAG2 precursor.	mito	0.04	stress
17	Os07t0219400-01	17062	23	0.88	Prolamin precursor.	chlo	0.24	not assigned
18	Os06t0625500-01	23788	32	0.87	Similar to Thioredoxin peroxidase.	chlo	0.05	redox
19	Os03t0327600-01	39254	85	0.85	Ricin B-related lectin domain containing protein.	cyto/nucl	0.01	not assigned
20	Os03t0793700-01	52436	408	0.83	RmlC-like jelly roll fold domain containing protein.	mito	0.38	development
21	Os08t0126300-01	36561	185	0.79	Similar to Glyceraldehyde-3-phosphate dehydrogenase (Fragment).	cyto	0.01	glycolysis
22	Os02t0601300-01	36716	241	0.79	Similar to Glyceraldehyde-3-phosphate dehydrogenase, cytosolic 3 (EC 1.2.1.12).	cyto	0	glycolysis
24	Os01t0191100-01	11714	9	0.76	Similar to Acidic ribosomal protein P2a-4 (Fragment).	chlo	0.01	protein

23	Os10t0167300-01	48226	85	0.76	Similar to Enolase 2 (EC 4.2.1.11)	chlo	0.04	glycolysis
25	Os02t0249800-01	56915	253	0.75	Glutelin precursor.	chlo/nucl	0.41	development
26	Os10t0542100-01	9457	5	0.75	Plant EC metallothionein-like protein, family 15 protein.	cyto	0.38	not assigned
27	Os03t0266300-01	17899	65	0.74	Class I low-molecular-weight heat shock protein 17.9.	cyto	0.03	stress
28	Os02t0169300-01	42196	48	0.74	Similar to Phosphoglycerate kinase, cytosolic (EC 2.7.2.3).	chlo	0.02	PS
29	Os09t0109600-01	7843	9	0.74	Conserved hypothetical protein.	chlo	0.09	not assigned
30	Os02t0699600-01	17820	13	0.72	Similar to 60S ribosomal protein L12.	cyto	0.03	protein
31	Os01t0705200-01	22119	22	0.72	Late embryogenesis abundant protein repeat containing protein.	nucl	0.22	not assigned
32	Os03t0424500-01	16434	26	0.72	Similar to 40S ribosomal protein S19-3.	cyto/nucl	0.18	protein
33	Os01t0686800-01	36665	46	0.70	Protein containing the WD-40 repeat, Innate immunity	cyto/nucl	0.01	development
34	Os03t0277300-01	71932	88	0.70	Heat shock protein 70.	cyto	0.28	stress
35	Os03t0427300-01	56550	118	0.70	Glutelin type-A III precursor.	chlo	0.37	development
36	Os02t0249600-01	56411	240	0.70	Similar to Glutelin.	chlo/nucl	0.43	development
37	Os12t0569200-01	17071	40	0.70	Conserved hypothetical protein.	extr	0.02	not assigned
38	Os05t0329100-01	16916	31	0.68	Prolamin.	chlo	0.26	not assigned
39	Os08t0191700-01	32875	50	0.68	Similar to Lactoylglutathione lyase (EC 4.4.1.5)	cyto	0.09	amino acid metabolism
40	Os01t0159600-01	10130	17	0.67	Small hydrophilic plant seed protein family protein.	nucl	0.36	not assigned
41	Os11t0199200-01	57047	65	0.66	Similar to Protein disulfide isomerase (Fragment).	E.R.	0	redox
42	Os10t0505900-01	45554	43	0.65	Conserved hypothetical protein.	nucl	0.12	not assigned
43	Os01t0124401-01	29253	103	0.65	Similar to Bowman-Birk type bran trypsin inhibitor.	extr	0.2	not assigned
44	Os05t0116100-01	23726	35	0.65	Dehydroascorbate reductase.	chlo	0.3	redox
45	Os03t0336100-01	36974	149	0.64	11-S plant seed storage protein family protein.	chlo	0.3	development
46	Os03t0277500-01	17773	16	0.63	Similar to Glyoxalase family protein, expressed.	nucl	0.13	Biodegradation of Xenobiotics
47	Os02t0814700-01	16392	17	0.63	Similar to Ribosomal Pr 117 (Fragment).	cyto	0.1	protein
48	Os05t0490100-01	12581	7	0.63	Similar to 60S ribosomal protein L30.	nucl	0.04	protein

50	Os03t0577000-01	25590	30	0.62	Similar to Ribosomal protein S3 (Fragment).	cyto	0.21	protein
49	Os05t0553000-02	59012	71	0.62	ATP synthase beta chain, mitochondrial precursor (EC 3.6.3.14).	mito	0.06	mitochondrial electron transport
51	Os05t0468800-01	18234	19	0.61	Phosphatidylethanolamine-binding protein PEBP domain containing protein.	cyto	0.02	not assigned
52	Os11t0210300-01	41699	133	0.60	Alcohol dehydrogenase 1.	cyto	0	misc
53	Os06t0341300-01	27905	30	0.59	Seed maturation protein domain containing protein.	cyto	0.12	development
54	Os10t0478200-01	35888	29	0.59	Cytoplasmic malate dehydrogenase.	cyto	0.08	TCA
55	Os02t0549600-01	20307	36	0.59	Similar to 40S ribosomal protein S10-1.	nucl	0.19	protein
56	Os01t0749000-01	28266	18	0.58	Protein of unknown function DUF1264 family protein.	cyto	0.1	not assigned
57	Os05t0542500-02	20502	28	0.58	LEA-like protein.	nucl	0.2	not assigned
58	Os08t0129200-02	19024	20	0.57	Similar to Cold shock protein-1.	mito /nucl	0.08	stress
59	Os03t0248600-01	48285	71	0.56	Similar to Enolase 2 (EC 4.2.1.11)	chlo	0.04	glycolysis
60	Os02t0250600-01	47344	46	0.55	Late embryogenesis abundant protein repeat containing protein.	nucl	0.23	not assigned
61	Os01t0835900-00	11402	17	0.55	Similar to Histone H4.	nucl	0.32	DNA
62	Os03t0712700-01	63138	41	0.54	Similar to Phosphoglucomutase, cytoplasmic 2 (EC 5.4.2.2)	cyto	0.03	not assigned
63	Os03t0200500-01	29880	28	0.53	40S ribosomal protein S3a (CYC07 protein).	cyto/nucl	0.4	protein
64	Os02t0162500-01	16410	11	0.53	Similar to 40S ribosomal protein S14.	cyto/nucl	0.3	protein
65	Os04t0486600-01	36921	170	0.53	Similar to Glyceraldehyde-3-phosphate dehydrogenase, cytosolic 3 (EC 1.2.1.12).	cyto	0.01	glycolysis
66	Os11t0115400-00	11766	26	0.52	Lipid transfer protein LPT IV.	extr	0.05	not assigned
67	Os01t0136100-01	16929	61	0.52	16.9 kDa class I heat shock protein 1.	cyto	0.07	stress
68	Os01t0136200-01	16947	59	0.52	16.9 kDa class I heat shock protein 1.	cyto	0.07	stress
69	Os07t0150200-01	15132	8	0.51	Similar to 40S ribosomal protein S12-1.	cyto	0.01	protein
70	Os07t0229900-01	15112	10	0.51	Ribosomal protein S12e domain containing protein.	chlo	0.02	protein
71	Os09t0553200-01	51821	38	0.51	Similar to UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9)	cyto	0	not assigned
72	Os04t0546500-01	15190	18	0.51	Similar to Oleosin.	nucl	0.01	lipid metabolism
73	Os05t0574400-01	35642	40	0.48	Similar to Malate dehydrogenase.	mito	0.12	TCA

74	Os08t0104400-01	10597	4	0.47	Conserved hypothetical protein.	chlo	0.07	not assigned
75	Os05t0499100-01	21497	30	0.47	26 kDa globulin (Alpha-globulin).	extr	0.45	not assigned
76	Os01t0728700-01	27724	27	0.45	Protein of unknown function DUF1264 family protein.	chlo	0.07	not assigned
77	Os01t0840100-01	71306	65	0.45	Heat shock protein Hsp70 family protein.	cyto	0.19	stress
78	Os03t0360700-01	15005	8	0.44	Similar to Protein-methionine-S-oxide reductase, PilB family.	chlo	0	RNA
79	Os01t0348900-01	15163	6	0.44	SalT gene product (Salt-induced protein).	cyto	0.01	misc
80	Os03t0177400-01	49604	62	0.44	EF-1 alpha.	cyto	0.06	protein
81	Os05t0323900-01	24982	13	0.43	Manganese-superoxide dismutase precursor (EC 1.15.1.1).	mito	0.03	redox
82	Os03t0663800-01	28776	105	0.43	Globulin 1 (Fragment).	vacu	0.63	development
83	Os12t0626500-00	21879	27	0.41	Similar to late embryogenesis abundant protein D-34.	cyto	0.08	not assigned
84	Os03t0343500-01	14520	7	0.40	Similar to 60S ribosomal protein L22-2.	cyto	0.06	protein
85	Os01t0328400-01	17885	26	0.40	Ubiquitin.	nucl	0.51	protein
86	Os07t0215500-01	17838	12	0.40	Allergenic protein.	extr	0.03	stress
88	Os01t0231700-01	11926	11	0.40	Similar to 60S acidic ribosomal protein P2-B (CaRP2B).	nucl	0.01	protein
87	Os12t0569300-01	23985	31	0.40	Thaumatococcus, pathogenesis-related family protein.	chlo	0.02	not assigned
89	Os02t0591700-01	24243	16	0.40	Similar to Candida glabrata strain CBS138 chromosome L complete sequence.	nucl	0.04	protein
90	Os02t0115900-01	73573	54	0.39	Endosperm lumenal binding protein.	E.R.	0.09	stress
91	Os02t0453600-01	28808	39	0.39	Similar to Glutelin.	chlo	0.48	development
92	Os03t0245800-02	26705	20	0.39	Similar to Heat shock protein 26.	chlo	0.2	stress
93	Os03t0305600-01	18416	10	0.39	Mitochondrial import inner membrane translocase, subunit Tim17/22 family protein.	chlo	0.21	protein
94	Os08t0559200-01	12061	12	0.39	Similar to Ribosomal protein S25 (40S ribosomal 25S subunit).	nucl	0.52	protein
95	Os01t0649100-01	35667	26	0.38	Malate dehydrogenase.	mito	0.18	TCA
96	Os01t0210500-01	23753	17	0.37	Similar to SOUL-like protein.	chlo	0.03	tetrapyrrole synthesis
97	Os07t0216700-01	17036	13	0.37	Bifunctional trypsin/alpha-amylase inhibitor domain containing protein.	chlo	0.02	not assigned
98	Os01t0276000-01	12584	10	0.37	Similar to 60S ribosomal protein L30.	cyto	0.08	protein
99	Os12t0464400-01	39255	32	0.36	Similar to Oxidoreductase, short chain dehydrogenase/reductase family protein, expressed.	chlo	0.1	misc

100	Os02t0249000-01	55226	43	0.35	Glutelin, Seed strage protein	E.R.	0.37	development
101	Os08t0116500-01	11133	9	0.35	Similar to 60S acidic ribosomal protein P1 (L12).	chlo /nucl	0	protein
102	Os11t0453900-01	15543	7	0.35	Dehydrin RAB 16D.	nucl	0.34	not assigned
104	Os07t0213800-01	17829	8	0.35	Similar to Allergenic protein.	chlo	0.03	stress
103	Os08t0117200-00	17874	10	0.35	Similar to 40S ribosomal protein S13 (Fragment).	nucl	0.41	protein
105	Os01t0124200-02	29198	30	0.34	Similar to Bowman Birk trypsin inhibitor.	extr	0.21	not assigned
106	Os04t0173800-01	24718	23	0.34	Lectin precursor (Agglutinin).	chlo	0.22	stress
107	Os03t0723400-01	18044	6	0.34	Similar to UFG2.	chlo	0.38	not assigned
108	Os03t0821100-01	71666	62	0.33	Similar to Non-cell-autonomous heat shock cognate protein 70.	cyto	0.25	stress
109	Os03t0820500-01	16280	6	0.33	Similar to WCOR719.	chlo	0.01	cell
110	Os07t0180900-01	44825	37	0.32	Similar to 60S ribosomal protein L4.	cyto /nucl	0.41	protein
111	Os07t0516200-01	18863	6	0.32	Similar to Endoribonuclease, L-PSP family.	chlo	0.01	RNA
112	Os03t0197300-01	71138	142	0.32	Similar to Cupin family protein, expressed.	chlo/nucl	0.75	development
113	Os04t0510900-01	35414	43	0.32	Similar to Embryo-specific protein 1 (ATS1).	chlo	0.05	development
114	Os02t0804100-01	6927	3	0.31	Similar to predicted protein.	nucl	0.38	not assigned
116	Os01t0938900-01	22079	13	0.31	Similar to Nascent polypeptide-associated complex alpha subunit-like protein 3	nucl	0.31	protein
115	Os06t0152100-01	14352	8	0.31	Similar to Profilin-2.	cyto	0.01	cell
117	Os02t0478700-01	9864	5	0.31	Ribosomal protein S27.	nucl	0.27	not assigned
118	Os03t0659300-01	15165	7	0.31	Glyoxalase/bleomycin resistance protein/dioxygenase domain containing protein.	cyto	0.03	Biodegradation of Xenobiotics
119	Os03t0699000-01	17211	4	0.30	Oleosin 18 kDa (OSE721).	plas	0.2	not assigned
120	Os03t0807800-01	30185	30	0.30	Similar to 40S ribosomal protein S2 (Fragment).	cyto	0.04	protein
121	Os01t0916600-01	15537	5	0.30	RNA recognition motif, glycine rich protein domain containing protein.	mito	0.01	RNA
122	Os03t0168100-01	41835	37	0.28	Late embryogenesis abundant protein repeat containing protein.	extr	0.23	development
123	Os01t0760600-01	50074	22	0.28	Aspartate aminotransferase, cytoplasmic (EC 2.6.1.1)	chlo	0.16	amino acid metabolism
124	Os08t0130500-01	34470	20	0.28	60S acidic ribosomal protein P0.	cyto	0.07	protein

125	Os03t0780600-01	50417	42	0.28	Tubulin beta-1 chain (Beta-1 tubulin).	chlo	0.16	cell
126	Os01t0866600-01	7831	3	0.26	Similar to bolA-like protein.	cyto	0.05	RNA
127	Os12t0632000-01	16130	7	0.26	Similar to Glycine-rich RNA-binding protein 1 (Fragment).	nucl	0.17	RNA
128	Os06t0221300-01	18450	4	0.26	Similar to Dehydration stress-induced protein.	extr	0.02	not assigned
129	Os07t0246200-01	48450	19	0.25	Similar to Calreticulin (Fragment).	vacu	0.08	signaling
130	Os10t0411700-01	8184	4	0.25	Similar to S28 ribosomal protein (Fragment).	cyto	0.1	protein
131	Os07t0219250-00	16984	16	0.25	Similar to cDNA, clone: J090058L24, full insert sequence.	nucl	0.22	not assigned
132	Os03t0750000-01	8481	2	0.24	Similar to ethylene-responsive protein.	cyto	0.02	not assigned
133	Os09t0568900-01	8449	4	0.24	Similar to predicted protein.	nucl	0.04	not assigned
134	Os04t0445100-01	23271	14	0.24	Similar to 22.7 kDa class IV heat shock protein precursor.	extr	0.12	stress
135	Os03t0341100-01	21118	3	0.24	Similar to 60S ribosomal protein L18.	nucl	0.27	protein
136	Os01t0654400-01	8528	10	0.24	Similar to Salt tolerant correlative protein.	mito	0.15	not assigned
137	Os02t0478600-01	14866	10	0.24	Similar to 40S ribosomal protein S15A.	cyto/nucl	0.09	protein
138	Os01t0205500-01	20978	8	0.23	Similar to 60S ribosomal protein L11-2 (L16). Splice isoform 2.	cyto	0.28	protein
140	Os02t0530600-01	93542	30	0.23	Poly(ADP-ribose) polymerase, regulatory region domain containing protein.	cyto/nucl	0.21	protein
139	Os03t0819600-01	23992	5	0.23	Chalcone isomerase (EC 5.5.1.6).	cyto	0.54	not assigned
141	Os03t0758800-01	17762	15	0.23	Similar to Eukaryotic translation initiation factor 5A-2	cysk	0.01	protein
142	Os08t0327700-01	15154	5	0.23	Late embryogenesis abundant (LEA) group 1 family protein.	nucl	0.2	development
143	Os01t0303300-01	17908	6	0.23	Similar to Stress-inducible membrane pore protein.	mito	0.3	protein
144	Os02t0519900-01	94987	48	0.23	Similar to Elongation factor EF-2 (Fragment).	cyto/nucl	0.16	protein
145	Os01t0184100-01	18133	21	0.23	Similar to 17.5 kDa class II heat shock protein.	cyto/nucl	0.05	stress
146	Os03t0182600-03	12620	10	0.22	Similar to 40S ribosomal protein SA.	cyto	0.2	protein
147	Os05t0519700-01	101062	30	0.22	Heat shock protein 101.	cyto	0.42	stress
148	Os03t0130300-01	9207	7	0.22	Similar to Cp-thionin.	extr	0.07	not assigned
149	Os03t0154700-01	22716	16	0.21	Similar to 40S ribosomal protein S9.	nucl	0.37	protein
150	Os05t0569500-01	29290	20	0.21	Similar to Embryo-specific protein.	cyto	0.11	not assigned

151	Os11t0247300-01	50390	19	0.20	Alfa-tubulin.	cyto /nucl	0.13	cell
152	Os02t0242600-01	57190	66	0.20	Similar to Glutelin.	vacu	0.39	development
153	Os06t0701100-02	47343	15	0.20	Eukaryotic initiation factor 4A (eIF4A) (eIF-4A).	cyto	0.37	DNA
154	Os03t0756000-01	23829	4	0.20	Similar to 60S ribosomal protein L13a-4.	chlo	0.51	protein
155	Os07t0662500-01	23842	9	0.20	Similar to Elongation factor 1-beta' (EF-1-beta').	cyto /nucl	0.1	protein
156	Os02t0753300-01	20315	11	0.20	Lipoxygenase, LH2 domain containing protein.	chlo	0.01	not assigned
157	Os05t0349800-01	10159	9	0.19	Embryonic abundant protein 1.	nucl	0.39	not assigned
159	Os05t0155100-01	21355	4	0.19	Similar to 60S ribosomal protein L18.	nucl	0.35	protein
158	Os07t0574800-01	50250	27	0.19	Tubulin alpha-1 chain.	cyto	0.13	cell
160	Os05t0474600-01	35852	19	0.19	Similar to Aldose reductase-related protein (EC 1.1.1.21).	E.R.	0.79	development
161	Os03t0760800-01	10589	3	0.18	Similar to GAST1 protein precursor.	extr	0.2	hormone metabolism
162	Os03t0293500-02	65761	38	0.18	Similar to Pyruvate decarboxylase isozyme 3 (EC 4.1.1.1) (PDC) (Fragment).	cyto	0.01	fermentation
163	Os06t0247500-01	61907	13	0.18	Similar to Pyrophosphate-fructose 6-phosphate 1-phosphotransferase (EC 2.7.1.90) (Fragment).	chlo	0.08	not assigned
164	Os03t0151800-02	90429	22	0.18	Similar to Cell division control protein 48 homolog A (AtCDC48a).	cyto/nucl	0.57	cell
165	Os03t0351500-01	15356	5	0.17	Similar to Superoxide dismutase.	cyto	0.03	redox
166	Os09t0252100-01	41397	15	0.17	Similar to Acetyl-CoA C-acetyltransferase.	chlo	0.01	secondary metabolism
167	Os03t0157900-01	45302	14	0.17	Phosphoserine aminotransferase, chloroplast precursor (EC 2.6.1.52) (PSAT).	chlo	0.05	amino acid metabolism
168	Os09t0324000-02	15553	4	0.17	Similar to Oleosin.	chlo	0	not assigned
170	Os01t0270100-01	27252	3	0.17	Similar to Cysteine protease inhibitor.	chlo	0.06	protein
169	Os04t0390700-01	39866	18	0.17	Short-chain dehydrogenase/reductase SDR domain containing protein.	chlo	0.14	misc
171	Os05t0350500-01	43570	17	0.17	Peptidase M24, structural domain domain containing protein.	cyto	0.29	protein
172	Os01t0652600-01	59986	12	0.16	Similar to Ketol-acid reductoisomerase, chloroplast precursor (EC 1.1.1.86)	chlo	0.15	amino acid metabolism
173	Os03t0408300-00	16101	10	0.16	Similar to 60S ribosomal protein L27a-3.	nucl	0.14	protein
174	Os08t0189100-01	23811	93	0.16	Similar to Germin-like protein precursor.	extr	0	stress
175	Os04t0402100-01	60920	21	0.16	Similar to Calnexin (Fragment).	plas	0.27	signaling

176	Os11t0116000-01	11889	6	0.16	Similar to Nonspecific lipid-transfer protein 1 (LTP 1) (Major allergen Pru d 3).	extr	0.02	lipid metabolism
177	Os03t0322900-00	36997	19	0.16	Late embryogenesis abundant protein repeat containing protein.	chlo	0.35	development
180	Os05t0501700-01	28532	8	0.16	Rossmann-like alpha/beta/alpha sandwich fold domain containing protein.	chlo	0.21	stress
179	Os10t0411800-01	16419	5	0.16	Similar to 40S ribosomal protein S17-3.	cyto /nucl	0.39	protein
178	Os11t0582400-01	49179	36	0.16	Similar to Embryo-specific protein.	extr	0.73	not assigned
181	Os02t0760300-01	12192	3	0.16	Similar to Immunophilin.	chlo	0	protein
182	Os01t0267900-01	16878	2	0.15	Similar to Calmodulin NtCaM3	cyto	0.03	signaling
183	Os03t0718100-01	42014	16	0.15	Actin 1.	cysk	0.05	cell
184	Os06t0133000-01	67004	18	0.15	Granule-bound starch synthase I, chloroplast precursor (EC 2.4.1.21).	chlo	0.05	major CHO metabolism
185	Os02t0489400-01	24928	11	0.15	Similar to 40S ribosomal protein S8.	chlo	0.69	protein
186	Os05t0169100-01	25112	8	0.15	Similar to 60S ribosomal protein L10 (QM protein homolog).	chlo	0.16	protein
188	Os04t0526600-01	21689	9	0.15	Similar to Alpha-amylase/subtilisin inhibitor (RASI).	vacu	0.05	stress
187	Os06t0547400-01	34498	4	0.15	Similar to Peroxidase P7 (EC 1.11.1.7) (TP7).	chlo	0.26	misc
190	Os07t0214600-01	17542	4	0.15	Similar to Seed allergenic protein RA17 precursor.	cyto	0.07	stress
189	Os10t0483000-01	17624	3	0.15	Similar to Transcription factor homolog BTF3-like protein.	cyto	0.31	RNA
192	Os02t0785800-01	12821	3	0.15	Similar to Ribosomal protein L35A.	cyto	0.14	protein
191	Os05t0595400-01	26092	8	0.15	Similar to Nucleoside diphosphate kinase III (EC 2.7.4.6)	chlo	0.03	nucleotide metabolism
195	Os02t0100300-01	44180	10	0.14	Similar to HSP associated protein like.	nucl	0.49	redox
193	Os03t0757900-01	53435	8	0.14	Similar to UDP-glucose 6-dehydrogenase (EC 1.1.1.22)	extr	0.01	cell wall
194	Os05t0346300-01	22350	8	0.14	Similar to 40S ribosomal protein S7.	cyto/nucl	0.17	protein
196	Os07t0186000-02	13319	6	0.14	Similar to Thioredoxin h isoform 1.	cyto	0	redox
197	Os08t0156800-01	13669	4	0.14	Similar to 60S ribosomal protein L34.	cyto	0.75	protein
199	Os01t0851700-01	94867	17	0.13	Similar to Cytosolic starch phosphorylase (Fragment).	cyto	0.29	major CHO metabolism
198	Os12t0623900-01	84874	22	0.13	Similar to Ethylene-responsive methionine synthase (Fragment).	cyto	0.12	amino acid metabolism
201	Os02t0130000-01	13826	3	0.13	Similar to SWIb domain-containing protein (Fragment).	mito	0.09	RNA
200	Os03t0390000-02	28269	8	0.13	Similar to Ribosomal protein s6 RPS6-2.	nucl	0.88	protein

202	Os06t0134000-01	14151	6	0.13	Similar to 40S ribosomal protein S20.	cyto	0.01	protein
203	Os01t0743500-01	64629	18	0.13	Cytosolic NADP malic enzyme.	cyto	0.21	TCA
204	Os03t0842900-01	39287	5	0.13	Similar to Steroleosin-B.	chlo	0.06	misc
205	Os04t0574200-01	44679	7	0.13	FAS1 domain domain containing protein.	plas	0.32	cell wall
206	Os01t0611000-01	40112	14	0.13	Protein of unknown function DUF642 domain containing protein.	chlo	0.04	not assigned
208	Os01t0823300-00	15381	6	0.12	Similar to Ribosomal protein S26.	chlo	0.42	protein
209	Os02t0622300-00	15435	3	0.12	Ribosomal protein L14 family protein.	cyto	0.24	protein
207	Os11t0451700-00	31233	11	0.12	Similar to Dehydrin DHN1 (M3) (RAB-17 protein).	nucl	0.22	not assigned
210	Os03t0101600-01	36833	5	0.12	Similar to Oxidoreductase, zinc-binding dehydrogenase family protein, expressed.	chlo	0.05	misc
212	Os01t0834500-01	15765	11	0.12	Similar to 40S ribosomal protein S23 (S12).	cyto	0.23	not assigned
213	Os04t0394200-01	48310	5	0.12	Similar to 2-oxoglutarate dehydrogenase E2 subunit.	mito	0.45	TCA
211	Os12t0478200-02	15693	10	0.12	GRAM domain containing protein.	nucl	0.22	hormone metabolism
214	Os05t0268500-01	54131	17	0.11	Similar to Serine carboxypeptidase 2.	chlo	0.05	protein
215	Os06t0167600-01	27180	3	0.11	Similar to Proteasome subunit alpha-3 (Fragment).	chlo	0.15	protein
217	Os02t0257200-01	32543	7	0.11	Conserved hypothetical protein.	plas	0.08	not assigned
219	Os03t0735300-01	32498	6	0.11	Alba, DNA/RNA-binding protein family protein.	nucl	0.25	RNA
220	Os04t0404400-01	32258	9	0.11	Similar to H0502B11.4 protein.	extr	0	stress
216	Os05t0469600-01	66083	22	0.11	Similar to Pyruvate decarboxylase (Fragment).	chlo	0.01	fermentation
218	Os11t0149200-00	15846	2	0.11	Conserved hypothetical protein.	cyto	0.01	not assigned
221	Os01t0783500-01	27781	5	0.11	Rossmann-like alpha/beta/alpha sandwich fold domain containing protein.	chlo	0.14	stress
223	Os08t0545200-01	39990	6	0.11	Alcohol dehydrogenase superfamily, zinc-containing protein.	cyto	0.01	misc
222	Os09t0501850-01	16394	2	0.11	Similar to FK506-binding protein 2-1 precursor (EC 5.2.1.8)	extr	0.09	cell
224	Os04t0605900-01	28401	11	0.11	Similar to 60S ribosomal protein L7-2.	cyto	0.53	not assigned
225	Os06t0727200-01	57064	9	0.11	Catalase isozyme B (EC 1.11.1.6) (CAT-B).	pero	0.13	redox
226	Os11t0455800-01	51812	4	0.11	Similar to Serine hydroxymethyltransferase.	cysk	0.01	C1-metabolism
230	Os01t0348700-01	17040	6	0.11	Similar to 60S ribosomal protein L23a (L25).	cyto	0.36	protein

232	Os01t0598600-01	51795	6	0.11	Peptidase A1 domain containing protein.	chlo	0.15	RNA
231	Os05t0156300-01	40429	7	0.11	Similar to protein disulfide isomerase.	chlo	0.12	redox
228	Os05t0584200-01	16706	4	0.11	Similar to Late embryogenesis abundant protein Lea14-A.	nucl	0.01	development
229	Os07t0492000-01	16851	2	0.11	Nucleoside diphosphate kinase I (EC 2.7.4.6)	cyto	0.01	nucleotide metabolism
227	Os10t0390500-01	34639	3	0.11	Similar to Alanine aminotransferase.	cyto	0.09	amino acid metabolism
233	Os07t0188800-01	57666	6	0.11	Similar to Methylmalonate-semialdehyde dehydrogenase (EC 1.2.1.27).	chlo	0.02	amino acid metabolism
234	Os05t0589600-01	41004	7	0.10	Similar to Nuclear RNA binding protein B (Fragment).	nucl	0.45	RNA
236	Os03t0807700-01	41248	7	0.10	Protein of unknown function DUF642 domain containing protein.	chlo	0.01	not assigned
240	Os03t0851000-01	17275	3	0.10	Similar to Transcription factor homolog BTF3-like protein.	cyto	0.31	RNA
235	Os05t0438800-01	41866	5	0.10	Similar to Actin 1.	cysk	0.01	cell
237	Os06t0507200-01	17405	2	0.10	Bifunctional inhibitor/plant lipid transfer protein/seed storage domain containing protein.	chlo	0.28	not assigned
238	Os09t0278000-00	17324	2	0.10	Hypothetical conserved gene.	cyto	0.06	not assigned
239	Os11t0454300-01	17315	20	0.10	Similar to Water-stress inducible protein RAB21.	nucl	0.25	not assigned
241	Os02t0196800-01	47645	7	0.10	Similar to Fumarylacetoacetase (Fragment).	cyto	0.07	amino acid metabolism
242	Os01t0531500-01	30505	5	0.10	Dienelactone hydrolase domain containing protein.	chlo	0.14	misc
243	Os06t0675700-01	96503	24	0.10	Similar to High pI alpha-glucosidase.	chlo	0.1	misc
246	Os03t0794700-01	17709	6	0.10	Similar to 40S ribosomal protein S18.	cyto	0.24	protein
247	Os04t0613600-00	18053	9	0.10	Similar to 40S ribosomal protein S11.	cyto/nucl	0.09	protein
248	Os05t0157200-01	18163	2	0.10	UspA domain containing protein.	cyto	0.01	stress
244	Os05t0576700-01	18145	2	0.10	Oleosin family protein.	plas	0.04	lipid metabolism
245	Os07t0206500-00	17923	4	0.10	13 kDa prolamin precursor.	extr	0.25	not assigned
249	Os09t0505600-01	24608	3	0.10	Proteasome subunit beta type 1 (EC 3.4.25.1)	chlo	0.09	protein
251	Os01t0860300-01	24837	4	0.10	Similar to Ribosomal protein L1.	cyto	0.16	protein
250	Os02t0797500-01	50547	7	0.10	Similar to Plastidic aspartate aminotransferase.	chlo	0.03	amino acid metabolism
252	Os12t0502200-01	25086	4	0.10	Similar to Low temperature-responsive RNA-binding protein.	nucl	0.22	RNA
253	Os06t0662000-01	68711	5	0.10	Similar to Vacuolar H ⁺ -ATPase subunit A (Fragment).	chlo	0.07	transport

255	Os01t0702500-01	19331	8	0.09	Similar to Dehydrin Rab25.	nucl	0.34	stress
254	Os03t0296400-01	38496	7	0.09	Similar to Eukaryotic translation initiation factor 2 subunit 1	cyto	0.25	protein
256	Os01t0172400-01	85659	14	0.09	Similar to Phospholipase D alpha 1.	chlo	0.25	lipid metabolism
257	Os03t0113700-01	72806	10	0.09	Similar to Heat shock 70 kDa protein, mitochondrial precursor.	mito	0.25	stress
263	Os01t0300200-01	66541	6	0.09	Similar to ATP-citrate lyase subunit B.	chlo	0.11	TCA
258	Os01t0542000-00	33660	4	0.09	Similar to DNA-damage-repair/toleration protein DRT102.	cyto	0.01	DNA
259	Os01t0817700-01	60980	6	0.09	Similar to 2,3-bisphosphoglycerate-independent phosphoglycerate mutase (EC 5.4.2.1)	cyto	0.03	not assigned
260	Os08t0338700-01	33755	4	0.09	Similar to Chaperone GrpE type 2.	chlo	0.63	protein
262	Os11t0579800-01	20050	2	0.09	Gar1 protein RNA-binding region family protein.	nucl	0.15	RNA
261	Os12t0207600-00	53704	10	0.09	Similar to ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit.	cyto	0.16	protein
264	Os03t0189600-01	41305	3	0.09	Similar to Alcohol dehydrogenase.	cyto	0	misc
266	Os05t0302700-01	41122	9	0.09	Similar to ATP/ADP carrier protein.	chlo	0.14	transport
265	Os06t0232000-01	41752	6	0.09	Similar to Pro-resilin.	nucl	0.6	not assigned
267	Os07t0568700-02	36012	8	0.09	Polygalacturonase inhibitor 1 precursor (Polygalacturonase-inhibiting protein) (Floral organ regulator 1).	chlo	0.25	cell wall
268	Os10t0177200-02	42732	3	0.09	EF-HAND 2 domain containing protein.	cyto	0.3	sitnallint
269	Os12t0145700-01	57862	8	0.08	Pyruvate kinase family protein.	cyto	0.04	lipid metabolism
270	Os12t0567700-01	28460	5	0.08	Similar to 60S ribosomal protein L2 (Fragment).	cyto	0.13	protein
273	Os01t0752300-01	21500	5	0.08	Similar to 60S ribosomal protein L18a-1.	nucl	0.38	protein
274	Os01t0829800-01	42046	12	0.08	Similar to Malate dehydrogenase precursor (EC 1.1.1.37).	chlo	0.03	TCA
272	Os03t0796000-02	21255	2	0.08	Similar to Ripening-associated protein (Fragment).	chlo	0	hormone metabolism
271	Os06t0264300-01	43107	3	0.08	Similar to RAD23, isoform I.	chlo	0.29	DNA
276	Os03t0212700-01	58829	10	0.08	Similar to Cytochrome C reductase-processing peptidase subunit I, MPP subunit I, P55.	mito	0.29	protein
277	Os09t0482100-01	80435	14	0.08	Similar to Heat shock protein 82.	nucl	0.53	stress
275	Os10t0548100-01	29200	2	0.08	Similar to DM280 protein.	chlo	0.06	not assigned
278	Os08t0345700-01	67910	11	0.08	Similar to Fructose-6-phosphate 1-phosphotransferase (Fragment).	cyto	0.12	not assigned

279	Os01t0328700-01	53009	10	0.08	FAD-dependent pyridine nucleotide-disulphide oxidoreductase domain containing protein.	chlo	0.13	TCA
280	Os04t0677500-01	55875	6	0.07	Pyruvate kinase (EC 2.7.1.40).	cyto	0.01	lipid metabolism
284	Os02t0774300-01	73081	7	0.07	Similar to Heat shock 70 kDa protein, mitochondrial precursor.	mito	0.29	stress
283	Os03t0695600-01	23634	4	0.07	Proteasome subunit beta type 2 (EC 3.4.25.1)	cyto	0.02	protein
281	Os06t0708500-01	24167	10	0.07	Similar to Peptidyl-prolyl cis-trans isomerase.	mito	0.05	cell
282	Os11t0104866-00	64410	8	0.07	Similar to Clathrin heavy chain.	cyto	0.3	not assigned
286	Os05t0304400-01	50074	6	0.07	Similar to GDP dissociation inhibitor protein OsGDI2.	cyto	0.14	signaling
285	Os07t0614500-01	24904	3	0.07	Similar to Elongation factor 1 beta 2.	cyto	0.05	protein
287	Os01t0896700-00	34773	14	0.07	Similar to 60S ribosomal protein L5.	mito	0.55	not assigned
290	Os02t0770000-01	26371	7	0.07	Beta 1 subunit of 20S proteasome.	cyto	0.02	protein
291	Os03t0146100-01	25740	2	0.07	Tonoplast intrinsic protein (Tonoplast water channel).	vacu	0	transport
289	Os06t0111500-01	52973	11	0.07	Cytosolic 6-phosphogluconate dehydrogenase.	chlo	0.03	OPP
288	Os07t0609000-01	26540	9	0.07	Stress responsive alpha-beta barrel domain containing protein.	chlo	0.03	not assigned
292	Os04t0650800-01	64153	3	0.06	Similar to Phosphoglycerate dehydrogenase.	mito	0.08	amino acid metabolism
293	Os05t0103200-01	26745	2	0.06	Cyclophilin-like domain containing protein.	chlo	0.04	cell
294	Os10t0492600-01	27496	7	0.06	Similar to Tonoplast membrane integral protein ZmTIP3-1.	mito	0.01	transport
295	Os09t0451500-02	47703	4	0.06	Thioredoxin domain 2 containing protein.	chlo	0.01	redox
296	Os02t0248800-01	56996	32	0.06	Similar to Glutelin type-B 2 precursor.	vacu	0.4	development
299	Os02t0537700-01	28307	5	0.06	Similar to 2-cys peroxiredoxin BAS1, chloroplast precursor (EC 1.11.1.15)	chlo	0.04	redox
300	Os03t0202200-01	29456	15	0.06	Porin-like protein.	cyto	0.01	transport
298	Os03t0851100-01	48564	19	0.06	Similar to Translational elongation factor EF-TuM.	mito	0.03	protein
297	Os04t0610600-01	28848	2	0.06	Similar to Cor14b protein precursor.	chlo	0.28	not assigned
301	Os09t0361400-01	29202	2	0.06	Outer mitochondrial membrane protein porin.	cyto	0.12	transport
303	Os02t0205200-01	39575	5	0.06	Similar to Unidentified precursor.	extr	0.09	not assigned
302	Os10t0155500-01	39620	4	0.06	Similar to Aldose 1-epimerase-like protein.	cyto	0.02	minor CHO metabolism
304	Os07t0410100-01	59248	10	0.06	Similar to Dihydrolipoamide S-acetyltransferase (EC 2.3.1.12).	mito	0.42	TCA

305	Os02t0187100-00	30010	4	0.06	Similar to cyclase.	plas	0	DNA
306	Os02t0669100-01	30904	2	0.06	Dehydrin family protein.	nucl	0.37	not assigned
307	Os04t0386700-01	29660	2	0.06	Similar to OSIGBa0148P16.6 protein.	plas	0.02	RNA
308	Os06t0486800-01	41543	5	0.06	Similar to Formate dehydrogenase, mitochondrial precursor (EC 1.2.1.2)	mito	0.01	C1-metabolism
309	Os12t0620400-01	31548	3	0.05	Methyl-CpG DNA binding domain containing protein.	nucl	0.57	RNA
310	Os01t0711000-01	54360	3	0.05	Similar to Vacuolar ATP synthase subunit B isoform 2 (EC 3.6.3.14)	cysk	0.14	mitochondrial electron transport
311	Os01t0937100-01	44500	5	0.05	Similar to Xylanase inhibitor precursor (Xylanase inhibitor TAXI-I).	chlo	0.18	protein
312	Os03t0340500-01	92501	5	0.05	Similar to Sucrose synthase (EC 2.4.1.13).	cyto	0.1	major CHO metabolism
314	Os04t0117900-01	45861	7	0.05	Amidase family protein.	cyto	0	protein
313	Os06t0726400-01	93747	3	0.05	Branching enzyme-I precursor (Starch-branching enzyme I)	chlo	0.17	major CHO metabolism
315	Os02t0817700-02	47370	3	0.05	Similar to 3-ketoacyl-CoA thiolase (Fragment).	chlo	0.05	amino acid metabolism
316	Os05t0155601-00	59100	8	0.05	Importin alpha-1b subunit.	nucl	0.64	protein
317	Os03t0143400-01	61292	7	0.05	Similar to mitochondrial chaperonin-60 [Oryza sativa (japonica cultivar-group)].	mito	0.06	protein
318	Os06t0538000-01	61316	3	0.05	Similar to T-complex protein 1, gamma subunit (TCP-1-gamma)	cyto	0.18	protein
319	Os09t0474300-01	75044	7	0.05	Similar to Heat-shock protein precursor.	chlo	0.49	stress
320	Os02t0575800-01	40366	2	0.04	Aldose-1-epimerase domain containing protein.	chlo	0.03	minor CHO metabolism
322	Os02t0735200-01	39405	4	0.04	Glutamine synthetase shoot isozyme (EC 6.3.1.2)	cyto	0.06	N-metabolism
325	Os02t0767500-01	39333	2	0.04	Mitochondrial phosphate transporter.	extr	0.03	transport
321	Os04t0390800-01	39547	7	0.04	NAD(P)-binding domain containing protein.	chlo	0.01	misc
324	Os06t0716700-02	93044	4	0.04	Similar to Heat shock protein 90.	vacu	0.44	stress
323	Os07t0622000-01	38913	20	0.04	Serine/threonine-protein kinase SAPK2 (EC 2.7.1.37)	cysk	0.1	protein
328	Os01t0118000-01	42253	2	0.04	Similar to Fructose-bisphosphate aldolase (EC 4.1.2.13) (Fragment).	chlo	0.06	PS
326	Os02t0815500-01	41652	4	0.04	Alcohol dehydrogenase class III (EC 1.1.1.1)	extr	0.01	misc
327	Os03t0610650-01	42114	2	0.04	Similar to cDNA clone:002-125-A07, full insert sequence.	plas	0.18	not assigned
329	Os09t0115400-01	71870	2	0.04	Similar to Poly(A)-binding protein.	nucl	0.38	RNA

331	Os01t0180800-01	93904	6	0.04	Heat shock protein Hsp70 family protein.	cyto	0.24	stress
330	Os10t0470900-01	45593	4	0.04	Nucleotide-binding, alpha-beta plait domain containing protein.	nucl	0.19	RNA
332	Os04t0670200-01	50964	7	0.03	Similar to Oryzain beta chain precursor (EC 3.4.22.-).	extr	0.05	protein
333	Os07t0134800-01	69494	3	0.03	Similar to Succinate dehydrogenase [ubiquinone] flavoprotein subunit, (EC 1.3.5.1)	mito	0.1	TCA
334	Os02t0523500-01	108515	5	0.03	Similar to 110 kDa 4SNC-Tudor domain protein (Fragment).	chlo	0.3	RNA
337	Os08t0440800-01	53963	2	0.03	Glyceraldehyde-3-phosphate dehydrogenase.	cyto	0.01	PS
335	Os09t0440300-01	55208	3	0.03	Similar to Aldehyde dehydrogenase family 7 member A1 (EC 1.2.1.3)	chlo	0.07	fermentation
336	Os11t0525600-01	114599	4	0.03	Similar to Alpha-mannosidase.	chlo	0.22	misc
338	Os02t0274100-01	79038	8	0.03	Similar to Peroxisomal fatty acid beta-oxidation multifunctional protein (MFP).	plas	0.06	lipid metabolism
341	Os02t0100100-01	62443	2	0.03	Thioredoxin domain domain containing protein.	E.R.	0.06	redox
343	Os02t0644100-01	65159	3	0.03	Similar to Heat shock protein STI (Stress inducible protein) (GmSTI).	mito	0.59	stress
340	Os04t0164900-01	62247	3	0.03	Similar to Starch debranching enzyme.	chlo/nucl	0.16	not assigned
339	Os07t0447800-01	58553	2	0.03	Alpha-D-phosphohexomutase, alpha/beta/alpha I, II and III domain containing protein.	chlo	0.06	glycolysis
342	Os08t0192900-01	60472	2	0.03	Nucleotide-binding, alpha-beta plait domain containing protein.	nucl	0.68	signaling
344	Os03t0136900-01	106862	8	0.03	Similar to Aconitate hydratase, cytoplasmic (EC 4.2.1.3)	chlo	0.04	TCA
345	Os03t0810600-01	72125	4	0.02	Miro-like domain containing protein.	plas	0.61	signaling
346	Os06t0303400-00	90373	10	0.02	Similar to aconitate hydratase, cytoplasmic.	cyto	0.08	TCA
347	Os05t0405000-01	103578	3	0.02	Orthophosphate dikinase precursor (EC 2.7.9.1).	chlo	0.11	not assigned
348	Os01t0226400-01	93590	6	0.02	ATPase, AAA-type, core domain containing protein.	vacu	0.76	protein
349	Os02t0218200-01	98904	7	0.02	Peptidase M1, membrane alanine aminopeptidase family protein.	cyto	0.05	protein

^aProtein ID is according to The Rice Annotation Project Database, ^bM.P. means number of matched peptide, the protein with >2 matched peptides were considered, ^cMol (%) is the percentage calculated using each emPAI of identified protein to divide the total emPAI of total identified proteins, ^dWoLFPSORT is protein location prediction software, ^eNucPred is protein location prediction software, ^fFunction were obtained using MapMan bin codes. *d* nucl, nuclear; cyto, cytoplasm; chlo, chloroplast; mito, mitochondria; E.R., endoplasmic reticulum; vacu, vacuole; cysk, cytoskeletal filaments; plas, plasma membrane, extr, extracellular. For results from NucPred, the consensus score is basically the fraction of predictors which vote "nuclear". For a discrete prediction, the user has to decide on a score threshold (preferably 0.8). Proteins score more than or equal to this threshold are predicted to spend time in the nucleus. *f* protein, protein synthesis/degradation/targeting/others; RNA, RNA processing/regulation of transcription; DNA, DNA synthesis/repair; cell, cell organization/vesicle transport; major CHO metabolism, major carbohydrates metabolism; TCA, tricarboxylic acid cycle; misc, miscellaneous; not assigned, unknown.

Supplemental Table 3. Nuclear proteins were identified in rice embryos after 24 h of imbibition

No.	Protein ID ^a	Mass(Da)	M.P. ^b	Mol (%) ^c	Description	WoLFPSORT ^d	NucPred ^e	Function ^f
1	Os05t0445500-01	14419	42	1.83	Similar to Acidic ribosomal protein (Fragment).	chlo	0	protein
2	Os02t0162500-01	16410	29	1.58	Similar to 40S ribosomal protein S14.	cyto/nucl	0.3	protein
3	Os02t0699600-01	17820	50	1.26	Similar to 60S ribosomal protein L12.	cyto	0.03	protein
4	Os10t0411800-01	16419	31	1.25	Similar to 40S ribosomal protein S17-3.	cyto /nucl	0.39	protein
5	Os02t0268100-01	57229	341	1.21	Similar to Glutelin (Fragment).	vacu	0.39	development
6	Os02t0249800-01	56915	361	1.18	Glutelin precursor.	chlo/nucl	0.41	development
7	Os01t0835900-00	11402	67	1.17	Similar to Histone H4.	nucl	0.32	DNA
8	Os07t0546700-01	8144	11	1.12	Similar to 60S ribosomal protein L38.	cyto	0.37	not assigned
9	Os03t0343500-01	14520	23	1.05	Similar to 60S ribosomal protein L22-2.	cyto	0.06	protein
10	Os02t0249600-01	56411	331	1.02	Similar to Glutelin.	chlo/nucl	0.43	development
11	Os10t0400200-01	56841	351	0.98	Glutelin type II precursor.	vacu	0.4	development
12	Os01t0686800-01	36665	82	0.98	Protein containing the WD-40 repeat, Innate immunity	cyto/nucl	0.01	development
13	Os03t0577000-01	25590	60	0.93	Similar to Ribosomal protein S3 (Fragment).	cyto	0.21	protein
14	Os01t0762500-00	56782	414	0.93	Glutelin subunit mRNA.	chlo	0.44	development
15	Os08t0117200-00	17874	46	0.93	Similar to 40S ribosomal protein S13 (Fragment).	nucl	0.41	protein
16	Os03t0424500-01	16434	34	0.91	Similar to 40S ribosomal protein S19-3.	cyto/nucl	0.18	protein
17	Os03t0182600-03	12620	21	0.90	Similar to 40S ribosomal protein SA.	cyto	0.2	protein
18	Os07t0214300-01	18423	22	0.88	Seed allergenic protein RAG2 precursor.	mito	0.04	stress
20	Os07t0229900-01	15112	37	0.82	Ribosomal protein S12e domain containing protein.	chlo	0.02	protein
19	Os07t0150200-01	15132	29	0.82	Similar to 40S ribosomal protein S12-1.	cyto	0.01	protein
21	Os01t0191100-01	11714	10	0.81	Similar to Acidic ribosomal protein P2a-4 (Fragment).	chlo	0.01	protein
22	Os01t0276000-01	12584	14	0.81	Similar to 60S ribosomal protein L30.	cyto	0.08	protein
23	Os02t0478700-01	9864	21	0.80	Ribosomal protein S27.	nucl	0.27	not assigned
24	Os07t0180900-01	44825	101	0.79	Similar to 60S ribosomal protein L4.	cyto /nucl	0.41	protein

25	Os03t0427300-01	56550	157	0.79	Glutelin type-A III precursor.	chlo	0.37	development
26	Os02t0814700-01	16392	57	0.77	Similar to Ribosomal Pr 117 (Fragment).	cyto	0.1	protein
28	Os03t0200500-01	29880	83	0.76	40S ribosomal protein S3a (CYC07 protein).	cyto/nucl	0.4	protein
29	Os12t0406200-01	29863	72	0.76	Similar to 40S ribosomal protein S3a (CYC07 protein).	cyto/nucl	0.35	protein
27	Os02t0287000-01	29912	63	0.76	Similar to 40S ribosomal protein S3a (CYC07 protein).	cyto/nucl	0.39	protein
30	Os11t0127900-01	16979	19	0.73	Similar to 40S ribosomal protein S16.	chlo	0.29	protein
31	Os08t0117300-01	17135	46	0.72	Similar to 40S ribosomal protein S13.	nucl	0.46	protein
32	Os05t0490100-01	12581	12	0.72	Similar to 60S ribosomal protein L30.	nucl	0.04	protein
33	Os03t0794700-01	17709	30	0.71	Similar to 40S ribosomal protein S18.	cyto	0.24	protein
34	Os07t0616600-02	33122	37	0.71	Similar to 40S ribosomal protein SA (p40) (Laminin receptor homolog).	cyto	0.19	protein
35	Os08t0326400-01	29457	59	0.70	60S ribosomal protein L7a.	chlo/nucl	0.4	protein
36	Os03t0327600-01	39254	97	0.69	Ricin B-related lectin domain containing protein.	cyto/nucl	0.01	not assigned
37	Os11t0482000-01	22307	50	0.68	Similar to 40S ribosomal protein S5.	cysk/nucl	0.19	protein
38	Os02t0249000-01	55226	103	0.67	Glutelin, Seed strage protein	E.R.	0.37	development
39	Os02t0591700-01	24243	51	0.65	Similar to Candida glabrata strain CBS138 chromosome L complete sequence.	nucl	0.04	protein
40	Os07t0674200-01	14465	18	0.64	Similar to 60S ribosomal protein L22-2.	cyto	0.05	protein
41	Os05t0499100-01	21497	48	0.64	26 kDa globulin (Alpha-globulin).	extr	0.45	not assigned
42	Os01t0752300-01	21500	28	0.64	Similar to 60S ribosomal protein L18a-1.	nucl	0.38	protein
43	Os05t0565000-01	21559	28	0.64	Similar to 60S ribosomal protein L18a-1.	cyto/nucl	0.41	protein
44	Os03t0756000-01	23829	30	0.62	Similar to 60S ribosomal protein L13a-4.	chlo	0.51	protein
46	Os09t0502000-01	15779	26	0.62	Similar to Ribosomal L32.	chlo	0.66	protein
45	Os02t0284600-01	15740	15	0.62	Similar to 60S ribosomal protein L27.	chlo/nucl	0.02	protein
47	Os09t0501200-01	15835	23	0.61	Similar to Ribosomal L32.	chlo	0.68	protein
48	Os06t0115500-01	24096	30	0.61	Similar to 60S ribosomal protein L13 (BBC1 protein homolog).	chlo	0.65	protein
49	Os03t0408300-00	16101	24	0.60	Similar to 60S ribosomal protein L27a-3.	nucl	0.14	protein
50	Os02t0549600-01	20307	48	0.59	Similar to 40S ribosomal protein S10-1.	nucl	0.19	protein

51	Os03t0336100-01	36974	231	0.59	11-S plant seed storage protein family protein.	chlo	0.3	development
52	Os08t0559200-01	12061	24	0.58	Similar to Ribosomal protein S25 (40S ribosomal 25S subunit).	nucl	0.52	protein
53	Os01t0205500-01	20978	31	0.57	Similar to 60S ribosomal protein L11-2 (L16). Splice isoform 2.	cyto	0.28	protein
54	Os07t0608500-01	26154	25	0.57	Similar to Ribosomal protein S3 (Fragment).	cyto	0.27	protein
55	Os01t0896700-00	34773	59	0.57	Similar to 60S ribosomal protein L5.	mito	0.55	not assigned
56	Os03t0576700-01	24056	22	0.57	Similar to 60S ribosomal protein L13 (BBC1 protein homolog).	chlo	0.65	protein
57	Os01t0896800-01	37754	59	0.55	Ribosomal protein L18/L5 domain containing protein.	mito	0.53	protein
58	Os03t0807800-01	30185	70	0.55	Similar to 40S ribosomal protein S2 (Fragment).	cyto	0.04	protein
59	Os03t0793700-01	52436	152	0.54	RmlC-like jelly roll fold domain containing protein.	mito	0.38	development
60	Os03t0154700-01	22716	53	0.54	Similar to 40S ribosomal protein S9.	nucl	0.37	protein
61	Os08t0428800-00	18660	26	0.54	Similar to High mobility group I/Y-2.	plas/nucl	0.12	DNA
62	Os07t0638300-01	24198	20	0.53	Similar to 1-Cys peroxiredoxin.	cyto /nucl	0.03	redox
63	Os03t0663800-01	28776	189	0.53	Globulin 1 (Fragment).	vacu	0.63	development
64	Os02t0235600-01	20994	25	0.52	Similar to 60S ribosomal protein L11-2 (L16). Splice isoform 2.	cyto/nucl	0.29	protein
65	Os01t0823300-00	15381	20	0.52	Similar to Ribosomal protein S26.	chlo	0.42	protein
66	Os05t0477300-03	15551	14	0.52	Ribosomal protein S26e domain containing protein.	chlo/nucl	0.36	protein
67	Os02t0821800-02	26896	47	0.51	Similar to Fibrillarin-2.	cyto/nucl	0.18	RNA
68	Os08t0116500-01	11133	26	0.51	Similar to 60S acidic ribosomal protein P1 (L12).	chlo /nucl	0	protein
69	Os02t0489400-01	24928	40	0.51	Similar to 40S ribosomal protein S8.	chlo	0.69	protein
70	Os04t0349500-01	25027	39	0.51	Similar to 40S ribosomal protein S8.	chlo/nucl	0.79	protein
71	Os01t0328400-01	17885	16	0.51	Ubiquitin.	nucl	0.51	protein
72	Os07t0213800-01	17829	8	0.51	Similar to Allergenic protein.	chlo	0.03	stress
73	Os01t0358400-01	29903	42	0.50	Similar to 40S ribosomal protein S4.	chlo	0.12	protein
74	Os02t0126700-01	10336	6	0.49	Similar to Small nuclear ribonucleoprotein homolog.	chlo	0.06	RNA
75	Os03t0796501-00	44632	47	0.49	Similar to 60S ribosomal protein L4 (L1).	cyto/nucl	0.21	protein
76	Os11t0168200-01	44862	61	0.48	60S ribosomal protein L3.	chlo	0.46	protein

77	Os04t0473400-01	24613	16	0.48	Similar to 60S ribosomal protein L6-B (L17) (YL16) (RP18).	mito/nucl	0.09	protein
78	Os02t0234800-01	31980	11	0.48	Similar to U2 small nuclear ribonucleoprotein A' (U2 snRNP-A').	cyto_nucl	0.29	RNA
79	Os08t0129200-02	19024	17	0.47	Similar to Cold shock protein-1.	mito /nucl	0.08	stress
80	Os02t0453600-01	28808	80	0.46	Similar to Glutelin.	chlo	0.48	development
81	Os03t0162200-01	14547	33	0.45	Similar to Histone H2A.	nucl	0.13	DNA
82	Os05t0155100-01	21355	19	0.44	Similar to 60S ribosomal protein L18.	nucl	0.35	protein
83	Os08t0156800-01	13669	14	0.43	Similar to 60S ribosomal protein L34.	cyto	0.75	protein
84	Os03t0266300-01	17899	14	0.43	Class I low-molecular-weight heat shock protein 17.9.	cyto	0.03	stress
85	Os03t0352300-01	61579	45	0.43	Similar to Nucleolar protein.	nucl	0.41	RNA
86	Os09t0402100-01	21739	6	0.43	PF1 protein.	nucl	0.32	DNA
87	Os05t0350500-01	43570	51	0.43	Peptidase M24, structural domain domain containing protein.	cyto	0.29	protein
88	Os05t0160200-01	17900	13	0.42	Ubiquitin.	nucl	0.5	protein
89	Os08t0530200-01	19585	25	0.41	Similar to 60S ribosomal protein L17.	chlo/nucl	0.56	protein
90	Os03t0350100-01	61141	45	0.41	SAR DNA-binding protein-2.	cyto/nucl	0.59	RNA
91	Os02t0242600-01	57190	103	0.41	Similar to Glutelin.	vacu	0.39	development
92	Os10t0564300-01	15633	13	0.40	Similar to 60S ribosomal protein L27.	chlo	0.02	protein
93	Os02t0229000-01	15796	30	0.40	Similar to 40S ribosomal protein S19-like.	nucl	0.25	protein
94	Os07t0613200-00	16007	14	0.39	Similar to 60S ribosomal protein L27a-3.	nucl	0.15	protein
95	Os05t0346300-01	22350	28	0.37	Similar to 40S ribosomal protein S7.	cyto/nucl	0.17	protein
96	Os03t0390000-02	28269	24	0.37	Similar to Ribosomal protein s6 RPS6-2.	nucl	0.88	protein
97	Os08t0234000-01	28493	22	0.37	Similar to 60S ribosomal protein L7-2.	cyto/nucl	0.62	protein
98	Os01t0348700-01	17040	12	0.37	Similar to 60S ribosomal protein L23a (L25).	cyto	0.36	protein
99	Os07t0622100-01	28683	25	0.36	Similar to Ribosomal protein s6 RPS6-2.	nucl	0.84	protein
100	Os02t0519900-01	94987	111	0.36	Similar to Elongation factor EF-2 (Fragment).	cyto/nucl	0.16	protein
101	Os02t0478600-01	14866	11	0.36	Similar to 40S ribosomal protein S15A.	cyto/nucl	0.09	protein
102	Os01t0834500-01	15765	24	0.36	Similar to 40S ribosomal protein S23 (S12).	cyto	0.23	not assigned

103	Os06t0507200-01	17405	9	0.35	Bifunctional inhibitor/plant lipid transfer protein/seed storage domain containing protein.	chlo	0.28	not assigned
104	Os03t0350300-01	62764	37	0.35	Similar to SAR DNA-binding protein-like protein.	cyto/nucl	0.62	RNA
105	Os12t0567700-01	28460	23	0.34	Similar to 60S ribosomal protein L2 (Fragment).	cyto	0.13	protein
106	Os11t0115400-00	11766	4	0.34	Lipid transfer protein LPT IV.	extr	0.05	not assigned
107	Os07t0215500-01	17838	15	0.34	Allergenic protein.	extr	0.03	stress
108	Os01t0231700-01	11926	13	0.33	Similar to 60S acidic ribosomal protein P2-B (CaRP2B).	nucl	0.01	protein
109	Os08t0130500-01	34470	33	0.33	60S acidic ribosomal protein P0.	cyto	0.07	protein
110	Os06t0221300-01	18450	12	0.33	Similar to Dehydration stress-induced protein.	extr	0.02	not assigned
112	Os07t0545400-01	13968	48	0.32	Protein H2A.	nucl	0.07	DNA
111	Os07t0545300-01	14036	27	0.32	Similar to Histone H2A.	nucl	0.08	DNA
113	Os06t0134000-01	14151	10	0.32	Similar to 40S ribosomal protein S20.	cyto	0.01	protein
114	Os02t0503400-01	14235	12	0.32	Similar to 60S ribosomal protein L35.	nucl	0.63	protein
115	Os12t0530000-01	14331	59	0.31	Similar to Histone H2A.	nucl	0.07	DNA
116	Os01t0723200-01	15766	22	0.31	Similar to 40S ribosomal protein S19-like.	nucl	0.23	protein
117	Os07t0109500-01	23885	17	0.31	Ribosomal protein L13 family protein.	chlo	0.52	protein
118	Os02t0115900-01	73573	29	0.31	Endosperm luminal binding protein.	E.R.	0.09	stress
119	Os08t0558800-01	17796	10	0.30	Similar to Ribosomal protein.	cyto/nucl	0.09	protein
120	Os02t0205200-01	39575	13	0.30	Similar to Unidentified precursor.	extr	0.09	not assigned
121	Os03t0197300-01	71138	232	0.30	Similar to Cupin family protein, expressed.	chlo/nucl	0.75	development
122	Os08t0558000-01	17942	10	0.30	Similar to Ribosomal protein.	cyto/nucl	0.11	protein
123	Os05t0169100-01	25112	22	0.29	Similar to 60S ribosomal protein L10 (QM protein homolog).	chlo	0.16	protein
124	Os11t0579800-01	20050	16	0.29	Gar1 protein RNA-binding region family protein.	nucl	0.15	RNA
125	Os03t0241200-00	14037	6	0.28	Similar to NHP2-like protein 1 (High mobility group-like nuclear protein 2 homolog 1).	cyto	0.05	protein
126	Os01t0860300-01	24837	15	0.27	Similar to Ribosomal protein L1.	cyto	0.16	protein
127	Os07t0639800-01	26828	10	0.27	Similar to Eukaryotic translation initiation factor 6 (Fragment).	cyto	0.01	protein
128	Os05t0597100-01	32698	22	0.27	Similar to Nucleolar histone deacetylase HD2-p39.	nucl	0.43	RNA

129	Os02t0804100-01	6927	6	0.26	Similar to predicted protein.	nucl	0.38	not assigned
130	Os03t0141000-01	9205	12	0.26	60S ribosomal protein L21.	cyto/nucl	0.27	protein
131	Os05t0268500-01	54131	24	0.25	Similar to Serine carboxypeptidase 2.	chlo	0.05	protein
132	Os02t0753300-01	20315	17	0.25	Lipoxygenase, LH2 domain containing protein.	chlo	0.01	not assigned
133	Os05t0368300-01	29758	26	0.25	Similar to 40S ribosomal protein S4, X isoform (Single copy abundant mRNA protein.	chlo	0.14	protein
134	Os02t0232400-01	54777	13	0.25	Similar to Citrate synthase.	cyto	0.39	gluconeotense
136	Os12t0133050-00	34559	27	0.25	Similar to 60S acidic ribosomal protein P0.	cyto	0.07	protein
135	Os02t0785800-01	12821	7	0.25	Similar to Ribosomal protein L35A.	cyto	0.14	protein
137	Os12t0569300-01	23985	15	0.25	Thaumatococcus, pathogenesis-related family protein.	chlo	0.02	not assigned
138	Os01t0949060-01	43964	11	0.24	Hypothetical conserved gene.	chlo	0.31	not assigned
139	Os06t0149400-01	42726	15	0.24	Similar to Chitinase A.	cyto/nucl	0.4	DNA
140	Os03t0758800-01	17762	12	0.24	Similar to Eukaryotic translation initiation factor 5A-2 (eIF-5A-2) (eIF-4D).	cysk	0.01	protein
141	Os08t0557100-01	21376	4	0.24	Similar to Nucleic acid-binding protein precursor.	chlo	0.05	RNA
142	Os07t0636000-01	66168	22	0.23	Similar to H/ACA ribonucleoprotein complex subunit 4 (EC 5.4.99.-)	cyto/nucl	0.48	DNA
143	Os04t0613600-00	18053	23	0.23	Similar to 40S ribosomal protein S11.	cyto/nucl	0.09	protein
144	Os05t0459900-01	12727	11	0.22	Similar to 60S ribosomal protein L36-1.	cyto	0.56	protein
145	Os01t0679700-02	10464	8	0.22	Similar to 60S ribosomal protein L37a.	cyto/nucl	0.18	protein
146	Os06t0319700-01	14282	5	0.22	Similar to 60S ribosomal protein L31.	cyto/nucl	0.28	protein
147	Os05t0140800-01	39249	14	0.21	Similar to Dormancy related protein (Fragment).	mito	0.3	misc
148	Os04t0683100-01	23410	9	0.21	Similar to Cleavage and polyadenylation specificity factor 5.	cyto/nucl	0.16	not assigned
149	Os10t0411700-01	8184	13	0.21	Similar to S28 ribosomal protein (Fragment).	cyto	0.1	protein
150	Os12t0569200-01	17071	5	0.21	Conserved hypothetical protein.	extr	0.02	not assigned
151	Os05t0552300-02	36828	16	0.21	Similar to Guanine nucleotide-binding protein beta subunit-like protein (GPB-LR) (RWD).	nucl	0.01	signaling
152	Os04t0164900-01	62247	25	0.21	Similar to Starch debranching enzyme.	chlo/nucl	0.16	not assigned
153	Os01t0937100-01	44500	18	0.20	Similar to Xylanase inhibitor precursor (Xylanase inhibitor TAXI-I).	chlo	0.18	protein
154	Os05t0589600-01	41004	15	0.20	Similar to Nuclear RNA binding protein B (Fragment).	nucl	0.45	RNA

155	Os03t0733400-01	81551	19	0.20	Zinc finger, BED-type predicted domain containing protein.	nucl	0.62	DNA
156	Os07t0262200-02	31935	13	0.20	Similar to Prohibitin.	chlo	0.2	mitochondrial electron transport
157	Os01t0502700-00	27401	82	0.20	Similar to Histone H2A.	nucl	0.18	DNA
158	Os03t0854400-01	18181	4	0.20	Ribonuclease III domain containing protein.	chlo	0.07	not assigned
159	Os01t0184100-01	18133	8	0.20	Similar to 17.5 kDa class II heat shock protein.	cyto/nucl	0.05	stress
160	Os06t0726400-01	93747	33	0.19	Branching enzyme-I precursor (Starch-branching enzyme I).	chlo	0.17	major CHO metabolism
161	Os01t0598600-01	51795	16	0.19	Peptidase A1 domain containing protein.	chlo	0.15	RNA
162	Os02t0288200-01	61601	21	0.19	Protein of unknown function DUF573 domain containing protein.	nucl	0.65	not assigned
163	Os11t0220800-01	25729	14	0.19	Similar to 60S ribosomal protein L10 (QM protein homolog).	chlo_mito	0.14	protein
164	Os06t0701100-02	47343	12	0.19	Eukaryotic initiation factor 4A (eIF4A) (eIF-4A).	cyto	0.37	DNA
165	Os03t0337800-01	24183	19	0.19	Similar to 60S ribosomal protein L19 (Fragment).	nucl	0.62	protein
167	Os03t0130300-01	9207	5	0.19	Similar to Cp-thionin.	extr	0.07	not assigned
166	Os01t0252300-01	9253	2	0.19	Conserved hypothetical protein.	extr	0.06	not assigned
168	Os03t0177400-01	49604	32	0.19	EF-1 alpha.	cyto	0.06	protein
169	Os02t0121100-01	23393	3	0.19	Zinc finger, CCHC-type domain containing protein.	nucl	0.11	stress
170	Os08t0430500-01	28979	7	0.19	Similar to 14-3-3-like protein S94.	plas/nucl	0.02	signaling
171	Os01t0710000-01	50593	16	0.18	Similar to WD-repeat protein RBAP1.	nucl	0.05	development
172	Os03t0345200-01	9305	4	0.18	40S ribosomal protein S21.	nucl	0.42	not assigned
173	Os01t0924900-01	56347	13	0.18	GTP-binding signal recognition particle SRP54, G-domain containing protein.	nucl	0.92	not assigned
174	Os07t0216700-01	17036	4	0.18	Bifunctional trypsin/alpha-amylase inhibitor domain containing protein.	chlo	0.02	not assigned
175	Os01t0136100-01	16929	4	0.18	16.9 kDa class I heat shock protein 1.	cyto	0.07	stress
176	Os06t0662000-01	68711	14	0.18	Similar to Vacuolar H ⁺ -ATPase subunit A (Fragment).	chlo	0.07	transport
177	Os06t0104400-01	48186	99	0.17	Similar to IQ calmodulin-binding motif family protein.	nucl	0.74	not assigned
178	Os03t0799000-01	29612	40	0.17	Similar to Histone H1.	nucl	0.35	DNA
179	Os08t0473600-01	49190	6	0.17	Alpha-amylase isozyme 3E precursor (EC 3.2.1.1) (1,4-alpha-D-glucan glucanohydrolase).	pero	0.01	major CHO metabolism
180	Os07t0112800-01	17983	14	0.17	Similar to Eukaryotic translation initiation factor 5A-4 (eIF-5A-4).	cysk/nucl	0.01	protein

181	Os05t0468800-01	18234	3	0.17	Phosphatidylethanolamine-binding protein PEBP domain containing protein.	cyto	0.02	not assigned
182	Os02t0622300-00	15435	5	0.17	Ribosomal protein L14 family protein.	cyto	0.24	protein
183	Os03t0341100-01	21118	18	0.16	Similar to 60S ribosomal protein L18.	nucl	0.27	protein
184	Os01t0663400-01	56473	13	0.16	Similar to Aspartic proteinase oryzasin 1 precursor (EC 3.4.23.-).	chlo/nucl	0.09	protein
185	Os02t0715400-00	10420	3	0.16	Conserved hypothetical protein.	chlo/nucl	0.05	not assigned
186	Os02t0601300-01	36716	11	0.16	Similar to Glyceraldehyde-3-phosphate dehydrogenase, cytosolic 3 (EC 1.2.1.12).	cyto	0	glycolysis
187	Os12t0632000-01	16130	4	0.16	Similar to Glycine-rich RNA-binding protein 1 (Fragment).	nucl	0.17	RNA
188	Os11t0104050-01	10740	3	0.16	Preprotein translocase Sec, Sec61-beta subunit, eukarya domain containing protein.	chlo	0.38	protein
189	Os03t0297100-01	22226	19	0.15	40S ribosomal protein S7.	cyto/nucl	0.19	protein
190	Os03t0836200-01	22038	3	0.15	Similar to RNA-binding protein RZ-1.	nucl	0.15	RNA
191	Os05t0567100-01	54723	8	0.15	Aspartic proteinase oryzasin 1 precursor (EC 3.4.23.-).	chlo	0.07	protein
193	Os05t0541900-01	14989	6	0.15	Similar to 60S ribosomal protein l28.	nucl	0.29	protein
192	Os04t0623700-01	15000	4	0.15	Similar to Signal recognition particle 14 kDa protein (SRP14).	nucl	0.39	protein
194	Os04t0661300-01	40460	19	0.15	Similar to H0112G12.10 protein.	mito/nucl	0.46	not assigned
195	Os04t0445100-01	23271	10	0.15	Similar to 22.7 kDa class IV heat shock protein precursor.	extr	0.12	stress
196	Os02t0137400-01	96565	12	0.14	Similar to Spliceosomal-like protein.	plas/nucl	0.34	RNA
197	Os11t0602200-01	90242	20	0.14	Similar to SET domain protein SDG111.	nucl	0.89	RNA
198	Os03t0579300-00	24163	13	0.14	60S ribosomal protein L19.	nucl	0.66	protein
199	Os10t0466300-01	58236	11	0.14	Similar to Yarrowia lipolytica chromosome C of strain CLIB99 of Yarrowia lipolytica.	nucl	0.27	RNA
200	Os05t0490700-01	74829	15	0.14	Similar to SET domain protein SDG111.	nucl	0.43	RNA
201	Os04t0173800-01	24718	3	0.14	Lectin precursor (Agglutinin).	chlo	0.22	stress
202	Os12t0502200-01	25086	4	0.14	Similar to Low temperature-responsive RNA-binding protein.	nucl	0.22	RNA
203	Os04t0462900-01	30840	4	0.13	Similar to prohibitin2.	cyto	0.01	mitochondrial electron transport
204	Os03t0799600-01	25545	6	0.13	Similar to ES43 like protein.	nucl	0.36	RNA
205	Os06t0342200-01	16500	5	0.13	Similar to Eukaryotic translation initiation factor 1A (EIF-1A) (EIF-4C).	nucl	0.16	protein
206	Os05t0595400-01	26092	6	0.13	Similar to Nucleoside diphosphate kinase III (EC 2.7.4.6) (NDK III) (NDP kinase III).	chlo	0.03	nucleotide metabolism

207	Os05t0555800-00	12811	3	0.13	Similar to 60S ribosomal protein L35a-3.	cyto/nucl	0.18	protein
208	Os10t0572900-02	26261	3	0.13	Protein of unknown function DUF296 domain containing protein.	nucl	0.67	RNA
209	Os06t0675700-01	96503	21	0.12	Similar to High pI alpha-glucosidase.	chlo	0.1	misc
210	Os04t0510900-01	35414	6	0.12	Similar to Embryo-specific protein 1 (ATS1).	chlo	0.05	development
211	Os03t0370500-02	65110	16	0.12	Similar to H/ACA ribonucleoprotein complex subunit 4 (EC 5.4.99.-) (Nucleolar protein NAP57 homolog) (Nopp-140 associated protein of 57 kDa homolog) (AtNAP57).	cyto/nucl	0.47	DNA
212	Os04t0376500-01	39644	5	0.12	Similar to Eukaryotic translation initiation factor 3 subunit 3 (eIF-3 gamma).	chlo/nucl	0.6	protein
214	Os07t0661800-01	35030	14	0.12	Similar to Nucleolar protein Nop56.	cyto	0	RNA
213	Os07t0202100-01	67302	12	0.12	Similar to ATP-dependent RNA helicase ded1.	mito/nucl	0.32	RNA
215	Os08t0189100-01	23811	3	0.12	Similar to Germin-like protein precursor.	extr	0	stress
216	Os01t0303300-01	17908	5	0.12	Similar to Stress-inducible membrane pore protein.	mito	0.3	protein
217	Os02t0248800-01	56996	72	0.12	Similar to Glutelin type-B 2 precursor.	vacu	0.4	development
218	Os03t0598800-02	24432	14	0.12	Similar to 60S ribosomal protein L15.	nucl	0.6	protein
219	Os11t0105400-01	26650	3	0.12	Ribosomal protein L10 family protein.	nucl	0.23	protein
220	Os05t0302700-01	41122	18	0.12	Similar to ATP/ADP carrier protein.	chlo	0.14	transport
221	Os02t0121300-01	18634	10	0.11	Cyclophilin 2.	cyto	0.01	cell
222	Os02t0102700-01	14386	7	0.11	Similar to AGL157Cp.	cyto	0.07	RNA
223	Os06t0724600-01	18720	3	0.11	Similar to Transformer-SR ribonucleoprotein (Fragment).	extr/nucl	0.46	RNA
224	Os09t0361400-01	29202	4	0.11	Outer mitochondrial membrane protein porin.	cyto	0.12	transport
225	Os08t0137200-01	48806	7	0.11	Actin/actin-like family protein.	cyto/nucl	0.24	cell
226	Os03t0735300-01	32498	5	0.11	Alba, DNA/RNA-binding protein family protein.	nucl	0.25	RNA
227	Os08t0549300-01	14645	2	0.11	Similar to Acyl carrier protein III, chloroplast precursor (ACP III).	chlo	0	lipid metabolism
228	Os06t0232000-01	41752	6	0.11	Similar to Pro-resilin.	nucl	0.6	not assigned
229	Os11t0247300-01	50390	13	0.11	Alfa-tubulin.	cyto /nucl	0.13	cell
230	Os01t0172400-01	85659	10	0.11	Similar to Phospholipase D alpha 1.	chlo	0.25	lipid metabolism
231	Os03t0761000-01	15085	2	0.11	SWIB/MDM2 domain containing protein.	chlo	0.33	RNA

232	Os03t0202200-01	29456	22	0.11	Porin-like protein.	cyto	0.01	transport
233	Os01t0905800-01	39141	4	0.10	Aldolase C-1.	cyto	0.05	PS
234	Os02t0788400-01	32160	2	0.10	Similar to Eukaryotic translation initiation factor 3 subunit-like protein.	cyto/nucl	0.1	protein
235	Os02t0257200-01	32543	10	0.10	Conserved hypothetical protein.	plas	0.08	not assigned
236	Os04t0405800-01	32574	3	0.10	Similar to OSIGBa0142C11.1 protein.	cyto/nucl	0.13	nucleotide metabolism
237	Os10t0321700-01	32282	3	0.10	Similar to Ribonucleoprotein like protein.	chlo/nucl	0.19	RNA
238	Os04t0404400-01	32258	4	0.10	Similar to H0502B11.4 protein.	extr	0	stress
239	Os06t0668200-01	42310	8	0.10	Similar to Phosphoglycerate kinase, cytosolic (EC 2.7.2.3).	chlo	0.01	PS
240	Os01t0851700-01	94867	15	0.10	Similar to Cytosolic starch phosphorylase (Fragment).	cyto	0.29	major CHO metabolism
241	Os09t0570850-00	16773	4	0.10	Similar to Histone H2B.	cyto/nucl	0.67	DNA
242	Os07t0600400-01	48200	2	0.09	WD40/YVTN repeat-like domain containing protein.	nucl	0.37	not assigned
243	Os02t0537700-01	28307	4	0.09	Similar to 2-cys peroxiredoxin BAS1, chloroplast precursor (EC 1.11.1.15).	chlo	0.04	redox
244	Os10t0478200-01	35888	4	0.09	Cytoplasmic malate dehydrogenase.	cyto	0.08	TCA
245	Os02t0771200-01	34494	8	0.09	Protein of unknown function DUF573 domain containing protein.	chlo/nucl	0.69	not assigned
246	Os02t0530600-01	93542	16	0.09	Poly(ADP-ribose) polymerase, regulatory region domain containing protein.	cyto/nucl	0.21	protein
247	Os07t0662500-01	23842	6	0.09	Similar to Elongation factor 1-beta' (EF-1-beta').	cyto /nucl	0.1	protein
248	Os09t0529900-01	37030	6	0.09	Pyruvate/Phosphoenolpyruvate kinase, catalytic core domain containing protein.	chlo	0.18	hormone metabolism
249	Os07t0422100-01	18333	2	0.09	AWPM-19-like family protein.	vacu	0	transport
250	Os06t0186900-01	52096	6	0.09	TIP49, C-terminal domain containing protein.	chlo	0.35	DNA
251	Os03t0812000-01	48808	6	0.09	DNA topoisomerase, type IIA, subunit A or C-terminal domain containing protein.	chlo	0.51	not assigned
252	Os02t0714600-01	36468	2	0.09	Ribose-phosphate pyrophosphokinase 4 (EC 2.7.6.1).	cyto/nucl	0.07	nucleotide metabolism
253	Os02t0782500-01	18706	3	0.08	Similar to Small heat stress protein class CIII.	cyto	0.39	stress
254	Os03t0212700-01	58829	11	0.08	Similar to Cytochrome C reductase-processing peptidase subunit I, MPP subunit I, P55.	mito	0.29	protein
255	Os03t0296400-01	38496	11	0.08	Similar to Eukaryotic translation initiation factor 2 subunit 1.	cyto	0.25	protein
256	Os02t0274100-01	79038	11	0.08	Similar to Peroxisomal fatty acid beta-oxidation multifunctional protein (MFP).	plas	0.06	lipid metabolism
257	Os07t0683600-00	39637	9	0.08	Similar to Osr40c1 protein.	nucl	0.03	not assigned

259	Os04t0446500-01	39476	3	0.08	Similar to OSIGBa0140O07.15 protein.	nucl	0.72	protein
258	Os03t0333300-01	30815	2	0.08	Similar to Eukaryotic translation initiation factor 2 beta subunit (eIF-2-beta) (P38).	nucl	0.45	protein
260	Os01t0837500-01	49866	5	0.08	Similar to Ruvb1 protein.	cyto	0.17	development
261	Os03t0313000-01	19672	2	0.08	Similar to NADH-ubiquinone oxidoreductase (Fragment).	mito/nucl	0.03	mitochondrial electron transport
262	Os09t0463700-01	39985	4	0.08	Similar to AHM1.	mito	0.53	not assigned
263	Os04t0103200-01	46904	7	0.08	Proteasome component region PCI domain containing protein.	cyto	0.12	protein
264	Os05t0227700-01	61803	7	0.08	Similar to Eukaryotic translation initiation factor 3 subunit 6-interacting protein.	cyto/nucl	0.27	not assigned
265	Os05t0126200-01	21440	2	0.07	Conserved hypothetical protein.	chlo	0.87	not assigned
266	Os06t0234100-01	68328	17	0.07	Peptidase S1C, HrtA/DegP2/Q/S family protein.	nucl	0.55	protein
267	Os05t0104800-01	31276	7	0.07	Similar to Eukaryotic translation initiation factor 3 subunit 5 (eIF-3 epsilon).	cyto	0.02	protein
268	Os01t0633100-01	58279	12	0.07	Similar to ADP-glucose pyrophosphorylase subunit SH2.	cyto/nucl	0.14	major CHO metabolism
269	Os03t0596900-01	77956	9	0.07	GTP-binding signal recognition particle SRP54, G-domain containing protein.	nucl	0.86	not assigned
271	Os09t0115400-01	71870	4	0.07	Similar to Poly(A)-binding protein.	nucl	0.38	RNA
270	Os05t0140500-01	22091	3	0.07	RNA binding motif protein 8 family protein.	nucl	0.57	RNA
272	Os06t0220000-01	28974	2	0.07	Similar to Phi-1 protein.	chlo	0.01	signaling
274	Os08t0512400-01	29716	3	0.07	Protein of unknown function DUF296 domain containing protein.	nucl	0.34	RNA
273	Os02t0221500-01	40241	2	0.07	Nucleotide-binding, alpha-beta plait domain containing protein.	nucl	0.26	RNA
275	Os05t0566500-01	65325	6	0.07	Similar to Initiation factor 3d (Fragment).	cysk/nucl	0.37	protein
276	Os08t0127900-01	58352	5	0.07	Similar to Globulin 1 (Fragment).	vacu/nucl	0.64	development
277	Os09t0565500-01	70370	4	0.07	Conserved hypothetical protein.	plas	0.23	not assigned
278	Os07t0209000-01	48417	4	0.07	Similar to Dolichyl-di-phosphooligosaccharide-protein glycotransferase (Oligosaccharyltransferase).	chlo	0.04	protein
279	Os01t0611000-01	40112	9	0.06	Protein of unknown function DUF642 domain containing protein.	chlo	0.04	not assigned
280	Os05t0155601-00	59100	4	0.06	Importin alpha-1b subunit.	nucl	0.64	protein
281	Os02t0158400-01	25239	4	0.06	ssDNA-binding transcriptional regulator family protein.	nucl	0.36	DNA
282	Os04t0434400-01	36870	8	0.06	Similar to H0823A09.7 protein.	extr	0.34	not assigned

283	Os12t0170700-01	57733	6	0.06	Conserved hypothetical protein.	cyto/nucl	0.86	not assigned
284	Os01t0975900-01	25361	4	0.06	Similar to Tonoplast membrane integral protein ZmTIP1-2.	vacu	0.01	transport
285	Os06t0336200-01	25169	3	0.06	Delta-tonoplast intrinsic protein.	plas	0	transport
286	Os07t0186400-01	25476	4	0.06	Similar to SHL1.	nucl	0.43	RNA
287	Os03t0146100-01	25740	6	0.06	Tonoplast intrinsic protein (Tonoplast water channel).	vacu	0	transport
288	Os04t0685200-01	34289	5	0.06	Peptidase aspartic, catalytic domain containing protein.	chlo	0.19	protein
289	Os03t0681900-01	34244	5	0.06	Similar to RGP-3 (Fragment).	nucl	0.25	RNA
290	Os12t0176800-01	51145	8	0.06	Similar to Heterochromatin protein (Fragment).	cyto/nucl	0.04	protein
291	Os06t0653800-01	38519	2	0.06	Similar to WD-repeat protein 57 (Prp8-binding protein) (hPRP8BP).	chlo	0.14	development
292	Os09t0551300-01	74352	9	0.06	Similar to predicted protein.	chlo/nucl	0.9	DNA
293	Os06t0715500-01	27445	2	0.06	Similar to Translocon-associated protein alpha subunit precursor (TRAP-alpha).	chlo	0.12	not assigned
294	Os01t0810000-01	27495	2	0.06	Utp11 family protein.	nucl	0.94	RNA
297	Os10t0492600-01	27496	8	0.06	Similar to Tonoplast membrane integral protein ZmTIP3-1.	mito	0.01	transport
296	Os02t0802500-01	80370	5	0.06	Similar to H(+)-translocating (Pyrophosphate-ENERGIZED) inorganic pyrophosphatase beta-1 polypeptide (EC 3.6.1.1) (Fragment).	vacu	0.02	transport
295	Os01t0659200-01	26784	2	0.06	Similar to Vacuolar ATP synthase subunit E (EC 3.6.3.14).	cyto	0.34	transport
298	Os06t0608300-01	111112	12	0.06	Similar to Small nuclear ribonucleoprotein component.	cyto/nucl	0.33	protein
299	Os08t0320100-01	36716	3	0.06	Nucleotide-binding, alpha-beta plait domain containing protein.	nucl	0.16	RNA
300	Os01t0639100-01	45912	6	0.05	Similar to Eukaryotic initiation factor 4A-3 (eIF4A-3) (eIF-4A-3).	cyto/nucl	0.45	DNA
301	Os04t0620700-01	75266	4	0.05	Nucleotide-binding, alpha-beta plait domain containing protein.	nucl	0.59	signaling
302	Os06t0718100-01	28475	5	0.05	Similar to Alpha-expansin precursor.	chlo	0.07	cell wall
303	Os02t0106966-00	30489	6	0.05	Similar to emb1507 (embryo defective 1507); ATP binding	cyto	0.75	not assigned
304	Os07t0603200-01	61920	3	0.05	WD40 repeat-like domain containing protein.	nucl	0.71	not assigned
305	Os05t0536200-01	29584	3	0.05	Voltage-dependent anion channel.	cyto	0.01	transport
306	Os03t0711400-01	137435	7	0.05	Similar to Coatomer alpha subunit.	mito/nucl	0.28	cell
307	Os03t0807700-01	41248	5	0.05	Protein of unknown function DUF642 domain containing protein.	chlo	0.01	not assigned

308	Os01t0907600-00	41150	5	0.05	Cysteine endopeptidase.	vacu	0.11	protein
309	Os05t0539700-01	41829	7	0.05	Similar to Nucleosome assembly protein 1.	cyto/nucl	0.38	DNA
310	Os05t0586700-00	32586	2	0.05	Conserved hypothetical protein.	plas	0.16	not assigned
311	Os08t0542100-01	31828	4	0.05	Similar to 60S ribosomal protein L7.	cyto/nucl	0.61	protein
312	Os07t0475800-01	33417	4	0.05	Eukaryotic rRNA processing family protein.	nucl	0.8	protein
313	Os11t0582400-01	49179	9	0.04	Similar to Embryo-specific protein.	extr	0.73	not assigned
314	Os05t0556100-01	69040	9	0.04	Similar to SDL5A.	cyto	0.68	misc
315	Os01t0120800-01	114224	7	0.04	Similar to Eukaryotic translation initiation factor 3 subunit 10 (eIF-3 theta).	cyto/nucl	0.91	protein
316	Os05t0564200-01	35070	2	0.04	U2 snRNP auxiliary factor, small subunit.	nucl	0.52	RNA
317	Os02t0756800-01	34675	2	0.04	Phosphate-induced protein 1 conserved region family protein.	chlo	0.03	signaling
318	Os10t0569200-01	83300	12	0.04	Six-bladed beta-propeller, TolB-like domain containing protein.	nucl	0.36	protein
319	Os03t0383800-02	78241	6	0.04	Nucleotide-binding, alpha-beta plait domain containing protein.	nucl	0.83	RNA
320	Os12t0288600-01	62680	6	0.04	Conserved hypothetical protein.	nucl	0.94	not assigned
321	Os03t0735100-01	89743	2	0.04	Quinoprotein amine dehydrogenase, beta chain-like domain containing protein.	chlo/nucl	0.28	signaling
322	Os03t0802700-01	67065	2	0.04	RH27 helicase (Fragment).	chlo/nucl	0.84	DNA
323	Os12t0609800-01	87650	8	0.04	WD40/YVTN repeat-like domain containing protein.	chlo/nucl	0.33	not assigned
324	Os01t0104800-01	73415	3	0.04	Sas10/Utp3 family protein.	cyto/nucl	0.85	not assigned
325	Os09t0482100-01	80435	7	0.04	Similar to Heat shock protein 82.	nucl	0.53	stress
326	Os09t0509000-01	43021	3	0.04	Similar to DAG protein.	chlo	0.46	development
328	Os07t0557500-01	76187	4	0.03	WRC domain containing protein.	nucl	0.87	protein
327	Os05t0558000-01	45670	2	0.03	Ribosomal protein L1 family protein.	cyto/nucl	0.64	protein
329	Os06t0693500-01	45807	5	0.03	Zinc finger, C2H2-like domain containing protein.	cysk/nucl	0.43	RNA
330	Os10t0470900-01	45593	3	0.03	Nucleotide-binding, alpha-beta plait domain containing protein.	nucl	0.19	RNA
331	Os02t0105500-01	45245	2	0.03	IQ calmodulin-binding region domain containing protein.	cyto/nucl	0.74	signaling
332	Os10t0573900-01	59418	4	0.03	NMD3 family protein.	chlo	0.37	not assigned
333	Os09t0553200-01	51821	3	0.03	Similar to UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9).	cyto	0	not assigned

334	Os01t0889000-01	73870	2	0.03	Tetratricopeptide-like helical domain containing protein.	nucl	0.91	protein
335	Os03t0854300-01	48374	6	0.03	Nucleotide-binding, alpha-beta plait domain containing protein.	nucl	0.86	RNA
336	Os08t0543900-00	49767	2	0.03	Similar to Transcription factor RF2b.	nucl	0.8	RNA
337	Os02t0523500-01	108515	7	0.03	Similar to 110 kDa 4Snc-Tudor domain protein (Fragment).	chlo	0.3	RNA
338	Os05t0519700-01	101062	5	0.03	Heat shock protein 101.	cyto	0.42	stress
339	Os08t0390000-01	69555	8	0.03	Moesin domain containing protein.	cyto/nucl	0.91	transport
340	Os01t0911200-01	75331	5	0.03	Ribophorin II family protein.	cyto/nucl	0.03	not assigned
341	Os06t0167000-02	131363	7	0.03	Similar to PRP8 protein (Fragment).	pero/nucl	0.57	RNA
342	Os01t0739000-01	54365	3	0.03	Similar to Mitochondrial processing peptidase.	mito	0.24	protein
343	Os11t0199200-01	57047	6	0.03	Similar to Protein disulfide isomerase (Fragment).	E.R.	0	redox
344	Os07t0224900-02	58295	2	0.03	WD40 repeat-like domain containing protein.	chlo/nucl	0.57	RNA
345	Os01t0183100-01	60637	2	0.03	Cytochrome cd1-nitrite reductase-like, C-terminal haem d1 domain containing protein.	cyto/nucl	0.54	development
346	Os05t0524400-01	63028	4	0.03	Phosphofructokinase family protein.	cysk	0.22	glycolysis
347	Os06t0644600-01	101847	2	0.03	Similar to predicted protein.	chlo/nucl	0.47	not assigned
348	Os01t0147200-01	59240	4	0.03	IWS1, C-terminal family protein.	nucl	0.91	RNA
349	Os08t0192900-01	60472	4	0.03	Nucleotide-binding, alpha-beta plait domain containing protein.	nucl	0.68	signaling
351	Os02t0612800-01	81708	6	0.02	AT hook, DNA-binding, conserved site domain containing protein.	nucl	0.75	not assigned
350	Os02t0103900-01	79132	5	0.02	U3 small nucleolar RNA-associated protein 6 domain containing protein.	nucl	0.85	not assigned
352	Os07t0124500-01	106606	3	0.02	Similar to Eukaryotic translation initiation factor 3 subunit 8 (eIF3 p110) (eIF3c).	nucl	0.83	protein
353	Os01t0275600-01	101545	2	0.02	Similar to Argonaute 4 protein.	nucl	0.72	RNA
354	Os02t0644100-01	65159	6	0.02	Similar to Heat shock protein STI (Stress inducible protein) (GmSTI).	mito	0.59	stress
355	Os03t0151800-02	90429	9	0.02	Similar to Cell division control protein 48 homolog A (AtCDC48a).	cyto/nucl	0.57	cell
356	Os05t0592600-01	135123	6	0.02	Translation initiation factor 2 related domain containing protein.	cyto/nucl	0.62	protein
357	Os06t0286351-01	176483	10	0.02	Armadillo-type fold domain containing protein.	nucl	0.82	not assigned
358	Os06t0305200-01	162656	7	0.01	Nucleoporin, non-repetitive/WGA-negative domain containing protein.	nucl	0.66	protein
359	Os09t0567700-01	107599	3	0.01	WD40 repeat-like domain containing protein.	nucl	0.51	development

360	Os05t0117864-01	127907	7	0.01	Conserved hypothetical protein.	chlo/nucl	0.93	RNA
361	Os05t0592400-01	122944	6	0.01	UV-damaged DNA binding protein.	chlo/nucl	0.12	stress
362	Os03t0743800-00	243940	6	0.01	Similar to predicted protein.	cyto	0.77	DNA

^aProtein ID is according to The Rice Annotation Project Database, ^bM.P. means number of matched peptide, the protein with >2 matched peptides were considered, ^cMol (%) is the percentage calculated using each emPAI of identified protein to divide the total emPAI of total identified proteins, ^dWoLFPSORT is protein location prediction software, ^eNucPred is protein location prediction software, ^fFunction were obtained using MapMan bin codes. *d* nucl, nuclear; cyto, cytoplasm; chlo, chloroplast; mito, mitochondria; E.R., endoplasmic reticulum; vacu, vacuole; cysk, cytoskeletal filaments; plas, plasma membrane, extr, extracellular. For results from NucPred, the consensus score is basically the fraction of predictors which vote “nuclear”. For a discrete prediction, the user has to decide on a score threshold (preferably 0.8). Proteins score more than or equal to this threshold are predicted to spend time in the nucleus. *f* protein, protein synthesis/degradation/targeting/others; RNA, RNA processing/regulation of transcription; DNA, DNA synthesis/repair; cell, cell organization/vesicle transport; major CHO metabolism, major carbohydrates metabolism; TCA, tricarboxylic acid cycle; misc, miscellaneous; not assigned, unknown.

Supplemental Table 4 -The probabilities of phosphorylation site assignment for nuclear phosphopeptides in rice embryos after 24 h of imbibition

Accession	Confidence Level	Protein Descriptions	Sequence	Modification s	phosphoRS		phosphoR		IonScor e
					Isoform Probability	phosphoRS Site Probabilities	S Binomial Peptide	q- Value	
Os01t0104800-01	High	Sas10/Utp3 family protein.	LSMQDFGLEDEGSDEEDR	S13(Phospho)	1	S(2): 0.0; S(13): 100.0	97	0	39
	High		NLETEVLQSQQVSSPAQSK	S14(Phospho)	0.453	T(4): 0.0; S(9): 0.0; S(13): 45.3	52	0	14
	Middle		sDtyALGmVmLQLLTAR	S1(Phospho)	1	S(1): 100.0; T(3): 100.0; Y(4): 1	75	0.015	18
	Low		LDFsGIVFGDWdyDDLd	S4(Phospho)	1	S(4): 100.0; Y(13): 100.0	25		11
	Low		VmLGIPLLEGNSPAScFPR	S12(Phospho)	0.729	S(12): 72.9; S(15): 27.1	16	0.287	13
Os01t0128400-01	High	Protein of unknown function DUF2359, TMEM214 domain containing protein.	IAAATAsAYSDDDDDSDEAQATRPEGE	S7(Phospho)	0.031	T(5): 0.2; S(7): 3.1; Y(9): 78.7;	63	0.005	28
	High		IAAATASAYSDDDDDSDEAQATRPEGE	S10(Phospho)	0.864	T(5): 0.0; S(7): 0.1; Y(9): 13.5;	106	0	79
	Low		ALsDQsEmLLRtmLEAGVLPDTASYR	S3(Phospho)	1	S(3): 100.0; S(6): 100.0; T(12):	57		11
	Low		AmGyNNPYDSSGtDDDLPPtQNRGLR	Y4(Phospho)	0.022	Y(4): 66.3; Y(8): 66.3; S(10): 40	1	0.568	12
	Low		ARSLPtAVLsGcAIALTsVLLDVtGmK	T6(Phospho)	0.042	S(3): 74.5; T(6): 31.4; S(10): 40	18	0.804	10
	Low		AsMMAAttVSPNtlcmAVEVtGARPK	S2(Phospho)	0.51	S(2): 98.1; T(7): 85.8; T(8): 85.	20		11
	Low		AtEsAStPIyNEyGEVEGRGIHMAK	T2(Phospho)	0.167	T(2): 83.3; S(4): 83.3; S(6): 83.	1	0.792	12
	Low		DDGIEMtHEDVESVmtKmGPDPFDHGK	T7(Phospho)	0.674	T(7): 76.5; S(13): 32.6; T(16): 9	21	0.568	23
	Low		EALPGPSKPTILDDSSDEssDDDVAF	S21(Phospho)	0.142	S(7): 19.3; T(10): 19.3; S(16): 2	8		16
	Low		MEGGGGGGTDMNAVDPGVVQHVLsM	S27(Phospho)	0.763	T(9): 0.1; S(24): 23.6; S(27): 76	33	0.3	11
	Low		mLEPsFGQPGEcFALQGSSGYVEIKLR	S5(Phospho)	0.646	S(5): 64.6; S(18): 15.7; S(19): 9	10	0.694	12
	Low		QGPSPGEQGsSTPAADVKAEGGPTAG	S4(Phospho)	0.018	S(4): 77.6; S(10): 15.0; S(11): 1	8	0.491	11
	Low		RNsDTLSGScLTGTLsGsGLDPssWR	S3(Phospho)	S16(Phospho) Too many isoforms			0.754	10
	Low		VSiGcELKDtMMmGADQYETEEETSK	T10(Phospho)	0.146	S(2): 68.4; T(10): 14.6; Y(18): 4	6		13
	Low		YRAVIVASALYLLSLGMLTAsSSSMAAQ	S21(Phospho)	0.084	Y(1): 1.0; S(8): 1.7; Y(11): 2.6;	10	0.618	10
Os01t0136000-00	Low	Similar to Cytosolic class I small heat-shock protein HSP17.5.	LIWstVKGLLDPK	S4(Phospho)	1	S(4): 100.0; T(5): 100.0	57	0.39	10
	Low		yGATELLLGLSVGEK	Y1(Phospho)	0.937	Y(1): 93.7; T(4): 5.7; S(11): 0.6	30	0.671	13

Os01t0191100-01	High High	Similar to Acidic ribosomal protein (Fragment). Similar to Acidic ribosomal protein P2a-4 (Fragment).	EEsDDDDMGFSLFD	S3(Phospho)	1 S(3): 100.0; S(10): 0.0	65	0	25
			VEEKEEsDDDMGFSLFD	S7(Phospho)	1 S(7): 100.0; S(14): 0.0	199	0	74
Os01t0205500-01	High	Similar to 60S ribosomal protein L11-2 (L16). Splice isoform 2.	VLEQLSGQsPVFSK	S9(Phospho)	0.994 S(6): 0.5; S(9): 99.4; S(13): 0.1	61	0.001	32
	Low		IADVsKLR	S5(Phospho)	1 S(5): 100.0	53		14
	Low		IALRsSVR	S5(Phospho)	0.907 S(5): 90.7; S(6): 9.3	56		11
	Low		IQASKAAALHGAAAAGAmLSQR	T8(Phospho):	0.943 S(4): 5.7; T(8): 96.1; S(21): 98.	23	0.391	11
	Low		IQtSLALR	T3(Phospho)	0.974 T(3): 97.4; S(4): 2.6	36		11
	Low		LARLVsSR	S6(Phospho)	0.5 S(6): 50.0; S(7): 50.0	31		12
	Low		LAsVRSLR	S3(Phospho)	0.983 S(3): 98.3; S(6): 1.7	51		12
	Low		RGLtVSLR	T4(Phospho)	0.998 T(4): 99.8; S(6): 0.2	56		13
	Low		SKAQsQATALASIDK	S5(Phospho)	0.737 S(1): 4.5; S(5): 73.7; T(8): 17.3	40		13
	Low		tlQLTLGR	T1(Phospho)	0.998 T(1): 99.8; T(5): 0.2	50		10
	Low		tlSKPLSR	T1(Phospho)	0.449 T(1): 44.9; S(3): 10.3; S(7): 44.	20		11
	Low		yHVmQAAKTLVNK	Y1(Phospho)	0.945 Y(1): 94.5; T(9): 5.5	35		13
Os01t0231700-01	High	Similar to 60S acidic ribosomal protein P2-B (CaRP2B).	SLSFLsLR	S6(Phospho)	0.496 S(1): 0.7; S(3): 49.6; S(6): 49.6	26	0.007	12
	Low		cVEWIPFKSsFR	S10(Phospho)	0.871 S(9): 12.9; S(10): 87.1	46	0.803	12
	Low		EQsRPVEAIVDRR	S3(Phospho)	1 S(3): 100.0	69		11
	Low		ISLsLRELtSLSR	S4(Phospho)	0 S(2): 99.9; S(4): 99.9; T(9): 0.1	19		15
	Low		mAVGVGATtPIDKER	T9(Phospho)	0.955 T(8): 4.5; T(9): 95.5	42	0.732	13
	Low		NsDVESGMNFySK	S2(Phospho)	0.14 S(2): 48.1; S(6): 48.1; Y(11): 4.	2		12
	Low		SAGAAAGPtAAAAAAVQK	T9(Phospho)	0.996 S(1): 0.4; T(9): 99.6	53		13
	Low		scSGYLGGGGSSSSsK	S1(Phospho)	0.007 S(1): 1.3; S(3): 0.6; Y(5): 1.3; S	12	0.531	13
Os01t0243100-01	Middle	Similar to Kinesin.	NLNLEVQQTDEPsSSAKLEK	S13(Phospho)	0.481 T(9): 1.9; S(13): 48.1; S(14): 48.	50	0.027	26
	Low		APESAGHPSSGIRyPHQIER	Y14(Phospho)	0.484 S(4): 3.1; S(9): 48.4; Y(14): 48.	49	0.682	12
	Low		ASMRWSNVAVmLGFVVGYR	Y18(Phospho)	0.998 S(2): 0.1; S(6): 0.1; Y(18): 99.8	35	0.763	11
	Low		ATSTVGAPPPSSLVPHtHDcK	T17(Phospho)	1 T(2): 0.0; S(3): 0.0; T(4): 0.0; S	64	0.698	19
	Low		ctVIGINLGTTYSWVGVYR	T2(Phospho)	0.042 T(2): 4.2; T(10): 5.2; T(11): 5.2	0	0.691	13
	Low		DGEMVVPtELDWAIRGTNR	T8(Phospho)	0.998 T(8): 99.8; T(17): 0.2	45	0.764	14
	Low		FNPFsGFQNPmYILKSPR	S5(Phospho)	1 S(5): 100.0; Y(12): 0.0; S(16): 0.	63	0.566	14
	Low		GIQmSYAAAVKTAGPsHEAVR	S16(Phospho)	0.493 S(5): 0.7; Y(6): 0.7; T(12): 49.3	30	0.467	17

Os01t0328400-01	Low	Ubiquitin.	GIITPTAAAFRTLAsGLcLSGK	T3(Phospho):	0.249 T(3): 64.3; T(5): 32.8; T(11): 40	13	0.747	13
	Low		GLQRQSTSMVSHISSPSNsR	S19(Phospho)	0.627 S(6): 0.3; T(7): 0.3; S(8): 0.3; S	25	0.766	15
	Low		GPLGQsAVSNGFTVtKIQmK	S6(Phospho)	0.103 S(6): 13.6; S(9): 48.5; T(13): 51	29	0.773	13
	Low		GWGcGWRNIQmLSsHLLK	S14(Phospho)	0.967 S(13): 3.3; S(14): 96.7	65	0.768	18
	Low		KLAEDNNVPLSSVmGtGPDGR	T16(Phospho)	0.992 S(11): 0.2; S(12): 0.6; T(16): 99	43	0.707	13
	Low		LPVIGHmHLVGsNPHVsLR	S12(Phospho)	1 S(12): 100.0; S(17): 100.0	13	0.44	17
	Low		mFAWPVPPRGWTVsPTTGR	S14(Phospho)	0.62 T(12): 21.5; S(14): 62.0; T(16):	22		10
	Low		NLAVSNtIDDQLAGVRAMDR	T7(Phospho)	0.5 S(5): 50.0; T(7): 50.0	79	0.083	16
	Low		NQVtEEGPYGFKILsQIR	T4(Phospho):	0.984 T(4): 99.2; Y(9): 1.6; S(15): 99.	38		11
	Low		QALYASKIcsYAQGMNIIK	S10(Phospho)	0.488 Y(4): 0.7; S(6): 1.8; S(10): 48.8	29		11
	Low		QGVISsSGTETGYLQDLIYK	S6(Phospho)	0.035 S(5): 0.9; S(6): 3.5; S(7): 3.5; T	13		11
	Low		QQELNYTQLQTPGAIDPsR	S18(Phospho)	0.747 Y(6): 10.3; T(7): 10.3; T(11): 4.	20		10
	Low		QQREsAEASLDLLSVDLER	S5(Phospho)	0.486 S(5): 48.6; S(9): 2.8; S(14): 48.	22		12
	Low		RAGIGGGAGcLGGVAAPeIFGAGR	T19(Phospho)	1 T(19): 100.0	23		11
	Low		RLSSDDVVAAVELSAATsPR	S19(Phospho)	0.567 S(3): 5.6; S(4): 5.6; S(15): 5.6;	12		13
	Low		sAANsRILNIsSQLGLLNK	S1(Phospho):	0.358 S(1): 85.8; S(5): 64.2; S(11): 89	17		13
	Low		SGGGEEAAEAGVGERAtAAVVSASR	T16(Phospho)	0.001 S(1): 99.9; T(16): 0.1; S(21): 0.	16	0.776	12
	Low		sHSSKALTNIGGQALEESSR	S1(Phospho)	0.825 S(1): 82.5; S(3): 7.5; S(4): 7.5;	35	0.365	14
	Low		SQTSQSfNHHIEmlsKLR	S15(Phospho)	0.78 S(1): 2.5; T(3): 4.6; S(4): 4.6; S	18	0.359	13
	Low		VESLPPPRPPLAFLsESR	S15(Phospho)	0.659 S(3): 1.2; S(15): 90.1; S(16): 79	26		12
Os01t0328400-01	Low		yMATIlmDsPKVVVLDIR	Y1(Phospho):	0.665 Y(1): 83.3; T(4): 33.5; S(9): 83.	30		12
	Low	Ubiquitin.	AGHPEVPVAEGsAEPLK	S12(Phospho)	1 S(12): 100.0	34	0.43	11
	Low		AIEAtVDDmPWEMIGSsR	T5(Phospho):	0.068 T(5): 20.6; S(16): 93.2; S(17): 8	7		11
	Low		LTVQHRMNDsIAswAsK	S10(Phospho)	0.21 T(2): 79.0; S(10): 89.3; S(13): 7	8		11
	Low		RPsAPTGGELLVPLRSSVLR	S3(Phospho)	0.985 S(3): 98.5; T(6): 1.5; S(16): 0.0	55	0.145	12
	Low		YGHRGAmGGGGVSDGYEGsK	S20(Phospho)	0.082 Y(1): 0.1; S(14): 22.9; Y(17): 68	23	0.722	15
Os01t0348700-01	Low	Similar to 60S ribosomal protein L23a (L25).	DFIIFSLsRTR	S8(Phospho)	0.438 S(6): 12.5; S(8): 43.8; T(10): 43	19	0.741	12
	Low		GGIARMLsQK	S8(Phospho)	1 S(8): 100.0	14		12
	Low		LAFLsYAATAAAGK	S5(Phospho)	0.798 S(5): 79.8; Y(6): 19.9; T(9): 0.3	32	0.613	11
	Low		LKNHESDsLALK	S8(Phospho)	0.964 S(6): 3.6; S(8): 96.4	40		11
Os01t0358400-01	Low	Similar to 40S ribosomal protein S4.	AHAtSPIHSLRLR	T4(Phospho)	0.838 T(4): 83.8; S(5): 15.9; S(9): 0.2	44		14
	Low		DsDKIMLAK	S2(Phospho)	1 S(2): 100.0	29	0.792	16
	Low		GLPVMKWtTR	T8(Phospho)	0.863 T(8): 86.3; T(9): 13.7	35		10
	Low		LEKQSNTTsLIPK	S9(Phospho)	0.425 S(5): 42.5; T(7): 7.5; T(8): 7.5;	40		12
	Low		LMGLItYHSR	T6(Phospho)	0.907 T(6): 90.7; Y(7): 6.7; S(9): 2.5	22	0.318	10
	Low		QLVAADtFR	T7(Phospho)	1 T(7): 100.0	23		12
Os01t0588700-01	Low	Protein of unknown function DUF572 family protein.	ALVVMQRQLyTHNSPGAFDALK	Y10(Phospho)	0.992 Y(10): 99.2; T(11): 0.6; S(14): 0	42	0.683	10
	Low		DDAsPIAGmVSESQHSQAPNAVTK	S4(Phospho)	0.006 S(4): 0.6; S(11): 1.8; S(13): 24.	4		14

	Low		ItALmDHLAmITVQSENsEK	T2(Phospho)	0.887 T(2): 100.0; T(12): 5.6; S(15): 5	52		17
	Low		MGLTcSTmMRTLISLSSHASR	T8(Phospho)	0.118 T(4): 33.6; S(6): 33.6; T(7): 11.	18	0.799	10
	Low		RSAGTPVIVmVADcADFDGsFPK	S20(Phospho)	1 S(2): 0.0; T(5): 0.0; S(20): 100.	63		16
	Low		SLLsRAcVGVSSSTAVAVSyHGVR	S4(Phospho)	0.187 S(1): 72.5; S(4): 20.8; S(11): 2.	35	0.682	11
Os01t0679700-03	Low	Similar to 60S ribosomal protein L37a.	sSGGGRPPAAQHIVR	S1(Phospho)	0.5 S(1): 50.0; S(2): 50.0	31		13
Os01t0686800-01	High	Protein containing the WD-40 repeat, Innate immunity	VVLFWRWAPVNGGAAGGGGGsGDGDE	S20(Phospho)	1 S(20): 100.0; S(26): 100.0; T(3	61	0	17
	Middle		GSSyMGSIYDARPTFEsYGVAHGSPDL	Y4(Phospho)	0.028 S(2): 22.4; S(3): 22.4; Y(4): 22.	0	0.021	13
	Low		AEGIQQLQHGDcEESsTAPLLAPHEsYR	S15(Phospho)	0.435 S(13): 20.7; S(15): 58.7; T(16):	33	0.774	15
	Low		AISIDMFEAGtDtSHLVLEyAmVELTR	T11(Phospho)	0.024 S(3): 91.0; T(11): 81.8; T(13): 2	18	0.403	13
	Low		ALEPILDmNDyLQIGtFVFTVVVEDNK	Y11(Phospho)	0.81 Y(11): 98.7; T(16): 82.3; T(20):	32	0.084	18
	Low		AtIsSPSATVEtmLDGFsRIGGVyR	T2(Phospho)	0.099 T(2): 49.0; S(4): 49.0; S(5): 49.	23		10
	Low		cRAAAGAAATTTTTGGGGGGGALVLE	T12(Phospho)	0.303 T(10): 5.9; T(11): 5.9; T(12): 30	24	0.233	13
	Low		cSPSYLATPSVSPSASTSALAAAATTsS	Y5(Phospho)	T27(Phospho) Too many isoforms		0.737	17
	Low		cyFLlImLFtMLHyINKItESQR	Y2(Phospho)	0.997 Y(2): 100.0; T(10): 100.0; Y(14	59	0.71	19
	Low		DELPTmVPASSGNLDDGVHGGAAEAA	S5(Phospho)	0.77 T(5): 77.0; S(10): 11.1; S(11): 1	25	0.394	16
	Low		DEttNAVDEAGNGTssSNQEAAIQEK	T3(Phospho)	0.428 T(3): 99.7; T(4): 99.7; T(14): 3.	51	0.081	14
	Low		DGSTtAstGtDDAYVYPLPHHPsk	T5(Phospho)	S7(Phospho)T Too many isoforms		0.601	11
	Low		DmcDEAILGTLLGscmtHNEVEVGR	S14(Phospho)	0.759 T(10): 24.1; S(14): 76.5; T(17):	28		11
	Low		ELAGLVFGsR	S9(Phospho)	1 S(9): 100.0	43	0.786	14
	Low		EQNmNASSSsDFLEDDRGLssGAVK	S10(Phospho)	0.596 S(7): 13.5; S(8): 13.5; S(9): 13.	54	0.589	12
	Low		ESTILETyKSLMmQDtGMPEDVR	Y8(Phospho)	0.083 S(2): 35.1; T(3): 35.1; T(7): 39.	7		11
	Low		EtGKmmAHGVDGEsTINELGKPSNSDI	T2(Phospho)	0.475 T(2): 98.2; S(14): 49.0; T(15): 4	29	0.354	15
	Low		GDcAAGLAsGEPVAAAGIGSVKPFdGV	S9(Phospho)	0.074 S(9): 24.7; S(19): 22.6; T(28): 7	1		14
	Low		GMAPmHPsIATPVRPSIAERRPtSk	S8(Phospho)	0.14 S(8): 72.8; T(11): 54.0; S(16): 6	7	0.778	10
	Low		GPLLtRGIMASAAAAPAPSPSPTAAAN	T5(Phospho)	0.377 T(5): 96.6; S(11): 4.9; S(20): 39	31	0.718	10
	Low		GQLEGyALmNAsEQyGmKRPSSADR	Y6(Phospho)	0.054 Y(6): 38.9; S(12): 54.1; Y(15): 5	0	0.184	12
	Low		GVEEsSLVTK	S5(Phospho)	0.82 S(5): 82.0; S(6): 14.8; T(9): 3.2	32	0.679	10
	Low		HGAAQVAAMSSPGQLHPTSSSFPQDcS	T18(Phospho)	0.341 S(10): 1.6; S(11): 4.1; T(18): 34	30	0.792	11
	Low		IMALQQIMSPFGKTDtASVLLEtITYIK	T16(Phospho)	0.121 S(9): 13.2; T(14): 30.7; T(16): 3	13	0.708	11
	Low		LAEMVEGLDLsHVRSLTAAGTElsDFK	S11(Phospho)	0.518 S(11): 70.4; S(15): 22.8; T(17):	29	0.355	16
	Low		LAsIAmDisAEQKGGFIGAtIASSLmR	S3(Phospho)	0.629 S(3): 100.0; S(9): 100.0; T(20):	43	0.646	10
	Low		LGAAPLPPsAAAEVEPtGSPSSSSSAA	S9(Phospho)	0.059 S(9): 27.3; T(17): 27.3; S(19): 2	4	0.524	23
	Low		LLFWGILLQGGYsHAPDDLsyGVDMk	S13(Phospho)	0.026 Y(12): 2.6; S(13): 2.6; S(20): 4	2	0.718	12
	Low		LPPAAPPSPGtsMEVEAAWPAsGLAAL	T11(Phospho)	0.64 S(9): 36.0; T(11): 75.0; S(12): 8	26	0.163	12
	Low		LPSMTHRWAVDQWLAIIDEAPHMLtAER	T24(Phospho)	0.798 S(3): 10.1; T(5): 10.1; T(24): 79	22	0.672	10
	Low		LtSYEVmSEVHsNIALGNAIGGEsDK	T2(Phospho)	0.391 T(2): 54.6; S(3): 25.3; Y(4): 25.	20	0.702	12
	Low		LVGAAMLALLYMVASFQGasGAAAGG	S29(Phospho)	0.479 Y(11): 4.7; S(15): 6.1; S(20): 6.	19	0.128	10
	Low		mAHKAAALVLLLVSvsVAAAASGDQES	S16(Phospho)	0.474 S(14): 47.4; S(16): 47.4; S(22):	32	0.511	13
	Low		mAsssKALLLLAVLLASAVLLAAAADQP	S3(Phospho)	0.992 S(3): 99.7; S(4): 99.7; S(5): 99.	32	0.79	15
	Low		mAVIHTEdTTGTGLVmRDSNNEASGtS	T26(Phospho)	0.1 T(6): 6.4; T(9): 6.4; T(10): 10.0	3	0.766	14
	Low		MAVITTSDDYDsPLAVRDSNDLADSMT	S12(Phospho)	0.549 T(5): 0.4; T(6): 2.3; S(7): 6.2; Y	36		13

Low		mDsGycRSALDyLELQPDLSALVR	S3(Phospho)	0.038 S(3): 54.6; Y(5): 54.6; S(8): 31.	3		12
Low		MFVADGGELLMAQsyAKNMGLyGER	S14(Phospho)	1 S(14): 100.0; Y(15): 100.0; Y(2	17	0.708	11
Low		mKGGQLtILGNPNSSVscsVHVQQR	T7(Phospho)	0.497 T(7): 99.8; S(15): 28.1; S(16): 2	33	0.805	10
Low		mKmsILMGVTQmNLGIVLsyFDAK	S4(Phospho)	0.263 S(4): 45.4; T(10): 73.7; S(19): 9	6		11
Low		mmLLGSPSSGGYGGKFAGASPAGGtT	T25(Phospho)	0.005 S(6): 43.2; S(8): 43.2; S(9): 43.	0	0.62	11
Low		MSPGAASNmDSSTEAFASPAGNAtT	T26(Phospho)	0.35 S(2): 6.0; S(7): 9.2; S(11): 9.2;	17	0.271	11
Low		MSSFGLVsSQTYFLARMLsDEEFGR	S8(Phospho)	0.064 S(2): 26.9; S(3): 26.9; S(8): 26.	3	0.473	11
Low		mtVTQLAAAGAAGGAsGGAAGAGGAP	T2(Phospho)	0.483 T(2): 51.7; T(4): 51.7; S(16): 96	51	0.698	11
Low		mVAAiTTTTATAATVAAmTTmmmTsGG	T5(Phospho)	0.047 T(5): 17.1; T(6): 17.1; T(7): 17.	11	0.776	16
Low		NALGctGVADRIPGTSALAMAsAsAIPQA	T6(Phospho)	0.979 T(6): 98.4; T(15): 0.9; S(16): 1.	51	0.123	13
Low		NFFPGsGAINEIGAGAGEHYsVNVPLDA	S6(Phospho)	0.108 S(6): 95.0; Y(20): 89.2; S(21): :	8		11
Low		NFKQAIDcytQFVDVGtMVSPTVYAR	Y9(Phospho)	0.797 Y(9): 94.4; T(10): 94.4; T(17): 8	49	0.726	16
Low		NSSNSVDFQWSPFPIEMsGVSAVIPSP	S18(Phospho)	0.371 S(2): 0.3; S(3): 0.3; S(5): 0.3; S	26		13
Low		NyGLFYPDGTPVYDVGLRGYLPPmDE	Y2(Phospho)	0.92 Y(2): 92.0; Y(6): 6.4; T(10): 0.7	31	0.729	15
Low		QGLAPLDRtINTGVGmVFLPQDENSmE	T9(Phospho)	0.853 T(9): 85.3; T(11): 7.3; S(24): 7.	25	0.318	11
Low		QHSVEYWmMASLQGGGGGGNGssSE	S22(Phospho)	0.433 S(3): 0.1; Y(6): 0.1; S(11): 4.5;	34	0.511	11
Low		QLAGADFLcDGVGGGGsER	S17(Phospho)	1 S(17): 100.0	38		12
Low		QLFGWAAmLKDmtlINFcHsTESMAR	T13(Phospho)	0.022 T(13): 81.9; S(19): 20.2; T(21):	33		12
Low		SAHSLPPLAsVPLPGQQYAREAEssPsR	S10(Phospho)	0.017 S(1): 23.3; S(4): 22.9; S(10): 2	5	0.729	18
Low		sEAEPsAmAGIDKSLFLELAMsAmDEL	S1(Phospho)	0.118 S(1): 54.9; S(6): 54.9; S(14): 5	2	0.446	12
Low		sGKPWKAFK	S1(Phospho)	1 S(1): 100.0	26	0.759	17
Low		SmSTVstPPLAsAsAAAPPAGPPPTTAT	S6(Phospho)	T7(Phospho)S Too many isoforms		0.335	17
Low		ssTEILSGDSQHVSksSAGIAsLLAQK	S1(Phospho)	S2(Phospho)S Too many isoforms			11
Low		TEAcRyAsLHDDmGSTDVLWSMLR	Y6(Phospho)	0.148 T(1): 26.8; Y(6): 37.0; S(8): 39.	6	0.749	10
Low		tsKAiPLtDVFAFGtFILEVTcGR	T1(Phospho)	0.14 T(1): 86.0; S(2): 86.0; T(5): 86.	4	0.435	11
Low		VAREMLQLGFGLsVASmEIMINGLcR	S13(Phospho)	0.712 S(13): 71.2; S(16): 28.8	26		10
Low		VEDELHSIEAcISsPsTTIEVVSDGLRR	S14(Phospho)	0.098 S(7): 1.5; S(13): 39.6; S(14): 39	26		10
Low		VGGAAsEASGVGVVVGSGSSSSDL	S6(Phospho)	0.067 S(6): 56.8; S(9): 37.7; S(21): 26	8	0.705	15
Low		VLRALePVsmGAGVIPAAcGGEGGDVM	S9(Phospho)	1 S(9): 100.0; Y(28): 100.0	19	0.622	10
Low		VssKIHCAmAALLLAILLPVsHAsGR	S2(Phospho)	1 S(2): 100.0; S(3): 100.0; S(21):	10	0.501	10
Low		VTIDVAsPEAGVIEKFIAsEGDtVTPGtK	S7(Phospho)	0.657 T(2): 10.0; S(7): 93.1; S(19): 92	29		14
Low		WAADAGHNLTAGDDFFTsvVKSyYk	S18(Phospho)	0.434 T(10): 0.4; T(17): 3.5; S(18): 47	50	0.66	13
Low		WGTWHRAMGDGAPGAGSALGGAGS	T32(Phospho)	0.307 T(3): 7.9; S(17): 30.7; S(24): 30	9	0.302	13

Os01t0723200-01	Low	Similar to 40S ribosomal protein S19-like.	MGtTVATNALLERK	T3(Phospho)	0.138 T(3): 13.8; T(4): 13.8; T(7): 72.	44		11
	Low		sFLVLIRGTHSmK	S1(Phospho)	0.719 S(1): 71.9; T(9): 20.8; S(11): 7.	19		11

Os01t0752300-01	Low	Similar to 60S ribosomal protein L18a-1.	AIPRI sPR	S6(Phospho)	1 S(6): 100.0	30		11
	Low		LPI tLPGR	T3(Phospho)	1 T(3): 100.0	39	0.718	17

Os01t0762500-00	Middle	Glutelin subunit mRNA.	EGMEsDEEIGRVPELGLEPGGASTSGR	S5(Phospho)	0.945 S(5): 94.5; S(23): 1.8; T(24): 1.	32	0.027	12
	Middle		EtLNIFPsQPmDGEPI tPKASMsAPPIA	T2(Phospho)	0.048 T(2): 71.4; S(8): 71.4; T(16): 71	0	0.036	12

Middle	GQVGVstAGNDGPDGFLHNGtPWtLTV. S5(Phospho)	0.018 S(5): 62.5; T(6): 62.5; S(7): 62.	0	0.014	12
Middle	QAVGVGcIIIMPHNVFLHsALVQSR S19(Phospho)	1 S(19): 100.0; S(24): 0.0	52	0.048	15
Low	AAAAAAGDEELESLLRNfHR T5(Phospho)	1 T(5): 100.0; S(14): 0.0	48	0.642	15
Low	AAGLTRIHALR T7(Phospho)	0.5 T(5): 50.0; T(7): 50.0	5	0.415	16
Low	AEFFyERGNFLASFLSAPAAAAAtdAASG Y5(Phospho)	0.314 Y(5): 62.9; S(13): 24.5; S(16): 1	13		12
Low	AESLcGAWVAsAEAAAAmAIASEVtEV S11(Phospho)	0.447 S(3): 10.3; S(11): 89.3; S(22): 1	34	0.052	11
Low	AGSGNSSDILSDSttQEVLPtEAVKPGGR T14(Phospho)	0.221 S(3): 13.7; S(6): 19.9; S(7): 19.	13	0.26	23
Low	AHRENDAMMLFQNILQsGssPSLsIYNsr S17(Phospho)	0.043 S(17): 66.9; S(19): 71.7; S(20):	1		10
Low	AIRtLSLSTFK T4(Phospho)	0.979 T(4): 97.9; S(6): 0.4; S(8): 0.4;	33	0.381	11
Low	ALAKLGPAAtPAR T10(Phospho)	1 T(10): 100.0	58		13
Low	APPsVAAAYPAFKPLIDGAsSNDVMLST S4(Phospho)	0.053 S(4): 70.7; Y(9): 61.4; S(20): 14	7	0.55	10
Low	AQEEVDsTIVIVGTGRWmAmGQAGFG(S7(Phospho)	0.652 S(7): 65.2; T(8): 32.1; T(14): 1.	21	0.527	12
Low	AsLGSFLAGR S2(Phospho)	0.842 S(2): 84.2; S(5): 15.8	31		10
Low	ATGIIALSDSsLK S11(Phospho)	0.759 T(2): 0.7; S(8): 5.1; S(10): 18.3	28		10
Low	ATSSsLTRR S5(Phospho)	0.466 T(2): 0.0; S(3): 0.2; S(4): 6.6; S	46	0.668	11
Low	cIGDGDGFTAyVPTtDPRESANVPLeVH Y11(Phospho)	0.232 T(9): 22.9; Y(11): 56.3; T(14): 3	18		10
Low	DDGTsMGKTyELGGPElyTVHELAEtMY S5(Phospho)	0.013 T(4): 28.6; S(5): 51.8; T(9): 51.	14	0.092	20
Low	DMDDTVmKTAIGVLGDLADTLGVHAGF S34(Phospho)	0.139 T(5): 0.2; T(9): 0.3; T(20): 13.9	28	0.751	15
Low	DmPPtPLPPETANTSPAPNGAtAGIRVEI T5(Phospho)	0.034 T(5): 43.8; T(11): 43.8; T(14): 4	2	0.754	17
Low	DPsVVTALiYmYAKcGMLDssVsLLyGVA S3(Phospho)	0.091 S(3): 51.6; T(6): 51.6; Y(10): 51	12	0.778	10
Low	EAVTLGVLMNtK T11(Phospho)	1 T(4): 0.0; T(11): 100.0	45		17
Low	EEFMHTLQYLTDLtmDNLsQssDLDNFL(T14(Phospho)	0.019 T(6): 66.1; Y(9): 55.9; T(11): 55	2		10
Low	ETEVLFLSGATAAAAsAGcGGGFPEAKSI S15(Phospho)	0.242 T(2): 47.4; S(7): 13.7; T(11): 8.	8		12
Low	EWAETWFISTLDDTSEPEGEAKNIVFPs S28(Phospho)	0.819 T(5): 0.5; S(9): 1.2; T(10): 1.2;	33		12
Low	FGHLtSIVNLGLDGSPIDGVPHDYK T5(Phospho)	0.617 T(5): 61.7; T(6): 18.7; S(7): 18.	39	0.727	11
Low	FIAsLIRDPVVASTmGSScILISmLSsGFII S4(Phospho)	T6(Phospho)S Too many isoforms		0.792	12
Low	FLsVVAEMGLPGFGVKDLEEGSmsSlVE S3(Phospho)	0.15 S(3): 100.0; S(22): 85.0; S(24):	29	0.766	11
Low	FmTPsGTAEQILNLGALGyRAPELANTA S5(Phospho)	0.04 T(3): 50.0; S(5): 30.2; T(7): 30.	8	0.766	21
Low	FNNTtPKPPPPPPPEPPTGPVSARR T5(Phospho)	0.74 T(4): 24.3; T(5): 74.0; T(19): 1.	35	0.399	11
Low	FstAAAAAAAscPisPcVTPRLAR S2(Phospho)	0.142 S(2): 82.8; T(3): 82.8; S(11): 82	0	0.803	10
Low	FSVMAIVAHAVVAsMLGP S14(Phospho)	1 S(2): 0.0; S(14): 100.0	58	0.388	11
Low	FtAENGVIK T2(Phospho)	1 T(2): 100.0	49		12
Low	GAIGFGVGGsGGGEDGGAGGLPVGAG S10(Phospho)	1 S(10): 100.0	58		17
Low	GcEVDaVDISGLSPNLAENLASPItLGVDI T24(Phospho)	0.348 S(10): 20.5; S(13): 22.4; S(22):	8		13
Low	GFGIKHQVDSHLFESDQGALmAVLVGY S28(Phospho)	0.497 S(10): 0.2; S(15): 0.3; Y(27): 49	26	0.774	11
Low	GHDGFQmVASAmSQDSVDGPQVSGcs S26(Phospho)	0.033 S(10): 24.7; S(13): 27.9; S(16):	5		11
Low	GPAAAAAAsPsPASPSPVSSPSsEEDEEt S8(Phospho)	0.059 S(8): 55.0; S(10): 44.0; S(13): 4	15	0.804	11
Low	GQQDFPcLQELAISNcLsLNsLSLYNmV/ S18(Phospho)	0.219 S(14): 29.4; S(18): 51.1; S(21):	12		11
Low	GQQQQTTTTNAAVATAEQEDAAPARD(T9(Phospho)	0.099 T(6): 17.4; T(7): 17.4; T(8): 29.	13		11
Low	GRPRGAtASSAHSAPPPQQQQQPTts. T7(Phospho)	0.041 T(7): 25.4; S(9): 25.4; S(10): 25	10	0.727	13
Low	GSGSSKAGASSASSSSsASASASAGC S16(Phospho)	0.006 S(2): 0.8; S(4): 0.8; S(5): 0.8; S	15	0.756	11
Low	GtPKLIEHFLtLSFNpVsVAAGtWHAAAL(T2(Phospho)	0.458 T(2): 95.9; T(11): 54.2; S(13): 5	42	0.804	12
Low	GtQTLAmLK T2(Phospho)	0.976 T(2): 97.6; T(4): 2.4	45		10
Low	IIsDcEsALTFLNNSLSILSTSVAREQGET S3(Phospho)	0.05 S(3): 9.8; S(7): 9.8; T(10): 9.1;	19		10
Low	IvAQPYIQEsK S10(Phospho)	0.998 Y(6): 0.2; S(10): 99.8	37	0.671	12
Low	IvVAGTRPNSAtADPAVAAsQLAFtsVsA. T12(Phospho)	0.038 T(6): 80.6; S(10): 79.6; T(12): 7	1		12
Low	KsIAHIVK S2(Phospho)	1 S(2): 100.0	45	0.776	11

Low	LAtAIMmLcyPNGEyKLVGNLPELFGDDY T3(Phospho)	0.497 T(3): 99.9; Y(10): 99.7; Y(15): 9	31	0.806	14
Low	LAVAAVVVFALLsLR S14(Phospho)	1 S(14): 100.0	67	0.149	15
Low	LLAGSVHVQSFDWVSPsVYGsGGKR S17(Phospho)	0.83 S(5): 0.0; S(10): 0.0; S(15): 1.2	45		11
Low	LLDDSmNsMHDAAtNfstELSSLEAMISE S8(Phospho)	0.006 S(5): 80.8; S(8): 22.5; T(14): 64	10	0.282	13
Low	LLPmLymLLmASTEYAQAFsNETDLDAL Y6(Phospho)	0.166 Y(6): 84.4; S(12): 16.2; T(13): 2	12	0.617	14
Low	LmGLMLDQAtLDDLlVsGDDGGVYDVN T10(Phospho)	0.721 T(10): 98.2; S(17): 73.9; Y(24):	33	0.519	13
Low	LNmtPtPsGTmPSTDWMAMVAGDGGGI T4(Phospho)	0.031 T(4): 38.1; T(6): 63.7; S(8): 64.	14	0.799	12
Low	LPAAttALVLAR T5(Phospho)	1 T(5): 100.0; T(6): 100.0	15	0.766	10
Low	LPQLLKEMAAmELKPDsVtystmlyAyAR S17(Phospho)	1 S(17): 100.0; T(19): 100.0; Y(2	1		12
Low	LsLLsmTVGLQNGGPmYEWAGAGITSV S2(Phospho)	0.787 S(2): 89.2; S(5): 89.2; T(7): 21.	37	0.155	11
Low	LsQSSILVVGAGGLGsPVAMyLAAcGVG S2(Phospho)	0.252 S(2): 41.9; S(4): 41.9; S(5): 41.	22	0.457	10
Low	LVAsgVPR S4(Phospho)	1 S(4): 100.0	10	0.804	14
Low	LVFHFDDGGADLDLPAENYmVLDGGsGf S25(Phospho)	0.106 Y(18): 50.1; S(25): 37.9; T(31):	5	0.735	12
Low	MAGNDWINSyLEAILDAGGAAGEISAAf Y10(Phospho)	0.793 S(9): 16.2; Y(10): 79.3; S(25): 4	27	0.731	15
Low	mARPsPVEASGGPVmGDITGGGGELR' S5(Phospho)	0.39 S(5): 48.4; S(10): 48.4; T(19): 1	11	0.766	15
Low	mDLSPNPDSPPSGGGNGGGGSSSsf S25(Phospho)	0.02 S(4): 11.7; S(9): 11.7; S(12): 11	3	0.507	10
Low	mEGVAAQFAGPILTIIVAAAvtFyAVsFr T22(Phospho)	0.068 T(14): 93.2; T(22): 63.8; Y(24):	2	0.715	18
Low	mmAEADADGDGFIsLDEFAALNATASG S14(Phospho)	0.892 S(14): 89.2; T(24): 5.4; S(26): 5	31	0.412	12
Low	MPVPTyGPPVASSEGQHSSSTGISSSSl Y6(Phospho)	S27(Phospho) Too many isoforms	0.792		13
Low	MPVPtYGPPVASSEGQHSSSTGISSSSl T5(Phospho)	S32(Phospho) Too many isoforms	0.653		13
Low	mQNEYGLAFIIFLGLPsFSSVIPWTsEKIt S17(Phospho)	0.234 Y(5): 1.1; S(17): 71.1; S(19): 21	32		13
Low	MTsAmAMSFLSTTAASSSQPLPARR S3(Phospho)	0.122 T(2): 6.3; S(3): 12.2; S(8): 12.2	11		10
Low	NDSVMALYNLSTVTDNLQTILsVQPIPSL Y8(Phospho)	0.061 S(3): 56.6; Y(8): 26.3; S(11): 10	15	0.502	14
Low	NDtFVAALK T3(Phospho)	1 T(3): 100.0	39		10
Low	NEVFcFGFEFVAVSVIQIFSITEGmEVHE S30(Phospho)	0.83 S(14): 1.2; S(20): 5.5; T(22): 11	27	0.803	12
Low	NISADTFVADAASVPPSGFWAPssLLPF S23(Phospho)	0.021 S(3): 24.2; T(6): 24.2; S(13): 41	4		10
Low	NiFGDHNvGLLtGDsAIINKDAQILIMtEILI T2(Phospho)	1 T(2): 100.0; T(12): 100.0; S(15):	16	0.65	16
Low	QGGmQQQVAMDRLAAGAMPVQYGMF S28(Phospho)	0.51 Y(22): 49.0; S(28): 87.8; Y(30):	14	0.806	10
Low	RALEAltGAVFQRPLISAVK T7(Phospho)	0.999 T(7): 99.9; S(18): 0.1	61		13
Low	RAVVtVR T5(Phospho)	1 T(5): 100.0	34		11
Low	RGLlsPR S5(Phospho)	1 S(5): 100.0	26		11
Low	RGLVsLR S5(Phospho)	1 S(5): 100.0	18	0.785	13
Low	RIASEVVAtILQALHmsETPLHFDFNSEIE T9(Phospho)	0.176 S(4): 55.1; T(9): 66.2; S(17): 46	16	0.702	10
Low	RsAHDFGPGVALGFDPAPsctNDGGYIL S2(Phospho)	0.842 S(2): 99.3; S(19): 91.6; T(21): 9	27	0.795	12
Low	SAMAtLVAAAFPSR T5(Phospho)	0.482 S(1): 48.2; T(5): 48.2; S(13): 3.	24		11
Low	scsRSNDmlyLPSVTQyVAPLTLTTPQAtf S1(Phospho)	S3(Phospho)Y Too many isoforms	0.803		14
Low	SGGMLLGRTLsVLItmtLGTAmAAR S11(Phospho)	0.17 S(1): 0.1; T(9): 5.3; S(11): 94.9	57		14
Low	slsLLEAIKccVstAlIcIGFTVLVDsILWR S1(Phospho)	0.118 S(1): 98.3; S(3): 98.6; S(13): 54	19		10
Low	sLQELDLGMGtiESYENFGMDFGMEVGi S1(Phospho)	0.034 S(1): 12.3; T(11): 31.4; S(14): 4	4	0.301	10
Low	SMTfIARPAVRR T5(Phospho)	0.972 S(1): 0.4; T(3): 2.3; T(5): 97.2	51		12
Low	sSASAPAPAKGGNASGAAVTK S1(Phospho)	0.475 S(1): 47.5; S(2): 47.5; S(4): 4.7	31	0.753	11
Low	SSTAVVmSSPDscltLSTQVEGNDcELDI S12(Phospho)	0.047 S(1): 26.3; S(2): 26.3; T(3): 19.	19	0.276	15
Low	STLSNSINLSTPIAvaASRTsVFPAR S22(Phospho)	0.146 S(1): 0.0; T(2): 0.0; S(4): 0.0; S	39	0.168	11
Low	SVTPTNDVVmtGPVAGADVQAAEtFR' T11(Phospho)	0.041 S(1): 54.1; T(3): 54.1; T(5): 44.	14	0.776	19
Low	TcGLGPAMPFAHRLLLQtDsEEVLGLVPi T18(Phospho)	0.278 T(1): 16.6; T(18): 61.1; S(20): 6	7		10
Low	TELSKsELIQK S6(Phospho)	0.132 T(1): 13.2; S(4): 73.6; S(6): 13.	32		10
Low	TKTPLSPTVAGsEPHPFsmsHGLGGSS S12(Phospho)	0 T(1): 46.3; T(3): 46.3; S(6): 49.	8	0.731	16

	Low		TLVmPYWVLcIALcIGTNSsAWLGtAALV S20(Phospho)	0.139 T(1): 26.6; Y(6): 18.4; T(17): 13	18		10
	Low		TPGTTpsscGASTLSVLGTILESGTDGEt S7(Phospho)	0.187 T(1): 6.1; T(4): 12.5; T(5): 12.5	32	0.708	10
	Low		TsHNNsGcPsQPLLVLVQNPsPKVstAAt S2(Phospho)	0.242 T(1): 60.8; S(2): 60.8; S(6): 89.	48	0.782	14
	Low		VAAAAAAWScEGGctARVAEAVVGESl T16(Phospho)	0.104 S(9): 48.5; T(16): 66.4; S(27): 7	7	0.761	10
	Low		VLHPIlccALSADLAAYGYLsR Y19(Phospho)	0.167 S(11): 0.0; Y(19): 99.8; Y(21): 8	62		10
	Low		VMIIIDYKLtYPSGtAtAVLINGFhtPHGDAR T9(Phospho)	0.129 Y(6): 9.1; T(9): 45.8; Y(10): 28.	31		10
	Low		VTAAAI FDSVARHGVTHmGGAPtVLsml T23(Phospho)	0.847 T(2): 0.4; S(9): 7.9; T(16): 7.8;	35		16
	Low		VTAAAI FDSVARHGVTHmGGAPTVLsml S9(Phospho)	0.101 T(2): 6.6; S(9): 82.4; T(16): 30.	18		11
	Low		VttGEmLVGPANAffmDEISTGLDSSItF T2(Phospho)	0.012 T(2): 40.9; T(3): 39.5; S(20): 46	1	0.782	12
	Low		VVEKPGIMSsTK S10(Phospho)	0.333 S(9): 33.3; S(10): 33.3; T(11): 3	15	0.46	13
	Low		VVVTtISIRLAPSPSSSPTSTTAPFPTP T5(Phospho)	0.365 T(4): 16.2; T(5): 36.5; S(7): 36.	21		11
	Low		WLDVGLYTSRIFmAVPGcstMVGPMntE S19(Phospho)	0.014 Y(7): 28.0; T(8): 43.2; S(9): 43.	1	0.802	10
	Low		WNcGWHicSNcQKPAFHmcYTctysLcK T23(Phospho)	0.069 S(9): 49.0; Y(20): 49.0; T(21): 4	3	0.806	13
	Low		YARPsIRAAmtVLQSNGLPVLpSk S5(Phospho)	0.169 Y(1): 10.1; S(5): 24.2; T(11): 63	23	0.733	15
	Low		YNEEWVDPsSPPVRNQSNTVLESISet S9(Phospho)	0.169 Y(1): 3.8; S(9): 16.9; S(10): 9.5	11	0.788	18
Os01t0815800-01	Low	Similar to 60S ribosomal protein L24-A (L30A) (RP29) (YL21).	tLEVKIAtPK T1(Phospho)	1 T(1): 100.0; T(8): 100.0	48	0.695	13
Os01t0823300-00	Low	Similar to Ribosomal protein S26.	AYLAATsSSVLVLDLK S7(Phospho)	0.091 Y(2): 0.7; T(6): 9.1; S(7): 9.1; S	30	0.421	10
	Low		DIDLmTQAsVSRaK S10(Phospho)	0.398 T(7): 20.4; S(10): 39.8; S(12): 3	6		12
	Low		DPLLGDGALVLPsGAR S14(Phospho)	1 S(14): 100.0	30	0.157	14
	Low		GEAGtGNVVEAVRHVR T5(Phospho)	1 T(5): 100.0	20	0.754	13
	Low		ISQPPsKILQSQAPR S6(Phospho)	0.998 S(2): 0.2; S(6): 99.8; S(11): 0.0	53	0.714	10
	Low		MISPsLILmMSPGTR S5(Phospho)	0.758 S(3): 20.6; S(5): 75.8; S(11): 2.	23		13
	Low		MVSIAGFGGLGKtTLAK T13(Phospho)	0.5 S(3): 0.0; T(13): 50.0; T(14): 50	39	0.337	14
	Low		NNLVGNVPDsLGLIPK S10(Phospho)	1 S(10): 100.0	8	0.727	11
	Low		RSPSSPPPGLDVAAGsR S16(Phospho)	0.652 S(2): 5.2; S(4): 5.2; S(5): 24.5;	17	0.799	12
	Low		SLLMLPAsGPKANGsK S8(Phospho)	0.982 S(1): 1.8; S(8): 98.3; S(15): 99.	35	0.803	12
	Low		VcVtGAGGFIGSWLVK T4(Phospho)	1 T(4): 100.0; S(12): 0.0	43	0.22	18
Os01t0835900-00	Middle	Similar to Histone H4.	ILGVLATsR S8(Phospho)	0.978 T(7): 2.2; S(8): 97.8	50	0.046	12
	Low		AAIPtIqYLIK T5(Phospho)	0.862 T(5): 86.2; Y(8): 13.8	50		13
	Low		ARALSVsPK S7(Phospho)	0.878 S(5): 12.2; S(7): 87.8	39	0.744	10
	Low		FIATLPSLrK T9(Phospho)	0.12 T(4): 44.0; S(7): 44.0; T(9): 12.	12	0.632	12
	Low		KVVNGAtIK T7(Phospho)	1 T(7): 100.0	42		10
	Low		LILtNLSR T4(Phospho)	0 T(4): 0.0; S(7): 100.0	33	0.11	12
	Low		LKSQIASLEsR S10(Phospho)	1 S(3): 0.0; S(7): 0.0; S(10): 100.	46	0.674	15
	Low		LVLfSkSLPSR S5(Phospho)	0.843 S(5): 84.3; S(7): 15.6; S(10): 0.	38	0.792	11
	Low		NAISsLGDELSK S5(Phospho)	0.496 S(4): 49.6; S(5): 49.6; S(11): 0.	33	0.524	13

Os01t0839500-00	Low Low	Histone-fold domain containing protein.	AAAIsvsNK VmRmVSEtSLLSPAK	S7(Phospho) T8(Phospho)	0.937 S(5): 6.3; S(7): 93.7 0.934 S(6): 3.0; T(8): 93.4; S(9): 3.0;	17 63	0.477 0.574	12 10
Os01t0851700-01	Low Low Low Low Low Low Low Low Low Low Low Low Low Low Low	Similar to Cytosolic starch phosphorylase (Fragment).	AVVIGVGSntAmGSIRDAMLR FSGDVFPKtDPGIVLAVTDR FtGAVGPHLVSLSHLPSSDGR HHHPLmTIVsNKPPTPSPK IPVssPQLAKHALEAHVTR KtLQsFDLLGmNVAFLK LLNGNRSILPATMTITmAsN LPTHPPSSSVLTPMAVtRSR mNIsLRtLFPPIFTFLK mRPEtRLDSAVFQLTPTR MSLIPLPGMVGLIPsGsKEK QQtAEAIvScIISSHFSSK tVVGTMREVVAEEGLMGLSR VAVQLNDtHPTLAIPELmR	T10(Phospho) T9(Phospho) T2(Phospho) S10(Phospho) S4(Phospho) T2(Phospho) S19(Phospho) T17(Phospho) S4(Phospho) T5(Phospho) S15(Phospho) T3(Phospho) T1(Phospho) T8(Phospho)	0.87 S(8): 10.8; T(10): 87.0; S(14): 2 0.955 S(2): 1.3; T(9): 95.5; T(18): 3.2 0.998 T(2): 99.8; S(11): 0.1; S(13): 0. 0.919 T(7): 7.0; S(10): 91.9; T(15): 0. 0.985 S(4): 99.2; S(5): 99.2; T(18): 1. 1 T(2): 100.0; S(5): 100.0 0.935 S(7): 0.0; T(12): 2.1; T(14): 2.1 0.5 T(3): 0.0; S(7): 0.0; S(8): 0.0; S 1 S(4): 100.0; T(7): 100.0; T(14): 0.986 T(5): 98.6; S(9): 0.5; T(15): 0.5 0.997 S(2): 0.3; S(15): 99.9; S(17): 99 0.2 T(3): 20.0; S(9): 20.0; S(13): 20 0.379 T(1): 37.9; T(5): 37.9; S(19): 24 0.994 T(8): 99.4; T(11): 0.6	24 28 36 36 24 79 37 47 46 27 36 1 2 44	0.713 0.713 0.574 0.573 0.756 0.784 0.577 0.803 0.763 0.804 0.702 0.743	11 14 14 22 12 11 11 12 14 15 16 12 12 12
Os01t0896700-00	Low Low	Similar to 60S ribosomal protein L5.	AAPTkLyITPNLVscNILLK AGLSDPNRPIASFmFGPtGVGK AsNILLDSDFNTKLSDFGLAK AtQVVFHELRApySFPFPR DFsGGGGGGGGATLsEmYQSARR FVVAaVVAVSLAMAAAAAAHDYGEAL HEIIsDGMHIPLPLDMDILR ITIGStPGAIEALVELLQSGSPR KSHtPSAIVIGSGFAGIAAANALR LAEKTESLTVAETGEPsFTGmK mAtmFAAVPSVVAmsLRNELR mmLKLfItINELsLVLQR MSPTtTVALPPsPPPLSVRAR MSPtTtTVALPPsPPPLSVRAR RSSsVNPVMLSSmAASPAANGAVK sTAPTGDPPVRVAVASGGGGmGLGK TPMtVtAPmQmAMtPSLANK VcVIAAAAAAKPVRVHssMyAsLR VESAVtQLtQLVsNLLAMHK VLDFtYGHGTANTALIYHHGK YEEsGRAYmLSGLSSHSWQR YEstEEDVNNmKMVMK	Y7(Phospho) T19(Phospho) S2(Phospho) T2(Phospho) S3(Phospho) S28(Phospho) S5(Phospho) T6(Phospho) T4(Phospho) S17(Phospho) T3(Phospho) T7(Phospho) T5(Phospho) T4(Phospho) S4(Phospho) S1(Phospho) T4(Phospho) S17(Phospho) T6(Phospho) T5(Phospho) S4(Phospho) S3(Phospho)	0.204 T(4): 72.8; Y(7): 21.2; T(9): 7.8 0.12 S(4): 12.0; S(12): 76.0; T(19): 1 0.489 S(2): 98.4; S(8): 2.0; T(12): 49. 0.833 T(2): 99.7; Y(13): 83.6; S(14): 1 0.44 S(3): 88.7; T(13): 55.2; S(15): 5 0.879 S(11): 0.3; Y(23): 11.9; S(28): 1 1 S(5): 100.0 0.603 T(2): 18.8; S(5): 18.8; T(6): 60. 0.447 S(2): 10.6; T(4): 44.7; S(6): 44. 0.189 T(5): 0.0; S(7): 0.0; T(9): 0.1; T 0.958 T(3): 95.8; S(10): 3.9; S(15): 0. 1 T(7): 100.0; T(9): 100.0; S(13): 0.129 S(2): 13.7; T(4): 70.1; T(5): 14. 0.726 S(2): 12.3; T(4): 73.4; T(5): 2.7 0.514 S(2): 18.8; S(3): 18.8; S(4): 51. 0.99 S(1): 99.5; T(2): 99.5; T(5): 1.0 0.879 T(1): 6.6; T(4): 94.0; T(6): 99.4 1 S(17): 100.0; S(18): 100.0; Y(2 0.976 S(3): 2.4; T(6): 98.2; T(9): 99.4 0.8 T(5): 80.0; Y(6): 19.4; T(10): 0. 0.618 Y(1): 17.1; S(4): 61.8; Y(8): 6.1 0.793 Y(1): 20.7; S(3): 89.6; T(4): 89.	25 12 36 41 41 27 33 28 51 37 25 17 55 84 18 54 49 26 42 31 15 78	 0.804 0.792 0.752 0.365 0.793 0.225 0.556 0.755 0.805 0.48 0.117 0.806 0.522 0.744 0.776 0.786 	10 14 13 10 14 12 12 10 13 14 11 14 12 10 14 15 14 12 13 10 15

	Low		yEsTEEDVNNmKMVMK	Y1(Phospho)	0.47 Y(1): 53.0; S(3): 94.1; T(4): 53.	88		17
Os01t0896800-01	High	Ribosomal protein L18/L5 domain containing protein.	AEsEGEAEGTTETHDVEGGISLPLSER	S3(Phospho)	0.998 S(3): 99.8; T(10): 0.1; T(11): 0.	78	0	20
	Low		AAPTKLyITPNLVscNILLK	Y7(Phospho)	0.204 T(4): 72.8; Y(7): 21.2; T(9): 7.8	25		10
	Low		AGLSDPNRPIASFMMGPtGVGK	T19(Phospho)	0.12 S(4): 12.0; S(12): 76.0; T(19): 1	12	0.804	14
	Low		AsNILLDSDFNTKLsDFGLAK	S2(Phospho)	0.489 S(2): 98.4; S(8): 2.0; T(12): 49.	36	0.792	13
	Low		AsTAAFLSTLAGSTSLGGATPASGGGS	S2(Phospho)	0.223 S(2): 49.0; T(3): 16.6; S(8): 16.	34		11
	Low		AtQVVFHELRApySFPFPR	T2(Phospho)	0.833 T(2): 99.7; Y(13): 83.6; S(14): 1	41		10
	Low		DDGSEARIPAsGGAcMRPGEIDISSK	S11(Phospho)	0.262 S(4): 73.3; S(11): 26.2; S(25): 0	22	0.563	18
	Low		DFsGGGGGGGATLsEmYQSARR	S3(Phospho)	0.44 S(3): 88.7; T(13): 55.2; S(15): 5	41	0.752	14
	Low		DGELKHGEQQAcSVLTLAcDSVNGGR	S13(Phospho)	0.927 S(13): 92.7; T(16): 6.6; S(21): 0	54	0.25	10
	Low		HEIIsDGMHIPLPLDMDILR	S5(Phospho)	1 S(5): 100.0	33	0.793	12
	Low		IGLscSmPLPK	S4(Phospho)	0.985 S(4): 98.5; S(6): 1.5	72		10
	Low		IQNAGTEVVEAKAGAGsAtLSmAYAAAF	S17(Phospho)	0.588 T(6): 4.9; S(17): 85.2; T(19): 70	29	0.279	14
	Low		ITIGStPGAIEALVELLQSGSPR	T6(Phospho)	0.603 T(2): 18.8; S(5): 18.8; T(6): 60.	28	0.225	10
	Low		KSHtPSAIVIGSGFAGIAAANALR	T4(Phospho)	0.447 S(2): 10.6; T(4): 44.7; S(6): 44.	51		13
	Low		LAETESLTVAETGEPsFTGmK	S17(Phospho)	0.189 T(5): 0.0; S(7): 0.0; T(9): 0.1; T	37	0.556	14
	Low		LGVNEKETSgGK	S9(Phospho)	0.951 T(8): 4.9; S(9): 95.1	39		12
	Low		mAPPPPPPTAtK	T11(Phospho)	0.827 T(9): 17.3; T(11): 82.7	29	0.773	18
	Low		mAtmFAAVPSVAmSLRNELR	T3(Phospho)	0.958 T(3): 95.8; S(10): 3.9; S(15): 0.	25	0.755	11
	Low		mDSAALsLTcAGLGGAEDDGGAVVGy	S7(Phospho)	0.204 S(3): 26.6; S(7): 20.4; T(9): 15.	2	0.784	11
	Low		mGSEmNVVmQtILVHMyIKcmR	T11(Phospho)	0.738 S(3): 26.2; T(11): 83.6; Y(17): 9	11	0.802	12
	Low		mmLKLfItINELsLVLQR	T7(Phospho)	1 T(7): 100.0; T(9): 100.0; S(13):	17	0.805	14
	Low		MSPTtTVALPPsPPPLSVRAR	T5(Phospho)	0.129 S(2): 13.7; T(4): 70.1; T(5): 14.	55	0.48	14
	Low		MSPtTTWALPPsPPPLSVRAR	T4(Phospho)	0.726 S(2): 12.3; T(4): 73.4; T(5): 2.7	84	0.117	12
	Low		NGLAVPMSNSIK	T11(Phospho)	0.488 S(8): 2.4; S(10): 48.8; T(11): 48	38		15
	Low		RSSsVNPVMLSSmAASPAANGAVK	S4(Phospho)	0.514 S(2): 18.8; S(3): 18.8; S(4): 51.	18	0.806	10
	Low		stAPTGDPPVRVAVASGGGGmGLGK	S1(Phospho)	0.99 S(1): 99.5; T(2): 99.5; T(5): 1.0	54	0.522	14
	Low		TPMtVtAPmQmAMtPSLANK	T4(Phospho)	0.879 T(1): 6.6; T(4): 94.0; T(6): 99.4	49	0.744	15
	Low		VESAvtQLtQLVsNLLAMHK	T6(Phospho)	0.976 S(3): 2.4; T(6): 98.2; T(9): 99.4	42		12
	Low		VLDfYtYGHGTANTALIYHHGK	T5(Phospho)	0.8 T(5): 80.0; Y(6): 19.4; T(10): 0.	31	0.776	13
	Low		VVKyNImSGTSMScPHVSAAtAVLLK	Y4(Phospho)	0.64 Y(4): 90.0; S(8): 13.2; T(10): 5.	30	0.742	12
	Low		YEEsGRAYmLSGLSSHWSQR	S4(Phospho)	0.618 Y(1): 17.1; S(4): 61.8; Y(8): 6.1	15	0.786	10
	Low		YEstEEDVNNmKMVMK	S3(Phospho)	0.793 Y(1): 20.7; S(3): 89.6; T(4): 89.	78		15
	Low		yEsTEEDVNNmKMVMK	Y1(Phospho)	0.47 Y(1): 53.0; S(3): 94.1; T(4): 53.	88		17
Os01t0924900-01	High	GTP-binding signal recognition particle SRP54, G-domain containing protein.	ASDAKPDsPPAGVDPPPPKEEAK	S8(Phospho)	1 S(2): 0.0; S(8): 100.0	116	0	52

	High		GVSQKPSQDTEEDDEPEVELESK	T9(Phospho)	0.497 S(3): 0.6; S(6): 49.7; T(9): 49.7	153	0	41
	High		GVSQKPsQDTEEDDEPEVELESK	S6(Phospho)	0.903 S(3): 0.1; S(6): 90.3; T(9): 9.6;	167	0	39
	High		KILTDLVHADYFQNmVyyK	Y17(Phospho)	1 T(4): 0.0; Y(11): 0.0; Y(17): 100.0	111	0.005	21
	Middle		GEWVVGmAQPM LATFLVtcR	T19(Phospho)	0.5 S(6): 0.0; T(15): 50.0; T(19): 50.0	62	0.047	12
	Middle		GVSQKPSQDTEEDDEPEVELESKK	T9(Phospho)	0.447 S(3): 10.7; S(6): 44.7; T(9): 44.7	53	0.048	14
	Low		AIPtILGsLKLtPSPPPsATPVr	T4(Phospho)	0.055 T(4): 100.0; S(8): 99.5; T(12): 100.0	45	0.546	14
	Low		AIPtILGsLKLTPsPPsATPVr	T4(Phospho)	0.819 T(4): 100.0; S(8): 100.0; T(12): 100.0	84	0.098	20
	Low		ALPLLPPAAPTssPPPsQRSR	S12(Phospho)	0.675 T(11): 26.8; S(12): 79.6; S(13): 79.6	37	0.804	10
	Low		ASAAmStLNLsSSPLTKQQLR	T7(Phospho)	0.017 S(2): 7.7; S(6): 10.4; T(7): 10.4	1		11
	Low		ESSQGD PATGSSGVQNGTVNALyK	Y23(Phospho)	0.946 S(2): 0.0; S(3): 0.0; T(9): 0.0; S(23): 0.0	70		11
	Low		ESSQGD PATGSSGVQNGtVNALYK	T18(Phospho)	0.307 S(2): 0.0; S(3): 0.0; T(9): 0.0; S(18): 0.0	52		23
	Low		IGNmTRFADtLsDTSPSSPAQR	T10(Phospho)	0.967 T(5): 3.1; T(10): 97.0; S(12): 99.0	73	0.761	10
	Low		KLsPPAsADmPQALPENDGEQR	S3(Phospho)	1 S(3): 100.0; S(7): 100.0	71		11
	Low		LRLIFILLYSSVsYyK	Y9(Phospho)	0.111 Y(9): 77.9; Y(10): 21.1; S(11): 21.1	27	0.789	11
	Low		mAALLmNTGAVsmPFPTTRTAAR	S12(Phospho)	0.576 T(8): 25.1; S(12): 57.6; T(17): 60.0	15	0.714	12
	Low		mASLASASAsL VFSTSSSKPR	S10(Phospho)	0.002 S(3): 3.4; S(6): 6.7; S(8): 5.7; S(10): 5.7	25	0.76	12
	Low		mQVtsAAAGmTVKVSTTPIFSK	T4(Phospho)	0 T(4): 6.8; S(5): 92.9; T(11): 1.0	3		18
	Low		MVNDGEQALTIAPAAAADSSsAEPAR	S20(Phospho)	0.934 T(10): 0.1; S(19): 6.5; S(20): 93.4	43	0.219	12
	Low		RPPSVAPNDDAsGPSPATARAVsR	S12(Phospho)	0.088 S(4): 1.8; S(12): 94.3; S(15): 7.0	25	0.803	19
	Low		RSGISSicYVLNVlySLLtGR	Y15(Phospho)	0.206 S(2): 0.1; S(5): 0.1; S(6): 0.1; Y(15): 0.1	33	0.451	11
	Low		tsSSNAAVLPRDSHSSSQRP HR	T1(Phospho)	0.906 T(1): 93.9; S(2): 93.9; S(3): 8.3	77	0.417	14
	Low		VGTstENVLLQSTsFGHADAPR	S4(Phospho)	0.333 T(3): 66.6; S(4): 66.6; T(5): 66.6	43		11
Os01t0949060-01	Low	Hypothetical conserved gene.	GLISGmVmGmVVGVALmAGWsR	S21(Phospho)	0.136 S(4): 86.4; S(21): 13.6	4		11
	Low		HSSSEDLSsLtINNLRI NHR	S8(Phospho)	0.032 S(2): 90.4; S(3): 3.2; S(7): 3.3;	59	0.412	14
	Low		RELtEAGGAGQH YGGAQGGALTGK	T4(Phospho)	0.687 T(4): 68.7; Y(13): 2.3; T(22): 29.0	19		11
	Low		WDNGAVsILPEYmHAYYIK	S7(Phospho)	0.988 S(7): 98.8; Y(12): 0.3; Y(16): 0.0	27	0.532	11
Os02t0105900-01	Low	Similar to 40S ribosomal protein S4.	LsLGGGmAARLK	S2(Phospho)	1 S(2): 100.0	22	0.732	16
	Low		mDtVAAAII LR	T3(Phospho)	1 T(3): 100.0	41	0.089	12
Os02t0115900-01	Low	Endosperm luminal binding protein.	AGGETPVLmSGAGHDAmAMARL tK	T23(Phospho)	0.971 T(5): 0.6; S(10): 2.3; T(23): 97.0	23	0.558	17
	Low		APPASAPSSSTSSASGSSTsATTLHR	S20(Phospho)	0.676 S(5): 0.1; S(8): 0.2; S(9): 0.2; S(20): 0.2	44		14
	Low		DNSSFKKPAQSSGNtIFI K	T15(Phospho)	0.1 S(3): 2.9; S(4): 38.5; S(11): 38.5	26	0.569	10
	Low		GTAALAI DTPPsWGR	S13(Phospho)	0.999 T(2): 0.0; T(10): 0.1; S(13): 99.0	54	0.3	15
	Low		LFstMQGFISVsGIER	S3(Phospho)	0.912 S(3): 99.1; T(4): 96.1; S(10): 8.0	50		10
	Low		mWASNSLNRLtPAssLPILR	T11(Phospho)	0.054 S(4): 71.7; S(6): 71.7; T(11): 71.7	7		11
	Low		mWAsNsLNRLtPASSLPILR	S4(Phospho)	0.869 S(4): 94.2; S(6): 94.2; T(11): 94.2	25		12
	Low		QANRASNFDTsILEMNT HVQK	S11(Phospho)	0.447 S(6): 10.5; T(10): 44.7; S(11): 44.7	46		11
	Low		RAsMLNmLGIsAGVAA YGEAR	S3(Phospho)	0.033 S(3): 11.8; S(11): 91.5; Y(19): 91.5	2		16
	Low		SHFLHTASTTtPRK	T11(Phospho)	0.973 S(1): 0.0; T(6): 0.0; S(8): 0.0; T(11): 0.0	63	0.602	12
	Low		sQFVTEVATIssVQHRNLVK	S1(Phospho)	0.837 S(1): 99.9; T(5): 9.8; T(9): 9.8;	56		10
	Low		SSPSISTtVPFAPHR	T8(Phospho)	0.673 S(1): 0.1; S(2): 0.1; S(4): 1.3; S(8): 1.3	32	0.329	12

	Low		SSPSISiTVPFAPHR	T7(Phospho)	0.438 S(1): 0.2; S(2): 0.2; S(4): 0.5; S	26	0.272	10
	Low		VVWTISsLIAASr	S7(Phospho)	0.695 T(4): 0.3; S(6): 14.8; S(7): 70.4	47	0.649	15
Os02t0130000-01	Low	Similar to SWIb domain-containing protein (Fragment).	LALtAAPPTQPRR	T4(Phospho)	0.967 T(4): 96.7; T(9): 3.3	26	0.743	14
Os02t0161200-01	High	Zinc finger, CCCH-type domain containing protein.	GANEEGSSVNEDLNERSpNTAATK	S17(Phospho)	0.965 S(7): 0.0; S(8): 0.1; S(17): 96.5	90	0.001	31
	High		GANEEGSSVNEDLNERSpNTAATK	T20(Phospho)	0.14 S(7): 0.0; S(8): 0.1; S(17): 85.4	85	0	36
	Low		AADPSSPGmAGAAVAAYGLRGsGmLG	S22(Phospho)	0.997 S(5): 0.0; S(6): 0.0; Y(17): 0.3;	64	0.596	12
	Low		AAtNNFNsKNILGEGGYGIVyK	T3(Phospho)	0.96 T(3): 99.7; S(8): 99.7; Y(17): 4.	33		13
	Low		EQILsSTNEKMTTSVPQGASSsK	S5(Phospho)	0.044 S(5): 13.1; S(6): 13.1; T(7): 57.	52		14
	Low		LAGMAPsPSLNRStFFSQPcSR	S7(Phospho)	0.383 S(7): 78.0; S(9): 21.1; S(13): 4.	43	0.603	11
	Low		LLtALVsEYLEWAQLSHtmK	T3(Phospho)	0.005 T(3): 60.9; S(7): 21.4; Y(9): 21.	2	0.773	13
	Low		MPSILPLARQLAsFLAPsPSVAR	S13(Phospho)	0.83 S(3): 3.0; S(13): 97.0; S(18): 8.	70	0.226	17
	Low		NASIsHEKVGSTQyTSAGSSSGAGK	S5(Phospho)	0.07 S(3): 47.1; S(5): 47.1; S(11): 1.	16	0.701	11
	Low		tTRiAYDQFTVTSGYETtNRP	T1(Phospho)	0.016 T(1): 12.0; T(2): 12.0; Y(6): 11.	5	0.76	12
Os02t0162500-01	Low	Similar to 40S ribosomal protein S14.	DGKIYVVDIAtR	T11(Phospho)	0.998 Y(5): 0.2; T(11): 99.8	33		10
	Low		DGLLLLcsTFNDRmsIPR	S8(Phospho)	0.927 S(8): 96.3; T(9): 7.3; S(15): 96.	49	0.612	10
	Low		GEtTGsyvVANPAItFRR	T3(Phospho)	0.124 T(3): 87.6; T(4): 87.6; S(6): 40.	32	0.067	10
	Low		GLHlyDLPGVTcLPESmQR	Y5(Phospho)	0.996 Y(5): 99.6; T(11): 0.2; S(16): 0.	34	0.439	11
	Low		LSmGNIItGALADAEeATKIAPK	T7(Phospho)	0.657 S(2): 6.9; T(7): 65.7; T(17): 27.	15		13
	Low		LtPDPTTVFYTSAIHSSR	T2(Phospho)	0.886 T(2): 88.6; T(6): 0.2; T(7): 0.1;	33		11
	Low		MAASItALSMKLLVDTNAQR	T5(Phospho)	0.74 S(4): 25.0; T(5): 86.9; T(6): 86.	73	0.726	12
	Low		MAASItALSMKLLVDTNAQR	S4(Phospho)	0.078 S(4): 52.7; T(5): 52.7; T(6): 75.	35	0.622	19
	Low		MADGANEDGGGsAAGERPMVAIK	S12(Phospho)	1 S(12): 100.0	51	0.479	10
	Low		MEHtPLtPEITLEqALANK	T4(Phospho)	0.333 T(4): 66.7; T(7): 66.7; T(11): 66.	14	0.65	13
	Low		MGDHTDIHGPAAGAsTVHGSASK	S15(Phospho)	0.592 T(5): 0.7; S(15): 59.2; T(16): 17	34	0.617	12
	Low		RNFEALLtDTVEHSDGIQR	T8(Phospho)	0.163 T(8): 16.3; T(10): 80.0; S(14): 3	39		10
	Low		SPVLSSPVVAADAeGYERER	S1(Phospho)	0.66 S(1): 66.0; S(5): 16.9; S(6): 16.	42	0.775	11
	Low		TTGPGRPPSVSGGRTASVcsDR	S20(Phospho)	0.929 T(1): 0.0; T(2): 0.0; S(9): 0.0; S	43		10
Os02t0175600-01	Low	Similar to 60S ribosomal protein L27a (Fragment).	ALcATVsASLR	S7(Phospho)	0.5 T(5): 0.0; S(7): 50.0; S(9): 50.0	48		11
	Low		tTAYVPQLQK	T1(Phospho)	0.333 T(1): 33.3; T(2): 33.3; Y(4): 33.	87		18
Os02t0235600-01	Low	Similar to 60S ribosomal protein L11-2 (L16). Splice isoform 2.	AtALDmAASGAHPAR	T2(Phospho)	0.201 T(2): 20.1; S(9): 79.9	24	0.691	11

	Low		IALRsSVR	S5(Phospho)	0.907 S(5): 90.7; S(6): 9.3	56		11
	Low		IQtSLALR	T3(Phospho)	0.974 T(3): 97.4; S(4): 2.6	36		11
	Low		KyNPATSScDTLV	Y2(Phospho)	1 Y(2): 100.0; T(6): 0.0; S(7): 0.0	66	0.741	11
	Low		LAsVRSLR	S3(Phospho)	1 S(3): 100.0; S(6): 0.0	62		12
	Low		LVEHPsktPTLR	S6(Phospho)	0.995 S(6): 99.8; T(8): 99.8; T(10): 0.	67	0.732	16
	Low		tlQLTLGR	T1(Phospho)	0.998 T(1): 99.8; T(5): 0.2	50		10
	Low		tlSKPLSR	T1(Phospho)	0.449 T(1): 44.9; S(3): 10.3; S(7): 44.	20		11
Os02t0242600-01	High	Similar to Glutelin.	AAsFNIIPSSTGAAK	S3(Phospho)	0.997 S(3): 99.7; S(9): 0.2; S(10): 0.1	38	0.006	19
	Low		ALLSssFVLPLR	S5(Phospho)	0.333 S(4): 66.7; S(5): 66.7; S(6): 66.	49	0.661	13
	Low		AQDSSSIVsPIR	S9(Phospho)	0.925 S(4): 0.3; S(5): 3.6; S(6): 3.6; S	39	0.776	13
	Low		AsLSGGSVGAGAGGGR	S2(Phospho)	0.779 S(2): 77.9; S(4): 17.6; S(7): 4.5	36	0.629	12
	Low		ATAQIISTVPDR	T5(Phospho)	0.45 T(2): 45.0; T(5): 45.0; S(7): 1.8	35	0.77	12
	Low		DGSsLGGIRELR	S4(Phospho)	0.987 S(3): 1.3; S(4): 98.7	77	0.539	10
	Low		ERGETALsQIR	S8(Phospho)	0.5 T(5): 50.0; S(8): 50.0	24		12
	Low		FsAHKcVLAAR	S2(Phospho)	1 S(2): 100.0	9	0.56	11
	Low		GETGQRsLQIFAK	S7(Phospho)	0.809 T(3): 19.1; S(7): 80.9	29		11
	Low		GGGGGsRATTGWELLR	S6(Phospho)	0.978 S(6): 97.8; T(9): 1.5; T(10): 0.7	29		10
	Low		GVDLmPQsKIR	S8(Phospho)	1 S(8): 100.0	34		11
	Low		IHDYSSILR	Y5(Phospho)	0.983 Y(5): 98.3; S(6): 1.5; S(7): 0.2	67	0.604	11
	Low		IQEDLTsGQLR	S7(Phospho)	0.84 T(6): 16.0; S(7): 84.0	37	0.555	12
	Low		ISVAMAEKsAPR	S9(Phospho)	0.5 S(2): 50.0; S(9): 50.0	14	0.436	12
	Low		KmmLLVAAPfTK	T11(Phospho)	1 T(11): 100.0	37	0.446	13
	Low		KsIAHIVK	S2(Phospho)	1 S(2): 100.0	45	0.776	11
	Low		LATFsGVDIPSFK	S5(Phospho)	0.937 T(3): 6.0; S(5): 93.7; S(11): 0.2	36	0.673	17
	Low		LSQSPGsSVKNR	S7(Phospho)	0.035 S(2): 0.1; S(4): 0.8; S(7): 3.5; S	32	0.788	10
	Low		QGDAIEtGSiIR	T7(Phospho)	0.985 T(7): 98.5; S(9): 1.5	73	0.45	12
	Low		QGDAIETGsIIR	S9(Phospho)	0.122 T(7): 87.8; S(9): 12.2	60	0.531	13
	Low		SDAPLKGPLsVR	S10(Phospho)	0.992 S(1): 0.8; S(10): 99.2	44		11
	Low		sIELAFLDHSK	S1(Phospho)	1 S(1): 100.0; S(10): 0.0	53	0.806	10
	Low		SSGTTALtALVFGR	T8(Phospho)	0.9 S(1): 0.4; S(2): 0.4; T(4): 4.6; T	40		14
	Low		SSILRsIQLR	S6(Phospho)	0.987 S(1): 0.6; S(2): 0.6; S(6): 98.7	46	0.285	11
	Low		sSSNVLLLALR	S1(Phospho)	0.098 S(1): 9.8; S(2): 9.8; S(3): 80.3	52		10
	Low		THPAHLGtAyLK	T8(Phospho)	0.992 T(1): 0.8; T(8): 99.6; Y(10): 99.	24	0.789	11
	Low		TSSSPPLSAVAsR	S12(Phospho)	0.206 T(1): 4.1; S(2): 4.1; S(3): 4.1; S	12	0.744	13
	Low		TSVDsGLSPAGLR	S5(Phospho)	0.987 T(1): 0.6; S(2): 0.6; S(5): 98.7;	60	0.551	16
	Low		TsVNVSVNGRAR	S2(Phospho)	0.446 T(1): 44.6; S(2): 44.6; S(6): 10.	28		11
	Low		VTSLKyLsLR	Y6(Phospho)	0.01 T(2): 49.5; S(3): 49.5; Y(6): 1.3	40	0.726	17
Os02t0248800-01	Low	Similar to Glutelin type-B 2 precursor.	AsAKLTLLHSmLK	S2(Phospho)	0.999 S(2): 99.9; T(6): 0.1; S(10): 0.0	66	0.802	12
Os02t0249000-01	Low	Glutelin, Seed strage protein	AAMaADGVSRFDLVPANVTAFEASAAE	S40(Phospho)	0.07 S(9): 22.4; T(19): 22.4; S(24): 2	3	0.668	11
	Low		ARWVTGTLLMLLSNVTWSLWIVLMSPL	S13(Phospho)	0.033 T(5): 24.1; T(7): 70.2; S(13): 3.	23		10
	Low		DTAFPMtERDR	T7(Phospho)	1 T(2): 0.0; T(7): 100.0	53		11
	Low		DyAGFSPILIK	Y2(Phospho)	1 Y(2): 100.0; S(6): 0.0	78	0.537	11

	Low		GA AAAASSPVEALFtAGIHHPQPSScS: T14(Phospho)	0.011	S(6): 13.5; S(7): 13.5; T(14): 12	0	0.164	11
	Low		IELTPGGVFLSVtK T13(Phospho)	0.997	T(4): 0.1; S(11): 0.2; T(13): 99.	47	0.513	10
	Low		KsIAHIVK S2(Phospho)	1	S(2): 100.0	45	0.776	11
	Low		KVsYGDILK S3(Phospho)	0.5	S(3): 50.0; Y(4): 50.0	40		13
	Low		LSGELPAsLGELR S8(Phospho)	0.958	S(2): 4.2; S(8): 95.8	40	0.54	11
	Low		LSGMTVAGNPLSVSSSAYSSLPTIIdS G: S27(Phospho)T29(Phospho)		Too many isoforms		0.49	22
	Low		LtVVGADAcYtKPyKTDVVVVSPGQtVDA T2(Phospho)	0.018	T(2): 60.7; Y(10): 60.7; T(11): 6	0	0.796	11
	Low		LVQtLGNDLR T4(Phospho)	1	T(4): 100.0	16		11
	Low		MFsPDVLSK S3(Phospho)	1	S(3): 100.0; S(8): 0.0	80	0.373	11
	Low		mGsIGVLTGNAGTIR S3(Phospho)	0.821	S(3): 82.1; T(8): 8.9; T(13): 8.9	22	0.246	17
	Low		mLsPEtEKALK S3(Phospho)	1	S(3): 100.0; T(6): 100.0	21	0.805	12
	Low		NAsPFPALHNQISNTSSLSEVAHAVAVK S3(Phospho)	0.006	S(3): 27.3; S(13): 27.3; T(15): 2	0	0.115	13
	Low		RADAVAAATAVGEPGVPDAAAASVVGI Y29(Phospho)	0.362	T(9): 12.5; S(23): 26.1; Y(29): 5	13	0.742	10
	Low		RDAFYLCaAFLAFHGLSLALLFAAsVsAs S25(Phospho)	0.06	Y(5): 43.7; S(17): 53.7; S(25): 5	2	0.804	11
	Low		RmGIGSHsER S6(Phospho)	1	S(6): 100.0; S(9): 100.0	68		14
	Low		sKYPLIDQGSSLR S1(Phospho)	0.974	S(1): 97.4; Y(3): 2.6; S(10): 0.0	60	0.696	11
	Low		sPAEWGAAAAEmEAEPAPSELNTTNS: S1(Phospho)	0.377	S(1): 37.7; S(19): 6.1; T(23): 10	8		14
	Low		tLIQPPSsMER T1(Phospho)	0.863	T(1): 100.0; S(7): 13.7; S(8): 86	51		12
	Low		VKEtFVTVPATLR T4(Phospho)	0.985	T(4): 98.5; T(7): 0.8; T(11): 0.8	53	0.629	12
	Low		yLSILNHLR Y1(Phospho)	0.857	Y(1): 85.7; S(3): 14.3	30		13
Os02t0249600-01	Middle	Similar to Glutelin.	sVDcVHGFLIyYAWtVScGQGTA VVIATC S1(Phospho)	0.107	S(1): 72.2; Y(11): 72.2; Y(12): 4	39	0.042	12
	Low		AAAAAAGGAsPDGADGAKRPAPAAAS: S10(Phospho)	0.362	S(10): 87.3; S(26): 45.8; S(27):	27		11
	Low		AcVPSIKLsVDAlIIYcsDWNPtNDLR S9(Phospho)	0.062	S(5): 21.5; S(9): 62.2; S(10): 26	23	0.805	13
	Low		AGNAtIAMPQsGNtItVSTATPVTALVDS\ T5(Phospho)S11(Phospho)		Too many isoforms		0.729	11
	Low		AGRLAEAGmMQMMPIQPSVTMWGs: S25(Phospho)	0.719	S(19): 26.1; T(21): 2.0; S(25): 7	28	0.72	11
	Low		AGyLTSSLKK Y3(Phospho)	0.676	Y(3): 67.6; T(5): 10.8; S(6): 10.	39		12
	Low		AKNLtLYSIAR T5(Phospho)	0.829	T(5): 82.9; Y(7): 8.5; S(8): 8.5	18	0.43	10
	Low		APSEVPEYFSGNmSGNLRTItYFDyATL: T21(Phospho)	0.004	S(3): 19.1; Y(8): 38.5; S(10): 38	4	0.49	13
	Low		AsAKLTLLHSmLK S2(Phospho)	0.999	S(2): 99.9; T(6): 0.1; S(10): 0.0	66	0.802	12
	Low		AyEEEQERIK Y2(Phospho)	1	Y(2): 100.0	40		14
	Low		cEmTGVVVDVGDGAtHIVPVADGyVIGs: T15(Phospho)	0.133	T(4): 86.7; T(15): 83.5; Y(24): 7	1	0.581	15
	Low		cLDtmtsKGLLPNTFTYNTVmTAYANVGf T4(Phospho)	0.891	T(4): 95.6; T(6): 95.6; S(7): 96.	46	0.67	21
	Low		cTDTVWPGVLSNAGsARLAtGFELPPG S15(Phospho)	0.162	T(2): 38.0; T(4): 40.7; S(11): 48	7		15
	Low		DAWAAGGGGsVVDtmDPRLEEYSGEE. S10(Phospho)	0.421	S(10): 58.7; T(14): 58.7; Y(22):	9	0.797	10
	Low		DGSmSQEIDIPGPVHSISMDVVGsLVTS S24(Phospho)	0.448	S(3): 2.6; S(5): 2.6; S(16): 1.6;	18		11
	Low		DTTSWNsmVSGSLFNGLAElSAYYFKE: S21(Phospho)	0.136	T(2): 9.0; T(3): 10.0; S(4): 10.0	2	0.231	11
	Low		DVAAGNyEyIDVVVTAVTAAGAGAAKsA Y7(Phospho)	0.617	Y(7): 93.2; Y(9): 93.2; T(15): 16	22	0.063	11
	Low		EDGIGVsEGEEDIsERALHSPSItmVFIVF S7(Phospho)	0.307	S(7): 99.2; S(14): 72.9; S(20): 5	29	0.233	10
	Low		EDyFYFsAtLELEPVGNLESVSPSPSPRf Y3(Phospho)	0.258	Y(3): 66.9; Y(5): 66.9; S(7): 66.	25	0.75	14
	Low		EEGQtmAPNQVAGEILsFFtRNNFTISDF T5(Phospho)	0.618	T(5): 99.7; S(17): 77.2; T(20): 7	31	0.433	10
	Low		EEVtSSEmLVETMMRTGDNDNANPTTT T4(Phospho)	0.288	T(4): 28.8; S(5): 28.8; S(6): 28.	20	0.515	11
	Low		EGPRMHDtNGLmSIsEtLsEYmLYLLVR S15(Phospho)	0.565	T(8): 0.4; S(13): 14.8; S(15): 86	45	0.156	12
	Low		EMsDAKIsPNAVTFVGLLSAYsNAGLmE S3(Phospho)	0.027	S(3): 32.5; S(8): 72.0; T(13): 38	3	0.804	17
	Low		EPSSPIPQAKALLPtSmAAGDMLGFFKP S4(Phospho)	0.523	S(3): 28.1; S(4): 73.5; T(15): 71	31	0.776	12
	Low		ETFNHLAsWLEDARQHANANmtVmLIGI S8(Phospho)	0.774	T(2): 22.6; S(8): 77.9; T(22): 99	29	0.519	14
	Low		ETVGLEGsANGQWWIDNIGKALDEGtsf S8(Phospho)	0.437	T(2): 56.3; S(8): 75.2; T(26): 84	8	0.771	12

Low	GEMGIQYVVLDMGAVGsIDTSGtsmLDE S17(Phospho)	0.046 Y(7): 54.7; S(17): 50.5; T(20): 4	0	0.38	10
Low	GGAPsMQASTHMFRTITPLGGSHHNS S5(Phospho)	0.046 S(5): 28.6; S(9): 28.6; T(10): 28	16		14
Low	GLGsNDIFDsQWIAPVQFEGLLDSEEE S4(Phospho)	0.952 S(4): 99.6; S(10): 95.5; S(24): 4	37	0.606	11
Low	GRAGDA t L I K T7(Phospho)	1 T(7): 100.0	23		11
Low	GR t EQAVL K T3(Phospho)	1 T(3): 100.0	33		10
Low	HAGDEAGMTYEEYmNSmASLFsRmVD S22(Phospho)	0.166 T(9): 16.6; Y(10): 30.2; Y(13): 1	8	0.782	11
Low	HAPNGTKsFcNAcGLmWANsKPIDL V Q t S8(Phospho)	0.413 T(6): 58.7; S(8): 58.7; S(20): 86	10	0.758	11
Low	HIEsLNsIDNFHDVGPSSV m ASPGGLQ S S4(Phospho)	0.971 S(4): 98.4; S(7): 98.4; S(17): 2.	35	0.115	12
Low	IQATAIlyFKR Y8(Phospho)	0.946 T(4): 5.4; Y(8): 94.6	30		12
Low	IsSsVYstRPVAVyEVDRVLLPmQIFR S2(Phospho)	0.179 S(2): 54.9; S(3): 54.9; S(4): 83.	28		10
Low	KLVMEILsHINK S8(Phospho)	1 S(8): 100.0	5	0.778	10
Low	KsIAHIVK S2(Phospho)	1 S(2): 100.0	45	0.776	11
Low	LEtVDLRR T3(Phospho)	1 T(3): 100.0	43		11
Low	LGsGPASTALK S3(Phospho)	0.333 S(3): 33.3; S(7): 33.3; T(8): 33.	32		12
Low	LLVtVQPK T4(Phospho)	1 T(4): 100.0	32		10
Low	MAAEDNI tGsGSGNGSSSNDHAPPPP T8(Phospho)	0.496 T(8): 66.6; S(10): 66.6; S(12): 1	22	0.271	10
Low	MALIA tGa tATATAAPVASPAASmAsEL T6(Phospho)	0.202 T(6): 94.1; T(9): 63.7; T(11): 30	29	0.462	19
Low	mASSGGA AISAGPTPPsAAAASSSVDW S17(Phospho)	0.294 S(3): 1.6; S(4): 1.6; S(10): 29.4	26	0.229	13
Low	mAtmNSTNPTLHLcSPAAGANVSGGGC T3(Phospho)	0.136 T(3): 25.5; S(6): 25.5; T(7): 25.	17		10
Low	mEmGsLLPHAASLFAVSmASLmIAADV: S5(Phospho)	0.051 S(5): 5.1; S(12): 90.9; S(17): 2.	16	0.102	24
Low	mEPKEAPPPPPQsPSSTEEEGMLSvt S14(Phospho)	0.066 S(14): 34.1; S(16): 34.1; S(17):	0	0.626	20
Low	mHsLVHDLAIsVSQNEHAIVGcENFTAT t S3(Phospho)	0.105 S(3): 38.2; S(11): 38.2; S(13): 1	1		14
Low	MLYAGcGIQmFQQITGIDATVYySPTIFR Y23(Phospho)	0.109 Y(3): 19.0; T(15): 19.0; T(20): 1	1	0.302	20
Low	MRNNyGIAVPQGNgmPNLAQNmPtFDF Y5(Phospho)	1 Y(5): 100.0; T(24): 100.0	6	0.741	13
Low	MSVIPSGSIRmMEEDGGAGAPSSed t V T26(Phospho)	0.173 S(2): 5.4; S(6): 4.8; S(8): 4.8; S	6	0.247	16
Low	mtAssLAAAASDGASSSSGSASAIVAGT T2(Phospho)	0.018 T(2): 28.6; S(4): 28.6; S(5): 28.	5	0.79	13
Low	mtPFsPHLVAAAAALLGVLAtAVAGGGt t T2(Phospho)	0.44 T(2): 99.4; S(5): 99.4; T(21): 92	25	0.37	11
Low	mTQImFETFNAPAmYVAIQA V L sLYAsGI Y15(Phospho)	0.034 T(2): 61.3; T(8): 61.3; Y(15): 45	0		11
Low	MtttTmPAAARTSAPGGFLEGESGISPS\ T2(Phospho)	0.244 T(2): 74.2; T(3): 74.2; T(4): 74.	39	0.347	11
Low	mVAGAEVmHQVVPLLEAsFHRR S18(Phospho)	1 S(18): 100.0	9	0.415	16
Low	mVRyWVFmGAsWMGFAsSMVMTLSLL Y4(Phospho)	0.036 Y(4): 38.9; S(11): 48.5; S(17): 1	0	0.771	13
Low	NALQtAVAyNAEADAWVPLPDMA t ERD t T5(Phospho)	1 T(5): 100.0; Y(9): 100.0; T(24):	30	0.552	12
Low	NGKPAAIQyGtGSIAGFFsEDsVtVGDLV Y9(Phospho)	0.125 Y(9): 87.5; T(11): 62.1; S(13): 1	6		13
Low	NsLVVQVTQTTLNLQSQLDAAsRELFEsE S2(Phospho)	0.009 S(2): 80.0; T(8): 41.9; T(10): 39	3		10
Low	NSPMmLLFPEG T t tNGDYLLPFKtGAFL T13(Phospho)	0.233 S(2): 0.4; T(12): 26.2; T(13): 56	29	0.476	10
Low	NTAtPNVmGFVK T4(Phospho)	0.98 T(2): 2.0; T(4): 98.0	24	0.737	18
Low	QAHRTISEAFPNQmPSmSEDSPPsGQI S24(Phospho)	0.72 T(5): 0.0; S(7): 0.0; S(16): 0.0;	51	0.272	15
Low	READDLHSVVsYfIEQEYnIIGLVGHSK S11(Phospho)	0.899 S(8): 1.9; S(11): 99.6; Y(12): 99	51	0.094	11
Low	RmVyLMIK Y4(Phospho)	1 Y(4): 100.0	19	0.792	12
Low	RPsQLPKAASLR S3(Phospho)	1 S(3): 100.0; S(10): 0.0	52		15
Low	RSLETcGVLAGtLK T12(Phospho)	0.955 S(2): 0.0; T(5): 4.5; T(12): 95.5	47		11
Low	SAKDnttQLEmVPGSSTTFDATYyGLVA T6(Phospho)	0 S(1): 1.5; T(6): 2.7; T(7): 5.5; S	2	0.804	12
Low	sEYLGSTQTDISVSGQAEKGAFDVLym\ S1(Phospho)	0.019 S(1): 24.7; Y(3): 20.0; S(6): 24.	1	0.805	13
Low	SFVIPLANySVDTTAsPVsFFEVS NAGQI Y9(Phospho)	0.072 S(1): 80.0; Y(9): 10.5; S(10): 10	29	0.508	10
Low	sGLLVFVPSPmLSR S1(Phospho)	0.744 S(1): 74.4; S(9): 15.8; S(13): 9.	10		13
Low	SNNQLEGVAMHASISSGKVASFDPDMDF S13(Phospho)	0.169 S(1): 6.5; S(13): 22.7; S(15): 2.	12	0.792	14
Low	sQLEAAGEFLsPRDFDGHGTHVASTAA S1(Phospho)	0.604 S(1): 99.5; S(11): 98.0; T(20): 1	33	0.169	12

	Low		ssPMPsPLQLsGcSLQELLLmSPPPGSA S1(Phospho)	0.712 S(1): 96.9; S(2): 96.9; S(6): 97.	35	0.62	11
	Low		SSSNsSNIFWQSFdyPTDTLFAKIGW S5(Phospho)	0.082 S(1): 25.8; S(2): 25.8; S(3): 25.	22	0.792	16
	Low		sSVQVATKEAmLPK S1(Phospho)	0.872 S(1): 87.2; S(2): 11.2; T(7): 1.6	74		11
	Low		StPmPPHQNQstVAPLHGHFQSSTGSV(T2(Phospho)	0.005 S(1): 98.6; T(2): 98.6; S(11): 75	23	0.375	21
	Low		sWQDIIDsLASDLEVPDYNmGAAESQQ(S1(Phospho)	0.923 S(1): 96.0; S(8): 96.0; S(11): 6.	38	0.805	12
	Low		tDGGPQsKAsAAPVIEDVEPSEmSLEEIf T1(Phospho)	0.534 T(1): 84.6; S(7): 69.8; S(10): 64	28	0.805	16
	Low		tPFFTPLPIImDSGGGGGDHAsHsAAAV, T1(Phospho)	0.156 T(1): 57.2; T(5): 57.2; S(13): 46	7		11
	Low		tsNsLAVVAVLVAtVAFSAAtFNVPGGYGD T1(Phospho)	0.018 T(1): 41.5; S(2): 60.3; S(4): 43.	0	0.77	10
	Low		TTGFSFAVSSNMLFTFLIAQAFLsMMcs(S24(Phospho)	0.912 T(1): 2.0; T(2): 2.0; S(5): 2.2; S	25	0.211	12
	Low		VAssAVATVLLNPAQSRLtsmsPPIAALIR S3(Phospho)	0.095 S(3): 93.1; S(4): 93.1; T(8): 18.	19		10
	Low		VGLVAVsAAGEVAmAyNtTgMFRACAtE S7(Phospho)	0.297 S(7): 90.0; Y(16): 70.3; T(18): 7	20	0.417	13
	Low		VLDEtIRR T5(Phospho)	1 T(5): 100.0	30		11
	Low		VPLyGAGGGMLLsssGGAVPLtLDFDLts(Y4(Phospho)	1 Y(4): 100.0; S(13): 100.0; S(14	1	0.429	12
	Low		WHVYsASSSASSSDADGAARLTAEVcn S5(Phospho)	0.455 Y(4): 45.5; S(5): 45.5; S(7): 4.4	48	0.752	11
	Low		yLHKEALK Y1(Phospho)	1 Y(1): 100.0	34	0.792	10
	Low		YLsLTSKQK S3(Phospho)	0.456 Y(1): 1.4; S(3): 45.6; T(5): 45.6	45		11
	Low		YSAWSSALSVGAAGKEtAGDAACDR T17(Phospho)	0.409 Y(1): 0.6; S(2): 1.4; S(5): 4.0; S	34	0.531	18
	Low		YScmLPVsTPASVAVWDDDDGGGGGDA S8(Phospho)	0.15 Y(1): 15.0; S(2): 15.0; S(8): 15.	21	0.792	13
Os02t0249800-01	Middle	Glutelin precursor.	sVDcVHGFLIyYAWtVScGQGTAUVIATG S1(Phospho)	0.107 S(1): 72.2; Y(11): 72.2; Y(12): 4	39	0.042	12
	Low		AAAAAAGGAsPDGADGAKRPAPAAAS: S10(Phospho)	0.362 S(10): 87.3; S(26): 45.8; S(27):	27		11
	Low		AcVPSIKLssVDAIIYcsDWNPItNDLR S9(Phospho)	0.062 S(5): 21.5; S(9): 62.2; S(10): 26	23	0.805	13
	Low		AGNAtIAMPQsGNIttVSTATPVtALVDS\ T5(Phospho)S11(Phospho)	Too many isoforms		0.729	11
	Low		AGRlAEAEgMqMMPIQPSVTMWGs(S25(Phospho)	0.719 S(19): 26.1; T(21): 2.0; S(25): 7	28	0.72	11
	Low		AGyLTSSLKK Y3(Phospho)	0.676 Y(3): 67.6; T(5): 10.8; S(6): 10.	39		12
	Low		AKNLtLYSIAR T5(Phospho)	0.829 T(5): 82.9; Y(7): 8.5; S(8): 8.5	18	0.43	10
	Low		APSEVPEYFSGNmSGNLRTItYFDyATL(T21(Phospho)	0.004 S(3): 19.1; Y(8): 38.5; S(10): 38	4	0.49	13
	Low		AsAKLTLLHSmLK S2(Phospho)	0.999 S(2): 99.9; T(6): 0.1; S(10): 0.0	66	0.802	12
	Low		AyEEEQERIK Y2(Phospho)	1 Y(2): 100.0	40		14
	Low		cEmTGVVVDVGdGAtHIVPVADGyVIGs: T15(Phospho)	0.133 T(4): 86.7; T(15): 83.5; Y(24): 7	1	0.581	15
	Low		cLDtmtsKGLLPNTFTYNTVmTAYANVGf T4(Phospho)	0.891 T(4): 95.6; T(6): 95.6; S(7): 96.	46	0.67	21
	Low		cTDTVWPGVLSNAGsARLAttGFELPPG S15(Phospho)	0.162 T(2): 38.0; T(4): 40.7; S(11): 48	7		15
	Low		DAWAAGGGGsVVDtmDPRLEEYSGEE S10(Phospho)	0.421 S(10): 58.7; T(14): 58.7; Y(22):	9	0.797	10
	Low		DGSmSQEIDIPGPVHSISMDVVGsLVTS S24(Phospho)	0.448 S(3): 2.6; S(5): 2.6; S(16): 1.6;	18		11
	Low		DTTSWNSmVSGSLFNGLAEIsAYYFKE(S21(Phospho)	0.136 T(2): 9.0; T(3): 10.0; S(4): 10.0	2	0.231	11
	Low		DVAAGNyEyIDVVVTAVTAAGAGAAKsA Y7(Phospho)	0.617 Y(7): 93.2; Y(9): 93.2; T(15): 16	22	0.063	11
	Low		EDGIGVsEGEEDIsERALHSPSItmVFIVf S7(Phospho)	0.307 S(7): 99.2; S(14): 72.9; S(20): 7	29	0.233	10
	Low		EDyFYfAtLELEPVGNLESVSPSPSPRI Y3(Phospho)	0.258 Y(3): 66.9; Y(5): 66.9; S(7): 66.	25	0.75	14
	Low		EEGQtmAPNQVAGEILsFFtRNNFTISDF T5(Phospho)	0.618 T(5): 99.7; S(17): 77.2; T(20): 7	31	0.433	10
	Low		EEVtSSEmLVETMMRTGDNDANPTTT T4(Phospho)	0.288 T(4): 28.8; S(5): 28.8; S(6): 28.	20	0.515	11
	Low		EGPRMHDtNGLmSIsEtIsEYmLYLLVR S15(Phospho)	0.565 T(8): 0.4; S(13): 14.8; S(15): 86	45	0.156	12
	Low		EMsDAKIsPNAVTFVGLLSAYsNAGLmE S3(Phospho)	0.027 S(3): 32.5; S(8): 72.0; T(13): 38	3	0.804	17
	Low		EPSsPIPQAKALLPtSmAAGDMLGFFKP S4(Phospho)	0.523 S(3): 28.1; S(4): 73.5; T(15): 71	31	0.776	12
	Low		ETFNHLAsWLEDARQHANANmtVmLIGI S8(Phospho)	0.774 T(2): 22.6; S(8): 77.9; T(22): 99	29	0.519	14
	Low		ETVGLEGsANGQWWIDNIGKALDEGtsf S8(Phospho)	0.437 T(2): 56.3; S(8): 75.2; T(26): 84	8	0.771	12
	Low		GEMGIQYVVLDMGAVGsIDTSGtsmLDE S17(Phospho)	0.046 Y(7): 54.7; S(17): 50.5; T(20): 4	0	0.38	10
	Low		GGAPsMQASTHMFRTITPLGGSHHNS(S5(Phospho)	0.046 S(5): 28.6; S(9): 28.6; T(10): 28	16		14

Low	GLGsNDIFDsQWIAPVQFEGLLDDSEEE(S4(Phospho):	0.952 S(4): 99.6; S(10): 95.5; S(24): 4	37	0.606	11
Low	GRAGDATLIK	1 T(7): 100.0	23		11
Low	GRtEQAVLK	1 T(3): 100.0	33		10
Low	HAGDEAGMTYEEYmNSmASLFSrMVD S22(Phospho)	0.166 T(9): 16.6; Y(10): 30.2; Y(13): 1	8	0.782	11
Low	HAPNGTKsFcNACGLmWANSKPIDLVT S8(Phospho):	0.413 T(6): 58.7; S(8): 58.7; S(20): 86	10	0.758	11
Low	HIEsLNsiDNFHDVGPSSVVMASPGGLQS S4(Phospho):	0.971 S(4): 98.4; S(7): 98.4; S(17): 2.	35	0.115	12
Low	IQATAIlyFKR	0.946 T(4): 5.4; Y(8): 94.6	30		12
Low	IsSsVYstRPVAVyEVDRVLLPmQIFR	0.179 S(2): 54.9; S(3): 54.9; S(4): 83.	28		10
Low	KLVMEILsHINK	1 S(8): 100.0	5	0.778	10
Low	KsIAHIVK	1 S(2): 100.0	45	0.776	11
Low	LEtVDLRR	1 T(3): 100.0	43		11
Low	LGsGPASTALK	0.333 S(3): 33.3; S(7): 33.3; T(8): 33.	32		12
Low	LLVIVQPK	1 T(4): 100.0	32		10
Low	MAAEDNItGsGSGNGSSSNDHAPPPP T8(Phospho):	0.496 T(8): 66.6; S(10): 66.6; S(12): 2	22	0.271	10
Low	MALIAtGAtATATAAPVASPAASmAsEL T6(Phospho):	0.202 T(6): 94.1; T(9): 63.7; T(11): 30	29	0.462	19
Low	mASSGGAAISAGPTPPsAAAASSSVDM S17(Phospho)	0.294 S(3): 1.6; S(4): 1.6; S(10): 29.4	26	0.229	13
Low	mAtmNSTNPTLHLcSPAAGANVSGGGC T3(Phospho):	0.136 T(3): 25.5; S(6): 25.5; T(7): 25.	17		10
Low	mDsTAcTtIVVFLLLPR	0.554 S(3): 63.8; T(4): 24.7; T(7): 20.	30	0.76	11
Low	mEmGsLLPHAASLFAVSmASLmIAADV S5(Phospho)	0.051 S(5): 5.1; S(12): 90.9; S(17): 2.	16	0.102	24
Low	mEPKEAPPPPPQsPSSTEEEGMLSVt S14(Phospho)	0.066 S(14): 34.1; S(16): 34.1; S(17):	0	0.626	20
Low	mHsLVHDLAIsVSQNEHAIVGcENFTAT S3(Phospho):	0.105 S(3): 38.2; S(11): 38.2; S(13): 3	1		14
Low	MLYAGcGIQmFQQITGIDATVYySPTIFR Y23(Phospho)	0.109 Y(3): 19.0; T(15): 19.0; T(20): 1	1	0.302	20
Low	MRRNyGIAVPQGNmPNLAQNmPtDF Y5(Phospho):	1 Y(5): 100.0; T(24): 100.0	6	0.741	13
Low	mRVGALAWNssLLssGsR	0.822 S(10): 17.8; S(11): 82.6; S(14):	47	0.752	18
Low	MSVIPSGSIRmMEEDGGAGAPSSedT V T26(Phospho)	0.173 S(2): 5.4; S(6): 4.8; S(8): 4.8; S	6	0.247	16
Low	mtAssLAAAASDGASSSSGSASAIVAGT T2(Phospho):	0.018 T(2): 28.6; S(4): 28.6; S(5): 28.	5	0.79	13
Low	mtPFsPHLVAAAAALLGVLAtAVAGGGtC T2(Phospho):	0.44 T(2): 99.4; S(5): 99.4; T(21): 92	25	0.37	11
Low	mTQImFETFNAPAmYVAIQAVALsLYAsGI Y15(Phospho)	0.034 T(2): 61.3; T(8): 61.3; Y(15): 45	0		11
Low	MtttTmPAAARTSAPGGFLEGESGISPS\ T2(Phospho):	0.244 T(2): 74.2; T(3): 74.2; T(4): 74.	39	0.347	11
Low	mVAGAEVmHQVVPLLEAsFHRR	1 S(18): 100.0	9	0.415	16
Low	mVRyWVFmGAsWMGFAsSMVMTLSLL Y4(Phospho):	0.036 Y(4): 38.9; S(11): 48.5; S(17): 3	0	0.771	13
Low	NALQtAVAYNAEADAWVPLPDMAterDt T5(Phospho):	1 T(5): 100.0; Y(9): 100.0; T(24):	30	0.552	12
Low	NGKPAAIQyGtGSIAGFFsEDsVtVGDLV Y9(Phospho):	0.125 Y(9): 87.5; T(11): 62.1; S(13): 3	6		13
Low	NsLVVQVTQTTLNLQSQLDAAsRELFEsE S2(Phospho):	0.009 S(2): 80.0; T(8): 41.9; T(10): 39	3		10
Low	NSPMmLLFPEGtTtNGDYLLPFKtGAFL T13(Phospho)	0.233 S(2): 0.4; T(12): 26.2; T(13): 56	29	0.476	10
Low	NTAtPNVmGFVK	0.98 T(2): 2.0; T(4): 98.0	24	0.737	18
Low	QAHRTISEAFPNQmPmSEDSPSsGQI S24(Phospho)	0.72 T(5): 0.0; S(7): 0.0; S(16): 0.0;	51	0.272	15
Low	READDLHSVVsYfIEQEYNIIGLVGHsK S11(Phospho)	0.899 S(8): 1.9; S(11): 99.6; Y(12): 99	51	0.094	11
Low	RmVyLMIK	1 Y(4): 100.0	19	0.792	12
Low	RPsQLPKAASLR	1 S(3): 100.0; S(10): 0.0	52		15
Low	RSLETcGVLAGtLK	0.955 S(2): 0.0; T(5): 4.5; T(12): 95.5	47		11
Low	SAKDnttQLEmVPGSSTTFDATYyGLVA T6(Phospho):	0 S(1): 1.5; T(6): 2.7; T(7): 5.5; S	2	0.804	12
Low	seYLGSTQTDISVSGQAEKGAFDVLym\ S1(Phospho):	0.019 S(1): 24.7; Y(3): 20.0; S(6): 24.	1	0.805	13
Low	SFVIPLANySVDTTAsPVsFFEVSNAQQL Y9(Phospho):	0.072 S(1): 80.0; Y(9): 10.5; S(10): 10	29	0.508	10
Low	sGLLVFVPSPmLSR	0.744 S(1): 74.4; S(9): 15.8; S(13): 9.	10		13
Low	SNNQLEGVAMHASISSGKVAsFPDMDF S13(Phospho)	0.169 S(1): 6.5; S(13): 22.7; S(15): 22	12	0.792	14
Low	sQLEAAGEFLsPRDFDGHGTHVASTAA S1(Phospho):	0.604 S(1): 99.5; S(11): 98.0; T(20): 3	33	0.169	12

	Low		ssPMPsPLQLsGcSLQELLLmSPPPGSA S1(Phospho):	0.712 S(1): 96.9; S(2): 96.9; S(6): 97.	35	0.62	11
	Low		SSSNsSNIFWQSFdyPTDTLFAgAKIGW S5(Phospho):	0.082 S(1): 25.8; S(2): 25.8; S(3): 25.	22	0.792	16
	Low		sSVQVATKEAmLPK S1(Phospho)	0.872 S(1): 87.2; S(2): 11.2; T(7): 1.6	74		11
	Low		StPmPPHQNQstVAPLHGHFQSSTGSV(T2(Phospho):	0.005 S(1): 98.6; T(2): 98.6; S(11): 75	23	0.375	21
	Low		sWQDIIDsLASDLEVPDYNmGAAESQQ(S1(Phospho):	0.923 S(1): 96.0; S(8): 96.0; S(11): 6.	38	0.805	12
	Low		tDGGPQsKAsAAPVIEDVEPSEmSLEEIf T1(Phospho):	0.534 T(1): 84.6; S(7): 69.8; S(10): 64	28	0.805	16
	Low		tPFFTPLPIImDSGGGGGDHAsHsAAAV, T1(Phospho):	0.156 T(1): 57.2; T(5): 57.2; S(13): 46	7		11
	Low		tsNsLAVVAVLVAtVAFSAAtFNVPGGYGD T1(Phospho):	0.018 T(1): 41.5; S(2): 60.3; S(4): 43.	0	0.77	10
	Low		TTGFSFAVSSNMLFTFLIAQAFLsMMcsf S24(Phospho)	0.912 T(1): 2.0; T(2): 2.0; S(5): 2.2; S	25	0.211	12
	Low		VAssAVATVLLNPAQSRLtsmsPPIAALIR S3(Phospho):	0.095 S(3): 93.1; S(4): 93.1; T(8): 18.	19		10
	Low		VGLVAVsAAGEVAmAyNtTGmFRACAtE S7(Phospho):	0.297 S(7): 90.0; Y(16): 70.3; T(18): 7	20	0.417	13
	Low		VLDEtIRR T5(Phospho)	1 T(5): 100.0	30		11
	Low		VPLyGAGGGLMLsssGGAVPLtLDFDLts(Y4(Phospho):	1 Y(4): 100.0; S(13): 100.0; S(14	1	0.429	12
	Low		WHVYsASSSASSSDADGAARLTAEVcn S5(Phospho)	0.455 Y(4): 45.5; S(5): 45.5; S(7): 4.4	48	0.752	11
	Low		yLHKEALK Y1(Phospho)	1 Y(1): 100.0	34	0.792	10
	Low		YLsLTSKQK S3(Phospho)	0.456 Y(1): 1.4; S(3): 45.6; T(5): 45.6	45		11
	Low		YSAWSSALSVGAAGKEtAGDAAcDR T17(Phospho)	0.409 Y(1): 0.6; S(2): 1.4; S(5): 4.0; S	34	0.531	18
	Low		YScmLPVsTPASVAVWDDDDGGGGGDA S8(Phospho)	0.15 Y(1): 15.0; S(2): 15.0; S(8): 15.	21	0.792	13
Os02t0257200-01	Middle	Conserved hypothetical protein.	TPAPVSGQVPPPPAGsYK S16(Phospho)	0.462 T(1): 5.4; S(6): 2.2; S(16): 46.2	24	0.018	16
	Middle		TPAPVSGQVPPPPAGsYK S16(Phospho)	0.172 T(1): 0.0; S(6): 0.0; S(16): 17.2	42	0.025	21
	Middle		TPAPVSGQVPPPPAGsYK S16(Phospho)	0.442 T(1): 10.7; S(6): 0.9; S(16): 44.	34	0.025	16
	Low		VtKLsAAPVVVALtK T2(Phospho):	1 T(2): 100.0; S(5): 100.0; T(15):	38	0.761	11
Os02t0268100-01	High	Similar to Glutelin (Fragment).	EsLAEAVSAVIGILGMQPcEGtDVVPsNS S2(Phospho):	0.403 S(2): 92.0; S(8): 8.0; T(22): 87.	43	0.007	11
	High		VSsPPPEPAPAVR S3(Phospho)	0.882 S(2): 11.8; S(3): 88.2	67	0.001	12
	Middle		QFGDIVVLNNALtIEGPDAGSARVGtAQc T13(Phospho)	0.995 T(13): 99.9; S(20): 0.5; T(25): 9	55	0.017	17
	Low		AAAVVmVVVVVLGMVSTSSAHVFVGA` Y39(Phospho)	0.928 S(16): 0.4; T(17): 0.4; S(18): 0.	36	0.708	11
	Low		AEEAAAASGsAVRmLLmDATAAMVAR S10(Phospho)	0.475 S(8): 47.5; S(10): 47.5; T(20): 4	19		11
	Low		AEEYAPVIFAQDAYKHVVSIDmLsGAEC S24(Phospho)	0.485 Y(4): 0.2; Y(14): 2.8; S(19): 48.	31	0.663	12
	Low		AGyLTSSLKK Y3(Phospho)	0.676 Y(3): 67.6; T(5): 10.8; S(6): 10.	39		12
	Low		ALLSssFVLPLR S5(Phospho):	0.333 S(4): 66.7; S(5): 66.7; S(6): 66.	49	0.661	13
	Low		AmAsTRMmIVR S4(Phospho)	0.5 S(4): 50.0; T(5): 50.0	19	0.768	12
	Low		AmVAAtmttTATAAttsVGAsAQELyAVtA, T6(Phospho)T8(Phospho)T	Too many NL-allowing PTMs		0.74	11
	Low		APAAEVssSAETTGSsAGsAPstAAAAA S7(Phospho)S8(Phospho)S	Too many NL-allowing PTMs		0.652	13
	Low		AQDSSSIVsPIR S9(Phospho)	0.925 S(4): 0.3; S(5): 3.6; S(6): 3.6; S	39	0.776	13
	Low		ARPLMSDVVETLEPLQGSGGSDGAVQ: S27(Phospho)	0.013 S(6): 38.3; T(11): 41.8; S(18): 5	2	0.615	12
	Low		AsFYLIYNATKTSLSMIPLPSYcSPSFTr S2(Phospho)	0.734 S(2): 73.4; Y(4): 19.3; Y(7): 5.4	50	0.083	22
	Low		AsLSGGSVGAGAGGGR S2(Phospho)	0.779 S(2): 77.9; S(4): 17.6; S(7): 4.5	36	0.629	12
	Low		ATAQtISTVPDR T5(Phospho)	0.45 T(2): 45.0; T(5): 45.0; S(7): 1.8	35	0.77	12
	Low		AtELKAGGVmFLVcLGRPsLHAcPTNQG T2(Phospho):	0.965 T(2): 98.9; S(19): 97.6; T(25): 9	20	0.611	15
	Low		ATtMIRMIGMAsATTATAVLIAmAAmPAI(T3(Phospho):	0.046 T(2): 69.5; T(3): 52.1; T(5): 57.1	10	0.624	20
	Low		AyEEEQERIK Y2(Phospho)	1 Y(2): 100.0	40		14
	Low		cFSVSSsVGLSPLSPTTVELAAAVVDDA S7(Phospho)	0.154 S(3): 35.3; S(5): 15.4; S(6): 15.	14	0.56	15
	Low		cVLRLLPVWASGIIFAAAYTQMTttFVLQ(T24(Phospho)	0.033 S(11): 40.5; Y(19): 50.4; T(20):	4	0.776	12

Low	DGSsLGGIRELR	S4(Phospho)	0.987 S(3): 1.3; S(4): 98.7	77	0.539	10
Low	DLASPLGLTANAQSAysANlcsQWGSF	Y17(Phospho)	0.159 S(4): 2.0; T(8): 4.3; T(10): 13.9	25		11
Low	DLELAmTtGIFIIPMTANIPVcMLDQcR	T8(Phospho)	0.758 T(7): 19.1; T(8): 75.8; T(16): 5.	58	0.549	13
Low	DsGGGGGASHKAASGSAPSGAAAANP	S2(Phospho)	0.009 S(2): 65.9; S(9): 33.3; S(14): 5.	2	0.776	12
Low	DsVtDGVIFmGALFFsVmmImFNGLSELF	S2(Phospho)	1 S(2): 100.0; T(4): 100.0; S(16):	0	0.588	11
Low	EEDQmsLSVGIVGAPNAGKSSLTNtmVt	S6(Phospho)	0.006 S(6): 61.2; S(8): 64.7; S(20): 3.	2	0.79	18
Low	EGGGQLQFPLDmDsIKLIIADLFsGGGET	S13(Phospho)	0.236 S(13): 71.3; S(23): 71.3; T(28):	1		10
Low	EGGtPVPVtDEIIVVLLFDmFTGASETSP	T4(Phospho)	0.029 T(4): 43.2; T(9): 43.0; T(22): 42	0	0.067	13
Low	ERGETALsQIR	S8(Phospho)	0.5 T(5): 50.0; S(8): 50.0	24		12
Low	EVPPVEATAPPAETSQLAtPPAETSQLA	T19(Phospho)	0.073 T(8): 8.2; T(14): 7.3; S(15): 6.9	0	0.589	11
Low	FADTLSDTsPsSPAQRfVSEDGVINSRP	S9(Phospho)	0.038 T(4): 80.1; S(6): 11.6; T(8): 19.	37		12
Low	FcRLAVAsPLSSGR	S8(Phospho)	0.981 S(8): 98.1; S(11): 1.0; S(12): 1.	42	0.165	16
Low	FISTIFPsAMMAADGGPLLGEWmSATA	S8(Phospho)	0.127 S(3): 4.0; T(4): 6.8; S(8): 12.7;	12	0.647	15
Low	FLlIFsPQLSRTLPSPLScGGR	S7(Phospho)	0.147 S(6): 4.8; S(7): 14.7; S(11): 49.	28	0.121	10
Low	FsAHKcVLAAR	S2(Phospho)	1 S(2): 100.0	9	0.56	11
Low	GGTTNQYANNAVNGyVQRSmSEmVVF	Y15(Phospho)	0.095 T(3): 11.3; T(4): 11.3; Y(7): 11.	9	0.406	10
Low	GRmLPEDtFAVRPR	T8(Phospho)	1 T(8): 100.0	27	0.803	14
Low	GSASHENIVAADFGPMPtHFLSSNQPLE	T18(Phospho)	0.098 S(2): 23.8; S(4): 63.0; T(18): 9.	15	0.669	10
Low	GsVHAcAVAARPAAsAmVSSRQAVEsKP	S2(Phospho)	0.546 S(2): 99.7; S(14): 93.1; S(18): 1	36	0.568	11
Low	GTPVTNTSSSAPTSLTNSSNLVLSdAD	S25(Phospho)	0.11 T(2): 7.2; T(5): 5.2; T(7): 7.2; S	6	0.792	10
Low	GTVGyLAPEWISGVAItPKVDVysYGmVI	Y5(Phospho)	0.026 T(2): 59.7; Y(5): 59.7; S(12): 54	3	0.764	13
Low	GVDLmPQsKIR	S8(Phospho)	1 S(8): 100.0	34		11
Low	GVGHGDmPIVVGEVGPWPTDGDKHAtA	T25(Phospho)	0.231 T(18): 14.8; T(25): 23.1; T(27):	6		11
Low	HAVFesDDGEDLNPMGIVEtVSSYVASE	S6(Phospho)	0.011 S(6): 31.4; T(20): 33.2; S(22): 3	0	0.191	10
Low	HKLLFILEmLDPFIDPSVsVmtDAMAFGE	S19(Phospho)	0.148 S(17): 85.2; S(19): 85.2; T(22):	3	0.475	12
Low	HLRttFDEVVAVTGDGtNDAPALHEADIG	T4(Phospho)	0.05 T(4): 43.5; T(5): 43.5; T(13): 54	0		11
Low	HYNEILRScNALDyHDFINSSITLLTK	Y14(Phospho)	0.563 Y(2): 0.3; S(8): 1.2; Y(14): 56.3	27		11
Low	IHDrySSILR	Y5(Phospho)	0.983 Y(5): 98.3; S(6): 1.5; S(7): 0.2	67	0.604	11
Low	ILAAGYAIFVAsSSSGSGSSsLAmLPAAAsV	S12(Phospho)	0.023 Y(6): 11.8; S(12): 31.7; S(13): 1	10	0.779	13
Low	IQATAIlyFKR	Y8(Phospho)	0.946 T(4): 5.4; Y(8): 94.6	30		12
Low	IQEDLTsGQLR	S7(Phospho)	0.84 T(6): 16.0; S(7): 84.0	37	0.555	12
Low	ISVAMAEKsAPR	S9(Phospho)	0.5 S(2): 50.0; S(9): 50.0	14	0.436	12
Low	KmmLLVAAPFtK	T11(Phospho)	1 T(11): 100.0	37	0.446	13
Low	KPISSAPPHSVPSNsR	S15(Phospho)	0.994 S(4): 0.0; S(5): 0.0; S(10): 0.1;	59		10
Low	KsIAHIVK	S2(Phospho)	1 S(2): 100.0	45	0.776	11
Low	KVLIFVNsIDsAFK	S8(Phospho)	1 S(8): 100.0; S(11): 100.0	75		14
Low	KyGEVVQGLTR	Y2(Phospho)	1 Y(2): 100.0; T(10): 0.0	50		15
Low	LAmSAAIGDFANTFAIAGVTSYLLAASF	S4(Phospho)	0 S(4): 5.3; T(14): 90.8; T(21): 23	5	0.111	17
Low	LATFsGVDIPSFK	S5(Phospho)	0.937 T(3): 6.0; S(5): 93.7; S(11): 0.2	36	0.673	17
Low	LFPstTSLHQELicFELPSLHSTFLDLLSA	S4(Phospho)	0.016 S(4): 23.8; T(5): 23.8; T(6): 23.	5		12
Low	LGYATEQLALYTGPtHGGLLNATFGNATI	T15(Phospho)	0.057 Y(3): 19.9; T(5): 14.3; Y(11): 19	6		10
Low	LLEDMDTKGLPVSSr	S14(Phospho)	0.909 T(6): 2.4; S(13): 6.7; S(14): 90.	25		12
Low	LLSLEPGPQKTAPmLLGFSEEHNVAFVt	S34(Phospho)	0.059 S(3): 22.5; T(11): 22.5; S(19): 2	2	0.689	11
Low	LLTYADHTASGRsLR	S13(Phospho)	0.943 T(3): 0.4; Y(4): 0.4; T(8): 0.4; S	36		14
Low	LNmAmPNPASERMEIDLAtmIGIVSLLYf	T19(Phospho)	0.15 S(10): 0.6; T(19): 15.0; S(25): 4	23	0.489	11
Low	LPEILTQLsVPAGsR	S9(Phospho)	0.5 T(6): 50.0; S(9): 50.0; S(14): 10	59		10
Low	LPSAVYMQRPLSATGEVVQQAAsssLA	S23(Phospho)	S24(Phospho) Too many isoforms	0.627		10

Low	LPSSsAAAsAAsAQPQPPPPsVVVVGAG(S5(Phospho):	0.006 S(3): 39.1; S(4): 46.6; S(5): 54.	3	0.711	10
Low	LRFEyLR Y5(Phospho)	1 Y(5): 100.0	41		12
Low	LRVLsHGDPAGK S5(Phospho)	1 S(5): 100.0	42		12
Low	LSQSPGsSVKNR S7(Phospho)	0.035 S(2): 0.1; S(4): 0.8; S(7): 3.5; S	32	0.788	10
Low	LssLQEDISLKEQSLLESELENIFQEHK S2(Phospho):	0.983 S(2): 99.0; S(3): 99.0; S(9): 1.4	46		11
Low	LTAYKSFSDLSPVLQFANFtVtQALLDEI/ T20(Phospho	0 T(2): 42.9; Y(4): 42.9; S(6): 28.	1	0.691	15
Low	LTLsLtsLSTDALFIIAQLPVLFLSLAFSVSA S4(Phospho)	0.004 T(2): 17.2; S(4): 32.0; T(6): 32.	1	0.379	10
Low	LVGDNLALNVQTVStVIsGFtIAmVANWk T15(Phospho	0.179 T(12): 71.5; S(14): 28.4; T(15):	19	0.711	13
Low	LYAPSASPLEQctsFEALAAHVWRAWVf T13(Phospho	0.977 Y(2): 0.1; S(5): 1.5; S(7): 1.5; T	55		12
Low	mAASPAAGAAAATVSSFVSPSsFsSVK S22(Phospho	0.017 S(4): 0.4; T(13): 5.4; S(15): 11.	19		11
Low	MAFIKVVFsVLLPVVVSmlVATTTmADH S9(Phospho)	0.417 S(9): 41.7; S(17): 41.7; T(22): 5	13	0.78	11
Low	mAPTVMVAEKPsiALsIALSGGRMS S13(Phospho	0.017 T(4): 11.0; S(13): 19.4; S(17): 3	4	0.775	12
Low	MASPLPTmEtIAHAtVLAIGTANPAKcVAc T10(Phospho	0.052 S(3): 42.0; T(7): 63.7; T(10): 59	10		11
Low	MAsSRVmAAAAASSSSSSPPPPPPAAA S3(Phospho)	0.494 S(3): 49.4; S(4): 49.4; S(13): 0.	30	0.353	12
Low	mASTTTTtAAAAARFTcLAPATRPASAS T8(Phospho)	0.185 S(3): 1.8; T(4): 1.8; T(5): 3.5; T	18	0.441	10
Low	mDTIMSPNSPRLAVMSsQLTDGGGEEI S17(Phospho	0.444 T(3): 0.5; S(6): 0.5; S(9): 2.6; S	37	0.446	13
Low	mEDQLQSQAQGGQGQQtEAIKyGHVF/ T17(Phospho	0.325 S(7): 20.5; T(17): 55.3; Y(22): 7	8	0.576	12
Low	mEGLVVsAAtGvmNSVLAKLtAFLGEEyI S7(Phospho)	0.178 S(7): 82.2; T(10): 36.5; S(15): 8	24	0.615	10
Low	mEISTVLGAILAEYAVtLVAMAVGFLVVC T17(Phospho	0.528 S(4): 14.8; T(5): 14.8; Y(14): 34	20	0.778	11
Low	mFcIAEPSYDKSLQQLQSFLsGLVSDEK S21(Phospho	0.521 S(8): 12.2; Y(9): 12.2; S(12): 6.	14		11
Low	mFVVtVGGssVMDLVVVVQDGFVVDGH T5(Phospho):	0.397 T(5): 73.8; S(9): 73.8; S(10): 72	8	0.638	10
Low	mSIADVLQASLEDELMVARESGLLAGS S30(Phospho	0.475 S(2): 0.2; S(10): 0.2; S(21): 2.3	25	0.683	12
Low	mTILVISDsTAQPK S9(Phospho)	0.624 T(2): 12.5; S(7): 12.5; S(9): 62.	40		11
Low	NLDTNMSGsNGHLIKLPSsSYFR S19(Phospho	0.129 T(4): 2.4; S(7): 1.2; S(9): 0.7; S	17		14
Low	NmYAFGcAtLASmTTILMGYNLALMSGC T9(Phospho)	0.415 Y(3): 41.5; T(9): 41.5; S(12): 16	36		12
Low	NPLTcLsLLAAFLLLsFsctsmVFAILKYtR S7(Phospho):	0.052 T(4): 70.7; S(7): 77.8; S(16): 83	5	0.776	12
Low	NTAtPNVmGFVK T4(Phospho)	0.98 T(2): 2.0; T(4): 98.0	24	0.737	18
Low	NTMIGPAPSPAAAAAAVSPScyAsPAA Y23(Phospho	0.016 T(2): 26.2; S(9): 63.0; S(19): 57	15	0.732	17
Low	QDmPEPPLLPQVPQEEVQtsIPAEQtKN T19(Phospho	1 T(19): 100.0; S(20): 100.0; T(2)	52	0.446	13
Low	QGDAIEtGSiIR T7(Phospho)	0.985 T(7): 98.5; S(9): 1.5	73	0.45	12
Low	QGDAIEtGSiIR S9(Phospho)	0.122 T(7): 87.8; S(9): 12.2	60	0.531	13
Low	QLFsGLSINYLKVVPSVAIGFTVyDsMK S4(Phospho)	0.38 S(4): 40.1; S(7): 12.4; Y(10): 40	38	0.561	13
Low	QLKGSNLTQSDVQsR S14(Phospho	0.984 S(5): 0.7; T(8): 0.3; S(10): 0.7;	30		12
Low	QLQSTGVHVLsNLPcLIDLTLTAQAtPED S11(Phospho	0.25 S(4): 10.3; T(5): 10.3; S(11): 80	23	0.148	10
Low	RADAVAAATAVGEPGVPDAAAASVVGI S42(Phospho	0.46 T(9): 0.5; S(23): 8.0; Y(29): 28.	28	0.474	15
Low	RMsPEELMAFGTGLmAVQAASVSAR S3(Phospho)	0.988 S(3): 98.8; T(12): 1.1; S(22): 0.	37	0.675	11
Low	RmVyLMIK Y4(Phospho)	1 Y(4): 100.0	19	0.792	12
Low	RNTVLALVSWLmLLALFITtATAsLPcR T20(Phospho	0.108 T(3): 13.7; S(9): 16.9; T(19): 34	6	0.661	13
Low	RPPPPRRPTGSSSTPYASPSPLSSSLSD T28(Phospho	0.343 T(9): 0.0; S(11): 0.0; S(12): 0.0	54	0.385	14
Low	RPsQLPKAASLR S3(Phospho)	1 S(3): 100.0; S(10): 0.0	52		15
Low	SAmVGYEFsDADsIRESDIGIAVADATD S9(Phospho):	0.689 S(1): 1.5; Y(6): 26.1; S(9): 75.0	41	0.773	13
Low	sAtsFYtYIRItYsstPFttsSmPSsPctPR S1(Phospho)T3(Phospho)S Too many NL-allowing PTMs			0.756	12
Low	ScEDGTTLAVEDmDWDALtVKGTcQIEI T19(Phospho	0.201 S(1): 7.8; T(6): 7.8; T(7): 7.8; T	22	0.768	10
Low	SDAPLKGPLsVR S10(Phospho	0.992 S(1): 0.8; S(10): 99.2	44		11
Low	sDKIASFGTTQPHK S1(Phospho)	0.997 S(1): 99.7; S(6): 0.2; T(9): 0.2;	53		10
Low	SEKPPGTsVLYVDK S8(Phospho)	0.831 S(1): 0.2; T(7): 15.9; S(8): 83.1	51	0.628	11
Low	sFGGLFLITGVVtsAMLLIyLAVFFYR S1(Phospho)	0.584 S(1): 100.0; T(9): 40.6; T(13): 8	46	0.719	12

Low	sFGGLFLITGVVtsAMLLIYLAVFFyR S1(Phospho)	0.079 S(1): 99.7; T(9): 20.0; T(13): 87	26	0.714	13
Low	SFHDcRPAFmQTGPTTAAsGsAYAEEFG S19(Phospho)	0.238 S(1): 1.8; T(12): 2.3; T(15): 10.	21	0.349	11
Low	sGGGDATPAEGDQVIVHcTTRTIDGIIVN S1(Phospho)	0.885 S(1): 88.5; T(7): 4.1; T(19): 1.7	38	0.331	15
Low	SHTmPsPMRsSASATAAAASDGEQVQc S6(Phospho)	0.091 S(1): 3.0; T(3): 7.1; S(6): 53.2;	26	0.805	10
Low	sIELAFLDHSK S1(Phospho)	1 S(1): 100.0; S(10): 0.0	53	0.806	10
Low	SKPKStsVAtENIDPtAmssQILASLSSSm T6(Phospho)S7(Phospho)	T Too many isoforms		0.588	11
Low	smGAVTSLLYGAEDSSIAGMVLDSAFtN S1(Phospho)	0.008 S(1): 30.4; T(6): 30.4; S(7): 30.	0	0.229	13
Low	SMPyVIGNETFEKLGITIGTtANLLVYLtV Y4(Phospho)T20(Phospho)	T Too many isoforms		0.218	18
Low	SNsLESSSTGAAAAPTTLTTSASTASVS S3(Phospho)	0.422 S(1): 42.2; S(3): 42.2; S(6): 7.1	25	0.566	12
Low	sQsNNTQQQGDEIcTTASGVRPVGFDA S1(Phospho)	0.242 S(1): 43.8; S(3): 43.8; T(6): 25.	12		12
Low	sSGAVSSTPSmRGTVcYVAPEYGGGGI S1(Phospho)	0.477 S(1): 48.0; S(2): 48.0; S(6): 1.7	43	0.549	11
Low	SSGTTALtALVFGR T8(Phospho)	0.9 S(1): 0.4; S(2): 0.4; T(4): 4.6; T	40		14
Low	sSIYDETIDMWALGcImAQLLGGQLLFR S1(Phospho)	0.173 S(1): 17.3; S(2): 17.3; Y(4): 32.	7	0.687	10
Low	stYEQAAGLASVPMVWVGEPQSLLING S1(Phospho)	0.242 S(1): 33.3; T(2): 33.3; Y(3): 33.	31		12
Low	tcPLPQAAtsGTR T1(Phospho)	0.731 T(1): 97.3; T(9): 94.1; S(10): 81	16	0.791	12
Low	tEMPLHAYtGGGLLPGRDAmADGAETf T1(Phospho)	1 T(1): 100.0; Y(8): 100.0; T(10):	3	0.776	11
Low	TEsNKNAGNAILYEcVETImGIEAtsGLR S3(Phospho)	0.607 T(1): 20.1; S(3): 79.7; Y(13): 0.	66	0.708	11
Low	tETVEAERISLDHTcPVVsDVSVPPLVGk T1(Phospho)	0.084 T(1): 47.9; T(3): 47.9; S(10): 5.	32	0.617	11
Low	tGLtHMPAsVAHScFRSPATLSLLAAFMt T1(Phospho)	0.01 T(1): 35.7; T(4): 35.7; S(9): 34.	0	0.804	10
Low	THPAHLGtAyLK T8(Phospho)	0.992 T(1): 0.8; T(8): 99.6; Y(10): 99.	24	0.789	11
Low	TIEHLtEVHSRGLELHAtAESK T6(Phospho)	0.043 T(1): 65.7; T(6): 65.7; S(10): 25	1		14
Low	TLANAAFYcAQGASSyLATAVVNVVNAF Y16(Phospho)	0.4 T(1): 1.8; Y(8): 8.1; S(14): 17.5	23	0.792	10
Low	tMsPAAAATGLALGVGGVAGAAAVGtG T1(Phospho)	0.567 T(1): 85.6; S(3): 72.3; T(9): 43.	19	0.716	13
Low	TmTTLSSsALLLtsssVQLRssPVLLLQPP: S7(Phospho)S8(Phospho)	T Too many isoforms		0.67	13
Low	TPAPGSPPPPHNPILDASSMsPsHGSSf S21(Phospho)	0.861 T(1): 0.0; S(6): 0.0; S(18): 2.2;	53	0.105	16
Low	TPAPGSPPPPHNPILDASSMSPsHGSSf S23(Phospho)	0.038 T(1): 0.6; S(6): 0.6; S(18): 28.0	18	0.089	14
Low	tQVLALPAPDGSmQNVGGDPFAASLSF T1(Phospho)	0.388 T(1): 38.8; S(12): 11.5; S(24): 8	9	0.179	10
Low	TSSSPPLSAVAsR S12(Phospho)	0.206 T(1): 4.1; S(2): 4.1; S(3): 4.1; S	12	0.744	13
Low	TSVDsGLSPAGLR S5(Phospho)	0.987 T(1): 0.6; S(2): 0.6; S(5): 98.7;	60	0.551	16
Low	TsVNVSVNGRAR S2(Phospho)	0.446 T(1): 44.6; S(2): 44.6; S(6): 10.	28		11
Low	TVANQVASsLsRAGNAmMPsGFASGIA S9(Phospho)	0.056 T(1): 12.0; S(8): 28.9; S(9): 68.	39		10
Low	VAtARLGGEPSR T3(Phospho)	0.996 T(3): 99.6; S(11): 0.4	37	0.748	12
Low	VcNEPPitALLVYLSPRHTSSSSSPAmP T8(Phospho)	0.066 T(8): 6.6; Y(13): 5.2; S(15): 5.2	1		10
Low	VLELAPctVGAsFQLPtKIsTSEETTAAR T8(Phospho)	0.054 T(8): 65.8; S(12): 65.8; T(17): 3	20	0.286	12
Low	VsETGWPSAGDANETGATPQNAARyN S2(Phospho)	0.845 S(2): 89.8; T(4): 10.0; S(8): 1.1	44	0.727	13
Low	VsSPPEPAPAVR S2(Phospho)	0.87 S(2): 87.0; S(3): 13.0	65	0.05	16
Low	VTSLKyLsLR Y6(Phospho)	0.01 T(2): 49.5; S(3): 49.5; Y(6): 1.3	40	0.726	17
Low	VVHGNIItAAVILNEIPQGTTEVFmTGAT T6(Phospho)	0.991 T(6): 99.9; T(8): 99.1; T(20): 0.	44	0.571	13
Low	WAALAIVAtQALSLLLATILRSmLSTPSA T9(Phospho)	0.876 T(9): 87.6; S(13): 8.3; T(18): 1.	27	0.177	14
Low	WcGVSVAAEEDDDAAVSATtTPPLPPL T20(Phospho)	0.626 S(5): 0.3; S(17): 7.8; T(19): 7.8	34	0.55	10
Low	yGEVGLAEVAGRALFEIEPENAGNFVsL Y1(Phospho)	0.457 Y(1): 89.3; S(27): 53.3; Y(32): 3	12	0.657	15
Low	YGNPTMFLsENGMDDPGNVTIAQGVH S9(Phospho)	0.406 Y(1): 16.0; T(5): 16.0; S(9): 67.	18	0.735	10
Low	YLsLTSKQK S3(Phospho)	0.456 Y(1): 1.4; S(3): 45.6; T(5): 45.6	45		11
Low	yLTGmATPVHTLGSIGIPmQGLVMEI Y1(Phospho)	0.089 Y(1): 8.9; T(3): 8.9; T(8): 11.7;	0	0.803	10
Low	YQNLHVPVTLmEcFLRVAEANtANNLEtr T22(Phospho)	0.123 Y(1): 64.7; T(9): 64.7; T(22): 54	3	0.638	15
Low	YVAKLAsEGTLR S7(Phospho)	0.974 Y(1): 1.3; S(7): 97.4; T(10): 1.3	40	0.304	15

Os02t0274100-01	Middle	Similar to Peroxisomal fatty acid beta-oxidation multifunctional protein (MFP).	ItGADFYHVMTAmVPLyVAMILAyGsVK	T2(Phospho)	0.067	T(2): 66.7; Y(7): 66.7; T(11): 66.7	0	0.046	10
Low	AEEVLQMmQDAGVRPKQTTycLVADAV		Y20(Phospho)	0.749	T(18): 5.5; T(19): 19.6; Y(20): 7.5	44	0.341	15	
Low	AQGtAPsAGGGAAVPTPSAAAAVSTTT		T4(Phospho)	S7(Phospho)	T	Too many isoforms		0.594	10
Low	DtVALLmNmNFVFQSGRyNGStVAlmGF		T2(Phospho)	0.046	T(2): 30.0; S(15): 59.4; Y(18): 6.0	1		11	
Low	GAcTtAPAsRPPPyPLsPSDLDAVSALLP		T5(Phospho)	0.592	T(4): 18.2; T(5): 86.4; S(9): 94.0	30	0.695	13	
Low	GNAGGsEcMsAlAGSyGYIAPEyAytLK		S6(Phospho)	0.035	S(6): 99.8; S(10): 99.7; S(15): 1.0	23	0.805	11	
Low	IcTYVQcTFLyVHyLHVSLYFDAAR		Y11(Phospho)	0.015	T(3): 59.8; Y(4): 59.8; T(8): 39.0	0	0.796	15	
Low	KLEsLPMmVQGLYsDDSSMQLESTTQF		S4(Phospho)	0.012	S(4): 99.9; Y(13): 0.2; S(14): 1.0	43	0.792	12	
Low	MDSmAIMVQHSGDDyLTAAmGSSPPRI		Y15(Phospho)	0.075	S(3): 0.6; S(11): 0.9; Y(15): 7.5	14	0.668	12	
Low	NGSAVLyMAHGGTNFGFYNGANtGQNI		T23(Phospho)	0.112	S(3): 0.7; Y(7): 0.7; T(13): 1.1;	12	0.485	12	
Low	NTMIGPAPSPAAAAAAVSPscYAsPAA		S21(Phospho)	0.648	T(2): 0.0; S(9): 0.7; S(19): 6.7;	62	0.688	11	
Low	SDVysYGmLILHmVGERENINASTESG		S Y4(Phospho)	0.002	S(1): 1.4; Y(4): 1.4; S(5): 1.7; Y	0	0.78	17	
Low	sGySLSRtAsMAALmAPMAGAFFLLLDPI		S1(Phospho)	0.097	S(1): 45.6; Y(3): 45.6; S(4): 65.0	18	0.29	12	
Low	SSGTNAAssVtDSLSSLVLNLSSSEAEI		S8(Phospho)	S9(Phospho)	T	Too many isoforms			11
Low	SVDLASELtHAWESTAmTLSDMVTMGV		T9(Phospho)	0.103	S(1): 34.9; S(6): 34.9; T(9): 10.0	5		11	
Low	TSRGTGVyASLFGVGAPeALVIGVVALL		Y8(Phospho)	0.678	T(1): 3.1; S(2): 3.1; T(5): 3.1; Y	36		13	
Low	TVGGGSTyFDVQFcLDALGSVGAGAGA	Y8(Phospho)	0.023	T(1): 72.7; S(6): 72.7; T(7): 72.0	10	0.732	10		
Os02t0284600-01	Low	Similar to 60S ribosomal protein L27.	GADtAKFLAEK	T4(Phospho)	1	T(4): 100.0	36	0.378	24
Os02t0287000-01	Low	Similar to 40S ribosomal protein S3a (CYC07 protein).	DSSQHsSNDLQEELKK	S7(Phospho)	0.743	S(2): 11.8; S(3): 11.8; S(6): 2.1	64	0.663	12
Low	IyGSLGTALPcPSEVAAK		Y2(Phospho)	0.841	Y(2): 84.1; S(4): 5.3; T(7): 5.3;	42		13	
Low	LLLPAsGR		S6(Phospho)	1	S(6): 100.0	18	0.21	11	
Low	mAVTAEVEsSPAATGKLR		S9(Phospho)	0.139	T(4): 72.1; S(9): 13.9; S(10): 1.0	44		10	
Os02t0288200-01	High	Protein of unknown function DUF573 domain containing protein.	EATTTAAsDDGTLVGSK	S8(Phospho)	0.805	T(3): 0.0; T(4): 0.1; T(5): 0.4; S	48	0	32
High	VTSTIAtDDDDGTTLGGSKR		T7(Phospho)	0.986	T(2): 0.1; S(3): 0.6; T(4): 0.6; T	74	0	17	
High	YNLAPEPSPsSK		S10(Phospho)	0.096	Y(1): 0.0; S(8): 89.3; S(10): 9.6	80	0.002	29	
High	YNLAPEPSPSSK		S8(Phospho)	0.948	Y(1): 0.0; S(8): 94.8; S(10): 2.6	55	0.001	15	
Middle	YNLAPEPSPSSK		S11(Phospho)	0.12	Y(1): 0.0; S(8): 75.9; S(10): 12.0	53	0.016	25	
Low	DYFIGSLLSGGGsVPR		S13(Phospho)	0.174	Y(2): 1.1; S(6): 1.1; S(9): 80.3;	36	0.062	12	

	Low		NVLsLWFDGLK	S4(Phospho)	1 S(4): 100.0	17	0.556	10
	Low		TFGAQGSSsTRGRPPK	S9(Phospho)	0.177 T(1): 0.0; S(7): 0.1; S(8): 0.4; S	34	0.792	16
	Low		VTSTIATDDDDGTLGGsKR	S17(Phospho)	0 T(2): 0.0; S(3): 0.0; T(4): 0.0; T	36	0.093	13
	Low		yFASFRGASQR	Y1(Phospho)	0.986 Y(1): 98.6; S(4): 0.3; S(9): 1.1	34		11
	Low		YGGIVKIASsK	S10(Phospho)	0.791 Y(1): 9.5; S(9): 17.1; S(10): 86.	29		11
Os02t0453600-01	High	Similar to Glutelin.	TASPFSSSSGSAAATK	S9(Phospho)	0.689 T(1): 0.1; S(3): 0.1; S(6): 2.0; S	37	0.005	19
	Middle		SAyMFLAPLQLcTPR	Y3(Phospho)	0.87 S(1): 13.0; Y(3): 87.0; T(14): 0.	63	0.044	10
	Low		AAAAIGGMLAsAAIKETR	S11(Phospho)	0.816 S(11): 99.6; T(17): 82.0; T(18):	34	0.792	10
	Low		AEVVLAMQIDVtRR	T12(Phospho)	1 T(12): 100.0	20		15
	Low		ALVsAsSSTTAVAALPGAAR	S4(Phospho):	0.455 S(4): 77.3; S(6): 58.0; S(7): 27.	24	0.793	14
	Low		AmIPEGARHMsLLAFGR	S11(Phospho)	1 S(11): 100.0	46		14
	Low		EQQQAAAAGVGVRsPGSGSK	S14(Phospho)	0.027 S(14): 2.7; S(17): 21.9; S(19): 1	11	0.76	10
	Low		ETAFNSELTALARANHK	T9(Phospho)	0.781 T(2): 0.3; S(6): 21.6; T(9): 78.1	27		11
	Low		EyEAFIVGRTEQK	Y2(Phospho)	0.994 Y(2): 99.4; T(10): 0.6	24		10
	Low		FGEREISINvYDK	Y11(Phospho)	0.973 S(7): 2.7; Y(11): 97.3	26		10
	Low		FIQVscLGASASSSR	S5(Phospho)	0.999 S(5): 99.9; S(10): 0.1; S(12): 0.	47		11
	Low		GssGGALLGRPHGPAP	S2(Phospho):	1 S(2): 100.0; S(3): 100.0	45		12
	Low		GVMNSAGGRLRPSTAGTQL	S13(Phospho)	0.777 S(5): 4.1; S(13): 77.7; T(14): 17	51		12
	Low		IALsLEAEsGGILVSVDK	S4(Phospho):	0.496 S(4): 99.1; S(9): 50.4; S(15): 50	22	0.448	17
	Low		LASRVTNsDQQILR	S8(Phospho)	0.922 S(3): 1.0; T(6): 6.8; S(8): 92.2	24		12
	Low		LRycDGGsFAGDSELR	Y3(Phospho):	0.946 Y(3): 99.7; S(8): 94.9; S(13): 5.	28	0.617	11
	Low		LVVtEGLGMQPVDTITK	T4(Phospho)	0.5 T(4): 99.9; T(14): 50.0; T(16): 5	36	0.764	10
	Low		QPIGFKIDtNSNIK	T9(Phospho)	0.966 T(9): 96.6; S(11): 3.4	48	0.774	15
	Low		QVVSEGANGLtIEKR	T11(Phospho)	0.5 S(4): 50.0; T(11): 50.0	20		10
	Low		sFDFKMAVLPQLsGVR	S1(Phospho):	1 S(1): 100.0; S(13): 100.0	66	0.654	10
	Low		sLSTTKDDsLFsN	S1(Phospho):	0.117 S(1): 89.8; S(3): 56.8; T(4): 20.	15	0.743	11
	Low		SMDLGAGtLSVVRLR	T8(Phospho)	0.828 S(1): 0.9; T(8): 82.8; S(10): 16.	37		11
	Low		SSLAAPGAVTSGRsLAR	S14(Phospho)	0.99 S(1): 0.0; S(2): 0.0; T(10): 0.5;	39		14
	Low		VERSSGtLIGsSIATIQK	T7(Phospho):	0.134 S(4): 3.8; S(5): 84.2; T(7): 82.0	46	0.64	14
	Low		VSTILNLELLEsNR	S12(Phospho)	0.99 S(2): 0.5; T(3): 0.5; S(12): 99.0	23		11
	Low		WSLQGKtALVTGGTR	T7(Phospho)	0.333 S(2): 0.0; T(7): 33.3; T(11): 33.	31	0.535	15
Os02t0478600-01	Low	Similar to 40S ribosomal protein S15A.	AtAAPAARR	T2(Phospho)	1 T(2): 100.0	29	0.772	12
	Low		ELALGAsGFSGmLPsSIGKLK	S7(Phospho):	0.292 S(7): 63.8; S(10): 29.6; S(15): 1	21	0.438	14
	Low		HAVtSPRPcRGLTLVsDGR	T4(Phospho):	0.802 T(4): 95.9; S(5): 4.1; T(13): 16.	57	0.703	14
	Low		ItNFTMR	T2(Phospho)	0.11 T(2): 11.0; T(5): 89.0	27	0.651	14
	Low		LARssIR	S4(Phospho):	1 S(4): 100.0; S(5): 100.0	70		12
	Low		LAsRsLR	S3(Phospho):	1 S(3): 100.0; S(5): 100.0	60		12
	Low		LSAYsSVR	S6(Phospho)	0.975 S(2): 0.3; Y(4): 0.3; S(5): 1.8; S	45		11
	Low		LVsNYMR	S3(Phospho)	0.891 S(3): 89.1; Y(5): 10.9	41		13
	Low		SWsHPIWVLmEPVFQMR	S3(Phospho)	0.829 S(1): 17.1; S(3): 82.9	36	0.683	32
	Low		WIDsVQISSGAYIGNIsIR	S4(Phospho):	0.907 S(4): 93.9; S(8): 3.2; S(9): 3.2;	35	0.376	15
Os02t0478700-01	Low	Ribosomal protein S27.	ALRVDAsAAADmTVLER	S7(Phospho)	0.122 S(7): 12.2; T(13): 87.8	4	0.776	14
	Low		DsVVALGGPTWtVPLGR	S2(Phospho):	0.445 S(2): 88.9; T(10): 55.5; T(12): 5	9	0.803	13

	Low		DVIGAGGFGsVYHGVLP	S10(Phospho)	0.928 S(10): 92.8; Y(12): 7.2	40	0.262	11
	Low		GGGGGGGASSVVVSAAAAAsRR	S20(Phospho)	0.475 S(9): 2.5; S(10): 2.5; S(14): 47.	25	0.777	11
	Low		GSVAAsGKHPVsFLAAAR	S6(Phospho):	0.219 S(2): 78.1; S(6): 69.8; S(12): 5;	1	0.743	13
	Low		IVVDGEsEVDLmVQTR	S7(Phospho)	0.217 S(7): 21.7; T(15): 78.3	17		11
	Low		LLsAQGANGQVfVK	S3(Phospho)	1 S(3): 100.0	56		10
	Low		LPSGKQIIALtLyK	T11(Phospho)	1 S(3): 0.0; T(11): 100.0; T(13): 1	62	0.792	18
	Low		MMLPPMGSSvVATRVpK	S9(Phospho)	0.499 S(8): 49.9; S(9): 49.9; T(13): 0.	39	0.46	12
	Low		NAGFRGPTPsFPLGNLR	S10(Phospho)	0.5 T(8): 50.0; S(10): 50.0	28	0.587	12
	Low		sATSLTSLPTRAAAR	S1(Phospho)	0.462 S(1): 46.2; T(3): 46.2; S(4): 7.6	54		12
	Low		SSHLLALGGHPPsPsLR	S13(Phospho)	0.978 S(1): 1.2; S(2): 1.2; S(13): 98.0	31		11
	Low		VIDVELtEAELEERR	T7(Phospho)	1 T(7): 100.0	24	0.806	10
	Low		VNGsLNLARAIGDMELK	S4(Phospho)	1 S(4): 100.0	30	0.788	11
Os02t0489400-01	Low	Similar to 40S ribosomal protein S8.	AtsGA AVLVSRTLPR	T2(Phospho):	0.994 T(2): 99.5; S(3): 99.5; S(10): 0.	40	0.774	11
	Low		EPQAsARSQHIVPR	S5(Phospho)	0.5 S(5): 50.0; S(8): 50.0	33	0.625	11
	Low		ItNFTMR	T2(Phospho)	0.5 T(2): 50.0; T(5): 50.0	37	0.665	25
	Low		LAsRsLR	S3(Phospho):	1 S(3): 100.0; S(5): 100.0	50	0.535	11
	Low		LLMGsSVADASAAARR	S5(Phospho)	0.189 S(5): 18.9; S(6): 12.2; S(11): 6;	4	0.778	14
	Low		LLPYGI NTSmLPKK	T6(Phospho)	0.167 Y(4): 83.2; T(6): 16.7; T(8): 0.0	33	0.723	14
	Low		LLYctGR	T5(Phospho)	0.121 Y(3): 87.9; T(5): 12.1	25		10
	Low		LSAYSsVR	S6(Phospho)	0.98 S(2): 0.3; Y(4): 0.3; S(5): 1.5; S	48		10
	Low		LVSNyMR	Y5(Phospho)	0.879 S(3): 12.1; Y(5): 87.9	42		20
	Low		mIAAVATsDKVVVEK	S8(Phospho)	0.263 T(7): 73.7; S(8): 26.3	10	0.447	11
	Low		NLLAsLPWsTRLK	S5(Phospho):	0.486 S(5): 97.1; S(9): 51.4; T(10): 51	32	0.774	11
	Low		RALtsVR	T4(Phospho):	1 T(4): 100.0; S(5): 100.0	44		10
	Low		SIVDAIEtGsNGRLK	T8(Phospho):	0.983 S(1): 1.7; T(8): 99.6; S(10): 98.	36	0.762	12
	Low		WsRLTPVGEPPSPR	S2(Phospho)	0.046 S(2): 4.6; T(5): 90.9; S(12): 4.6	22		10
Os02t0503400-01	Low	Similar to 60S ribosomal protein L35.	GALAI sAK	S6(Phospho)	1 S(6): 100.0	25	0.434	11
	Low		IIStIGK	T4(Phospho)	0.883 S(3): 11.7; T(4): 88.3	39	0.752	16
	Low		II sTIGK	S3(Phospho)	0.5 S(3): 50.0; T(4): 50.0	31		13
	Low		IsTLLGK	S2(Phospho)	0.5 S(2): 50.0; T(3): 50.0	26		11
	Low		LEtLKK	T3(Phospho)	1 T(3): 100.0	29		13
	Low		RLItVK	T4(Phospho)	1 T(4): 100.0	42	0.776	11
	Low		RLLsLK	S4(Phospho)	1 S(4): 100.0	56		10
	Low		RLVtIK	T4(Phospho)	1 T(4): 100.0	47		10
	Low		sLLTLGK	S1(Phospho)	0.5 S(1): 50.0; T(4): 50.0	26		11
Os02t0519900-01	High	Similar to Elongation factor EF-2 (Fragment).	EQMTPLsDFEDKL	S7(Phospho)	1 T(4): 0.0; S(7): 100.0	81	0.001	41
	Low		AI VEYATSNAlTDIVVGAS tRNtFIR	T20(Phospho)	0.411 Y(5): 8.0; T(7): 11.0; S(8): 15.7	17	0.732	10
	Low		DNS EDLSsTSSALSPSPAKNSGYGYAD	S8(Phospho)	0.306 S(3): 30.6; S(7): 30.6; S(8): 30.	27		11
	Low		EQSTAGIDVISGGVGDmEKLGI sEsFK	S23(Phospho)	0.867 S(3): 6.1; T(4): 6.1; S(11): 4.5;	23	0.792	10
	Low		FGLPFPNLEcGLQVsPSEIMKGASER	S15(Phospho)	0.422 S(15): 42.2; S(17): 42.2; S(24):	4	0.391	13

	Low		GHTKVVVSALAVDHTGSR	T3(Phospho)	0.947 T(3): 94.7; S(7): 5.3; T(14): 0.0	44	0.742	15
	Low		HsPSmESPLEFQYSIVcNFKYGVK	S2(Phospho)	0.466 S(2): 46.6; S(4): 46.6; S(7): 5.0	23	0.276	13
	Low		LAEKTESLTVaETGEPsftGmK	T19(Phospho)	0.831 T(5): 0.0; S(7): 0.0; T(9): 0.0; T	62		11
	Low		LPEAGGGssVsLEAVEQcSGGWRSRLR	S8(Phospho)	0.129 S(8): 52.3; S(9): 70.9; S(11): 70	8	0.8	11
	Low		LtsDSGKVLVANNVIPASWKPGVTYR	T2(Phospho)	0.671 T(2): 77.9; S(3): 77.9; S(5): 20.	26		11
	Low		LyQAsSISQNNLPTIRsIDmVsR	Y2(Phospho)	0.762 Y(2): 98.1; S(5): 79.3; S(6): 20.	51	0.735	11
	Low		mGAKGGmATAAGTAVLVYLVLsGR	S22(Phospho)	0.028 T(9): 47.2; T(13): 2.8; Y(18): 47	13		10
	Low		NYITYAtTLLQDK	T7(Phospho)	0.667 Y(2): 0.1; T(4): 11.1; Y(5): 11.1	50	0.731	10
	Low		QRLYNQsGNGmADYTLdVSyAAQLR	S7(Phospho)	0.979 Y(4): 2.0; S(7): 97.9; Y(14): 0.0	50	0.405	11
	Low		RAVLLSAAPDSSsASAGAAAsLFGR	S13(Phospho)	0.664 S(6): 0.0; S(11): 3.5; S(12): 14.	56	0.604	13
	Low		RPstGAAAAISGDLDfLPTyTTYGSR	S3(Phospho)	0.507 S(3): 94.6; T(4): 96.0; S(11): 5.	35	0.551	19
	Low		ScAStsGNK	T5(Phospho)	0.431 S(1): 4.2; S(4): 53.5; T(5): 53.5	27	0.618	10
	Low		sKPsALVGWFDKK	S1(Phospho)	1 S(1): 100.0; S(4): 100.0	66		11
	Low		SLITNEIsIQNtNVsPLDPK	S8(Phospho)	0.777 S(1): 11.9; T(4): 20.7; S(8): 82.	33	0.459	12
	Low		SSGTLIGssIATIQK	S8(Phospho)	0.815 S(1): 16.5; S(2): 15.0; T(4): 1.1	57		11
	Low		SVALQGVAAPPsGGSTmGsLRFR	S12(Phospho)	0.917 S(1): 0.2; S(12): 99.1; S(15): 2.	52	0.759	12
	Low		TcILmEVLHLHLIVVRQLDtcHK	T20(Phospho)	1 T(1): 0.0; T(20): 100.0	36		10
	Low		tEIIGLKGR	T1(Phospho)	1 T(1): 100.0	68	0.467	13
	Low		tmYSQSSQFHGGLTQSLGLRK	T1(Phospho)	0.719 T(1): 71.9; Y(3): 20.8; S(4): 6.5	37		14
	Low		TVILAVSLsVGIVAmAMIVTcSyLVr	S9(Phospho)	0.195 T(1): 15.3; S(7): 15.3; S(9): 61.	11	0.474	13
	Low		YLIDVGEEKDtAcAAILSmAR	T11(Phospho)	0.744 Y(1): 24.0; T(11): 74.4; S(18): 1	25		11
	Low		YmYFVERyLSVLK	Y8(Phospho)	0.434 Y(1): 2.8; Y(3): 43.4; Y(8): 43.4	33		11
Os02t0523500-02	High	Similar to RNA binding protein Rp120.	LQIWQYGDVEsDEEEQAPAAR	S11(Phospho)	0.87 Y(6): 13.0; S(11): 87.0	96	0	30
	Low		FGITSAGDGALQGTsSGGETKQGDGH	S15(Phospho)	0.289 T(4): 2.6; S(5): 2.6; T(14): 28.9	38	0.206	10
	Low		SSAAsRSWFDDLAVLGLHMyK	S5(Phospho)	0.709 S(1): 5.3; S(2): 5.3; S(5): 71.0;	37		11
	Low		VAAAsLPLSIGtPPVAGcFISSTGR	S4(Phospho)	0.086 S(4): 28.5; S(8): 43.0; T(11): 38	7		12
	Low		WRsLWYLLPELDFVSTADAR	S3(Phospho)	0.915 S(3): 91.5; Y(6): 8.4; S(15): 0.1	32	0.801	13
Os02t0549600-01	High	Similar to 40S ribosomal protein S10-1.	GGAPAEFQPsFR	S10(Phospho)	1 S(10): 100.0	88	0	36
	Low		AVDMFKPSyK	Y9(Phospho)	0.979 S(8): 2.1; Y(9): 97.9	48		12
	Low		EAIvSAPAGGGEK	S5(Phospho)	1 S(5): 100.0	28	0.786	12
	Low		HSFHDSSKLK	S7(Phospho)	0.461 S(2): 7.9; S(6): 46.1; S(7): 46.1	9	0.469	13
	Low		IKMIDLgstK	S8(Phospho)	1 S(8): 100.0; T(9): 100.0	45	0.792	12
	Low		MILLsTLTFTKR	S5(Phospho)	0.734 S(5): 73.4; T(6): 12.1; T(8): 12.	42	0.792	14
	Low		MsQLGAQGTGNSESTK	S2(Phospho)	0.934 S(2): 93.4; T(9): 4.9; S(12): 1.4	35	0.744	13
	Low		NKFSGAESAFK	S4(Phospho)	0.846 S(4): 84.6; S(8): 15.4	32	0.777	12
	Low		NKFSGAESAFK	S8(Phospho)	0.995 S(4): 0.5; S(8): 99.5	46	0.801	24
	Low		QFtYEELKK	T3(Phospho)	0.757 T(3): 75.7; Y(4): 24.3	12	0.591	13
	Low		QFtYKELEK	T3(Phospho)	0.832 T(3): 83.2; Y(4): 16.8	29	0.495	13
	Low		SASsVGLPLSLR	S4(Phospho)	0.748 S(1): 12.6; S(3): 12.6; S(4): 74.	49	0.589	16
	Low		SPAPQVDRVsK	S10(Phospho)	0.731 S(1): 26.9; S(10): 73.1	9		11
	Low		SSGDsPLQLGPK	S5(Phospho)	0.724 S(1): 6.9; S(2): 20.7; S(5): 72.4	23	0.176	17

	Low		SSGHGRLtNTR	T8(Phospho)	0.158 S(1): 4.4; S(2): 4.4; T(8): 15.8;	12	0.806	12
	Low		SSSGSVPRsPmR	S9(Phospho)	0.544 S(1): 4.2; S(2): 13.8; S(3): 13.8	21		11
	Low		SSSGsVPRSPmR	S5(Phospho)	0.184 S(1): 6.8; S(2): 6.8; S(3): 6.8; S	10		13
	Low		SsSGSVPRSPmR	S2(Phospho)	0.229 S(1): 22.9; S(2): 22.9; S(3): 22.	11		12
	Low		tTAEPEPGLLR	T1(Phospho)	0.5 T(1): 50.0; T(2): 50.0	38		12
	Low		VSHQAGSSsFTR	S9(Phospho)	0.523 S(2): 11.9; S(7): 11.9; S(8): 11.	27		10
	Low		VSSLTNGHQsR	S10(Phospho)	0.759 S(2): 1.5; S(3): 4.8; T(5): 17.8;	31	0.792	11
		Similar to Candida glabrata strain CBS138 chromosome L complete sequence.						
Os02t0591700-01	Low		ANGKADtASKPR	T7(Phospho)	0.969 T(7): 96.9; S(9): 3.1	42		10
	Low		EGGRiVGAGVVS	T5(Phospho)	0.084 T(5): 8.4; S(12): 91.6	9	0.802	17
	Low		ELGAGsARELK	S6(Phospho)	1 S(6): 100.0	37	0.779	14
	Low		LAsNPAAFLRR	S3(Phospho)	1 S(3): 100.0	66	0.737	10
	Low		QGsnVTGKALIK	S3(Phospho)	0.5 S(3): 50.0; T(6): 50.0	15	0.803	11
	Low		RSSsAASDPPLK	S4(Phospho)	0.067 S(2): 2.5; S(3): 6.7; S(4): 6.7; S	12		10
	Low		sFLSAAIYKK	S1(Phospho)	0.998 S(1): 99.8; S(4): 0.2; Y(8): 0.0	39	0.576	11
	Low		sKHNLtVIPK	S1(Phospho)	1 S(1): 100.0; T(6): 100.0	47	0.582	11
	Low		SsQVDRPTLK	S2(Phospho)	0.487 S(1): 48.7; S(2): 48.7; T(8): 2.6	31	0.251	11
	Low		sSQVDRPTLK	S1(Phospho)	0.852 S(1): 85.2; S(2): 14.8; T(8): 0.0	47	0.318	14
	Low		VIDAIMPtLR	T8(Phospho)	1 T(8): 100.0	41	0.629	11
		Similar to 60S ribosomal protein L12.						
Os02t0699600-01	Low		AAELKyGTLLsLQK	Y6(Phospho)	0.448 Y(6): 55.2; T(8): 55.2; S(11): 85	40		16
	Low		ELQAPtRPILK	T6(Phospho)	1 T(6): 100.0	4	0.347	10
	Low		GRLyEFSNVNsTR	Y4(Phospho)	0.603 Y(4): 81.3; S(7): 34.0; S(11): 7	25	0.607	11
	Low		LSLLGVGSFENSPsSR	S14(Phospho)	0.445 S(2): 0.0; S(8): 0.3; S(12): 44.5	41		16
	Low		RLHIPLPsSR	S8(Phospho)	0.5 S(8): 50.0; S(9): 50.0	33	0.792	13
	Low		SLEVNRNGtDVLGLK	T9(Phospho)	0.775 S(1): 22.5; T(9): 77.5	16		10
	Low		SSLPVtPVGdHR	T6(Phospho)	0.333 S(1): 33.3; S(2): 33.3; T(6): 33.	14	0.663	12
	Low		VGDKtFDawLDQVR	T5(Phospho)	1 T(5): 100.0	34		11
		Similar to Eukaryotic translation initiation factor 3 subunit-like protein.						
Os02t0788400-01	High		DLAPQTEAFVDRPPTADGSGPPGGAVK	T15(Phospho)	0.996 T(6): 0.0; T(15): 99.6; S(19): 0.	102	0	46
	Low		DDPTTYLVtFDDDGAKYLPLPtK	T9(Phospho)	0.467 T(4): 17.6; T(5): 17.6; Y(6): 17.	34	0.617	16
	Low		DIKVPEALyGGTGNyAsALFLTAak	Y9(Phospho)	0.304 Y(9): 46.7; T(12): 46.7; Y(15): 1	25		12
	Low		ELLIWVSISEIVLsPsGtKLvFR	S14(Phospho)	0.068 S(7): 10.6; S(9): 63.2; S(14): 2	14	0.638	10
	Low		FEVDsLGNTSSTVMYGPADGAYEPR	S5(Phospho)	0.056 S(5): 5.6; T(9): 40.3; S(10): 14.	14	0.785	11
	Low		GmFGNTVVMDDVLTEGPAATsVLGR	S22(Phospho)	0.333 T(6): 0.0; T(14): 0.0; T(20): 33.	54	0.76	13

	Low		LGDNsLATLDLSRPtmSPERPER	S5(Phospho)	0.276 S(5): 68.2; T(8): 29.5; S(12): 19.5	16	0.723	15
	Low		LQILRSITHsHALSNTSILmDASK	S10(Phospho)	0.052 S(6): 0.5; T(8): 0.2; S(10): 5.2;	33	0.55	13
	Low		MAAAAVmVssASGLLAMLQEPAAELK	S9(Phospho)	0.944 S(9): 97.2; S(10): 97.2; S(12): 97.2;	44	0.434	15
	Low		MAGLRPVDVEIEPGttMHIWVPK	T15(Phospho)	1 T(15): 100.0; T(16): 100.0	27	0.562	12
	Low		mAIPTLVLLPtWGTGHLmSLLDAGK	T11(Phospho)	0.362 T(5): 36.2; T(11): 36.2; T(14): 10.0;	23	0.747	13
	Low		mAMLLASLLSPSPLPTTTTssTSPR	S20(Phospho)	0.356 S(7): 0.0; S(10): 0.2; S(12): 0.2	49	0.292	12
	Low		mmNLQtLDLKGTYVSQLPsGITK	T6(Phospho)	0.632 T(6): 98.2; T(12): 2.2; Y(13): 2.0;	40		13
	Low		mPLASmSNLTSicGTPRGAGGIPsSR	S24(Phospho)	0.467 S(5): 0.7; S(7): 0.7; T(10): 0.5;	20		15
	Low		mTTIQtlSgIEIsGSLATFAGIIR	T6(Phospho)	0.051 T(2): 35.5; T(3): 35.5; T(6): 35.5;	48	0.566	14
	Low		NEPDSAKVTmQTESVAQPNEADsAK	S23(Phospho)	0.998 S(5): 0.0; T(9): 0.1; T(12): 0.1;	41		13
	Low		PSSTIRsISITASDDDDAAAAGAPSAAPR	S7(Phospho)	0.181 S(2): 2.3; S(3): 2.3; T(4): 2.3; S(5): 2.3;	33		11
	Low		QLNGsWPAGLPANGsLAVStRHNR	S5(Phospho)	0.002 S(5): 0.8; S(15): 99.8; S(19): 99.8;	3		11
	Low		RPsgGGGTLPsAGSSGRGAGcGSVAPSI	S3(Phospho)	0.333 S(3): 45.7; T(7): 45.7; S(10): 5.0;	37	0.265	12
	Low		SASPDELERHVSPsNNGHGPPVDGK	S12(Phospho)	0.991 S(1): 0.3; S(3): 0.7; S(12): 99.5	39		10
	Low		sEKEAAAAAGELDAAAAAEVNAAADAA	S1(Phospho)	1 S(1): 100.0	60	0.393	12
	Low		TlmQLmsVDGLtRENVAsHLQK	S7(Phospho)	0.189 T(1): 81.1; S(7): 65.4; T(12): 88.0;	5	0.8	13
	Low		TSSSTVNGGGISSGAADStLARsTAAR	T20(Phospho)	0.001 T(1): 26.6; S(2): 26.6; S(3): 26.6;	8	0.792	15
	Low		VPPPATPPPAALPDsLTAQDALSAAAF	S15(Phospho)	0.698 T(6): 7.7; S(15): 69.8; T(17): 22.0;	35	0.659	14
	Low		yGAAsAQYALLEYASGAPVQFSYR	Y1(Phospho)	0.67 Y(1): 89.4; S(5): 75.3; Y(8): 29.0;	27	0.478	11
Os02t0821800-01	Low	Similar to Fibrillarin-2.	AsEAAALAmRR	S2(Phospho)	1 S(2): 100.0	11	0.806	13
	Low		AttADAGGSNINDPLLPHHPmDEIVtLLk	T2(Phospho)	0.889 T(2): 95.0; T(3): 95.0; S(9): 11.0;	28	0.77	11
	Low		EHVLIsIFANAGcAFGNNGNAyAVmIVDIIR	S6(Phospho)	1 S(6): 100.0; Y(21): 100.0	47	0.348	10
	Low		ETAAYLSmLAItsEVImyPATTTQTGRGR	T12(Phospho)	0.007 T(2): 25.2; Y(5): 32.3; S(7): 32.0;	0	0.683	13
	Low		FLFLQIVmKFAsIPsVsVssSIIVLLR	S12(Phospho)	0.241 S(12): 92.4; S(15): 92.4; S(17): 92.4;	8	0.806	12
	Low		FWyYAHGGmLNPVDGSLVFSDQIREA/	Y3(Phospho)	0.756 Y(3): 75.6; Y(4): 17.0; S(16): 5.0;	19	0.532	14
	Low		KYASFSPSSSSSTmAAASPSPISAAAAA/	T34(Phospho)	0.937 Y(2): 0.2; S(4): 0.2; S(6): 0.3; S(7): 0.3;	26		13
	Low		LtSEQKSEIK	T2(Phospho)	0.968 T(2): 96.8; S(3): 3.0; S(7): 0.2	48	0.787	11
	Low		mtAPPMWLPFGWAELEPHV	T2(Phospho)	1 T(2): 100.0; T(18): 100.0	1	0.804	10
	Low		mVLSGEGSDELLGGyLYFHFAPNKEEF	Y15(Phospho)	0.202 S(4): 0.1; S(8): 1.7; Y(15): 20.2	39	0.093	12
	Low		NYMKQAFVsLtSIEELTISGSFLTYLsK	S9(Phospho)	0.003 Y(2): 2.2; S(9): 9.5; T(11): 22.1	16		10
	Low		NYYItAIAGATNGSSLVvmSKGTPYTQQ	T5(Phospho)	0.234 Y(2): 23.4; Y(3): 23.4; T(5): 23.0;	11	0.806	13
	Low		QPAWPMADGTPWGGTSGHPFTTtGLP	T23(Phospho)	0.65 T(10): 2.4; T(15): 2.4; S(16): 2.0;	40		10
	Low		stQPsSPSTSPcSSPSVPSDANTmPLVH	S1(Phospho)T2(Phospho)	S Too many isoforms		0.585	12
	Low		tARGGATSAGSAR	T1(Phospho)	0.983 T(1): 98.3; T(7): 0.7; S(8): 0.7;	29	0.752	11
	Low		TGEPsQHPLPAAQAERGQPsSVTPTAS	S5(Phospho)	0.131 T(1): 75.7; S(5): 24.1; S(20): 56.0;	32	0.803	13
	Low		TTPtGASSAGESVGKAASVAmVIVSAA	T4(Phospho)	0.013 T(1): 19.7; T(2): 19.7; T(4): 19.7;	1	0.674	21
	Low		tVGVDLGGGSVMqAmLSNTAANAF	T1(Phospho)	0.039 T(1): 26.7; S(11): 51.3; Y(16): 3.0;	8	0.802	12
	Low		VHsAITNGSTVGATVDSIDVAmQNFsElf	S3(Phospho)	0.273 S(3): 36.3; T(6): 36.3; S(9): 15.0;	14	0.806	10
	Low		VIAtLLLSVISHGAYPAmGSAWEEEDF/	T4(Phospho)	0.025 T(4): 22.2; T(5): 22.2; S(9): 44.0;	9	0.803	12
	Low		VVsEQWVDDsLDLGemADADRVLYRP\	S3(Phospho)	0.989 S(3): 100.0; S(10): 99.0; Y(24): 99.0;	42	0.806	10
	Low		YLsMLPVDPK	S3(Phospho)	0.5 Y(1): 50.0; S(3): 50.0	46	0.743	14
	Low		YMFVYVsNsIsFMASIAVIMLLLSKSVR	S7(Phospho)	0.342 Y(1): 32.1; Y(5): 32.1; S(7): 83.0;	52		14
Os03t0154700-01	Low	Similar to 40S ribosomal protein S9.	KLEAMAVGYRPsALR	S12(Phospho)	0.768 Y(9): 23.2; S(12): 76.8	22	0.742	11
	Low		LKsLHTLR	S3(Phospho)	0.974 S(3): 97.4; T(6): 2.6	37		13

Os03t0177400-01	Low	EF-1 alpha.	RsPLGTR	S2(Phospho)	0.999 S(2): 99.9; T(6): 0.1	46	0.806	16
	Low		sGLSADLLAK	S1(Phospho)	0.967 S(1): 96.7; S(4): 3.3	41	0.263	13
	Low		SGLsADLLAK	S4(Phospho)	0.097 S(1): 90.3; S(4): 9.7	61	0.163	29
	Low		SLsPARR	S3(Phospho)	0.148 S(1): 85.2; S(3): 14.8	21	0.745	15
	Low		VKNTesGLGSSSDLLR	S6(Phospho)	0.758 T(4): 15.9; S(6): 75.8; S(10): 3.	42	0.639	12
	Low		VLPELNGKLTGmAFFR	T10(Phospho)	1 T(10): 100.0	40		11
	Low		LGGsDVAVTK	S4(Phospho)	0.812 S(4): 81.2; T(9): 18.8	26	0.786	12
Os03t0182600-02	Low	Similar to 40S ribosomal protein SA.	DVTSTKPQsTNGDGRQQSmPK	S9(Phospho)	0.468 T(3): 1.2; S(4): 3.7; T(5): 1.2; S	29	0.806	17
	Low		EEVSTALsQLVPTIFSMsMK	S8(Phospho)	0.007 S(4): 0.5; T(5): 0.8; S(8): 1.3; T	10		13
	Low		EySNSWTEPLTPSTNQK	Y2(Phospho)	0.843 Y(2): 84.3; S(3): 15.3; S(5): 0.2	47	0.59	15
	Low		FLQTKFVGAGsK	S11(Phospho)	0.774 T(4): 22.6; S(11): 77.4	23	0.805	11
	Low		GQAWVVFSEITAATNAFR	S8(Phospho)	0.277 S(8): 27.7; T(11): 27.7; T(14): 4	2		15
	Low		GtSSLcDASAAATSGLtGIR	T2(Phospho)	0.106 T(2): 15.4; S(3): 15.4; S(4): 15.	29	0.486	15
	Low		KmWDEEEEVQsPLAFK	S11(Phospho)	1 S(11): 100.0	61	0.7	15
	Low		LTHLNLsSNSItGELQDDLK	S7(Phospho)	0.337 T(2): 3.8; S(7): 78.2; S(8): 18.8	25		11
	Low		LtNIGETGGmKEsAEVLK	T2(Phospho)	0.993 T(2): 99.3; T(7): 0.7; S(13): 100	62	0.079	18
	Low		mKPRLLSDSGAsScNSGAK	S12(Phospho)	0.497 S(7): 0.0; S(9): 0.1; S(12): 49.7	58	0.722	10
	Low		SAAPVDPVAQVEVLPsAGERGR	S17(Phospho)	0.325 S(1): 67.5; S(17): 32.5	7		14
Os03t0197300-01	Low	Similar to Cupin family protein, expressed.	AAAAAsGMGARLR	S5(Phospho)	1 S(5): 100.0	57		10
	Low		AMVLsPNIMR	S5(Phospho)	1 S(5): 100.0	36	0.47	12
	Low		AQALPIAFLAELLKPIATGmTSFGGK	T6(Phospho)	1 T(6): 100.0; T(18): 0.0; T(21): 0	51		11
	Low		ATSEGDLmAAVsARPR	S12(Phospho)	0.647 T(2): 17.6; S(3): 17.6; S(12): 64	27	0.628	12
	Low		DGGtYIEAILPGAAADQGTGK	T4(Phospho)	0.5 T(4): 50.0; Y(5): 50.0; T(18): 0.	31		11
	Low		DLAAVHGPLmMLQLGETPLVVVsR	S24(Phospho)	0.485 T(17): 2.9; S(23): 48.5; S(24): 4	17	0.615	11
	Low		DPNANIImLATGTGIAPFRsFLWK	S20(Phospho)	1 T(11): 0.0; T(13): 0.0; S(20): 100	50		13
	Low		EASLELNsLR	S8(Phospho)	0.5 S(3): 50.0; S(8): 50.0	32		11
	Low		ELVtPRAmAVAVVLSVVlcFVGmR	T4(Phospho)	0.922 T(4): 92.2; S(15): 7.8	19		12
	Low		EREsVIIMR	S4(Phospho)	1 S(4): 100.0	36	0.3	11
	Low		ESFsAAVDAALELLGGDGAR	S4(Phospho)	0.948 S(2): 5.2; S(4): 94.8	43	0.786	13
	Low		EVAAMARVSGtHHVLGVPHLLGELR	T11(Phospho)	0.853 S(9): 14.7; T(11): 85.3	20		11
	Low		FIVANPsWKLAMK	S7(Phospho)	1 S(7): 100.0	50		10
	Low		GNVetGSVREIIVQSGLPATR	T5(Phospho)	0.661 T(5): 66.1; S(7): 3.5; S(15): 3.5	18		18
	Low		GTAAALAIIDTPPsWGR	S13(Phospho)	0.842 T(2): 0.0; T(10): 15.8; S(13): 84	46	0.364	12
	Low		IADVsVVS LGTAAAI AVLADELttLR	S5(Phospho)	0.008 S(5): 5.1; S(8): 31.8; T(11): 37.	1		14
	Low		IADVSVVSLGTAAAI AVLADELttLR	T23(Phospho)	0.982 S(5): 0.1; S(8): 0.7; T(11): 1.3;	39		16
	Low		KIVLIPAsTDDENVK	S8(Phospho)	0.5 S(8): 50.0; T(9): 50.0	53	0.138	21
	Low		KIVLIPAsTDDENVK	T9(Phospho)	0.5 S(8): 50.0; T(9): 50.0	31	0.759	12
	Low		LAsSTVGFPFR	S3(Phospho)	0.467 S(3): 46.7; S(4): 46.7; T(5): 6.7	51		11
	Low		LEVVDLSsNR	S8(Phospho)	0.857 S(7): 14.3; S(8): 85.7	38		10
	Low		LGmTPPSRtR	T9(Phospho)	0.154 T(4): 3.4; S(7): 81.2; T(9): 15.4	30	0.628	13
	Low		LQIADVEtVAAGDIVK	T8(Phospho)	1 T(8): 100.0	36		11
	Low		LsVSMGSMELPSQGADVIK	S2(Phospho)	0.015 S(2): 1.5; S(4): 3.6; S(7): 13.9;	3	0.068	11

	Low		MALSWPsAIR	S7(Phospho)	0.988 S(4): 1.2; S(7): 98.8	33		12
	Low		mAtVPEPLIWEIVK	T3(Phospho)	1 T(3): 100.0	52		10
	Low		MGPTGNtGLKR	T7(Phospho)	0.153 T(4): 84.7; T(7): 15.3	32		12
	Low		MRINPsQTKPIQTK	S6(Phospho)	0.951 S(6): 95.1; T(8): 3.4; T(13): 1.6	22		11
	Low		MRPsPLmKR	S4(Phospho)	1 S(4): 100.0	28		11
	Low		MRsSDGLPIR	S3(Phospho)	0.5 S(3): 50.0; S(4): 50.0	40	0.656	12
	Low		MRSsDGLPIR	S4(Phospho)	0.136 S(3): 86.4; S(4): 13.6	35	0.509	15
	Low		NFsFMPENETVMVQHR	S3(Phospho)	0.5 S(3): 50.0; T(10): 50.0	55	0.659	10
	Low		NLMtRsIAIVPSLIVSIIIGSSGAGR	T4(Phospho)	0.918 T(4): 99.1; S(6): 92.6; S(12): 7.	45		11
	Low		QMDNmPAVAsPTMNKR	S10(Phospho)	0.971 S(10): 97.1; T(12): 2.9	68		11
	Low		RAmPSPPPHGPmsLmASR	S13(Phospho)	0.987 S(5): 0.7; S(13): 98.7; S(17): 0.	40	0.628	11
	Low		RDPVPSPRPSPGMILsPR	S16(Phospho)	0.959 S(6): 0.1; S(10): 4.0; S(16): 95.	48		10
	Low		RLLSISVAAVAETPR	T5(Phospho)	0.853 S(4): 14.6; T(5): 85.3; S(6): 0.1	49		10
	Low		RsQDGS�TLR	S2(Phospho)	0.442 S(2): 44.2; S(6): 44.2; T(8): 11.	23	0.313	11
	Low		sAlcNAVVAAR	S1(Phospho)	1 S(1): 100.0	33		11
	Low		SILDAVsGSVPTASMSRR	S7(Phospho)	0.793 S(1): 1.2; S(7): 79.3; S(9): 18.0	50	0.171	12
	Low		SsmRHSVLDPGILR	S2(Phospho)	0.489 S(1): 48.9; S(2): 48.9; S(6): 2.2	48	0.378	11
	Low		SSPSISTvPFAPHR	T8(Phospho)	0.748 S(1): 0.0; S(2): 0.0; S(4): 0.1; S	46	0.312	14
	Low		TAAAAAAsQLTR	S8(Phospho)	0.018 T(1): 97.9; S(8): 1.8; T(11): 0.3	12	0.737	11
	Low		tAtPMLLQPISGAGAGARR	T1(Phospho)	0.196 T(1): 39.3; T(3): 80.4; S(11): 80.	20		13
	Low		TLALsKmAANPALMSQHAALK	S5(Phospho)	0.777 T(1): 14.6; S(5): 77.7; S(15): 7.	15		15
	Low		TLIRcyFSPVYSTGQR	Y6(Phospho)	0.463 T(1): 2.9; Y(6): 46.3; S(8): 46.3	37		12
	Low		tLVVAHGAGyVFDDVPGGSSR	T1(Phospho)	0.872 T(1): 98.2; Y(10): 88.1; S(19): 0.	23	0.652	17
	Low		VDVYsyGVVLELVsGR	S5(Phospho)	0.977 Y(4): 2.3; S(5): 97.7; Y(6): 99.9	76		17
	Low		VDVySYGVVLELVsGR	Y4(Phospho)	0.078 Y(4): 50.6; S(5): 50.6; Y(6): 82.	38		11
	Low		VIDPGNtEVGRItNNIR	T7(Phospho)	1 T(7): 100.0; T(13): 100.0	53		14
	Low		VPVAGGDPDGKSAAIPtR	T18(Phospho)	0.5 S(13): 50.0; T(18): 50.0	36	0.641	18
	Low		VRFGAVsyNMVLDALGR	S7(Phospho)	1 S(7): 100.0; Y(8): 100.0	80		16
	Low		VVsLAAsLmKLGScsLR	S3(Phospho)	0.123 S(3): 37.0; S(7): 87.7; S(13): 8.	4	0.754	12
	Low		YHRSLGVQVVIGGtR	T14(Phospho)	0.999 Y(1): 0.0; S(4): 0.1; T(14): 99.9	39		11
	Low		YKPDLS EGKTQEGK	S6(Phospho)	0.26 Y(1): 69.2; S(6): 26.0; T(10): 4.	8	0.57	14
	Low		YPSmRSLLNvymDDSK	Y11(Phospho)	0.818 Y(1): 0.0; S(3): 0.0; S(6): 0.0; Y	42	0.215	12
Os03t0200500-02	Low	Similar to 40S ribosomal protein S3a.	GtRYVItAAADTGtIK	T2(Phospho)	0.428 T(2): 55.7; Y(4): 55.7; T(7): 85.	29		12
	Low		HQASsSSGAAASASPPSPPAK	S5(Phospho)	0.348 S(4): 12.5; S(5): 34.8; S(6): 34.	25		10
	Low		LLLPAsGR	S6(Phospho)	1 S(6): 100.0	18	0.21	11
Os03t0219300-01	High	Similar to Tubulin alpha-2 chain (Alpha-2 tubulin).	TVQFVDWcPtGFK	T10(Phospho)	1 T(1): 0.0; T(10): 100.0	106	0	62
Os03t0249900-01	High	Conserved hypothetical protein.	ASSDtDDDDDDFIVSK	T5(Phospho)	0.727 S(2): 13.7; S(3): 13.7; T(5): 72.	55	0	20
	Low		AsLtTNVGLSTPAAAASSLVRPVAGAGR	S2(Phospho)	0.014 S(2): 8.9; T(3): 4.2; T(5): 7.6; S	24	0.726	11
	Low		EsTScSARPLGSLISVLMNVVTTLR	S2(Phospho)	0.466 S(2): 46.6; T(3): 46.6; S(4): 3.4	42	0.719	15

	Low		EWLNVAFIDVGHASMQVsIVGYKK	S18(Phospho)	0.988 S(14): 0.2; S(18): 98.8; Y(22): 1	58	0.734	16
	Low		GtQHAQSVGsARIGEGQTLIGAGHNR	T2(Phospho)	0.846 T(2): 92.3; S(7): 15.4; S(10): 92	47	0.776	12
	Low		HQItVGsTVSINLPVVNQVFSSNR	T4(Phospho)	0.134 T(4): 32.1; S(7): 73.7; T(8): 63.	28	0.806	13
	Low		HQITVGstVSINLPVVNQVFSSNR	S7(Phospho)	0.072 T(4): 72.0; S(7): 54.6; T(8): 31.	9	0.796	12
	Low		IQsALGYmAPEFtcRtVNVTEK	S3(Phospho)	0.081 S(3): 51.6; Y(7): 52.7; T(13): 67	0	0.511	12
	Low		LVVYEYVATGSFsAMLHGKIAEK	S13(Phospho)	0.709 Y(4): 0.3; Y(6): 0.4; T(9): 3.8; S	29	0.802	12
	Low		mDHyPGVGHGESLALcATTkDyR	Y4(Phospho)	0.842 Y(4): 94.7; S(12): 3.5; T(18): 3.	37		10
	Low		NmHDQVDHsKPFsSGSPPPGsTLR	S14(Phospho)	0.208 S(9): 0.9; S(13): 36.6; S(14): 36	48		11
	Low		NmHDQVDHsKPFsSGSPPPGsTLR	S13(Phospho)	0.019 S(9): 2.4; S(13): 6.6; S(14): 6.6	28		11
	Low		SAAISGAsLVLsSPPAPGARPPQPRPAR	S8(Phospho)	0.3 S(1): 11.9; S(5): 25.6; S(8): 61.	22	0.792	12
	Low		sEDGSEEAAsVLPKPLAAIVTGARsR	S1(Phospho)	0.407 S(1): 68.7; S(5): 37.4; T(21): 31	15	0.743	12
	Low		SLSPKVLtLVEmESNTNTAPFPQR	T8(Phospho)	0.048 S(1): 41.3; S(3): 41.3; T(8): 4.8	6	0.806	13
	Low		SMAWYAKTntQVPEVVLVPsGsR	T10(Phospho)	0.02 S(1): 13.7; Y(5): 42.5; T(8): 69.	12	0.577	12
	Low		TALRLsEVGNAAVVVNPsTmQIIAK	S6(Phospho)	0.323 T(1): 48.7; S(6): 48.7; S(18): 68	14	0.739	10
	Low		TAPAPMPLPPAQAPVWsPAPAPAATQF	S17(Phospho)	0.987 T(1): 0.4; S(17): 98.7; T(25): 0.	36		15
	Low		TLVAVGLmLGmILGFLSGSVFFsYK	S23(Phospho)	0.249 T(1): 0.3; S(17): 24.9; S(19): 24	20	0.652	11
	Low		TSILGDtIGyVKELmDR	T7(Phospho)	0.158 T(1): 68.3; S(2): 16.1; T(7): 16.	29		11
	Low		VAEEmRPPPPPPPARAEQHGTGtVR	T23(Phospho)	0.251 T(21): 74.9; T(23): 25.1	23		10
	Low		WKHLILNtTPTTPIEPcEWLNK	T8(Phospho)	0.393 T(8): 39.3; T(9): 39.3; T(11): 10	26	0.776	10
	Low		yWSSMVTcLVGVFQtALVGIIIR	Y1(Phospho)	0.347 Y(1): 38.8; S(3): 38.8; S(4): 15.	23	0.321	13
Os03t0277300-01	Low	Heat shock protein 70.	GTAAALAIIDTPPsWGR	S13(Phospho)	0.967 T(2): 0.0; T(10): 3.3; S(13): 96.	52	0.298	14
	Low		SHFLHTASTTtPRK	T11(Phospho)	0.973 S(1): 0.0; T(6): 0.0; S(8): 0.0; T	63	0.602	12
	Low		SSPSISiTVPFAPHR	T7(Phospho)	0.438 S(1): 0.2; S(2): 0.2; S(4): 0.5; S	26	0.272	10
Os03t0327600-01	High	Ricin B-related lectin domain containing protein.	ILPWGDEAYAGGsANAPR	S13(Phospho)	1 Y(9): 0.0; S(13): 100.0	136	0	34
	Low		AlSGEQLRELAAGLEtSGHR	S3(Phospho)	0.086 S(3): 31.4; T(16): 77.2; S(17): 9	11	0.715	15
	Low		ALQHsKVK	S5(Phospho)	1 S(5): 100.0	40		12
	Low		AMEGQAsALHEmSAQLR	S7(Phospho)	0.924 S(7): 92.4; S(13): 7.6	28		10
	Low		APEHHDHELTLTAGKEsFR	S17(Phospho)	0.782 T(10): 9.3; T(12): 12.5; S(17): 7	10		11
	Low		ATIPAMATPMsGGRCAPR	S11(Phospho)	0.839 T(2): 11.2; T(8): 4.9; S(11): 83.	21		11
	Low		DVPVVLADEAAPSGtAPR	T15(Phospho)	0.814 S(13): 18.6; T(15): 81.4	41		10
	Low		GRSQAIAsPPLPetGQR	S8(Phospho)	0.856 S(3): 14.4; S(8): 87.6; T(14): 98	18		15
	Low		HAIsGDQIAIVIGtVTDDKR	S4(Phospho)	0.469 S(4): 93.8; T(14): 53.1; T(16): 5	23	0.691	11
	Low		HITASREAIISVVEsPetR	S15(Phospho)	0.868 T(3): 5.0; S(5): 5.0; S(11): 6.5;	32	0.709	11
	Low		IELLALsHANKAER	S7(Phospho)	1 S(7): 100.0	16		12
	Low		ILPtPELK	T4(Phospho)	1 T(4): 100.0	38		10
	Low		mEIKDEETtAEVAMVVQSR	T9(Phospho)	0.99 T(8): 0.9; T(9): 99.0; S(18): 0.1	49	0.682	11
	Low		mStnQGvQLR	T3(Phospho)	0.916 S(2): 8.4; T(3): 91.6	82	0.771	13
	Low		NcPFSLcINicPNtIVPR	T14(Phospho)	1 S(5): 0.0; T(14): 100.0	61	0.762	20
	Low		NRmASQPATNAsKPATVQMR	S12(Phospho)	0.231 S(5): 3.7; T(9): 3.7; S(12): 23.1	17	0.054	16
	Low		NSALmIsRTLAMAYVmDQK	S7(Phospho)	0.152 S(2): 25.4; S(7): 15.2; T(9): 10.	3	0.602	12
	Low		RDPSEMVsIK	T9(Phospho)	0.854 S(4): 0.0; S(8): 14.6; T(9): 85.4	47		10
	Low		RHGAASGGStGTTRPFSTPSSR	T10(Phospho)	0.736 S(6): 0.0; S(9): 0.5; T(10): 73.6	77	0.088	21

	Low		sARLVcAPK	S1(Phospho)	1 S(1): 100.0	42	0.776	12
	Low		sIQRLELPGTETQSSPVR	S1(Phospho)	0.08 S(1): 85.9; T(11): 13.0; T(13): 1	9	0.691	13
	Low		SWsHPIWVLmEPVFQmR	S3(Phospho)	0.257 S(1): 74.3; S(3): 25.7	11	0.483	15
	Low		TAATRVPItFVDVTtMSER	T9(Phospho)	0.459 T(1): 0.0; T(4): 0.0; T(9): 99.5;	51	0.741	14
	Low		TIGFQLIDDKyPR	Y11(Phospho)	0.989 T(1): 1.1; Y(11): 98.9	40	0.491	12
	Low		tVALVGGSGSGKstVIALLER	T1(Phospho)	0.826 T(1): 98.0; S(8): 13.1; S(10): 6.	34	0.261	14
	Low		VMVDALVRsRPFLHmAcR	S9(Phospho)	1 S(9): 100.0	11	0.679	10
	Low		ymGAQVEISVDFLTEK	Y1(Phospho)	0.899 Y(1): 89.9; S(9): 3.7; T(14): 6.4	17	0.732	11
Os03t0336100-01	Middle	11-S plant seed storage protein family protein.	VcLLGcGVSTGLGAVWNtAK	T18(Phospho)	1 S(9): 0.0; T(10): 0.0; T(18): 100	43	0.042	15
	Low		AKPSAAAGGSsHPPYFEmIK	S11(Phospho)	0.682 S(4): 4.0; S(10): 4.0; S(11): 68.	24		12
	Low		DAGVsAKDIDEVLLVGGmTR	S5(Phospho)	0.994 S(5): 99.4; T(19): 0.6	24		10
	Low		DGKATMESPsSIPTLK	S10(Phospho)	0.287 T(5): 28.7; S(8): 10.0; S(10): 28	19		12
	Low		DGKATMESPsSIPTLK	S8(Phospho)	0.478 T(5): 15.5; S(8): 47.8; S(10): 15	19		10
	Low		EAtLDAATIAGLNVmR	T3(Phospho)	0.5 T(3): 50.0; T(8): 50.0	35		13
	Low		EDAsALIQSTEEIKK	S4(Phospho)	0.053 S(4): 5.3; S(9): 47.4; T(10): 47.	14	0.724	14
	Low		EFIFSSSFTGDKQtLAQR	T14(Phospho)	0.999 S(5): 0.0; S(6): 0.0; S(7): 0.0; T	64		15
	Low		ERLVVVEFAASHsVNsSR	S13(Phospho)	0.029 S(11): 93.9; S(13): 6.7; S(16): 4	25	0.685	15
	Low		FEtSHVLGALLASsPLLAR	T3(Phospho)	0.248 T(3): 50.0; S(4): 50.0; S(13): 50	27	0.078	11
	Low		FVsAFRSsELLAVR	S3(Phospho)	0.68 S(3): 90.9; S(7): 32.0; S(8): 77.	16		10
	Low		GyVGDPEATAATITPDGWLK	Y2(Phospho)	1 Y(2): 100.0; T(9): 0.0; T(12): 0.	59		11
	Low		IVAsNTGSGVYK	S4(Phospho)	0.79 S(4): 79.0; T(6): 20.2; S(8): 0.7	31	0.573	15
	Low		KEDAsALIQSTEEIK	S5(Phospho)	0.993 S(5): 99.3; S(10): 0.3; T(11): 0.	30		11
	Low		LPLPSGASRSADAYtR	T15(Phospho)	0.498 S(5): 0.0; S(8): 0.2; S(10): 0.2;	38	0.456	20
	Low		MAsgmVVSASmGVMKPLLTK	S3(Phospho)	0.827 S(3): 82.7; S(8): 17.0; S(10): 0.	46	0.659	12
	Low		MLItRAPR	T4(Phospho)	1 T(4): 100.0	50		15
	Low		MPSsPWIPTAGAPPPR	S4(Phospho)	0.852 S(3): 14.8; S(4): 85.2; T(9): 0.0	63		13
	Low		RPPPPPsPPPsHPHRSggK	S7(Phospho)	0.66 S(7): 90.0; S(11): 76.0; S(16): 1	18		10
	Low		SDVYSFGMLVLEmVsGRR	S15(Phospho)	0.429 S(1): 19.0; Y(4): 19.0; S(5): 19.	14		14
	Low		TAGAALPtPFLDRsAVAAPR	T8(Phospho)	0.458 T(1): 54.2; T(8): 69.5; S(14): 76	4	0.804	12
	Low		TtAERINSFR	T2(Phospho)	0.497 T(1): 49.7; T(2): 49.7; S(8): 0.6	24		12
	Low		tTAERINSFR	T1(Phospho)	0.788 T(1): 78.8; T(2): 20.0; S(8): 1.2	21		11
	Low		TTtAKRPLAVAGVSGSGDsGR	T3(Phospho)	0.022 T(1): 6.6; T(2): 6.6; T(3): 11.4;	9	0.564	13
	Low		VADsMLVNTALMLIYVtK	S4(Phospho)	0.468 S(4): 49.6; T(9): 49.6; Y(15): 6.	41		15
	Low		YmWLIPsLR	S7(Phospho)	0.999 Y(1): 0.1; S(7): 99.9	36		12
Os03t0337800-01	Low	Similar to 60S ribosomal protein L19 (Fragment). 60S ribosomal protein L19.	AAmVLDLLSLIGAyAAGtsR	Y14(Phospho)	0.506 S(9): 49.4; Y(14): 78.4; T(18): 8	6	0.33	12
	Low		ALSSPWSPRAVQAR	S4(Phospho)	0.978 S(3): 2.2; S(4): 97.8; S(7): 0.0	60		10
	Low		ASMRWSNVAVmLGFVVGyR	Y18(Phospho)	1 S(2): 0.0; S(6): 0.0; Y(18): 100.	64		10
	Low		AVFAAmATsGGYGYGGLQHFR	S9(Phospho)	0.952 T(8): 4.8; S(9): 95.2; Y(12): 0.0	56		11
	Low		DADEmVDILVAAtFSALHDK	T13(Phospho)	0.5 T(13): 50.0; S(15): 50.0	29		15

	Low		EFPEATIMRPATmiGtEDR	T16(Phospho	0.648 T(6): 7.6; T(12): 27.6; T(16): 64	13		11
	Low		EGMGLGVsGQGmLDPIPVK	S8(Phospho)	1 S(8): 100.0	32	0.618	20
	Low		EisSSGGLSAPAPAPAAGAAGR	S3(Phospho)	0.067 S(3): 6.7; S(4): 20.1; S(5): 66.5	21	0.658	11
	Low		EmHisEAYPISTAPGSAGKAK	S5(Phospho)	0.483 S(5): 48.3; Y(8): 48.3; S(11): 0.	32	0.535	12
	Low		GKVWLDPNEVNEISMANsR	S18(Phospho)	0.904 S(14): 9.6; S(18): 90.4	31	0.806	14
	Low		GRQGAASVsELHSmVQMLSR	S9(Phospho)	0.212 S(7): 76.6; S(9): 21.2; S(13): 2.	29	0.646	10
	Low		KLDLGASGFsGsLPsSLGSLK	S10(Phospho)	0 S(7): 4.8; S(10): 94.0; S(12): 1.	26	0.803	14
	Low		KsAFEASYMVLAIVGQGGmGK	S2(Phospho)	0.333 S(2): 33.3; S(7): 33.3; Y(8): 33.	1	0.659	11
	Low		LARyAVYDtDFGLGRPmK	Y4(Phospho)	0.381 Y(4): 61.9; Y(7): 61.9; T(9): 76.	2	0.629	12
	Low		MLMsLKLNSTPEItSR	S4(Phospho)	0.763 S(4): 98.4; S(9): 1.8; T(10): 2.4	32		12
	Low		MPLSYsAAAAAAPsPLAAR	S6(Phospho)	0.779 S(4): 4.5; Y(5): 17.7; S(6): 78.0	39	0.689	21
	Low		NSALmISRtLAMAYVMDQK	T9(Phospho)	0.254 S(2): 1.2; S(7): 11.4; T(9): 25.4	16		11
	Low		QALYASKIcsYAQGMNIK	S10(Phospho)	0.395 Y(4): 10.5; S(6): 10.5; S(10): 39	36		15
	Low		QGVISSsGTETGYLQDLIYK	S7(Phospho)	0.104 S(5): 1.3; S(6): 33.7; S(7): 10.4	28		10
	Low		RHGAASGGSTTGtRPFSTPSSR	T13(Phospho)	0.568 S(6): 0.4; S(9): 2.3; T(10): 18.0	35	0.804	11
	Low		ScVSDsAQRRGPVDPLR	S6(Phospho)	0.146 S(1): 42.7; S(4): 42.7; S(6): 14.	13	0.601	12
	Low		sNVVQTPVHQmGSVsSLPSK	S1(Phospho)	0.091 S(1): 86.3; T(6): 72.1; S(13): 8.	14	0.803	14
	Low		VRMTTWtAPPLPR	T7(Phospho)	0.82 T(4): 3.1; T(5): 14.9; T(7): 82.0	43		10
Os03t0343500-01	Low	Similar to 60S ribosomal protein L22-2.	FPTPEARLK	T3(Phospho)	1 T(3): 100.0	67		11
	Low		LSSIPGNVGsK	S10(Phospho)	0.791 S(2): 1.7; S(3): 19.2; S(10): 79.	32		11
	Low		yGtVKIQEDAmK	Y1(Phospho)	1 Y(1): 100.0; T(3): 100.0	46		11
Os03t0350100-01	High	SAR DNA-binding protein-2.	TYNPAADLVLGQStEETPKKPEGASK	T14(Phospho)	0.302 T(1): 0.0; Y(2): 0.0; S(13): 30.2	36	0.005	11
	High		TYNPAADLVLGQSTEEtPKKPEGASK	T17(Phospho)	0.497 T(1): 0.0; Y(2): 0.0; S(13): 0.3;	60	0	20
	Low		AHGAPVmRLQLGLsPAVVIssPGAAR	S14(Phospho)	1 S(14): 100.0; S(20): 100.0; S(2	18		15
	Low		ALAGGALsmHVAyFLAIsCLGyGLLGVLK	S8(Phospho)	1 S(8): 100.0; Y(13): 100.0; S(18	1		13
	Low		AQFPSPNEYSSFMGDFsTATGIATFTMM	Y9(Phospho)	0.038 S(5): 76.3; Y(9): 11.8; S(10): 9.	29		11
	Low		AQyAATAGAsKicsAFDIVIAK	Y3(Phospho)	0.936 Y(3): 99.0; T(6): 6.4; S(10): 99.	53		10
	Low		AQyPsPNEYSSFMGDFSTATGIATFTMM	Y3(Phospho)	0.012 Y(3): 56.2; S(5): 20.3; Y(9): 19.	21	0.094	12
	Low		ASLNcIDDESTGGLsQVRsLTVFGVLAI	S16(Phospho)	0.262 S(2): 0.5; S(11): 26.6; T(12): 12	29		13
	Low		ATNVLLDQDHNPYVSDYGLSALmsFPIS	Y13(Phospho)	0.066 T(2): 84.9; Y(13): 10.1; S(15): 2	26		10
	Low		cHTyMMMkQVVATTSGTQPPWsTLLM	Y4(Phospho)	0.013 T(3): 3.4; Y(4): 3.4; T(13): 24.0	22	0.497	12
	Low		cVHVLENGAIVSAsSsAFGFPGstPLHL	S15(Phospho)	0.016 S(13): 59.2; S(15): 78.9; S(16):	4	0.56	14
	Low		DGGVHGGGGmVcGLKQRPQGVSmTVR	T23(Phospho)	0.793 S(21): 20.7; T(23): 79.3	49		12
	Low		DMGHNPAGSACWTSNVAtIFcccGRGRF	T18(Phospho)	0.941 S(9): 0.3; T(13): 1.6; S(14): 4.0	44	0.673	10
	Low		DNAsssPAsILLFALIGAtAttAAFGQLRR	S4(Phospho)	1 S(4): 100.0; S(5): 100.0; S(6): 1	51		12
	Low		DtFMYKGAAFcSLEcR	T2(Phospho)	0.996 T(2): 99.6; Y(5): 0.4; S(13): 0.0	76	0.203	11
	Low		DVVVESALVDLYAKcGAVDYAYSVFEA	S28(Phospho)	0.503 S(6): 7.5; Y(12): 7.5; Y(20): 12.	16	0.692	22
	Low		EEEEEEGVscGicLTDAR	S9(Phospho)	0.998 S(9): 99.8; T(15): 0.2	51	0.729	11
	Low		EFVKGMtLTPtPSSR	T7(Phospho)	0.718 T(7): 79.3; T(8): 19.1; T(11): 90	48		13
	Low		EGcYLDINFIvLcNLSttPPAtAAGtIILK	T17(Phospho)	0.073 Y(4): 66.2; S(16): 56.1; T(17): 5	2	0.804	12
	Low		EHQLAAAtAPVAIPGVALAEtEELKEEQs	T8(Phospho)	0.19 T(8): 98.4; T(21): 60.3; S(29): 6	13	0.767	12
	Low		EIKPVsDGEERSsSSLR	S6(Phospho)	0.5 S(6): 77.9; S(12): 22.4; S(13): 6	33	0.225	14
	Low		EIVyGAtGAEYSIPPKITFPASEAttFEDVt	Y4(Phospho)	0.009 Y(4): 96.6; T(7): 94.0; Y(11): 30	15		10

Low	EKEATsSGNIHAssGDGMK	S6(Phospho)	0.005 T(5): 35.2; S(6): 81.9; S(7): 81.	17	0.786	11
Low	EQLLGsVDLNsVGEsLEPDVR	S6(Phospho)	1 S(6): 100.0; S(11): 100.0; S(15)	65		10
Low	EsPEsmRSVAGALSPLALAVASYASGA	S2(Phospho)	0.007 S(2): 31.3; S(5): 31.3; S(8): 30.	1	0.792	14
Low	EsSAAGGAAAAAAQQRSR	S2(Phospho)	0.5 S(2): 50.0; S(3): 50.0; S(18): 0.	53		14
Low	EsSPLPAMASAAAAAAEWEEAERK	S2(Phospho)	0.823 S(2): 82.3; S(3): 17.7; S(10): 0.	54		12
Low	FAIGAYARsFLDNPItctSGLGSsYLAGVF	Y6(Phospho)	0.062 Y(6): 90.1; S(9): 90.1; T(15): 7.	12	0.792	11
Low	FEcQTTGPPGSEVcAtEGR	T16(Phospho)	0.001 T(5): 3.4; T(6): 3.4; S(11): 93.0	16	0.803	11
Low	FGHLYAAAsTRPGNGVSVTSVLGGTSD	S9(Phospho)	0.003 Y(5): 47.9; S(9): 47.9; T(10): 3.	0	0.612	12
Low	FQsTALEALEDITALYYDEERDElyTGNR	S3(Phospho)	0.516 S(3): 72.2; T(4): 23.1; T(13): 3.	31		11
Low	FSNGKNmPDIIseHLGAEPVLPYLSPELI	S12(Phospho)	0.649 S(2): 0.5; S(12): 64.9; Y(23): 2.	24	0.715	11
Low	GFFKAsVLATGLImNNILR	S6(Phospho)	0.776 S(6): 77.6; T(10): 22.4	24	0.232	16
Low	GGEAmAPIESTtGGtLLVR	T12(Phospho)	0.682 S(10): 16.1; T(11): 16.1; T(12):	33		12
Low	GGGSGALPYGPsScPAAAAAAQQREGI	S12(Phospho)	0.322 S(4): 3.3; Y(9): 32.2; S(12): 32.	40	0.285	11
Low	GLETAtGAIAGLDDDAmmEEFVK	T6(Phospho)	0.5 T(4): 50.0; T(6): 50.0	39		15
Low	GLRNQLtELIsGLGAQDLGPmsLGLsHSI	T7(Phospho)	0.111 T(7): 75.3; S(11): 75.3; S(22): 6	4		12
Low	GRmLsPALASGLIcGDGVGsILLsmLtLm	S5(Phospho)	0.188 S(5): 81.2; S(10): 81.2; S(20): 7	2	0.774	14
Low	GSLLPVTTDWEAASLEAWPWAVsscR	S24(Phospho)	0.698 S(2): 10.5; T(8): 10.5; T(9): 10.	15	0.56	10
Low	GVGSPPTGVPSLQIEAQGDVIPcGGANF	T7(Phospho)	0.333 S(4): 33.3; T(7): 33.3; S(11): 3.	45	0.529	24
Low	GVGSPPTGVPSLQIEAQGDVIPcGGANF	S11(Phospho)	0.989 S(4): 0.1; T(7): 1.0; S(11): 98.9	64	0.798	11
Low	HLPSPRPSTTFSTSPHSYTAfSSSFAA	S29(Phospho)	0.464 S(4): 0.9; S(8): 0.9; T(9): 1.0; T	30	0.056	17
Low	HsGsDPDmVKITVAGGNVNGGAAASET	S2(Phospho)	0.3 S(2): 68.1; S(4): 49.8; T(12): 4.	18		11
Low	HVIsEsPPERDLTSSSHNLPcENEPcYS	S4(Phospho)	0.069 S(4): 82.0; S(6): 14.4; T(13): 3.	34	0.618	12
Low	IEAASIDDsPPPPSLPGGmGVsLLK	S9(Phospho)	0.016 S(5): 11.7; S(9): 89.6; S(14): 9.	13		10
Low	IGEIVDQHsEsYKQSR	S9(Phospho)	0.744 S(9): 93.8; S(11): 80.0; Y(12): 1	26	0.792	11
Low	IGPcLYVIDtFsAAADFLPDR	T10(Phospho)	0.983 Y(6): 1.7; T(10): 98.7; S(12): 9.	25	0.48	10
Low	IGVERsEAAALGADLIIMTIsAVDGWtEDI	S6(Phospho)	0.074 S(6): 66.9; T(19): 60.8; S(21): 5	1	0.805	11
Low	ImcsSNILKLGYNLQcDLHQLSQSyGELK	S4(Phospho)	0.123 S(4): 43.3; S(5): 33.2; Y(12): 2.	4	0.792	14
Low	IMEmDEEIQLLVGSNQIAETtFQMGSNI	T22(Phospho)	0.483 S(14): 28.0; T(21): 28.0; T(22):	18	0.341	12
Low	INFPGGGtHFHtGADKYIVHLAQmLNFP	T8(Phospho)	0.474 T(8): 94.7; T(12): 52.6; Y(17): 5	16	0.287	11
Low	ItANcVAPGATATDMFFAGKSEER	T2(Phospho)	0.944 T(2): 94.4; T(11): 2.7; T(13): 2.	38	0.68	15
Low	LDsGPLHThATGPtHAVGPTDQQ	S3(Phospho)	0.168 S(3): 93.1; T(8): 60.2; T(11): 2.	32		12
Low	LKQQEILEDsDEEYDEIIQDsGEQEVK	S11(Phospho)	1 S(11): 100.0; Y(15): 100.0; S(2	12	0.761	11
Low	LmIENLEGLPAcSQILtRMQsGVGVALtD	T17(Phospho)	0.281 S(13): 71.9; T(17): 78.1; S(21):	2	0.729	19
Low	LNPstNLGLALAssFssSSRPEQPELPGA	S4(Phospho)	0.031 S(4): 67.4; T(5): 59.4; S(13): 7.	5	0.713	14
Low	LNsLDLSGNDLSGAVPASLAALKLssLNr	S3(Phospho)	0.591 S(3): 59.8; S(7): 19.2; S(12): 1.	39	0.738	15
Low	LQmSQISmFLAQSGPMsMsLVARsTmE	S17(Phospho)	0.003 S(4): 84.1; S(7): 72.4; S(13): 1.	8	0.733	11
Low	LsQIPcLLYTSSESAGDsVVslsLVEKR	S2(Phospho)	S Too many isoforms			0.792
Low	LVttSYPLVLVLVGEEGAGSNGMTAtss	T3(Phospho)	0.005 T(3): 45.2; T(4): 45.2; S(5): 45.	2	0.56	11
Low	mAAAAAEGGGGGGGAUVDPSYVPDS	T28(Phospho)	0.21 Y(17): 0.9; S(20): 2.4; Y(21): 6.	44		12
Low	mASKPGPLtQWPWHNLGNyK	T9(Phospho)	0.211 S(3): 78.9; T(9): 93.0; Y(19): 2.	20	0.485	12
Low	mGAAASAAFSATcQTAGKATMAAADV	T30(Phospho)	0.721 S(6): 0.1; S(10): 0.0; T(12): 0.1	41	0.662	19
Low	mGtsTsAEVQNNVQGTR	T3(Phospho)	0.778 T(3): 89.6; S(4): 89.6; T(5): 22.	90	0.478	16
Low	mLPPLLTtVHEQTGmLPPAWMGTLTG	S31(Phospho)	0.133 T(7): 1.3; T(8): 1.4; T(13): 3.9;	25	0.556	12
Low	MPVWVWSHQLLSNAMFTSDistETTtVFI	S21(Phospho)	0.062 S(7): 16.3; S(12): 16.3; T(17): 1	4	0.792	11
Low	MsATmDAVMPGAAGAHNATAAAAAGR	S2(Phospho)	0.427 S(2): 42.7; T(4): 42.7; T(19): 1.	23		14
Low	mTDIHTNENySNSAVSPVNVVPPsGAA	Y10(Phospho)	0.001 T(2): 47.3; T(6): 47.3; Y(10): 3.	24	0.34	17
Low	mTTTTtAAAAALtssVGDGPPPsRSTTT	T16(Phospho)	T13(Phospho) Too many isoforms			0.722
Low						12

Low	mVFTFMAYLAFTWStVVLGGYVssLQF T15(Phospho	0.012 T(4): 50.4; Y(8): 35.4; T(12): 35	0	0.2	13
Low	mVHLsTSITIsETPPEHWQK S5(Phospho):	0.427 S(5): 72.1; T(6): 23.0; S(7): 16.	53	0.617	14
Low	mVIASAAFSAGASASsGsAAAAAADPsF S16(Phospho	0.026 S(5): 31.0; S(9): 31.0; S(13): 5	22	0.105	23
Low	mVTtRGmAATAsAAEGYER T4(Phospho):	0.002 T(3): 0.9; T(4): 1.6; T(10): 52.0	4	0.719	15
Low	NAsKLLNYtVQVPAAGTTR S3(Phospho):	0.149 S(3): 64.7; Y(8): 64.7; T(9): 36.	7	0.805	11
Low	NyyItAIAGATNGSSSLVVMsKGTPTYTQqS Y2(Phospho)Y3(Phospho)T Too many isoforms		0.75		14
Low	QTETAIAKAAHGGGAAGtPFAR T18(Phospho	0.926 T(2): 3.7; T(4): 3.7; T(18): 92.6	17	0.749	11
Low	RAQSLSVHLLDmVILTLLAtGsAtAASMA T20(Phospho	0.01 S(4): 9.0; S(6): 28.6; T(16): 61.	6	0.792	12
Low	RIAPtFGSDHSINNALcWsPDGQFLAVP(T5(Phospho):	0.158 T(5): 50.9; S(8): 50.9; S(11): 50	0	0.062	10
Low	RsPsSPPPGLDVAAGSR S2(Phospho):	0.211 S(2): 63.3; S(4): 36.7; S(5): 50.	17		16
Low	sAAAGDPAssLPPYLLRPFAQK S1(Phospho):	0.961 S(1): 99.9; S(9): 99.5; S(10): 90	34	0.683	12
Low	SASssAtAAAAAAGNtHNSINFLNVLISLI(S4(Phospho)S5(Phospho)T Too many isoforms		0.493		10
Low	sAstVsTATTTSTTTTTTTPRLGAVALS(S1(Phospho)S3(Phospho)T Too many isoforms		0.301		14
Low	sGHGDTNVSTTTTFTETPTSVLMSGGLI S1(Phospho)S24(Phospho) Too many isoforms		0.684		12
Low	SLDFPTPSRcHDDTyNstNsTNLHILEK Y15(Phospho	0.001 S(1): 54.9; T(6): 25.4; S(8): 26.	2	0.75	14
Low	smsFPSIVDLLKDsLK S1(Phospho):	0.289 S(1): 71.1; S(3): 71.1; S(6): 71.	3	0.805	11
Low	SScKQQQPPsPAAVAsVAAAIVSSYS(S10(Phospho)S11(Phospho) Too many isoforms				11
Low	ssLGADLRPTEDScGPmNSINQPcVNVIt S1(Phospho):	1 S(1): 100.0; S(2): 100.0; T(10):	55		14
Low	SSLGAFGAcGGFAAtAAAAGDAAssMt T16(Phospho	0.025 S(1): 45.2; S(2): 45.2; S(4): 53.	2	0.414	18
Low	sTMIGAmANFLDyDVYDLDTSVKNNsE S1(Phospho)	0.07 S(1): 66.2; T(2): 66.2; Y(13): 40	11	0.608	12
Low	SVISYLGmDLYKLVEMLsLmYDFLyTK S19(Phospho	0.036 S(1): 29.0; S(4): 29.0; Y(5): 29.	1		11
Low	SWLPLLcRGsNGtDAPVLsSK S10(Phospho	0.808 S(1): 0.1; S(10): 99.9; T(13): 90	51	0.804	14
Low	TAAyISQEDLHAGEmtVR Y4(Phospho):	0.654 T(1): 24.2; Y(4): 73.3; S(6): 13.	21	0.209	12
Low	TDQMDSPTDPFIWPGQLGFAYTLQtRA T25(Phospho	0.033 T(1): 44.3; S(6): 36.5; T(8): 36.	0	0.792	11
Low	TGcAKssAPLASSIAVAER S6(Phospho):	0.823 T(1): 4.1; S(6): 88.0; S(7): 88.0	32	0.773	14
Low	TLAFPAGVcPTVGVGHHISGGGFGtLmf T25(Phospho	0.849 T(1): 0.2; T(11): 0.9; S(19): 13.	26	0.256	12
Low	VALLctQGSPHQRPpMsK T6(Phospho):	0.796 T(6): 99.7; S(9): 20.4; S(17): 80	30	0.089	12
Low	VKVfVsSEQAIDLTDtVYGLIYLLDYEmR S6(Phospho)	0.036 S(6): 26.3; S(7): 26.3; T(14): 20	0		12
Low	VVLItGASSGIGEELAyQYAsK T5(Phospho):	0.165 T(5): 49.3; S(8): 49.3; S(9): 37.	17		10
Low	VVNPSSmGAILcGHKQMSEIEITR S6(Phospho)	0.5 S(5): 50.0; S(6): 50.0; S(18): 0.	54	0.56	14
Low	WFtIASLLEYVVLVSPSR T3(Phospho)	0.993 T(3): 99.3; S(6): 0.5; Y(10): 0.2	35		12
Low	YLGLGSGmKNSAALLSGtPIShsVGPDLI T18(Phospho	0.008 Y(1): 29.3; S(6): 33.2; S(11): 30	3	0.773	12

Os03t0352300-01	Low	Similar to Nucleolar protein.	cLVFLPFRsSAPSSAASALFEyPR S9(Phospho):	0.754 S(9): 75.5; S(10): 18.2; S(13): 4	58		16
	Low		cLVFLPFRSSAPsSAASALFEyPR S13(Phospho	0.165 S(9): 56.5; S(10): 16.5; S(13): 1	35		12
	Low		EcGISIADRPsyAFAsRVIsRPtK S16(Phospho	0.165 S(5): 0.5; S(11): 16.8; Y(12): 60	37	0.783	17
	Low		GANQASTtKLLK T8(Phospho)	0.982 S(6): 0.4; T(7): 1.3; T(8): 98.2	35		11
	Low		GAsEIVLAAcDK S3(Phospho)	1 S(3): 100.0	39	0.703	13
	Low		KsTDAVMIR S2(Phospho)	0.794 S(2): 79.4; T(3): 20.6	25	0.522	11
	Low		LDFHNFVFsmKASNPVImVQAYR S9(Phospho)	0.87 S(9): 88.3; S(13): 13.0; Y(22): 9	24	0.694	12
	Low		LEGIAKSyK Y8(Phospho)	0.5 S(7): 50.0; Y(8): 50.0	51		12
	Low		LEGIAKsYK S7(Phospho)	0.5 S(7): 50.0; Y(8): 50.0	59		12
	Low		LGGsFTSEGmKELVGLTLQcVSTsAR S4(Phospho):	0.748 S(4): 91.3; T(6): 4.4; S(7): 4.4;	70		21
	Low		LKSQIASLEsR S10(Phospho	1 S(3): 0.0; S(7): 0.0; S(10): 100.	40	0.741	16
	Low		LPALsPSPAR S5(Phospho)	0.984 S(5): 98.4; S(7): 1.6	31		10
	Low		mMAWRsLsLVAFmAAVAAAAAAGDDI S6(Phospho):	1 S(6): 100.0; S(8): 100.0	10	0.662	11

	Low		mQSDAVARsPR	S9(Phospho)	0.5 S(3): 50.0; S(9): 50.0	21	0.628	11
	Low		QATAssHLRAGmLLFVsYADGLALR	S5(Phospho)	0.032 T(3): 66.9; S(5): 66.9; S(6): 66.	18		12
	Low		SANsSSmVTTASTSYSTPPAHGGGAGI	S4(Phospho)	0.323 S(1): 2.8; S(4): 32.3; S(5): 32.3	52		19
	Low		sANSSSmVTTASTSYSTPPAHGGGAGI	S1(Phospho)	0.599 S(1): 59.9; S(4): 13.2; S(5): 13.	56		14
	Low		SGDStANKLK	T5(Phospho)	0.499 S(1): 0.3; S(4): 49.9; T(5): 49.9	48	0.784	15
	Low		SMQLADmNtPSQSLEEVmAIIQEAR	T9(Phospho)	0.427 S(1): 0.5; T(9): 42.7; S(11): 14.	26		10
	Low		SYIGPDsTGDTSDDEDDEIVPEEISR	S7(Phospho)	0.569 S(1): 13.7; Y(2): 13.7; S(7): 56.	56	0.141	13
	Low		TGIKFPAFLEDDsSPStTVLVGMGFK	S14(Phospho)	0.165 T(1): 0.0; S(13): 49.7; S(14): 49.	67		11
	Low		yGGMGtLLVNK	Y1(Phospho)	1 Y(1): 100.0; T(6): 100.0	34	0.093	11
Os03t0352450-00	High	Hypothetical conserved gene.	NLDGAsDDDEVDAYSNQITEEHYR	S6(Phospho)	1 S(6): 100.0; Y(14): 0.0; S(15): 0.	53	0.003	20
	Low		EGMEsDEEIGRVPELGLPPGGASTSGR	S5(Phospho)	0.986 S(5): 98.6; S(23): 0.5; T(24): 0.	24	0.057	17
	Low		LStMDVDMVELPASmPNFSTVmRR	T3(Phospho)	0.708 S(2): 27.0; T(3): 70.8; S(14): 1.	21		10
	Low		SLLcSEVDEGVIFHsVEQLNLyK	S15(Phospho)	0.937 S(1): 3.6; S(5): 4.1; S(15): 96.2	19	0.792	15
	Low		tGGKPsGSVILsGDGTAtIAIYWR	T1(Phospho)	0.042 T(1): 95.5; S(6): 95.5; S(8): 10.	50	0.052	14
Os03t0379500-01	Low	Similar to 40S ribosomal protein S9.	SQVALLEsK	S8(Phospho)	0.5 S(1): 50.0; S(8): 50.0	11		12
Os03t0383800-03	High	Nucleotide-binding, alpha-beta plait domain containing protein.	LEPPPPAAAPISPAItPK	T15(Phospho)	0.468 S(12): 6.3; T(15): 46.8; T(16): 4	93	0	28
	High		LEPPPPAAAPIsPATTPK	S12(Phospho)	0.47 S(12): 47.0; T(15): 47.0; T(16):	97	0	29
	High		LKLEPPPPAAAPIsPATTPK	S14(Phospho)	0.998 S(14): 99.8; T(17): 0.2; T(18): 0	120	0	28
	Low		AAGDmANTSTKTSESsGK	S16(Phospho)	0.206 T(8): 3.0; S(9): 7.3; T(10): 7.3;	15	0.806	10
	Low		RcGSGGGESAAAATsPPAR	S15(Phospho)	0.765 S(4): 0.4; S(9): 0.6; T(14): 22.5	25	0.218	14
	Low		VAsGsPVHLLtIPK	S3(Phospho)	1 S(3): 100.0; T(4): 100.0; S(5): 1	26	0.57	13
Os03t0390000-02	Low	Similar to Ribosomal protein s6 RPS6-2.	ADLALStVHALLGVIRK	T7(Phospho)	0.972 S(6): 2.8; T(7): 97.2	67		17
	Low		AKLtGAAAGSIVLVtR	T4(Phospho)	0.25 T(4): 75.0; S(10): 75.0; T(15): 7	11	0.803	15
	Low		DALKSLNtHILIVAR	T9(Phospho)	0.989 S(5): 1.1; T(9): 98.9	55		19
	Low		DDAGNPAWcAGEtQAAR	T13(Phospho)	1 T(13): 100.0	11	0.752	16
	Low		DNGGFLDtLASVLLK	T8(Phospho)	0.761 T(8): 76.1; S(11): 23.9	25		14
	Low		DPAItRAAAAIVEK	T4(Phospho)	1 T(4): 100.0	48		12
	Low		FGcsAsRLsISTSTR	S4(Phospho)	0.017 S(4): 35.3; S(6): 35.3; S(9): 35.	0		14
	Low		GGGGAASLQLMtaAGARNGK	T12(Phospho)	0.958 S(7): 4.2; T(12): 95.8	25	0.76	11
	Low		GRHHAAEHAGVEVVsR	S15(Phospho)	1 S(15): 100.0	61	0.404	13
	Low		HsAGQGKPsNMSSEHR	S2(Phospho)	0.476 S(2): 79.5; S(9): 61.2; S(12): 29	12		14
	Low		IATGPRSGDGAVAVLAsR	T3(Phospho)	0.229 T(3): 24.4; S(7): 77.1; S(17): 98	17	0.365	12
	Low		ILVctPQAEVAIcWK	T5(Phospho)	1 T(5): 100.0	32	0.605	10
	Low		KSSAGISSILSIGsGPK	S15(Phospho)	0.315 S(2): 6.8; S(3): 6.8; S(7): 10.6;	7		16
	Low		LDLPTPEsPmsTTLNR	S11(Phospho)	0.2 T(5): 20.0; S(8): 20.0; S(11): 20	33	0.632	15

	Low		REDGtADILPLLAAsR	T5(Phospho):	1 T(5): 100.0; S(15): 100.0	57	0.769	12
	Low		RSARPatHPPAVYPR	T7(Phospho)	0.991 S(2): 0.9; T(7): 99.1; Y(13): 0.0	53		10
	Low		ssPPQVPVtSEPPPAK	S1(Phospho):	0.056 S(1): 99.8; S(2): 99.8; T(9): 6.0	33	0.796	12
	Low		tMLTDVVGVQLSTRR	T1(Phospho)	0.932 T(1): 93.2; T(4): 4.5; S(12): 1.1	20	0.806	12
	Low		VAHLGVHLGGDAADGsVGR	S16(Phospho)	1 S(16): 100.0	31	0.743	11
Os03t0390400-01	High	Similar to Cytochrome c oxidase subunit 6b.	MDMELSSSSsAASVFASSSATSPPLGR	S10(Phospho)	0.184 S(6): 18.4; S(7): 18.4; S(8): 18.4	33	0.008	10
	High		ysHVMHISSTVSGELDDHLQSWDALR	Y1(Phospho):	0.811 Y(1): 84.7; S(2): 91.5; S(8): 12.2	41	0.002	13
	Middle		GIEVItmLWALATHGTGIARPDDEVPEGt	T6(Phospho)	0.821 T(6): 82.1; T(13): 8.4; T(15): 8.4	21	0.012	12
	Middle		YDmASFPIQItsQsSPQADGASAGSQWf	T11(Phospho)	0.175 Y(1): 3.3; S(5): 8.8; T(11): 88.6	36	0.033	13
	Low		AAELmRLAGsAcSPQPAHAAALPEmPl	S10(Phospho)	1 S(10): 100.0; S(13): 100.0	2	0.748	11
	Low		AISIDmFEAGTDTsHLVLEyAMVELtR	S14(Phospho)	0.299 S(3): 0.5; T(11): 25.6; T(13): 53.2	29		12
	Low		AISIDMFEAGtDtSHLVLEyAmVELTR	T11(Phospho)	0.126 S(3): 0.7; T(11): 57.2; T(13): 57.2	31	0.697	11
	Low		AMtNsAVARTSVAtFmmPPmDcLVGPAk	T3(Phospho):	0.547 T(3): 84.0; S(5): 67.8; T(10): 33.2	33	0.494	13
	Low		AMtTPRPVAEDASEFEKFQAMIYSTAMt	T3(Phospho)	0.476 T(3): 47.6; T(4): 47.6; S(13): 1.1	20	0.593	11
	Low		AScAsPSSRLHGNAAGGGAGGSAtAMN	S5(Phospho):	0.254 S(2): 11.6; S(5): 29.5; S(7): 29.5	31	0.54	10
	Low		ATctEYtIFMsADNtSRSSNmyIGK	T4(Phospho)T7(Phospho)	S Too many isoforms		0.802	11
	Low		cDIMVVHAGAGANGVAAATAAPSmAGf	S30(Phospho)	0.666 T(19): 9.7; S(23): 23.7; S(30): 6.0	17	0.188	14
	Low		csAVsELAPtAsAAYGALLGGGAFayVR	S2(Phospho):	0.969 S(2): 100.0; S(5): 100.0; T(10): 100.0	49		12
	Low		cSPSyLATPSVSPSASTSALAAAATTtsS	Y5(Phospho)T27(Phospho)	Too many isoforms		0.411	12
	Low		cyFLLImLFtMLHyINKItESQR	Y2(Phospho):	0.998 Y(2): 100.0; T(10): 100.0; Y(14): 100.0	74	0.747	19
	Low		DcLAcSGcITSAETVMLEKQsLGDFITR	S21(Phospho)	0.238 S(6): 2.4; T(10): 2.4; S(11): 2.4	10		12
	Low		DGVGETFIGVGAGAGAGVGsSLtGDGG	S20(Phospho)	0.069 T(6): 7.7; S(20): 34.4; S(21): 34.4	6	0.48	14
	Low		DmGEDDTPAScPsmRPSGRQLTSLYGf	S13(Phospho)	0.404 T(7): 18.9; S(10): 18.9; S(13): 4.0	15	0.803	12
	Low		DSGGGGGASHKAASGSAPsGAAAANP	S19(Phospho)	0.154 S(2): 5.7; S(9): 8.0; S(14): 8.0;	5	0.602	13
	Low		EEMetsLPLsRFAELNLVITNatSR	T5(Phospho):	0.438 T(5): 100.0; S(6): 100.0; S(10): 100.0	45	0.723	14
	Low		EFmsFMAPAmTAGEIIEESKNFFFAGK	S4(Phospho)	0.832 S(4): 83.2; T(11): 15.7; S(19): 15.7	19	0.689	11
	Low		EmTSGsELRPsQVAGEPAVQItGGRDGI	S6(Phospho):	0.004 T(3): 98.7; S(4): 98.7; S(6): 97.7	8	0.778	10
	Low		EPYQmPVAtGEIPAAAtAGFYGNLADVRR	Y3(Phospho):	0.3 Y(3): 70.0; T(9): 80.0; T(16): 80.0	4		10
	Low		FtELLLDPsVRPKGEFNLVsWEsR	T2(Phospho):	1 T(2): 100.0; S(9): 100.0; S(20): 100.0	56	0.438	10
	Low		FTYAELEEAtEGFKsQIGSGGFGcVyR	T10(Phospho)	0.02 T(2): 95.1; Y(3): 89.2; T(10): 4.0	25		10
	Low		GFSASmKGPEVPPDLsFTGAALPSNPS	S16(Phospho)	0.115 S(3): 3.2; S(5): 3.2; S(16): 11.5	12	0.763	12
	Low		GGGGAATAVQGSmPmTTTDSRptAPG	T23(Phospho)	0.063 T(7): 0.8; S(12): 3.3; T(16): 12.0	12	0.601	10
	Low		GLLPLPLPPPtTAVAGGDGSAGVAGEK	T11(Phospho)	0.782 T(11): 78.2; T(12): 21.2; S(20): 21.2	59	0.387	18
	Low		IMDRsSHGGDGDGEAMNtSEcFLDVLLF	S5(Phospho):	0.673 S(5): 76.7; S(6): 25.8; T(18): 88.0	38		10
	Low		ItSAFPKVLNLsNNNFsGVIPQDIGQLK	T2(Phospho):	0.433 T(2): 56.7; S(3): 56.7; S(12): 93.3	15	0.503	16
	Low		LARVMHLHsSELsAWNLVSAAPAVSP	S9(Phospho):	0.529 S(9): 80.8; S(10): 31.5; S(13): 6.0	35	0.726	14
	Low		LDHVDsARVsPFtYAQIlmLsASANK	S6(Phospho):	0.61 S(6): 99.8; S(10): 98.0; T(13): 6.0	41	0.459	11
	Low		LEWyQIVEGEHALWDGVSQPYRETIR	Y4(Phospho)	0.908 Y(4): 90.8; S(18): 2.5; Y(21): 3.0	16		10
	Low		LLFLDEPTsGLDSAASFHVMSRITDLAAI	S9(Phospho)	0.321 T(8): 14.1; S(9): 32.1; S(13): 32.1	17	0.754	12
	Low		LLFSNPPLVSSAtctPAMATNGAAAVt	T15(Phospho)	0.721 S(4): 0.0; S(12): 2.2; S(13): 6.9	46	0.145	13
	Low		LQWNLtIPTPyVFImMLSASADNKSDK	T6(Phospho):	0.284 T(6): 49.5; T(9): 49.5; Y(11): 63.0	12	0.429	10
	Low		LTARGISAEDPNGtVVWSTPAFAsPVAA	T14(Phospho)	0.007 T(2): 22.5; S(7): 73.8; T(14): 21.0	14	0.601	11
	Low		mAAAAARQTVcVtGAGGFmASSHVELL	T13(Phospho)	0.782 T(9): 6.5; T(13): 82.4; S(21): 8.0	29	0.171	17
	Low		MASsSPLccyLLLFFVVVVVLTGScRAR	S4(Phospho):	0.206 S(3): 40.8; S(4): 40.8; S(5): 40.8	16		11

Low	mAsSSssWLVLsAALcIGALPAsHAAR S3(Phospho):	0.069 S(3): 66.6; S(4): 66.6; S(5): 66.	6	0.761	16
Low	mASYGVdIRPAAAAAGGGGAGAGAAG T8(Phospho):	0.045 S(3): 57.7; Y(4): 57.7; T(8): 45.	1		10
Low	mGLAGSAFATDDMAMdyVYDYmLHVL` Y17(Phospho):	0.378 S(6): 5.2; T(10): 5.2; Y(17): 37.	30	0.722	21
Low	mGNAAAVPsScASADAAPSttPtiKLLIAK S9(Phospho):	0.029 S(9): 46.2; S(10): 46.2; S(13): 4	8	0.806	13
Low	mGQRAsAAVVGfAGSATSGGPAATDE S6(Phospho):	0.95 S(6): 95.0; S(15): 2.7; T(17): 0.	29		11
Low	MIVATAtIPFFPsFHRPRFRPGGLPR T7(Phospho):	0.925 T(5): 7.5; T(7): 92.6; S(13): 100	50	0.066	11
Low	MmLPmsSAcSGGQFPGASPHGIIPKQF: S6(Phospho):	0.202 S(6): 44.6; S(7): 44.6; S(10): 30	7	0.803	14
Low	mtLSAVPLPNTGMLLYAGNHWIGKTHD: T2(Phospho):	0.774 T(2): 77.4; S(4): 21.8; T(11): 0.	47	0.411	12
Low	mTTTTTAAAAALTSSVGDGPPPSRSTT T30(Phospho):	0.056 T(2): 0.0; T(3): 0.0; T(4): 0.0; T	26	0.762	11
Low	NALGctGVADRIPGTSALAMAsAsAIPQA T6(Phospho):	0.076 T(6): 99.2; T(15): 23.2; S(16): 6	29	0.803	12
Low	NPVASSPSVSEGsAHAAALAsPTAADSI S13(Phospho):	0.028 S(5): 34.5; S(6): 34.5; S(8): 34.	1	0.727	10
Low	NtYDHLLFsRSSLLSVyADmSVtcK T2(Phospho):	0.231 T(2): 50.7; Y(3): 50.7; S(9): 94.	72		10
Low	QAQTPcLLYtSESAGENVAcLySLAEK T4(Phospho):	0.127 T(4): 92.4; Y(9): 54.3; T(10): 22	27		13
Low	QEVTTMNLPIsFRPKDFGsAMWDMIR S11(Phospho):	0.153 T(4): 54.2; T(5): 54.2; S(11): 45	0	0.549	13
Low	QGDtnFYLCeVsSNmVIDATNKGnmsR S12(Phospho):	0.925 T(4): 0.3; Y(7): 2.4; S(12): 94.8	43	0.743	19
Low	QIPyNSIIYKAfGQENPDsLTDYGCQK Y4(Phospho):	0.759 Y(4): 75.9; S(6): 18.9; Y(9): 5.2	39	0.367	15
Low	QLSQGGELtIVWLMAEHAGLFLVNktR T9(Phospho):	0.205 S(3): 72.9; T(9): 21.1; T(10): 7.	26		10
Low	QPRVsLWEIEPLTTFPMYPsPFPLR S5(Phospho):	0.108 S(5): 96.8; T(13): 47.7; T(14): 4	14	0.486	18
Low	RQILESYQVYGDsIMGQYGPsrPNVR Y10(Phospho):	0.027 S(6): 53.3; Y(7): 53.3; Y(10): 8;	34	0.579	11
Low	sHGHVAMGWVPQITILAHAAVGAFLTH: S1(Phospho):	0.929 S(1): 92.9; T(14): 7.1; T(26): 0.	41	0.204	12
Low	SHNLLFDWDFTGAGAGKDDDEyTYGF Y23(Phospho):	0.568 S(1): 0.2; T(12): 0.5; Y(23): 56.	28	0.186	13
Low	sIIQTLNATQGAfETADsmtPFdVAVR S1(Phospho):	0.083 S(1): 49.5; T(5): 49.5; T(9): 1.1	47	0.727	10
Low	sPITVAImFSIGmILFsGFLVPKMPK S1(Phospho):	0.483 S(1): 48.4; T(4): 48.4; S(10): 3.	46	0.298	15
Low	sVAVVVVGgGDGtAsWSVSVGGDHGG S1(Phospho):	0.009 S(1): 89.3; T(13): 78.1; S(15): 7	3	0.664	11
Low	tAsSASPSSDLVVSPVAWPATGGGGPA T1(Phospho):	0.023 T(1): 27.9; S(3): 27.9; S(4): 27.	13	0.614	10
Low	tLsNSMETVLTVTGLyYWFVAIEsVK T1(Phospho):	0.034 T(1): 99.0; S(3): 99.0; S(5): 2.0	54	0.454	14
Low	TTQTAlmDILLSLLEFAsSYNSTSNLR S19(Phospho):	0.092 T(1): 0.7; T(2): 0.7; T(5): 1.4; S	12		10
Low	TVDtFEAAAAmFPGGmImPPPAPGSKD T4(Phospho):	0.369 T(1): 36.9; T(4): 36.9; S(25): 26	3	0.706	13
Low	VAFLPGQPRsPQmSQFSGYItVNSQNG S10(Phospho):	0.058 S(10): 44.3; S(14): 41.7; S(17):	0	0.339	15
Low	VsEAEDVSAlsEctVKLWVMAALLK S2(Phospho):	0.413 S(2): 58.7; S(9): 58.7; S(12): 8;	33		13
Low	VSGmISQHAAPGcDAATIAGmAsALtDY S23(Phospho):	0.055 S(2): 34.3; S(6): 34.3; T(17): 27	4	0.665	11
Low	VsHDAVSScHDAFVRsAQAAALsAAAAAA S2(Phospho):	0.893 S(2): 91.0; S(7): 8.5; S(8): 2.7;	34	0.806	10
Low	VtLSDVEVSGNENLNLTSSSANSdHsMf T2(Phospho):	0.399 T(2): 47.2; S(4): 47.2; S(9): 5.5	25	0.707	10
Low	WGTWHRAMGDGAPGAGSALGGAGsA S24(Phospho):	0.076 T(3): 42.4; S(17): 42.4; S(24): 7	6	0.632	13
Low	yMVFyVSNSIsFMAsIAVImLLsK Y1(Phospho):	0.729 Y(1): 98.6; Y(5): 74.4; S(7): 20.	46		12

Os03t0392400-01	High	Heat shock protein DnaJ, N-terminal domain containing protein.	GININEEAQsTDGATR	S10(Phospho)	0.909 S(10): 90.9; T(11): 9.1; T(15): 0	113	0	42
	High		GININEEAQsTDGATR	T11(Phospho)	0.5 S(10): 50.0; T(11): 50.0; T(15):	67	0	40
	Middle		RQPsPPLQQPAAEEK	S4(Phospho)	1 S(4): 100.0	92	0.019	11

Os03t0403100-01	High	Similar to DNA-directed RNA polymerase subunit.	TEEEEAPAAKDPNASLPsPTYR	S18(Phospho	0.317 T(1): 0.0; S(15): 4.9; S(18): 31.	83	0.003	25
	High		TEEEEAPAAKDPNASLPsPTYr	Y21(Phospho	0.447 T(1): 0.0; S(15): 0.6; S(18): 10.	61	0.002	23
	Middle		DPNASLPsPTYR	S8(Phospho)	0.879 S(5): 0.2; S(8): 87.9; T(10): 10.	76	0.036	21
	Middle		NAstSSDMSSLASQGPPNNPASLR	S3(Phospho)	0.614 S(3): 61.4; T(4): 12.4; S(5): 12.	63	0.01	13
	Low		RLGVGDDAEGGGsK	S13(Phospho	1 S(13): 100.0	84		14
	Low		VSPAENSEVEtR	T11(Phospho	0.998 S(2): 0.0; S(7): 0.1; T(11): 99.8	38		11
Os03t0408300-00	Low	Similar to 60S ribosomal protein L27a-3.	ALcATVsASLR	S7(Phospho)	0.5 T(5): 0.0; S(7): 50.0; S(9): 50.0	48		11
	Low		tTAYVPQLQK	T1(Phospho)	0.333 T(1): 33.3; T(2): 33.3; Y(4): 33.	87		18
Os03t0424500-01	Low	Similar to 40S ribosomal protein S19-3.	KSLVSEsVR	S7(Phospho)	0.985 S(2): 0.0; S(5): 1.5; S(7): 98.5	58	0.432	15
Os03t0427300-01	High	Glutelin type-A III precursor.	FKDLIPQSGsPPR	S10(Phospho	0.968 S(8): 3.2; S(10): 96.8	55	0.003	11
	Low		ADLAsKtLtsSADAtFtyDtLLIAtGssVIK	S5(Phospho)T7(Phospho)T	Too many NL-allowing PTMs		0.778	12
	Low		AGKyPNALLSFSSGPR	Y4(Phospho)	0.295 Y(4): 29.5; S(10): 29.5; S(12): :	13		10
	Low		AKASASVsPK	S8(Phospho)	0.818 S(4): 3.2; S(6): 15.0; S(8): 81.8	35		12
	Low		AKASAsVSPK	S6(Phospho)	0.817 S(4): 3.2; S(6): 81.7; S(8): 15.1	38		16
	Low		ASVFQEPISAALSALsLLVQFNGWLsFFI	S16(Phospho	0.178 S(2): 11.2; S(9): 9.3; S(13): 12.	17	0.731	11
	Low		AtLSSKPQPVAktEK	T2(Phospho)	0.795 T(2): 79.9; S(4): 16.4; S(5): 4.1	39		11
	Low		ATVsKVEVVGMGDR	S4(Phospho)	0.994 T(2): 0.6; S(4): 99.4	57	0.758	14
	Low		DQtLSRIK	T3(Phospho)	0.896 T(3): 89.6; S(5): 10.4	48		14
	Low		DRDPPmRPVsGALSR	S10(Phospho	0.081 S(10): 8.1; S(14): 91.9	12	0.633	11
	Low		DRTAHAAPDGLSSTSEATTLQLEySYLs	Y24(Phospho)S28(Phospho	Too many isoforms			12
	Low		ELIRmSNtSIIR	T8(Phospho)	0.159 S(6): 80.5; T(8): 15.9; S(9): 3.6	35	0.755	13
	Low		ELVtATTR	T4(Phospho)	0.999 T(4): 99.9; T(6): 0.1	41		10
	Low		EsILASVAR	S2(Phospho)	1 S(2): 100.0; S(6): 0.0	75		25
	Low		EVGNItSLK	T6(Phospho)	0.5 T(6): 50.0; S(7): 50.0	46		11
	Low		EVGNITsLK	S7(Phospho)	0.023 T(6): 97.7; S(7): 2.3	30		10
	Low		FQIHKAyGsTNHLPsAHtcFNQLDLPEytS	Y7(Phospho)	0.119 Y(7): 47.0; S(9): 80.8; T(10): 80.	30	0.682	11
	Low		FVVDVDAWMDLsVAGEtDSISDTVsYtDI	S12(Phospho	0.002 S(12): 88.1; T(17): 10.3; S(19):	35	0.055	16
	Low		GGQLcPNDIATyNLIIQGLGQMGAeva	Y12(Phospho	0.249 T(11): 48.8; Y(12): 48.8; S(30):	16	0.742	15
	Low		GGsIITEIR	S3(Phospho)	0.972 S(3): 97.2; T(6): 2.8	16		10
	Low		GLDASALAALPVtAyR	T13(Phospho	0.981 S(5): 1.9; T(13): 98.7; Y(15): 98.	23	0.649	12
	Low		GsyALGPYLssKLLAEIPIGAAPLIFGsIL	S2(Phospho)	0.018 S(2): 69.9; Y(3): 69.9; Y(8): 56.	2	0.776	17
	Low		GTIGYAPPEYGAGNmVSTHGDIYSyGIL	Y25(Phospho	0.41 T(2): 1.5; Y(5): 2.3; Y(10): 2.3;	24	0.637	11
	Low		GiVcYVAPEyGGGGPLSEKcDIYSFGVLI	T2(Phospho)	0.049 T(2): 35.4; Y(5): 29.3; Y(10): 29.	1	0.697	12
	Low		HtAHSAAAAALPPR	T2(Phospho)	0.5 T(2): 50.0; S(5): 50.0	40	0.487	11
	Low		IAIEQFPTIDKTntEK	T14(Phospho	0.002 T(8): 99.7; T(12): 0.1; T(14): 0.1	20	0.74	11

Low	IGmIKALAEStsPAVHQINtVAASISGFLr	T12(Phospho)	0.013 S(11): 42.9; T(12): 36.6; S(13):	0	0.126	11
Low	KDDtAAVLK	T4(Phospho)	1 T(4): 100.0	43		11
Low	KsIAHIVK	S2(Phospho)	1 S(2): 100.0	45	0.776	11
Low	KTTLENMWLETlMALIGEQFDESEElcG	S32(Phospho)	0.328 T(2): 14.7; T(3): 14.7; T(11): 14	4	0.715	12
Low	KVDTcAAVmPNGSVATQMGTlAsTSFVS	T20(Phospho)	0.017 T(4): 37.5; S(13): 22.3; T(16): 1	2	0.804	14
Low	LEItGGLSR	T4(Phospho)	1 T(4): 100.0; S(8): 0.0	69		14
Low	LGAIDTAKLLQVTsmDR	S14(Phospho)	0.182 T(6): 0.0; T(13): 81.8; S(14): 18	44		11
Low	LGVpVtVAWRVtYLLPsLGVVsGmTASG	T6(Phospho)	0.013 T(6): 78.7; T(12): 53.6; Y(13): 5	3		13
Low	LPDttVDAEAVVSIPAsRPDVsaAPSAS	S17(Phospho)	0.018 T(4): 46.6; T(5): 46.6; S(13): 57	5		11
Low	LQRSMPPDtIGAR	T9(Phospho)	0.5 S(4): 50.0; T(9): 50.0	26	0.773	16
Low	LRALATAFDNIWPGAAPAsAYLAmVSTs	S19(Phospho)	0.144 T(6): 6.0; S(19): 31.0; Y(21): 30	18	0.799	11
Low	LREALtDK	T6(Phospho)	1 T(6): 100.0	54		11
Low	LSDmIGSASDTTSGTVAASNtGVGtsARl	T21(Phospho)	T25(Phospho) Too many isoforms		0.754	11
Low	LsGNAHVKEIR	S2(Phospho)	1 S(2): 100.0	78	0.77	18
Low	LSQAEtAIK	T6(Phospho)	0.031 S(2): 96.9; T(6): 3.1	23	0.107	16
Low	LYYEGmmMSQPPPsAAsAssAsssGAG	S14(Phospho)	S15(Phospho) Too many NL-allowing PTMs		0.549	10
Low	mAlSLRPFAYIANEILQSTSTNcFVSsEsF	S4(Phospho)	0.557 S(4): 91.3; Y(10): 8.3; S(18): 0.	42	0.804	11
Low	mEGVIRGNVDGGGsGPTVVAGMGAtA\	S14(Phospho)	0.453 S(14): 54.7; T(17): 54.7; T(25):	20		10
Low	MEGVIRGNVDGGGSGPtVVAGmGAtAv	T17(Phospho)	0.708 S(14): 29.2; T(17): 72.3; T(25):	24	0.16	12
Low	mELTmAstmSLALLVLSAAYVLVALR	T8(Phospho)	0.657 T(4): 15.3; S(7): 15.3; T(8): 65.	66		15
Low	mGANADPTGVLLGGPHHRNPSPAPAL/	S21(Phospho)	0.917 T(8): 8.3; S(21): 97.2; S(33): 97	18	0.403	15
Low	MGLQsLRR	S5(Phospho)	1 S(5): 100.0	23	0.467	18
Low	mLLIPLIAysGLQQAFVWAVFTK	Y10(Phospho)	0.991 Y(10): 99.6; S(11): 99.5; T(23):	26	0.175	11
Low	mWVLMNAEAVASELRVVLGSVAtAmD\	T23(Phospho)	0.816 S(12): 1.2; S(20): 16.8; T(23): 8	32	0.581	12
Low	NDPDVDTDsSTQVGFFcGSPpVRANNF	S9(Phospho)	0.283 T(7): 14.5; S(9): 28.3; S(10): 14	15	0.326	11
Low	NsLSNGLLK	S2(Phospho)	0.994 S(2): 99.4; S(4): 0.6	40	0.792	11
Low	NTAtPNVmGFVK	T4(Phospho)	0.979 T(2): 2.1; T(4): 97.9	28	0.7	12
Low	QALKtSGLK	T5(Phospho)	0.872 T(5): 87.2; S(6): 12.8	37	0.63	10
Low	QmAALLEGTEAAyCTASGmsAISSVLMQ	S19(Phospho)	0.139 T(8): 7.7; Y(12): 10.0; T(14): 20	5		12
Low	QsVVHLLVALAEDGtATGDLFLDDGESP	S2(Phospho)	0.057 S(2): 67.5; T(15): 43.0; T(17): 3	1	0.777	13
Low	QYPSRVtTLNLR	T7(Phospho)	0.475 Y(2): 2.5; S(4): 2.5; T(7): 47.5;	26	0.574	11
Low	QyRDGIDNLLVLLIGGIPIAmPtVLSVTm/	Y2(Phospho)	0.185 Y(2): 100.0; T(23): 96.7; S(26):	37	0.776	12
Low	RLSsQINK	S4(Phospho)	0.87 S(3): 13.0; S(4): 87.0	47		11
Low	RTGEtVAVK	T5(Phospho)	0.5 T(2): 50.0; T(5): 50.0	28		11
Low	RTPPSsPAAGTGAAASGGR	S6(Phospho)	0.377 T(2): 3.3; S(5): 37.7; S(6): 37.7	31		11
Low	SDLIIVDTsGRHK	S9(Phospho)	0.333 S(1): 33.3; T(8): 33.3; S(9): 33.	20		10
Low	sGVGEMIVSSVARR	S1(Phospho)	0.421 S(1): 42.1; S(9): 15.9; S(10): 42	10	0.569	10
Low	sIDVGGTALK	S1(Phospho)	0.992 S(1): 99.2; T(7): 0.8	40		11
Low	SKLPLLLVLAVvtAAVsSAWLPSPASAA/	T13(Phospho)	0.039 S(1): 19.6; T(13): 58.8; S(17): 2	12	0.768	11
Low	sLEILGASR	S1(Phospho)	1 S(1): 100.0; S(8): 0.0	50		16
Low	SMAAsLEQEATDSsESGARR	S4(Phospho)	0.017 S(1): 73.4; S(4): 64.0; T(10): 21	3	0.284	12
Low	sPQHQNIGMSPSPISPRTTSGASTPLT	S1(Phospho)	0.722 S(1): 72.2; S(10): 7.9; S(12): 2.	19	0.506	12
Low	SYMLEDfNsIGMLGyVmAGVVAGILsAL	S9(Phospho)	0.214 S(1): 45.5; Y(2): 45.5; S(9): 52.	12		10
Low	tIDLNGKK	T1(Phospho)	1 T(1): 100.0	56		10
Low	tKAAAASGLR	T1(Phospho)	1 T(1): 100.0; S(7): 0.0	40		12
Low	tLGmIMNETLR	T1(Phospho)	0.5 T(1): 50.0; T(9): 50.0	13	0.147	11
Low	tRLQDTVK	T1(Phospho)	0.5 T(1): 50.0; T(6): 50.0	25		13

	Low		TRMitNEPINPR	T5(Phospho)	0.998 T(1): 0.2; T(5): 99.8	43	0.75	13
	Low		TRPDRGATEEsVK	S11(Phospho)	0.853 T(1): 0.0; T(8): 14.7; S(11): 85.	41	0.688	10
	Low		TsTSSASAAASRAK	S2(Phospho)	0.384 T(1): 38.4; S(2): 38.4; T(3): 7.6	43	0.493	12
	Low		TWMPFSINGLTSLSTGSRTSYGTtLTSG T24(Phospho)		0.18 T(1): 0.9; S(6): 1.2; T(11): 3.4;	28		12
	Low		VEDEsVQSSDDLTLADPFPLSAyTLVN S5(Phospho)		0.025 S(5): 30.6; S(8): 30.6; S(9): 30.	5	0.756	13
	Low		VfATAFFSmLEGPMHNFQTIVmcmQ T3(Phospho)		0.317 T(3): 31.7; T(5): 31.7; S(9): 31.	12	0.529	10
	Low		VKTMVPSVVAsmAGGIER	S11(Phospho)	0.532 T(3): 18.1; S(7): 28.6; S(11): 53	7		13
	Low		VmGtHGyAAPEYImTGHlTAKSDVYSF T4(Phospho)		0.127 T(4): 12.7; Y(7): 10.1; Y(12): 11	3	0.776	12
	Low		VTTLHGKsQEQR	S9(Phospho)	0.999 T(2): 0.0; T(3): 0.0; S(9): 99.9	39		10
	Low		WTIDLSPGVEVEELAGADHmAMcsKPR S24(Phospho)		0.333 T(2): 33.3; S(6): 33.3; S(24): 33	2	0.64	10
	Low		YSDAmWASTAPIEDISFVAAtRTGFLQL T21(Phospho)		0.325 Y(1): 15.3; S(2): 8.0; S(8): 8.0;	13	0.621	11
Os03t0577000-01	Low	Similar to Ribosomal protein S3 (Fragment).	AmPRAPPAAPNLQsLK	S14(Phospho)	1 S(14): 100.0	32	0.686	12
	Low		IWSLsEGRMLR	S5(Phospho)	0.111 S(3): 88.9; S(5): 11.1	60	0.685	10
	Low		lySKIWK	Y2(Phospho)	0.911 Y(2): 91.1; S(3): 8.9	42		12
	Low		KSLSTDHDsVVR	S9(Phospho)	0.508 S(2): 16.4; S(4): 16.4; T(5): 16.	16		10
	Low		KsVPDGNsVLDGR	S2(Phospho)	0.997 S(2): 99.7; S(8): 0.3	40		11
	Low		LDMKSALQQSWItR	T13(Phospho)	0.204 S(5): 6.5; S(10): 73.1; T(13): 20	19	0.407	13
	Low		LKsSIFDK	S3(Phospho)	0.973 S(3): 97.3; S(4): 2.7	40		10
	Low		MLASVVDtSKHR	T8(Phospho)	0.5 S(4): 0.1; T(8): 50.0; S(9): 50.0	51		11
	Low		RmVEVLsIVGmGGLGK	S7(Phospho)	1 S(7): 100.0	28	0.805	12
	Low		yQSLSVLK	Y1(Phospho)	0.984 Y(1): 98.4; S(3): 0.8; S(5): 0.8	34		11
Os03t0579300-00	Low	60S ribosomal protein L19.	AAMVLDLLSLIGAyAAGtsR	Y14(Phospho)	0.506 S(9): 49.4; Y(14): 78.4; T(18): 8	6	0.33	12
	Low		ASMRWSNVAVmLGFVVGyR	Y18(Phospho)	1 S(2): 0.0; S(6): 0.0; Y(18): 100.	64		10
	Low		AVFAAmATsGGYGYGGLQHRF	S9(Phospho)	0.952 T(8): 4.8; S(9): 95.2; Y(12): 0.0	56		11
	Low		DADEmVDILVAAtFSALHDK	T13(Phospho)	0.5 T(13): 50.0; S(15): 50.0	29		15
	Low		EFPEATIMRPATmIGtEDR	T16(Phospho)	0.648 T(6): 7.6; T(12): 27.6; T(16): 64	13		11
	Low		EGMGLGVsGQGmLDPIPVK	S8(Phospho)	1 S(8): 100.0	32	0.618	20
	Low		ElSSGGLSAPAPAPAAGAAGR	S3(Phospho)	0.067 S(3): 6.7; S(4): 20.1; S(5): 66.5	21	0.658	11
	Low		EmHIsEAYPISTAPGSAGKAK	S5(Phospho)	0.483 S(5): 48.3; Y(8): 48.3; S(11): 0.	32	0.535	12
	Low		GKVLWDPNEVNEISMAnsR	S18(Phospho)	0.904 S(14): 9.6; S(18): 90.4	31	0.806	14
	Low		GRQGAASVsELHSmVQMLSR	S9(Phospho)	0.212 S(7): 76.6; S(9): 21.2; S(13): 2.	29	0.646	10
	Low		KLDLGASGFsGsLPsSLGSLK	S10(Phospho)	0 S(7): 4.8; S(10): 94.0; S(12): 1.	26	0.803	14
	Low		KsAFEASYMVLAlVGQGGmGK	S2(Phospho)	0.333 S(2): 33.3; S(7): 33.3; Y(8): 33.	1	0.659	11
	Low		LARyAVYDtDFGLGRPmK	Y4(Phospho)	0.381 Y(4): 61.9; Y(7): 61.9; T(9): 76.	2	0.629	12
	Low		MLMsLKLNSTPEItSR	S4(Phospho)	0.763 S(4): 98.4; S(9): 1.8; T(10): 2.4	32		12
	Low		MPLSYsAAAAAAPsPLAAR	S6(Phospho)	0.779 S(4): 4.5; Y(5): 17.7; S(6): 78.0	39	0.689	21
	Low		NSALmISRtLAMAYVMDQK	T9(Phospho)	0.254 S(2): 1.2; S(7): 11.4; T(9): 25.4	16		11
	Low		QALYASKIcsYAQGMNIiK	S10(Phospho)	0.395 Y(4): 10.5; S(6): 10.5; S(10): 39	36		15
	Low		QGVISsGTETGYLQDLiYK	S7(Phospho)	0.104 S(5): 1.3; S(6): 33.7; S(7): 10.4	28		10
	Low		RHGAASGGSTTGtRPFPSTPSSR	T13(Phospho)	0.568 S(6): 0.4; S(9): 2.3; T(10): 18.0	35	0.804	11
	Low		ScVSDsAQRGRPVDPLR	S6(Phospho)	0.146 S(1): 42.7; S(4): 42.7; S(6): 14.	13	0.601	12
	Low		sNVVQTPVHQmGSVsSLPSK	S1(Phospho)	0.091 S(1): 86.3; T(6): 72.1; S(13): 8.	14	0.803	14

Os03t0596900-01	High	GTP-binding signal recognition particle SRP54, G-domain containing protein.	LLDFIAEPHAMADSGHsDDQGSNSR	S22(Phospho	0.838 S(14): 0.1; S(17): 0.6; S(22): 8	85	0	25
	High		LLDFIAEPHAMADSGHsDDQGSNSR	S17(Phospho	0.861 S(14): 0.0; S(17): 86.1; S(22): 1	136	0	41
	High		LLDFIAEPHAMADsGHsDDQGSNSR	S14(Phospho	0.5 S(14): 50.0; S(17): 50.0; S(22):	105	0	28
	Low		AAFDPPVGEGFFGtclSGcLATATAR	T14(Phospho	0.939 T(14): 93.9; S(17): 5.8; T(22): 0	48		13
	Low		HGPPNAGAHAAPsPVGQGSSSDDGAD	S13(Phospho	0.73 S(13): 73.0; S(19): 15.0; S(20):	20		11
	Low		HGPPNAGAHAAPsPVGQGGSsSDDGAD	S20(Phospho	0.445 S(13): 0.0; S(19): 44.5; S(20): 4	52		13
	Low		mIcSSSGAAPFSKIMSVmLTPsTR	T20(Phospho	0.278 S(4): 4.3; S(5): 4.3; S(6): 5.4; S	17	0.792	15
	Low		mPPsSAATTGGAVHKPIImPPEsER	S4(Phospho)	0.467 S(4): 46.8; S(5): 46.8; T(8): 3.3	52	0.603	15
	Low		MSPAmLQASSLcVSAALsGAAsRPGR	S18(Phospho	0.985 S(2): 0.0; S(9): 0.1; S(10): 0.1;	52	0.665	10
	Low		RtVsVTPNAAAPtPGEQGVAmEQGK	T2(Phospho)	0.682 T(2): 84.1; S(4): 84.1; T(6): 31.	44	0.285	14
	Low		VyGVtLILMAAcAIGSGLsFGSsR	Y2(Phospho)	0.794 Y(2): 99.9; T(5): 99.6; S(16): 7.	42		10
	Low		yLDPNLKLLtGymNVLASTLEK	Y1(Phospho)	0.048 Y(1): 98.0; T(10): 33.0; Y(12): 3	20	0.792	10
Os03t0598800-02	Low	Similar to 60S ribosomal protein L15.	APELAAsKKPsPSFK	S7(Phospho)	0.934 S(7): 99.8; S(11): 93.6; S(13): 6	30		10
	Low		LGIQKGtR	T7(Phospho)	1 T(7): 100.0	34		11
Os03t0648400-01	Low	Similar to DnaJ protein.	NYQAPsEKISAR	S6(Phospho)	0.495 Y(2): 49.5; S(6): 49.5; S(10): 1.	26		10
Os03t0663800-01	High	Globulin 1 (Fragment).	sINSPPRPQDNETcLSPTDK	S1(Phospho)	0.814 S(1): 81.4; S(4): 18.6; T(13): 0.	50	0.001	10
	Middle		LLPPFHQASsLLR	S10(Phospho	0.855 S(9): 14.5; S(10): 85.5	56	0.021	20
	Low		AGNAtIAMPQsGNtItVSTATPVTALVDS\	T5(Phospho)S11(Phospho)	Too many isoforms		0.765	12
	Low		AHEPTSLASYGLSISPLSKDAAmGLVVs	S28(Phospho	0.851 T(5): 1.3; S(6): 1.3; S(9): 1.3; Y	31	0.708	11
	Low		AKLtVFVAILAVAAAAAAAVstttAHGVA\	T4(Phospho)	1 T(4): 100.0; S(22): 100.0; T(23)	11	0.7	12
	Low		ALIFTQMTKmLDILEEFINLyGtyLR	Y21(Phospho	0.331 T(5): 6.2; T(8): 12.7; Y(21): 80.	23	0.773	10
	Low		ALLVGISYAATGYELKGtVNDVNcmsFLI	T18(Phospho	0.464 S(7): 12.8; Y(8): 14.3; T(11): 18	13		10
	Low		ANSWTKIsNVIFVDsPPGTGFTYATTAE	S8(Phospho)	0.77 S(3): 3.9; T(5): 10.1; S(8): 86.0	44		10
	Low		APMDDLsILAVLTScHAGLVsEGLGIFyR	S7(Phospho)	0.205 S(7): 99.5; T(13): 74.4; S(14): 7	33	0.373	10
	Low		APSIABAEATAAARAPVDLVtVLDVSGS	T21(Phospho	0.37 S(3): 17.6; T(10): 10.0; T(21): 7	20	0.351	12
	Low		APsIAVAEATAAARAPVDLVTVLDVSGS	S3(Phospho)	0.01 S(3): 99.3; T(10): 86.2; T(21): 1	14	0.663	18
	Low		AsLIIFILsFMIFIsAISLGGVGIsNMIGK	S2(Phospho)	0.768 S(2): 99.1; S(9): 97.0; S(15): 86	26	0.612	19
	Low		AYALADSSLDPStsATVVSLLEDALRcP5	T13(Phospho	0.249 Y(2): 0.6; S(7): 2.7; S(8): 6.0; S	34	0.785	12
	Low		AyVHDDQQSTsKPItmSSVPPLGDILILI	Y2(Phospho)	0.102 Y(2): 58.8; S(9): 17.3; T(10): 17	13		11
	Low		cGVGDDDVERPVsVALsPGAQGGVVSf	S17(Phospho	0.809 S(13): 12.8; S(17): 80.9; S(26):	26	0.772	12
	Low		cIPPLASDsEssAsSPTTSPAAAAAALPG	S9(Phospho)	0.013 S(7): 45.0; S(9): 45.0; S(11): 38	6		11
	Low		cPGVVScADVLALAARDAVImAGGPYYC	T31(Phospho	0.434 S(6): 4.6; Y(26): 8.7; Y(27): 43.	16	0.712	11
	Low		csFTNTTTSDNRYHLELWIPIIGQPFDK	S2(Phospho)	0.452 S(2): 45.2; T(4): 45.2; T(6): 1.6	25	0.543	12
	Low		cSFtNTTTSDNRYHLELWIPIIGQPFDK	T4(Phospho)	0.209 S(2): 78.5; T(4): 20.9; T(6): 0.2	47	0.242	12
	Low		DAWTALVNEYGLQEENAYLQKEmDIDlc	Y18(Phospho	0.708 T(4): 14.6; Y(10): 14.6; Y(18): 7	13		12
	Low		DAYRAIVPALcDAGMLDEAtHVLYSmLW	T20(Phospho	0.479 Y(3): 0.0; T(20): 47.9; Y(24): 4.	44	0.095	24

Low	DAYRAIVPALcDAGMLDEATHVLYsmLV S25(Phospho)	0.671 Y(3): 0.3; T(20): 23.6; Y(24): 9.	26	0.654	11
Low	DFPDRPPVmFDFtNAAAVNRNMsLMVt T13(Phospho)	0.494 T(13): 100.0; S(23): 98.7; T(27)	48	0.31	14
Low	DFtDVSEKLLGIPGSSHVGTyGHNALHA T3(Phospho)	0.123 T(3): 85.7; S(6): 13.6; S(15): 38	24	0.632	12
Low	DGINENNTVLsFHDLMRIHMPPYDDAVI S11(Phospho)	0.681 T(8): 26.5; S(11): 68.1; Y(23): 5	21	0.777	12
Low	DIGNLVNLQYLSLANNStGsLPsSFSKL T19(Phospho)	0.139 Y(10): 0.9; S(12): 0.9; S(17): 10	42	0.626	12
Low	DKNyTAHDmPAFLAAAGLPEFEVtLYEt Y4(Phospho)	0.045 Y(4): 73.4; T(5): 73.4; T(24): 71	1	0.799	15
Low	DLDStAcLAmFSGLQLKPEFSAVAKHmL T5(Phospho)	0.669 S(4): 28.4; T(5): 66.9; S(12): 3.	22	0.458	13
Low	DLGsGLsQMQLHtSGYPINPDLFFVLEQ S4(Phospho)	0.177 S(4): 63.8; S(7): 63.8; T(13): 71	5	0.803	10
Low	DSFSRNAtQIAtQLcGFVtIVAGTFLLHK T8(Phospho)	0.043 S(2): 56.4; S(4): 45.5; T(8): 58.	2		10
Low	EANIHKFisALPQGyETQVGESGVQLSG S9(Phospho)	0.777 S(9): 98.2; Y(15): 79.4; T(17): 2	47		10
Low	EDGIGVsEGEEDIsERALHSPSItmVFIVF S7(Phospho)	0.797 S(7): 99.9; S(14): 94.6; S(20): 1	47	0.771	12
Low	EDVFATPLEHNssmMFPESLNFSSAVP S12(Phospho)	0.188 T(6): 30.3; S(12): 49.1; S(13): 5	16	0.615	13
Low	EEVTSSmLVETMMRtGDND DANPTTT T16(Phospho)	0.019 T(4): 0.7; S(5): 0.5; S(6): 0.5; T	8	0.784	10
Low	EFmEALQAGADVSmIGQFGVGFySAYL Y23(Phospho)	0.385 S(13): 11.5; Y(23): 38.5; S(24):	32		11
Low	EGPRmHDtNGLMsIsETLSEYmLYLLVR T8(Phospho)	0.147 T(8): 99.0; S(13): 76.4; S(15): 3	34	0.509	11
Low	ELsNYLymVVHPLmLsSSTmAIKR S3(Phospho)	0.222 S(3): 97.3; Y(5): 52.7; Y(7): 52.	59	0.691	12
Low	EPPTSHVTNAFsSDSDASVEEGGADAC S12(Phospho)	0.448 T(4): 0.4; S(5): 1.6; T(8): 1.6; S	35	0.142	12
Low	EQPSQPPPmVHTELLcRPHsSLLSsQP S20(Phospho)	0.121 S(4): 13.8; T(12): 16.0; S(20): 4	7		10
Low	EQRQGVDSsAVcGGQSTMSTAVGFIPT S9(Phospho)	0.734 S(8): 25.8; S(9): 73.4; S(16): 0.	42		11
Low	EtMGLMVtLLAVGVFYVAMALVAVSDEc T2(Phospho)	0.034 T(2): 81.3; T(8): 18.7; Y(16): 11	8	0.806	11
Low	EVWVITAcMDLIKATtSHYDGTAVAIDSE T22(Phospho)	0.653 T(6): 0.0; T(15): 2.6; T(16): 2.6	45		14
Low	EVWVITAcMDLIKATtSHYDGTAVAIDSE T16(Phospho)	0.021 T(6): 21.5; T(15): 39.5; T(16): 2	3	0.802	14
Low	EyEGGSGGGGGGGRGAAAAPAVVP Y2(Phospho)	0.764 Y(2): 76.4; S(7): 23.6	45	0.157	10
Low	FAHGGYIPVAMsAVLmGVmGVWHyVH S12(Phospho)	0.012 Y(6): 98.8; S(12): 73.5; Y(24): 1	7	0.776	11
Low	FEcsQmPHPLLDHITFVDTPGVLSGEKQ S4(Phospho)	0.008 S(4): 0.8; T(15): 2.4; T(19): 4.2	0	0.671	13
Low	FEcSQMPHPLLEHITFVDTPGVLSGEKQ T19(Phospho)	0.884 S(4): 0.1; T(15): 0.4; T(19): 88.	35		17
Low	FEcSQMPHPLLEHITFVDTPGVLSGEKQ T15(Phospho)	0.555 S(4): 20.5; T(15): 55.5; T(19): 2	30		10
Low	FFGVKtPHTGVQMfNAMLScIQDWNIA T6(Phospho)	0.493 T(6): 49.3; T(9): 49.3; S(19): 1.	44	0.361	11
Low	FISTIFPsAMMAADGGPLLGEWMsATA S8(Phospho)	0.386 S(3): 10.7; T(4): 10.7; S(8): 73.	18	0.164	17
Low	FKIFDLAVGALsGPsHSDVPVLHAVYs S12(Phospho)	0.174 S(12): 92.8; S(15): 87.5; S(17):	21	0.277	11
Low	FLQmQLtLGPtRYAytDLTAITGHFGEK T7(Phospho)	0.098 T(7): 82.0; T(11): 82.0; Y(13): 6	22	0.591	15
Low	FNQNLRSLSFGHSSPPSPASYGQNGL Y29(Phospho)	1 S(7): 0.0; S(9): 0.0; S(13): 0.0;	82		10
Low	FPsDsSVDAGALySFARLLALLLEDSSI S3(Phospho)	0.453 S(3): 98.4; S(5): 95.5; S(6): 50.	44	0.613	11
Low	FSEDYRASISTPSLTSLtLYKPDAsVP SL T18(Phospho)	0.07 S(2): 3.5; Y(5): 3.1; S(8): 3.8; S	15		12
Low	FVTTLVPSvGLsTAETLRK S8(Phospho)	0.558 T(3): 10.2; T(4): 10.2; S(8): 75.	26	0.567	11
Low	FVTTLVPSvGLsTAETLRK S8(Phospho)	0.837 T(3): 0.0; T(4): 0.0; S(8): 99.3;	73		14
Low	FWITGcGsRFVLFfSNsGNHLFFSGTGE S8(Phospho)	0.684 T(4): 8.1; S(8): 89.8; S(15): 22.	33	0.688	25
Low	GAlmDTQAVADAcAsGHVAGYGGDVW S15(Phospho)	0.996 T(6): 0.1; S(15): 99.6; Y(21): 0.	42		12
Low	GATLWWyPSSmsNKssVisFYPGEDER Y7(Phospho)	0.007 T(3): 57.2; Y(7): 57.2; S(9): 54.	0	0.179	12
Low	GFVKWSmSmSTAASsSASAVRPPPTW S15(Phospho)	0.067 S(6): 33.4; S(8): 14.2; S(10): 14	10	0.806	13
Low	GKDDVsGEIALIADGmNmItEtAVGGHA S6(Phospho)	1 S(6): 100.0; T(20): 100.0; T(22)	39	0.629	12
Low	GLGsNDIFDSQWIAPVQFEGLDDsEEEE S4(Phospho)	0.26 S(4): 99.1; S(10): 74.0; S(24): 1	26	0.735	12
Low	GLmFNGRTHPAHLGtAYLK T15(Phospho)	0.255 T(8): 49.0; T(15): 25.5; Y(17): 2	6	0.776	13
Low	GPGDGVySGSTcKQGEIEAVVIAtGVHf Y7(Phospho)	0.131 Y(7): 13.8; S(8): 13.8; S(10): 3	24	0.743	11
Low	GssEmtATEVAALLDLKPHPEGGYTET S2(Phospho)	0.86 S(2): 97.1; S(3): 97.1; T(6): 91.	44	0.434	11
Low	GVSTVmVSySSWNGVKMHANHHLitDF Y9(Phospho)	0.357 S(3): 1.9; T(4): 1.9; S(8): 36.1;	31	0.776	10
Low	GyTctGAQVmNVIFVVLIGLLASGQASP Y2(Phospho)	0.06 Y(2): 24.1; T(3): 24.1; T(5): 25.	4		11

Low	GyTcTGAQVmNVIFVVLIGLLASGQASP Y2(Phospho):	0.179 Y(2): 37.6; T(3): 37.6; T(5): 23.	11		11
Low	HcKFmsmQYPILFPYGEDGYHENITYR S6(Phospho)	0.893 S(6): 89.3; Y(9): 6.5; Y(15): 1.7	24		10
Low	HGGPGEELEEDVGVAyLLGVAAAmVG/ Y16(Phospho)	0.402 Y(16): 96.7; S(28): 83.7; Y(29):	25	0.213	15
Low	HLAAcETmGSATTlcSDKTGTLtNHmtV T24(Phospho)	0.018 T(7): 33.0; S(10): 27.4; T(12): 1	2		10
Low	HQDKIIFLDLsNNQMNGAIPPAWAWETW S11(Phospho)	0.733 S(11): 73.3; T(26): 26.7	26		12
Low	HQPSPPLIAAcDYADImyLIDVLtLTLGR Y18(Phospho)	0.464 S(4): 20.6; Y(13): 20.6; Y(18): 6	32	0.68	12
Low	HsTFYWHLSDDLPLVDLLGSIHESmSELG/ S2(Phospho)	0.082 S(2): 8.2; T(3): 8.2; Y(5): 16.9;	13	0.803	12
Low	IGGsNmQLDPDsIPVVsAK S4(Phospho):	1 S(4): 100.0; S(12): 100.0; S(17)	23	0.366	12
Low	IIAEFDPEVAAERAAQANHDGEtPLYVA T23(Phospho)	0.5 T(23): 50.0; Y(26): 50.0	21	0.647	14
Low	ILGVEVmQQLstGYSDWAVVHFVcDyVF S11(Phospho)	0.104 S(11): 54.7; T(12): 54.7; Y(14):	27	0.546	11
Low	IPHHPIsFsFsFLPPQASPPALAPAAAAA S7(Phospho):	0.569 S(7): 86.8; S(9): 86.8; S(11): 8;	8		11
Low	IQVSSITDTHMLQGGPAVDtIVyDMVLE Y23(Phospho)	0.5 S(4): 7.9; S(5): 7.9; T(7): 7.9; T	14	0.161	12
Low	ISENyYPPLSAWsHLSSGRASVNAATPE Y5(Phospho):	0.565 S(2): 8.1; Y(5): 67.3; Y(6): 22.9	35	0.803	14
Low	KcNtAmAPPQAVDTPATAAGGVELTSLI T4(Phospho):	0.135 T(4): 25.1; T(14): 64.2; T(17): 1	22	0.592	11
Low	KELPTPSLSScPcSAPTTPPSAsTGAPP' S23(Phospho)	0.013 T(5): 30.2; S(7): 30.2; S(9): 12.	11	0.689	13
Low	KFEGQtNLTEPWyGTYSVEAVTPSIIQI T6(Phospho):	0.662 T(6): 95.6; T(9): 6.1; Y(13): 68.	46	0.763	12
Low	KPQyTINIsNsSAQSLVTLGKIQEYNWK Y4(Phospho):	0.005 Y(4): 77.7; T(5): 77.7; S(9): 26.	9	0.776	12
Low	KPSIWDTFtHQGYSPGGAIADVSADQYI T9(Phospho)	0.732 S(3): 2.8; T(7): 2.8; T(9): 73.2;	24	0.512	10
Low	KWsmFfGGVTFLAGSalNGAAtDVmML S3(Phospho):	0.899 S(3): 90.5; T(10): 4.9; S(15): 5.	33	0.804	14
Low	LAQDVLTVPVSSvSsEsAFSLcGRIIEDR S12(Phospho)	0.012 T(7): 28.0; S(11): 46.4; S(12): 4	7	0.478	12
Low	LASASAAGGWAAPPAMKQPSTAALI S29(Phospho)	0.152 S(3): 1.3; S(5): 1.3; S(22): 3.1;	21	0.534	16
Low	LcDGGDGGGGsGLRLFGVQVHVAAGG S11(Phospho)	1 S(11): 100.0	22		11
Low	LDAlHDVAPVSAPPAGAAVVVGGGGEs S27(Phospho)	0.627 S(11): 7.9; S(27): 62.7; S(30): ;	19		11
Low	LEVSLQNvcEGHtLLFALDGSPsELLFEF T13(Phospho)	0.849 S(4): 7.3; T(13): 91.3; S(21): 8.	30	0.719	14
Low	LFAARLVLAPGTPPSNSTTSyNItMtLSLF Y21(Phospho)	0.019 T(12): 25.2; S(15): 25.2; S(17):	5	0.596	15
Low	LFVLVLIMcSTTAlTctNGGAGDGGEGl T18(Phospho)	0.884 S(10): 2.9; T(11): 2.9; T(12): 2.	48		14
Low	LGVGcIDLyQHRIIDStVPVEItMGELK Y9(Phospho):	0.684 Y(9): 98.1; Y(10): 98.1; S(16): ;	24	0.759	13
Low	LHLEDISDTLyTRPSVLAGAASATtRSPS Y11(Phospho)	0.028 S(7): 45.0; T(9): 45.0; Y(11): 5.	34		12
Low	LKHRPAPDIVsYNTVLAGYsAQGDEEGf S11(Phospho)	0.052 S(11): 35.3; Y(12): 35.3; T(14):	8	0.759	19
Low	LLSNDWmAQENAVtALLNLSIFEPNKG S4(Phospho):	0.202 S(4): 40.4; T(15): 79.8; S(21): ;	4	0.655	11
Low	LLNAtLLPALLVcVAsIAATLSTYnsLFY T5(Phospho):	0.534 T(5): 99.9; S(16): 99.4; T(20): 1	54	0.489	19
Low	LLNAtLLPALLVcVAsIAATLSTYnsLFy T5(Phospho):	0.711 T(5): 99.3; S(16): 92.3; T(20): 6	40	0.803	12
Low	LMGLMLDQAtLDDLLVSGDDGGVYDVN T10(Phospho)	0.645 T(10): 64.5; S(17): 24.9; Y(24):	20	0.334	13
Low	LmmTHVLRcsSQSGGVTDVSMGQGNE S10(Phospho)	0.056 T(4): 2.2; S(10): 5.6; S(11): 5.6	7	0.662	13
Low	LmNHGPWQGAsSYNSIAVR S11(Phospho)	0.866 S(11): 86.6; S(12): 13.0; Y(13):	64	0.276	14
Low	LNVDSFAGDSFSPSWFNPESLPtLRmm T23(Phospho)	0.852 S(5): 0.8; S(10): 2.8; S(12): 2.8	22	0.483	13
Low	LPYmDPEFNtGELTTLSDVYsLGVILR T10(Phospho)	0.074 Y(3): 14.0; T(10): 31.0; T(11): ;	8	0.471	16
Low	LSFYNYGQEDVTLYsMVTTHVRSLNIFR S15(Phospho)	0.184 S(2): 0.0; Y(4): 0.0; Y(6): 0.1; T	35	0.803	14
Low	LsISEFsAFGSLSNVGAmVGAIASGQmA S2(Phospho):	0.306 S(2): 46.8; S(4): 46.8; S(7): 67.	17		13
Low	LTARWAPLPLPPGsGLAPQDtDWVtGG S14(Phospho)	0.912 T(2): 8.8; S(14): 93.6; T(21): 98	22	0.158	10
Low	LtLAMDVYsFGVVMLEMLTGKTAAGLVs T2(Phospho):	0.196 T(2): 91.6; Y(8): 54.4; S(9): 25.	24	0.776	10
Low	mAAmAAAAATtTKK T10(Phospho)	0.727 T(9): 6.6; T(10): 90.4; T(11): 81	36	0.411	10
Low	mAAPPPLSGTGKPPtLPFsLKKPPPMf T16(Phospho)	0.487 S(9): 23.8; T(11): 42.0; T(16): 6	20		14
Low	MAEAGSTPAGmAtVATSAEAPDPGALE T13(Phospho)	0.419 S(6): 0.3; T(7): 0.5; T(13): 41.9	34		10
Low	MAEVPsDLVsRPELsHcMMSATGEVERI S6(Phospho):	0.709 S(6): 94.9; S(10): 89.5; S(15): ;	27	0.593	14
Low	MAMLGSSsAVVLELMtMGyQSAAYLGEI S8(Phospho):	0.029 S(6): 23.3; S(7): 64.2; S(8): 35.	27	0.632	13
Low	MAQGIAPsAGGGAAVPtPSAAAOSTT T5(Phospho)S8(Phospho)T Too many isoforms		0.15		14

Low	MASLTTTTAAASSPAALPAAsTAPASS` S21(Phospho)	0.022 S(3): 0.4; T(5): 0.4; T(6): 0.4; T	23		11
Low	mAsLTTTTAAASSPAALPAASTTAPASS S3(Phospho)	0.046 S(3): 13.8; T(5): 13.8; T(6): 31.	23	0.099	10
Low	MATLAALMAAAAAAAtAAGAVTFDATN` T16(Phospho)	0.265 T(3): 50.0; T(16): 26.5; T(22): 9	10		10
Low	mAVmHSsFtWKHWIGLAVTSAAYFLPY` S7(Phospho)	0.903 S(6): 8.5; S(7): 92.2; T(9): 96.8	54		11
Low	MDAEMAAPALAAAHLLDsPMRPQVsRy S18(Phospho)	0.788 S(18): 99.1; S(25): 79.1; Y(27):	45	0.803	12
Low	MDtISGmFRPVFDRIRPSIASAAELSFsR T3(Phospho)	0.244 T(3): 49.1; S(5): 49.1; S(18): 1.	35		11
Low	mDTISGmFRPVFDRIRPSIASAAELsFSF S18(Phospho)	0.058 T(3): 9.8; S(5): 9.8; S(18): 17.1	10	0.33	13
Low	MDtKLGALALmLPLLYPTSSSSAAFVAc` T3(Phospho)	0.311 T(3): 98.0; Y(16): 32.2; T(18): 3	31		10
Low	mDTKLGALALMLPLLYPtSSSAAFVAc` T18(Phospho)	0.023 T(3): 68.7; Y(16): 37.1; T(18): 2	2		13
Low	mEGcmPsDANYAPLTPVsFLERAAVVY` S7(Phospho)	0.057 S(7): 78.1; Y(11): 15.3; T(15): 8	14		12
Low	mELLVLStLDWRmAAVTPFDyLPcLSSR T8(Phospho)	0.225 S(7): 41.5; T(8): 41.5; T(17): 34	11	0.792	12
Low	mELQFQKPTQQQsQQQcHYQVPTVT S13(Phospho)	0.819 T(9): 16.0; S(13): 81.9; Y(20): 0	39	0.691	15
Low	MGAKALHsAPcWsVsssHHVDCVMPWR S8(Phospho)	1 S(8): 100.0; S(13): 100.0; S(15)	7	0.653	11
Low	MGTLLRPRPLAHAAGAGDatPstAHAV` T20(Phospho)	0.086 T(3): 38.8; T(20): 75.0; S(22): 7	3		10
Low	mGyIAPNLsAIVGsAVAsK Y3(Phospho)	1 Y(3): 100.0; S(9): 100.0; S(14):	15	0.806	14
Low	MIGRFSQFLSLDAGGESLLFmGsEFENI S23(Phospho)	0.457 S(6): 13.3; S(10): 27.7; S(17):	8	0.803	11
Low	mLLTtPFVsSPVRVQGNGSGSPWAc` T5(Phospho)	0.008 T(4): 7.9; T(5): 7.9; S(9): 44.6;	4		12
Low	mLsLyGIAKSNFLDGILTAQYSENDINLR S3(Phospho)	0.415 S(3): 87.5; Y(5): 53.8; S(10): 5	40		11
Low	MNTMIGPAPSPAAAAAAVSPscYAsP` S22(Phospho)	0.06 T(3): 21.3; S(10): 48.0; S(20): 2	16	0.646	13
Low	mPPPAADmENGAVGSPAEEVEAGAsP S25(Phospho)	0.506 S(15): 1.1; S(25): 50.6; S(28):	18	0.776	14
Low	mPPPAADmENGAVGSPAEEVEAGAsP S28(Phospho)	0.187 S(15): 38.5; S(25): 18.7; S(28):	15		11
Low	mQYHSLsLANQAGmEVDIVANGGSDP` S7(Phospho)	0.25 Y(3): 25.0; S(5): 25.0; S(7): 25.	2		13
Low	MRPITTASHPNSTSLccscSYPPyLPSKR S18(Phospho)	0.09 T(5): 0.1; T(6): 0.2; S(8): 0.3; S	39	0.696	13
Low	msFGMcGGDEVGAGLAVFsSVVGETAm S2(Phospho)	0.232 S(2): 99.8; S(19): 23.3; S(20): 0	29	0.488	13
Low	mSGGVEPETPPGSSSGGSTPVGGKPF S32(Phospho)	0.486 S(2): 0.0; T(9): 0.4; S(13): 0.4;	32	0.561	10
Low	msGGVEPETPPGSSSGGSTPVGGKPP S2(Phospho)	0.158 S(2): 15.8; T(9): 39.0; S(13): 15	22	0.69	15
Low	mSSSAATSTYAEsVAScRAPAPATPRPI S13(Phospho)	0.043 S(2): 9.7; S(3): 9.7; S(4): 9.7; T	2	0.608	11
Low	mTDIHTNENYSNSAVSPVNVVPPSGAA S32(Phospho)	0.909 T(2): 0.0; T(6): 0.0; Y(10): 0.0;	37	0.218	10
Low	mTELLSLsASSLDDEILDGSLNPAPQcL S8(Phospho)	0.394 T(2): 4.3; S(6): 1.6; S(8): 42.1;	35	0.327	10
Low	MTIDQcGDILIWGFGATGsNSMHRLES S20(Phospho)	0.734 T(2): 0.6; T(18): 11.3; S(20): 73	29		15
Low	MTLSTLTdtsVLSALNIIK T9(Phospho)	0.939 T(2): 0.0; S(4): 0.4; T(5): 0.1; T	55	0.474	16
Low	MVIAsAAFSAGASASSGSAAAAAADPSI S5(Phospho)	0.034 S(5): 24.9; S(9): 24.9; S(13): 24	0	0.464	13
Low	NFISLGGPHAGTAsVPLcGsGIFcILADSI S14(Phospho)	0.217 S(4): 1.1; T(12): 11.9; S(14): 84	32		12
Low	NFISLGGPHAGTAsVPLcGsGIFcILADSL T12(Phospho)	0.171 S(4): 12.3; T(12): 73.6; S(14): 7	23		12
Low	NISSGGLsVPsIASRMNLsgNIGSGGLN` S8(Phospho)	0.545 S(3): 10.0; S(4): 18.4; S(8): 78.	48		11
Low	NISSGGLSVPSIAsRmNLsGNIGSGGLN` S14(Phospho)	0.021 S(3): 21.5; S(4): 31.9; S(8): 43.	5	0.528	11
Low	NSIAAAAPSSRPAAAAAATTPTGVNAD` S35(Phospho)	0.429 S(2): 1.7; S(9): 1.7; S(10): 1.7;	14		10
Low	NSIKSVIFDMFTAGTgTlSSTLGWGMSE T17(Phospho)	0.086 S(2): 3.7; S(5): 22.0; T(12): 22.	19	0.549	11
Low	NsVGEsAALETLEQVMAQALTLVNTDR` S2(Phospho)	0.928 S(2): 95.9; S(6): 95.9; T(11): 6.	31	0.238	15
Low	NTAWsYHNGGSWPTLLWQLtVAcIKVD S5(Phospho)	0.297 T(2): 8.3; S(5): 30.5; Y(6): 30.5	45	0.583	11
Low	QAEEEyGFPsGAsGPVALPcDEDHFRD Y6(Phospho)	0.497 Y(6): 99.5; S(10): 50.3; S(13): 9	46	0.49	20
Low	QASNmVGELIAtIsPsTPAKKPAGSAAG` T12(Phospho)	0.11 S(3): 15.5; T(12): 43.3; S(14): 7	10	0.587	11
Low	QDPsHsIKAlcIVHNETAtGVtNDLsAVR S4(Phospho)	0.459 S(4): 100.0; S(6): 100.0; T(17):	40	0.776	12
Low	QmAVAASTEALAVAAAAAtARAPQHHiIf T18(Phospho)	0.966 S(7): 0.9; T(8): 2.5; T(18): 96.6	46	0.154	12
Low	QPpALVILLQFAIAmFVMDtWQYFMHR S3(Phospho)	0.397 S(3): 79.5; T(20): 60.3; Y(23): 6	4	0.804	11
Low	QQsNIIsIVGFGGLGKtLANSLLQELEAK S3(Phospho)	0.196 S(3): 89.6; S(7): 80.4; T(17): 80	5	0.35	13
Low	QtFmDATEFLsPQmGtEDLLLHAYWAK T2(Phospho)	0.059 T(2): 37.9; T(7): 48.7; S(11): 61	0	0.682	14

Low	QWEFLQSLWVLDIRD TNWDWILsPsK	S23(Phospho)	0.994 S(7): 0.0; T(16): 0.6; S(23): 99.	49	0.419	11
Low	READDLHSVsyFIEQEyNIIGLVGHsK	S11(Phospho)	0.949 S(8): 1.5; S(11): 98.8; Y(12): 9.	48	0.761	11
Low	RLDLPTPEsPmsttLNR	S12(Phospho)	0.992 T(6): 0.4; S(9): 0.6; S(12): 99.6	37	0.792	12
Low	RmRPGLtFGVsNIEIALVTLLyHFDWK	T7(Phospho)	0.461 T(7): 96.1; S(11): 96.1; T(19): 5	21		16
Low	RPALSLSPsALtMAEsAKPTPQLELFNSM	S9(Phospho)	0.139 S(5): 34.2; S(7): 34.2; S(9): 48.	11		12
Low	RPHGQGGVAATsPTVSSGGDGVTLRL	S12(Phospho)	0.398 T(11): 39.8; S(12): 39.8; T(14):	34	0.098	16
Low	RPsAPTGGELLVPLRSSVLR	S3(Phospho)	0.899 S(3): 89.9; T(6): 9.9; S(16): 0.1	32	0.128	11
Low	RPstssRPSQIVTAVISAA SPISSAPPPTIf	S3(Phospho)T4(Phospho)	S Too many isoforms		0.792	11
Low	RSSSVDRPRPTSNAAGG DALGPNG	T29(Phospho)	T30(Phospho) Too many isoforms		0.676	12
Low	RTLQEILHsFQGHGGAIFNGDEsMEAtIT	S9(Phospho)	0.462 T(2): 20.4; S(9): 82.6; S(23): 86	15	0.799	12
Low	RVLDLAtsANEEVHVVLr	T7(Phospho)	1 T(7): 100.0; S(8): 100.0	25	0.704	12
Low	RVsEmSAAsGGGAGAPVQVGHAFAAA	S3(Phospho)	0.077 S(3): 87.8; S(6): 92.3; S(9): 19.	5	0.77	14
Low	RVtsLAsEFPDIELsHMYVDNAAMQLIR	T3(Phospho)	0.103 T(3): 66.4; S(4): 82.3; S(7): 66.	5	0.793	16
Low	SAAAACLAALcSSTSDLtVRIIDEssLHLt	T19(Phospho)	0.607 S(1): 3.6; S(13): 8.4; S(14): 15.	27	0.761	15
Low	sAAPtPyTAAIPEYRVVLVKPEEAmHINK	S1(Phospho)	0.306 S(1): 81.3; T(5): 81.3; Y(7): 62.	19		13
Low	sAlmGAQIAyMITHHQTVIVDHDmPVPf	S1(Phospho)	0.038 S(1): 20.2; Y(10): 57.0; T(13): 6	2	0.804	13
Low	SANDVDMPLPAVELQFHGtNHANPLPTR	T18(Phospho)	0.373 S(1): 31.7; T(18): 66.1; T(26): 4	8	0.766	15
Low	SDIVAVAINLDQAGASHHAtsFTSTSSPF	T20(Phospho)	0.399 S(1): 0.6; S(16): 22.3; T(20): 62	42	0.601	12
Low	SDmsPNtVEcENMSQLLKEWGVFSLES	S4(Phospho)	0.315 S(1): 52.5; S(4): 52.5; T(7): 68.	14	0.652	12
Low	siVLDGSHTLLYGYGGFGMNmTPHFS	S1(Phospho)	0.325 S(1): 74.2; S(7): 22.8; T(10): 5.	40	0.569	17
Low	SLSALDsRPGALSK	S7(Phospho)	0.643 S(1): 13.7; S(3): 8.2; S(7): 64.3	11	0.208	12
Low	SmDDYyDtLDAFLFYLPDPEAAPVVELP	Y6(Phospho)	0.011 S(1): 2.9; Y(5): 2.9; Y(6): 10.5;	22	0.483	15
Low	SNNQLEGVAMHAsISGKVASFPMDF	S13(Phospho)	0.042 S(1): 70.8; S(13): 16.6; S(15): 1	4	0.803	13
Low	SPGAVEKLNVLtR	T13(Phospho)	1 S(1): 0.0; T(13): 100.0	47		10
Low	SPLsFNLPWtRTMPVSAHQFVSIHPcMV	S4(Phospho)	0.164 S(1): 23.8; S(4): 58.1; T(10): 37	12	0.439	11
Low	SQQcSPVAMAEQQQITESPRSSQVstG	S25(Phospho)	0.416 S(1): 8.1; S(5): 8.1; T(16): 13.0	22		13
Low	sRGLLLSGESyAGHYIPQLTDVLLtHNEK	S1(Phospho)	0.004 S(1): 29.6; S(7): 70.2; S(10): 49	17		11
Low	SSmMSIAIyLLAtSLTAclTVKLVEyAK	Y9(Phospho)	0.217 S(1): 20.2; S(2): 20.2; S(5): 19.	29		12
Low	SSmMSIAIyLLAtSLTAclTVKLVEyAK	Y9(Phospho)	0.055 S(1): 35.1; S(2): 35.1; S(5): 15.	21		14
Low	ssSACSLASGLNFGtGKQAMPEAAGAVf	S1(Phospho)	0.091 S(1): 36.3; S(2): 36.3; S(3): 63.	38	0.765	12
Low	sstGLsIGVGVSsAAAsLILIVImAlFIIRK	S1(Phospho)	0.021 S(1): 70.4; S(2): 70.4; T(3): 70.	1		16
Low	SSTSNSIStPQQVKVKPSPK	T9(Phospho)	0.326 S(1): 10.6; S(2): 10.6; T(3): 10.	19	0.445	11
Low	STPmPPHQNQstVAPLHGHFQsSTGSV	S11(Phospho)	0.003 S(1): 11.3; T(2): 11.3; S(11): 12	3	0.567	13
Low	sVEFmPFsLsFSLTISAVVWFLYGLLIK	S1(Phospho)	0.136 S(1): 99.7; S(8): 80.9; S(10): 3.	43	0.334	11
Low	SWQDIIDSLAsDLEVPDYNmGAAESQQI	S8(Phospho)	0.76 S(1): 11.2; S(8): 88.6; S(11): 89	24	0.763	12
Low	sWYVDANLHLWLDPKSVAtSGGLVAYD	S1(Phospho)	0.239 S(1): 49.6; Y(3): 49.6; S(16): 2.	43	0.232	16
Low	SWyVDANLHLWLDPKSVAtsGGLVAYC	Y3(Phospho)	0.201 S(1): 50.0; Y(3): 50.0; S(16): 5.	34	0.44	14
Low	TAAALAKPsKDSSLESAPVTR	S9(Phospho)	0.223 T(1): 76.0; S(9): 22.3; S(12): 1.	27	0.605	11
Low	TDsNISNVAGSMTPSASVLVFWTicPHci	S3(Phospho)	0.141 T(1): 8.9; S(3): 14.1; S(6): 14.1	6	0.541	11
Low	TGIAGAARWPHAILASSSSSSSSSSSSS	S23(Phospho)	0.046 T(1): 2.7; S(16): 4.6; S(17): 4.6	3	0.427	13
Low	tGLVLSSPAFAAmARPGMAASLTELAA\	T1(Phospho)	0.683 T(1): 70.3; S(6): 14.8; S(7): 14.	33		12
Low	tIGPNAIGAVIGHGECsSNVELSEQELQm\	T1(Phospho)	0.851 T(1): 85.1; S(17): 8.7; S(22): 3.	18	0.743	14
Low	TIGSGTNGNGISNPANTsIRsTTSSPTQI	S18(Phospho)	0.251 T(1): 0.0; S(4): 0.0; T(6): 0.0; S	46		11
Low	TIGSGTNGNGISNPANTsIRsTTSSPTQII	S21(Phospho)	0.145 T(1): 0.2; S(4): 0.2; T(6): 0.1; S	39		11
Low	tPFFtPLPIImDSGGGGGDHASHsAAAVf	T1(Phospho)	0.09 T(1): 59.1; T(5): 63.1; S(13): 56	1	0.361	18
Low	tPPPTPcSPTSPTADTAvtcASSPSSASf	T1(Phospho)	0.013 T(1): 2.0; T(5): 5.3; S(8): 15.1;	26	0.484	12
Low	TTmLNTALNSILPVSSsLRVLDLsciEtK	S17(Phospho)	0.598 T(1): 0.6; T(2): 0.6; T(6): 2.2; S	35	0.56	13

Low			ttQTALVGFFGGTIGDIIVGVRGWELtVEf T1(Phospho)	0.096 T(1): 62.7; T(2): 62.7; T(4): 62.7	1	0.773	12
Low			tWANWVDsNVDPAtTRVFFmSISTTHMF T1(Phospho)	0.068 T(1): 53.1; S(8): 39.0; T(14): 39.0	8	0.776	10
Low			VFFTNsGSEANDSQVKIVWYyNNALGR S6(Phospho)	0.232 T(4): 48.9; S(6): 48.9; S(8): 2.2	33	0.362	10
Low			VGPIVIAsAGLGmLAGVAmANR S8(Phospho)	1 S(8): 100.0	43	0.489	10
Low			VGSISKLDSETmHSIENyQSELLsDGVLI Y18(Phospho)	0.026 S(3): 13.8; S(5): 13.8; S(9): 18.0	4	0.57	17
Low			VLLAHLEPAASPAAPAITAsAcAAGD S22(Phospho)	0.097 S(11): 52.9; T(20): 28.0; S(22): 2.0	4		12
Low			VPGVGFVYsSTTNGVPPmFAHFVtNFP S9(Phospho)	0.005 Y(8): 70.9; S(9): 54.3; S(10): 2.0	2	0.198	10
Low			VttPEPLAATTPVLTEAAADSAAKTTTEA T2(Phospho)	0.922 T(2): 94.9; T(3): 94.9; T(10): 3.0	39	0.628	11
Low			VVDtAtPSSQPTSGQDANAGHPSPPSc T4(Phospho)	0.227 T(4): 70.9; T(6): 39.5; S(8): 39.5	27	0.658	16
Low			WGcNNGQAcIAPDYVITtKSFAPELVDSI T18(Phospho)	0.491 Y(14): 0.4; T(17): 1.1; T(18): 4.9	42	0.582	11
Low			WHVYSASSSASsSDADGAARLTAEVcn S12(Phospho)	0.047 Y(4): 15.1; S(5): 15.1; S(7): 15.1	26	0.748	13
Low			WLLtIlIPNYPmLNFMLTTAlyVAVsHR T4(Phospho)	0.072 T(4): 40.9; Y(9): 50.7; T(17): 4.9	3	0.781	13
Low			WmPIPPtQGNQIFVNLGDQVEVIsNGIY T7(Phospho)	0.745 T(7): 99.9; S(24): 74.6; Y(28): 2.0	35	0.385	11
Low			WmPIPPtQGNQIFVNLGDQVEVIsNGIY T7(Phospho)	0.948 T(7): 100.0; S(24): 5.2; Y(28): 9.0	55	0.14	11
Low			WQNDNSEIGKPLNAEVmELDLLsLDsV S23(Phospho)	0.134 S(6): 86.6; S(23): 68.4; S(26): 4.0	4		14
Low			WSLFLItTNVGGVGIlITK T7(Phospho)	0.614 S(2): 0.3; T(7): 78.4; T(8): 21.8	42	0.519	12
Low			yGFSmSDmPSLLKWcNVSVPmAALALL Y1(Phospho)	0.972 Y(1): 97.2; S(4): 1.7; S(6): 0.5;	51		12
Low			yGmDISLGVSDDGVLPMIQPTKPQKG Y1(Phospho)	0.108 Y(1): 11.2; S(6): 11.2; S(10): 7.0	21	0.513	11
Low			yTVTWYTLsAAVTFMAAK Y1(Phospho)	0.086 Y(1): 70.7; T(2): 24.2; T(4): 24.0	25		11
Low			YVKASTAHLGKPAAGGGQsDDmVDFD S19(Phospho)	0.181 Y(1): 18.2; S(5): 18.2; T(6): 18.0	15	0.774	11
Low			YYYAMGFDHTVRTFsFTTPPKPAPDAP S15(Phospho)	0.108 Y(1): 10.8; Y(2): 10.8; Y(3): 4.0	27		14

Os03t0718500-00	High	Homeodomain-related domain containing protein.	GGGDVGVLsPAMGGDGEDDEEVR S10(Phospho)	1 S(10): 100.0	112	0	29
Low			AAStSAATAMARHAVTMPVPTR S3(Phospho)	0.249 S(3): 55.3; T(4): 55.3; S(5): 55.0	27	0.357	10
Low			EDGTHtQGHNLsLtWPPPK T6(Phospho)	0.751 T(4): 24.9; T(6): 76.6; S(12): 9.9	26		12
Low			MRPMMSMATsAAAPLRMAPtR T20(Phospho)	0.07 S(6): 31.0; T(9): 31.0; S(10): 31.0	33	0.747	13
Low			MyNPPsAQEMTYKDHVQR Y2(Phospho)	1 Y(2): 100.0; S(6): 100.0; T(11): 1.0	51		11
Low			QTPPSAPQtASPLtPPGPISR T9(Phospho)	0.006 T(2): 76.9; S(5): 76.9; T(9): 15.0	10	0.526	12
Low			sSmSEASSLSVSFAISLGMSKR S1(Phospho)	0.428 S(1): 42.8; S(2): 42.8; S(4): 12.0	38	0.558	13

Os03t0726100-02	High	Similar to Alpha-tubulin.	TIQFVDWcPtGFK T10(Phospho)	1 T(1): 0.0; T(10): 100.0	128	0	48
Low			TRVVFVSmAYtTK T11(Phospho)	0.329 T(1): 0.0; S(7): 1.3; Y(10): 66.2	35		13

Os03t0733400-01	High	Zinc finger, BED-type predicted domain containing protein.	LALTPAVGtDNDGEGTVERPSK T9(Phospho)	0.955 T(4): 0.9; T(9): 95.5; T(16): 2.6	40	0	23
High			LMLNsDGELEEEQETHAER S5(Phospho)	1 S(5): 100.0; T(15): 0.0	62	0.006	20
Low			AtDGFsSTNLVGSgtFGFVYK T2(Phospho)	0.448 T(2): 78.7; S(6): 53.8; S(7): 26.0	19	0.602	12
Low			AWPGsGATNDANSSRGTTTHDK S5(Phospho)	0.497 S(5): 49.7; T(8): 10.7; S(13): 1.0	14	0.712	11
Low			FYAAAAYAGFGAGGAtSSSAIsR T16(Phospho)	0.012 Y(2): 71.2; Y(7): 71.2; T(16): 1.0	0	0.478	12
Low			GGWsVAGNtLVEAGVGRtDVK S4(Phospho)	1 S(4): 100.0; T(9): 100.0; T(18): 1.0	37	0.77	12
Low			KDEIPAsPADNQsILVSLSSR S7(Phospho)	1 S(7): 100.0; S(13): 0.0; S(17): 0.0	70		13

	Low		LEmLVLMENGLFGPIPDSLGDcKtLr	T24(Phospho	0.631 S(18): 36.9; T(24): 81.5; T(26):	28	0.265	11
	Low		LPFNPSTNHDNGTSNGTTNsR	S20(Phospho	0.915 S(6): 0.0; T(7): 0.0; T(13): 1.2;	55	0.165	11
	Low		LsQAAFGEAmLHTIGYIYAR	S2(Phospho)	0.175 S(2): 17.5; T(13): 47.5; Y(16): 1	18	0.099	11
	Low		MALATNSAAVSGGAAAAAsSAPQPR	S19(Phospho	0.473 T(5): 3.7; S(7): 0.4; S(11): 1.2;	40	0.132	15
	Low		MPNVQVADVSNLTAGITVyKK	Y19(Phospho	0.788 S(10): 0.0; T(13): 4.0; T(17): 17	53	0.792	12
	Low		mtlDLSmPGsSGLLDDVGGKK	T2(Phospho)	0.573 T(2): 78.3; S(6): 26.0; S(10): 74	34	0.784	10
	Low		SLRGGRPtTVALPLTQEPpMK	S8(Phospho)	0.433 S(1): 0.3; S(8): 43.3; T(9): 13.1	29	0.729	11
	Low		SsAsAmAAPLLLvvvvvvrTR	S2(Phospho)	0.333 S(1): 66.7; S(2): 66.7; S(4): 66.	39	0.707	11
	Low		ssRPRAAGcSVVAscPVVSK	S1(Phospho)	0.231 S(1): 99.1; S(2): 99.1; S(10): 74	24		11
	Low		VFDMMTKAGFRPDHAtFLSILsAcAHK	T16(Phospho	0.716 T(6): 2.6; T(16): 77.8; S(19): 26	30	0.447	11
	Low		VPRGSFACAPAPsGGVIVAGGGSr	S13(Phospho	0.984 S(5): 1.6; S(13): 98.4; S(23): 0.	49	0.683	17
	Low		VStssVFSEGLASAFGSPKSK	T3(Phospho)	0.063 S(2): 85.2; T(3): 60.9; S(4): 60.	24	0.649	12
	Low		yLVNTRPDLAYSVGyVsR	Y1(Phospho)	0.026 Y(1): 97.9; T(5): 85.1; Y(11): 52	22		10
	Low		YYDAVmPyLKAILMNATDK	Y8(Phospho)	0.167 Y(1): 0.3; Y(2): 0.3; Y(8): 16.7;	30	0.792	13
Os03t0743400-01	Low	Similar to H2A protein.	EATyKLSLK	Y4(Phospho)	0.72 T(3): 14.0; Y(4): 72.0; S(7): 14.	33		12
	Low		IPtPSAITPR	T3(Phospho)	0.813 T(3): 81.3; S(5): 18.1; T(8): 0.6	27	0.562	11
	Low		LKItsLGLK	T4(Phospho)	1 T(4): 100.0; S(5): 100.0	45		12
	Low		LKVtYLK	T4(Phospho)	0.991 T(4): 99.1; Y(5): 0.9	60		10
	Low		yLEASTKLK	Y1(Phospho)	0.438 Y(1): 43.8; S(5): 12.3; T(6): 43.	19		13
Os03t0756000-01	Low	Similar to 60S ribosomal protein L13a-						
	Low	4.	KSLVSEsVR	S7(Phospho)	0.5 S(2): 0.0; S(5): 50.0; S(7): 50.0	80	0.743	10
			MLLGGRGFNAsgR	S11(Phospho	1 S(11): 100.0	50		13
Os03t0758800-01	Low	Similar to Eukaryotic translation						
	Low	initiation factor 5A-2 (eIF-5A-2) (eIF-						
		4D).	EEVSStLINTR	T6(Phospho)	0.965 S(4): 0.6; S(5): 2.9; T(6): 96.5;	50	0.32	16
			mQtDIAGELVR	T3(Phospho)	1 T(3): 100.0	21		11
Os03t0787300-01	Low	Similar to DnaJ homolog.						
	Low		ANTGSTAGssAHGELGSVFSEQTLQSF	S9(Phospho)	0.075 T(3): 9.7; S(5): 9.7; T(6): 18.9;	13	0.209	14
	Low		cAmLSLsSAGGNDcGASVsSAIVGWILQ	S7(Phospho)	0.089 S(5): 33.5; S(7): 33.5; S(8): 33.	5	0.48	13
	Low		EtWPAEPNHGSAAAVVAStAAsGGGG	T2(Phospho)	0.224 T(2): 74.3; S(11): 49.8; S(19): 4	8	0.689	11
	Low		FAFAcAILAsmtSILLGYDIGVmSGAsLYII	S10(Phospho	0.073 S(10): 70.0; T(12): 42.1; S(13):	16	0.577	10
	Low		GDANIGGLQNHPYyHNvYGmLMAKsT\	S25(Phospho	0.167 Y(13): 16.7; Y(14): 16.7; Y(18):	2	0.803	10
	Low		GmQNGQKItFPGEADEAPDTVTGDIIFF	T9(Phospho)	0.028 T(9): 2.8; T(20): 83.8; T(22): 13	12	0.767	12
	Low		HGGGsGAGAGNsSGDSPLLLLPmLDDt	S5(Phospho)	0.133 S(5): 45.0; S(12): 45.0; S(13): 4	5	0.743	26
	Low		IsEYEDYHVGIpFGtFLTVGGFLNFmLTG	S2(Phospho)	0.15 S(2): 47.7; Y(4): 47.7; Y(7): 47.	15	0.291	15
	Low		KRPpSDGssPPHAVDDAAAAsIGSAGA	S8(Phospho)	0.496 S(5): 18.1; S(8): 77.7; S(9): 79.	23	0.55	15
	Low		LPLPLSLcNNstFLPNNsTPTSPISHSPG	S12(Phospho	0.035 S(7): 17.7; S(12): 41.8; T(13): 4	11	0.165	11
	Low		LsDPSSRLQVIGHPHpVVVTATEAASc	S2(Phospho)	0.035 S(2): 16.4; S(5): 16.4; S(6): 16.	34		11
	Low		MPFtPGPySGVStLALVARAsALGVGVV	T4(Phospho)	0.052 T(4): 62.5; Y(8): 62.5; S(9): 62.	9	0.477	10

	Low		mssSVVVSASGSGSGGGGGGGGA S2(Phospho):	0.233 S(2): 54.5; S(3): 54.5; S(4): 54.	19	0.519	15	
	Low		MTDIHTNENySNSAVSPVNVVPPSGAA Y10(Phospho):	0.475 T(2): 14.0; T(6): 14.0; Y(10): 47	24	0.589	16	
	Low		MTGALAMmPStssPYPLLAPPTcSSRLP T11(Phospho):	0.012 T(2): 36.0; S(10): 36.0; T(11): 3	0		11	
	Low		RIAAGLTNIIVPAPVSSSsALAsEFVsTyV S19(Phospho):	S23(Phospho) Too many isoforms		0.702	11	
	Low		sNSLESSTGAAAAPTTLTTSASTASVS S1(Phospho):	0.008 S(1): 10.6; S(3): 10.6; S(6): 10.	0	0.211	11	
	Low		sSNILLsQNLDGcVsEFLAQLmTIPPAP S1(Phospho):	0.127 S(1): 62.7; S(2): 62.7; S(7): 62.	2	0.567	11	
	Low		STVHHAAAAARHTSATANAAAAPAGTsP S26(Phospho):	S28(Phospho) Too many isoforms		0.753	15	
	Low		tAtNVGAAASATyKPRVEMASSAVSVtIK T1(Phospho):	0.007 T(1): 45.2; T(3): 45.2; S(10): 35	5	0.774	14	
	Low		VGVGHmVymsGLtcTLSSTNKLEVAWtE Y8(Phospho):	0.018 Y(8): 25.1; S(10): 35.0; T(13): 5	8		14	
	Low		VQsQFssILHLNEDDLLRIAHSDTLLsGK S3(Phospho):	0.329 S(3): 99.6; S(6): 99.5; S(7): 99.	26	0.569	14	
Os03t0793700-01	Low	RmIC-like jelly roll fold domain containing protein.	AARAYDLAALK	Y5(Phospho)	1 Y(5): 100.0	31	0.786	12
	Low		AFDLQIGSFtLRQIK	T6(Phospho)	0.848 T(6): 97.8; S(8): 15.2; T(10): 87	54		14
	Low		AGsDDPDAPAWLHGLKR	S3(Phospho)	1 S(3): 100.0	25		10
	Low		ALcATVsASLR	S7(Phospho)	0.998 T(5): 0.0; S(7): 99.8; S(9): 0.2	64	0.132	13
	Low		APRVVVSPAAAmGsR	S14(Phospho)	1 S(7): 0.0; S(14): 100.0	63		19
	Low		AVRITSLPHPPAHGHR	T4(Phospho)	0.156 T(4): 15.6; T(5): 15.6; S(6): 68.	27		10
	Low		cEPAVVHGDVKAsNVLLDEAMsAK	S13(Phospho)	1 S(13): 100.0; S(22): 100.0	17		10
	Low		cPALVVVVPRtsTLLPPsmHHK	T11(Phospho)	0.171 T(11): 35.8; S(12): 82.9; T(13):	32		11
	Low		cPALVVVVPRtsTLLPPsmHHK	T11(Phospho)	0.579 T(11): 82.0; S(12): 93.9; T(13):	28		11
	Low		DAGDTSAAAAPtPARLR	T14(Phospho)	1 T(5): 0.0; S(6): 0.0; T(14): 100.	62		13
	Low		DAVsiSMK	S4(Phospho)	0.5 S(4): 50.0; S(6): 50.0	40	0.708	13
	Low		DVTITAYsKMGVYALQAADILsK	Y7(Phospho)	0.075 T(3): 4.3; T(5): 51.8; Y(7): 51.8	21	0.598	10
	Low		EDNTPtyLINAK	T6(Phospho)	0.131 T(4): 86.9; T(6): 86.9; Y(7): 26.	29	0.659	11
	Low		ELtGSYPQNITVVsYDFK	T3(Phospho):	0.589 T(3): 87.8; S(5): 6.2; Y(6): 6.2;	44	0.714	13
	Low		ELVDEIKEIGQALLPSTGtK	T19(Phospho)	0.784 S(16): 4.2; T(17): 17.4; T(19): 7	49	0.759	17
	Low		EVmVGsKGVik	S6(Phospho)	1 S(6): 100.0	47		11
	Low		FLAAVsAAPDPDLTNFR	S6(Phospho)	0.982 S(6): 98.2; T(14): 1.8	32		11
	Low		FVPDKAFtGAPASVAAGK	T8(Phospho)	0.998 T(8): 99.8; S(13): 0.2	38	0.769	13
	Low		GDFsIRVINWGAVImSVVLPDSR	S4(Phospho)	0.2 S(4): 77.3; T(8): 33.1; S(16): 22	10		11
	Low		GFFLALSAAALYRLILsLVELAYK	S17(Phospho)	0.917 S(7): 7.8; Y(12): 0.3; S(17): 91.	43	0.391	12
	Low		GFmLISRHtAAPsLLYTVLLcR	T9(Phospho):	0.047 S(6): 72.6; T(9): 22.4; S(13): 28	6		10
	Low		GRPLDFAsTAK	S8(Phospho)	0.5 S(8): 50.0; T(9): 50.0	33	0.354	11
	Low		GSVAAsGKHVPsFLAAAR	S6(Phospho):	0.687 S(2): 31.3; S(6): 72.6; S(12): 96	16	0.767	11
	Low		GYVITSAtLNSAPR	T8(Phospho)	0.147 Y(2): 1.0; T(5): 14.7; S(6): 69.4	28	0.291	11
	Low		HPsQHTPNNGGGPGVMGSGPRGTFLR	S3(Phospho)	0.901 S(3): 90.1; T(6): 9.8; S(18): 0.0	37		16
	Low		IAActAHALEYLHEVcSPPVLHK	T5(Phospho)	0.905 T(5): 90.5; Y(11): 9.3; S(17): 0.	38	0.225	21
	Low		IAAsEAAARSAK	S4(Phospho)	0.995 S(4): 99.5; S(10): 0.5	26	0.762	11
	Low		IDPTGSANtKR	T9(Phospho)	0.993 T(4): 0.0; S(6): 0.6; T(9): 99.3	49		11
	Low		IFMQQLsHR	S7(Phospho)	1 S(7): 100.0	51		14
	Low		IGGtVAAsLLMRVPLR	T4(Phospho):	1 T(4): 100.0; S(8): 100.0	62	0.583	20
	Low		ImAsSHRVSR	S4(Phospho)	0.461 S(4): 46.1; S(5): 46.1; S(9): 7.8	34		11
	Low		INWASFsmGDRR	S7(Phospho)	0.952 S(5): 4.8; S(7): 95.2	40	0.804	11
	Low		IQLAQGALEDASGKLAsAMsLMVGAK	S17(Phospho)	0.973 S(12): 2.7; S(17): 97.9; S(20): 9	54	0.806	10

Low	ISHIATSGAHTAAItDSGELYTWGR	T15(Phospho	0.2 S(2): 0.0; T(6): 0.0; S(7): 0.0; T	48		14
Low	ISHIATSGAHTAAITDSGELYTWGR	T11(Phospho	0.855 S(2): 0.2; T(6): 0.1; S(7): 0.7; T	46		11
Low	ITPKSPGSDVAAEtAAAmAAASLVyK	T14(Phospho	0.028 T(2): 0.1; S(5): 0.1; S(8): 0.6; T	23	0.753	14
Low	IYRPtFAGFVDVDIAK	T5(Phospho)	0.222 Y(2): 77.8; T(5): 22.2	21	0.575	12
Low	KWLPQsYLK	S6(Phospho)	0.871 S(6): 87.1; Y(7): 12.9	45	0.725	10
Low	LAAAAVGEGGAtr	T12(Phospho	1 T(12): 100.0	20		12
Low	LDIAVGSAEGLAYmHsR	S16(Phospho	0.791 S(7): 7.2; Y(13): 13.7; S(16): 79	15	0.777	13
Low	LLFGGTGNLSgK	S10(Phospho	0.851 T(6): 14.9; S(10): 85.1	14	0.634	11
Low	LLLPQDAAASASASRAAtPAsFsTR	T18(Phospho	0.003 S(10): 84.3; S(12): 70.8; S(14):	2	0.792	15
Low	LNVGGNAlSPSKDtGGYR	T14(Phospho	0.073 S(9): 62.5; S(11): 26.5; T(14): 7	4		12
Low	LsLLAAtELRVLVAVtGPScTVGQ	S2(Phospho)	0.436 S(2): 100.0; T(7): 99.9; T(16): 4	38		10
Low	LSSTALRPLAQPATATAtAtAFSASR	T18(Phospho	0.005 S(2): 13.7; S(3): 13.7; T(4): 7.9	13	0.621	14
Low	LSVFNYNLVsQLsLK	S10(Phospho	1 S(2): 0.0; Y(6): 0.0; S(10): 100.	82	0.571	17
Low	LtGVPcKIFK	T2(Phospho)	1 T(2): 100.0	87		14
Low	LtSEQKSEIK	T2(Phospho)	0.997 T(2): 99.7; S(3): 0.3; S(7): 0.0	55	0.464	10
Low	mALHLILAALLGELQIGsRmGsLL	S18(Phospho	1 S(18): 100.0; S(22): 100.0	13	0.643	13
Low	MELGFMIRLsPR	S10(Phospho	1 S(10): 100.0	8	0.357	11
Low	NAIEVGvFTGySLLAtALALPDDGK	Y11(Phospho	0.252 T(9): 47.4; Y(11): 47.4; S(12): 4	7		10
Low	NAIEVGvFTGysLLAtALALPDDGK	Y11(Phospho	0.286 T(9): 30.5; Y(11): 63.2; S(12): 5	14		10
Low	NcALLPsLSAsLHTLK	S7(Phospho)	0.404 S(7): 86.9; S(9): 18.1; S(11): 4	51		14
Low	NVENLEKAtK	T9(Phospho)	1 T(9): 100.0	43	0.792	13
Low	PPPPAPPsVER	S8(Phospho)	1 S(8): 100.0	34		11
Low	QADLPsLLssYIVQVVIHYFDK	S9(Phospho)	0.022 S(6): 80.8; S(9): 46.8; S(10): 19	32		11
Low	QLDsAAVAGRR	S4(Phospho)	1 S(4): 100.0	33		11
Low	QLyHVtTKTITLGGAK	Y3(Phospho)	0.471 Y(3): 95.2; T(6): 51.6; T(7): 51.	27		11
Low	QPASLsLSmVSAQAPESVVNSLPcK	S6(Phospho)	0.493 S(4): 0.7; S(6): 49.3; S(8): 49.3	51	0.169	12
Low	QtIVVSGHHGK	T2(Phospho)	1 T(2): 100.0; S(6): 0.0	54	0.117	12
Low	RPLAAGEAAPcsVAAAWAGRR	S12(Phospho	1 S(12): 100.0	10		11
Low	RVVsLYTEIGVGQNAK	S4(Phospho)	0.923 S(4): 92.3; Y(6): 5.9; T(7): 1.8	32	0.792	13
Low	scPSGLLLPcSLVLDVsISFSKR	S1(Phospho)	0.418 S(1): 50.0; S(4): 50.0; S(11): 7.	37		12
Low	sDLEAPIAIRPTSETVMYPYFSK	S1(Phospho)	1 S(1): 100.0; T(12): 0.0; S(13): 0	62		13
Low	sDVENQSEFINFLAVEVKNAAYK	S1(Phospho)	1 S(1): 100.0; S(7): 0.0; Y(22): 0.	77		16
Low	sIDPNSRWVVTNAILYGNTsLSK	S1(Phospho)	0.417 S(1): 97.6; S(6): 2.3; T(11): 0.2	46		12
Low	SmYLSsLGVPPVNGFYPGAVQYPR	S6(Phospho)	0.935 S(1): 0.4; Y(3): 0.4; S(5): 5.5; S	59		13
Low	SmYLSsLGVPPVNGFYPGAVQYPR	S5(Phospho)	0.39 S(1): 11.0; Y(3): 11.0; S(5): 39.	49		11
Low	SQPTQQQRGFGFSGVGAAAAAAPsP	S25(Phospho	0.155 S(1): 52.2; T(4): 27.2; S(13): 5.	6		10
Low	sSADDRDPAAVVLGR	S1(Phospho)	0.845 S(1): 84.5; S(2): 15.5	43	0.803	10
Low	SSHLLALGGHPPsPsLR	S13(Phospho	0.984 S(1): 0.9; S(2): 0.9; S(13): 99.0	26	0.062	13
Low	tARGGATSAGSAR	T1(Phospho)	0.999 T(1): 99.9; T(7): 0.0; S(8): 0.0;	48	0.121	21
Low	tKGPTLASmLK	T1(Phospho)	0.997 T(1): 99.7; T(5): 0.3; S(8): 0.0	62	0.76	15
Low	tKLFPPANFK	T1(Phospho)	1 T(1): 100.0	45	0.396	10
Low	tLISRNSIMK	T1(Phospho)	1 T(1): 100.0; S(4): 0.0; S(7): 0.0	47	0.542	18
Low	TmLAKALANAAGAsFLNISMASMTSK	S14(Phospho	0.059 T(1): 91.9; S(14): 5.9; S(19): 0.	11	0.645	23
Low	tTAYVPQLQK	T1(Phospho)	0.479 T(1): 47.9; T(2): 47.9; Y(4): 4.2	80		15
Low	ttLGGLLALGySVVVSFKR	T1(Phospho)	0.787 T(1): 99.9; T(2): 99.9; Y(11): 78	38	0.782	13
Low	TtTAKVVsQmLGLQAIEVNASDSR	T2(Phospho)	0.441 T(1): 45.0; T(2): 45.0; T(3): 10.	54		13
Low	TtTAKVVSQmLGLQAIEVNAsDSR	T2(Phospho)	0.233 T(1): 47.6; T(2): 47.6; T(3): 5.0	31		12

	Low		tVTNVGQGSAARYSVAVVEPMGVSVK	T1(Phospho)	0.729	T(1): 93.2; T(3): 6.9; S(9): 78.0	48		10
	Low		TYGPVmlMKMGLTTTVISSGDAAR	T13(Phospho)	0.237	T(1): 6.6; Y(2): 11.8; T(13): 23.	11		13
	Low		tYVPQSR	T1(Phospho)	0.864	T(1): 86.4; Y(2): 13.4; S(6): 0.2	31	0.803	12
	Low		VEAsDLsAQQsRFLIPQAAAsLR	S4(Phospho)	0.025	S(4): 3.4; S(7): 97.5; S(11): 99.	26	0.233	15
	Low		VEINERImGssK	S10(Phospho)	1	S(10): 100.0; S(11): 100.0	44	0.806	12
	Low		VGLDVTVGtGsFAAR	S11(Phospho)	0.851	T(6): 7.5; T(9): 7.5; S(11): 85.1	29		15
	Low		VGyTFTtDALDALYKK	T7(Phospho)	0.435	Y(3): 16.4; T(4): 16.4; T(6): 16.	14		10
	Low		VLMAAGDtFRAAAR	T8(Phospho)	1	T(8): 100.0	35		11
	Low		VMQTILsLGNALNQGtARGsAVGFR	S7(Phospho)	0.204	T(4): 0.6; S(7): 20.6; T(16): 79.	41	0.474	13
	Low		VPSPpCAAArSGWAVPmVsVRPAR	S11(Phospho)	0.498	S(3): 50.2; S(11): 50.2; S(19): 5	26		11
	Low		VSEGPVRPsAATPsETLPLAWVDR	S9(Phospho)	0.057	S(2): 25.8; S(9): 25.8; T(12): 35	2		11
	Low		VTSPQASGsTAMALScRLDLGER	S10(Phospho)	0.672	T(2): 0.3; S(3): 0.3; S(8): 8.6; S	36	0.693	16
	Low		WDPDsSLDVRLPSGGGAAsASVAALR	S5(Phospho)	0.007	S(5): 6.9; S(6): 6.9; S(13): 10.9	14	0.563	11
	Low		WDPSSSLDVRLPSGGGAAsASVAALR	S19(Phospho)	0.93	S(5): 0.1; S(6): 0.1; S(13): 6.8;	47	0.492	21
	Low		YELIHtFLK	T6(Phospho)	1	Y(1): 0.0; T(6): 100.0	49	0.581	11
	Low		YGPLMQLRFGsFPVVVGSSAEmAR	S11(Phospho)	0.04	Y(1): 92.6; S(11): 4.0; S(18): 2.	8		13
Os03t0799000-01	High	Similar to Histone H1.	DVLPSPSsNQNNSSLPFVR	S8(Phospho)	0.434	S(5): 10.0; S(7): 43.4; S(8): 43.	47	0	18
	Low		AEELIGsGLPYtIVRPGGmERPtDAFK	S8(Phospho)	0.241	S(8): 77.3; Y(12): 75.9; T(13): 7	0	0.309	11
	Low		AFGLssLARGGTPLPPTSSR	S5(Phospho)	0.786	S(5): 88.6; S(6): 88.6; T(12): 15	26	0.479	13
	Low		AGAtAATPmDIDAAAPPPGAAAK	T4(Phospho)	0.944	T(4): 94.4; T(7): 5.6	56	0.284	17
	Low		ALSNTGMsEKLAGMYsSVK	S8(Phospho)	0.464	S(3): 2.4; T(5): 19.7; S(8): 64.8	36	0.803	14
	Low		ALVRHVfMmNsNDGSEHAVAALLAVcl	S11(Phospho)	0.352	S(11): 67.6; S(12): 67.6; S(16):	0	0.792	11
	Low		AMTNSAVARtsVAtFmmPPmDcLVGPAt	T10(Phospho)	0.434	T(3): 27.0; S(5): 45.8; T(10): 65	30		11
	Low		ANVVDGATAATTRASAEQyR	Y19(Phospho)	0.999	T(8): 0.0; T(11): 0.0; T(12): 0.1	47	0.66	10
	Low		DELRAEAAAAAsGsGSGSGSR	S13(Phospho)	0.31	S(13): 54.0; S(15): 54.0; S(17):	25	0.574	11
	Low		DGLIsAEELGtVLESLGLR	S5(Phospho)	0.969	S(5): 100.0; T(11): 96.9; S(15):	64	0.17	13
	Low		DLAYLQMKsIAsAVLLR	Y4(Phospho)	1	Y(4): 100.0; S(9): 100.0; S(12):	50	0.729	11
	Low		DLESKLQTAsmWLMNLR	S10(Phospho)	0.908	S(4): 0.6; T(8): 8.6; S(10): 90.8	30	0.778	10
	Low		EcGAsHASNLASAKDtSGSK	S5(Phospho)	0.328	S(5): 90.8; S(8): 15.0; S(12): 35	27	0.713	11
	Low		ERLtcGIPmSMGPTIFLL	T4(Phospho)	0.908	T(4): 90.8; S(10): 8.4; T(14): 0.	24	0.742	11
	Low		GLDVTLTGsGtNGAmPtTLSPtILNVIWR	S9(Phospho)	0.03	T(5): 75.7; T(7): 85.2; S(9): 18.	23	0.636	10
	Low		GMRLSVTLGtALIDmYsK	T10(Phospho)	0.495	S(5): 0.0; T(7): 0.2; T(10): 99.0	45	0.719	13
	Low		GMRLSVTLGtALIDmySK	T10(Phospho)	0.499	S(5): 0.0; T(7): 0.2; T(10): 99.8	57	0.803	13
	Low		GTPATVVVYDtFmPWVPR	T11(Phospho)	0.386	T(2): 38.6; T(5): 7.2; Y(9): 15.7	15	0.526	12
	Low		HLKDHQsmNLLALMNDR	S7(Phospho)	1	S(7): 100.0	9	0.304	17
	Low		HSVmYDLERLLVGmsNR	S15(Phospho)	0.333	S(2): 33.3; Y(5): 33.3; S(15): 35	0		10
	Low		LGIvtSLSVSWAPDVYDPPVTsGsHtVK	T5(Phospho)	0.098	T(5): 97.5; S(6): 14.1; S(8): 55.	39	0.638	14
	Low		LRsGDEGGGGWDAYGNGVMR	S3(Phospho)	1	S(3): 100.0; Y(14): 0.0	67	0.224	11
	Low		LSGAMDAAHtDIDSPFSPGEssQsHDTI	S21(Phospho)	0.012	S(2): 25.7; T(10): 41.9; S(14): 5	1	0.75	11
	Low		LSGGTDLtGVGLATAAAGNPK	T8(Phospho)	0.132	S(2): 23.4; T(5): 61.5; T(8): 70.	20	0.628	11
	Low		mAPtAPTAAKSASPSPsQPsGK	T4(Phospho)	0.049	T(4): 44.2; T(7): 44.2; S(11): 51	1	0.607	10
	Low		MLTLLSVAGNALsGEIPPsLSNcPLEQLK	S13(Phospho)	0.07	T(3): 25.7; S(6): 64.1; S(13): 75	12		11
	Low		NMSLVSPALmtWsRyVLPcstATLK	T11(Phospho)	0.079	S(3): 26.8; S(6): 66.5; T(11): 57	23		15
	Low		REsPAAYARPFLLtHSR	S3(Phospho)	0.123	S(3): 24.8; Y(7): 74.5; T(14): 50	19	0.74	12
	Low		RmDMQTtQDyPSSGANSR	Y10(Phospho)	0.155	T(6): 15.5; T(7): 15.5; Y(10): 15	0	0.504	10
	Low		sALAAAEQTVSTAGSAlmSNR	S1(Phospho)	0.106	S(1): 10.6; T(9): 22.8; S(11): 22	1	0.483	11

	Low		SFHDLSSSyEAHEHDGMSAAESsmKVY	Y9(Phospho)	0.129	S(1): 9.1; S(6): 9.1; S(7): 27.3;	34		12
	Low		SGKLMATSGVLTDDPSGVyR	Y19(Phospho)	0.979	S(1): 0.0; T(7): 0.0; S(8): 0.0; T	41	0.715	11
	Low		sLETAVyRtPtLIPPR	S1(Phospho)	0.499	S(1): 50.1; T(4): 50.1; Y(7): 99.	60	0.329	11
	Low		SSKDFAWyDIATFLAYR	Y8(Phospho)	0.126	S(1): 42.9; S(2): 42.9; Y(8): 12.	18	0.774	13
	Low		SVKTTWTPmNGGVTNQPyR	Y17(Phospho)	0.977	S(1): 0.0; T(4): 0.0; T(6): 0.0; T	37		10
	Low		TDIEHsVVVsDYAQmDR	S6(Phospho)	0.167	T(1): 66.0; S(6): 66.0; S(10): 42	5	0.584	10
	Low		VTAKssAAAAATVSSTDVLPV	S5(Phospho)	0.86	T(2): 10.1; S(5): 92.5; S(6): 92.	44	0.714	12
	Low		YDmASFPIQItsQsSPQADGASAGSQWf	T11(Phospho)	0.017	Y(1): 83.3; S(5): 74.8; T(11): 16	23	0.541	17
	Low		ylsLRDNclSGTIPPSLGNLSLLELR	Y1(Phospho)	0.163	Y(1): 71.7; S(3): 71.7; S(10): 38	17	0.731	11
Os03t0801600-02	Low	Similar to vacuolar protein sorting 35.	cNLsLSFALAmLFIsLLGRSILR	S4(Phospho)	0.339	S(4): 61.8; S(6): 38.2; S(15): 61	11	0.804	15
	Low		EtQADYLtTFQmATVRTASPLEK	T2(Phospho)	0.534	T(2): 89.4; Y(6): 20.0; T(8): 23.	28	0.743	11
	Low		EWLNVAFIDVGHASMQVSIVGyKK	Y22(Phospho)	0.742	S(14): 2.9; S(18): 22.8; Y(22): 1	28	0.792	10
	Low		FSmsVQGLLAPLGESSKPRVQSMAR	S4(Phospho)	0.11	S(2): 16.9; S(4): 11.0; S(15): 8.	3	0.572	12
	Low		GsIELANIEATSPISSSLRisIKPK	S2(Phospho)	0.062	S(2): 41.0; T(11): 29.5; S(12): 2	5	0.806	14
	Low		KNtASVLTSSMSVSScEADLAGLMR	T3(Phospho)	0.035	T(3): 56.2; S(5): 38.6; T(8): 17.	5	0.806	11
	Low		TAPAPMPLPPAQAPVWsPAPAPAATQF	S17(Phospho)	0.94	T(1): 1.1; S(17): 94.0; T(25): 4.	26	0.527	12
Os03t0807800-01	Low	Similar to 40S ribosomal protein S2 (Fragment).	DsVLGFSVNVPGTTAK	S2(Phospho)	0.002	S(2): 0.2; S(7): 99.8; T(13): 0.0	22	0.688	12
	Low		KPyLHESRRR	Y3(Phospho)	0.998	Y(3): 99.8; S(7): 0.2	37		10
	Low		KVLIFVNsIDsAFK	S8(Phospho)	1	S(8): 100.0; S(11): 100.0	63	0.761	15
	Low		LVARVsDIItR	S6(Phospho)	1	S(6): 100.0; T(10): 100.0	23		13
	Low		NGSIRSGsK	S8(Phospho)	0.862	S(3): 0.6; S(6): 13.3; S(8): 86.2	36		11
	Low		SSAPASSPsLLSPASGSR	S9(Phospho)	0.845	S(1): 0.3; S(2): 0.3; S(6): 4.2; S	42	0.708	11
	Low		VTDDGsQGIQGLMIR	S6(Phospho)	0.5	T(2): 50.0; S(6): 50.0	47	0.07	15
	Low		WLIIMNK	T3(Phospho)	1	T(3): 100.0	36		11
	Low		yIQNITIPSALIDK	Y1(Phospho)	0.488	Y(1): 48.8; T(6): 48.8; S(9): 2.3	42		13
Os03t0839100-01	Middle	Ubiquinone biosynthesis hydroxylase, UbiH/UbiF/VisC/COQ6 domain containing protein.	FLPsGPIALLPIGDNYsNIVWtMSPEESLI	S4(Phospho)	0.05	S(4): 51.5; Y(16): 51.5; S(17): 5	0	0.033	13
	Low		EYERAIDVVDGAVLSDNVtESFsALAAV	T19(Phospho)	0.349	Y(2): 4.4; S(15): 13.4; T(19): 52	15	0.657	18
	Low		LEILVNNAAVsGmEHAQRVDTNEEQFV	S11(Phospho)	0.891	S(11): 89.1; T(21): 10.9	23		13
Os04t0162533-00	Middle	Os04t0162533-00	GFFLALSAAALYRLILsLVELAYK	S17(Phospho)	0.789	S(7): 0.0; Y(12): 0.0; S(17): 78.	45	0.038	24
	Low		QTSEDNmETAVTVmKsTYNFYR	S16(Phospho)	0.145	T(2): 0.0; S(3): 0.0; T(9): 0.2; T	33	0.198	13
Os04t0349500-01	Low	Similar to 40S ribosomal protein S8.	ALSVPmVRsFNVSR	S9(Phospho)	0.493	S(3): 1.3; S(9): 49.3; S(13): 49.	26		11

Os04t0419600-01	Low	AmGlyRR	Y5(Phospho)	1 Y(5): 100.0	35	0.763	10
	Low	ItATGLLGLTNDsFR	T2(Phospho)	0.824 T(2): 82.4; T(4): 17.6; T(10): 0.1	49	0.089	17
	Low	ITNFtMR	T5(Phospho)	0.122 T(2): 87.8; T(5): 12.2	29	0.677	13
	Low	KFsVDMR	S3(Phospho)	1 S(3): 100.0	26	0.803	13
	Low	KtPPPPPLAAATAmAK	T2(Phospho)	0.5 T(2): 50.0; T(12): 50.0	7	0.806	11
	Low	LARssIR	S4(Phospho)	1 S(4): 100.0; S(5): 100.0	69		17
	Low	LAsRsLR	S3(Phospho)	1 S(3): 100.0; S(5): 100.0	69	0.713	17
	Low	LSAYSsVR	S6(Phospho)	0.94 S(2): 2.0; Y(4): 2.0; S(5): 2.0; S	39		12
	Low	LVsNYMR	S3(Phospho)	0.114 S(3): 11.4; Y(5): 88.6	26	0.778	13
	Low	mAsVTLQDGAFENLK	S3(Phospho)	0.5 S(3): 50.0; T(5): 50.0	50	0.718	11
	Low	RsAsLLR	S2(Phospho)	1 S(2): 100.0; S(4): 100.0	29	0.372	10
	Low	sRIsALR	S1(Phospho)	1 S(1): 100.0; S(4): 100.0	43		15
	Low	sRLsLAR	S1(Phospho)	1 S(1): 100.0; S(4): 100.0	28		15
	Low	TQsFIMR	S3(Phospho)	0.114 T(1): 88.6; S(3): 11.4	26	0.707	13
	Low	VWKyMR	Y4(Phospho)	1 Y(4): 100.0	36		11
	Low	WSRLtPVGEPPSPR	T5(Phospho)	0.959 S(2): 0.8; T(5): 95.9; S(12): 3.3	45		10
	Low	AEARAMVISGFAGLLAGAcsmAlGEFVs	S20(Phospho)	0.395 S(9): 60.5; S(20): 79.8; S(28): 1	4	0.805	10
	Low	AsVWcLsAsAsAAAPVAAAAAAPGPLGA	S2(Phospho)	0.975 S(2): 99.5; S(7): 99.1; S(9): 98.	36	0.669	11
	Low	AVTIPVmcASGLssVtAPmAVTAGAAGVC	S13(Phospho)	0.009 T(3): 61.8; S(10): 40.6; S(13): 5	2	0.386	11
	Low	cAVELGIPtItIHGLGGAAtVPDLmAALsLP	T9(Phospho)	1 T(9): 100.0; T(10): 100.0; T(19)	26		12
	Low	EASLLDPVVVEAAPDSLdGLmAEmDTn	S30(Phospho)	0.497 S(3): 0.0; S(16): 0.0; T(26): 0.6	41		11
	Low	FTGHPAGITTTLQRVGAGmAtccLHMVVA	T20(Phospho)	0.538 T(2): 1.5; T(9): 22.4; T(10): 22.	23	0.694	12
	Low	GDYStsDAVAMFGsLVVPHNLFLHsSLVI	T5(Phospho)	0.001 Y(3): 26.5; S(4): 26.5; T(5): 26.	1	0.333	11
	Low	GLAFVtMGsEEEEALsALNHLNsTTLNDR	T6(Phospho)	0.034 T(6): 93.7; S(9): 93.7; S(15): 2.	12		11
	Low	GLFGtATAPELsQtVsAPPKLGVEMGGA	T5(Phospho)	0.624 T(5): 78.2; T(7): 37.6; S(12): 96	25	0.759	10
	Low	GRWQscsPHKPVHGGWQEVEVAmAA	S5(Phospho)	0.95 S(5): 97.5; S(7): 97.5; T(26): 5.	16	0.752	15
	Low	GYcYPPREPIDYsLVGLyHytVLEITSK	S13(Phospho)	0.007 Y(2): 88.5; Y(4): 88.5; Y(12): 7.	19	0.368	11
	Low	LLQGIPQLsKALFQSQImLGmVtPQMMC	S9(Phospho)	0.311 S(9): 94.3; S(15): 68.9; T(23): 3	14	0.647	18
	Low	LLQGQQAQDtPAGMVLNQRPAERmVs	T10(Phospho)	0.091 T(10): 93.7; S(26): 11.1; S(27):	18	0.752	14
	Low	LTAEQVINGGDLANGEEQSVsKyAAVH	T7(Phospho)	0.484 T(2): 33.5; T(7): 67.2; S(19): 28	21	0.805	10
	Low	MAGLVIGYLAVQLSLmsLLLcPsSSTAQ	S17(Phospho)	0.625 Y(8): 0.3; S(14): 0.9; S(17): 92.	38		10
	Low	MAPAAEVsSSAETTGSAGSAPSTAA	S9(Phospho)	0.259 S(8): 25.9; S(9): 25.9; S(10): 1.	25	0.229	10
	Low	MEADGGELRLGPFGDTCALVsVLFscLG	S21(Phospho)	0.403 T(16): 59.7; S(21): 80.6; S(25):	13	0.605	12
	Low	mNSPFLKVntQGGGcPSSFLcEHdtFAL	T10(Phospho)	0.043 S(3): 26.6; T(10): 26.6; S(17): 3	0		10
	Low	mPPLLGVyDFtAGLPPsPPTGVSAYTAGI	Y8(Phospho)	0.02 Y(8): 68.3; T(11): 42.5; S(17): 3	11		11
	Low	MPQRStVtWNSmIFGLANSgHcQEAVG	T6(Phospho)	0.324 S(5): 22.4; T(6): 67.5; T(8): 53.	34	0.75	13
	Low	mSVSTsNVAHQAAVRPEWAWyAWAAssI	S6(Phospho)	0.145 S(2): 56.4; S(4): 14.5; T(5): 14.	56	0.115	10
	Low	NYFIGSVLsGGGsvPAAQASPAAWVsm	S9(Phospho)	0.002 Y(2): 29.4; S(6): 70.6; S(9): 70.	14	0.661	20
	Low	RGWLLLLLLAQSQPtISLLSHFFcScYFG	T15(Phospho)	0.745 S(12): 22.2; T(15): 74.5; S(17):	34	0.74	14
	Low	RYLDIMVsEGLEItQPALDPDLstDIHHR	S8(Phospho)	0.082 Y(2): 91.8; S(8): 22.5; T(14): 95	7	0.804	10
	Low	SDVYSyGVLLLLLVtGKPVAQGDDDG	Y6(Phospho)	0.062 S(1): 35.3; Y(4): 35.3; S(5): 15.	23		17
	Low	SSLSADPVAAAmHAGIPsAsMsVAGsAs	S20(Phospho)	0.521 S(1): 3.9; S(2): 3.9; S(4): 3.0; S	40	0.805	10
	Low	sYISGYQASKDDmTVFTSLPSAPAASyV	S1(Phospho)	Y27(Phospho) Too many isoforms		0.538	10
	Low	VAGGSWNPNVYGdGGGSASmPIASHC	S32(Phospho)	0.32 S(5): 0.5; Y(11): 0.5; S(17): 1.5	18		10
	Low	VAMFRySSVElyTtckPQTTLQFDNPcR	Y6(Phospho)	0.056 Y(6): 19.6; S(7): 48.6; S(8): 48.	26		12
	Low	VFVSAAsGsVGsLVGQFAKLAgcYVVGc	S7(Phospho)	0.133 S(4): 66.1; S(7): 66.1; S(9): 66.	17		15
	Low	VGNPQFIASmTVSPNASYsAGctNAPFV	S19(Phospho)	0.029 S(9): 18.5; T(11): 26.2; S(13): 2	3		11

	Low		VLHMTLVKQmEmmETLEAMQHHyQSS Y23(Phospho		0.146 T(5): 15.0; T(15): 18.3; Y(23): 3	7	0.792	12
	Low		VTELETEEEAPHPHESAVmsGAAAAAVA S19(Phospho		0.355 T(2): 4.7; T(6): 10.8; S(15): 10.	19	0.592	14
	Low		WFSPLEcGGGGGRLPGAPtMLYLPGIDt T19(Phospho		0.04 S(3): 95.5; T(19): 4.0; Y(22): 0.	10	0.796	14
Os04t0421900-01	High	Similar to H0525E10.11 protein.	LITDASVSsPVSR	S9(Phospho)	0.99 T(3): 0.0; S(6): 0.0; S(8): 0.1; S	108	0	35
	Low		LLDIISWENTk	T10(Phospho)	0.998 S(6): 0.2; T(10): 99.8	51		16
Os04t0446500-01	High	Similar to OSIGBa0140007.15 protein.	TPPAESLEsEDEDGFPVSFSISK	S9(Phospho)	0.964 T(1): 0.0; S(6): 3.5; S(9): 96.4;	77	0	47
	Low		KGANmAltGAtAmDANFFR	T8(Phospho)	1 T(8): 100.0; T(11): 100.0	10	0.758	13
	Low		TPNLLTGFPsFAKPSAsSLR	S17(Phospho)	0.433 T(1): 0.0; T(6): 0.0; S(10): 1.3;	38		12
Os04t0473400-01	Low	Similar to 60S ribosomal protein L6-B (L17) (YL16) (RP18).	ELGAGsARELK	S6(Phospho)	1 S(6): 100.0	37	0.779	14
	Low		sFLSAAIYKK	S1(Phospho)	0.998 S(1): 99.8; S(4): 0.2; Y(8): 0.0	39	0.576	11
	Low		sSQVDRPTLK	S1(Phospho)	0.852 S(1): 85.2; S(2): 14.8; T(8): 0.0	47	0.318	14
Os04t0486600-01	High	Similar to Glyceraldehyde-3-phosphate dehydrogenase, cytosolic 3 (EC 1.2.1.12).	AAsFNIIPSSTGAAK	S3(Phospho)	1 S(3): 100.0; S(9): 0.0; S(10): 0.	95	0	31
	Low		DQNPAASSSAPTTPPPATttdDSPAAs	T19(Phospho)	0.241 S(7): 3.0; S(8): 3.0; S(9): 4.6; T	24	0.792	12
	Low		FILETNtGGGGGRR	T7(Phospho)	0.841 T(5): 15.9; T(7): 84.1	51		12
	Low		LPVHHPPQAsGSAGGGGGGGGGGGG	S10(Phospho)	0.544 S(10): 83.3; S(12): 45.6; S(30):	11	0.374	11
	Low		MPsTAAAAAEMEPEPDHTKPSTSAAA	S3(Phospho)	0.763 S(3): 76.3; T(4): 23.6; T(19): 0.	39		13
	Low		NPEEIPWGETGAEFVVEsTGVFtDKDK	S18(Phospho)	0.324 T(10): 2.7; S(18): 66.3; T(19): 6	32	0.25	15
	Low		RTSLLmAsQVWK	S8(Phospho)	0.996 T(2): 0.2; S(3): 0.2; S(8): 99.6	38	0.802	12
	Low		StKSSLLRPHtK	T2(Phospho)	0.441 S(1): 44.1; T(2): 44.1; S(4): 5.9	62		11
	Low		TADSDGGEGDENVsPsLGsKRPAAs	S14(Phospho)	0.656 T(1): 26.6; S(4): 26.6; S(14): 79	29		11
Os04t0501600-01	High	AT hook, DNA-binding, conserved site domain containing protein.	ALRPTMsALIK	S7(Phospho)	0.981 T(5): 1.9; S(7): 98.1	58	0.002	15
	High		ELsPETDDGDnKLPPETGNR	S3(Phospho)	0.875 S(3): 87.5; T(6): 12.5; T(17): 0.	116	0	37
	High		QQEDTPPDEDtDEDLSLK	T11(Phospho)	0.975 T(5): 0.0; T(11): 97.5; S(16): 2.	80	0	26
	High		QQEDTPPDEDtDEDLSLKDIVSPK	T11(Phospho)	0.995 T(5): 0.3; T(11): 99.5; S(16): 0.	46	0	21
	High		TGAAADETPPVPLQsQETQDPNEPK	S16(Phospho)	0.827 T(1): 0.0; T(8): 0.0; S(16): 82.7	67	0.009	20
	Low		ALRPtMSALIK	T5(Phospho)	0.946 T(5): 94.6; S(7): 5.4	27	0.624	20

Low		AmEtGsVTIQVAGYSRtK	T4(Phospho)	0.866	T(4): 98.2; S(6): 94.0; T(8): 7.6	45		11
Low		ANPLSNGHGGmDtIAGLLAsLMEVVR	T13(Phospho)	0.97	S(5): 3.0; T(13): 97.3; S(20): 99.0	39		12
Low		AsAsAGPNDLAI TGsAMRPK	S2(Phospho)	0.671	S(2): 92.2; S(4): 96.9; T(13): 32.0	28		11
Low		EmFTSEYFQsIAVGSASTTIPLYR	S10(Phospho)	0.094	T(4): 4.9; S(5): 4.9; Y(7): 2.8; S(10): 99.9	9	0.372	13
Low		GDASEtAAAAALPPsPQGP GPPRRR	T6(Phospho)	0.3	S(4): 70.0; T(6): 70.0; T(7): 70.0	30		13
Low		GtyVsQLPsGITKLESLR	T2(Phospho)	0.962	T(2): 99.7; Y(3): 99.7; S(5): 99.0	34	0.214	12
Low		IWIsREEsmLDPGGNVVLMWNR	S4(Phospho)	1	S(4): 100.0; S(8): 100.0	46		11
Low		LAPSGSGTWsSLGTVAGAGPyVVSEQF	S10(Phospho)	0.099	S(4): 5.1; S(6): 9.2; T(8): 9.0; S(10): 99.9	18	0.411	15
Low		MAGstSGGGGALSAQAAAALGEGIGLVI	S4(Phospho)	0.146	S(4): 64.2; T(5): 35.8; S(6): 35.0	17		11
Low		RSstPSSSTPSGGGGGAASRPR	S3(Phospho)	0.08	S(2): 45.4; S(3): 45.4; T(4): 19.0	36		13
Low		RtPAsMPTsAPAGPGLFLPR	T2(Phospho)	0.482	T(2): 98.2; S(5): 98.2; T(8): 51.0	32		12
Low		RtPAsMPtSAPAGPGLFLPR	T2(Phospho)	0.779	T(2): 99.9; S(5): 99.2; T(8): 78.0	35		16
Low		ScSVLDIGTGSGRLsQQLAK	S15(Phospho)	0.669	S(1): 3.0; S(3): 1.4; T(9): 21.1; S(15): 99.9	23	0.802	11
Low		SPIlSTHPVsEFLtssGTSAGERK	S10(Phospho)	0.022	S(1): 81.1; S(5): 81.1; T(6): 79.0	30	0.729	14
Low		TTPPPPtPPsPPsPPASSRR	T7(Phospho)	0.566	T(1): 18.3; T(2): 18.3; T(7): 63.0	38		13
Low		VDSYDTESGDEVVLMDAAGAPAFtVR	T24(Phospho)	1	S(3): 0.0; Y(4): 0.0; T(6): 0.0; S(24): 99.9	58	0.734	17
Low		VIAEFmtPAMVIMLEEARK	T7(Phospho)	1	T(7): 100.0	16	0.803	13
Low		VyIGLVASPEQDSAWmFQK	Y2(Phospho)	0.791	Y(2): 79.1; S(8): 10.4; S(13): 10.4	16	0.335	14
Low		yGELVGAcYAALEEDPSSPR	Y1(Phospho)	0.792	Y(1): 79.2; Y(9): 11.1; S(17): 4.0	23		12

Os04t0543200-01	High	Nucleotide-binding, alpha-beta plait domain containing protein.	RQPsPPLQQPAAEEK	S4(Phospho)	1	S(4): 100.0	94	0	17
	Low		RTNAATASGDLaTAVR	T13(Phospho)	0.365	T(2): 2.1; T(6): 12.4; S(8): 36.5	19		17
	Low		tFDEAAA VINRALER	T1(Phospho)	1	T(1): 100.0	62		15
	Low		TWVGsMQELGLEVVK	S5(Phospho)	0.5	T(1): 50.0; S(5): 50.0	56		16
	Low		WKLETLEtGLSGEGR	T8(Phospho)	0.904	T(5): 2.5; T(8): 90.4; S(11): 7.1	26	0.712	13
Os04t0605900-01	Low	Similar to 60S ribosomal protein L7-2.	tEIIGLKGR	T1(Phospho)	1	T(1): 100.0	42	0.687	12
	Low		yPAHITLLR	Y1(Phospho)	1	Y(1): 100.0; T(6): 0.0	76	0.156	22
Os04t0635900-01	High	DNA repair exonuclease family protein.	SVTAQSNLNsFSDDDEDTR	S10(Phospho)	0.5	S(1): 0.0; T(3): 0.0; S(6): 0.0; S(10): 99.9	82	0	34
	Low		EtAAVAGGGGGGSLHsKTLLK	T2(Phospho)	0.222	T(2): 66.6; S(13): 33.4; S(16): 5.0	11	0.35	19
	Low		LtTsvSPHLSSGGVmDER	T3(Phospho)	0.502	T(2): 4.8; T(3): 50.2; T(4): 14.9	35	0.74	12
	Low		NIESNLSSNGstNPQTSR	S11(Phospho)	0.029	S(4): 3.4; S(7): 3.4; S(8): 4.8; S(11): 99.9	9		14
Os04t0671800-02	High	Similar to H0624F09.12 protein.	INESSLAsPER	S9(Phospho)	0.999	S(4): 0.0; S(5): 0.1; S(9): 99.9	74	0	33
	Low		AVLGLStAFSPPR	T7(Phospho)	0.333	S(6): 33.3; T(7): 33.3; S(10): 33.3	8	0.604	13
	Low		KNIASAYSLLR	Y7(Phospho)	0.827	S(5): 17.3; Y(7): 85.6; S(8): 97.0	40		16
	Low		NRSSPTsNLSPR	S7(Phospho)	0.434	S(3): 2.1; S(4): 9.0; T(6): 43.4;	38		11
	Low		VEQLDVVEsAAR	S9(Phospho)	1	S(9): 100.0	50		14

Os04t0679400-03	High Low Low	Similar to H0801D08.15 protein.	VDsEGVMcGATFK sIGADymSKLVK tcVNLPmFLLGK	S3(Phospho) S1(Phospho) T1(Phospho)	1 S(3): 100.0; T(11): 0.0 0.617 S(1): 80.9; Y(6): 80.9; S(8): 38. 1 T(1): 100.0	55 15 37	0 0.803 0.594	21 10 10
Os05t0113900-01	Low Low Low	Similar to Histone H2A.	LGVsLEK LKvtYLK WAsLIR	S4(Phospho) T4(Phospho) S3(Phospho)	1 S(4): 100.0 0.991 T(4): 99.1; Y(5): 0.9 1 S(3): 100.0	60 60 20	0.545 0.653	11 10 10
Os05t0160200-01	Low Low	Ubiquitin.	REVALlCtLsLPLsLGEQR SAMVDssMYDPDRYFLR	S9(Phospho) S6(Phospho)	1 S(9): 100.0; S(13): 100.0 0.691 S(1): 0.1; S(6): 84.1; S(7): 84.1	35 50	0.652 0.652	11 12
Os05t0169100-01	Low Low	Similar to 60S ribosomal protein L10 (QM protein homolog).	APPsAVQIEAAR tAFmLAAVLTR	S4(Phospho) T1(Phospho)	1 S(4): 100.0 0.885 T(1): 88.5; T(10): 11.5	41 16		13 12
Os05t0176000-01	Low Low	Similar to fibrillarin-2.	ADTRSSPFIsALELVsLDDSMYNTTDFDI AsEAAALAmRR EcPATVscADILALAARDGVAMLGPsVA ETSELPayDmPTGDLGLNHsGNPSNLN GFytYDAFIAAANSFPAGTSGGsAELIR KGSmNGGVSAIVDEIPYLTsFLsNPQyQ LDVRDnsDIYSNDDITSPVIEDDNtsTPK LScDTcGEPtTRDVcLVPGPDSCTNLPGI LiSEQKSEIK mELcVRAsSLLLGLLLQLLSSVDVVsAA mSNNsmAtstILLFLLAVGGLAAAHGDTIF MTQsFRGtPQGVNLsLINGsMVSGVETL NEVINGAVRGtVsGVIGcIFSGLLAAsGA PVNLLVTYRWEVNFSSVLtPGQGGSpyR tARGGATSAGSAR YLsMLPVDPK YVcmLsNGDVTVDPTGAGEVISGWDLGII	S10(Phospho) S2(Phospho) T5(Phospho) Y8(Phospho) Y3(Phospho) S20(Phospho) T25(Phospho) T10(Phospho) T2(Phospho) S8(Phospho) S5(Phospho) S4(Phospho) T11(Phospho) S16(Phospho) T1(Phospho) S3(Phospho) S6(Phospho)	0.139 T(3): 26.5; S(5): 26.5; S(6): 26. 1 S(2): 100.0 1 T(5): 100.0; S(7): 100.0; S(27): 0.026 T(2): 50.5; S(3): 50.5; Y(8): 62. 0.583 Y(3): 78.6; T(4): 78.6; Y(5): 38. 0.365 S(3): 5.3; S(9): 3.4; Y(17): 29.7 0.333 S(7): 0.0; Y(10): 0.0; S(11): 0.0 0.096 S(2): 3.7; T(5): 3.7; T(10): 9.6; 0.968 T(2): 96.8; S(3): 3.0; S(7): 0.2 0.06 S(8): 15.2; S(9): 15.2; S(20): 4 0.552 S(2): 41.4; S(5): 74.3; T(8): 92. 0.008 T(2): 51.4; S(4): 51.4; T(8): 51. 0.061 T(11): 76.1; S(13): 73.8; S(21): 0.332 T(7): 0.0; Y(8): 0.4; S(15): 66.5 0.983 T(1): 98.3; T(7): 0.7; S(8): 0.7; 0.5 Y(1): 50.0; S(3): 50.0 0.53 Y(1): 21.8; S(6): 53.0; T(10): 21	12 11 51 12 35 28 44 5 48 14 23 8 1 62 29 46 19	0.726 0.806 0.599 0.794 0.588 0.743 0.787 0.806 0.713 0.629 0.763 0.752 0.743	12 13 18 12 10 11 10 15 11 12 19 12 11 11 14 11
Os05t0295100-01	High Low	Hypothetical conserved gene.	ELDGVGLAEESPPPGSSLGK DHSAAAMANKPslAVAAASR	S11(Phospho) S12(Phospho)	0.999 S(11): 99.9; S(16): 0.1; S(17): 0 0.986 S(3): 0.7; S(12): 98.6; S(19): 0.	82 40	0	51 11
Os05t0302700-01	Low Low Low Low Low	Similar to ATP/ADP carrier protein.	APsIAVAEAtAAARAPVDLVTVLDSGSr AsPATsSAVLVVVLVATLAAGGANAATF cGVLLmSLFVFFTTTMsVsFTLRETQSR DIGNLVNLQYLSLANNSLTGsLPsSFSKL EDTHLTITGARGtPGYAAPELWmPLPVt	S3(Phospho) S2(Phospho) S17(Phospho) T19(Phospho) T13(Phospho)	0.9 S(3): 98.0; T(10): 90.7; T(21): 5 0.159 S(2): 93.4; T(5): 63.9; S(6): 63. 0.014 S(7): 62.4; T(13): 31.2; T(14): 1 0.078 Y(10): 0.1; S(12): 0.2; S(17): 1 0.309 T(3): 12.8; T(6): 12.8; T(8): 31.	30 31 1 48 24	0.187 0.8	11 11 16 10 11

Low	FDSELLTAFTSSyLiAGLLtTFLASSVTAR S12(Phospho	0.004 S(3): 10.8; T(7): 76.5; T(10): 49	23	0.249	15
Low	GGGGEAFTMTSNIAGtRGYTAPEYLEHt T16(Phospho	0.413 T(8): 7.6; T(10): 17.1; S(11): 7.	25	0.173	16
Low	GPSIWDTFTHNHPEKIANGsNGDIAIDsy S20(Phospho	0.045 S(3): 39.8; T(7): 39.8; T(9): 51.	3		11
Low	GVSTVmVSySSWNGVKMHANHHLLtDF Y9(Phospho)	0.248 S(3): 0.3; T(4): 0.3; S(8): 24.9;	38	0.56	12
Low	HIVQmcmNVILVsIELGQFPVSVNyVSK S13(Phospho	0.872 S(13): 91.2; S(23): 9.8; Y(25): 9	35	0.188	17
Low	HVLLmDPVLGtGNsANQAIELLISSGVPE T11(Phospho	0.993 T(11): 99.8; S(14): 99.4; S(24):	33		11
Low	IVGMyWDDmNGTNIISAEFTSsmRTmM Y5(Phospho)	0.025 Y(5): 6.4; T(12): 60.9; S(16): 26	11		11
Low	LLGEGLGScSVQELQELEVQLEKsLcsIF S24(Phospho	0.963 S(8): 2.0; S(10): 2.0; S(24): 97.	27	0.617	19
Low	LPTGKPLDGS�KSSGNtsAsVVSQSNgc T17(Phospho	0.004 T(3): 7.2; S(10): 4.5; S(13): 12.	9	0.406	12
Low	LVEsATTSTSGRSVASAAAVGDALVSEI S4(Phospho)	0.017 S(4): 1.7; T(6): 1.7; T(7): 1.7; S	0		11
Low	mDTISGMFRPVFDRIRPSIAsAAELsFSF S21(Phospho	0.631 T(3): 7.0; S(5): 2.6; S(18): 21.2	38	0.741	12
Low	mEASTLstyLPLAmVLVQLGLAGLNVm: S7(Phospho)	0.229 S(4): 45.9; T(5): 45.9; S(7): 45.	39	0.465	14
Low	MIGRFSQFLSLDAGGEsLLFmGSEFENI S17(Phospho	0.081 S(6): 0.9; S(10): 1.6; S(17): 8.1	11	0.792	11
Low	MQESQAmQEKmLEESTEmDEGLLMsE S25(Phospho	0.25 S(4): 25.0; S(15): 25.0; T(16): 2	2		11
Low	mQESTQtLGIGSVLIVTVTFGAmFALPGt T7(Phospho)	0.092 S(4): 41.2; T(5): 25.2; T(7): 25.	10		13
Low	mTELLSLSAsSLDDEILDGSLNPAPQcL S10(Phospho	0.578 T(2): 2.7; S(6): 1.2; S(8): 19.2;	34	0.11	12
Low	NISSGGLSVPSIAsRmNLsGNVGSGLL S14(Phospho	0.056 S(3): 34.6; S(4): 34.6; S(8): 34.	12		10
Low	NLmAVLATNEDQLsASsAATSKAQDAAI S14(Phospho	0.151 T(8): 2.3; S(14): 34.2; S(16): 58	20	0.789	16
Low	NSVtWsAMIGGyGmQGDSAGSIDLFNEI T4(Phospho)	0.057 S(2): 53.7; T(4): 53.7; S(6): 86.	13	0.713	14
Low	RFSHVcTAPVDSDDsSIVTGAHLEVVS H15(Phospho	0.373 S(3): 1.6; T(7): 14.9; S(12): 14.	23	0.789	11
Low	sTmmAASMLLFLVLVLAGIVTATTTTDDs S1(Phospho)	0.008 S(1): 44.9; T(2): 44.9; S(7): 45.	0	0.713	10
Low	SVIFVsFGsGGALPTEHmRELALGLELS S6(Phospho)	0.629 S(1): 34.1; S(6): 81.2; S(9): 81.	46	0.723	15
Low	sYMTQGLVNGGINVPMMSSSPIFANAP. S1(Phospho)	0.471 S(1): 47.1; Y(2): 47.1; T(4): 5.5	29	0.644	17
Low	symtQGLVNGGINVPMMSSsPIFANAPA S1(Phospho)	0.674 S(1): 99.7; Y(2): 99.7; T(4): 99.	50	0.622	21
Low	tmRLAAAVVVMVVVAAAAMSVEAELSV T1(Phospho)	0.091 T(1): 99.8; S(20): 9.2; S(26): 72	25	0.735	14
Low	tsSSLLSGGQQGmGSGGGMPLPSQSPFt T1(Phospho)	0.023 T(1): 43.6; S(2): 43.6; S(3): 43.	14		10
Low	TTQSyLEQTAGPWITSRLSGPPELDITC Y5(Phospho)	0.325 T(1): 4.2; T(2): 4.2; S(4): 23.8;	33	0.744	13
Low	VAAAAAAAtAKDK T9(Phospho)	1 T(9): 100.0	26		11
Low	VDWKAIAIsR S9(Phospho)	1 S(9): 100.0	59	0.755	16
Low	VLHLSDTDDSDAdmDLNTSTsMELsTAGI S20(Phospho	0.02 S(5): 15.9; T(7): 12.7; S(10): 11	7	0.737	13
Low	VYAMSKsPSWIADPDFPPWFELLDLSQ S7(Phospho)	0.383 Y(2): 6.3; S(5): 15.0; S(7): 38.3	25		11
Low	WGcNNGQAcIAPDYVITtKSFAPELVDSI T18(Phospho	0.699 Y(14): 0.2; T(17): 14.9; T(18): 6	61		13
Low	YNYtPDTVGKTGVQVHTDSGFLTVLQEI T4(Phospho)	0.311 Y(1): 31.1; Y(3): 31.1; T(4): 31.	32	0.053	13
Low	YsmVITPKNWNLFsVNVAMAGTGlyQL: S2(Phospho)	0.085 Y(1): 49.3; S(2): 49.3; T(6): 1.8	20	0.54	11

Os05t0350500-01	High	Peptidase M24, structural domain domain containing protein.	VTSHSLQELQPtKSIEDNAEIK T12(Phospho	0.954 T(2): 0.0; S(3): 0.0; S(5): 0.1; T	73	0.001	28
	Middle		EVLDQMPSPK S8(Phospho)	1 S(8): 100.0	56	0.011	16
	Low		DLLVAGVVDA sR S11(Phospho	1 S(11): 100.0	62	0.308	11
	Low		EIVPSsPGGWPGIEPALVQTLPLlTR S6(Phospho)	0.434 S(5): 50.0; S(6): 50.0; T(20): 12	26	0.741	16
	Low		ELLDNSsYEVKLSVVscISEITR S7(Phospho)	0.025 S(6): 40.3; S(7): 40.3; Y(8): 11.	28	0.749	11
	Low		mAASLQEFAGGAFIEQGELtKYGNVK T20(Phospho	0.333 S(4): 33.3; T(20): 33.3; Y(22): 3	7		14
	Low		mFHGSPAAVAASAAVAEMRFtTGGSS T21(Phospho	0.501 S(5): 2.0; S(12): 8.2; T(21): 50.	22	0.659	15

	Low		RLFLSTSGGSSsVGLsTGLQRPSCLK	S12(Phospho)	0.089 S(5): 6.9; T(6): 6.9; S(7): 6.9; S	26		11
Os05t0367100-01	High	Ribosome biogenesis protein Nop16 domain containing protein.	APVDEFEPVDSGsDLESDDLK	S13(Phospho)	0.98 S(11): 2.0; S(13): 98.0; S(17): 0	108	0	56
	Middle		LHtPGATAHGADGDATPTeR	T3(Phospho)	0.804 T(3): 98.6; T(7): 1.4; T(17): 1.1	53	0.04	18
	Low		DPAsAAySMASMLVLVLFRR	S4(Phospho)	0.483 S(4): 96.6; Y(7): 51.7; S(8): 51.	40		11
	Low		EAEDVAAAsFGADITVLAVsPR	S9(Phospho)	0.998 S(9): 100.0; T(15): 0.2; S(20): 0	75	0.205	19
	Low		ENIVTASTLQssAsLTcQVT	S11(Phospho)	0.006 T(5): 3.5; S(7): 3.5; T(8): 2.5; S	12	0.439	11
	Low		GyEDEEDGKcAIPTDSDIEK	Y2(Phospho)	0.999 Y(2): 99.9; T(14): 0.0; S(16): 0.	44	0.773	12
	Low		HLASAEEmssVTAISLSLQAK	S9(Phospho)	0.007 S(4): 0.8; S(9): 2.4; S(10): 2.1;	10	0.682	10
	Low		RDSGNSSGGGGGSySPHSLPGtR	Y14(Phospho)	0.236 S(3): 0.7; S(6): 4.7; S(7): 10.5;	29	0.477	15
	Low		tsAATDLAGAGcFLtEPSGKR	T1(Phospho)	0.401 T(1): 79.5; S(2): 79.5; T(5): 45.	22	0.432	19
Os05t0445500-01	High	Similar to Acidic ribosomal protein (Fragment).	EEsDDDMGFSLFD	S3(Phospho)	1 S(3): 100.0; S(10): 0.0	65	0	25
	High		VEEKESDDDMGFSLFD	S7(Phospho)	1 S(7): 100.0; S(14): 0.0	197	0	77
	Middle		LsSPELQPSGGISFPSSVAAHRPK	S2(Phospho)	0.48 S(2): 48.0; S(3): 48.0; S(9): 3.7	36	0.046	14
	Low		EDSPHQNGSASPFSNGstK	S17(Phospho)	0.755 S(3): 0.2; S(9): 2.1; S(11): 2.1;	41	0.673	11
	Low		EYFQKDsEVSvVEmADK	S7(Phospho)	0.976 Y(2): 2.4; S(7): 97.6; S(10): 0.0	63	0.729	12
	Low		GsISmMNNLLIGFADGGVRVVVVR	S2(Phospho)	0.5 S(2): 50.0; S(4): 50.0	33	0.754	12
	Low		GVLHRAVVGGEQsR	S13(Phospho)	1 S(13): 100.0	58		14
	Low		HsLPSAHScPGRPRSSPARPPLR	S2(Phospho)	0.251 S(2): 25.1; S(5): 12.3; S(8): 12.	8		10
	Low		IsEGAVKPAAATPEETLPLAWVDR	S2(Phospho)	0.03 S(2): 3.0; T(12): 85.3; T(16): 11	3	0.731	11
	Low		MGVLRAAVPLQPEADLVLaTGGER	T20(Phospho)	1 T(20): 100.0	18	0.62	10
Os05t0459900-01	Low	Similar to 60S ribosomal protein L36-1.	AAAsAISAAVK	S4(Phospho)	0.843 S(4): 84.3; S(7): 15.7	11		14
	Low		LEKtSQTVK	T4(Phospho)	0.493 T(4): 49.3; S(5): 49.3; T(7): 1.5	35	0.707	11
Os05t0499100-01	Low	26 kDa globulin (Alpha-globulin).	AAAAsTSRWSAVSPR	S5(Phospho)	0.888 S(5): 88.8; T(6): 7.9; S(7): 2.8;	30	0.632	11
	Low		ASLSGGsVGAGAGGGR	S7(Phospho)	0.909 S(2): 4.6; S(4): 4.6; S(7): 90.9	44	0.762	15
	Low		HPtAIHRcLR	T3(Phospho)	1 T(3): 100.0	57	0.223	15
	Low		IFRsSsVLQK	S4(Phospho)	0.843 S(4): 97.5; S(5): 15.7; S(6): 86.	36		12
	Low		KSAsPPSPPPPPQEAk	S4(Phospho)	0.455 S(2): 8.9; S(4): 45.5; S(7): 45.5	34	0.415	11
	Low		LDcHsGRSYHLK	S5(Phospho)	0.952 S(5): 95.2; S(8): 2.4; Y(9): 2.4	54		12
	Low		LSRNSGWsFR	S8(Phospho)	0.954 S(2): 0.4; S(5): 4.2; S(8): 95.4	33		12
	Low		READEsILLSK	S6(Phospho)	0.5 S(6): 50.0; S(10): 50.0	28	0.745	10
	Low		sAQATVGRGASLDER	S1(Phospho)	0.997 S(1): 99.7; T(5): 0.2; S(11): 0.1	34		11
	Low		SFGARVstIVK	S7(Phospho)	1 S(1): 0.0; S(7): 100.0; T(8): 100	45		11
	Low		TAPPPAIVITAsRR	T7(Phospho)	0.902 T(1): 6.2; T(7): 92.1; T(10): 3.9	31	0.77	11

	Low		VEEtTDVAKLR	T4(Phospho)	0.5	T(4): 50.0; T(5): 50.0	35		11
	Low		yPNtKLAESLK	Y1(Phospho)	0.458	Y(1): 54.2; T(4): 91.6; S(9): 54.	35		11
	Low		yVEMmKAENVSR	Y1(Phospho)	1	Y(1): 100.0; S(11): 0.0	98		23
Os05t0520100-00	High	Similar to MPPN domain containing protein.	AAAVDFSPDAAASELLLPVASSPsPR	S24(Phospho)	0.723	S(7): 0.1; S(13): 0.1; S(21): 6.6	37	0.002	32
	Low		FNKAGPQtPISNAGSPGNPSTPASSR	T8(Phospho)	0.77	T(8): 77.0; S(11): 7.7; S(15): 4.	20	0.746	15
	Low		GtAllyRLVHAIAGcSFLHVAFR	T2(Phospho)	0.988	T(2): 99.8; Y(5): 99.0; S(15): 1.	42		10
	Low		tPVAVNEEDtESGLLLGFLSQLK	T1(Phospho)	0.728	T(1): 99.2; T(10): 73.4; S(12): 2	26		12
	Low		VAEGSsAKsLELVTNVAISEVEVK	S6(Phospho)	0.067	S(5): 93.2; S(6): 97.8; S(9): 8.9	33		10
Os05t0524400-01	High	Phosphofructokinase family protein.	NAsSVSLADAAYVK	S3(Phospho)	0.882	S(3): 88.2; S(4): 11.5; S(6): 0.3	73	0	61
	Low		IsRDSYPNLR	S2(Phospho)	0.057	S(2): 5.7; S(5): 47.2; Y(6): 47.2	52	0.35	10
	Low		ISRDSyPNLR	Y6(Phospho)	0.495	S(2): 1.0; S(5): 49.5; Y(6): 49.5	57		12
	Low		LLDTLSRtLPIR	T8(Phospho)	0.333	T(4): 33.3; S(6): 33.3; T(8): 33.	17	0.653	11
	Low		TctGLGLQSRK	T3(Phospho)	0.852	T(1): 14.8; T(3): 85.2; S(9): 0.0	44	0.736	13
	Low		VSVNsSMLDLR	S5(Phospho)	0.484	S(2): 3.2; S(5): 48.4; S(6): 48.4	26		11
	Low		VTISVcDLsAR	S9(Phospho)	0.926	T(2): 1.9; S(4): 5.6; S(9): 92.6	24		11
Os05t0540800-01	High	Homeodomain-like containing protein.	FIDAPPsPPQSK	S7(Phospho)	0.979	S(7): 97.9; S(11): 2.1	65	0	32
	Low		RAPSSsPSSRRPR	S5(Phospho)	0.109	S(4): 37.1; S(5): 10.9; S(6): 4.0	11	0.5	11
	Low		VAVsAAVAAARAVK	S4(Phospho)	1	S(4): 100.0	30	0.804	10
Os05t0576700-01	High	Oleosin family protein.	LGYAPAASADsPSTTLR	S11(Phospho)	0.895	Y(3): 0.0; S(8): 9.4; S(11): 89.5	138	0	39
	Low		FTRIILTHASASAscR	S14(Phospho)	0.982	T(2): 0.1; T(7): 0.7; S(10): 0.3;	35		10
	Low		RsPSPSPSPSPAPAAASAR	S2(Phospho)	0.855	S(2): 85.5; S(4): 7.1; S(6): 2.4;	32		13
	Low		tLSSLDEFVLVSVGAVKK	T1(Phospho)	0.778	T(1): 77.8; S(3): 20.2; S(4): 1.8	41		11
Os05t0592600-03	High	Hypothetical conserved gene.	LLAEIDDtSPPTEEAEPVEEVPA PDADD.	T8(Phospho)	0.447	T(8): 44.7; S(9): 44.7; T(12): 10	76	0	49
	Low		AAsttGLLLILLLLVAFTVcNYsSLKLstR	S3(Phospho)	0.011	S(3): 65.0; T(4): 65.0; T(5): 65.	0	0.277	11
	Low		AGmAKGLGIGctYGIACmsWALVFWYAC	T12(Phospho)	0.303	T(12): 63.6; Y(13): 63.6; S(19):	12	0.765	12
	Low		AKEsPmPDPSelfFTNVyVNDcGLEsFG\	S4(Phospho)	0.42	S(4): 52.2; S(10): 5.3; T(14): 50	31	0.804	10
	Low		AmPSGGLSMDGPPTTLsGtGIDRmAFLL	T19(Phospho)	0.213	S(4): 10.1; S(8): 29.9; T(14): 11	15		18
	Low		AQAGNtcAVSFDWkcSGlcDSVENmQW	T6(Phospho)	0.273	T(6): 27.3; S(10): 27.3; S(16): 1	2	0.805	12
	Low		AQFPsPNEYSSFMGDFSTATGIATFTMI	S5(Phospho)	0.218	S(5): 21.8; Y(9): 11.8; S(10): 1.	5		11
	Low		AQssDLIsVSSKHlIAETPHVDNIVcPELF	S3(Phospho)	0.09	S(3): 66.2; S(4): 51.6; S(8): 51.	5		11
	Low		ASmDSSEGIIVNsFVELEPLcFDGWSRn	S13(Phospho)	0.19	S(2): 19.0; S(5): 19.0; S(6): 19.	2		11
	Low		ASSSSTSNSAISsVVAAsAVATTTPGAGS	S13(Phospho)	0.005	S(2): 4.4; S(3): 4.4; S(4): 14.7;	8	0.459	11
	Low		AVSsPVKPiNAADtTSPNDKNVLVEQGY	S4(Phospho)	0.029	S(3): 40.7; S(4): 40.7; T(9): 40.	6	0.792	12
	Low		DEADYSVLSHINsVtssVAKISIDATPDLA	S13(Phospho)	0.012	Y(5): 41.2; S(6): 41.2; S(9): 43.	2	0.803	12
	Low		EAtEVFREmVatGcEPNmHtYIMLLQGHl	T3(Phospho)	0.469	T(3): 98.9; T(12): 94.9; T(20): 5	16		11
	Low		EDAVMFMSVLQAQNGQATEDmGcsNIF	S24(Phospho)	0.096	S(8): 47.5; T(18): 37.5; S(24): 3	1	0.792	14

Low	EEVPVDSATQHLLLEENNHLNQAIE T26(Phospho)	0.387 S(8): 7.7; T(10): 14.9; T(26): 38	8		12
Low	ELTFEDLGDDLAPEGSLMAAQSPNLcTL S16(Phospho)	0.256 T(3): 23.1; S(16): 25.6; S(22): 2	0	0.233	12
Low	EVmSSWDtAGNGTNmPAPVlcQWTGV: T8(Phospho)	0.202 S(4): 14.9; S(5): 14.9; T(8): 20.	3	0.645	11
Low	FVQETImDQVAsMFLWPKtLEVPIMDPS S12(Phospho)	0.244 T(5): 42.8; S(12): 54.0; T(19): 5	3		11
Low	GASEDFIVYGQEKPMDSGSyLDPLAEG: S19(Phospho)	0.051 S(3): 66.9; Y(9): 24.9; S(17): 50	24		11
Low	GEVSALGAAELVAAAYssPsFGVGYLGsN S16(Phospho)	0.007 S(4): 4.8; Y(15): 93.0; S(16): 90	17		11
Low	HGGVTGFRmVVEAQVIMEAVAtAVGAA T22(Phospho)	0.24 T(5): 76.0; T(22): 76.0; S(31): 7	0	0.526	18
Low	HSSSASSAASyGSDVsFmNHsPAAALP: Y11(Phospho)	S16(Phospho) Too many isoforms		0.065	12
Low	IELcTVLLSNcFHElcGstYAHVNFtAR S18(Phospho)	0.177 T(5): 9.5; S(9): 7.8; S(18): 37.1	30	0.274	13
Low	IIGSQPPmVGTDAsQSSAHAGLWNFPS S14(Phospho)	0.17 S(4): 17.0; T(11): 17.0; S(14): 1	4	0.088	21
Low	KPVDmsRPGGQENLVsWARPLLtNVVsl S6(Phospho):	1 S(6): 100.0; S(16): 100.0; T(23)	4	0.759	12
Low	KRPPSDGssPPHAVDDAAAAsIGSAGA: S8(Phospho):	0.042 S(5): 51.3; S(8): 56.1; S(9): 56.	8	0.56	13
Low	LIDVPMsNcINsGINKVYILtQFNSASLNR S12(Phospho)	0.3 S(7): 16.0; S(12): 69.5; Y(18): 2	19		17
Low	LLsPIPSMSPIPSIAsDIVFARssRPAAAQ S3(Phospho):	0.025 S(3): 58.4; S(7): 58.4; S(9): 53.	1	0.109	12
Low	LLTVDKFTmVVAGsmGYIDPVFYmTG S15(Phospho)	0.143 T(3): 14.3; T(9): 14.3; S(15): 14	0	0.116	10
Low	LPAsSSTLVTMESTEAFGLEAADVKyVt S4(Phospho)	0.039 S(4): 30.2; S(5): 30.2; S(6): 30.	6	0.792	11
Low	LPATSANPAGmPSTPScRAVFIAtssLttP T24(Phospho)	S25(Phospho) Too many isoforms		0.594	11
Low	LVYNQYSWTQmAsIIFLDsPVGsGFSYA S13(Phospho)	0.192 Y(3): 8.1; Y(6): 8.1; S(7): 8.1; T	32	0.569	13
Low	MAGGYGVEWFQVVyGKAEQAsAVLSQ Y14(Phospho)	0.212 Y(5): 54.5; Y(14): 54.5; S(21): 5	2	0.786	12
Low	mAssSGSGGSASVSAATAAAGGSsAAE S3(Phospho)	S4(Phospho)S Too many isoforms		0.421	12
Low	mAtEEVVPEVPVTEVEAAAAEEAVEET: T3(Phospho)	0.427 T(3): 42.7; T(13): 42.7; T(27): 7	11	0.768	11
Low	mLPPLLTTVHEQTGMLPPAWMGTLTG: T32(Phospho)	0.126 T(7): 15.1; T(8): 15.1; T(13): 15	8		15
Low	mmLLVAAPFTKEsFtmPEMFHHGsMAL: S13(Phospho)	0.25 T(10): 75.0; S(13): 75.0; T(15):	2	0.374	12
Low	MNPtsyLPASAAPWIELSTTGLGyNTAtG T4(Phospho)	S5(Phospho)Y Too many isoforms			11
Low	MQsLQELsGITVYDEcSTNSLLELGNLNs S3(Phospho):	0.157 S(3): 52.5; S(8): 52.5; T(11): 32	13		13
Low	MSEIFSSALsVDVESLMEmFSGGPLEHI S10(Phospho)	0.306 S(2): 12.3; S(6): 12.3; S(7): 12.	14		12
Low	mSPVSPPLPRcSsLLmGmGGsGMGsSL S13(Phospho)	0.011 S(2): 68.7; S(5): 68.7; S(12): 50	4	0.792	10
Low	mSSSSSSsALLmAALLscGAmGsTA: S8(Phospho)	S9(Phospho)S Too many isoforms		0.421	11
Low	MTRGTTScEPsGsGLDAAsLLSRPFsAT S11(Phospho)	0.04 T(2): 10.1; T(5): 16.6; T(6): 16.0	18		11
Low	MVFiFMAYLAFiWSTVLLGGyVSSLQR T4(Phospho):	0.039 T(4): 46.4; Y(8): 46.4; T(12): 46	11		14
Low	mYSANHWGGsFEIAADGAAEDDHSRN S10(Phospho)	0.326 Y(2): 32.6; S(3): 32.6; S(10): 32	16		11
Low	NLSSISSSAASPsPLsPADGFLcVKDGVl S13(Phospho)	0.367 S(3): 12.8; S(4): 12.8; S(6): 12.	19	0.718	14
Low	QsGINNPLEKIDVELNQmAQNcmtLAsm S2(Phospho):	1 S(2): 100.0; T(24): 100.0; S(27)	25		12
Low	RAsIIVAAVIAAcVLLVcMtTssVVDAAAA: S3(Phospho)	0.339 S(3): 66.1; T(20): 89.3; T(21): 6	10	0.742	11
Low	RVsNTQPALLALHAAmILDLFGLmGAY: S3(Phospho):	0.076 S(3): 24.5; T(5): 24.5; Y(27): 75	0	0.787	13
Low	SATSFYTTYIRITYSStPFttSSmPSSPcTi T17(Phospho)	T20(Phospho) Too many isoforms			10
Low	sFGyFYGFLiITAAmSIGmSLPFFIGSAF: S1(Phospho)	0.013 S(1): 26.4; Y(4): 26.4; Y(6): 26.	12		11
Low	sISILSDAGLmAMFsLGLFMALQPsIIAc S1(Phospho):	0.201 S(1): 54.2; S(3): 54.2; S(6): 46.	5		13
Low	ssGFsNEYiVITILVAAEGVHKLPsINGSG S1(Phospho):	0.016 S(1): 81.1; S(2): 81.1; S(5): 81.	2	0.785	14
Low	syEQAVAWKVLSDDDAPHcLAFMLVNW S1(Phospho):	0.957 S(1): 97.6; Y(2): 97.6; S(12): 3.	24	0.778	16
Low	tERsSAVGIAmAGFQLGNtIGLLSPiImSl T1(Phospho):	0.058 T(1): 81.1; S(4): 72.9; S(5): 72.	2	0.486	13
Low	tNAVmLQVVPWGHmEHPSmVFYGGP: T1(Phospho)	0.291 T(1): 29.1; S(18): 35.4; Y(22): 3	0		13
Low	TWFGGFVGMmIFGASEVSRNVDLGDD T29(Phospho)	0.229 T(1): 8.4; S(15): 22.9; S(18): 22	7	0.449	21
Low	tyILLGFmLFmFIVAVAVLMAssGHRSTK T1(Phospho):	0.067 T(1): 66.7; Y(2): 66.7; S(22): 66	0	0.781	22
Low	VGSISKLDSEtmHsIENYQSELLSDGVLL T11(Phospho)	0.027 S(3): 21.9; S(5): 21.9; S(9): 21.	0	0.483	18
Low	VISDSPENmSTTTSMPSAASAsGEDC S24(Phospho)	0.069 S(3): 6.9; S(5): 6.9; S(10): 6.9;	3		11
Low	VLPsMVEYKFWTQsFAVGDDLYVMETC S4(Phospho):	0.067 S(4): 33.3; Y(8): 33.3; T(12): 33	0	0.803	12

	Low		VmLmEKtLLNPIFLVALMMYsLLIGNSLs(T7(Phospho):	0.422 T(7): 99.9; Y(20): 48.5; S(21): 4	42	0.673	12	
	Low		VSVSVSQKGVLAGYPPSNGmFsPEAts; S22(Phospho)T26(Phospho)	Too many isoforms		0.805	11	
	Low		VVHNYSFDIHVIENcGIKVAGFHADtMH T26(Phospho)	0.856 Y(5): 7.2; S(6): 7.2; T(26): 85.6	11	0.805	13	
	Low		WYEHWTSNLVYDGDmIVLQGQEKIFLs S27(Phospho)	0.014 Y(2): 68.2; T(6): 39.0; S(7): 39.	0	0.585	13	
	Low		YHELPtAGHLFPITEGMPDLIVRsMLLTD T6(Phospho):	0.243 Y(1): 27.8; T(6): 61.5; T(14): 25	9		10	
Os05t0596200-03	High	Similar to cDNA clone:001-104-D04, full insert sequence.	VDYsDDDDDFIVK	S4(Phospho)	0.99 Y(3): 1.0; S(4): 99.0	104	0	33
	Low		LIWstVKGLLDPK	S4(Phospho)	1 S(4): 100.0; T(5): 100.0	51	0.145	29
Os05t0597100-01	High	Similar to Nucleolar histone deacetylase HD2-p39.	VSQPAEEDEMDFDsEEVEDEEEEEK	S14(Phospho)	1 S(2): 0.0; S(14): 100.0	246	0	79
	Middle		MISsSSSSTGTPASASESPPSPTSPNLL	S4(Phospho)	0.186 S(3): 18.6; S(4): 18.6; S(5): 18.	36	0.028	12
	Low		AAASTSTDAVVSPsPsAfTSAFSLRR	S15(Phospho)	0.016 S(4): 24.1; T(5): 24.1; S(6): 24.	6		10
	Low		AGLsDPNRPIASFmFMGPTGVGktELAk	S4(Phospho)	0.607 S(4): 77.7; S(12): 22.0; T(19): 2	35	0.11	12
	Low		ATPASSPssAARsHtsATSSAPSSTPPR	S8(Phospho)S9(Phospho)	S Too many isoforms		0.722	10
	Low		DEmHsAEWgtYPGNEDSDLMPAAQDK	S5(Phospho)	0.15 S(5): 39.1; T(10): 60.9; Y(11): 6	4	0.735	11
	Low		DQNLGLNQVAFDDstmPAPAcscTGK	S14(Phospho)	0.488 S(14): 98.8; T(15): 98.8; S(22):	21		12
	Low		EWVFEstMNGTDtYGVtTtGFGGAAHR	S6(Phospho)	0.016 S(6): 51.4; T(7): 51.4; T(11): 44	3	0.783	14
	Low		FFPIRNAVEIGWDSVAyltsTDADR	Y17(Phospho)	0.425 S(14): 2.7; Y(17): 96.6; T(19): 8	41	0.773	11
	Low		GGSIAVEDAADSVLVsPsGNFscGFyK	S16(Phospho)	0.77 S(3): 6.4; S(12): 20.0; S(16): 8	23	0.295	17
	Low		GsDHGVPVssANASNSQISATSSVTsDNF	S2(Phospho)S8(Phospho)	S Too many isoforms			18
	Low		HGmGEFsGmATTGALySGQVmPltsR	S7(Phospho)	0.093 S(7): 89.4; T(11): 30.5; T(12): 5	16	0.501	12
	Low		HPWNstLAHYtQYKSsELSDcVK	S5(Phospho)	0.014 S(5): 49.4; T(6): 49.4; Y(10): 49	0	0.19	10
	Low		LLyTSGmPVVLLSSAVSSLYVVSQALYF	Y3(Phospho)	0.42 Y(3): 42.0; T(4): 42.0; S(5): 14.	29		10
	Low		LtyVPSTGDVVVDcSPSAVGDGATATRC	T2(Phospho)	0.139 T(2): 31.9; Y(3): 31.9; S(6): 31.	20	0.541	11
	Low		LVsDYmAMPTQHTSNdANPAAtMAGyK	S3(Phospho)	0.026 S(3): 88.0; Y(5): 12.0; T(10): 18	18	0.615	10
	Low		mASSSSSPSSDPSLEtVAPHAAVTGt	T18(Phospho)	0.126 S(3): 2.5; S(4): 2.5; S(5): 5.3; S	15	0.509	11
	Low		McsIPssLsNPPNATDsPPAFAAIPK	S3(Phospho)	0.088 S(3): 63.6; S(6): 83.6; S(7): 83.	3	0.308	11
	Low		mGTPPYAATAHALPTSAMVMAAtAR	S21(Phospho)	0.063 T(3): 53.9; Y(6): 53.9; T(9): 16.	15	0.414	14
	Low		MHDtNGLMsiSETLSEYmLYLLVR	T4(Phospho):	0.787 T(4): 99.5; S(9): 79.0; S(11): 16	51	0.653	11
	Low		mPGEVVEEEVAtVPRGsEGtEEEEK	T12(Phospho)	1 T(12): 100.0; S(17): 100.0; T(2	60		12
	Low		NPYGYGsLDstKQNGHHSyGSIGSPK	S7(Phospho)	0.084 Y(3): 30.9; Y(5): 30.9; S(7): 55.	17	0.354	10
	Low		QALmTTPVLAmPDFtEPFVVETDASDK	T15(Phospho)	0.147 T(5): 41.9; T(6): 41.9; T(15): 14	13	0.419	10
	Low		RSPHAGAcVYGHGDLLAAAGASAAGS\	T30(Phospho)	0.788 S(2): 0.0; Y(10): 0.0; S(22): 1.6	34	0.692	10
	Low		sFQDSATTVSPGSVVGQASPDIIIGAADI	S1(Phospho)	0.338 S(1): 33.8; S(5): 33.8; T(7): 13.	14	0.093	12
	Low		sLAtFLLPDEVMMGGsGNALPVTAssR	S1(Phospho)	0.007 S(1): 51.8; T(4): 51.8; S(15): 98	0	0.792	13
	Low		sPsRPDEADPAADFGsHPtDQELVTK	S1(Phospho):	0.46 S(1): 100.0; S(3): 100.0; S(16):	43	0.393	10
	Low		sSLFDMmATDmSPAPNcPVLPPsMGK	S1(Phospho):	0.383 S(1): 39.5; S(2): 39.5; T(9): 16.	25		11
	Low		TMSAIAGsyGyIAPEYAFTmKVTEK	S8(Phospho)	0.096 T(1): 59.1; S(3): 59.1; S(8): 59.	29	0.733	15
	Low		VAPmSTISGITLLTTFGVtDItsLQEK	T19(Phospho)	0.106 S(5): 11.9; T(6): 11.9; S(8): 14.	23	0.449	12
	Low		YFHLysYmmPsFQPGAMPHLER	Y5(Phospho):	0.123 Y(1): 40.9; Y(5): 69.1; S(6): 71.	8	0.735	12

Os06t0104400-01	Low	Similar to IQ calmodulin-binding motif family protein.	AEMPSsVTGKAPTmPTK	S6(Phospho)	0.414 S(5): 10.8; S(6): 41.4; T(8): 41.	31	0.669	12
	Low		AVVIGVGSNtAmGSIRDAMLR	T10(Phospho)	0.316 S(8): 36.8; T(10): 31.6; S(14): 3	0	0.746	11
	Low		clTGLsGVmDGLVVHGYLEVK	S6(Phospho)	0.989 T(3): 1.1; S(6): 98.9; Y(17): 0.0	53		11
	Low		FTGAVGPHLVSLsHLPSSDGR	S13(Phospho)	0.905 T(2): 5.7; S(11): 1.6; S(13): 90.	47	0.617	13
	Low		RNVLSTMLstSTVILFGSK	S9(Phospho)	0.123 S(5): 10.2; T(6): 22.3; S(9): 53.	18	0.792	11
	Low		WFIDIDIVsMQRVLQR	S10(Phospho)	1 S(10): 100.0	23	0.583	10
	Low		WFRIsPIVEGKPEAFTEK	S5(Phospho)	0.893 S(5): 89.3; T(16): 10.7	26	0.535	13
Os06t0115500-01	Low	Similar to 60S ribosomal protein L13 (BBC1 protein homolog).	AGDSTAEELATAtQVQGDYmPIARGEK	T13(Phospho)	0.058 S(4): 3.7; T(5): 3.7; T(11): 3.7;	6	0.806	13
	Low		FDsGGNLIQPayDIVSIIGSGLR	S3(Phospho)	0.844 S(3): 100.0; Y(12): 84.4; S(16):	68	0.623	16
	Low		GDGSTMPRVATAADMsVVEAPSSSSSI	S16(Phospho)	0.885 S(4): 0.0; T(5): 0.0; T(11): 0.0;	56	0.575	15
	Low		GtVDPWPGAVPTALRAcAHLADVAsGR	T2(Phospho)	0.67 T(2): 76.2; T(12): 33.0; S(25): 9	27	0.652	13
	Low		LLVmAGADIAATsAEGKsAMSIIR	S13(Phospho)	0.985 T(12): 1.4; S(13): 98.9; S(18): 9	67		12
	Low		RmssTASLSLSFLPVPLSSSSSSmVR	S3(Phospho)	0.02 S(3): 18.3; S(4): 18.3; T(5): 34.	8	0.803	11
	Low		sPPAAALLVtEPTPPVVASGsPPR	S1(Phospho)	0.749 S(1): 100.0; T(10): 99.8; T(13):	42		11
Os06t0149400-01	High	Similar to Chitinase A.	LQSLAGQHTDVLEALsPNVR	S16(Phospho)	1 S(3): 0.0; T(9): 0.0; S(16): 100.	101	0	16
	Low		APsFPLsFAPQSADEATAHK	S3(Phospho)	0.189 S(3): 50.0; S(7): 50.0; S(12): 4	4	0.17	15
	Low		mKsHQmLESEdMQLLR	S3(Phospho)	0.868 S(3): 86.8; S(9): 13.2	13	0.561	11
	Low		NVmNNKDtLNtInNLIPK	T8(Phospho)	1 T(8): 100.0; T(11): 100.0	17	0.763	13
Os06t0221300-01	Low	Similar to Dehydration stress-induced protein.	TSVVtILR	T5(Phospho)	0.1 T(1): 45.0; S(2): 45.0; T(5): 10.	11	0.63	15
Os06t0234100-01	High	Peptidase S1C, HrtA/DegP2/Q/S family protein.	GRPEPPSDAGAAPHAPPsPPR	S18(Phospho)	1 S(7): 0.0; S(18): 100.0	203	0	54
	Low		AMsRLPVDtMmPVMIVFHEK	S3(Phospho)	0.981 S(3): 98.1; T(9): 1.9	18		10
	Low		AtDGFSAAANLIGVGSFGSVYK	T2(Phospho)	0.811 T(2): 81.1; S(6): 18.8; S(15): 0.	49		19
	Low		DLAPmTSRLVcLDGELPVsK	S19(Phospho)	0.333 T(6): 33.3; S(7): 33.3; S(19): 3	4	0.763	11
	Low		DNPGsDLAGETAAALAAASIVFR	S5(Phospho)	0.928 S(5): 92.8; T(11): 3.8; S(19): 3.	15		11
	Low		DPENTTLVILDNLDImQIR	T18(Phospho)	0.975 T(5): 0.9; T(6): 1.7; T(18): 97.5	25		11
	Low		DVVVGAGFsGHGFKmGPAVGR	S9(Phospho)	1 S(9): 100.0	55		14
	Low		IcAAVDVADEGIVtVmLAVEK	T14(Phospho)	1 T(14): 100.0	11	0.766	11
	Low		IHGRSsQGtSVVAPVSAMKPK	S6(Phospho)	0.28 S(5): 26.1; S(6): 64.2; T(9): 50.	20	0.56	14
	Low		LAVDVLDRVVAAAAAGGAtGPsR	T19(Phospho)	1 T(19): 100.0; S(22): 100.0	25		15
	Low		LGLtAVVVVsSAEAAREAYTK	T4(Phospho)	0.306 T(4): 53.1; T(5): 53.1; S(10): 6	19	0.802	10
	Low		mAAAtNAAAAAAAAPAPATPVPR	T5(Phospho)	0.983 T(5): 98.3; T(21): 1.7	24	0.584	13

	Low		mARGVSYVsAAQLVPmLR	Y7(Phospho)	0.501 S(6): 49.9; Y(7): 79.7; S(9): 70.	5		13
	Low		mNSTLALSVATAGIKAtsTK	T17(Phospho)	0.446 S(3): 0.0; T(4): 0.0; S(8): 0.1; T	40		17
	Low		QGGIKYtItGNPSYNmVMVK	T9(Phospho)	0.955 Y(6): 1.4; T(7): 1.4; T(9): 95.5;	38		11
	Low		RGRPEPPSDAGAAPHAPPSPPR	S19(Phospho)	1 S(8): 0.0; S(19): 100.0	81		13
	Low		RPGGGGGAAAAtTDWRAFDK	T13(Phospho)	0.5 T(13): 50.0; T(14): 50.0	23		10
	Low		TIELDDVTFHQcVNLR	T16(Phospho)	1 T(1): 0.0; T(8): 0.0; T(16): 100.0	44		12
	Low		VEKyHFLEAmSTITPAAHR	Y4(Phospho)	0.867 Y(4): 86.7; S(11): 3.8; T(12): 3.	16		10
Os06t0507200-01	Low	Bifunctional inhibitor/plant lipid transfer protein/seed storage domain containing protein.	EEPTGTGPLsR	S10(Phospho)	0.165 T(4): 16.5; T(6): 67.0; S(10): 16	23	0.05	11
	Low		EVLDQMPsPK	S8(Phospho)	1 S(8): 100.0	66		16
	Low		LQQQPATVtR	T9(Phospho)	0.85 T(7): 15.0; T(9): 85.0	39		12
Os06t0555400-01	Low	Similar to 40S ribosomal protein S19-like.	MGtTVATNALLERK	T3(Phospho)	0.138 T(3): 13.8; T(4): 13.8; T(7): 72.	44		11
	Low		sFLVLIRGTHSmK	S1(Phospho)	0.719 S(1): 71.9; T(9): 20.8; S(11): 7.	19		11
Os06t0698859-01	High	Similar to C2H2 zinc-finger protein SERRATE (Fragment).	GsSKETDPLSGAPVAHPVSSESR	S2(Phospho)	0.493 S(2): 49.3; S(3): 49.3; T(6): 1.4	82	0.003	21
	High		GSsKETDPLSGAPVAHPVSSESR	S3(Phospho)	0.494 S(2): 49.4; S(3): 49.4; T(6): 1.1	50	0.006	21
	Low		LTWAHSPLGPTLSFSPSAsGRK	S19(Phospho)	0.377 T(2): 3.1; S(6): 2.6; T(11): 9.9;	12	0.726	12
	Low		VLELSNDPsPGyNIEQLAKK	S9(Phospho)	0.223 S(5): 77.7; S(9): 92.1; Y(12): 30	22		16
Os06t0724600-02	High	Similar to transformer-2 protein.	RsPPPMYPSYR	S2(Phospho)	0.896 S(2): 89.6; Y(7): 10.4; S(9): 0.0	68	0.009	15
	High		sPPPMYPSYR	S1(Phospho)	1 S(1): 100.0; Y(6): 0.0; S(8): 0.0	84	0.003	28
	Low		AASSDSASAAAtGK	T12(Phospho)	0.965 S(3): 0.2; S(4): 0.5; S(6): 0.5; S	29		10
	Low		FGSGGGGGGsLADR	S10(Phospho)	0.987 S(3): 1.3; S(10): 98.7	20		10
	Low		NITVEKsR	S7(Phospho)	1 T(3): 0.0; S(7): 100.0	44	0.742	19
	Low		sPPPEEEEGKA	S1(Phospho)	1 S(1): 100.0	42		10
Os07t0150200-01	High	Similar to 40S ribosomal protein S12-1.	GALsDLKTGVQLsLDEFER	S4(Phospho)	0.5 S(4): 50.0; T(8): 50.0; S(13): 10	81	0.002	18
	High		GALSDLKtGVQLsLDEFER	T8(Phospho)	0.985 S(4): 1.5; T(8): 98.5; S(13): 100	111	0.008	16
	Low		AASsFHRPtSQPSPTFNR	S5(Phospho)	0.041 S(3): 24.3; T(4): 24.3; S(5): 24.	0		10
	Low		AcLTLTtVQLPKLYSGGR	T7(Phospho)	0.723 T(4): 8.3; T(5): 22.9; T(7): 91.6	47		11
	Low		APESAGHPSSGGIRyPHQIER	Y14(Phospho)	0.996 S(4): 0.0; S(9): 0.3; Y(14): 99.6	58		11
	Low		APESAGHPSSGGIRYPHQIER	S4(Phospho)	0.419 S(4): 41.9; S(9): 16.3; Y(14): 4.	21	0.672	14

Low	ASMRWSNVAVmLGFVVGYR	Y18(Phospho)	0.997 S(2): 0.1; S(6): 0.2; Y(18): 99.7	35	0.734	13
Low	ATSTVGAPPPSSLVPHHDcK	T17(Phospho)	0.998 T(2): 0.0; S(3): 0.0; T(4): 0.0; S	46	0.802	19
Low	ctVIGINLGTYSWVGYYR	T2(Phospho)	0.088 T(2): 8.8; T(10): 15.3; T(11): 30	4		12
Low	DVSFEQLGLNmsTVYVLLD	S12(Phospho)	0.694 S(3): 0.1; S(12): 69.4; T(13): 15	37	0.774	13
Low	EIPtLLSTSPPEsPLASPsR	T4(Phospho)	0.02 T(4): 5.0; S(7): 5.0; T(8): 5.0; S	17		12
Low	EIPTLLSTsPPEsPLASPSR	S9(Phospho)	0.018 T(4): 9.0; S(7): 9.0; T(8): 14.7;	6		10
Low	ELALGAsGFSGmLPSsIGKLK	S7(Phospho)	0.411 S(7): 85.9; S(10): 6.2; S(15): 54	29	0.721	13
Low	EVKSlyVSGQNDmQLR	Y6(Phospho)	0.555 S(4): 22.3; Y(6): 55.5; S(8): 22.	8	0.805	10
Low	FEILQLtGSFTmAEEGGRR	T7(Phospho)	0.829 T(7): 82.9; S(9): 17.0; T(11): 0.	58	0.702	13
Low	FNPFsGFQNPmYILKSPR	S5(Phospho)	1 S(5): 100.0; Y(12): 0.0; S(16): 0	63	0.254	11
Low	FTDEQLATMPesLHATLVR	S12(Phospho)	0.5 T(2): 0.0; T(8): 50.0; S(12): 50.	49		11
Low	FVPEVDGPGLNAAsARGGAVmK	S14(Phospho)	1 S(14): 100.0	26	0.792	11
Low	GLQRQSTSMVSHISSPSNsR	S19(Phospho)	0.732 S(6): 0.0; T(7): 0.0; S(8): 0.0; S	40	0.806	16
Low	GmEyLHAQGVHRLDK	Y4(Phospho)	1 Y(4): 100.0	21	0.611	10
Low	GPLGQSAVsNGFTVtKIQmK	S9(Phospho)	0.249 S(6): 49.9; S(9): 49.9; T(13): 50	31		10
Low	GPLGQsAVSNGFTVtKIQmK	S6(Phospho)	0.223 S(6): 47.6; S(9): 47.6; T(13): 52	21	0.792	12
Low	GsGVELVLGYLRPQAAPR	S2(Phospho)	0.914 S(2): 91.4; Y(10): 8.6	20	0.417	16
Low	GWGcGWRNIQmLSsHLLK	S14(Phospho)	0.982 S(13): 1.8; S(14): 98.2	37	0.806	11
Low	IALsLEAESGGILVsVDK	S4(Phospho)	0.024 S(4): 99.1; S(9): 97.6; S(15): 3.	13	0.225	11
Low	IGGYIGGGNWKSAHGTAHyGR	Y19(Phospho)	0.77 Y(4): 0.0; S(12): 2.0; T(16): 21.	39		12
Low	IKEmLGSLDsLEFPTGK	S10(Phospho)	0.055 S(7): 92.9; S(10): 5.5; T(15): 1.	10	0.8	11
Low	IstmNSLLPVLEmSIKNR	S2(Phospho)	0.333 S(2): 66.7; T(3): 66.7; S(6): 66.	45	0.473	12
Low	LAaVVsSSASIAKSDtAAR	S6(Phospho)	0.007 S(6): 54.0; S(7): 54.0; S(8): 70.	2	0.788	12
Low	LLAYtSTHGTGNWtSVPQR	T5(Phospho)	0.098 Y(4): 24.9; T(5): 24.9; S(6): 24.	13	0.356	13
Low	LLmNGySEGHLVLSHFPTK	Y6(Phospho)	0.378 Y(6): 37.8; S(7): 37.8; S(14): 10	14		11
Low	LPVIGHmHLVGsNPHVsLR	S12(Phospho)	1 S(12): 100.0; S(17): 100.0	27	0.743	19
Low	LQSAGsFLmKVFGALAVK	S6(Phospho)	0.5 S(3): 50.0; S(6): 50.0	8	0.092	17
Low	LVImsTEGQQTGTTLTK	S5(Phospho)	0.412 S(5): 41.2; T(6): 41.2; T(11): 2.	20	0.117	10
Low	LVVIEGLGMQPVdITK	T4(Phospho)	0.418 T(4): 83.6; T(14): 58.2; T(16): 5	11	0.724	15
Low	MASAGRPpAWNAAARPIR	T17(Phospho)	1 S(3): 0.0; T(17): 100.0	45	0.161	12
Low	MDTAAGDDASLLPLPAASSsLR	S20(Phospho)	0.53 T(3): 1.6; S(10): 4.4; S(18): 20.	18	0.73	13
Low	MDVLPsSicTmYNLQTLR	S6(Phospho)	0.499 S(6): 49.9; S(7): 49.9; T(10): 0.	78	0.54	10
Low	mIAFGANRtlyLNGAVVPR	T9(Phospho)	1 T(9): 100.0; Y(11): 100.0	61		11
Low	MKsAIGIGTLmDGLGDtIR	S3(Phospho)	0.817 S(3): 99.6; T(9): 18.3; T(18): 82	43	0.806	12
Low	mTSVFDaVTSTLIDRSADK	T14(Phospho)	0.436 T(2): 0.1; S(3): 0.1; T(9): 0.1; S	34	0.649	10
Low	NLAVsNTIDDQLAGVRAMDR	S5(Phospho)	0.5 S(5): 50.0; T(7): 50.0	38	0.624	14
Low	NLAVSNtIDDQLAGVRAMDR	T7(Phospho)	0.893 S(5): 10.7; T(7): 89.3	29	0.753	11
Low	NLNLEVgQTDEPsSSAKLEK	S13(Phospho)	0.466 T(9): 0.2; S(13): 46.6; S(14): 46	71	0.773	13
Low	NMTIcAATTSIVVPAsLcSR	S16(Phospho)	0.028 T(3): 0.2; T(8): 69.5; T(9): 13.4	35		11
Low	NQVtEEGPYGFKILsQIR	T4(Phospho)	0.966 T(4): 97.0; Y(9): 3.4; S(15): 99.	35		11
Low	NSALmISRLAMAYVMDQK	T9(Phospho)	0.041 S(2): 1.2; S(7): 1.8; T(9): 4.1; Y	6		11
Low	QAtKVVESmTAYGFEPDLR	T3(Phospho)	0.5 T(3): 50.0; S(8): 50.0; T(10): 0.	56	0.358	11
Low	QGVISsSGTETGYLQDLIYK	S6(Phospho)	0.142 S(5): 7.1; S(6): 14.2; S(7): 14.2	11	0.776	15
Low	QLsYFcYVVDATRcLEK	S3(Phospho)	0.422 S(3): 42.2; Y(4): 13.4; Y(7): 42.	21		10
Low	QQELNYTQLQTPGAIDPsR	S18(Phospho)	0.999 Y(6): 0.0; T(7): 0.0; T(11): 0.1;	46		10
Low	RLSSDDVVAAVELSAATsPR	S19(Phospho)	0.792 S(3): 3.1; S(4): 8.1; S(15): 1.4;	25	0.804	15
Low	sAANsRILNIsSQLGLLNK	S1(Phospho)	0.802 S(1): 99.9; S(5): 99.9; S(11): 80	36		12

	Low		scVLcHHLTVLPGPENIGR	S1(Phospho)	0.745 S(1): 74.5; T(9): 25.5	5		11
	Low		sHSSKALTNIGGQALEESSR	S1(Phospho)	0.589 S(1): 58.9; S(3): 17.9; S(4): 17.	27	0.793	16
	Low		SIMLQIDSKSQVSAssLR	S16(Phospho)	0.441 S(1): 0.0; S(8): 0.6; S(10): 1.3;	41		11
	Low		sLSPAAASSAVHALHHtGAHR	S1(Phospho)	0.084 S(1): 62.5; S(3): 62.5; S(8): 26.	8	0.651	10
	Low		sPtHLLHLPPIALLR	S1(Phospho)	1 S(1): 100.0; T(3): 100.0; S(12):	59		13
	Low		SsIsPmPPIYSSSLKQIVK	S2(Phospho)	0.333 S(1): 66.6; S(2): 66.6; S(4): 66.	42	0.364	18
	Low		SWsHPIWVLmEPVFQMR	S3(Phospho)	0.834 S(1): 16.6; S(3): 83.4	44	0.792	19
	Low		SWYLVDLPGYGFAAASQsAR	S18(Phospho)	0.794 S(1): 0.0; Y(3): 0.0; Y(10): 0.2;	42	0.755	14
	Low		SWYLVDLPGYGFAAAsQSAR	S16(Phospho)	0.493 S(1): 0.1; Y(3): 0.1; Y(10): 1.2;	27		11
	Low		tLVASELLGAAAPGMAVVGR	T1(Phospho)	0.912 T(1): 91.2; S(5): 8.8	17		13
	Low		tNSVVDPSEPKILDASSASR	T1(Phospho)	0.736 T(1): 73.6; S(3): 20.3; S(8): 6.0	43	0.554	13
	Low		tVsSAVVAVPVYFNDAR	T1(Phospho)	0.326 T(1): 52.0; S(3): 72.9; S(4): 55.	13	0.732	10
	Low		VAAVLDWFcTtLLDVtR	T12(Phospho)	0.868 T(11): 13.2; T(12): 86.8; T(17):	63	0.745	13
	Low		VESLPPRPPLAFLssESR	S15(Phospho)	0.779 S(3): 0.0; S(15): 95.6; S(16): 8;	45		13
	Low		VSRPAtdGTDNGFGmTmSK	T6(Phospho)	0.307 S(2): 12.8; T(6): 30.7; T(8): 30.	12	0.668	10
	Low		WIDSVQISSGAYIGNIsIR	S4(Phospho)	0.947 S(4): 95.2; S(8): 2.4; S(9): 2.4;	55	0.601	14
Os07t0167200-01	High	Similar to Zinc finger POZ domain protein (Fragment).	MDDDAGDASPPPAAGVGAtAAQSRD	T20(Phospho)	0.998 S(9): 0.1; T(20): 99.8; S(24): 0.	62	0.009	22
	Low		AMSLDTFLmITPFGPTGecLLMtLmT	T23(Phospho)	0.62 S(3): 11.0; T(6): 12.1; T(11): 15	19	0.793	13
	Low		cPGVVScADVLALAARDAVIMAGGPYY	T31(Phospho)	0.714 S(6): 2.8; Y(26): 9.2; Y(27): 16.	16	0.792	15
	Low		DLmQMASKSSSTAQNcVLLPSSAtATV	T24(Phospho)	0.109 S(7): 10.9; S(9): 10.9; S(10): 10	2	0.719	11
	Low		EAGEGDRPKALPLSAAAGGHSFLsPA	S25(Phospho)	0.05 S(14): 50.0; S(21): 50.0; S(25):	0	0.195	11
	Low		EcPAtdVscADILALAARDGVAMLGPsVA	T5(Phospho)	1 T(5): 100.0; S(7): 100.0; S(27):	56		16
	Low		EFSLDNLLFIWDEIFSSPNHsycADIK	S21(Phospho)	0.169 S(3): 22.7; S(16): 32.3; S(17): 4	6	0.805	13
	Low		ELQKLtyVEANQNGNtIEELGsLtQLR	T6(Phospho)	1 T(6): 100.0; Y(7): 100.0; T(16):	17		11
	Low		FFDSAPAEmaAIPDISSAsVPDSAcAlccI	S19(Phospho)	0.116 S(4): 68.4; S(16): 5.5; S(17): 1.	14	0.433	13
	Low		FImAPIAScGSGGISRcYTAAtTAATmAS	T22(Phospho)	0.107 S(8): 12.9; S(11): 12.9; S(15): 9	0	0.549	14
	Low		IGEQyVsELLGmSFLQYSSSLVPDyTGLR	Y5(Phospho)	0.022 Y(5): 35.7; S(7): 35.7; S(13): 3	1		10
	Low		lyMTPRMPPPsPPsAVtSSAAATmELMP	Y2(Phospho)	0.004 Y(2): 83.8; T(4): 14.1; S(11): 44	15	0.732	11
	Low		LEEAGPVSPFASSLAAGFsGVVAAAAs	S19(Phospho)	0.176 S(8): 20.8; S(12): 20.8; S(13): 1	8	0.741	11
	Low		LFLEYMVRMGycVIASFtiYLDsSFR	Y11(Phospho)	0.087 Y(5): 16.0; Y(11): 73.7; S(16): 4	13	0.805	17
	Low		LIVtsAtLDAEKFSGYFFNcNIFTIPGR	T4(Phospho)	0.05 T(4): 53.9; S(5): 53.9; T(7): 53.	1	0.792	11
	Low		mAtLsyalcFAIVAGAIAsLWAmLSSRK	T3(Phospho)	0.172 T(3): 88.7; S(5): 84.5; Y(6): 83.	10	0.509	11
	Low		MsYYDtAANLAETsGIQDLVDVDVFLDAI	S2(Phospho)	0.236 S(2): 40.7; Y(3): 40.7; Y(4): 40.	43	0.792	13
	Low		MVAEEEsPstASGGGMPiGLPAADKLmC	S7(Phospho)	0.528 S(7): 84.3; S(9): 84.3; T(10): 84	44	0.11	11
	Low		PVNLLVtyRWEVNFSSVLTPGQGsPyR	Y8(Phospho)	0.005 T(7): 0.6; Y(8): 1.3; S(15): 82.2	23	0.75	12
	Low		QmssFsFLATRTPAAGIGSHsHQRPHF	S3(Phospho)	0.195 S(3): 99.8; S(4): 99.8; S(6): 97.	45	0.711	11
	Low		TLTYycGSmTNAAMVImssNcPNLEVFR	S18(Phospho)	0.042 T(1): 15.7; T(3): 15.7; Y(4): 15.	4	0.729	12
	Low		YcLQqYGGVGSAILMTtRDQGVaQLmG	Y6(Phospho)	0.05 Y(1): 25.3; Y(6): 29.1; S(11): 29	1	0.395	11
Os07t0173700-00	Low	40S ribosomal protein S18.	ASEEVmAtRR	T8(Phospho)	1 S(2): 0.0; T(8): 100.0	69		10
	Low		DLsFRGEGER	S3(Phospho)	1 S(3): 100.0	28	0.792	10
	Low		LVtIDLHR	T3(Phospho)	1 T(3): 100.0	60		13

	Low		RTSNILSAsSK	S9(Phospho)	0.487 T(2): 0.9; S(3): 0.9; S(7): 0.9; S	23	0.806	12
	Low		sQLGLtKPNK	S1(Phospho)	1 S(1): 100.0; T(6): 100.0	52	0.792	13
	Low		ssPPIWSLAK	S1(Phospho)	1 S(1): 100.0; S(2): 100.0; S(7): 1	60	0.782	13
	Low		TFQRGLLSsR	S9(Phospho)	0.5 T(1): 0.0; S(8): 50.0; S(9): 50.0	35	0.785	12
Os07t0180900-01	Low	Similar to 60S ribosomal protein L4.	EAsKIFVPGGAK	S3(Phospho)	1 S(3): 100.0	29	0.74	12
	Low		FIQVsSLGASASSPsRmLR	S5(Phospho)	0.347 S(5): 49.0; S(6): 49.0; S(10): 3.	36	0.204	18
	Low		GSHPGGLEsIFDssLK	S9(Phospho)	0.51 S(2): 49.0; S(9): 83.7; S(13): 8;	5		14
	Low		IASRGGDALPSFSNGsGLPWK	S16(Phospho)	0.981 S(3): 0.0; S(11): 1.5; S(13): 0.4	55		16
	Low		KGsySHSLmDDADIR	S3(Phospho)	0.167 S(3): 50.0; Y(4): 50.0; S(5): 50.	2	0.584	24
	Low		LHcQALNSlyAGTGVIPIFR	Y10(Phospho)	0.789 S(8): 17.0; Y(10): 78.9; T(13): 4	41		12
	Low		LVmGTssFSVKR	S6(Phospho)	0.697 T(5): 5.6; S(6): 84.6; S(7): 84.6	43	0.394	12
	Low		SDMSPNtVEcENmSQLLK	T7(Phospho)	0.436 S(1): 23.2; S(4): 23.2; T(7): 43.	8	0.792	11
	Low		sGTDKAGsGGASELGmGGR	S1(Phospho)	0.264 S(1): 50.0; T(3): 50.0; S(8): 64.	8		18
	Low		SSSGNPLGGtTQDELGNR	T10(Phospho)	0.488 S(1): 0.8; S(2): 0.8; S(3): 0.8; T	34		11
	Low		VLKQIGAYADAeK	Y8(Phospho)	1 Y(8): 100.0	71	0.223	13
	Low		VQPGRtYLLR	T6(Phospho)	0.5 T(6): 50.0; Y(7): 50.0	56		15
Os07t0215500-01	Low	Allergenic protein.	IVGtSGGyRPR	T4(Phospho)	0.809 T(4): 82.2; S(5): 19.1; Y(8): 98.	30	0.674	16
	Low		tPGFPAGPLGGGGR	T1(Phospho)	1 T(1): 100.0	33		10
Os07t0229900-01	High	Ribosomal protein S12e domain containing protein.	GALSDLKtGVQLsLDEFER	T8(Phospho)	0.985 S(4): 1.5; T(8): 98.5; S(13): 100	111	0.008	16
	Low		AASTsFHRPtSQPSPTFNR	S5(Phospho)	0.041 S(3): 24.3; T(4): 24.3; S(5): 24.	0		10
	Low		AcLTTLtVQLPKLYSGGR	T7(Phospho)	0.723 T(4): 8.3; T(5): 22.9; T(7): 91.6	47		11
	Low		APESAGHPSSGGIRYPHQIER	S4(Phospho)	0.419 S(4): 41.9; S(9): 16.3; Y(14): 4;	21	0.672	14
	Low		ASMRWSNVAVmLGFVVGYR	Y18(Phospho)	0.997 S(2): 0.1; S(6): 0.2; Y(18): 99.7	35	0.734	13
	Low		ATSTVGAPPPSSSLVPHtHDcK	T17(Phospho)	0.998 T(2): 0.0; S(3): 0.0; T(4): 0.0; S	37	0.636	19
	Low		ctVIGINLGTtYSWVGvYR	T2(Phospho)	0.088 T(2): 8.8; T(10): 15.3; T(11): 30	4		12
	Low		DVSFEQLGLNmSTVYVLLD	S12(Phospho)	0.171 S(3): 0.0; S(12): 17.1; T(13): 17	28	0.751	16
	Low		EIPTLLSTsPPEsPLASPSR	S9(Phospho)	0.018 T(4): 9.0; S(7): 9.0; T(8): 14.7;	6		10
	Low		ELALGAsGFSGmLPSsIGKLK	S7(Phospho)	0.04 S(7): 8.9; S(10): 2.9; S(15): 94.	34	0.432	14
	Low		FEILQLtGSFTmAEeGGRR	T7(Phospho)	0.971 T(7): 97.1; S(9): 2.9; T(11): 0.0	66	0.609	11
	Low		FNPFsGFQNPmYILKSPR	S5(Phospho)	0.997 S(5): 99.7; Y(12): 0.2; S(16): 0.	34	0.472	13
	Low		FTDEQLATMPESLHATLVR	S12(Phospho)	0.5 T(2): 0.0; T(8): 50.0; S(12): 50.	49		11
	Low		FVPEVDGPGLNAAAsARGGAVmK	S14(Phospho)	1 S(14): 100.0	26	0.792	11
	Low		GLQRQSTSMVSHISSPSNsR	S19(Phospho)	0.784 S(6): 0.2; T(7): 0.3; S(8): 0.3; S	33	0.802	17
	Low		GPLGQsAVSNGFTVtKIQmK	S6(Phospho)	0.223 S(6): 47.6; S(9): 47.6; T(13): 52	21	0.792	12
	Low		GWGcGWRNIQmLSsHLLK	S14(Phospho)	0.945 S(13): 5.5; S(14): 94.5	49		11
	Low		IGGYIGGGNWKSAGHTAHyGR	Y19(Phospho)	0.631 Y(4): 1.4; S(12): 10.8; T(16): 24	18	0.805	13
	Low		IstmNSLLPVLEmSIKNR	S2(Phospho)	0.995 S(2): 99.7; T(3): 99.7; S(6): 0.5	53	0.722	11
	Low		LLAYtSTHGTGNWtSVPQR	T5(Phospho)	0.098 Y(4): 24.9; T(5): 24.9; S(6): 24.	13	0.356	13
	Low		LLmNGySEGHLVLSHFPTK	Y6(Phospho)	0.378 Y(6): 37.8; S(7): 37.8; S(14): 10	14		11
	Low		LPVIGHmHLVGsNPHVSLR	S12(Phospho)	1 S(12): 100.0; S(17): 100.0	13		11

Os07t0545400-01	Low	Protein H2A.	MDTAAGDDASLLPLPAASSsLR	S20(Phospho	0.53 T(3): 1.6; S(10): 4.4; S(18): 20.	18	0.73	13
	Low		MDVLPsSicTmYNLQTLR	S6(Phospho)	0.431 S(6): 43.1; S(7): 43.1; T(10): 6.	64	0.093	11
	Low		mTSVFDaVTVSTLIDRSADK	T14(Phospho	0.436 T(2): 0.1; S(3): 0.1; T(9): 0.1; S	34	0.649	10
	Low		NLAVSNtiDDQLAGVDRAMDR	T7(Phospho)	0.893 S(5): 10.7; T(7): 89.3	29	0.753	11
	Low		NLNLEVQGQTDEPsSSAKLEK	S13(Phospho	0.695 T(9): 14.8; S(13): 69.5; S(14): 1	48	0.508	17
	Low		NQVtIEGPyGFKILsQIR	T4(Phospho)	0.966 T(4): 97.0; Y(9): 3.4; S(15): 99.	35		11
	Low		NSALmISRtLAMAYVMDQK	T9(Phospho)	0.041 S(2): 1.2; S(7): 1.8; T(9): 4.1; Y	6		11
	Low		QGVISsSGTETGYLQDLIYK	S6(Phospho)	0.142 S(5): 7.1; S(6): 14.2; S(7): 14.2	11	0.776	15
	Low		RLSSDDDVVAVELSAATsPR	S19(Phospho	0.364 S(3): 17.8; S(4): 17.8; S(15): 10	9		11
	Low		sAANsRILNisSQLGLLNK	S1(Phospho)	0.827 S(1): 99.8; S(5): 99.2; S(11): 8	54		11
	Low		sHSSKALTNIGGQALEESSSR	S1(Phospho)	0.169 S(1): 16.9; S(3): 65.7; S(4): 16.	34	0.62	13
	Low		sPtHLLHLPPsPIALLR	S1(Phospho)	1 S(1): 100.0; T(3): 100.0; S(12):	59		13
	Low		SsIsPmPPIYSSSLKQIVK	S2(Phospho)	0.333 S(1): 66.6; S(2): 66.6; S(4): 66.	42	0.364	18
	Low		SWsHPIWVLmEPVFQMR	S3(Phospho)	0.5 S(1): 50.0; S(3): 50.0	29	0.752	12
	Low		SWYLVLDLPGYGFAAAsQSAR	S16(Phospho	0.493 S(1): 0.1; Y(3): 0.1; Y(10): 1.2;	27		11
	Low		tHLtAAFGRGSPAAAAER	T1(Phospho)	0.852 T(1): 89.8; T(4): 95.5; S(11): 14	14	0.732	12
	Low		tNSVVDPSEPKILDASSASR	T1(Phospho)	0.736 T(1): 73.6; S(3): 20.3; S(8): 6.0	43	0.554	13
	Low		tVsSAVVAVPVYFNDAQRR	T1(Phospho)	0.326 T(1): 52.0; S(3): 72.9; S(4): 55.	13	0.732	10
	Low		VAAVVDWFcTtLLDVtR	T12(Phospho	0.207 T(11): 79.3; T(12): 79.3; T(17):	17		11
	Low		VESLPPPRPPLAFLsESR	S15(Phospho	0.679 S(3): 11.2; S(15): 83.2; S(16): 8	20		11
Os07t0557500-01	Low	WRC domain containing protein.	WIDsVQISSGAYIGNIsIR	S4(Phospho)	0.59 S(4): 61.8; S(8): 19.0; S(9): 19.	27	0.563	13
	Low		DDAmATASSLFLAsPVATAPTAR	S14(Phospho	0.475 T(6): 23.3; S(8): 12.5; S(9): 7.3	14	0.588	13
	Low		LKVtYLK	T4(Phospho)	0.991 T(4): 99.1; Y(5): 0.9	60		10
	Low		SPsIRmAPAPSsSLAtAGHGK	S3(Phospho)	0.016 S(1): 91.2; S(3): 91.2; S(11): 50	2	0.764	21
	Low		sVAyDVEDVLDELDAALIK	S1(Phospho)	1 S(1): 100.0; Y(4): 100.0	30	0.764	10
	Low		tRAssVLmQLIScGSVsVK	T1(Phospho)	0.334 T(1): 74.8; S(4): 74.8; S(5): 74.	11	0.665	13
	Low		VKGATAAAAAAsSGIVAtGVQR	T5(Phospho)	0.791 T(5): 99.5; S(14): 80.1; S(15): 2	48	0.563	11
	Low							
Os07t0557500-01	High	WRC domain containing protein.	AGDRGDsPPPLPDHLR	S7(Phospho)	1 S(7): 100.0	125	0	25
	High		ISPGSSEPAASLPsPVTTK	S14(Phospho	0.954 S(2): 0.0; S(5): 0.0; S(6): 0.0; S	79	0	33
	High		IsPGSSEPAASLPsPVTTK	S2(Phospho)	0.984 S(2): 98.4; S(5): 1.3; S(6): 0.3;	57	0	37
	High		NVNASPAsPPAATSDVTR	S8(Phospho)	1 S(5): 0.0; S(8): 100.0; T(13): 0.	133	0	46
	High		VSSPPPEPAPAVR	S3(Phospho)	0.879 S(2): 12.1; S(3): 87.9	73	0.003	18
	Middle		GDsPPPLPDHLR	S3(Phospho)	1 S(3): 100.0	63	0.025	22
	Middle		ISPGSSEPAASLPsPVTTk	S2(Phospho)	0.006 S(2): 96.4; S(5): 3.0; S(6): 0.6;	44	0.047	17
	Low		ANsHRPFLLRP	S3(Phospho)	1 S(3): 100.0	66		15
	Low		ASPPPPAAAAAsPK	S13(Phospho	0.998 S(2): 0.2; S(13): 99.8	33		17
	Low		EWGGtSVAAATRPRSR	T5(Phospho)	0.801 T(5): 80.1; S(6): 19.2; T(11): 0.	31	0.683	11
	Low		IEASGAtVDPRtSDASNSK	T7(Phospho)	0.76 S(4): 19.0; T(7): 76.0; T(12): 1.	28		11
	Low		ISPGSSEPAAsLPsPVTTK	S11(Phospho	0 S(2): 79.7; S(5): 16.6; S(6): 3.7	27	0.182	14
	Low		ItGGHPLAIVVLAgLLR	T2(Phospho)	1 T(2): 100.0	16	0.729	10
	Low		QmLPAVGmAGAGYtVTR	T14(Phospho	0.869 Y(13): 12.8; T(14): 86.9; T(16):	80		20
	Low		sAKPmKPPVRtYTK	S1(Phospho)	0.333 S(1): 100.0; T(11): 33.3; Y(12):	42		12
	Low		VEQAPSESmISAtPAMK	T14(Phospho	0.996 S(6): 0.0; S(8): 0.1; S(11): 0.3;	55		11
	Low		YVAKLAsEGTLR	S7(Phospho)	0.947 Y(1): 1.1; S(7): 94.7; T(10): 4.2	37	0.42	17

Os07t0574800-01	High	Tubulin alpha-1 chain.	TVQFVDWcPiGFK	T10(Phospho	1 T(1): 0.0; T(10): 100.0	89	0	49
	Low		cItGLSGVmDGLVVHGyLVK	T3(Phospho)	0.5 T(3): 50.0; S(6): 50.0; Y(17): 0.	60	0.379	20
	Low		FTGAVGPHLVSLsHLPSSDGR	S13(Phospho	0.928 T(2): 2.2; S(11): 2.2; S(13): 92.	45	0.705	11
	Low		GySGSHVATVGSVVVTNLTGK	Y2(Phospho)	0.449 Y(2): 44.9; S(3): 44.9; S(5): 4.6	36	0.618	15
	Low		HHHPLmTIVsNKPPTPSPK	S10(Phospho	0.198 T(7): 73.9; S(10): 19.8; T(15): 6	22	0.367	13
	Low		KtLQsFDLLGmNVAFLK	T2(Phospho):	1 T(2): 100.0; S(5): 100.0	48	0.76	11
	Low		LLNGNRSILPATMTITmAsN	S19(Phospho	0.464 S(7): 0.7; T(12): 17.6; T(14): 17	21	0.735	13
	Low		RAtAPPAAPPAGAAPGGR	T3(Phospho)	1 T(3): 100.0	28	0.776	11
	Low		REVALlCtLsLPLsLGEQR	S9(Phospho):	1 S(9): 100.0; S(13): 100.0	37	0.735	11
	Low		SYVILETGPLADtsQSKK	T14(Phospho	0.119 S(1): 0.0; Y(2): 0.0; T(8): 87.6;	72	0.631	10
	Low		WFRIsPIVEGKPEAFTEK	S5(Phospho)	0.999 S(5): 99.9; T(16): 0.1	35	0.619	11
Os07t0607800-01	High	Similar to leucine-rich repeat family protein.	AVEAALQAAGEGSSsPAR	S15(Phospho	0.831 S(13): 2.6; S(14): 14.2; S(15): 1	71	0	32
	Low		sVLAPLPTIYsGAFR	S1(Phospho):	0.398 S(1): 90.2; T(8): 17.1; Y(10): 46	23	0.674	10
Os07t0613200-00	Low	Similar to 60S ribosomal protein L27a-3.	ESAVTWsAmIGGyVR	S7(Phospho):	0.497 S(2): 0.2; T(5): 50.2; S(7): 50.2	44	0.8	10
	Low		EVSsEEEEAGGGDELRR	S4(Phospho)	0.831 S(3): 16.9; S(4): 83.1	39	0.474	13
	Low		FQLSARAssASAAAAAR	S8(Phospho):	0.874 S(4): 0.4; S(8): 99.4; S(9): 88.0	72	0.148	15
	Low		LDGYESLLYltSWR	T11(Phospho	0.673 Y(4): 3.4; S(6): 0.9; Y(9): 14.2;	38	0.695	13
	Low		mRAVSPSPSPsTcGGGR	S11(Phospho	0.471 S(5): 0.7; S(7): 0.7; S(9): 4.5; S	28	0.691	17
	Low		RPsiPLIKcPScGVK	S3(Phospho)	1 S(3): 100.0; S(11): 0.0	64	0.804	12
	Low		ScSHWLTSDLAEGGIS	S8(Phospho)	0.029 S(1): 47.1; S(3): 47.1; T(7): 2.9	25	0.79	12
	Low		SLLLLtsGWWGLsR	T6(Phospho):	0.071 S(1): 52.2; S(2): 52.2; T(6): 76.	17	0.29	11
Os07t0616600-02	Middle	Similar to 40S ribosomal protein SA (p40) (Laminin receptor homolog).	VEtPPPPSYGFHNLDLDR	T3(Phospho)	1 T(3): 100.0; S(8): 0.0; Y(9): 0.0	65	0.028	15
	Low		EySNSWTEPLTPSTNQK	Y2(Phospho)	0.843 Y(2): 84.3; S(3): 15.3; S(5): 0.2	47	0.59	15
	Low		FLQTKFGVAGsK	S11(Phospho	0.774 T(4): 22.6; S(11): 77.4	23	0.805	11
	Low		GQAWVVFfsEITAATNAFR	S8(Phospho)	0.277 S(8): 27.7; T(11): 27.7; T(14): 4	2		15
	Low		GtSSLcDASAAATSGLtGIR	T2(Phospho):	0.106 T(2): 15.4; S(3): 15.4; S(4): 15.	29	0.486	15
	Low		KmWDEEEEVQsPLAFK	S11(Phospho	1 S(11): 100.0	61	0.7	15
	Low		LtNIGETGGmKEsAEVLK	T2(Phospho):	0.993 T(2): 99.3; T(7): 0.7; S(13): 100	62	0.079	18
	Low		mKPRLLSDSGAsScNSGAK	S12(Phospho	0.497 S(7): 0.0; S(9): 0.1; S(12): 49.7	58	0.722	10
	Low		mKQsSPFTFLSPmHR	S4(Phospho)	0.376 S(4): 37.6; S(5): 37.6; T(8): 12.	20	0.719	14
	Low		VQDIVLPGNLlVTGVsK	T11(Phospho	0.497 T(11): 99.4; T(13): 50.3; S(16):	45		12

Os07t0622100-01	Low	Similar to Ribosomal protein s6 RPS6-2.	ADLALStVHALLGVIRK	T7(Phospho)	0.993 S(6): 0.7; T(7): 99.3	60		16
	Low		DPAtRAAAAAVEK	T4(Phospho)	1 T(4): 100.0	35		11
	Low		ILVctPQAEVAIcWK	T5(Phospho)	1 T(5): 100.0	32	0.605	10
	Low		VAHLGVHLGGDAADGsVGR	S16(Phospho)	1 S(16): 100.0	31	0.743	11
Os07t0674200-01	Low	Similar to 60S ribosomal protein L22-2.	TVGRPLLPtR	T9(Phospho)	0.992 T(1): 0.8; T(9): 99.2	21	0.115	11
Os08t0116500-01	High	Similar to 60S acidic ribosomal protein P1 (L12).	EEAKEEsDDDMGFSLFD	S7(Phospho)	1 S(7): 100.0; S(14): 0.0	96	0	36
	High		EEsDDDMGFSLFD	S3(Phospho)	1 S(3): 100.0; S(10): 0.0	39	0.001	14
	Low		AEGVISEMREHGIPP NATVYNayLDGLLI Y20(Phospho)		0.749 S(6): 0.6; T(18): 24.6; Y(20): 76.0	36		11
	Low		APsIARAcAAPVAALFGAsS	S3(Phospho):	0.31 S(3): 61.9; S(19): 69.0; S(20): 6.0	0	0.304	10
	Low		AtELKAGGVmFLVcLGRPsLHAcPTNQGT2(Phospho):		0.756 T(2): 84.2; S(19): 91.4; T(25): 2.0	15	0.791	14
	Low		AVAAmcSAGMEGVRHGAAAVASVPAA S29(Phospho)		0.387 S(7): 2.9; S(22): 19.6; S(27): 38.0	14	0.69	11
	Low		DVPLGLISSmSSItVvycLMSLALVGMQFT14(Phospho)		0.042 S(8): 27.3; S(9): 43.5; S(11): 4.0	6	0.629	17
	Low		EYsNSWTEPLTPSTNQK	S3(Phospho)	0.416 Y(2): 41.6; S(3): 41.6; S(5): 8.4	52	0.767	13
	Low		GsASHENIVAADF GPMPT HFLSSNQPLI S2(Phospho)		0.498 S(2): 49.8; S(4): 49.8; T(18): 0.0	31	0.779	12
	Low		IEcPRPcWIsPcPLPTNLDEsRANtR	S10(Phospho)	0.887 S(10): 95.0; T(16): 11.3; S(21): 0.0	26	0.799	12
	Low		KIHTPVVysESSVNWR	Y8(Phospho):	0.012 T(4): 0.0; Y(8): 6.9; S(9): 6.9; S(10): 0.0	25		11
	Low		KLsDMIGsAsDttSGTVAASNtGVGtsAR	S3(Phospho):	0.005 S(3): 70.0; S(8): 75.2; S(10): 75.0	0	0.803	15
	Low		KmWDEEEEVQsPLAFK	S11(Phospho)	1 S(11): 100.0	82	0.314	14
	Low		LLLIQFRTSGEGYLSPsGAVtsPTGSSPT S17(Phospho)		0.392 T(8): 1.7; S(9): 1.7; Y(13): 4.1; S(14): 0.0	34	0.803	11
	Low		LLLSLLMTAAASYLAYAVHDMPSVsTGL S25(Phospho)		0.405 S(4): 0.0; T(8): 0.0; S(12): 0.3; S(13): 0.0	37	0.09	11
	Low		LTPPLLSYSLSSVsDARLLLPLVtHsLR	S14(Phospho)	0.057 T(2): 12.0; S(7): 14.9; Y(8): 14.0	13	0.755	15
	Low		mAASPTGSSSSAPAAAAAAAEAtDGP T24(Phospho)		0.016 S(4): 20.7; T(6): 20.7; S(8): 20.0	2	0.55	18
	Low		MASGSSSSNDAAADLtVLVDDFyFSVLS T16(Phospho)		0.611 S(3): 2.9; S(5): 2.9; S(6): 2.9; S(7): 0.0	24	0.378	12
	Low		mAsSRVMAAAAASSSSPPPPPPAAA S3(Phospho)		0.862 S(3): 86.2; S(4): 13.0; S(13): 0.0	32	0.621	13
	Low		RsPSELHDDVSSSSTATHLTGPVWPAS S2(Phospho)		0.371 S(2): 37.1; S(4): 37.1; S(11): 4.0	35	0.682	18
	Low		sFGGLFLITGVVtsAMLLIYLAVFFyR	S1(Phospho)	0.102 S(1): 99.7; T(9): 65.8; T(13): 65.0	29	0.55	19
	Low		SSPAAGVsFsstARGsGAsAAtADtGIDSF S8(Phospho):		0.005 S(1): 74.6; S(2): 74.6; S(8): 78.0	3		14
	Low		SSSSSAGGSHAGLALAATAMALSGTL S31(Phospho)		0.935 S(1): 0.0; S(2): 0.0; S(3): 0.0; S(4): 0.0	45	0.516	13
	Low		sVGLAMSLSAQGVGSyASSALVSAIDW. S1(Phospho)		0.055 S(1): 45.3; S(7): 27.2; S(9): 27.0	15	0.446	13
	Low		SyLVWNAVGC LGVsAIsDLVREVEAIQK Y2(Phospho):		0.5 S(1): 50.0; Y(2): 50.0; S(14): 10.0	49		11
	Low		tNSEGSFFAGPLYDDIGYVEASKAGYt T1(Phospho)		0.104 T(1): 10.4; S(3): 10.4; S(6): 10.0	25		10
	Low		VNDIHSEmsARGLsPNLVTYGALIAGWc S9(Phospho):		0.084 S(6): 33.8; S(9): 33.8; S(14): 4.0	0		12
	Low		YFFWDSFHPTeKVN R	T10(Phospho)	0.85 Y(1): 2.1; S(6): 12.8; T(10): 85.0	62	0.452	10
	Low		ySTESVVHTNEEKmLGK	Y1(Phospho)	0.244 Y(1): 24.4; S(2): 24.4; T(3): 24.0	12	0.741	12
Os08t0117200-00	Low	Similar to 40S ribosomal protein S13 (Fragment).	DGVVVSLsPSER	S8(Phospho)	0.921 S(6): 3.9; S(8): 92.1; S(10): 3.9	40		11

	Low		GLRsLAVAR	S4(Phospho)	1 S(4): 100.0	47		13
	Low		IGVKStAIR	T6(Phospho)	0.894 S(5): 10.6; T(6): 89.4	48	0.538	12
	Low		LsRIETHmAR	S2(Phospho)	0.959 S(2): 95.9; T(6): 4.1	31		10
	Low		MLsGDVTLPA PK	S3(Phospho)	0.993 S(3): 99.3; T(7): 0.7	46		13
	Low		SFGARVstIVK	S7(Phospho)	1 S(1): 0.0; S(7): 100.0; T(8): 100.0	55		11
	Low		TPTtPSSSKPAR	T4(Phospho)	0.486 T(1): 1.2; T(3): 48.6; T(4): 48.6	58	0.702	11
Os08t0117300-01	High	Similar to 40S ribosomal protein S13.	TAA sDVEEMIMK	S4(Phospho)	0.999 T(1): 0.1; S(4): 99.9	122	0	62
	Low		AAVTtTAGGKVVVR	T5(Phospho)	0.333 T(4): 33.3; T(5): 33.3; T(6): 33.3	4	0.743	11
	Low		DGRAsPLAGDTLR	S5(Phospho)	1 S(5): 100.0; T(11): 0.0	50	0.752	14
	Low		DGSSALSAEsIcK	S10(Phospho)	0.729 S(3): 4.7; S(4): 17.6; S(7): 4.7;	38		11
	Low		GLRsLAVAR	S4(Phospho)	1 S(4): 100.0	47		13
	Low		IGVKStAIR	T6(Phospho)	0.894 S(5): 10.6; T(6): 89.4	48	0.538	12
	Low		mLQELFKtFR	T8(Phospho)	1 T(8): 100.0	75		13
	Low		SAtARGGGGGGAPT LR	T3(Phospho)	0.495 S(1): 49.5; T(3): 49.5; T(13): 1.1	25	0.127	12
	Low		sATARGGGGGGAPT LR	S1(Phospho)	0.772 S(1): 77.2; T(3): 18.1; T(13): 4.1	40	0.159	18
Os08t0127700-01	High	Similar to Pre-mRNA-splicing factor SLU7.	DGEEGDENVAsEEEEDEEDGLKIDEAK	S11(Phospho)	1 S(11): 100.0	97	0	51
	Middle		FltAtAFAsAAVGTALNQVILPEIRK	T3(Phospho)	0.539 T(3): 84.6; T(5): 84.6; S(9): 84.6	9	0.037	13
	Low		APsFARsAPsVPSmtssAGALscK	S3(Phospho)	0.231 S(3): 93.9; S(7): 76.9; S(10): 76.9	9	0.592	13
	Low		AsENEIsNRMA sVtLQDGAFENLK	S2(Phospho)	1 S(2): 100.0; S(7): 100.0; S(12): 100.0	12	0.19	12
	Low		GyMFHIDEIILLWEAEGFVsSNGR	Y2(Phospho)	0.76 Y(2): 95.8; S(20): 80.2; S(21): 80.2	13		10
	Low		HVsHLFLGYPGHTmSLEKtPDLcK	S3(Phospho)	0.062 S(3): 46.4; Y(9): 46.4; T(13): 46.4	2		11
	Low		IlGLVGmRPTSLHDcGRDsDDDDFR	S19(Phospho)	0.648 T(10): 17.6; S(11): 17.6; S(19): 17.6	12	0.803	12
	Low		IYDtDPTVLNALANTGIKVmVmLPNK	T4(Phospho)	0.195 Y(2): 19.5; T(4): 19.5; T(7): 16.1	1	0.792	11
	Low		LmssSSSDDEyDEDSRNLFssR	S3(Phospho)	0.008 S(3): 55.6; S(4): 55.6; S(5): 55.6	0	0.235	13
	Low		MAAVGScLLGAISGDtLyVANLGDSR	T17(Phospho)	0.161 S(6): 3.3; S(14): 28.8; T(17): 57.1	14	0.804	10
	Low		mLSTLPFSAmIVLSTLVAPAA tPLSGSR	T22(Phospho)	0.66 S(3): 0.8; T(4): 0.8; S(8): 0.8; S(11): 0.8	23	0.154	10
	Low		MsVSAFAAVAIAAAAssPsRPLVIAPR	S2(Phospho)	0.492 S(2): 50.8; S(4): 50.8; S(16): 98.4	44	0.596	12
	Low		mVsAA sEVAASAAAGPSSSSSDAsPP	S3(Phospho)	0.011 S(3): 27.1; S(6): 27.1; S(12): 49.1	9	0.694	16
	Low		sAAA AKQsSQPPPPPSMDGGEPFYVVF	S1(Phospho)	0.709 S(1): 96.7; S(8): 73.5; S(9): 22.1	43		10
	Low		SYTAVLAALVAHsHLsLARSLLADmR	S13(Phospho)	0.055 S(1): 39.4; Y(2): 39.4; T(3): 39.4	0	0.479	13
	Low		VAtNAYTLAVWFTAsADATVAWTANR	T3(Phospho)	0.196 T(3): 33.6; Y(6): 33.6; T(7): 33.6	30	0.474	26
	Low		VFDssVEtlttGtWQALGsAWK	S4(Phospho)	1 S(4): 100.0; S(5): 100.0; T(8): 100.0	0	0.106	14
	Low		VLLDHDP SLGKtFGQSNVTP LITAAIR	T12(Phospho)	0.08 S(8): 1.8; T(12): 8.0; S(16): 61.1	11	0.603	12
	Low		VVIDGNLItGmGLGtVIDFsLAIKK	T9(Phospho)	1 T(9): 100.0; T(15): 100.0; S(20): 100.0	30	0.539	12
Os08t0129200-02	Low	Similar to Cold shock protein-1.	DSsQHSSNDLQEELKK	S3(Phospho)	0.498 S(2): 49.8; S(3): 49.8; S(6): 0.2	84	0.683	14
	Low		IEATTGGGGGGGAADtGGSPRR	T15(Phospho)	0.468 T(4): 4.7; T(5): 46.8; T(15): 46.8	29	0.442	11
Os08t0130500-01	High	60S acidic ribosomal protein P0.	EEPEEEsDGD LGMSLFD	S7(Phospho)	1 S(7): 100.0; S(14): 0.0	46	0	29
	High		EVAVNDFmPATSAyETIR	Y14(Phospho)	0.333 T(11): 33.3; S(12): 33.3; Y(14): 33.3	69	0.003	12

High	KEEPEEEsDGDGLGMSLFD	S8(Phospho)	1 S(8): 100.0; S(15): 0.0	125	0	66
Middle	AVFAAmATSGGyGYGGLQHR	Y12(Phospho)	0.981 T(8): 0.6; S(9): 0.6; Y(12): 98.1	39	0.037	12
Middle	EASHAEIYETAItHNSR	T13(Phospho)	0.437 S(3): 0.0; Y(9): 1.9; T(11): 1.9;	47	0.029	12
Middle	LSVTALMATGIGNAALMVIsVAIsVAmFV	S20(Phospho)	0.973 S(2): 1.0; T(4): 1.1; T(9): 1.7; S	31	0.02	14
Low	AASFNTRGsLsFDMATASFDLGGVGVG	S9(Phospho)	0.076 S(3): 10.1; T(6): 10.1; S(9): 62.	18		14
Low	AcLHDGGLLQGSRFHPQLsTlyNVGQSy	S19(Phospho)	0.059 S(12): 77.4; S(19): 22.9; T(20):	13	0.75	11
Low	AGDtKPtEsAIVGSTVTGHLLHIDGYSt	T4(Phospho)T5(Phospho)	T Too many isoforms		0.529	11
Low	AIGGSLTAVPGLSDmIDDTVNSIVsDmLI	S25(Phospho)	0.301 S(5): 9.1; T(7): 9.1; S(13): 6.0;	9	0.766	12
Low	AKELssmGFTIVWSPPPTDsVsPEGyMP	S5(Phospho)	0.027 S(5): 75.7; S(6): 75.7; T(10): 60	5	0.732	12
Low	ALPAITTCPFYTTSWAGRGSHVNLtAG	T26(Phospho)	0.732 T(6): 3.6; T(7): 3.6; Y(12): 3.6;	19	0.652	11
Low	AMEVLTVMVMPNcFTYNSIMHGyCSSG	S29(Phospho)	0.546 T(6): 0.0; T(15): 0.0; Y(16): 0.0	53	0.64	15
Low	ANKPyYGiDFPGSKPtGRFsNGFNADy	Y5(Phospho)	0.171 Y(5): 56.5; Y(6): 56.5; S(13): 5	16	0.708	13
Low	APPVRDVLGDDVsLLcQSTHRPASSAA	S13(Phospho)	0.06 S(13): 79.9; S(18): 17.1; T(19):	15	0.367	11
Low	AQFPSPNEYSSfMgGDFsTATGIATFTmr	S11(Phospho)	0.014 S(5): 7.7; Y(9): 7.7; S(10): 10.5	2	0.762	11
Low	AQPPLPSGPPPHVSTSFSAAsssLHLPA	S21(Phospho)S22(Phospho)	T Too many isoforms			11
Low	AQSGNPSSVAsVSVEAGPK	S12(Phospho)	0.651 S(4): 19.5; S(8): 6.5; S(9): 6.5;	29		12
Low	ASASASDGASSaIVAGtVNGYHVLKIVc	S12(Phospho)T18(Phospho)	T Too many isoforms		0.56	12
Low	ASYQDPSLPSLVPymTSR	Y14(Phospho)	0.166 S(2): 0.0; Y(3): 0.0; S(7): 1.1; S	34	0.729	10
Low	ATLHtVcFMEFLVGVmR	T5(Phospho)	0.733 T(2): 26.7; T(5): 73.3	13	0.499	11
Low	ATNFPTVDQyGDYLIGLLQsNLNSLyKm	Y10(Phospho)	0.268 T(2): 8.9; T(6): 21.6; Y(10): 59.	25	0.077	11
Low	ATSSeQLPDsEKTNPPTVPPISESPVQG	S4(Phospho)	0.204 T(2): 39.1; S(3): 39.1; S(4): 39.	43	0.131	12
Low	ATTINVNsrAR	S8(Phospho)	0.708 T(2): 21.4; T(3): 7.8; S(8): 70.8	18		11
Low	AVSPRPTHAAtsAAAsNTEGHGGAA/	T12(Phospho)	0.075 S(3): 21.0; T(7): 21.0; T(9): 21.	16		11
Low	cAAAGEVVGSAAGVGRsAGMEVAIAAtA/	S17(Phospho)	0.492 S(10): 50.8; S(17): 50.8; T(26):	28	0.456	11
Low	cHtyMMMKQVVATTSGTQPPWSTLLMC	T3(Phospho)	0.816 T(3): 89.9; Y(4): 89.9; T(13): 14	40	0.359	11
Low	cHYMMMKQVVATTSGTQPPWStLLMQ	T3(Phospho)	0.093 T(3): 48.2; Y(4): 48.2; T(13): 6.	36	0.503	15
Low	cLAPEASAVMNGRLIsVWAVDEssILAFs	S16(Phospho)	0.17 S(7): 50.3; S(16): 50.3; S(23): 0	9	0.397	11
Low	cLsEAFLADGAEHDPGYEAVTVALEKyA	S3(Phospho)	0.899 S(3): 97.6; Y(17): 5.4; T(21): 5.	22		10
Low	cNATsLPGyYLNLPsIsVPDLRyPvvVSR	S5(Phospho)	0.029 T(4): 91.2; S(5): 82.5; Y(9): 19.	23		10
Low	cVRQVISEVVAItLLVfVtCgAASlyGEDr	T12(Phospho)	0.083 S(7): 68.7; T(12): 49.7; T(19): 6	1	0.415	11
Low	DAFLEILQENSGALPGFsGHIFGHNGLQ	S18(Phospho)	0.99 S(11): 1.0; S(18): 99.4; Y(29): 9	56	0.589	14
Low	DcLETISDGISTGTRTSLDSQNILIsMSSc	S26(Phospho)	0.598 T(5): 0.0; S(7): 0.0; S(11): 0.0;	39	0.682	16
Low	DDDDGAQLGNGGVILVLFtIPTGFALFs	T20(Phospho)	0.033 T(20): 98.4; T(22): 96.7; S(28):	16	0.786	11
Low	DDGSSVFSKitAFEEELR	T11(Phospho)	1 S(4): 0.0; S(5): 0.0; S(8): 0.0; T	73	0.731	17
Low	DDTVDPAPQDmRHVLSDLsFDLAtEGs	S20(Phospho)	0.225 T(3): 11.8; S(16): 23.7; S(20): 9	11		12
Low	DKFLVQsVVVDDGLsAK	S7(Phospho)	1 S(7): 100.0; S(15): 100.0	23	0.772	10
Low	DNFMEVAVtKDYFHLGQsFPSVIEEIKPf	T9(Phospho)	0.154 T(9): 37.6; Y(12): 37.6; S(18): 7	10		12
Low	DQtLNQLLTEMdGFDSDMKVIVmAAtNF	T3(Phospho)	0.636 T(3): 65.6; T(9): 18.5; S(16): 18	21		14
Low	DTVGQyESHmAftMPGLYRVVHGIDVFI	Y6(Phospho)	0.613 T(2): 10.2; Y(6): 82.7; S(8): 30.	37		13
Low	DTWANEAVAQTIRSNFIFWQVyHDtSEC	Y22(Phospho)	0.875 T(2): 0.3; T(11): 1.1; S(14): 3.5	44		14
Low	DYDGtVVWQsDSNSIDVQYAQLLDTGN	T5(Phospho)	0.02 Y(2): 11.9; T(5): 11.9; S(10): 21	2	0.743	11
Low	EEGGcsNASVsDxAPPQRHAPHPIALAT	S6(Phospho)	0.269 S(6): 49.3; S(9): 49.3; S(11): 60	11	0.438	11
Low	EEREMEAAAAAGVQLGtsKPQIATQAEm	T17(Phospho)	0.641 T(17): 76.8; S(18): 91.0; T(24):	34	0.06	15
Low	ELFGGAmDLEESLSMLVMLQEAsDYmE	S23(Phospho)	0.105 S(12): 18.3; S(14): 18.3; S(23):	8	0.775	10
Low	EmAIAIVGLGGssGEADVRRGGVGAAG	S13(Phospho)	1 S(13): 100.0; S(14): 100.0; T(3)	5	0.652	12
Low	ENPPASKASVESmPTVtIAAsHVGADSt	T17(Phospho)	0.038 S(6): 24.2; S(9): 24.2; S(12): 2	4	0.715	10
Low	ESENSALEdANAPLEDtRNASDAASLSE	S5(Phospho)	0.085 S(2): 83.0; S(5): 16.4; T(17): 58	20	0.776	15

Low	ETmANTVAETLHVHSSDGsFSGFAAGG S16(Phospho)	0.037 T(2): 16.0; T(6): 16.0; T(10): 15	3	0.756	11
Low	EVDSLmVAQNIVQQItDFNVRsGMLAE T17(Phospho)	0.994 S(4): 0.6; T(17): 99.6; S(23): 99	29	0.094	10
Low	FASGVsMVAsVSLAISYPTIAAAPHmFL† S6(Phospho)	0.077 S(3): 40.9; S(6): 40.9; S(10): 40	11	0.778	10
Low	FASGVSmVAsVSLAISYPTIAAAPHMFL† S10(Phospho)	0.057 S(3): 23.5; S(6): 23.5; S(10): 3	9	0.712	11
Low	FDAQIDVSKNALLSDVclStSAAPtyLPG† T20(Phospho)	0.341 S(8): 0.9; S(14): 20.5; S(19): 20	41	0.372	15
Low	FDSPAAsPYATALsSPRGR S7(Phospho)	0.567 S(3): 3.2; S(7): 68.3; Y(9): 14.2	52	0.746	15
Low	FDsQLLTAFtSSLYVAGLLTtFAAsRVtA(S3(Phospho)T21(Phospho)	Too many isoforms		0.803	14
Low	FGGtLALSmAFIAVmyGLFGAMGyLAFG T4(Phospho)	0.882 T(4): 88.9; S(8): 11.8; Y(16): 99	32	0.761	12
Low	FILFDSVSVSGATyLHNSTSFVyKtVVNt† Y14(Phospho)Y23(Phospho)	Too many isoforms		0.641	11
Low	FRcPEVLFPQPSMIGmEsAGIHETTYNSlr S17(Phospho)	0.669 S(11): 25.1; S(17): 66.9; T(23):	30	0.195	19
Low	FSMRMGTSyFGLYIEPPASSSGGGGVA S8(Phospho)	0.351 S(2): 20.3; T(7): 37.3; S(8): 59.	27		12
Low	FsMRMGTSyFGLYIEPPASSSGGGGVA S2(Phospho)	0.219 S(2): 69.5; T(7): 39.0; S(8): 39.	25		12
Low	GDYStsDAVAMFGsLVVPHNLFLHSSLV T5(Phospho)	0.022 Y(3): 21.1; S(4): 21.1; T(5): 30.	6	0.768	11
Low	GHVVAvtGDGtNDAPALHEADIGLSmGI T7(Phospho)	0.261 T(7): 73.7; T(11): 73.7; S(25): 4	7	0.168	11
Low	GLGWETNSDsLR S10(Phospho)	0.989 T(6): 0.0; S(8): 1.1; S(10): 98.9	75	0.572	16
Low	GLQFIGNMSVAmDDQtAAPAsGsVVS† T17(Phospho)	0.027 S(10): 42.9; T(17): 61.3; S(22):	6	0.755	16
Low	GMAAtAGEGLEWGMmAFGPGLtVETm† T4(Phospho)	0.333 T(4): 66.7; T(22): 66.7; T(25): 6	1	0.465	12
Low	GmGIVGGKGGHGGGSSDSESGGDLA† T31(Phospho)	0.963 S(15): 0.4; S(16): 0.7; S(18): 0.	27		10
Low	GNDAAANVYDQAVIDSMVATLVERVsc† T8(Phospho)	0.657 T(8): 66.8; Y(9): 27.2; S(16): 5.	28	0.806	13
Low	GNyVitsEELEEIMEEcmRVWFEFIR Y3(Phospho)	1 Y(3): 100.0; T(6): 100.0; S(7): 1	3	0.645	12
Low	GRmcSsAAPcLPLPPPPPLLLmTWLcsS S5(Phospho)	0.33 S(5): 72.0; S(6): 27.2; T(23): 8.	18	0.556	12
Low	GScNFNNLSMITTSDPsQGTcRFQIEIDT S17(Phospho)	0.538 S(2): 18.9; S(9): 2.9; T(12): 7.1	31	0.175	16
Low	GsGDGcQPKPLSPmAEGLR S2(Phospho)	0.987 S(2): 98.7; S(13): 1.3	31	0.63	13
Low	GSTLQVmGIIAASSGEWSVIGGTGEFsr S27(Phospho)	0.324 S(2): 11.3; T(3): 11.3; S(13): 15	14	0.572	15
Low	GtLPPDDVp†DTHDQKPDGTSTEKLET† T2(Phospho)	0.089 T(2): 64.2; T(10): 60.3; T(12): 2	10	0.806	11
Low	GTSVGQmISAYLANEsELDDRTIHLLFs† S16(Phospho)	0.014 T(2): 47.2; S(3): 47.2; S(9): 30.	3	0.772	10
Low	GVLASDQt†ADNATAALVAQNAYnMYL T8(Phospho)	0.309 S(5): 53.4; T(8): 53.4; T(10): 69	40		11
Low	GvtFGEYVSEFSsSNGTFLKPPFcASVm T3(Phospho)	0.087 T(3): 20.4; Y(7): 20.4; S(9): 20.	12	0.682	12
Low	GVTSSLNSGDGcFSNTASTDVADmGsF S26(Phospho)	0.015 T(3): 1.3; S(4): 1.3; S(5): 1.6; S	11	0.682	11
Low	GyAGAAAVAGsIGYGsAAAAAAAmGGY Y2(Phospho)	0.343 Y(2): 95.6; S(11): 76.6; Y(14): 1	23		11
Low	GYcYPPREPIDYsLVGLyHytVLEITSK S13(Phospho)	0.187 Y(2): 0.5; Y(4): 0.5; Y(12): 80.3	50	0.804	13
Low	GyFEDRRPAsNMDPYVVTGMIAEtLLW Y2(Phospho)	0.337 Y(2): 99.9; S(10): 77.5; Y(15): 1	42	0.691	11
Low	GYLGAKSWPPDGLSSSSsGEAAAD† S19(Phospho)	0.686 Y(2): 4.2; S(7): 4.2; S(13): 1.9;	31	0.189	16
Low	HASSSTQVVAsAtSTSTSTVAMVNPcS† S11(Phospho)	0.03 S(3): 22.6; S(4): 22.6; S(5): 17.	23	0.772	13
Low	HDGGTPDEGGDPAtAVEAVTNmSGEA† T14(Phospho)	0.935 T(5): 0.2; T(14): 93.5; T(20): 3.	44	0.537	18
Low	HEAGGSSPRADPTAcGTVEAGtDLGGN T22(Phospho)	0.58 S(6): 5.1; S(7): 3.3; T(13): 8.4;	18	0.663	11
Low	HEAGSSPRADPTAcGTVEAGTDLGG† S34(Phospho)	0.197 S(6): 9.6; S(7): 9.6; T(13): 13.3	6		11
Low	HGVEAyQGVLFGLELDMMPsNKtPSL† Y6(Phospho)	0.263 Y(6): 99.4; S(21): 68.8; T(24): 2	27	0.504	16
Low	HHPsLLFFRTpQVGPAYGsGGLEEGD S19(Phospho)	0.011 S(4): 80.2; T(10): 85.2; Y(17): 2	3	0.717	13
Low	HHVAMNyLFAsWLLLQTcSQcRSFAPM† Y7(Phospho)	0.926 Y(7): 96.1; S(11): 94.6; T(17): 3	28	0.708	16
Low	HlyDAVAQYVVNGAmKGINGTIFAYGV† Y3(Phospho)	0.02 Y(3): 55.5; Y(9): 54.9; T(21): 49	0	0.743	16
Low	HLNLSVNSFTGSmPATYGyLPSLQVLs† Y19(Phospho)	0.005 S(5): 37.6; S(8): 37.6; T(10): 37	0		12
Low	HLSRAyNFsNGVAFGDGFVEVLAATQT† Y6(Phospho)	0.073 S(3): 92.5; Y(6): 77.9; S(9): 29.	29	0.166	13
Low	HMFKsAIEscYLFQGVsDsLIVQLVAEMK S5(Phospho)	0.483 S(5): 96.9; S(9): 51.7; Y(11): 5	50	0.773	13
Low	HPscGVSSREHPTQLGTcSAQEPPTS S3(Phospho)	0.603 S(3): 60.3; S(7): 21.7; S(8): 8.5	28	0.764	15
Low	HSGsDPDmVKItVAGGNVNGGAAASET S4(Phospho)	0.25 S(2): 40.9; S(4): 40.9; T(12): 56	14		14
Low	HsIlmYDLIAGPSKASLMQSSIPAPcsLtc† S2(Phospho)	0.018 S(2): 37.5; Y(6): 37.5; S(13): 3	0		10

Low	HtymLILScQDSSYLHScFMGGKQAHQL T2(Phospho)	0.209 T(2): 45.2; Y(3): 45.2; S(8): 27.	15	0.541	11
Low	IGAGmALsVAAmAAAAtVEGR S8(Phospho)	1 S(8): 100.0; T(17): 100.0	44	0.365	10
Low	IILTKMTAFITILDDIFDTYAttEESMmLAK T22(Phospho)	0.041 T(4): 0.9; T(7): 4.0; T(11): 4.0;	21		12
Low	IPsGSQLETIYNQHPDIYNGNsGLcGPPL S3(Phospho)	0.25 S(3): 36.2; S(5): 36.2; T(9): 17.	15		12
Low	KyPALysGtALmFFLsFLQMAVVALAIDR Y2(Phospho)	1 Y(2): 100.0; Y(6): 100.0; S(7): 1	16	0.69	10
Low	LDDAREVIVWNIAPsNWNFGTTYTsNIN T8(Phospho)	0.021 T(8): 70.4; S(15): 30.8; T(21): 6	4	0.746	12
Low	LDDGcPTTDTLQLAHPTLsLMDAHIVYIM T17(Phospho)	0.01 T(7): 1.3; T(8): 1.3; T(10): 20.6	17	0.224	15
Low	LGGtSAETYEkTVEVLTK T4(Phospho)	0.386 T(4): 38.6; S(5): 38.6; T(8): 15.	16		10
Low	LGLTTAVVVsSR S10(Phospho)	0.112 T(4): 43.7; T(5): 43.7; S(10): 11	15	0.313	13
Low	LGMtNMYPstTLLGDKSSEMSGLPIDE T5(Phospho)	0.01 T(5): 17.4; Y(8): 23.7; S(10): 31	7	0.791	12
Low	LGVVRAAsAEVAAPDAAAAAPGYtsDSL S8(Phospho)	0.104 S(8): 96.1; Y(23): 47.7; T(24): 4	19	0.806	11
Low	LHVVCpsGAANAGQGDtSRSHNAGAGA S7(Phospho)	0.13 S(7): 97.1; T(17): 45.1; S(18): 4	20		10
Low	LKAVmAsDGYEHLVtsFPSIAtEILAMFA S7(Phospho)	0.177 S(7): 97.8; Y(10): 10.1; T(15): 4	27	0.803	10
Low	LLFPVAAGIWDFLsGGGAGGAAAsLA S14(Phospho)	1 S(14): 100.0; S(25): 100.0	41	0.291	15
Low	LLHHLNLAGNNIsGTIPRGLsNLtAmtQtK S13(Phospho)	0.182 S(13): 74.5; T(15): 81.8; S(21):	2		10
Low	LLsPKAtTVVLLDTGsLsVsLALcsPPPLR S3(Phospho)	0.073 S(3): 92.2; T(7): 55.0; T(8): 55.	24	0.806	11
Low	LLYtsGMPVLLssAVssLYVVSQALYRR T4(Phospho)	S5(Phospho)S Too many isoforms		0.508	10
Low	LMIENLEGLPAcsQILtRmQSGVGVALtD S13(Phospho)	0.12 S(13): 81.1; T(17): 39.2; S(21):	5	0.792	11
Low	LmSDIGDMmNIQVIVEGSmNSSNPYFN S28(Phospho)	0.388 S(3): 0.0; S(18): 1.5; S(21): 12.	39	0.649	11
Low	LmSSNSRSTmVltcFFtEtLALQAEIHK T10(Phospho)	0.028 S(3): 40.8; S(4): 40.8; S(6): 40.	16	0.747	11
Low	LNPstNLGLALAsFsSSsRPEQPELPGA S4(Phospho)	0.033 S(4): 86.7; T(5): 82.1; S(13): 63	6		11
Low	LNsLDLSGNDLSGAVPASLAALKLssLnr S3(Phospho)	0.673 S(3): 86.3; S(7): 9.2; S(12): 20.	33	0.774	13
Low	LQAASPHGDSSNGAPAtttMAATAAVAAI S11(Phospho)	0.338 S(5): 18.1; S(10): 44.4; S(11): 4	34	0.735	10
Low	LQGLcLPcPssAPLATHSSELSLAKATSy S10(Phospho)	0.01 S(10): 32.4; S(11): 45.9; T(16):	3	0.691	10
Low	LQWcVDAVPDsTyTLTTTDTPRLLGmStl S11(Phospho)	0.006 S(11): 5.1; T(12): 5.1; Y(13): 11	40	0.414	16
Low	LRVFLFPAsGsEAAAAGAsGSGSHLAA S9(Phospho)	0.02 S(9): 29.2; S(11): 74.7; S(19): 1	27	0.761	11
Low	LsFAFNGLtGslPGELAtLsGVEILYASSNF S2(Phospho)	0.199 S(2): 78.2; T(9): 80.9; S(11): 80	14	0.337	10
Low	LsFKWDAGscssASSsAMysPLsAVsAP S2(Phospho)	0.055 S(2): 74.3; S(9): 74.3; S(11): 74	20	0.806	15
Low	LSGMTVAGNPLSVSSSAySSLPTIIDsGt Y18(Phospho)	S27(Phospho)S Too many isoforms			13
Low	LsKIGssDsGAAAsGAAAGAGGGVGGG S2(Phospho)	1 S(2): 100.0; S(6): 100.0; S(7): 1	12	0.573	16
Low	LsNLVEVALyNTSLsGLIPssIGNLtNLNR S2(Phospho)	0.011 S(2): 98.6; Y(10): 97.7; T(12): 9	8	0.776	10
Low	LsQMssTLIPISASGLHRALPSGLSTTLs S2(Phospho)	S5(Phospho)S Too many isoforms		0.786	11
Low	LstTHAAVRHPPPCAAPTAAAAAAIAS S2(Phospho)	0.023 S(2): 40.7; T(3): 40.7; T(4): 40.	0	0.206	13
Low	LTNSEGstVRPPtIVQAsVLEVGNHQPSI S7(Phospho)	0.229 T(2): 44.6; S(4): 44.6; S(7): 67.	18	0.746	18
Low	mAAAAAEGGGGGGGAVIDPSYVPDs S25(Phospho)	0.711 Y(17): 2.0; S(20): 0.9; Y(21): 0.	44	0.758	15
Low	mAAAAAEGGGGGGGAVIDPSYVPDs S28(Phospho)	0.154 Y(17): 10.2; S(20): 10.2; Y(21):	19	0.507	10
Low	MAccGRQSYGGVAELGHGGPAQVLAs S26(Phospho)	0.894 S(8): 5.3; Y(9): 5.3; S(26): 89.4	21	0.662	13
Low	mADKNGLLLLsTIAAVTLssLsLAAVAsP S11(Phospho)	0.02 S(11): 93.5; T(12): 93.5; T(17):	28		11
Low	mAETALSMARSMMLGGAIsAAsAAAGEE S18(Phospho)	0.067 T(4): 33.4; S(7): 33.4; S(11): 33	0		10
Low	mAGTLLQPVALGttFAGR T13(Phospho)	0.938 T(4): 6.2; T(13): 96.9; T(14): 96	28		11
Low	mALIssFLicLAsPGIGSSSSsARFLsPF S5(Phospho)	S6(Phospho)S Too many isoforms		0.724	10
Low	MAScLsVLLLLcLALAGsVsGQQLSATFY S6(Phospho)	0.012 S(3): 29.2; S(6): 68.7; S(18): 13	12		11
Low	mAVEEsPPPPPsPPPPPsPQPAAEV S6(Phospho)	0.25 S(6): 99.8; S(12): 75.0; S(13): 1	37	0.803	24
Low	mEGGKmSSmGmDAASASVtVPPmQm T19(Phospho)	0.724 S(7): 0.3; S(8): 0.3; S(15): 6.1;	41	0.673	13
Low	mEMAIAIVGLGGSSGEADVRRGGVGAA S15(Phospho)	0.321 S(14): 26.0; S(15): 32.1; T(33):	3	0.589	16
Low	mGAAASAAFSATcQTAGKATMAAAIDV T30(Phospho)	0.732 S(6): 0.2; S(10): 0.1; T(12): 0.1	33	0.507	14
Low	mGAAASAAFSATcQTAGKATmAAAIDV T29(Phospho)	0.029 S(6): 8.5; S(10): 9.4; T(12): 11.	5	0.707	11

Low	mGEVQLAVRFtcSSLLNmmHLysQPLLP T11(Phospho)	0.09 T(11): 59.4; S(13): 59.4; S(14):	4	0.533	21
Low	mLKsVStGGGASGAAAAAAER S4(Phospho)	0.773 S(4): 82.1; S(6): 22.4; T(7): 95.	52	0.708	11
Low	mLKSVstGGGASGAAAAAAER S6(Phospho)	0.989 S(4): 1.1; S(6): 99.1; T(7): 99.8	73	0.577	11
Low	MLScYFTtVGFyFSTLLTVVTVYVFLYGR T8(Phospho)	0.196 S(3): 11.5; Y(5): 11.5; T(7): 21.	19		11
Low	MsFytGIIIHDLmDSGTLGPAKEVHGyAD S2(Phospho)	0.929 S(2): 98.8; Y(4): 98.2; T(5): 94.	35	0.691	14
Low	MstmTmSALPLAAPAtAAAAAAGAFaHIL S2(Phospho)	0.15 S(2): 44.5; T(3): 69.6; T(5): 69.	16		10
Low	mtDIHTNENYSNSAVSPVNVVPPSGAAI T2(Phospho)	0.009 T(2): 88.1; T(6): 11.0; Y(10): 2.	26	0.618	12
Low	mTTTTTAAAAALTSSVGDGPPPSRsttlt S25(Phospho)T26(Phospho)	Too many isoforms		0.776	13
Low	MVAVAAATTTTmLtaAMK T14(Phospho)	0.247 T(7): 8.6; T(8): 8.6; T(9): 24.7; T	21	0.744	17
Low	mVIASAAFSAGASASsGsAAAAAADPsF S16(Phospho)	0.198 S(5): 6.6; S(9): 8.4; S(13): 33.6	61	0.49	16
Low	myHLLTsSGLKPDQYtWsALLSALYRSG Y2(Phospho)S8(Phospho)T	Too many isoforms		0.683	10
Low	NETEQmVRLVsPSGETGmLVVDsVVPE S11(Phospho)	0.108 T(3): 17.0; S(11): 25.0; S(13): 4	4	0.786	11
Low	NGILAmLDERTGDIILANPAIGEtLAVPPF T15(Phospho)	0.383 T(11): 61.7; T(15): 77.2; T(21):	5	0.31	10
Low	NIEMDDVLGLNySNQAQQSACvQPAAsG Y12(Phospho)	0.52 Y(12): 66.0; S(13): 36.6; S(19):	17	0.776	10
Low	NIHEMPsstQYIPKLTLDGmEIQVVEIK T4(Phospho)	0.072 T(4): 64.9; S(8): 67.6; S(9): 68.	1		10
Low	NIHEMPssTQyIPKLTLDGmEIQVVEIK T4(Phospho)	0.079 T(4): 58.6; S(8): 77.4; S(9): 77.	9	0.743	12
Low	NPNAVItLHsLIKLEGWESLVTIISsDMR T7(Phospho)	0.097 T(7): 71.1; S(10): 71.1; S(19): 6	2	0.123	11
Low	NQQLLLKsyADtINtsILESATSAEILcR S8(Phospho)	0.335 S(8): 80.1; Y(9): 80.1; T(12): 80	25	0.804	14
Low	NtVsWTAMISGFALHNRVEPClHLFAsm T2(Phospho)	0.035 T(2): 17.7; S(4): 50.0; T(6): 50.	32		11
Low	NVDDVENDGyLTGLGPQISDALTINGmF Y10(Phospho)	0.747 Y(10): 74.7; T(12): 24.9; S(19):	40	0.392	16
Low	NVmNMSQADQGALWQsVMKGNLDGyr S16(Phospho)	0.055 S(6): 0.7; S(16): 16.7; Y(25): 60	15	0.804	16
Low	NVVsWttAIAGFVQDDEPVSAMLLREM S4(Phospho)	0.299 S(4): 89.6; T(6): 70.1; T(7): 70.	33	0.532	10
Low	QAANAIPSTPLSQVRDQVtstcINILQsYR T19(Phospho)	0.468 S(8): 2.5; T(9): 2.5; S(12): 3.1;	36		11
Low	QENAVVQTcVVAcASMTYSGGFGsyLL/ S24(Phospho)	0.844 T(8): 2.4; S(15): 3.7; T(17): 3.7	27	0.679	12
Low	QNKAtAQVVASIGIIILGTIsAALGtYssVI T5(Phospho)	0.039 T(5): 50.5; T(6): 50.5; S(12): 32	10	0.806	10
Low	RLFLtASAWIsFLCcFLymAVQVSFAGFR T5(Phospho)	0.071 T(5): 57.1; S(7): 57.1; S(11): 57	0	0.478	14
Low	RLTLVPGAmTWLsAGVsDVLEVSDDEGI T10(Phospho)	0.1 T(3): 60.0; T(10): 60.0; S(13): 6	0	0.349	13
Low	RPQQAsYLtYRPAFSGLFALGRSQHHtA S6(Phospho)	0.007 S(6): 51.2; Y(7): 51.2; T(9): 52.	1	0.55	11
Low	RSSSSAASAsPASASTANSVVTASmS S10(Phospho)	0.028 S(2): 2.2; S(3): 2.2; S(4): 2.2; S	2		11
Low	RsVDLAsELtHAWESTAmTlSDMVTMG S2(Phospho)	0.92 S(2): 99.0; S(7): 96.3; T(10): 94	37	0.754	12
Low	RtPAGEssAQNNsIAAAAAAASVLPtIS T2(Phospho)	0.049 T(2): 49.0; S(7): 75.9; S(8): 75.	15		11
Low	SAAATLQsARAR S8(Phospho)	0.965 S(1): 0.2; T(5): 3.3; S(8): 96.5	41		16
Low	SAHLNQmASIAQLQmAVSscPPsTGG S20(Phospho)	0.01 S(1): 44.6; S(9): 44.6; S(19): 1.	2	0.708	10
Low	SASsAtAAAAAAGNtHNSINFLNVLISLI/ S4(Phospho)S5(Phospho)T	Too many isoforms		0.752	13
Low	SATPsEVEAFytSLISNYSAAITELYGmG. S5(Phospho)	0.023 S(1): 37.6; T(3): 37.6; S(5): 37.	14	0.59	11
Low	SDSLTLAPSPPCAAAAmQQHASSNAtIA T26(Phospho)	0.626 S(1): 0.1; S(3): 0.1; T(5): 0.1; S	46		12
Low	sDVySyGVLLLELVtGKPVAAQGDdDGN/ S1(Phospho)	0.021 S(1): 36.6; Y(4): 36.6; S(5): 32.	4	0.446	11
Low	SFLVQGdDPItSGTGGEsIYGAPFADEI T10(Phospho)	0.257 S(1): 2.1; T(10): 61.3; S(12): 28	25	0.776	10
Low	SGLDYAMmTGGDVAPLGsEAVtKIHQIF S18(Phospho)	0.603 S(1): 16.9; Y(5): 16.9; T(9): 17.	14	0.693	15
Low	SGLSALEEtLEGQtVIVGPsGVGKsSLIN T9(Phospho)	0.021 S(1): 52.3; S(4): 52.3; T(9): 60.	4	0.779	12
Low	sGsLAIAsLdSLLDLLSGFILWFTAfSK S1(Phospho)	0.683 S(1): 99.5; S(3): 99.5; S(9): 98.	35	0.462	15
Low	sLKNmVsQDPsILLGTTPQGNTcLHISSII S1(Phospho)	0.223 S(1): 83.4; S(7): 83.4; S(11): 30	21	0.756	13
Low	SmGPNWQINLNYNLtWILSVdAGFyyLLI T15(Phospho)	0.251 S(1): 16.5; Y(12): 26.0; T(15): 5	12		11
Low	SMSSARVIYDSIsEPDLVssTALISGyTMI S13(Phospho)S19(Phospho)	Too many isoforms		0.758	18
Low	sPLAHYDSSLRVayAGGEVGSmyIPAG/ S1(Phospho)	0.073 S(1): 26.6; Y(6): 26.6; S(8): 26.	12	0.683	14
Low	sPMPMQSSHEGHNLSPLVQGGtMAGG. S1(Phospho)	0.415 S(1): 51.9; S(7): 21.9; S(8): 21.	13	0.352	13
Low	SPSESWLSRALPsVssNPPATsFLGIHV S13(Phospho)	0.041 S(1): 25.4; S(3): 25.4; S(5): 25.	15	0.396	11

Low	SQHsLmDLQDAAtLGSLLSSLMQHcDPPC S4(Phospho)	0.06 S(1): 17.4; S(4): 30.9; T(12): 20.	11		12
Low	sQIGLVGQEPVLFstSIIENVmmGKENAtI S1(Phospho)	0.272 S(1): 95.2; S(14): 72.8; T(15): 7.	11	0.446	12
Low	ssAVALLVAtSSPRcScSLSALITSPPNW S1(Phospho)	0.106 S(1): 100.0; S(2): 100.0; T(10):	62	0.142	25
Low	ssAVALLVATSSPRcScSLSALITSPPNW S1(Phospho)	0.599 S(1): 99.7; S(2): 99.7; T(10): 0.	49	0.752	13
Low	SSDsNsISSALSQTTPVLR S4(Phospho)	0.583 S(1): 22.0; S(2): 22.0; S(4): 66.	51	0.361	13
Low	sslGADLRPTEDScGpmNSINQPcVNVV S1(Phospho)	0.985 S(1): 98.9; S(2): 98.9; T(10): 0.	31	0.227	11
Low	SSTPPAAssAsAsPtPtPAsAsmSTSSSLF S8(Phospho)S9(Phospho)	S Too many isoforms		0.446	12
Low	stIIVPAGsSGEEGWAEFRNVLEINNEA S1(Phospho)	0.247 S(1): 74.8; T(2): 74.8; S(9): 74.	24	0.721	11
Low	StMIGAmANFLDYDVYDLDLtsVKNNSEI T2(Phospho)	0.001 S(1): 71.8; T(2): 28.8; Y(13): 84.	5		10
Low	stSSSTTLSSSTAPPPSSSPSPTRsDtL S1(Phospho)T2(Phospho)	S Too many isoforms		0.629	15
Low	sVmNLPEANsTEFDNNAKTPcVIFMPEG S1(Phospho)	0.093 S(1): 94.7; S(10): 73.2; T(11): 4.	10		13
Low	sVVGIALVFVAtVAIVAFVVFncADGmDs S1(Phospho)	0.304 S(1): 83.5; T(12): 69.6; S(29): 7.	3	0.451	13
Low	sYTRPGSAALAGLMWPAPVRNAVALsV S1(Phospho)	0.362 S(1): 36.5; Y(2): 36.5; T(3): 13.	36	0.749	12
Low	tAGGLILtEttKEKPSIGtVVAVGPGLDDE T1(Phospho)	0.585 T(1): 77.7; T(8): 95.9; T(10): 95.	26	0.631	14
Low	TAGGWTScTTSACsATPTRsTSSPSPTf S20(Phospho)	0.039 T(1): 9.8; T(6): 9.8; S(7): 9.8; T	5	0.603	15
Low	TALDcVAGAAWTAGESAtSLEAWADEV T18(Phospho)	0.479 T(1): 2.2; T(12): 8.2; S(16): 18.	19	0.171	10
Low	TGGyIEGNISIsGYPKK Y4(Phospho)	0.64 T(1): 15.1; Y(4): 70.3; S(10): 18.	39	0.776	11
Low	TGGyIEGSINIsGYPKK Y4(Phospho)	0.153 T(1): 3.7; Y(4): 16.2; S(8): 80.1	37		10
Low	TImSSSPTstLmSPPKSPSPSESPPLSPD S9(Phospho)	0.112 T(1): 7.7; S(4): 13.1; S(5): 23.5	20		12
Low	TImSSSPTstLmSPPKSPSPSESPPLSPD S9(Phospho)T10(Phospho)	T Too many isoforms		0.758	15
Low	tMKPEGsAKNEGVDVANVTSSSTNLIASC T1(Phospho)	0.005 T(1): 8.9; S(7): 21.4; T(19): 55.	16	0.48	12
Low	TmPSmHGcKWSPPVsLAVNNsLYVMEI S15(Phospho)	0.145 T(1): 12.7; S(4): 12.7; S(11): 30.	13	0.804	17
Low	TMQLLcVLPMPSSsLAsFVtAVRWVPPS S14(Phospho)	0.092 T(1): 19.2; S(12): 46.5; S(13): 4.	17		12
Low	tmsEEGAKPLPEETTTVSSKNSIVAAAAI T1(Phospho)	0.051 T(1): 44.2; S(3): 44.2; T(14): 31	16	0.764	12
Low	tNAIsDFLNLWsAHAPVQLQGSI LDW IQK T1(Phospho)	1 T(1): 100.0; S(5): 100.0; S(12):	62	0.741	12
Low	tPIPGAAPVPRsSSAAAGGR T1(Phospho)	0.669 T(1): 98.8; S(12): 67.7; S(13): 2	26	0.806	12
Low	tsFRVPVGVGPGSPAPLGmSISGDGAVI T1(Phospho)	0.981 T(1): 99.4; S(2): 99.4; S(13): 1.	47	0.706	11
Low	tsGmQLssVILRSTMSIASLVLLSAQRPL S1(Phospho)S2(Phospho)	S Too many isoforms		0.084	12
Low	TVNKLssEYLVIHDEYHTcsVQNmVLcR S6(Phospho)	0.128 T(1): 63.3; S(6): 79.4; S(7): 33.	26	0.753	12
Low	VEmLLLSAIPSLVDtWtmAFGFVPIDDL T15(Phospho)	0.281 S(7): 36.9; S(11): 47.3; T(15): 5	5	0.444	15
Low	VFVSAAsGsVGsLVGQFAKLAgcyVVGc S7(Phospho)	0.262 S(4): 43.3; S(7): 74.7; S(9): 80.	13		11
Low	VGmLVFsAESDcLYAAEmEAARPGAYLI S7(Phospho)	0.436 S(7): 88.8; S(10): 8.0; Y(14): 4.	25	0.225	10
Low	VLPsMVEYKFWtQsFAVGDDLYVmETG S4(Phospho)	0.779 S(4): 92.6; Y(8): 22.0; T(12): 92.	52	0.731	12
Low	VsLRPPQVLSVQtALPGMAAMmPsPs S2(Phospho)	0.707 S(2): 97.9; S(11): 29.3; T(14): 7	26		10
Low	VVPDEytLAaVVsASAtLPAmFGGKPLH Y6(Phospho)	0.2 Y(6): 80.0; T(7): 80.0; S(13): 80.	0	0.428	11
Low	VyHHHPVSPSTmQGSLARPSIHAGsAsI Y2(Phospho)	0.013 Y(2): 7.3; S(8): 22.0; S(10): 22.	12	0.41	10
Low	WLPPtGVQVGSFLFRGVGDPTTPmWAs T5(Phospho)	0.014 T(5): 5.8; S(11): 5.8; T(20): 31.	3	0.766	13
Low	WtGsFDAVQVYTLGEAAsWRDVPAPAC T2(Phospho)	0.18 T(2): 97.6; S(4): 97.6; Y(11): 29.	27	0.799	13
Low	yGILVDSLDMVEVNGSSYSGDGYEtItIE Y1(Phospho)	0.004 Y(1): 32.5; S(7): 60.8; S(16): 50.	5	0.804	11
Low	YHmQDIFGAGSEtSatLEWVmAELIRN T13(Phospho)	0.187 Y(1): 0.0; S(11): 14.3; T(13): 44.	40	0.772	15
Low	YHmQDIFGAGsETSAtLEWVMAELIRNI S11(Phospho)	0.047 Y(1): 0.8; S(11): 83.4; T(13): 83.	23		11
Low	yLmSFVEGGGGGDDGRQLR Y1(Phospho)	0.5 Y(1): 50.0; S(4): 50.0	45	0.775	11

Os08t0137300-01	Middle	Protein of unknown function DUF604 family protein.	AtTTTLAHVVFGIASSR	T2(Phospho)	0.307 T(2): 53.4; T(3): 53.4; T(4): 30.	31	0.04	24
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	Low		LLEWYwIVLSLTYmA	Y5(Phospho)	0.98	Y(5): 98.0; S(10): 0.7; T(12): 0.	25	0.691	10
	Low		LtTSNSASASSPPAAAPEEK	T2(Phospho)	0.436	T(2): 43.6; T(3): 43.6; S(4): 10.	47	0.324	13
	Low		NRPATGGKESPPQPPEVR	S10(Phospho)	0.962	T(5): 3.8; S(10): 96.2	55	0.616	12
Os08t0154600-01	High	Similar to Topoisomerase I.	IEQPGDDsEDDKPLASR	S8(Phospho)	1	S(8): 100.0; S(16): 0.0	88	0	34
	High		KPAVGSGTANDsDDDKPLSLK	S12(Phospho)	0.847	S(6): 3.8; T(8): 1.6; S(12): 84.7	30	0.001	28
	Low		APQtSSSTTTAKPANTtK	T4(Phospho)	0.72	T(4): 89.8; S(5): 5.5; S(6): 1.8;	41	0.082	15
	Low		GGGVVRcsAGPVSGGmIsK	S8(Phospho)	0.983	S(8): 98.5; S(13): 1.7; S(18): 9.	45	0.77	14
	Low		GGSGmVYKGILPNnttVAIK	T15(Phospho)	0.735	S(3): 4.5; Y(7): 23.5; T(15): 86.	21	0.504	15
	Low		RPTtATAmWAAtRWR	T4(Phospho)	0.658	T(3): 16.8; T(4): 67.4; T(6): 18.	31		11
	Low		TSGPKLSASDAAsPsmR	S14(Phospho)	0.012	T(1): 0.6; S(2): 0.6; S(7): 0.6; S	13		13
	Low		tSSEILVRSTmPVLSSsPK	T1(Phospho)	0.022	T(1): 35.9; S(2): 35.9; S(3): 32.	9	0.793	14
	Low		TTsVLSAVGLtEcPSNR	S3(Phospho)	0.199	T(1): 23.8; T(2): 23.8; S(3): 51.	12		15
	Low		TtSVLSAVGLTEcPsNR	T2(Phospho)	0.084	T(1): 44.5; T(2): 44.5; S(3): 10.	29	0.365	14
Os08t0178300-02	High	Hypothetical conserved gene.	QALGDGDIsPPR	S9(Phospho)	1	S(9): 100.0	80	0.005	37
	Low		MPtNQREPPR	T3(Phospho)	1	T(3): 100.0	21		15
Os08t0191700-01	High	Similar to Lactoylglutathione lyase (EC 4.4.1.5) (Methylglyoxalase) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase).	TTVIELtYNYGVTEYTK	T7(Phospho)	0.767	T(1): 1.0; T(2): 1.0; T(7): 76.7; T	47	0.001	15
	Low		GGAtIDDELASIGQQIAKK	T4(Phospho)	1	T(4): 100.0; S(11): 100.0	41		11
	Low		LGLGScVPVANSVLNmYGK	S12(Phospho)	0.237	S(5): 0.2; S(12): 23.7; Y(17): 7.	21	0.701	15
	Low		SAAVESITSTAVKtGcQER	T14(Phospho)	0.929	S(1): 0.7; S(6): 0.1; T(8): 2.1; S	39		13
	Low		SLITNsAADVYLSQMPER	S6(Phospho)	0.138	S(1): 13.8; T(4): 72.4; S(6): 13.	54		14
	Low		TTTTTTTtGAGTGRAAAAAAGGK	T8(Phospho)	0.632	T(1): 0.2; T(2): 0.2; T(3): 0.5; T	36	0.385	14
	Low		TVmPsILYLDHRDFGSK	S5(Phospho)	0.23	T(1): 73.6; S(5): 23.0; Y(8): 3.2	20		12
	Low								
Os08t0234000-01	Low	Similar to 60S ribosomal protein L7-2.	EAsATALLAK	S3(Phospho)	0.5	S(3): 50.0; T(5): 50.0	47		22
	Low		EATAAAsLLK	S7(Phospho)	0.967	T(3): 3.3; S(7): 96.7	37		10

	Low		GsTVEVIAAK	S2(Phospho)	0.839 S(2): 83.9; T(3): 16.1	30		11	
	Low		KKPAAASsSK	S8(Phospho)	0.756 S(7): 12.2; S(8): 75.6; S(9): 12.	35		14	
	Low		KTsVSLPSR	S3(Phospho)	0.884 T(2): 11.6; S(3): 88.4; S(5): 0.1	57		13	
	Low		SEsLNALLK	S3(Phospho)	0.5 S(1): 50.0; S(3): 50.0	42		15	
	Low		sGAPQRAMAASATSK	S1(Phospho)	0.179 S(1): 17.9; S(11): 57.9; T(13): 1	17	0.503	13	
	Low		sGLSADLLAK	S1(Phospho)	0.998 S(1): 99.8; S(4): 0.2	66		14	
	Low		SPsSDKILK	S3(Phospho)	0.466 S(1): 46.6; S(3): 46.6; S(4): 6.7	33		17	
	Low		SSLLPAPsRR	S8(Phospho)	1 S(1): 0.0; S(2): 0.0; S(8): 100.0	56	0.792	29	
	Low		tAGVSNGKIK	T1(Phospho)	0.832 T(1): 83.2; S(5): 16.8	26	0.732	13	
	Low		TAGVsNGKIK	S5(Phospho)	0.85 T(1): 15.0; S(5): 85.0	39		11	
	Low		tEIIGLKGR	T1(Phospho)	1 T(1): 100.0	42	0.687	12	
Os08t0326400-01	Low	60S ribosomal protein L7a.	AEGEsGGVVALK	S5(Phospho)	1 S(5): 100.0	25	0.201	16	
	Low		APsRHGGHGLK	S3(Phospho)	1 S(3): 100.0	12	0.763	11	
	Low		DEKsLFHLK	S4(Phospho)	1 S(4): 100.0	45	0.582	12	
	Low		GDIQLtQVSR	T6(Phospho)	0.973 T(6): 97.3; S(9): 2.7	47	0.582	12	
	Low		GLNAtAAGRER	T5(Phospho)	1 T(5): 100.0	38	0.591	14	
	Low		GPMGRSPSsLK	S9(Phospho)	0.859 S(6): 0.5; S(8): 13.6; S(9): 85.9	43	0.773	10	
	Low		KtVALVGR	T2(Phospho)	1 T(2): 100.0	34	0.555	14	
	Low		LQVLGLGtALK	T8(Phospho)	1 T(8): 100.0	55		11	
	Low		NQRtiDELK	T4(Phospho)	1 T(4): 100.0	42		11	
	Low		SSPsDKLLLVK	S4(Phospho)	0.952 S(1): 2.4; S(2): 2.4; S(4): 95.2	50		10	
	Low		VLNAtEAVNK	T5(Phospho)	1 T(5): 100.0	40		14	
Os08t0390000-01	High	Moesin domain containing protein.	SATAGGAEESEEAESDAKsDEAEAQEE	S19(Phospho)	0.59 S(1): 1.0; T(3): 1.0; S(9): 19.5;	46	0.005	30	
	High		sRGLsYssLsmALGGLFIWtHtYSLmQK	S1(Phospho)	0.011 S(1): 71.2; S(5): 71.2; Y(6): 71.	3	0.005	13	
	Middle		SPPVILADFLPHVITVVGssIsPDFPEtAR	S19(Phospho)	0.074 S(1): 24.9; T(15): 61.4; S(19): 6	11	0.034	11	
	Low		AAPLLLSitILALVVVAssTHGtMANGVFQ	T8(Phospho)	0.044 S(7): 78.0; T(8): 86.5; S(18): 58	4	0.653	14	
	Low		AAPsLtVSDGALPTVSDGALPTASSsDD	S4(Phospho)	0.128 S(4): 76.7; T(6): 43.0; S(8): 75.	31		10	
	Low		AllmDmFVGGsDTTtMmAWtmAELINHF	S11(Phospho)	0.067 S(11): 66.7; T(13): 66.7; T(14):	0	0.261	13	
	Low		AlmSNEEFDNLKEELMWEGSSVvmLsF	S26(Phospho)	0.56 S(4): 13.7; S(20): 13.7; S(21): 1	6	0.568	11	
	Low		ALRPWtAEGMcRYVANGGmGEPMGGI	T6(Phospho)	0.09 T(6): 9.0; Y(13): 9.9; S(32): 81.	0	0.715	11	
	Low		AsIIVAAVIAAcVLLVcMttSsVVDAAAAAP	S2(Phospho)	0.202 S(2): 80.8; T(19): 79.8; T(20): 7	0	0.776	12	
	Low		cVEENFISLLGSVTSYGRHQHtAAttTGH	T22(Phospho)	0.181 S(8): 2.6; S(12): 14.1; T(14): 6.	35	0.759	10	
	Low		DAPLPsSASSGHGLAATssFPGsssPsAt	S6(Phospho)	S18(Phospho) Too many isoforms			0.756	16
	Low		DcLETISDGISTGTRTSLDSQNILIsMSSC	S26(Phospho)	0.238 T(5): 4.2; S(7): 3.5; S(11): 3.1;	9	0.597	11	
	Low		DLHLmIsILNGYYSESPELEDAtAttVARR	S7(Phospho)	0.098 S(7): 13.0; Y(12): 29.8; Y(13): 1	22	0.28	12	
	Low		DLNLALILmHALLcMSTFtyLmcIcAcKR	T19(Phospho)	0.259 S(16): 40.8; T(17): 40.8; T(19):	11	0.569	10	
	Low		DtSDRGQVKPPSGLSLAEyLDLsFNEAsI	T2(Phospho)	0.19 T(2): 50.1; S(3): 50.1; S(12): 38	16	0.719	14	
	Low		EALRyYsIESTIALAVSFMINLFVttVFAK	Y5(Phospho)	0.018 Y(5): 49.0; Y(6): 49.0; S(7): 49.	1		10	
	Low		EDYHREINWQNPLGMVVSTLstsMALKF	S21(Phospho)	0.052 Y(3): 13.2; S(18): 64.9; T(19): 6	10	0.459	10	
	Low		EEADDAPPPWRPsKPAAAI DGSSGPLA	S13(Phospho)	0.635 S(13): 66.7; S(22): 18.9; S(23):	17	0.776	12	
	Low		EsDtGLAPPsQWDLVsDKQMMQEEQPL	S2(Phospho)	1 S(2): 100.0; T(4): 100.0; S(10):	9		11	
	Low		EVFGKsVIAEPsNVIYLssILNtEGPIPSHK	S6(Phospho)	0.046 S(6): 68.3; S(12): 68.3; Y(16): 1	0	0.168	11	

Low	FiPFsANAVVLLtIGPAVLGVGPssGKPA(T2(Phospho):	0.746 T(2): 98.6; S(5): 98.6; T(13): 98.6	26	0.157	10
Low	FWcQyWIIVSmVIAcEsFVSWmPMYGEI Y5(Phospho):	0.109 Y(5): 36.2; S(10): 36.2; S(17): 36.2	7	0.378	11
Low	GGGGGcVNNISSVAGsVGmPALAVYsV S16(Phospho):	0.022 S(11): 43.8; S(12): 38.8; S(16): 38.8	0		11
Low	GINIALFSFSVTVSsFANVGLVPtNENMA S15(Phospho):	0.274 S(8): 22.6; S(10): 22.6; T(12): 22.6	14	0.652	10
Low	GIQLEtSMGsVEFAsMVAALLGmsQGITI S7(Phospho):	0.041 T(6): 60.4; S(7): 60.4; S(10): 60.4	4		10
Low	GMTTVNNEAGVHAsMVSDYESALmVAI S14(Phospho):	0.124 T(3): 31.8; T(4): 31.8; S(14): 31.8	9	0.776	13
Low	GsLSQYNLLTLLGYSSSNcTAcSNAVLsE S2(Phospho):	0.015 S(2): 16.1; S(4): 16.1; Y(6): 16.1	0	0.759	13
Low	GsmSTPAAsANGGQVLLLPFPAAQGH T S2(Phospho):	0.07 S(2): 39.8; S(4): 61.5; T(5): 65.0	7	0.747	22
Low	GSTPSLsPARALstAAVTADAPAAAAAA S7(Phospho):	0.064 S(2): 38.4; T(3): 38.4; S(5): 38.4	13	0.13	16
Low	GVAIGNGMtHPVTQVtHADIAYFmGLIN T9(Phospho):	0.1 T(9): 60.0; T(13): 60.0; T(16): 60.0	0		11
Low	GWKVVHDLsGsAVAAAFmATPFVAAS S10(Phospho):	0.286 S(10): 96.7; S(12): 68.8; T(21): 68.8	28	0.763	14
Low	HGVEAyQGVLFGLELDMMPsNKtPSLI Y6(Phospho):	0.673 Y(6): 98.9; S(21): 27.5; T(24): 27.5	27	0.526	17
Low	HHHcARPDpSssSPssPsssssPssR S10(Phospho)S11(Phospho)	Too many NL-allowing PTMs		0.758	12
Low	KsLSLPISTASLHPLLsALPsAPAFALFAE S2(Phospho):	0.059 S(2): 43.2; S(4): 43.2; S(8): 35.0	7	0.713	14
Low	LEDyPEASGVEVStIDsFQGREADAVVIS Y4(Phospho):	0.144 Y(4): 50.1; S(8): 50.1; S(13): 50.1	13	0.352	14
Low	LFGDQAQSDAVLDDVScmLGCtRssLH S24(Phospho):	0.015 S(8): 85.3; S(16): 73.5; T(22): 73.5	1	0.708	10
Low	LFYFAGADTTSVLLtWtMLLLSmHPEWÇ T15(Phospho):	0.067 Y(3): 19.8; T(9): 21.9; T(10): 21.9	3		12
Low	LGSACQDWGFFQLVNHGVDEQVVNE S29(Phospho):	0.496 S(3): 0.8; S(29): 49.6; T(30): 49.6	18		12
Low	LGWNVELGAVIYSGVVVtALsYYMQmW T18(Phospho):	0.037 Y(12): 40.7; S(13): 40.7; T(18): 40.7	5	0.691	11
Low	LMEAQEFEGILSNNQTVNsDFyNWNKV S19(Phospho):	0.837 S(12): 2.7; T(16): 14.4; S(19): 14.4	21	0.417	17
Low	LPFyHSFWNHtTRPsLDLAKELIsMFTA Y4(Phospho):	0.065 Y(4): 17.9; S(6): 17.9; T(11): 44.0	21	0.776	13
Low	LPGcVPIHAHDLPSsMLADRSsATyAGLI S15(Phospho):	0.037 S(14): 40.9; S(15): 40.9; S(21): 40.9	10	0.691	14
Low	LRLILAPSSGTsmyMDcSsIVssPPLcLQ T3(Phospho)Y15(Phospho)	Too many isoforms		0.779	13
Low	LSGEIPTALSNLsGLmHLDLDTNmLSG S32(Phospho):	0.304 S(2): 6.5; T(7): 6.5; S(10): 6.2; S(11): 6.2	7		11
Low	LtFTQLIEATNGFSTAsLIGsGGFGEVFK T2(Phospho):	0.04 T(2): 38.8; T(4): 38.8; T(10): 38.8	12	0.543	13
Low	LVDAIAAAAAstAEAAVNISRQItGPmtI S11(Phospho):	0.09 S(11): 87.1; S(12): 66.6; T(13): 66.6	4	0.691	13
Low	LVVDWVPstDLEDstATVAPDAYNTAWS S8(Phospho):	0.025 S(8): 47.0; T(9): 47.0; S(14): 47.0	4	0.642	11
Low	MADAAAATVPGEASSSSSAAAttVLDsL T22(Phospho)T23(Phospho)	Too many isoforms		0.682	11
Low	MIPTsVLWGyFAymAIDSLPGNQFWER S5(Phospho):	0.209 T(4): 70.6; S(5): 70.6; Y(10): 70.6	10	0.531	13
Low	MPGDsmLWISSFVcLMAIAKYFEGAY Y26(Phospho):	0.332 S(5): 0.1; S(10): 0.1; S(11): 0.3	29	0.618	15
Low	msLFGsPTVLMAGPAANHfVFSNQDLIF S2(Phospho):	0.048 S(2): 49.0; S(6): 49.0; T(8): 49.0	0		14
Low	NAITHDPQKsLmSWNDSNHLcSWEGV S10(Phospho):	0.46 T(4): 15.9; S(10): 46.0; S(13): 46.0	16	0.727	12
Low	NEsDyTVLSHVTsVcLGIDKISVDAtPELs S3(Phospho):	0.011 S(3): 42.6; Y(5): 42.6; T(6): 42.6	2		10
Low	NPEVDQsGSNGLIQTmAMcGyLPmm S7(Phospho):	0.069 S(7): 56.9; S(9): 56.9; T(15): 72.0	2		11
Low	QcPGsNWcGYGNstAAsSDDDDASFsD S5(Phospho):	0.067 S(5): 59.4; Y(10): 59.4; S(13): 59.4	14	0.708	10
Low	QsLsYLDGTLPGDFGFDPLGLSDPEG T2(Phospho):	0.07 S(2): 49.4; S(4): 49.4; Y(5): 48.0	23		12
Low	QsSPSPSSSAGASQGETLPRGSEmIPP S2(Phospho):	0.038 S(2): 27.3; S(3): 15.1; S(5): 15.1	8	0.653	13
Low	RHsGDPLALLWtIALMcTHLFFLISSLsR S3(Phospho):	0.121 S(3): 83.8; T(12): 50.8; T(19): 50.8	10	0.691	11
Low	RLVttsYPLVLVLVGEEEGAGSNGmTAT T4(Phospho):	0.023 T(4): 50.3; T(5): 50.3; S(6): 46.0	6	0.776	12
Low	RTTTSMVILcLVILSLtVDSATAAQcGccIS T17(Phospho):	0.067 T(2): 15.0; T(3): 15.0; T(4): 15.0	2	0.691	12
Low	SFcLVDCPNLVSLstEGLNQctVLEKLHIK S14(Phospho):	0.093 S(1): 65.9; S(12): 59.4; S(14): 59.4	1		12
Low	sFSLVELEAATNDFEVSNMMMQDSHG S1(Phospho):	0.883 S(1): 88.3; S(3): 11.4; T(11): 0.0	33	0.763	11
Low	sGDGDGTVLAmHRHDisFAGFTNGSHH S1(Phospho):	0.349 S(1): 51.9; T(7): 51.9; S(17): 72.0	19	0.691	17
Low	SIGssIFYcmLGMAAWLNtmLIELVNrvT S4(Phospho):	0.051 S(1): 50.0; S(4): 50.0; S(5): 50.0	0		11
Low	SNmGEGMIIGVLDDGIAAGHPsFDAAG S22(Phospho):	0.5 S(1): 50.0; S(22): 50.0	0		11
Low	SPSPRNSTSLsSSQGGGGADSTGVA S12(Phospho):	0.084 S(1): 5.1; S(3): 5.1; S(7): 5.1; T(12): 5.1	2	0.653	11
Low	sQNVARLVQtmDscELScLDSNDSWsLF S1(Phospho):	0.075 S(1): 60.7; T(10): 60.7; S(13): 60.7	7	0.761	10

	Low		SSKSTIDLFTAAAGsPVAAHsIMsPPQFn S15(Phospho)	0.133 S(1): 32.5; S(2): 32.5; S(4): 32.	10	0.774	12	
	Low		ssRsIVNsHNHFSNPTLLSLPAVATTILHE S1(Phospho)	0.018 S(1): 45.9; S(2): 45.9; S(4): 45.	4	0.39	11	
	Low		SSSGIRSLASLTSFTTSTMsPYAtAsAVD S20(Phospho)	T24(Phospho) Too many isoforms		0.256	11	
	Low		STAFSLLSPSNSYPRMEDINTTstSQSS T23(Phospho)	S24(Phospho) Too many isoforms		0.535	13	
	Low		STDDLFLTEQEAAGDGLVAAGmSAAGf T31(Phospho)	0.409 S(1): 2.1; T(2): 2.1; T(8): 1.9; S	14	0.776	10	
	Low		syntQGLVNGGINVPMMSsPIFANAPA S1(Phospho)	0.575 S(1): 99.7; Y(2): 99.7; T(4): 99.	34	0.697	13	
	Low		tADIGQmImVREEDDPAPEGIEytHGLTP T1(Phospho)	0.904 T(1): 97.2; Y(23): 99.2; T(24): 9	30	0.761	13	
	Low		tPRPMmGAPGNGYNSGGSGHGtGAG T1(Phospho)	0.044 T(1): 76.0; Y(13): 34.3; S(15): 3	6		11	
	Low		TQWYHFtAIVIAgMGFFTDAYDLFSIsLV T7(Phospho)	0.034 T(1): 24.9; Y(4): 24.9; T(7): 24.	0	0.403	12	
	Low		TRVVFQSTFYHTmtDGsLcGPVIDDASL T14(Phospho)	0.111 T(1): 12.0; S(7): 14.0; T(8): 14.	9	0.691	15	
	Low		TSsAIsAGVAGWstASGAAATMRPKSDI S3(Phospho)	0.007 T(1): 44.2; S(2): 44.2; S(3): 44.	0		10	
	Low		VAAmtMcAAVAVLLVL TstMAAAAGDGD T5(Phospho)	0.155 T(5): 72.1; T(17): 61.0; S(18): 6	4	0.145	13	
	Low		VAGDGtTcAtVLTQAILtEGcKAVAAGVN T6(Phospho)	0.129 T(6): 57.6; T(7): 57.6; T(10): 58	2	0.662	11	
	Low		VsLyGLLQSTTNQGRAIAAGTVsALAALI S2(Phospho)	0.011 S(2): 53.1; Y(4): 53.1; S(9): 53.	2		12	
	Low		WFmPacLLASTFVyFVQSMHttRYGIWR Y14(Phospho)	0.029 S(10): 42.9; T(11): 42.9; Y(14):	0		14	
	Low		WIAEGyAsGSESNsLEEmGELFHKLSs Y6(Phospho)	0.054 Y(6): 29.3; S(8): 29.3; S(10): 29	4		11	
	Low		WLREtAQQNQsTSyQVLVTGsLHLVGD T5(Phospho)	0.034 T(5): 57.9; S(11): 57.9; T(12): 5	2	0.722	11	
	Low		YGVmENETTETSTSGcGsLILEMGALSf S18(Phospho)	0.104 Y(1): 10.4; T(8): 10.4; T(9): 10.	3	0.777	14	
	Low		ysNVGtmFQEAPSLPmDTVAGLVDELv Y1(Phospho)	0.029 Y(1): 58.9; S(2): 58.9; T(6): 58.	2		10	
Os08t0428800-00	High	Similar to High mobility group I/Y-2.	DPNAPPPPPKPSsPRPR	S13(Phospho)	0.5 S(12): 50.0; S(13): 50.0	114	0	46
	High		DPNAPPPPPKPsSPRPR	S12(Phospho)	0.5 S(12): 50.0; S(13): 50.0	62	0	20
	Low		ADELEtKVR	T6(Phospho)	1 T(6): 100.0	69	0.76	16
	Low		DLsSASGPPPADLPTLLR	S3(Phospho)	0.509 S(3): 50.9; S(4): 16.4; S(6): 16.	21	0.127	10
	Low		DWSKLPVDALsAVFMK	S11(Phospho)	0.941 S(3): 5.9; S(11): 94.1	29		10
	Low		DWsKLPVDALsAVFMK	S3(Phospho)	0.966 S(3): 96.6; S(11): 3.4	24		13
	Low		ILAGLGFDQAMQARStK	T16(Phospho)	0.813 S(15): 18.7; T(16): 81.3	10		11
	Low		mPAKNAVsYGAIISGLAK	S8(Phospho)	0.104 S(8): 10.4; Y(9): 13.6; S(14): 76	1	0.805	13
	Low		RAALHVLGcGsPVADQR	S11(Phospho)	1 S(11): 100.0	14	0.776	21
	Low		SGsNKSAISK	S3(Phospho)	0.414 S(1): 12.6; S(3): 41.4; S(6): 41.	17		11
	Low		sGSNKSAISK	S1(Phospho)	0.811 S(1): 81.1; S(3): 18.0; S(6): 0.6	27		12
	Low		STLPPTPAVQVPPmLsR	S16(Phospho)	0.999 S(1): 0.0; T(2): 0.0; T(6): 0.1; S	42		14
	Low		WVSWQmIMKILVtR	T13(Phospho)	0.996 S(3): 0.4; T(13): 99.6	31	0.741	12
Os08t0512400-02	High	Similar to AT-hook protein 1.	AVPTAGMGPNsPPSR	S11(Phospho)	0.5 T(4): 0.0; S(11): 50.0; S(14): 50	113	0	50
	High		AVPTAGMGPNsPPsR	S14(Phospho)	0.916 T(4): 0.0; S(11): 8.4; S(14): 91.	132	0	53
	High		DLFGMPKsPPAAAAAPPQSVR	S8(Phospho)	1 S(8): 100.0; S(19): 0.0	95	0	22
	Low		FRySYWNsSQSYVLTK	Y3(Phospho)	0.961 Y(3): 97.6; S(4): 1.2; Y(5): 1.2;	104		10
	Low		MELHPLVVSAAAADsTSPRR	S15(Phospho)	0.153 S(9): 54.1; S(15): 15.3; T(16): 1	30	0.746	15
	Low		mtTALFLRcGcLAAAPALR	T2(Phospho)	0.5 T(2): 50.0; T(3): 50.0	40	0.772	12
	Low		SFsGILtGSSELDfSTPRK	S3(Phospho)	0.798 S(1): 13.1; S(3): 82.4; T(7): 94.	77	0.741	17
	Low		SIFWsTQADItANTTmVK	S5(Phospho)	0.108 S(1): 70.0; S(5): 31.1; T(6): 21.	16	0.75	13
	Low		SIVLQIDsKSQQVSAAsALR	S8(Phospho)	0.099 S(1): 3.9; S(8): 48.1; S(10): 48.	26	0.806	11
	Low		syAAIIVAVSSSmPLtsR	S1(Phospho)	0.016 S(1): 80.7; Y(2): 80.7; S(10): 60	3	0.526	14

Os08t0528900-01	High	Similar to Transcriptional activator FHA1.	YLSPEDWsPTETK	S8(Phospho)	0.988 Y(1): 0.0; S(3): 0.0; S(8): 98.8;	98	0	36
Os08t0533700-01	High Low	Similar to cation cation antiporter.	EVESSYEGEKPGSPISLSSGLR DyPSELQLRALEQVNLsPR	S16(Phospho) Y2(Phospho):	0.435 S(4): 0.0; S(5): 0.0; Y(6): 0.1; S 0.245 Y(2): 89.1; S(4): 75.5; S(17): 3;	49 10	0	29 11
Os08t0558000-01	Middle Low	Similar to Ribosomal protein.	MFILPScSPsAAISR AsNLSSGMLGSLATSIK	S10(Phospho) S2(Phospho)	0.25 S(6): 25.0; S(8): 25.0; S(10): 2; 0.997 S(2): 99.7; S(5): 0.1; S(6): 0.1;	36 37	0.032 0.568	10 13
Os08t0558800-01	Middle Low Low	Similar to Ribosomal protein.	MFILPScSPsAAISR AsNLSSGMLGSLATSIK sDPIIQTLTPmsPK	S10(Phospho) S2(Phospho) S1(Phospho):	0.25 S(6): 25.0; S(8): 25.0; S(10): 2; 0.997 S(2): 99.7; S(5): 0.1; S(6): 0.1; 0.058 S(1): 98.0; T(7): 94.2; S(12): 7.	36 37 7	0.032 0.568	10 13 11
Os08t0559200-01	Low Low Low Low Low Low	Similar to Ribosomal protein S25 (40S ribosomal 25S subunit).	DATGKVAHsAGSsLR FLAGGDGEGVDVTGsR GATAmQPPSSSsLMR MPLPLAPAsPHPPGR sDGmMYALASFLSK VERPHPDsEWER	S9(Phospho): S15(Phospho) S12(Phospho) S9(Phospho) S1(Phospho) S8(Phospho)	0.068 T(3): 6.3; S(9): 14.8; S(12): 89. 0.5 T(13): 50.0; S(15): 50.0 0.492 T(3): 0.0; S(9): 0.3; S(10): 1.4; 1 S(9): 100.0 0.684 S(1): 68.4; Y(6): 21.9; S(10): 1. 1 S(8): 100.0	12 21 56 52 21 66	0.48 0.467 0.443 0.234 0.766	13 14 13 12 12 11
Os09t0115400-03	Low Low Low	Hypothetical conserved gene.	AAVTTtAGGKVVVR LTsIGGEIGITLR SAtARGGGGGAPT LR	T6(Phospho) S3(Phospho) T3(Phospho)	0.42 T(4): 42.0; T(5): 16.0; T(6): 42.0 0.818 T(2): 17.7; S(3): 81.8; T(11): 0. 0.836 S(1): 16.4; T(3): 83.6; T(13): 0.	15 31 47	0.489 0.697 0.064	14 12 20
Os09t0372400-02	High Low Low	Conserved hypothetical protein.	LGLPEAEEDMFADsPKDK cLDsPPAsPAAPPPPPQGR SKPAAAAADTtstALVAASK	S14(Phospho) S4(Phospho): T11(Phospho)	1 S(14): 100.0 1 S(4): 100.0; S(8): 100.0 0.005 S(1): 96.4; T(10): 13.7; T(11): 2	71 27 3	0.002	27 16 14
Os09t0402100-01	High Low Low Low Low Low Low Low	PF1 protein.	DAAAAAAPAPAPAAsSPRPR ATLTMQPIGPLPSTKQEGtR cITGLsGVmDGLVVHGYLVK FPLASPPPAItSAGAGGWSARK sDILIQVPNGAATGSDAAQAVK sNAWQIKVNSISGTIDSWK WFRIsPIVEGKPEAFTEK	S19(Phospho) T19(Phospho) S6(Phospho) T10(Phospho) S1(Phospho) S1(Phospho) S5(Phospho)	0.5 S(19): 50.0; S(20): 50.0 0.996 T(2): 0.0; T(4): 0.0; S(13): 0.1; 0.995 T(3): 0.4; S(6): 99.5; Y(17): 0.1 0.429 S(5): 0.5; T(10): 42.9; T(11): 42 0.986 S(1): 98.6; T(13): 0.3; S(15): 1. 0.785 S(1): 78.5; S(10): 7.6; S(12): 4. 0.999 S(5): 99.9; T(16): 0.1	71 59 50 35 60 15 40	0 0.297 0.803 0.798 0.611	26 13 10 16 13 11 19

Os09t0413500-01	Low	Similar to 60S ribosomal protein L34.	KEAAAAAsTPTtTIR KEAAAAAsPTTTIR	S8(Phospho)	0.665 S(8): 81.9; T(9): 16.0; T(11): 17	53	0.588	10
	Low			S8(Phospho)	0.005 S(8): 3.7; T(9): 16.8; T(11): 82.	34	0.757	10
Os09t0485900-01	Low	Similar to 60S ribosomal protein L9 (Gibberellin-regulated protein GA).	HRLGGLyLR yPAHITLLR	Y7(Phospho)	1 Y(7): 100.0	32	0.439	13
	Low			Y1(Phospho)	0.998 Y(1): 99.8; T(6): 0.2	43	0.325	13
Os09t0491708-01	High	Protein of unknown function DUF296 domain containing protein.	MVPMSGTGPSsPPSR DDLLANPNQsTGR DNSsFKKPAQSSGNTIFIK ERLVVVEFAAsHsVNSSR FEILSLsGSFLLSENGGHR GDGALGAGSGAGGEGsAAK GRTVVIEQsFGAPK MPTsGPDAmQPALR SSETSPAPAAAAAGsGR tHPVVAYLRKPK VANSSEGGPTRGsGGR	S11(Phospho)	0.898 S(5): 0.0; T(7): 0.2; S(10): 10.1	108	0	47
	Low			S11(Phospho)	0.859 S(10): 12.2; S(11): 85.9; T(12):	65		14
	Low			S4(Phospho)	0.5 S(3): 50.0; S(4): 50.0; S(11): 0.	64	0.268	15
	Low			S11(Phospho)	0.023 S(11): 80.0; S(13): 20.0; S(16):	26	0.803	13
	Low			S7(Phospho)	0.529 S(5): 8.1; S(7): 52.9; S(9): 19.5	18	0.463	10
	Low			S16(Phospho)	0.787 S(9): 21.3; S(16): 78.7	28	0.09	10
	Low			S9(Phospho)	0.991 T(3): 0.9; S(9): 99.1	46	0.358	14
	Low			S4(Phospho)	0.862 T(3): 13.8; S(4): 86.2	51		12
	Low			S15(Phospho)	1 S(1): 0.0; S(2): 0.0; T(4): 0.0; S	51		11
	Low			T1(Phospho)	1 T(1): 100.0; Y(7): 100.0	58		10
	Low			S13(Phospho)	0.942 S(4): 0.8; S(5): 1.5; T(10): 3.4;	24	0.704	11
Os09t0502000-01	Low	Similar to Ribosomal L32.	GtSKVyATIGLDK tGSGKTTLLsTLFR	T2(Phospho)	0.701 T(2): 83.9; S(3): 16.7; Y(6): 83.	45		19
	Low			T1(Phospho)	0.326 T(1): 47.4; S(3): 47.4; T(6): 9.7	25	0.792	17
Os09t0551300-01	Low	Similar to predicted protein.	NtIDtARssssTIGNSGSsK NTQLLDISsLHVATLmVYNSINK PATPTIIGALLGLGtQmySNALRK VLWKHNvYGItpTIGSAHYLLK yGPVIsTIPQQLSRQFNmVSS	T2(Phospho)	0.006 T(2): 82.0; T(5): 48.7; S(8): 92.	6	0.766	13
	Low			S9(Phospho)	0.823 T(2): 0.2; S(8): 17.2; S(9): 82.3	58		10
	Low			T15(Phospho)	0.826 T(3): 0.0; T(5): 0.0; T(15): 99.2	69		16
	Low			T11(Phospho)	0.033 Y(8): 11.2; T(11): 22.8; T(13): 5	10	0.755	12
	Low			Y1(Phospho)	0.494 Y(1): 99.1; S(6): 50.1; T(7): 50.	45		11
Os09t0565500-01	High	Conserved hypothetical protein.	HATPAPASAPAAAMADPASPATGELsP HATPAPASAPAAAMADPAsPATGELsPI LAATLLsSPGANsSPASAADAHQAVAR AVLRMHsGVWSGsPcVSAYLLSR ELRGtGITANAVAPGSTGTPmmYTgK ELRGtGItANAVAPGSTGTPmmYTgK	S26(Phospho)	1 T(3): 0.0; S(8): 0.0; S(19): 0.0;	92	0	53
	High			S19(Phospho)	0.5 T(3): 0.0; S(8): 0.0; S(19): 50.0	81	0	49
	Middle			S7(Phospho)	0.067 T(4): 10.4; S(7): 10.4; S(8): 8.9	28	0.024	10
	Low			S7(Phospho)	0.053 S(7): 95.3; S(11): 5.3; S(13): 7.	19		11
	Low			T5(Phospho)	0.845 T(5): 84.5; T(8): 15.5; S(16): 0.	79		11
	Low			T8(Phospho)	0.746 T(5): 25.3; T(8): 74.6; S(16): 0.	37		11

	Low		FKLQLQsLmEtLSSTEPHYIR	S7(Phospho)	0.027	S(7): 90.2; T(11): 82.2; S(13): 6	9		13
	Low		HssIGGGGGVETASTmGIGGGWQLAW	S2(Phospho)	1	S(2): 100.0; S(3): 100.0; T(12):	67	0.232	15
	Low		IcAVVEADGRYItNSGmLMQLK	T14(Phospho)	0.668	Y(12): 23.8; T(14): 66.8; S(16):	23		14
	Low		IEDAGGFVMWAGTWRVGGVLAVsR	T13(Phospho)	1	T(13): 100.0; S(23): 100.0	13		10
	Low		ITtQTGTGtCIAIAGVALYsYIKAK	T3(Phospho)	0.103	T(2): 7.1; T(3): 31.0; T(5): 31.0	42	0.253	10
	Low		MASSVAAAStFLGTRLADPAPQsGR	S3(Phospho)	0.038	S(3): 4.1; S(4): 4.1; S(10): 4.0;	20		20
	Low		RVGGVWLALGSSAIAGGGVGGssWPR	S12(Phospho)	0.914	S(11): 8.6; S(12): 91.8; S(22): 9	49	0.755	17
	Low		RVGVVLPLAVSDDGGtLtVyEHR	T16(Phospho)	0.964	S(11): 3.6; T(16): 97.2; T(18): 9	36		13
	Low		sGQQLNFtIIGDRMDVR	S1(Phospho)	1	S(1): 100.0; T(8): 100.0	79	0.373	10
	Low		tVNLtNGEANLGSFFFTESSHGKR	T1(Phospho)	0.999	T(1): 99.9; T(5): 99.9; S(13): 0.	47		13
	Low		VVIRPASSAsGGGLAQyFLmtRR	S10(Phospho)	0.711	S(7): 22.0; S(8): 7.6; S(10): 71.	34		14
Os09t0570850-00	High	Similar to Histone H2B.	TGAAADETPPVVPLQSQEtQDPNEPK	T19(Phospho)	0.5	T(1): 0.0; T(8): 0.0; S(16): 50.0	88	0	45
	Low		KPAATATAAAPSAmSKGFPSYIsPAPR	S15(Phospho)	0.06	T(5): 39.8; T(7): 20.8; S(12): 20	9	0.713	10
	Low		NGSNmVTPLGSPAVMAEtRGHGHGA	T19(Phospho)	0.04	S(3): 60.5; T(7): 27.2; S(11): 8.	0		13
	Low		QtEGNNYLLVIMKDQYANYVVQK	T2(Phospho)	0.298	T(2): 29.8; Y(7): 29.8; Y(16): 29	22	0.792	17
Os10t0400200-01	Middle	Glutelin type II precursor.	QALGDGDIsPPR	S9(Phospho)	1	S(9): 100.0	36	0.02	21
	Low		AAGGHQLAKELsVTQLVAIGVGsTIGAG	S12(Phospho)	0.504	S(12): 85.0; T(14): 15.1; S(23):	31	0.691	11
	Low		AALtALAPEAPyLAAGTMSGAVDMLFSA	T4(Phospho)	0.031	T(4): 88.2; Y(12): 16.1; T(17): 9	25		10
	Low		AALtAMAGAAATLALSKEQcGVSVR	T4(Phospho)	0.722	T(4): 80.9; T(5): 80.9; T(13): 18	27	0.792	11
	Low		AsLGSFLAGR	S2(Phospho)	0.842	S(2): 84.2; S(5): 15.8	31		10
	Low		ATGIIALSDSsLK	S11(Phospho)	0.759	T(2): 0.7; S(8): 5.1; S(10): 18.3	28		10
	Low		ATSSsLTRR	S5(Phospho)	0.466	T(2): 0.0; S(3): 0.2; S(4): 6.6; S	46	0.668	11
	Low		cKLLTPcMVDGLDDLMQyTVGR	Y19(Phospho)	0.494	T(5): 1.2; Y(19): 49.4; T(20): 49	26		11
	Low		cRPLSTAEIsNGcSSIVQIDPSHETELQF	S10(Phospho)	0.22	S(5): 0.0; T(6): 0.1; S(10): 22.0	49	0.318	13
	Low		csAVNPPSPSSAAASMLATSLAGsLLF	S2(Phospho)	0.058	S(2): 80.6; S(8): 16.0; S(11): 8.	20		11
	Low		EAVTLGVLMNtK	T11(Phospho)	1	T(4): 0.0; T(11): 100.0	45		17
	Low		EPALIVDGAVIDAHAALcERFNSTVR	T5(Phospho)	0.992	T(5): 99.2; S(22): 0.4; T(23): 0.	25	0.711	10
	Low		FLsVVAEMGLPGFGVKDLEEGsmSsIVE	S3(Phospho)	0.716	S(3): 100.0; S(22): 78.4; S(24):	50		11
	Low		FSVMAIVAHAVVAsMLGP	S14(Phospho)	1	S(2): 0.0; S(14): 100.0	58	0.388	11
	Low		FtAENGVIK	T2(Phospho)	1	T(2): 100.0	49		12
	Low		FtMVLVPTLNLDTGTPDSAFFTQAGR	T2(Phospho)	0.999	T(2): 99.9; T(8): 0.1; T(14): 0.0	51		12
	Low		GFGIKHQVDSHLFESDQGALmAVLVGY	S28(Phospho)	0.497	S(10): 0.3; S(15): 0.4; Y(27): 49	28	0.776	15
	Low		GGETIAAVINILSAAIYIsNAAPDLQsFsQ	Y17(Phospho)	0.092	T(4): 77.2; S(13): 54.8; Y(17): 4	9		10
	Low		GMAAAQSGSVPAALALSSGHtMPsVGL	T21(Phospho)	0.649	S(8): 0.6; S(17): 18.8; S(18): 18	31	0.741	13
	Low		GREAAASLAAAAAAAAAAsSGDQQC	S21(Phospho)	0.499	S(7): 0.3; S(21): 49.9; S(22): 49	45		11
	Low		GTIGYAPPEYGAGNtVSTLGDlySYGILV	T15(Phospho)	0.019	T(2): 8.0; Y(5): 10.6; Y(10): 12.	4	0.507	17
	Low		GtQTLAmLK	T2(Phospho)	0.976	T(2): 97.6; T(4): 2.4	45		10
	Low		HLGmVADEDSPLsAPSVLTEVVRSssP	S10(Phospho)	0.027	S(10): 55.5; S(13): 60.4; S(16):	1	0.766	10
	Low		HPQLFYEAKLyNALQGGSsGIANVK	Y11(Phospho)	0.746	Y(6): 25.4; Y(11): 77.4; S(18): 9	29		13
	Low		IVAQPYYIQEsK	S10(Phospho)	0.998	Y(6): 0.2; S(10): 99.8	37	0.671	12
	Low		KsIAHIVK	S2(Phospho)	1	S(2): 100.0	45	0.776	11
	Low		LLVFTTIVPLVFVYTLGmYIstAISLFRLT	Y15(Phospho)	0.015	T(5): 29.2; T(6): 67.7; Y(15): 28	20		13
	Low		LMtDVPFGVLLSGGLDsSLVASVVS	T3(Phospho)	0.06	T(3): 98.1; S(12): 85.6; S(17): 6	31	0.792	16
	Low		LPAAttALVLAR	T5(Phospho)	1	T(5): 100.0; T(6): 100.0	15	0.766	10
	Low		LQVTRLtAAHtIEQAPGQSPAQAAmGVC	T7(Phospho)	0.409	T(4): 44.8; T(7): 66.2; T(11): 68	16	0.735	17

Low		LtFSGsLKHR	T2(Phospho)	0.333 T(2): 66.7; S(4): 66.7; S(6): 66.7	19		11
Low		LVAsGVPR	S4(Phospho)	1 S(4): 100.0	10	0.804	14
Low		mAAVWtAAAmAR	T6(Phospho)	1 T(6): 100.0	60		10
Low		mAGsssLAsPHsLLLLPLLLLFLLVAAAIGS	S4(Phospho)	0.53 S(4): 85.6; S(5): 85.6; S(6): 85.6	14		10
Low		mDmLISAVASDLVSRFisyLVHK	S18(Phospho)	0.878 S(6): 0.1; S(10): 0.6; S(14): 11.1	49	0.568	11
Low		mEttGGGGSPKEAVVPSAASGDTtLGR	T3(Phospho)	0.024 T(3): 52.4; T(4): 52.4; S(9): 93.3	26	0.49	18
Low		mLVDDVVGfTSLEFLQHHLShccKEVyl	S9(Phospho)	0.047 S(9): 39.0; T(10): 39.0; S(11): 39.0	7		11
Low		MPLDRtPLIPHQDAGAsAQALFLR	T6(Phospho)	1 T(6): 100.0; S(17): 100.0	53	0.531	12
Low		NDtFVAALK	T3(Phospho)	1 T(3): 100.0	39		10
Low		QAmSQVLVEANGVtRtLVLNRPK	S4(Phospho)	1 S(4): 100.0; T(14): 100.0; T(16): 100.0	25	0.456	11
Low		QEmFLEDINLTASDGAGNStVLPIR	T20(Phospho)	0.628 T(11): 6.0; S(13): 6.0; S(19): 25.0	16	0.49	10
Low		RAVVtVR	T5(Phospho)	1 T(5): 100.0	34		11
Low		RGLLSPR	S5(Phospho)	1 S(5): 100.0	26		11
Low		RGLVsLR	S5(Phospho)	1 S(5): 100.0	18	0.785	13
Low		RHGGsLLAAAAVAAtPK	S5(Phospho)	1 S(5): 100.0; T(15): 100.0	24	0.665	15
Low		RIEASIDDSPPPPsLPGGmGVsLLK	S10(Phospho)	0.06 S(6): 93.9; S(10): 26.3; S(15): 100.0	29	0.073	11
Low		SAMAtLVAAAFPSR	T5(Phospho)	0.482 S(1): 48.2; T(5): 48.2; S(13): 3.0	24		11
Low		SKNFAVSLAELIsAAGKPNNSGEAsR	S13(Phospho)	0.828 S(1): 0.1; S(7): 0.2; S(13): 91.3	40		11
Low		sLPAsAAcRPDVETyTLLLTsvVR	S1(Phospho)	0.953 S(1): 96.5; S(5): 96.5; T(14): 3.0	49	0.26	17
Low		sLPASAAcRPDVETyTLLLTsvVR	S1(Phospho)	0.011 S(1): 93.6; S(5): 93.6; T(14): 3.0	12	0.055	14
Low		SMTFtARPAVRR	T5(Phospho)	0.972 S(1): 0.4; T(3): 2.3; T(5): 97.2	51		12
Low		sSASAPAPAKGGNASGAATK	S1(Phospho)	0.475 S(1): 47.5; S(2): 47.5; S(4): 4.7	31	0.753	11
Low		sVVSPSAAQVGGGSSAR	S1(Phospho)	0.891 S(1): 89.1; S(4): 5.4; S(6): 5.4	40	0.35	21
Low		tAGsAREsLGSmAGVVTlVTSiLLLLSGS	T1(Phospho)S4(Phospho)	S Too many isoforms		0.477	12
Low		TELSKsELIQK	S6(Phospho)	0.132 T(1): 13.2; S(4): 73.6; S(6): 13.2	32		10
Low		TNQDVVVsEMGIAAGAALPGGPAGPAC	S8(Phospho)	0.339 T(1): 33.9; S(8): 33.9; S(34): 16.0	3	0.744	11
Low		tPlVATTTpAAAAAtAAAAEVKPAKR	T1(Phospho)	0.007 T(1): 97.3; T(3): 97.3; T(6): 34.1	30		10
Low		TTLENmWLETlMAlIGEQFDEsEEIcGV	S22(Phospho)	0.216 T(1): 7.2; T(2): 7.2; T(10): 6.0; S(10): 6.0	6		10
Low		VcQVVVAAVcKFNvAPPDDmsLLYELPL	S21(Phospho)	0.431 S(21): 43.1; Y(24): 19.0; S(31): 19.0	19		11
Low		VPLPLLLmTNTADGVGGDtSGcDIFK	T19(Phospho)	0.12 T(9): 38.0; T(11): 38.0; T(19): 100.0	6	0.092	10
Low		VPPPSdSSPIsGGEPVVSvSSPTesGy	S5(Phospho)S26(Phospho)	S Too many isoforms		0.628	13
Low		VtWVVDPKGtPGDttFTtIAAALEK	T2(Phospho)	0.98 T(2): 100.0; T(10): 98.0; T(14): 100.0	66		13
Low		VtWVVDPKGtPGDttFTtIAAALEK	T2(Phospho)	0.646 T(2): 100.0; T(10): 14.3; T(14): 100.0	55		13
Low		VVEKPGIMSSTK	S10(Phospho)	0.333 S(9): 33.3; S(10): 33.3; T(11): 3.0	15	0.46	13

Os10t0411700-01	Low	Similar to S28 ribosomal protein (Fragment).	DKsTPVSASEmK	S3(Phospho)	0.394 S(3): 39.4; T(4): 39.4; S(7): 14.0	11		12
	Low		SKsLESTESDGR	S3(Phospho)	0.067 S(1): 2.7; S(3): 6.7; S(6): 19.4	12	0.796	14
	Low		TIDsEKDGQFR	S4(Phospho)	0.715 T(1): 28.5; S(4): 71.5	8	0.711	10

Os10t0411800-01	Low	Similar to 40S ribosomal protein S17-3.	GASLSAQNASGWtPLMVAR	T13(Phospho)	0.548 S(3): 11.2; S(5): 11.2; S(10): 2.0	12		11
	Low		GFFHcVVsgDGsLLVYR	S8(Phospho)	0.821 S(8): 82.1; S(12): 17.8; Y(16): 0.0	43	0.783	12
	Low		IGEIVDQHsEsYKQSR	S9(Phospho)	0.934 S(9): 96.7; S(11): 96.7; Y(12): 0.0	45	0.76	10
	Low		IGTWGGNGGGRVDLSVLPR	S15(Phospho)	0.848 T(3): 15.2; S(15): 84.8	17	0.803	12

Low	IPLAGGPQAGDsSGAmPKDK	S12(Phospho)	0.969 S(12): 96.9; S(13): 3.1	47	0.806	12
Low	KFLHVGsEALLEQsmK	S7(Phospho)	1 S(7): 100.0; S(14): 100.0	62		10
Low	LLEWyWIVLSLTYmA	Y5(Phospho)	0.837 Y(5): 83.7; S(10): 1.2; T(12): 7.	26	0.617	11
Low	LLsHGGLLR	S3(Phospho)	1 S(3): 100.0	45		19
Low	msKSAGAAAGPTAAAAAAVQK	S2(Phospho)	0.688 S(2): 68.8; S(4): 15.6; T(12): 15	12	0.752	15
Low	RVLVtGGNGFIGsWIVR	T5(Phospho)	1 T(5): 100.0; S(13): 100.0	47		10
Low	tIANSSSGNLGLNHTVFGK	T1(Phospho)	0.43 T(1): 43.0; S(5): 20.2; S(6): 20.	13	0.333	11
Low	tLPLRLPR	T1(Phospho)	1 T(1): 100.0	23	0.776	10
Low	VGQPELAGAGHQLGVsSGPR	S16(Phospho)	0.5 S(16): 50.0; S(17): 50.0	9		10
Low	WGMIIHTGLLMPPsSPR	S14(Phospho)	0.574 T(7): 21.3; S(14): 57.4; S(15): 2	16	0.691	11

Os10t0466300-01	Middle	Similar to Yarrowia lipolytica chromosome C of strain CLIB99 of Yarrowia lipolytica.	DKPItAPssAmLAIsNsSNFVLsDLEGHtF	T5(Phospho)	0.228 T(5): 93.7; S(8): 93.7; S(9): 93.	9	0.015	13
	Middle		sLSELFHSFmPcIASSASLLSSSsEHLIIE	S1(Phospho)	0.022 S(1): 20.0; S(3): 20.0; S(8): 20.	0	0.024	13
	Middle		WcGGAAAsDDDTTAAPmPSLGSgsAAL	S7(Phospho)	0.013 S(7): 41.1; T(11): 41.1; T(12): 4	0	0.021	11
	Low		AGALVETPSISALQRGHSAFILsHLstQsL	S23(Phospho)	0.194 T(7): 31.7; S(9): 31.7; S(11): 31	18		11
	Low		AGLIDEAmEMIssMPmEADtyVWGGILAt	S12(Phospho)	1 S(12): 100.0; S(13): 100.0; T(2)	3	0.629	11
	Low		AKLmFLEAYEPGWtASQQLGWISSLM	T14(Phospho)	0.526 Y(9): 15.2; T(14): 52.6; S(16): 1	14		10
	Low		APTPPAAAAAPAAPPAPsGLPSWPLL	S19(Phospho)	0.338 T(3): 16.2; S(19): 33.8; S(23): 3	5	0.749	11
	Low		ASLNcIDDESTGGLsQVR	S16(Phospho)	1 S(2): 0.0; S(11): 0.0; T(12): 0.0	74		14
	Low		AsSIHLIEGKLYLLLLGTtALsLVtPLLfk	S2(Phospho)	0.073 S(2): 50.2; S(3): 50.2; Y(12): 25	22	0.55	23
	Low		AtmLsELALAGNsIAGEVPQLGSLNKLEr	T2(Phospho)	0.25 T(2): 75.0; S(5): 75.0; S(13): 75	0		11
	Low		AycsFVVEHsLWVVmPFmTEGscLHLmk	Y2(Phospho)	0.2 Y(2): 80.0; S(4): 80.0; S(10): 80	0		11
	Low		cAAAGEVVGsAAGVGRsAGmEVAIAAtA	S10(Phospho)	1 S(10): 100.0; S(17): 100.0; T(2)	5		11
	Low		cGPFGLcDADAAAtSFcGcVDGFTAASP	T14(Phospho)	0.129 T(14): 45.6; S(15): 45.6; T(24):	4	0.336	12
	Low		cTSPmAAtsAAEsAAccFcmAsssDcHER	T8(Phospho)	S9(Phospho)S Too many NL-allowing PTMs		0.673	11
	Low		DGPEGDDtHVSTRVmGTHGYAAPEYInr	T8(Phospho)	0.125 T(8): 12.5; S(11): 12.5; T(12): 1	0		10
	Low		DIIAtGGIDtNAVLFDRPSGQILcTLtGHsK	T5(Phospho)	0.244 T(5): 88.6; T(10): 78.4; S(19): 5	13	0.541	10
	Low		DQIYDIFQLPPKIQVGVFsATmPPEALE	S20(Phospho)	0.319 Y(4): 18.1; S(20): 31.9; T(22): 3	4	0.803	10
	Low		DTVtIELAPAttAIDDDVDGDQPPTTMAT	T11(Phospho)	0.008 T(2): 33.5; T(4): 33.5; T(11): 28	0		10
	Low		DVIsWtGLLNGyMEFGLVDmAMDVFDRl	S4(Phospho)	1 S(4): 100.0; T(6): 100.0; Y(12):	7	0.516	11
	Low		DVntLANFVSEVSLTLHDNNTAySLlISN	T4(Phospho)	0.122 T(4): 53.8; S(10): 13.3; S(13): 1	20		15
	Low		EFsmNyImVGYtLDKDyRPyPsSDPPK	S3(Phospho)	0.078 S(3): 82.8; Y(6): 82.8; Y(11): 5	7	0.405	10
	Low		EsNtNVHVESVFFSAVEQLTKMNPpPVF	S2(Phospho)	0.436 S(2): 79.8; T(4): 73.2; S(10): 73	9		11
	Low		FGGVLPDSLSNLStsLQtLsLQYNTISGRl	T14(Phospho)	S15(Phospho) Too many isoforms		0.254	10
	Low		GAHDPALWLAAPFiFEELDSLVLKAAL	T14(Phospho)	0.269 T(14): 26.9; S(20): 18.3; Y(23):	2	0.745	10
	Low		GAYNAFQlLQKVfMgATVAFcAtAGIPAI	T8(Phospho)	0.167 Y(3): 50.0; T(8): 50.0; T(17): 50	0	0.054	12
	Low		GNsRALAtVsAIIDGTGSVGAALGPLLTG	S3(Phospho)	0.006 S(3): 38.1; T(8): 38.1; S(10): 61	14	0.804	11
	Low		GyVDPESFSAGHVSEAGDVYSFGVVLL	Y2(Phospho)	0.096 Y(2): 47.7; S(7): 34.9; S(9): 28.	5	0.203	10
	Low		IFNsYVNLlIsALPGSmEDEANIDGLGNK	S4(Phospho)	0.498 S(4): 99.8; Y(5): 99.8; S(11): 50	28		10
	Low		IPHTYVSSNcFAAYFcPNLSQLTSFLPPK	S20(Phospho)	0.144 T(4): 14.4; Y(5): 14.4; S(7): 14.	5		11
	Low		KDFEPDsGHWsLRPLWSQMIDFPQDF	S7(Phospho)	0.394 S(7): 78.8; S(11): 60.6; S(17): 6	3	0.713	13

Low		LFGKtHcImPLHSGMASLSSDSLVCaES\ T5(Phospho)	0.089	T(5): 31.3; S(13): 17.9; S(17): 1	7	0.799	13
Low		LKKPALAYmmGWLGVVAsDTTNVcW\ S18(Phospho)	0.242	Y(8): 24.2; S(18): 24.2; T(20): 1	3	0.806	11
Low		LtAnSMyGcLGFsNSRFYAKPLAELITLQ T2(Phospho)	0.34	T(2): 91.0; S(5): 52.9; Y(7): 52.	37	0.597	22
Low		mMDPSsssAAVPAAAPAVGDGGGGGG S6(Phospho)	0.011	S(5): 44.3; S(6): 44.3; S(7): 44.	7	0.686	14
Low		MTADTVTTTtAAVAEHpAtSLSPSSPHp T10(Phospho)	0.232	T(2): 7.2; T(5): 7.2; T(7): 7.2; T	21	0.405	11
Low		MTASANGDTDEtSGLTTPRScEVPLcSS T12(Phospho)	0.647	T(2): 0.3; S(4): 0.3; T(9): 0.9; T	33		10
Low		NFADGLTTFKTATFAAQGDGFMAIGmG T31(Phospho)	0.722	T(7): 4.9; T(8): 4.9; T(11): 9.1; T	13	0.645	22
Low		NVQPyDVFLSEPHVSftGIIGAVAsGSFC Y5(Phospho)	0.027	Y(5): 41.5; S(10): 41.5; S(15): 4	0	0.611	14
Low		NVSQLSEVFPDvDmVFGNGQKLsLSPE S23(Phospho)	0.659	S(3): 1.9; S(6): 1.9; S(23): 65.9	17	0.109	12
Low		QAGENSIDcSLVAPAALVLFmVmmYtPsi Y25(Phospho)	0.147	S(6): 59.5; S(10): 59.5; Y(25): 6	5	0.482	12
Low		QNVsQHdLSNDFFSLFLDKSMTySsAlf S4(Phospho)	0.005	S(4): 35.3; Y(7): 59.5; S(10): 64	2	0.806	14
Low		QPtmPLPtNcHcRsMPTPQsLPHPPVtAR T3(Phospho)	0.178	T(3): 82.2; T(8): 82.2; S(14): 82	1	0.423	14
Low		QRssMALQDVEEEASANMFAATTDSEN S3(Phospho)	0.057	S(3): 27.7; S(4): 27.7; S(15): 20	4	0.443	14
Low		SENYSSsVsDDEALNAmeELLPKAsAVY Y4(Phospho)	0.007	S(1): 41.9; Y(4): 41.9; S(5): 41.	1	0.803	10
Low		SESTFVQQLARPLAEyMsLPASQySVLC Y16(Phospho)	0.028	S(1): 32.9; S(3): 32.9; T(4): 32.	3	0.532	13
Low		SLGELDLSSNALtGGIPVELGGcsGLLKL S9(Phospho)	0.03	S(1): 44.1; S(8): 44.1; S(9): 44.	1	0.802	11
Low		SNImNYSSPSNFRSGsmK S16(Phospho)	0.989	S(1): 0.0; Y(6): 0.1; S(7): 0.1; S	53	0.736	11
Low		ssIsYFLVAmLLcNGFGFIVsAQVVGGS S1(Phospho)	0.017	S(1): 62.5; S(2): 62.5; S(4): 62.	0		12
Low		tEMVAIAGILLGVFVAVTgtYtsLLQIIAtF T1(Phospho)	0.023	T(1): 71.7; T(19): 82.9; T(21): 7	1	0.44	11
Low		tSGIHGGGPGGPLLSQITQtmQIPLTYAE T1(Phospho)	0.054	T(1): 27.9; S(2): 27.9; S(15): 27	2	0.601	10
Low		TTYNSSQyGILNQEGmFLAsyFVsSDLFk Y3(Phospho)Y8(Phospho)		S Too many isoforms		0.57	15
Low		TYAFKmYDEmISSGFtPcLTTYNALLNVI T16(Phospho)	0.094	T(1): 13.1; Y(2): 13.1; Y(7): 9.4	1	0.741	12
Low		tyYIGAPSESVEQDVmHSYSmAfGGGG T1(Phospho)	0.067	T(1): 28.0; Y(2): 28.0; Y(3): 28.	6		12
Low		VKDcFDIDAAeEGSAmSLltPAmEEFyV T12(Phospho)	0.1	T(12): 60.0; S(15): 60.0; S(18):	0	0.113	12
Low		VSStQLLYqSAPYQAAILFATGPFVDQLL T4(Phospho)	0.019	S(2): 35.6; S(3): 35.6; T(4): 35.	3	0.368	11
Low		VtVPFmVLHGTADRvtDPLASQDLYNEA T2(Phospho)	0.03	T(2): 54.5; T(11): 58.6; T(16): 5	1	0.69	12
Low		VVNPPNNTSLtFLGmVVVmDDPLtERPC T11(Phospho)	0.654	T(8): 21.2; S(9): 21.2; T(11): 79	18	0.764	19
Low		VVVsESGWPSAEGIGASmDNARAYNQ S4(Phospho)	0.139	S(4): 42.0; S(6): 42.0; S(10): 3:	4	0.806	11
Low		VyLmRVPDASSLGALPAASLVKPtSLAE Y2(Phospho)	0.048	Y(2): 37.9; S(10): 37.9; S(11): 3	5	0.304	12
Low		WsRTQSTNISWLYRPLSSltGLcPQVIsR S2(Phospho)S18(Phospho)		Too many isoforms		0.103	13
Low		ysGGsLAAARtLGsGTADIAINWsGGMHt Y1(Phospho)	0.288	Y(1): 91.5; S(2): 91.5; S(5): 91.	8	0.422	13

Os10t0466700-01	Low	Similar to 60S ribosomal protein L17.	AGLLsAAERAGLSLsAVER S5(Phospho)	0.229	S(5): 98.8; S(13): 77.1; S(15): 1	24		10
	Low		ASMSKsSLR S7(Phospho)	0.872	S(2): 0.0; S(4): 1.7; S(6): 11.1;	45		11
	Low		ASMSKsSLR S6(Phospho)	0.487	S(2): 0.5; S(4): 2.0; S(6): 48.7;	28		10
	Low		cAKmIPVmlWGtlIMR T12(Phospho)	1	T(12): 100.0	8	0.678	11
	Low		EIFLDLLsKLDENcNK S8(Phospho)	1	S(8): 100.0	49	0.203	11
	Low		HKVMAFVGIFTGFGsVGR S15(Phospho)	0.5	T(11): 50.0; S(15): 50.0	10		13
	Low		HLASGAGtPR T8(Phospho)	0.5	S(4): 50.0; T(8): 50.0	26		10
	Low		LHNAASPR T3(Phospho)	0.999	T(3): 99.9; S(7): 0.1	42		16
	Low		LItSLPR T3(Phospho)	0.985	T(3): 99.8; S(4): 98.7; S(5): 1.5	55		11
	Low		mILFLIscsMSVRGK S8(Phospho)	0.425	S(8): 57.5; S(10): 84.9; S(12): 1	17	0.776	13
	Low		PRPNetPR T6(Phospho)	1	T(6): 100.0	40		13
	Low		RADAAAAAAAMEPLVPGAtr T19(Phospho)	1	T(19): 100.0	30		10
	Low		RGAEPsPR S7(Phospho)	1	S(7): 100.0	47		17
	Low		VcsGTQVQTLRFAFPAK S3(Phospho)	0.446	S(3): 44.6; T(5): 44.6; T(9): 10.	31		17

	Low		VGTAIQQDLPKVmtmMR	T14(Phospho	0.5 T(3): 50.0; T(14): 50.0	19		10
	Low		VyGDFLPR	Y2(Phospho)	1 Y(2): 100.0	36		13
	Low		VyTRTGNR	Y2(Phospho)	0.489 Y(2): 48.9; T(3): 48.9; T(5): 2.1	30		14
	Low		yPPKEsADAAVLVAATLR	Y1(Phospho)	1 Y(1): 100.0; S(6): 100.0; T(16):	63	0.398	13
	Low		ySPPPVVEVVAEKtISR	Y1(Phospho)	0.726 Y(1): 81.5; S(2): 22.8; T(14): 89	35	0.773	15
	Low		yVLDPGFR	Y1(Phospho)	1 Y(1): 100.0	38		10
Os11t0137100-01	Low	Similar to predicted protein.	APGDADFEFsVGSHPMmAADQLISKGF	S10(Phospho	0.26 S(10): 26.0; S(13): 26.0; S(24):	7	0.766	14
	Low		ASNNTINNtPSVGPKDWSGSFLWDSR	T9(Phospho)	0.459 S(2): 15.4; T(5): 15.4; T(9): 45.	29	0.249	10
	Low		LmMPPIKNSVLPSsGVWtHFWR	S14(Phospho	0.697 S(9): 2.7; S(13): 29.2; S(14): 78	44		14
	Low		mLVYEymHNQSLDtFIFDEGKR	Y6(Phospho)	0.128 Y(4): 19.9; Y(6): 19.9; S(11): 78	9	0.515	17
	Low		TSSIDTINGSGGAGNNNFDSFsEAGWS	S22(Phospho	0.446 T(1): 1.0; S(2): 1.0; S(3): 1.0; T	18		13
Os11t0168200-01	Low	60S ribosomal protein L3.	EHVTGLGPKLSEtVK	T12(Phospho	0.403 T(4): 40.3; S(10): 19.5; T(12): 4	8		12
	Low		FLKSsAGGFLGDLVK	S5(Phospho)	0.5 S(4): 50.0; S(5): 50.0	39	0.596	12
	Low		ISTyIRTPVsGALVSR	Y4(Phospho)	0.159 S(2): 17.4; T(3): 64.6; Y(4): 18.	28	0.799	10
	Low		MLLSYYHyHRR	Y8(Phospho)	0.668 S(4): 14.6; Y(5): 14.6; Y(6): 4.0	21	0.615	11
	Low		MVPTAISHKNTSAVsTR	S15(Phospho	0.625 T(4): 0.1; S(7): 0.5; T(11): 4.6;	41		10
	Low		sKINGLK	S1(Phospho)	1 S(1): 100.0	59		13
	Low		sYNLRSDSTILLR	S1(Phospho)	0.5 S(1): 50.0; Y(2): 50.0; S(6): 0.0	44		14
	Low		VEPtVRDVLAFHR	T4(Phospho)	1 T(4): 100.0	53		12
Os11t0174700-00	Middle	Os11t0174700-00	WVmDAMVDAteLWSLDayTGHGLPR	T10(Phospho	0.95 T(10): 99.7; S(14): 0.3; Y(18): 9	75	0.013	22
	Low		ATmAssGAAAAAMAVFLAmALVLsGTE/	S5(Phospho)	0.365 T(2): 25.7; S(5): 86.3; S(6): 86.	27	0.617	12
	Low		EmTGsGIFAAGEVEEDEsANASATPVf	S5(Phospho)	0.447 T(3): 30.4; S(5): 65.6; S(19): 68	16		10
	Low		FIEmEHFLIPtVEPtQEPTQGRR	T11(Phospho	1 T(11): 100.0; T(15): 100.0; T(16)	53		10
	Low		ILFsGsIHYPRstPEmWDGLIEK	S4(Phospho)	0.071 S(4): 28.4; S(6): 92.9; Y(9): 92.	11		12
	Low		ISDFGDLASVAfFGFRGEALsSLcALGK	T12(Phospho	0.441 S(2): 2.1; S(9): 49.4; T(12): 49.	33	0.105	11
	Low		LEPGVQLKDTMMmGADyyQtEAER	Y17(Phospho	0.813 T(10): 18.7; Y(17): 95.2; Y(18):	13	0.643	16
	Low		mEVTEEGLtNLtyLQcIIKETLR	T9(Phospho)	0.001 T(4): 99.9; T(9): 99.4; T(12): 50	11	0.731	17
	Low		mtVtQLAAAGAAGGASGGAAGAGGAP/	T2(Phospho)	0.987 T(2): 99.4; T(4): 99.4; S(16): 1.	35	0.106	15
	Low		PssAATASAAGQSmSVSNVvtPAGEDeI	S2(Phospho)	0.125 S(2): 51.1; S(3): 51.1; T(6): 51.	18	0.612	13
	Low		QLTKWLySDEQGSTVItVsGmGGLGK	Y7(Phospho)	0.01 T(3): 56.1; Y(7): 33.8; S(8): 33.	3	0.805	19
	Low		tAsLLPIMIttsSPSSQPVRQLQQR	T1(Phospho)	0.043 T(1): 70.7; S(3): 70.7; T(10): 61	6	0.572	11
	Low		yLIGDKPLmDMVDPtLKSVPEEQVR	Y1(Phospho)	0.443 Y(1): 88.6; T(15): 55.7; S(18): 5	6	0.803	12
	Low		yTTPVPPmPTmLASLmHastsALVK	Y1(Phospho)	0.013 Y(1): 50.4; T(2): 50.4; T(3): 50.	0	0.483	14
Os11t0303500-01	High	Nucleotide-binding, alpha-beta plait domain containing protein.	ATNTGScAsFSDVDEDIPEK	S9(Phospho)	0.999 T(2): 0.0; T(4): 0.0; S(6): 0.0; S	133	0	29
	High		ATNTGScASFsDVDEDIPEK	S11(Phospho	0.888 T(2): 0.0; T(4): 0.0; S(6): 0.0; S	99	0	50
	Low		EPPAPAAAsRQcDAcGDDVR	S9(Phospho)	1 S(9): 100.0	19		14
	Low		IsLSNFAmDSINsDLsKK	S2(Phospho)	0.904 S(2): 98.0; S(4): 5.5; S(10): 4.8	32	0.483	12

	Low		KMEtEDQSLVHDyNPEK	T4(Phospho)	0.995 T(4): 99.5; S(8): 0.5; Y(13): 100.0	77		10
	Low		KMETEDQsLVHDyNPEK	S8(Phospho)	0.052 T(4): 94.8; S(8): 10.5; Y(13): 94.8	23		15
	Low		mmTRAsMGAMEGAADVVR	S6(Phospho)	0.948 T(3): 5.2; S(6): 94.8	37	0.792	11
	Low		MtsVVHDSVSGNHGADERQK	T2(Phospho)	0.825 T(2): 88.1; S(3): 94.4; S(9): 17.0	18	0.62	13
Os11t0482000-01	Low	Similar to 40S ribosomal protein S5.	ADVcFSLsTPtDLVIHRSQVPK	S8(Phospho)	0.098 S(6): 15.2; S(8): 38.8; T(9): 37.0	7	0.467	10
	Low		ANcNLASLGVQRsRPPTPQHGGAR	S13(Phospho)	0.066 S(7): 0.2; S(13): 6.6; T(17): 93.0	40		11
	Low		IGADGYsRmLLFHGNVLQPNVAR	S7(Phospho)	0.839 Y(6): 16.1; S(7): 83.9	63		14
	Low		mARDVLAIPATsVAsEAAFSTGER	S12(Phospho)	0.311 T(11): 64.5; S(12): 64.5; S(15): 0.0	19		11
	Low		SEGASSSSASSAGAGGAHRSAPGAs	S26(Phospho)	0.963 S(1): 0.0; S(5): 0.0; S(6): 0.0; S(26): 0.0	37	0.803	12
	Low		VTYIAPPQPPSPVPEESEEGsPSR	S21(Phospho)	0.707 T(2): 0.0; Y(3): 0.0; S(11): 0.0; S(21): 0.0	70	0.132	17
	Low		WQAQDLAtIVPtLDPAGLDLLSK	T8(Phospho)	1 T(8): 100.0; T(12): 100.0; S(22): 0.0	58	0.657	13
	Low		YLsNHFYVGGSSYAGKVIIMK	S3(Phospho)	0.498 Y(1): 49.8; S(3): 49.8; Y(7): 0.2	53		12
	Low		YsVNGVSHVNPDTPLKVADyYK	S2(Phospho)	0.023 Y(1): 12.4; S(2): 12.4; S(7): 29.0	1	0.735	16
Os12t0165900-01	High	Hypothetical conserved gene.	VPFFADDEESPAtPK	T13(Phospho)	0.999 S(10): 0.1; T(13): 99.9	109	0	47
	Low		EVmVGsKGVik	S6(Phospho)	1 S(6): 100.0	53		10
	Low		IVGTsGGYRPR	S5(Phospho)	0.18 T(4): 1.4; S(5): 18.0; Y(8): 80.6	26	0.395	12
	Low		LtGVPcKIFK	T2(Phospho)	1 T(2): 100.0	93	0.802	19
	Low		LVKSsKPEmK	S5(Phospho)	0.981 S(4): 1.9; S(5): 98.1	61	0.584	18
	Low		NRGVLLsEFK	S7(Phospho)	1 S(7): 100.0	48		11
	Low		tKLFPPANFK	T1(Phospho)	1 T(1): 100.0	53	0.673	13
	Low		tLISRNSIMK	T1(Phospho)	0.891 T(1): 89.1; S(4): 5.5; S(7): 5.5	26	0.509	12
Os12t0166000-00	High	Conserved hypothetical protein.	VPFFADDEESPAtPK	T13(Phospho)	1 S(10): 0.0; T(13): 100.0	101	0	35
Os12t0167900-01	Low	60S ribosomal protein L3.	VEPtVRDVLAFHR	T4(Phospho)	1 T(4): 100.0	53		12
Os12t0170700-01	Low	Conserved hypothetical protein.	tsDLSSLsLVSK	T1(Phospho)	0.779 T(1): 85.3; S(2): 85.3; S(5): 12.0	29		11
Os12t0256300-01	High	Similar to Schizosaccharomyces pombe (Fragment).	KEPtPPLPPPPPLPELIPGR	T4(Phospho)	1 T(4): 100.0	125	0	41
	Low		mPLIFALsSLIKGtPFTLSK	S9(Phospho)	0.64 S(8): 18.3; S(9): 81.5; T(14): 78.0	41	0.322	11
Os12t0288600-01	High	Conserved hypothetical protein.	DVLPSPsSNQNSSLPFVR	S7(Phospho)	0.468 S(5): 46.8; S(7): 46.8; S(8): 6.5	92	0	23
	High		DVLPsPSSNQNNSSLPFVR	S5(Phospho)	0.999 S(5): 99.9; S(7): 0.0; S(8): 0.0	102	0	48
	Low		ARPAFVDAsGAALSFAGLR	S9(Phospho)	0.998 S(9): 99.9; T(10): 99.8; S(15): 0.0	44		11
	Low		EGcyLVsLmAtDATLIK	Y4(Phospho)	0.031 Y(4): 25.6; S(7): 80.5; T(11): 96.0	2	0.125	14
	Low		VVEtstSSSWFLASPFR	T4(Phospho)	0.075 T(4): 21.5; S(5): 58.4; T(6): 58.0	23	0.765	15

Os12t0406200-01	Low	Similar to 40S ribosomal protein S3a (CYC07 protein).	LLLPAsGR	S6(Phospho)	1 S(6): 100.0	18	0.21	11
Os12t0481100-01	High High Low Low	Similar to cDNA clone:J033010C22, full insert sequence.	EMLEDEsEDEEEAK FDPDGsDDDGAASAAAGR RDVVTWNSMIsGYSR SLAAsmANLNIEVmNR	S7(Phospho) S6(Phospho) S11(Phospho) S5(Phospho)	1 S(7): 100.0 1 S(6): 100.0; S(14): 0.0 0.322 T(5): 1.7; S(8): 1.7; S(11): 32.2 0.5 S(1): 50.0; S(5): 50.0	102 131 26 29	0 0 0.313 0.575	58 57 17 12
Os12t0502200-01	Low Low	Similar to Low temperature-responsive RNA-binding protein.	RAHtADEAAAVLR SIYAPLSPsLTAR	T4(Phospho) S9(Phospho)	1 T(4): 100.0 0.481 S(1): 1.8; Y(3): 1.8; S(7): 48.1;	38 40	0.714	13 13
Os12t0530000-01	High Low Low Low Low Low Low	Similar to Histone H2A.	DKADIGSAsQEF ITSNNGSGSGSDK LKVtYLK SLLDHLEQtAAAAAsGGAAGLRK sRsTTPASPAGR tLLNPPPsLR	S9(Phospho) T2(Phospho) T4(Phospho) T9(Phospho): S1(Phospho): T1(Phospho):	0.989 S(7): 1.1; S(9): 98.9 0.902 T(2): 90.2; T(3): 6.8; S(4): 2.3; 0.991 T(4): 99.1; Y(5): 0.9 0.986 S(1): 1.4; T(9): 99.6; S(14): 99. 0.112 S(1): 25.3; S(3): 74.1; T(4): 74. 1 T(1): 100.0; S(8): 100.0	94 29 60 36 27 53	0.002 0.77	29 11 10 13 10 17
Os12t0567700-01	High High Low Low Low Low Low Low Low Low Low	Similar to 60S ribosomal protein L2 (Fragment).	ASGsPPVPVMHsPPRPVTVK DAAAAAAPAPAPAAPAsSPRPR AIDPVLsEFAIVPPDFmSR AtAAGAPPDAAAFNALLAALsR GPPPPPGQARAAtAAGALGAELR IGAGMtLSVAAmAAAATVEGRR LAcRsIFGTSTGFTDmLVK mALAFAGKsVAVsAISMIVR mFIGHRsMVLSLAMSPDGR TQAGETAAGKYPLNVtAEGSR TRVSPASPAsAR	S4(Phospho): S19(Phospho) S7(Phospho) T2(Phospho): T13(Phospho) T6(Phospho) S5(Phospho) S9(Phospho): S7(Phospho) T16(Phospho) S10(Phospho)	0.471 S(2): 52.4; S(4): 52.4; S(12): 94. 0.807 S(19): 80.7; S(20): 19.3 0.5 S(7): 50.0; S(18): 50.0 1 T(2): 100.0; S(21): 100.0 1 T(13): 100.0 0.671 T(6): 67.1; S(8): 29.9; T(17): 3. 0.42 S(5): 42.0; T(9): 14.5; S(10): 14. 0.83 S(9): 99.2; S(13): 83.8; S(16): 1. 0.486 S(7): 48.6; S(11): 48.6; S(15): 1. 0.134 T(1): 35.2; T(6): 35.2; Y(11): 13. 0.767 T(1): 0.7; S(4): 4.9; S(7): 17.8;	33 48 21 13 34 14 24 58 43 14 26	0 0 0.455 0.714 0.803 0.612 0.711 0.776 0.562	13 13 11 10 13 11 14 10 10 15 13
Os12t0579000-01	High High Low	Leo1-like protein family protein.	DVFGESDEDEPAPYR VMQNDAAGMDsEDEAYQQRPVASR ImDPVKIFEGNsNHSGsQVGNWR	S6(Phospho) S11(Phospho) S12(Phospho)	1 S(6): 100.0; Y(14): 0.0 0.835 S(11): 83.5; Y(16): 16.5; S(23): 0.433 S(12): 86.7; S(15): 56.7; S(17):	94 64 34	0 0	32 38 11

Low	LyNLDWHtsAAKNEcTAAFGK	Y2(Phospho)	0.283 Y(2): 84.9; T(8): 71.7; S(9): 71.	9	0.752	16
Low	mDmGISSTFAsLIsAAAsVGMLTK	S12(Phospho)	0.024 S(6): 51.4; S(7): 51.4; S(8): 53.	5		17
Low	RtPPAPTcsAPPAsR	T2(Phospho)	0.83 T(2): 100.0; T(7): 17.0; S(9): 97	53		15
Low	SVLIFDLGGNTFDIsIIAIDNGVFK	S15(Phospho)	0.874 S(1): 1.9; T(11): 10.7; S(15): 87	29	0.563	12
Low	YWVTEMHVDGFRFDLAsImtR	S17(Phospho)	0.013 Y(1): 49.7; T(4): 49.7; S(17): 50	4	0.805	11

Supplemental Table 5. Nuclear phosphoproteins identified in rice embryos after 24 h of imbibition

No.	Protein ID ^a	Description	Score	M.P. ^b	M.P.P. ^c	MW(kDa)	Calc. pI	Function ^d
1	Os01t0104800-01	Sas10/Utp3 family protein.	67.77	1	1	73.2	5.49	not assigned
2	Os01t0128400-01	Protein of unknown function DUF2359, TMEM214 domain containing protein	107.61	1	1	63.3	8.75	not assigned
3	Os01t0191100-01	Similar to Acidic ribosomal protein P2a-4 (Fragment).	498.28	3	2	11.6	4.32	protein
4	Os01t0205500-01	Similar to 60S ribosomal protein L11-2 (L16). Splice isoform 2.	422.16	4	1	20.8	9.92	protein
5	Os01t0226400-01	ATPase, AAA-type, core domain containing protein.	35.1	1	1	93.4	8.18	protein
6	Os01t0243100-01	Similar to Kinesin	35.1	1	1	10	8.18	cell
7	Os01t0851700-01	Similar to Cytosolic starch phosphorylase (Fragment).	60.66	2	1	94.4	7.24	major CHO metabolism
8	Os01t0924900-01	GTP-binding signal recognition particle SRP54, G-domain containing protein.	224.43	3	3	56.2	6.47	not assigned
9	Os02t0161200-01	Zinc finger, CCCH-type domain containing protein.	31.04	1	2	49	9.11	RNA
10	Os02t0257200-01	Conserved hypothetical protein.	35.17	2	2	32.3	9.47	not assigned
11	Os02t0288200-01	Protein of unknown function DUF573 domain containing protein	70.56	3	1	61.5	6.07	not assigned
12	Os02t0519900-01	Similar to Elongation factor EF-2 (Fragment).	442.39	9	1	94	6.16	protein
13	Os02t0523500-02	Similar to RNA binding protein Rp120.	39.41	1	1	44.2	5.6	RNA
14	Os02t0549600-01	Similar to 40S ribosomal protein S10-1.	140.94	4	1	20.3	9.76	protein
15	Os02t0550700-01	Similar to Nucleolar autoantigen-like protein	21.92	1	1	43.2	6.14	RNA
16	Os02t0788400-01	Similar to Eukaryotic translation initiation factor 3 subunit-like protein.	69.71	2	1	32	8.5	protein
17	Os03t0219300-01	Similar to Tubulin alpha-2 chain (Alpha-2 tubulin).	89.41	2	1	50	5.25	cell
18	Os03t0249900-01	Conserved hypothetical protein	40.18	3	1	35.1	8.73	not assigned
19	Os03t0327600-01	Ricin B-related lectin domain containing protein.	245.88	8	1	38.8	6.8	not assigned
20	Os03t0337800-01	Similar to 60S ribosomal protein L19 (Fragment).	85.36	3	1	24.1	11.39	protein
21	Os03t0350100-01	SAR DNA-binding protein-2.	387.34	9	3	61	8.82	RNA
22	Os03t0352450-00	Hypothetical conserved gene.	20.19	1	1	52.2	9.54	not assigned
23	Os03t0383800-02	Nucleotide-binding, alpha-beta plait domain containing protein.	39.86	4	3	78.1	4.7	RNA
24	Os03t0383800-03	Nucleotide-binding, alpha-beta plait domain containing protein.	26.64	3	3	31.6	9.03	RNA

25	Os03t0392400-01	Heat shock protein DnaJ, N-terminal domain containing protein.	41.61	1	1	42.4	6.9	stress
26	Os03t0403100-01	Similar to DNA-directed RNA polymerase subunit.	25.18	2	3	130	8.62	RNA
27	Os03t0579300-00	Similar to 60S ribosomal protein L19 (Fragment).	72.84	3	1	24.1	11.31	protein
28	Os03t0596900-01	GTP-binding signal recognition particle SRP54, G-domain containing protein.	34.76	1	3	77.8	5.14	not assigned
29	Os03t0663800-01	Globulin 1 (Fragment).	3212.39	5	1	28.4	10.04	development
30	Os03t0718500-00	Homeodomain-related domain containing protein.	28.58	1	1	24.3	7.93	RNA
31	Os03t0726100-02	Similar to Alpha-tubulin.	68.47	2	1	41.5	5.19	cell
32	Os03t0733400-01	Zinc finger, BED-type predicted domain containing protein.	42.31	2	1	80.9	5.33	DNA
33	Os03t0787300-01	Similar to DnaJ homolog.	61.19	2	1	46.7	6.19	stress
34	Os03t0839100-01	Ubiquinone biosynthesis hydroxylase, UbiH/UbiF/VisC/COQ6 domain containing protein.	0	1	1	55.6	7.77	misc
35	Os04t0103200-01	Proteasome component region PCI domain containing protein.	24.63	1	1	46.3	5.24	protein
36	Os04t0162533-00	Unknown	24.63	1	1	10.3	5.24	not assigned
37	Os04t0419600-01	Histone H3.	24.69	2	1	30.5	11.82	DNA
38	Os04t0421900-01	Similar to H0525E10.11 protein.	40.98	1	1	122.7	6.02	not assigned
39	Os04t0446500-01	Similar to OSIGBa0140O07.15 protein.	68.29	2	1	39.3	4.97	protein
40	Os04t0486600-01	Similar to Glyceraldehyde-3-phosphate dehydrogenase, cytosolic 3 (EC 1.2.1.12).	41.55	3	2	36.7	6.81	glycolysis
41	Os04t0486600-02	Similar to Glyceralde-3-phosphate dehydrogenase.	41.55	2	1	25	7.93	glycolysis
42	Os04t0501600-01	AT hook, DNA-binding, conserved site domain containing protein.	81.77	4	4	92.5	6.43	not assigned
43	Os04t0501600-02	Nucleotide-binding, alpha-beta plait domain containing protein.	95.68	3	2	67.9	8.6	not assigned
44	Os04t0543200-01	Nucleotide-binding, alpha-beta plait domain containing protein.	0	1	1	86.6	5.87	RNA
45	Os04t0635900-01	DNA repair exonuclease family protein.	47.92	2	1	79.1	6.38	DNA
46	Os04t0671800-02	Similar to H0624F09.12 protein.	32.8	1	1	45.4	5.97	RNA
47	Os04t0679400-03	Similar to H0801D08.15 protein.	32.79	1	1	10.7	6.51	hormone metabolism
48	Os05t0295100-01	Hypothetical conserved gene	54.83	1	1	42.9	6.4	not assigned
49	Os05t0302700-01	Similar to ATP/ADP carrier protein.	35.72	2	2	41	9.74	transport
50	Os05t0350500-01	Peptidase M24, structural domain domain containing protein.	174.63	4	1	43.2	7.08	protein

51	Os05t0367100-01	Ribosome biogenesis protein Nop16 domain containing protein.	75.78	1	1	21.1	9.67	not assigned
52	Os05t0445500-01	Similar to Acidic ribosomal protein (Fragment).	477.23	6	3	14.4	4.27	protein
53	Os05t0445500-02	Similar to 60S acidic ribosomal protein p2b (Fragment).	438.76	5	3	7.6	4.22	protein
54	Os05t0494800-01	Hypothetical protein	75.78	1	1	7.6	4.22	not assigned
55	Os05t0520100-00	Similar to MPPN domain containing protein.	31.9	1	1	34.7	9.86	not assigned
56	Os05t0524400-01	Phosphofructokinase family protein.	68.3	2	2	62.5	6.9	glycolysis
57	Os05t0540800-01	Homeodomain-like containing protein.	32.05	1	1	49.3	9.51	RNA
58	Os05t0576700-01	Oleosin family protein.	68.22	1	1	18.1	9.7	lipid metabolism
59	Os05t0592600-03	Hypothetical conserved gene.	48.7	2	1	32.5	4.64	protein
60	Os05t0596200-03	Similar to cDNA clone:001-104-D04, full insert sequence.	35.99	1	1	18.2	9.96	not assigned
61	Os05t0597100-01	Similar to Nucleolar histone deacetylase HD2-p39.	316.59	4	2	32.5	4.68	RNA
62	Os06t0115500-01	Similar to 60S ribosomal protein L13 (BBC1 protein homolog).	139.65	4	1	24	10.99	protein
63	Os06t0149400-01	Similar to Chitinase A.	46.34	2	1	42.6	4.48	DNA
64	Os06t0234100-01	Peptidase S1C, HrtA/DegP2/Q/S family protein.	79.35	3	2	68	8.75	protein
65	Os06t0698859-01	Similar to C2H2 zinc-finger protein SERRATE (Fragment).	10	2	2	79.9	8.85	RNA
66	Os06t0724600-02	Sas10/Utp3 family protein.Similar to transformer-2 protein.	29.22	2	2	31.6	10.54	RNA
67	Os07t0167200-01	Similar to Zinc finger POZ domain protein (Fragment).	21.51	1	1	46.1	5.53	protein
68	Os07t0180900-01	Similar to 60S ribosomal protein L4.	353.84	6	1	44.7	10.54	protein
69	Os07t0557500-01	WRC domain containing protein.	143.01	4	4	74.8	4.82	protein
70	Os07t0574800-01	Tubulin alpha-1 chain.	80.86	2	1	49.6	5.06	cell
71	Os07t0607800-01	Similar to leucine-rich repeat family protein.	31.68	1	1	51.8	3.93	not assigned
72	Os08t0116500-01	Similar to 60S acidic ribosomal protein P1 (L12).	76.29	4	2	11.1	4.51	protein
73	Os08t0117300-01	Similar to 40S ribosomal protein S13.	226.19	3	1	17.1	10.54	protein
74	Os08t0127700-01	Similar to Pre-mRNA-splicing factor SLU7.	50.57	1	1	62	5.88	RNA
75	Os08t0130500-01	60S acidic ribosomal protein P0.	242.92	7	4	34.4	5.49	protein
76	Os08t0137300-01	Protein of unknown function DUF604 family protein	50.57	1	1	42	5.88	not assigned

77	Os08t0154600-01	Similar to Topoisomerase I.	44.57	2	2	102.6	9.54	DNA
78	Os08t0178300-02	Hypothetical conserved gene.	36.42	1	1	50	9.82	not assigned
79	Os08t0191700-01	Similar to Lactoylglutathione lyase (EC 4.4.1.5)	50.57	1	1	32.8	9.82	amino acid metabolism
80	Os08t0328300-01	ENT domain containing protein.	34.69	1	1	50.3	7.66	not assigned
81	Os08t0390000-01	Moesin domain containing protein	10.69	1	1	50.3	7.66	transport
82	Os08t0428800-00	Similar to High mobility group I/Y-2.	70.46	3	3	18.7	10.46	DNA
83	Os08t0512400-02	Similar to AT-hook protein 1.	153.37	2	2	35.2	10.07	RNA
84	Os08t0528900-01	Similar to Transcriptional activator FHA1.	36.21	1	1	38.1	7.69	RNA
85	Os08t0533700-01	Similar to cation cation antiporter.	10	1	1	26.4	5.83	transport
86	Os09t0369500-01	Conserved hypothetical protein	36.21	1	1	41.4	5.83	not assigned
87	Os09t0372400-02	Conserved hypothetical protein.	30.39	2	1	47.3	4.61	not assigned
88	Os09t0402100-01	PF1 protein.	40.3	3	1	21.7	9.95	DNA
89	Os09t0491708-01	Protein of unknown function DUF296 domain containing protein.	46.37	2	2	35.5	10.14	RNA
90	Os09t0565500-01	Conserved hypothetical protein.	67.47	2	2	70	7.46	not assigned
91	Os09t0570850-00	Similar to Histone H2B.	45.18	1	1	16.8	9.55	DNA
92	Os10t0466300-01	Similar to Yarrowia lipolytica chromosome C of strain CLIB99 of Yarrowia lipolytica.	29.8	2	1	57.8	6.39	RNA
93	Os11t0174700-00	Unknown	10	1	1	37.9	6.07	not assigned
94	Os11t0247300-01	Alfa-tubulin.	84.67	3	1	49.7	4.96	cell
95	Os11t0303500-01	Nucleotide-binding, alpha-beta plait domain containing protein.	33.59	1	1	77.6	9.76	RNA
96	Os12t0165900-01	Hypothetical conserved gene.	68.04	2	1	98.7	8.31	protein
97	Os12t0166000-00	Conserved hypothetical protein.	34.9	1	1	75.2	9.64	protein
98	Os12t0256300-01	Similar to Schizosaccharomyces pombe (Fragment).	40.76	1	1	90	7.8	protein
99	Os12t0288600-01	Conserved hypothetical protein.	59.79	1	1	62.3	7.09	not assigned
100	Os12t0481100-01	Similar to cDNA clone:J033010C22, full insert sequence.	111.67	2	2	89.5	5.43	DNA
101	Os12t0530000-01	Similar to Histone H2A.	531.28	3	1	14.3	10.2	DNA
102	Os12t0579000-01	Leo1-like protein family protein.	47.08	2	2	75.9	4.69	RNA

^aProtein ID is according to The Rice Annotation Project Database, ^bM.P. means number of matched peptide, ^cM.P.P. means number of matched phosphopeptide, ^dFunction were obtained using MapMan bin codes. *d* protein, protein synthesis/degradation/targeting/folding; RNA, RNA processing/regulation of transcription; DNA, DNA synthesis/repair; cell, cell organization/vesicle transport; major CHO metabolism, major carbohydrates metabolism; misc, miscellaneous; not assigned, unknown.

Supplemental Table 6. Nuclear phosphoproteins identified in rice embryos during early stage of germination

No.	Protein ID ^a	Description	M.P.P. ^b	Ratio_0	StdDev_0	PValue_0	Ratio_12	StdDev_12	PValue_12	Ratio_24	StdDev_24	PValue_24
1	Os01t0896700-00	Similar to 60S ribosomal protein L5.	4	1	0.229	1	14.267	0.509	0.0831	12.866	0.197	0.0000
2	Os01t0896800-01	Ribosomal protein L18/L5 domain containing protein.	4	1	0.229	1	14.267	0.509	0.0831	12.866	0.197	0.0000
3	Os08t0512400-01	Protein of unknown function DUF296 domain containing protein.	2	1	0.400	1	55.609	0.783	0.0965	6.752	0.329	0.0033
4	Os08t0512400-02	Similar to AT_hook protein 1.	4	1	0.289	1	28.402	0.549	0.0055	5.076	0.285	0.0004
5	Os06t0234100-01	Peptidase S1C_ HrtA/DegP2/Q/S family protein.	1	1	0.493	1	36.110	1.133	0.1978	3.457	1.935	0.5419
6	Os08t0246001-01	Hypothetical gene.	1	1	0.570	1	1.534	0.582	0.1747	0.987	0.903	0.9751
7	Os01t0962600-01	Similar to 40S ribosomal protein S10_1.	1	1	1.740	1	6.837	1.761	0.2371	0.950	1.080	0.9312
8	Os02t0549600-01	Similar to 40S ribosomal protein S10_1.	1	1	1.740	1	6.837	1.761	0.2371	0.950	1.080	0.9312
9	Os07t0557500-01	WRC domain containing protein.	5	1	0.106	1	1.700	0.510	0.0017	0.600	0.143	0.0000
10	Os04t0501600-01	AT hook_ DNA_binding_ conserved site domain containing protein.	6	1	0.223	1	10.264	0.461	0.2846	0.470	0.229	0.0000
11	Os04t0501600-02	Similar to H0311C03.6 protein.	6	1	0.223	1	10.264	0.461	0.2846	0.470	0.229	0.0000
12	Os03t0327600-01	Ricin B_related lectin domain containing protein.	2	1	0.873	1	2.200	1.069	0.1284	0.433	0.753	0.2335
13	Os09t0565500-01	Conserved hypothetical protein.	2	1	0.614	1	1.781	0.777	0.7400	0.344	0.549	0.0830
14	Os11t0303500-01	Nucleotide_binding_ alpha_beta plait domain containing protein.	2	1	0.551	1	3.197	0.844	0.5207	0.335	0.392	0.0881
15	Os02t0744650-00	Similar to CSLA1_cellulose synthase_like family A; mannan synthase.	2	1	0.281	1	2.301	0.493	0.3279	0.269	0.255	0.0015
16	Os06t0724600-02	Similar to transformer_2 protein.	1	1	1.161	1	1.762	1.480	0.5008	0.257	0.730	0.1565
17	Os03t0403100-01	Similar to DNA_directed RNA polymerase subunit.	2	1	0.661	1	4.808	1.069	0.3346	0.241	0.340	0.0622
18	Os03t0733400-01	Zinc finger_ BED_type predicted domain containing protein.	1	1	0.185	1	1.712	0.744	0.6220	0.198	0.187	0.0005
19	Os02t0161200-01	Zinc finger_ CCCH_type domain containing protein.	6	1	0.136	1	2.994	0.759	0.0000	0.191	0.467	0.0003
20	Os06t0532101-00	Hypothetical protein.	1	1	0.948	1	0.830	0.990	0.6698	0.159	1.110	0.0856
21	Os09t0491708-01	Protein of unknown function DUF296 domain containing protein.	1	1	0.686	1	0.469	1.784	0.3127	0.157	0.465	0.0506
22	Os07t0574800-01	Tubulin alpha_1 chain.	2	1	0.082	1	0.247	0.672	0.0000	0.137	1.051	0.0155
23	Os03t0350100-01	SAR DNA_binding protein_2.	7	1	0.083	1	0.031	0.371	0.0000	0.124	0.177	0.0000
24	Os01t0924900-02	Similar to BRI1_KD interacting protein 112 (Fragment).	5	1	0.058	1	0.663	0.285	0.0000	0.113	0.057	0.0000

25	Os01t0924900-01	GTP_binding signal recognition particle SRP54_ G_domain containing protein.	7	1	0.057	1	0.594	0.270	0.0000	0.113	0.057	0.0000
26	Os03t0383800-02	Nucleotide_binding_ alpha_beta plait domain containing protein.	8	1	0.196	1	0.208	0.521	0.0000	0.106	0.350	0.0005
27	Os02t0204300-01	Similar to Fgenesh protein 41.	3	1	0.282	1	0.783	0.844	0.0007	0.098	0.323	0.0008
28	Os02t0759800-01	Similar to GAMYB_binding protein (Fragment).	3	1	0.482	1	0.584	1.042	0.1347	0.070	0.561	0.0286
29	Os02t0759800-02	Similar to pre_mRNA_splicing factor prp45.	3	1	0.482	1	0.584	1.042	0.1347	0.070	0.561	0.0286
30	Os01t0959000-01	Nucleotide_binding_ alpha_beta plait domain containing protein.	1	1	0.514	1	0.247	0.963	0.0166	0.065	1.043	0.0132
31	Os05t0295100-01	Hypothetical conserved gene.	1	1	1.386	1	0.331	1.564	0.2314	0.061	0.852	0.1435
32	Os05t0295100-02	Protein of unknown function DUF1253 family protein.	1	1	1.386	1	0.331	1.564	0.2314	0.061	0.852	0.1435
33	Os05t0524400-01	Phosphofructokinase family protein.	2	1	0.361	1	0.875	0.661	0.9939	0.061	0.475	0.0024
34	Os05t0105900-01	Nucleotide_binding_ alpha_beta plait domain containing protein.	1	1	0.186	1	0.375	0.814	0.0451	0.058	0.175	0.0032
35	Os03t0350300-01	Similar to SAR DNA_binding protein_like protein.	4	1	0.189	1	0.014	0.579	0.0000	0.051	0.420	0.0001
36	Os03t0249900-01	Conserved hypothetical protein.	7	1	0.116	1	0.358	0.378	0.0000	0.044	0.217	0.0000
37	Os01t0125700-01	Conserved hypothetical protein.	1	1	2.114	1	6.954	2.055	0.2743	0.041	2.789	0.2565
38	Os01t0744300-01	Similar to Casein kinase_like protein.	1	1	0.472	1	0.664	0.885	0.5325	0.041	0.570	0.0107
39	Os02t0709900-01	Conserved hypothetical protein.	2	1	0.702	1	0.452	1.039	0.2040	0.041	0.956	0.0386
40	Os08t0117300-01	Similar to 40S ribosomal protein S13.	3	1	0.171	1	0.249	0.611	0.1569	0.033	0.337	0.0036
41	Os05t0445500-01	Similar to Acidic ribosomal protein (Fragment).	6	1	0.116	1	0.170	0.382	0.0000	0.029	0.201	0.0000
42	Os05t0445500-02	Similar to 60S acidic ribosomal protein p2b (Fragment).	6	1	0.116	1	0.170	0.382	0.0000	0.029	0.201	0.0000
43	Os02t0288200-01	Protein of unknown function DUF573 domain containing protein.	13	1	0.171	1	0.014	0.402	0.0000	0.029	0.246	0.0000
44	Os05t0596200-03	Similar to cDNA clone:001_104_D04_ full insert sequence.	2	1	0.805	1	2.819	0.940	0.4973	0.023	0.885	0.0707
45	Os03t0596900-01	GTP_binding signal recognition particle SRP54_ G_domain containing protein.	3	1	0.525	1	0.215	0.742	0.0295	0.020	0.922	0.0121
46	Os05t0367100-01	Ribosome biogenesis protein Nop16 domain containing protein.	3	1	0.166	1	0.320	0.706	0.0111	0.020	0.539	0.0814
47	Os12t0165900-01	Hypothetical conserved gene.	2	1	0.567	1	0.554	0.718	0.0856	0.018	0.437	0.0212
48	Os12t0166000-00	Conserved hypothetical protein.	2	1	0.567	1	0.554	0.718	0.0856	0.018	0.437	0.0212
49	Os01t0191100-01	Similar to Acidic ribosomal protein P2a_4 (Fragment).	4	1	0.122	1	0.199	0.432	0.0003	0.017	0.220	0.0000
50	Os02t0529700-01	Similar to Acidic ribosomal protein P2a_4 (Fragment).	4	1	0.122	1	0.199	0.432	0.0003	0.017	0.220	0.0000

51	Os03t0811500-01	Zinc finger_ HIT_type domain containing protein.	1	1	1.811	1	0.770	1.796	0.7443	0.016	2.005	0.2004
52	Os05t0597100-01	Similar to Nucleolar histone deacetylase HD2_p39.	7	1	0.182	1	0.051	0.317	0.0000	0.015	0.205	0.0000
53	Os12t0288600-01	Conserved hypothetical protein.	2	1	0.170	1	0.046	0.875	0.1723	0.014	0.711	0.0003
54	Os04t0446500-01	Similar to OSIGBa0140O07.15 protein.	4	1	0.072	1	0.071	0.354	0.0000	0.014	0.108	0.0000
55	Os04t0446500-02	Similar to FK506_binding protein 2 precursor (EC 5.2.1.8)	4	1	0.072	1	0.071	0.354	0.0000	0.014	0.108	0.0000
56	Os01t0505700-01	Conserved hypothetical protein.	1	1	1.693	1	0.189	1.838	0.2356	0.014	1.160	0.1812
57	Os07t0203300-01	Nucleic acid_binding_ OB_fold domain containing protein.	1	1	1.085	1	0.158	1.474	0.1062	0.014	1.127	0.0877
58	Os04t0306800-01	RNA recognition motif_ RNP_1 domain containing protein.	1	1	1.334	1	0.087	1.957	0.1376	0.012	1.383	0.1242
59	Os04t0306800-02	Similar to OSIGBa0096F13.9 protein.	1	1	1.334	1	0.087	1.957	0.1376	0.012	1.383	0.1242
60	Os01t0128400-01	Protein of unknown function DUF2359_ TMEM214 domain containing protein.	2	1	0.125	1	0.289	0.914	0.0241	0.010	0.383	0.0000
61	Os07t0603200-01	WD40 repeat_like domain containing protein.	3	1	0.347	1	0.154	0.606	0.0062	0.010	0.577	0.0028
62	Os08t0130500-01	60S acidic ribosomal protein P0.	2	1	0.270	1	0.307	0.657	0.0023	0.009	0.613	0.0003
63	Os08t0130500-02	Similar to 60S acidic ribosomal protein p0.	2	1	0.270	1	0.307	0.657	0.0023	0.009	0.613	0.0003
64	Os11t0135400-00	60S acidic ribosomal protein P0.	2	1	0.270	1	0.307	0.657	0.0023	0.009	0.613	0.0003
65	Os12t0133050-00	Similar to 60S acidic ribosomal protein P0.	2	1	0.270	1	0.307	0.657	0.0023	0.009	0.613	0.0003
66	Os08t0528900-01	Similar to Transcriptional activator FHA1.	1	1	0.838	1	0.214	1.505	0.0626	0.009	1.476	0.0547
67	Os12t0481100-01	Similar to cDNA clone:J033010C22_ full insert sequence.	2	1	0.358	1	0.101	0.823	0.0012	0.008	0.346	0.0014
68	Os03t0249900-02	Hypothetical conserved gene.	3	1	0.504	1	0.846	0.778	0.9613	0.007	0.318	0.0092
69	Os08t0129200-02	Similar to Cold shock protein_1.	1	1	0.668	1	0.041	1.755	0.0348	0.007	1.204	0.0356
70	Os09t0551300-01	Similar to predicted protein.	9	1	0.424	1	0.048	0.610	0.0745	0.006	0.462	0.2504
71	Os09t0551300-02	Bacterial Fmu (Sun)/eukaryotic nucleolar NOL1/Nop2p domain containing protein.	9	1	0.424	1	0.048	0.610	0.0745	0.006	0.462	0.2504
72	Os01t0224500-01	Conserved hypothetical protein.	3	1	1.011	1	0.371	1.057	0.3761	0.005	1.007	0.1231
73	Os01t0582400-01	Similar to Multidomain cyclophilin type peptidyl_prolyl cis_trans isomerase.	3	1	0.121	1	0.098	0.423	0.0000	0.004	0.318	0.0000
74	Os08t0154600-01	Similar to Topoisomerase I.	2	1	0.256	1	0.064	1.404	0.0022	0.003	1.008	0.0029
75	Os08t0127700-01	Similar to Pre_mRNA_splicing factor SLU7.	3	1	0.174	1	0.092	0.648	0.0002	0.003	0.826	0.0257
76	Os04t0480400-01	Similar to OSIGBa0158F13.7 protein.	3	1	0.131	1	0.005	0.738	0.0023	0.003	0.625	0.3703

77	Os07t0636000-01	Similar to H/ACA ribonucleoprotein complex subunit 4 (EC 5.4.99._)	2	1	0.384	1	0.004	0.496	0.0022	0.002	0.760	0.0022
78	Os07t0633200-01	Similar to SC35_like splicing factor SCL30a_30a kD.	1	1	0.753	1	0.002	2.109	0.0443	0.002	0.530	0.0443
79	Os05t0560600-01	Homeodomain_like containing protein.	1	1	0.852	1	0.019	1.076	0.0618	0.002	1.262	0.0590
80	Os12t0579000-01	Leo1_like protein family protein.	1	1	0.451	1	0.687	0.888	0.6026	0.002	1.034	0.0085
81	Os12t0527800-01	Zinc finger_ RING/FYVE/PHD_type domain containing protein.	3	1	0.317	1	0.144	0.629	0.0004	0.002	0.668	0.0005
82	Os03t0352450-00	Hypothetical conserved gene.	1	1	1.032	1	0.323	1.396	0.1373	0.002	1.383	0.0787
83	Os01t0104800-01	Sas10/Utp3 family protein.	3	1	0.065	1	0.055	0.410	0.0000	0.001	0.336	0.0000
84	Os05t0490000-01	KRR1 interacting protein 1 domain containing protein.	4	1	0.096	1	0.009	0.797	0.0005	0.001	0.517	0.2361
85	Os07t0644300-02	Similar to XPA_binding protein 2 (Adapter protein ATH_55).	1	1	0.205	1	0.013	1.762	0.0026	0.001	1.098	0.0035
86	Os08t0116500-01	Similar to 60S acidic ribosomal protein P1 (L12).	3	1	0.160	1	0.138	0.595	0.0215	0.001	0.639	0.0037
87	Os09t0103400-01	Conserved hypothetical protein.	2	1	0.191	1	0.006	1.320	0.0004	0.001	1.320	0.0004
88	Os10t0559700-01	Similar to Agenet domain containing protein_ expressed.	4	1	0.504	1	0.004	0.865	0.0081	0.000	1.118	0.0080
89	Os10t0559700-02	Similar to Agenet domain containing protein_ expressed.	4	1	0.504	1	0.004	0.865	0.0081	0.000	1.118	0.0080
90	Os03t0219300-01	Similar to Tubulin alpha_2 chain (Alpha_2 tubulin).	1	1	0.082	1	0.073	0.716	0.0000	0.000	1.784	0.0070
91	Os02t0523500-01	Similar to 110 kDa 4SNc_Tudor domain protein (Fragment).	1	1	0.349	1	0.026	1.403	0.0032	0.000	1.952	0.0814
92	Os02t0523500-02	Similar to RNA binding protein Rp120.	1	1	0.349	1	0.026	1.403	0.0032	0.000	1.952	0.0814
93	Os07t0408100-01	WD40 repeat_like domain containing protein.	1	1	1.103	1	0.125	2.276	0.0962	0.000	2.284	0.0883
94	Os02t0591800-01	Brix domain containing protein.	1	1	0.397	1	0.000	1.931	0.0129	0.000	1.931	0.0129
95	Os08t0467600-00	Hypothetical conserved gene.	2	1	0.630	1	0.000	0.919	0.6979	0.000	0.912	0.2607
96	Os02t0771200-01	Protein of unknown function DUF573 domain containing protein.	11	1	0.144	1	0.024	0.505	0.0259	0.000	0.327	0.9972
97	Os02t0728700-01	Ribosomal RNA_processint protein 7 domain containing protein.	4	1	0.115	1	0.026	0.458	0.0000	0.000	0.552	0.5965
98	Os08t0192900-01	Nucleotide_binding_ alpha_beta plait domain containing protein.	11	1	0.050	1	0.003	0.376	0.1053	0.000	0.314	1.0000
99	Os01t0109700-01	Similar to Paired amphipathic helix repeat_containing protein / transcription regulator_related.	1	1	0.938	1	0.167	1.610	0.0755	0.000	1.000	1.0000
100	Os03t0343700-01	Brix domain containing protein.	1	1	1.160	1	0.026	1.447	0.1005	0.000	1.000	1.0000
101	Os02t0301000-01	Zinc finger_ RING/FYVE/PHD_type domain containing protein.	3	1	0.260	1	0.010	0.949	0.0005	0.000	0.577	1.0000

102	Os08t0532400-01	Similar to AT.I.24_7 protein.	1	1	0.411	1	0.006	1.937	0.0137	0.000	1.000	1.0000
103	Os03t0726100-01	Similar to Tubulin alpha_1 chain (Alpha_1 tubulin).	1	1	0.157	1	0.004	1.811	0.0019	0.000	1.000	1.0000
104	Os03t0726100-02	Similar to Alpha_tubulin.	1	1	0.157	1	0.004	1.811	0.0019	0.000	1.000	1.0000
105	Os11t0247300-01	Alfa_tubulin.	1	1	0.157	1	0.004	1.811	0.0019	0.000	1.000	1.0000
106	Os05t0519500-02	WD40/YVTN repeat_like domain containing protein.	1	1	0.401	1	0.003	1.429	0.0058	0.000	1.000	1.0000
107	Os03t0110400-01	Similar to nuclear matrix protein_related.	1	1	0.743	1	0.000	1.000	1.0000	0.000	1.000	1.0000
108	Os06t0698859-01	Similar to C2H2 zinc_finger protein SERRATE (Fragment).	1	1	0.409	1	0.000	1.000	1.0000	0.000	1.000	1.0000
109	Os06t0275900-01	Forkhead_associated domain containing protein.	1	1	0.156	1	0.000	1.000	1.0000	0.000	1.000	1.0000
110	Os06t0275900-02	Similar to FHA domain protein.	1	1	0.156	1	0.000	1.000	1.0000	0.000	1.000	1.0000
111	Os02t0766700-01	Similar to Absciscic acid responsive elements_binding factor (ABA_responsive element binding protein 2) (AREB2).	1	1	0.618	1	0.000	1.000	1.0000	0.000	1.000	1.0000
112	Os06t0211200-01	Similar to Absciscic acid responsive elements_binding factor (ABA_responsive element binding protein 1) (AREB1).	1	1	0.618	1	0.000	1.000	1.0000	0.000	1.000	1.0000
113	Os09t0456200-01	Similar to BZIP transcription factor ABI5.	1	1	0.618	1	0.000	1.000	1.0000	0.000	1.000	1.0000
114	Os02t0565000-01	Homeodomain_like containing protein.	1	1	0.795	1	0.000	1.000	1.0000	0.000	1.000	1.0000
115	Os03t0708900-01	Zinc finger_RanBP2_type domain containing protein.	1	1	0.224	1	0.000	1.000	1.0000	0.000	1.000	1.0000

^aProtein ID is accordint to The Rice Annotation Project Database, ^bM.P.P. means number of matched phosphopeptide.

Supplemental Table 7. The probabilities of phosphorylation site assignment for nuclear phosphopeptides in rice embryos during early stage of germination

No.	Protein ID ^a	Description	M.P.P. ^b	Ratio_0	StdDev_0	PValue_0	Ratio_12	StdDev_12	PValue_12	Ratio_24	StdDev_24	PValue_24
1	Os06t0234100-01	Peptidase S1C_ HrtA/DegP2/Q/S family protein.	1	1	0.492919	1	36.11041	1.13269	0.197771	3.457322	1.935045	0.541873
		RTRPEPPSDATAAPHAPPSPPR+Phospho(19)	1	0.492919	1	36.11041	1.13269	0.197771	3.457322	1.935045	0.541873	0
2	Os08t0512400-02	Similar to AT_hook protein 1.	4	1	0.289151	1	28.40185	0.548853	0.005505	5.07571	0.284603	0.000426
		AVPTATMTPNSPPSR+Phospho(11)	3	0.510058	1	69.61356	0.912254	0.095355	7.945661	0.496959	0.046109	0
		AVPTATMTPNSPPSR+Phospho(14)	2	0.645682	1	16.27102	1.528893	0.205195	5.818563	0.439274	0.008022	0
		DLFTMPKSPAAAAAPPQSVR+Phospho(8)	1	1.054297	1	2.722583	0.861726	0.061028	0.188139	0.755025	0.11554	0
		SPPAAAAAPPQSVR+Phospho(1)	1	0.455562	1	0.019962	1.706173	0.01626	0.005116	0.857448	0.017012	0
3	Os01t0896700-00	Similar to 60S ribosomal protein L5.	4	1	0.229473	1	14.26698	0.508612	0.083096	12.86558	0.196937	8.81E-06
		LNALNSSATADDDEEEDDE+Phospho(6)	1	0.631609	1	4.089508	1.341531	0.330018	0.014986	1.552409	0.03222	0
		LNALNSSATADDDEEEDDE+Phospho(7)	1	0.631609	1	4.089508	1.341531	0.330018	0.014986	1.552409	0.03222	0
4	Os01t0896800-01	Ribosomal protein L18/L5 domain containing protein.	4	1	0.229473	1	14.26698	0.508612	0.083096	12.86558	0.196937	8.81E-06
		LNALNSSATADDDEEEDDE+Phospho(6)	1	0.631609	1	4.089508	1.341531	0.330018	0.014986	1.552409	0.03222	0
		LNALNSSATADDDEEEDDE+Phospho(7)	1	0.631609	1	4.089508	1.341531	0.330018	0.014986	1.552409	0.03222	0
5	Os04t0501600-01	AT hook_ DNA_binding_ conserved site domain containing protein.	6	1	0.223193	1	10.26439	0.461481	0.284596	0.469936	0.228932	1.57E-05
		ELSPETDDTDNKLPPETTNR+Phospho(3)	4	0.35113	1	27.06246	0.790591	0.222594	0.723455	0.315833	0.001829	0
		QQEDTPPEDETDDELSTK+Phospho(11)	1	0.52999	1	1.010305	1.191305	0.986819	0.157869	0.617782	0.027195	0
		QQEDTPPEDETDDELSTK+Phospho(16)	1	0.603739	1	1.048844	1.230099	0.940317	0.161453	0.600213	0.037693	0
		QQEDTPPEDETDDELSTK+Phospho(5)	2	0.678131	1	0.133541	1.496464	0.034006	0.000946	1.231154	0.031546	0
		QQEDTPPEDETDDELSTKDIVSPK+Phospho(11)	1	0.757519	1	2.67628	1.248213	0.337888	0.283854	0.816554	0.069964	0
		QQEDTPPEDETDDELSTKDIVSPK+Phospho(5)	1	0.757519	1	2.67628	1.248213	0.337888	0.283854	0.816554	0.069964	0
6	Os01t0125700-01	Conserved hypothetical protein.	1	1	2.114293	1	6.954111	2.05516	0.274331	0.041388	2.789197	0.256521
		ENANLIDADDSELR+Phospho(11)	1	2.114293	1	6.954111	2.05516	0.274331	0.041388	2.789197	0.256521	0
7	Os01t0962600-01	Similar to 40S ribosomal protein S10_1.	1	1	1.740245	1	6.837108	1.760834	0.237148	0.950299	1.080216	0.931224

		TTAPAEFQPSFR+Phospho(10)	1	1.740245	1	6.837108	1.760834	0.237148	0.950299	1.080216	0.931224	0
8	Os02t0549600-01	Similar to 40S ribosomal protein S10_1.	1	1	1.740245	1	6.837108	1.760834	0.237148	0.950299	1.080216	0.931224
		TTAPAEFQPSFR+Phospho(10)	1	1.740245	1	6.837108	1.760834	0.237148	0.950299	1.080216	0.931224	0
9	Os03t0403100-01	Similar to DNA_directed RNA polymerase subunit.	2	1	0.661022	1	4.808104	1.069062	0.33456	0.241077	0.340285	0.062236
		TEEEEAPAAKDPNASLPSPTYR+Phospho(20)	1	0.934826	1	4.808104	1.511881	0.31918	0.241077	0.481236	0.106594	0
		TEEEEAPAAKDPNASLPSPTYR+Phospho(21)	1	0.934826	1	4.808104	1.511881	0.31918	0.241077	0.481236	0.106594	0
10	Os11t0303500-01	Nucleotide_binding_ alpha_beta plait domain containing protein.	2	1	0.550892	1	3.19684	0.844354	0.520717	0.335376	0.391816	0.088131
		ATNTTSCASFSDVDEIPEK+Carbamidomethyl(7)Phospho(11)	3	0.679352	1	3.382344	1.003902	0.47558	0.332211	0.477005	0.131	0
		ATNTTSCASFSDVDEIPEK+Carbamidomethyl(7)Phospho(9)	1	0.941417	1	2.748355	1.560951	0.419011	0.34194	0.686988	0.133274	0
11	Os02t0161200-01	Zinc finger_ CCCH_type domain containing protein.	6	1	0.136386	1	2.994013	0.758803	1.19E-06	0.19075	0.466915	0.000274
		TANEETSSVNEDLNERSPNTAATK+Phospho(17)	2	0.190805	1	0.057058	1.320884	0.000272	0.00945	1.167899	0.000379	0
		TANEETSSVNEDLNERSPNTAATK+Phospho(20)	1	0.292306	1	0.114339	1.878204	0.004435	0.01561	1.501655	0.006384	0
		TANEETSSVNEDLNERSPNTAATK+Phospho(23)	1	0.292306	1	0.114339	1.878204	0.004435	0.01561	1.501655	0.006384	0
		TANEETSSVNEDLNERSPNTAATK+Phospho(7)Phospho(17)	1	0.963056	1	0.119869	2.208672	0.070055	0	0	1	0
		TANEETSSVNEDLNERSPNTAATK+Phospho(7)Phospho(20)	1	1.171098	1	27.0688	2.31446	0.436439	0.88345	1.016983	0.789201	0
		TANEETSSVNEDLNERSPNTAATK+Phospho(8)Phospho(17)	1	0.963056	1	0.119869	2.208672	0.070055	0	0	1	0
12	Os05t0596200-03	Similar to cDNA clone:001_104_D04_ full insert sequence.	2	1	0.805178	1	2.818894	0.939969	0.497342	0.022637	0.884824	0.070724
		RVDYSDDDDFIVK+Phospho(5)	2	0.929071	1	3.338694	1.132506	0.344575	0.013027	1.32842	0.076911	0
		VDYSDDDDDFIVK+Phospho(4)	1	1.613845	1	1.667936	1.685202	0.537191	0.0303	1.18627	0.172832	0
13	Os02t0744650-00	Similar to CSLA1_cellulose synthase_like family A; mannan synthase.	2	1	0.281196	1	2.301067	0.492918	0.327885	0.269123	0.255324	0.001456
		WEFVNANDCLLTRMQEMSMDYHFK+Carbamidomethyl(9)Phospho(18)Phospho(21)	2	0.397671	1	2.301067	0.697092	0.314598	0.269123	0.361083	0.012179	0
		)Oxidation(17)										
		WEFVNANDCLLTRMQEMSMDYHFK+Carbamidomethyl(9)Phospho(18)Phospho(21)	2	0.397671	1	2.301067	0.697092	0.314598	0.269123	0.361083	0.012179	0
		)Oxidation(19)										
14	Os03t0733400-01	Zinc finger_ BED_type predicted domain containing protein.	1	1	0.185177	1	1.712272	0.743561	0.622031	0.197736	0.187141	0.000533
		LALTPAVTTDNDTETTVVERPSK+Phospho(9)	2	0.185177	1	1.712272	0.743561	0.622031	0.197736	0.187141	0.000533	0

15	Os07t0557500-01	WRC domain containing protein.	5	1	0.106109	1	1.700232	0.509798	0.001681	0.600387	0.143333	9.99E-08
		ATDRTDSPPLPDHLR+Phospho(7)	1	0.119516	1	0.392933	0.98669	0.098267	0.046302	0.175649	0.001208	0
		TDSPPLPDHLR+Phospho(3)	1	0.31144	1	0.128208	1.110048	0.001972	0.005019	0.543214	0.008058	0
		ISPTSSEPAASLPSPVTTK+Phospho(14)	1	1.938805	1	0.401178	1.878821	0.401845	0.100246	1.294921	0.249084	0
		ISPTSSEPAASLPSPVTTK+Phospho(2)Phospho(18)	1	0.466688	1	0.302017	1.135819	0.029089	0.004543	0.677314	0.017821	0
		NVNASPASPPAATSDVTR+Phospho(8)	3	0.523982	1	5.982289	1.025669	0.333186	2.736856	0.314692	0.000101	0
16	Os01t0924900-01	GTP_binding signal recognition particle SRP54_G_domain containing protein.	7	1	0.056828	1	0.594343	0.27004	9.69E-08	0.112638	0.056517	6.18E-12
		TVSKPSQDTEEDDEPEVELESK+Phospho(3)	1	0.301099	1	0.790458	1.046596	0.662285	0.154277	0.298661	0.009166	0
		TVSKPSQDTEEDDEPEVELESK+Phospho(6)	4	0.13769	1	0.696215	0.529081	0.683928	0.129379	0.14018	4.54E-06	0
		TVSKPSQDTEEDDEPEVELESK+Phospho(9)	3	0.161335	1	0.703909	0.610986	0.659881	0.131457	0.161014	5.71E-05	0
		HIIEEVINMSDDEETEDNAEDDKDK+Phospho(11)	4	0.322995	1	0.008501	0.927176	0.000673	9.38E-06	2.044975	0.543226	0
		HIIEEVINMSDDEETEDNAEDDKDK+Phospho(9)	1	0.625849	1	0.008155	1.926344	0.031423	0.000127	2.044975	0.031132	0
17	Os03t0249900-01	Conserved hypothetical protein.	7	1	0.115812	1	0.358115	0.377573	2.43E-05	0.044198	0.216525	7.41E-07
		ASSDTDDDDDFIVSK+Phospho(2)	1	0.872542	1	0.846254	1.347583	0.782454	0.006801	0.551419	0.058709	0
		ASSDTDDDDDFIVSK+Phospho(3)	1	0.872542	1	0.846254	1.347583	0.782454	0.006801	0.551419	0.058709	0
		ASSDTDDDDDFIVSK+Phospho(5)	1	0.872542	1	0.846254	1.347583	0.782454	0.006801	0.551419	0.058709	0
		DEDDSTDDDDYHVPLSR+Phospho(5)	3	0.233379	1	0.010553	0.779501	0.000493	0.00018	1.97675	0.246887	0
		KDEDDSTDDDDYHVPLSR+Phospho(6)	2	0.159128	1	0.028341	0.791111	0.000102	0.000162	1.304352	0.000211	0
18	Os01t0191100-01	Similar to Acidic ribosomal protein P2a_4 (Fragment).	4	1	0.122044	1	0.198767	0.431906	0.000275	0.017029	0.219956	1.99E-06
		EESDDDMTFSLFD+Phospho(3)	1	0.598724	1	0.122693	1.181066	0.025803	0.001166	0.935146	0.028661	0
		EESDDDMTFSLFD+Phospho(3)Oxidation(7)	1	3.421376	1	0	0	1	0	0	1	0
		VEEKEESDDMTFSLFD+Phospho(7)	4	0.172269	1	0.248292	0.552892	5.55E-05	0.015277	0.247967	2.61E-05	0
		VEEKEESDDMTFSLFD+Phospho(7)Oxidation(11)	1	0.180876	1	0.443832	1.638431	0.295141	0.045165	0.664823	0.001585	0
19	Os02t0529700-01	Similar to Acidic ribosomal protein P2a_4 (Fragment).	4	1	0.122044	1	0.198767	0.431906	0.000275	0.017029	0.219956	1.99E-06
		EESDDDMTFSLFD+Phospho(3)	1	0.598724	1	0.122693	1.181066	0.025803	0.001166	0.935146	0.028661	0
		EESDDDMTFSLFD+Phospho(3)Oxidation(7)	1	3.421376	1	0	0	1	0	0	1	0

20	Os05t0445500-01	VEEKEESDDDMTFSLFD+Phospho(7)	4	0.172269	1	0.248292	0.552892	5.55E-05	0.015277	0.247967	2.61E-05	0
		VEEKEESDDDMTFSLFD+Phospho(7)Oxidation(11)	1	0.180876	1	0.443832	1.638431	0.295141	0.045165	0.664823	0.001585	0
		Similar to Acidic ribosomal protein (Fragment).	6	1	0.115693	1	0.170423	0.382338	1.16E-05	0.028809	0.201281	1.08E-07
		EESDDDMTFSLFD+Phospho(3)	1	0.598724	1	0.122693	1.181066	0.025803	0.001166	0.935146	0.028661	0
		EESDDDMTFSLFD+Phospho(3)Oxidation(7)	1	3.421376	1	0	0	1	0	0	1	0
		VEEKEESDDDMTFSLFD+Phospho(7)	4	0.172269	1	0.248292	0.552892	5.55E-05	0.015277	0.247967	2.61E-05	0
21	Os01t0582400-01	VEEKEESDDDMTFSLFD+Phospho(7)Oxidation(11)	1	0.180876	1	0.443832	1.638431	0.295141	0.045165	0.664823	0.001585	0
		Similar to Multidomain cyclophilin type peptidyl_prolyl cis_trans isomerase.	3	1	0.120695	1	0.098031	0.423189	5.59E-11	0.003745	0.31795	1.63E-08
		ELEHDSSETDDYPDENEEFDNR+Phospho(6)	3	0.199245	1	0.114166	0.662447	5.68E-06	0.001402	0.560303	0.000108	0
		ELEHDSSETDDYPDENEEFDNR+Phospho(8)	3	0.199245	1	0.114166	0.662447	5.68E-06	0.001402	0.560303	0.000108	0
22	Os04t0446500-01	Similar to OSIGBa0140O07.15 protein.	4	1	0.072403	1	0.070987	0.354175	9.9E-20	0.014075	0.1079	7.77E-16
		TPPAESLESEDEDTFPVSFSESK+Phospho(1)	4	0.132358	1	0.057272	0.676799	2.23E-08	0.011433	0.198503	2.85E-06	0
		TPPAESLESEDEDTFPVSFSESK+Phospho(6)	4	0.132358	1	0.057272	0.676799	2.23E-08	0.011433	0.198503	2.85E-06	0
		TPPAESLESEDEDTFPVSFSESK+Phospho(9)	5	0.116168	1	0.063712	0.614835	3.33E-10	0.011994	0.174843	1.84E-07	0
23	Os01t0104800-01	Sas10/Utp3 family protein.	3	1	0.065237	1	0.054625	0.409828	7.73E-13	0.001174	0.3364	2.4E-09
		LSMQDFTLEDTESDEEDR+Phospho(13)	4	0.220518	1	0.037639	0.929485	1.66E-05	0.000675	0.645333	0.001322	0
		NAYYDATEQSTDEDDYEEAR+Phospho(10)	4	0.169418	1	0.023952	0.601225	8.29E-06	0.000213	0.90433	0.000387	0
		NAYYDATEQSTDEDDYEEARR+Phospho(10)	2	0.074625	1	0.106116	0.701886	9.01E-06	0.001629	0.437995	1.31E-05	0
24	Os05t0597100-01	Similar to Nucleolar histone deacetylase HD2_p39.	7	1	0.182433	1	0.050705	0.317211	2.88E-07	0.015257	0.205489	8.44E-08
		VSQPAEEDEMDFDSEEEVEEEEEK+Phospho(14)	9	0.305847	1	0.07767	0.502737	0.001076	0.004745	0.32046	0.000267	0
		VSQPAEEDEMDFDSEEEVEEEEEK+Phospho(14)Oxidation(10)	5	0.52605	1	0.061986	0.683897	0.02169	0.034459	0.429897	0.018564	0
		VSQPAEEDEMDFDSEEEVEEEEEKIIPAPR+Phospho(14)	2	0.374071	1	0.017061	0.978306	0.004633	0.001173	0.578524	0.004537	0
25	Os03t0350100-01	SAR DNA_binding protein_2.	7	1	0.08287	1	0.031329	0.370994	9.1E-15	0.123938	0.176693	2.49E-14
		TYNPAADLVLTQSTEETPKKPETASK+Phospho(13)	1	0.347028	1	0.002628	1.269109	0.009923	0.008789	1.129597	0.009929	0
		TYNPAADLVLTQSTEETPKKPETASK+Phospho(14)	1	0.347028	1	0.002628	1.269109	0.009923	0.008789	1.129597	0.009929	0
		TYNPAADLVLTQSTEETPKKPETASK+Phospho(17)	2	0.307016	1	0.007307	0.926114	0.003111	0.017054	0.635384	0.003163	0

26	Os02t0728700-01	Ribosomal RNA_processing protein 7 domain containing protein.	4	1	0.11453	1	0.025599	0.458442	6.28E-08	2.2E-05	0.55174	0.59651
		SSQTDSDDMLELLTSK+Phospho(1)	1	0.250589	1	0.028539	1.019552	0.004174	0	0	1	0
		SSQTDSDDMLELLTSK+Phospho(2)	1	0.250589	1	0.028539	1.019552	0.004174	0	0	1	0
		SSQTDSDDMLELLTSK+Phospho(4)	1	0.250589	1	0.028539	1.019552	0.004174	0	0	1	0
		SSQTDSDDMLELLTSK+Phospho(6)	2	0.187442	1	0.021066	0.730877	0.00031	0.000253	1.873262	0.039676	0
27	Os02t0771200-01	Protein of unknown function DUF573 domain containing protein.	11	1	0.143548	1	0.023754	0.504949	0.025929	3.8E-05	0.327298	0.997177
		TAESDSSTEEEEEEEEEDLVR+Phospho(12)	1	1.133463	1	0.036321	1.776717	0.097664	0	0	1	0
		TAESDSSTEEEEEEEEEDLVR+Phospho(4)	2	1.360431	1	0.004091	1.330101	0.188091	0	0	1	0
		TAESDSSTEEEEEEEEEDLVR+Phospho(4)Phospho(12)	2	1.351054	1	0.090652	1.562207	0.221474	0	0	1	0
		TAESDSSTEEEEEEEEEDLVR+Phospho(4)Phospho(6)	3	0.260977	1	8.52E-05	1.993328	0.266478	0	0	1	0
		TAESDSSTEEEEEEEEEDLVR+Phospho(4)Phospho(7)	3	0.260977	1	8.52E-05	1.993328	0.266478	0	0	1	0
		TAESDSSTEEEEEEEEEDLVR+Phospho(6)	2	1.360431	1	0.004091	1.330101	0.188091	0	0	1	0
		TAESDSSTEEEEEEEEEDLVR+Phospho(6)Phospho(12)	2	1.351054	1	0.090652	1.562207	0.221474	0	0	1	0
		TAESDSSTEEEEEEEEEDLVR+Phospho(6)Phospho(7)	3	0.260977	1	8.52E-05	1.993328	0.266478	0	0	1	0
		TAESDSSTEEEEEEEEEDLVR+Phospho(7)	2	1.360431	1	0.004091	1.330101	0.188091	0	0	1	0
		RPTPPPPPPVASSEETASTSDSESEEEEEESPLAQAPVVSNK+Phospho(19)	1	1.423021	1	0.001092	2.443561	0.135562	0.00106	2.443561	0.135555	0
		RPTPPPPPPVASSEETASTSDSESEEEEEESPLAQAPVVSNK+Phospho(26)	1	1.423021	1	0.001092	2.443561	0.135562	0.00106	2.443561	0.135555	0
28	Os02t0288200-01	Protein of unknown function DUF573 domain containing protein.	13	1	0.171018	1	0.013552	0.401673	1.19E-05	0.0288	0.245968	2.6E-05
		TAASSDEEEEEEDSDTDYAQTFQLR+Phospho(15)	1	1.131334	1	0.000396	2.297718	0.092217	0.000286	2.297718	0.092199	0
		TAASSDEEEEEEDSDTDYAQTFQLR+Phospho(17)	2	0.802014	1	0.001186	1.229433	0.049481	4.55E-05	2.297718	0.311984	0
		TAASSDEEEEEEDSDTDYAQTFQLR+Phospho(19)	2	0.802014	1	0.001186	1.229433	0.049481	4.55E-05	2.297718	0.311984	0
		TAASSDEEEEEEDSDTDYAQTFQLR+Phospho(20)	1	1.137125	1	0.001502	1.455278	0.093213	0	0	1	0
		VTTTDEETEEVETDSSESEPEPEPVKK+Phospho(15)	2	0.578023	1	0.015773	1.513757	0.018792	0.000549	0.746063	0.018362	0
		VTTTDEETEEVETDSSESEPEPEPVKK+Phospho(15)Phospho(18)	1	0.782367	1	0.052204	2.106933	0.046258	0.000196	1.300537	0.047427	0
		VTTTDEETEEVETDSSESEPEPEPVKK+Phospho(16)	1	0.818713	1	0.005978	2.141407	0.052064	8.9E-05	2.141407	0.051583	0
		VTTTDEETEEVETDSSESEPEPEPVKK+Phospho(18)	2	0.578023	1	0.015773	1.513757	0.018792	0.000549	0.746063	0.018362	0

		YNLAPEPSPSSK+Phospho(10)	1	0.757357	1	0.0611	1.828658	0.043929	0.051083	0.568878	0.049114	0
		YNLAPEPSPSSK+Phospho(11)	1	0.757357	1	0.0611	1.828658	0.043929	0.051083	0.568878	0.049114	0
		YNLAPEPSPSSK+Phospho(8)	1	0.757357	1	0.0611	1.828658	0.043929	0.051083	0.568878	0.049114	0
29	Os08t0192900-01	Nucleotide_binding_alpha_beta plait domain containing protein.	11	1	0.050329	1	0.003076	0.375817	0.105307	5.64E-06	0.314173	1
		TKPASSDSESDDDEMEDEKPAAPVK+Phospho(10)	1	0.588043	1	0.027208	2.026072	0.026617	0	0	1	0
		TKPASSDSESDDDEMEDEKPAAPVK+Phospho(10)Phospho(12)	1	0.13766	1	0	0	1	0	0	1	0
		TKPASSDSESDDDEMEDEKPAAPVK+Phospho(12)	1	0.588043	1	0.027208	2.026072	0.026617	0	0	1	0
		TKPASSDSESDDDEMEDEKPAAPVK+Phospho(6)Phospho(10)	1	0.13766	1	0	0	1	0	0	1	0
		TKPASSDSESDDDEMEDEKPAAPVK+Phospho(6)Phospho(12)	1	0.13766	1	0	0	1	0	0	1	0
		TKPASSDSESDDDEMEDEKPAAPVK+Phospho(6)Phospho(8)	1	0.13766	1	0	0	1	0	0	1	0
		TKPASSDSESDDDEMEDEKPAAPVK+Phospho(8)	1	0.588043	1	0.027208	2.026072	0.026617	0	0	1	0
		TKPASSDSESDDDEMEDEKPAAPVK+Phospho(8)Phospho(10)	2	0.107427	1	0	0	1	0	0	1	0
		TKPASSDSESDDDEMEDEKPAAPVK+Phospho(8)Phospho(10)Phospho(12)	1	2.057063	1	0.00101	2.760582	0.234537	0.000436	2.760582	0.234355	0
		TKPASSDSESDDDEMEDEKPAAPVK+Phospho(8)Phospho(12)	2	0.107427	1	0	0	1	0	0	1	0

^aProtein ID is according to The Rice Annotation Project Database, ^bM.P.P. means number of matched phosphopeptide.

Supplemental Table 8.Comparison of the proteome data in this study with transcriptome data in Narsai et al. (2009) in rice embryo.

No.	Protein ID ^d	Mass(Da)	M.P. ^b	Mol (%) ^c	Description	WoLFPSORT ^d	NucPred ^e	Function ^f
1	Os01t0147900-01	27274	89	1.95	Triosephosphate isomerase, cytosolic (EC 5.3.1.1)	cyto	0.03	PS
2	Os01t0905800-01	39141	236	1.36	Aldolase C-1.	cyto	0.05	PS
3	Os05t0140800-01	39249	114	1.28	Similar to Dormancy related protein (Fragment).	mito	0.3	misc
4	Os07t0638300-01	24198	99	1.26	Similar to 1-Cys peroxiredoxin.	cyto /nucl	0.03	redox
5	Os02t0268100-01	57229	222	1.25	Similar to Glutelin (Fragment).	vacu	0.39	development
6	Os04t0508300-01	11938	23	1.25	Glutaredoxin.	chlo	0.03	redox
7	Os02t0121300-01	18634	80	1.22	Cyclophilin 2.	cyto	0.01	cell
8	Os05t0445500-01	14419	23	1.2	Similar to Acidic ribosomal protein (Fragment).	chlo	0	protein
9	Os01t0762500-00	56782	308	1.1	Glutelin subunit mRNA.	chlo	0.44	development
10	Os10t0400200-01	56841	282	1.06	Glutelin type II precursor.	vacu	0.4	development
11	Os01t0675100-01	17337	21	1	Similar to peroxiredoxin.	cyto	0.01	redox
12	Os01t0276300-01	24470	21	0.96	Similar to Group 3 late embryogenesis abundant protein (Fragment).	mito	0.44	not assitned
13	Os03t0159600-01	27174	30	0.94	Similar to Rab28 protein.	cyto	0.02	not assitned
14	Os10t0563700-01	16769	23	0.91	Similar to Nucleoside diphosphate kinase I (EC 2.7.4.6)	cyto	0.02	nucleotide metabolism
15	Os06t0668200-01	42310	86	0.91	Similar to Phosphoglycerate kinase, cytosolic (EC 2.7.2.3).	chlo	0.01	PS
16	Os07t0214300-01	18423	25	0.89	Seed allergenic protein RAG2 precursor.	mito	0.04	stress
17	Os07t0219400-01	17062	23	0.88	Prolamin precursor.	chlo	0.24	not assitned
18	Os06t0625500-01	23788	32	0.87	Similar to Thioredoxin peroxidase.	chlo	0.05	redox
19	Os03t0327600-01	39254	85	0.85	Ricin B-related lectin domain containing protein.	cyto/nucl	0.01	not assitned
20	Os03t0793700-01	52436	408	0.83	RmlC-like jelly roll fold domain containing protein.	mito	0.38	development
21	Os08t0126300-01	36561	185	0.79	Similar to Glyceraldehyde-3-phosphate dehydrogenase (Fragment).	cyto	0.01	tlycolysis
22	Os02t0601300-01	36716	241	0.79	Similar to Glyceraldehyde-3-phosphate dehydrogenase, cytosolic 3 (EC 1.2.1.12).	cyto	0	tlycolysis
24	Os01t0191100-01	11714	9	0.76	Similar to Acidic ribosomal protein P2a-4 (Fragment).	chlo	0.01	protein
23	Os10t0167300-01	48226	85	0.76	Similar to Enolase 2 (EC 4.2.1.11)	chlo	0.04	tlycolysis
25	Os02t0249800-01	56915	253	0.75	Glutelin precursor.	chlo/nucl	0.41	development
26	Os10t0542100-01	9457	5	0.75	Plant EC metallothionein-like protein, family 15 protein.	cyto	0.38	not assitned
27	Os03t0266300-01	17899	65	0.74	Class I low-molecular-weight heat shock protein 17.9.	cyto	0.03	stress
28	Os02t0169300-01	42196	48	0.74	Similar to Phosphoglycerate kinase, cytosolic (EC 2.7.2.3).	chlo	0.02	PS
29	Os09t0109600-01	7843	9	0.74	Conserved hypothetical protein.	chlo	0.09	not assitned
30	Os02t0699600-01	17820	13	0.72	Similar to 60S ribosomal protein L12.	cyto	0.03	protein
31	Os01t0705200-01	22119	22	0.72	Late embryogenesis abundant protein repeat containing protein.	nucl	0.22	not assitned
32	Os03t0424500-01	16434	26	0.72	Similar to 40S ribosomal protein S19-3.	cyto/nucl	0.18	protein
33	Os01t0686800-01	36665	46	0.7	Protein containing the WD-40 repeat, Innate immunity	cyto/nucl	0.01	development
34	Os03t0277300-01	71932	88	0.7	Heat shock protein 70.	cyto	0.28	stress
35	Os03t0427300-01	56550	118	0.7	Glutelin type-A III precursor.	chlo	0.37	development
36	Os02t0249600-01	56411	240	0.7	Similar to Glutelin.	chlo/nucl	0.43	development
37	Os12t0569200-01	17071	40	0.7	Conserved hypothetical protein.	extr	0.02	not assitned
38	Os05t0329100-01	16916	31	0.68	Prolamin.	chlo	0.26	not assitned
39	Os08t0191700-01	32875	50	0.68	Similar to Lactoylglutathione lyase (EC 4.4.1.5)	cyto	0.09	amino acid metabolism
40	Os01t0159600-01	10130	17	0.67	Small hydrophilic plant seed protein family protein.	nucl	0.36	not assitned
41	Os11t0199200-01	57047	65	0.66	Similar to Protein disulfide isomerase (Fragment).	E.R.	0	redox
42	Os10t0505900-01	45554	43	0.65	Conserved hypothetical protein.	nucl	0.12	not assitned
43	Os01t0124401-01	29253	103	0.65	Similar to Bowman-Birk type bran trypsin inhibitor.	extr	0.2	not assitned
44	Os05t0116100-01	23726	35	0.65	Dehydroascorbate reductase.	chlo	0.3	redox
45	Os03t0336100-01	36974	149	0.64	11-S plant seed storage protein family protein.	chlo	0.3	development
46	Os03t0277500-01	17773	16	0.63	Similar to Glyoxalase family protein, expressed.	nucl	0.13	Biodetradation of Xenobiotics
47	Os02t0814700-01	16392	17	0.63	Similar to Ribosomal Pr 117 (Fragment).	cyto	0.1	protein
48	Os05t0490100-01	12581	7	0.63	Similar to 60S ribosomal protein L30.	nucl	0.04	protein
50	Os03t0577000-01	25590	30	0.62	Similar to Ribosomal protein S3 (Fragment).	cyto	0.21	protein
49	Os05t0553000-02	59012	71	0.62	ATP synthase beta chain, mitochondrial precursor (EC 3.6.3.14).	mito	0.06	mitochondrial electron transport
51	Os05t0468800-01	18234	19	0.61	Phosphatidylethanolamine-binding protein PEBP domain containing protein.	cyto	0.02	not assitned
52	Os11t0210300-01	41699	133	0.6	Alcohol dehydrogenase 1.	cyto	0	misc
53	Os06t0341300-01	27905	30	0.59	Seed maturation protein domain containing protein.	cyto	0.12	development
54	Os10t0478200-01	35888	29	0.59	Cytoplasmic malate dehydrogenase.	cyto	0.08	TCA
55	Os02t0549600-01	20307	36	0.59	Similar to 40S ribosomal protein S10-1.	nucl	0.19	protein
56	Os01t0749000-01	28266	18	0.58	Protein of unknown function DUF1264 family protein.	cyto	0.1	not assitned
57	Os05t0542500-02	20502	28	0.58	LEA-like protein.	nucl	0.2	not assitned
58	Os08t0129200-02	19024	20	0.57	Similar to Cold shock protein-1.	mito /nucl	0.08	stress
59	Os03t0248600-01	48285	71	0.56	Similar to Enolase 2 (EC 4.2.1.11)	chlo	0.04	tlycolysis
60	Os02t0250600-01	47344	46	0.55	Late embryogenesis abundant protein repeat containing protein.	nucl	0.23	not assitned
61	Os01t0835900-00	11402	17	0.55	Similar to Histone H4.	nucl	0.32	DNA
62	Os03t0712700-01	63138	41	0.54	Similar to Phosphoglucomutase, cytoplasmic 2 (EC 5.4.2.2)	cyto	0.03	not assitned
63	Os03t0200500-01	29880	28	0.53	40S ribosomal protein S3a (CYC07 protein).	cyto/nucl	0.4	protein
64	Os02t0162500-01	16410	11	0.53	Similar to 40S ribosomal protein S14.	cyto/nucl	0.3	protein
65	Os04t0486600-01	36921	170	0.53	Similar to Glyceraldehyde-3-phosphate dehydrogenase, cytosolic 3 (EC 1.2.1.12).	cyto	0.01	tlycolysis
66	Os11t0115400-00	11766	26	0.52	Lipid transfer protein LPT IV.	extr	0.05	not assitned
67	Os01t0136100-01	16929	61	0.52	16.9 kDa class I heat shock protein 1.	cyto	0.07	stress
68	Os01t0136200-01	16947	59	0.52	16.9 kDa class I heat shock protein 1.	cyto	0.07	stress
69	Os07t0150200-01	15132	8	0.51	Similar to 40S ribosomal protein S12-1.	cyto	0.01	protein
70	Os07t0229900-01	15112	10	0.51	Ribosomal protein S12e domain containing protein.	chlo	0.02	protein
71	Os09t0553200-01	51821	38	0.51	Similar to UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9)	cyto	0	not assitned
72	Os04t0546500-01	15190	18	0.51	Similar to Oleosin.	nucl	0.01	lipid metabolism
73	Os05t0574400-01	35642	40	0.48	Similar to Malate dehydrogenase.	mito	0.12	TCA
74	Os08t0104400-01	10597	4	0.47	Conserved hypothetical protein.	chlo	0.07	not assitned
75	Os05t0499100-01	21497	30	0.47	26 kDa globulin (Alpha-globulin).	extr	0.45	not assitned

76	Os01t0728700-01	27724	27	0.45	Protein of unknown function DUF1264 family protein.	chlo	0.07	not assitned
77	Os01t0840100-01	71306	65	0.45	Heat shock protein Hsp70 family protein.	cyto	0.19	stress
78	Os03t0360700-01	15005	8	0.44	Similar to Protein-methionine-S-oxide reductase, PilB family.	chlo	0	RNA
79	Os01t0348900-01	15163	6	0.44	SalT gene product (Salt-induced protein).	cyto	0.01	misc
80	Os03t0177400-01	49604	62	0.44	EF-1 alpha.	cyto	0.06	protein
81	Os05t0323900-01	24982	13	0.43	Manganese-superoxide dismutase precursor (EC 1.15.1.1).	mito	0.03	redox
82	Os03t0663800-01	28776	105	0.43	Globulin 1 (Fragment).	vacu	0.63	development
83	Os12t0626500-00	21879	27	0.41	Similar to late embryogenesis abundant protein D-34.	cyto	0.08	not assitned
84	Os03t0343500-01	14520	7	0.4	Similar to 60S ribosomal protein L22-2.	cyto	0.06	protein
85	Os01t0328400-01	17885	26	0.4	Ubiquitin.	nucl	0.51	protein
86	Os07t0215500-01	17838	12	0.4	Allergenic protein.	extr	0.03	stress
88	Os01t0231700-01	11926	11	0.4	Similar to 60S acidic ribosomal protein P2-B (CaRP2B).	nucl	0.01	protein
87	Os12t0569300-01	23985	31	0.4	Thaumatococcus, pathogenesis-related family protein.	chlo	0.02	not assitned
89	Os02t0591700-01	24243	16	0.4	Similar to Canavalia glauca strain CBS130 chromosome L complete sequence.	nucl	0.04	protein
90	Os02t0115900-01	73573	54	0.39	Endosperm luminal binding protein.	E.R.	0.09	stress
91	Os02t0453600-01	28808	39	0.39	Similar to Glutelin.	chlo	0.48	development
92	Os03t0245800-02	26705	20	0.39	Similar to Heat shock protein 26.	chlo	0.2	stress
93	Os03t0305600-01	18416	10	0.39	Mitochondrial import inner membrane translocase, subunit Tim17/22 family protein.	chlo	0.21	protein
94	Os08t0559200-01	12061	12	0.39	Similar to Ribosomal protein S25 (40S ribosomal 25S subunit).	nucl	0.52	protein
95	Os01t0649100-01	35667	26	0.38	Malate dehydrogenase.	mito	0.18	TCA
96	Os01t0210500-01	23753	17	0.37	Similar to SOUL-like protein.	chlo	0.03	tetrapyrrole synthesis
97	Os07t0216700-01	17036	13	0.37	Bifunctional trypsin/alpha-amylase inhibitor domain containing protein.	chlo	0.02	not assitned
98	Os01t0276000-01	12584	10	0.37	Similar to 60S ribosomal protein L30.	cyto	0.08	protein
99	Os12t0464400-01	39255	32	0.36	Similar to Oxidoreductase, short chain dehydrogenase/reductase family protein, expressed.	chlo	0.1	misc
100	Os02t0249000-01	55226	43	0.35	Glutelin, Seed strage protein	E.R.	0.37	development
101	Os08t0116500-01	11133	9	0.35	Similar to 60S acidic ribosomal protein P1 (L12).	chlo /nucl	0	protein
102	Os11t0453900-01	15543	7	0.35	Dehydrin RAB 16D.	nucl	0.34	not assitned
104	Os07t0213800-01	17829	8	0.35	Similar to Allergenic protein.	chlo	0.03	stress
103	Os08t0117200-00	17874	10	0.35	Similar to 40S ribosomal protein S13 (Fragment).	nucl	0.41	protein
105	Os01t0124200-02	29198	30	0.34	Similar to Bowman Birk trypsin inhibitor.	extr	0.21	not assitned
106	Os04t0173800-01	24718	23	0.34	Lectin precursor (Agglutinin).	chlo	0.22	stress
107	Os03t0723400-01	18044	6	0.34	Similar to UFG2.	chlo	0.38	not assitned
108	Os03t0821100-01	71666	62	0.33	Similar to Non-cell-autonomous heat shock cognate protein 70.	cyto	0.25	stress
109	Os03t0820500-01	16280	6	0.33	Similar to WCOR719.	chlo	0.01	cell
110	Os07t0180900-01	44825	37	0.32	Similar to 60S ribosomal protein L4.	cyto /nucl	0.41	protein
111	Os07t0516200-01	18863	6	0.32	Similar to Endoribonuclease, L-PSP family.	chlo	0.01	RNA
112	Os03t0197300-01	71138	142	0.32	Similar to Cupin family protein, expressed.	chlo/nucl	0.75	development
113	Os04t0510900-01	35414	43	0.32	Similar to Embryo-specific protein 1 (ATS1).	chlo	0.05	development
114	Os02t0804100-01	6927	3	0.31	Similar to predicted protein.	nucl	0.38	not assitned
116	Os01t0938900-01	22079	13	0.31	Similar to Inascent polypeptide-associated complex alpha subunit-like protein 2	nucl	0.31	protein
115	Os06t0152100-01	14352	8	0.31	Similar to Profilin-2.	cyto	0.01	cell
117	Os02t0478700-01	9864	5	0.31	Ribosomal protein S27.	nucl	0.27	not assitned
118	Os03t0659300-01	15165	7	0.31	Glyoxalase/bleomycin resistance protein/dioxygenase domain containing protein.	cyto	0.03	Biotradation of Xenobiotics
119	Os03t0699000-01	17211	4	0.3	Oleosin 18 kDa (OSE721).	plas	0.2	not assitned
120	Os03t0807800-01	30185	30	0.3	Similar to 40S ribosomal protein S2 (Fragment).	cyto	0.04	protein
121	Os01t0916600-01	15537	5	0.3	RNA recognition motif, glycine rich protein domain containing protein.	mito	0.01	RNA
122	Os03t0168100-01	41835	37	0.28	Late embryogenesis abundant protein repeat containing protein.	extr	0.23	development
123	Os01t0760600-01	50074	22	0.28	Aspartate aminotransferase, cytoplasmic (EC 2.6.1.1)	chlo	0.16	amino acid metabolism
124	Os08t0130500-01	34470	20	0.28	60S acidic ribosomal protein P0.	cyto	0.07	protein
125	Os03t0780600-01	50417	42	0.28	Tubulin beta-1 chain (Beta-1 tubulin).	chlo	0.16	cell
126	Os01t0866600-01	7831	3	0.26	Similar to bolA-like protein.	cyto	0.05	RNA
127	Os12t0632000-01	16130	7	0.26	Similar to Glycine-rich RNA-binding protein 1 (Fragment).	nucl	0.17	RNA
128	Os06t0221300-01	18450	4	0.26	Similar to Dehydration stress-induced protein.	extr	0.02	not assitned
129	Os07t0246200-01	48450	19	0.25	Similar to Calreticulin (Fragment).	vacu	0.08	signalint
130	Os10t0411700-01	8184	4	0.25	Similar to S28 ribosomal protein (Fragment).	cyto	0.1	protein
131	Os07t0219250-00	16984	16	0.25	Similar to cDNA, clone: J090058L24, full insert sequence.	nucl	0.22	not assitned
132	Os03t0750000-01	8481	2	0.24	Similar to ethylene-responsive protein.	cyto	0.02	not assitned
133	Os09t0568900-01	8449	4	0.24	Similar to predicted protein.	nucl	0.04	not assitned
134	Os04t0445100-01	23271	14	0.24	Similar to 22.7 kDa class IV heat shock protein precursor.	extr	0.12	stress
135	Os03t0341100-01	21118	3	0.24	Similar to 60S ribosomal protein L18.	nucl	0.27	protein
136	Os01t0654400-01	8528	10	0.24	Similar to Salt tolerant correlative protein.	mito	0.15	not assitned
137	Os02t0478600-01	14866	10	0.24	Similar to 40S ribosomal protein S15A.	cyto/nucl	0.09	protein
138	Os01t0205500-01	20978	8	0.23	Similar to 60S ribosomal protein L11-2 (L16). Splice isoform 2.	cyto	0.28	protein
140	Os02t0530600-01	93542	30	0.23	Poly(ADP-ribose) polymerase, regulatory region domain containing protein.	cyto/nucl	0.21	protein
139	Os03t0819600-01	23992	5	0.23	Chalcone isomerase (EC 5.5.1.6).	cyto	0.54	not assitned
141	Os03t0758800-01	17762	15	0.23	Similar to Eukaryotic translation initiation factor 5A-2	cysk	0.01	protein
142	Os08t0327700-01	15154	5	0.23	Late embryogenesis abundant (LEA) group 1 family protein.	nucl	0.2	development
143	Os01t0303300-01	17908	6	0.23	Similar to Stress-inducible membrane pore protein.	mito	0.3	protein
144	Os02t0519900-01	94987	48	0.23	Similar to Elongation factor EF-2 (Fragment).	cyto/nucl	0.16	protein
145	Os01t0184100-01	18133	21	0.23	Similar to 17.5 kDa class II heat shock protein.	cyto/nucl	0.05	stress
146	Os03t0182600-03	12620	10	0.22	Similar to 40S ribosomal protein SA.	cyto	0.2	protein
147	Os05t0519700-01	101062	30	0.22	Heat shock protein 101.	cyto	0.42	stress
148	Os03t0130300-01	9207	7	0.22	Similar to Cp-thionin.	extr	0.07	not assitned
149	Os03t0154700-01	22716	16	0.21	Similar to 40S ribosomal protein S9.	nucl	0.37	protein
150	Os05t0569500-01	29290	20	0.21	Similar to Embryo-specific protein.	cyto	0.11	not assitned
151	Os11t0247300-01	50390	19	0.2	Alfa-tubulin.	cyto /nucl	0.13	cell
152	Os02t0242600-01	57190	66	0.2	Similar to Glutelin.	vacu	0.39	development
153	Os06t0701100-02	47343	15	0.2	Eukaryotic initiation factor 4A (eIF4A) (eIF-4A).	cyto	0.37	DNA
154	Os03t0756000-01	23829	4	0.2	Similar to 60S ribosomal protein L13a-4.	chlo	0.51	protein
155	Os07t0662500-01	23842	9	0.2	Similar to Elongation factor 1-beta' (EF-1-beta').	cyto /nucl	0.1	protein
156	Os02t0753300-01	20315	11	0.2	Lipoxygenase, LH2 domain containing protein.	chlo	0.01	not assitned

157	Os05t0349800-01	10159	9	0.19	Embryonic abundant protein 1.	nucl	0.39	not assitned
159	Os05t0155100-01	21355	4	0.19	Similar to 60S ribosomal protein L18.	nucl	0.35	protein
158	Os07t0574800-01	50250	27	0.19	Tubulin alpha-1 chain.	cyto	0.13	cell
160	Os05t0474600-01	35852	19	0.19	Similar to Aldose reductase-related protein (EC 1.1.1.21).	E.R.	0.79	development
161	Os03t0760800-01	10589	3	0.18	Similar to GAST1 protein precursor.	extr	0.2	hormone
162	Os03t0293500-02	65761	38	0.18	Similar to Pyruvate decarboxylase isozyme 3 (EC 4.1.1.1) (PDC) (Fragment).	cyto	0.01	metabolism
163	Os06t0247500-01	61907	13	0.18	Similar to Pyrophosphate-fructose 6-phosphate 1-phosphotransferase (EC 2.7.1.90) (Fragment).	chlo	0.08	fermentation
164	Os03t0151800-02	90429	22	0.18	Similar to Cell division control protein 48 homolog A (AtCDC48a).	cyto/nucl	0.57	not assitned
165	Os03t0351500-01	15356	5	0.17	Similar to Superoxide dismutase.	cyto	0.03	cell
166	Os09t0252100-01	41397	15	0.17	Similar to Acetyl-CoA C-acetyltransferase.	chlo	0.01	redox
167	Os03t0157900-01	45302	14	0.17	Phosphoserine aminotransferase, chloroplast precursor (EC 2.6.1.52) (PSAT).	chlo	0.05	secondary
168	Os09t0324000-02	15553	4	0.17	Similar to Oleosin.	chlo	0	metabolism
170	Os01t0270100-01	27252	3	0.17	Similar to Cysteine protease inhibitor.	chlo	0.06	amino acid
169	Os04t0390700-01	39866	18	0.17	Short-chain dehydrogenase/reductase SDR domain containing protein.	chlo	0.14	metabolism
171	Os05t0350500-01	43570	17	0.17	Peptidase M24, structural domain domain containing protein.	cyto	0.29	protein
172	Os01t0652600-01	59986	12	0.16	Similar to Ketol-acid reductoisomerase, chloroplast precursor (EC 1.1.1.86)	chlo	0.15	amino acid
173	Os03t0408300-00	16101	10	0.16	Similar to 60S ribosomal protein L27a-3.	nucl	0.14	metabolism
174	Os08t0189100-01	23811	93	0.16	Similar to Germin-like protein precursor.	extr	0	protein
175	Os04t0402100-01	60920	21	0.16	Similar to Calnexin (Fragment).	plas	0.27	stress
176	Os11t0116000-01	11889	6	0.16	Similar to Nonspecific lipid-transfer protein 1 (LTP 1) (Major allergen Pru d 3).	extr	0.02	sitnallint
177	Os03t0322900-00	36997	19	0.16	Late embryogenesis abundant protein repeat containing protein.	chlo	0.35	lipid
180	Os05t0501700-01	28532	8	0.16	Rossmann-like alpha/beta/alpha sandwich fold domain containing protein.	chlo	0.21	metabolism
179	Os10t0411800-01	16419	5	0.16	Similar to 40S ribosomal protein S17-3.	cyto /nucl	0.39	development
178	Os11t0582400-01	49179	36	0.16	Similar to Embryo-specific protein.	extr	0.73	stress
181	Os02t0760300-01	12192	3	0.16	Similar to Immunophilin.	chlo	0	protein
182	Os01t0267900-01	16878	2	0.15	Similar to Calmodulin NtCaM3	cyto	0.03	not assitned
183	Os03t0718100-01	42014	16	0.15	Actin 1.	cysk	0.05	protein
184	Os06t0133000-01	67004	18	0.15	Granule-bound starch synthase I, chloroplast precursor (EC 2.4.1.21).	chlo	0.05	sitnallint
185	Os02t0489400-01	24928	11	0.15	Similar to 40S ribosomal protein S8.	chlo	0.69	cell
186	Os05t0169100-01	25112	8	0.15	Similar to 60S ribosomal protein L10 (QM protein homolog).	chlo	0.16	major CHO
188	Os04t0526600-01	21689	9	0.15	Similar to Alpha-amylase/subtilisin inhibitor (RASI).	vacu	0.05	metabolism
187	Os06t0547400-01	34498	4	0.15	Similar to Peroxidase P7 (EC 1.11.1.7) (TP7).	chlo	0.26	protein
190	Os07t0214600-01	17542	4	0.15	Similar to Seed allergenic protein RA17 precursor.	cyto	0.07	stress
189	Os10t0483000-01	17624	3	0.15	Similar to Transcription factor homolog BTF3-like protein.	cyto	0.31	misc
192	Os02t0785800-01	12821	3	0.15	Similar to Ribosomal protein L35A.	cyto	0.14	RNA
191	Os05t0595400-01	26092	8	0.15	Similar to Nucleoside diphosphate kinase III (EC 2.7.4.6)	chlo	0.03	protein
195	Os02t0100300-01	44180	10	0.14	Similar to HSP associated protein like.	nucl	0.49	nucleotide
193	Os03t0757900-01	53435	8	0.14	Similar to UDP-glucose 6-dehydrogenase (EC 1.1.1.22)	extr	0.01	metabolism
194	Os05t0346300-01	22350	8	0.14	Similar to 40S ribosomal protein S7.	cyto/nucl	0.17	redox
196	Os07t0186000-02	13319	6	0.14	Similar to Thioredoxin h isoform 1.	cyto	0	cell wall
197	Os08t0156800-01	13669	4	0.14	Similar to 60S ribosomal protein L34.	cyto	0.75	protein
199	Os01t0851700-01	94867	17	0.13	Similar to Cytosolic starch phosphorylase (Fragment).	cyto	0.29	major CHO
198	Os12t0623900-01	84874	22	0.13	Similar to Ethylene-responsive methionine synthase (Fragment).	cyto	0.12	metabolism
201	Os02t0130000-01	13826	3	0.13	Similar to SWIb domain-containing protein (Fragment).	mito	0.09	amino acid
200	Os03t0390000-02	28269	8	0.13	Similar to Ribosomal protein s6 RPS6-2.	nucl	0.88	metabolism
202	Os06t0134000-01	14151	6	0.13	Similar to 40S ribosomal protein S20.	cyto	0.01	RNA
203	Os01t0743500-01	64629	18	0.13	Cytosolic NADP malic enzyme.	cyto	0.21	protein
204	Os03t0842900-01	39287	5	0.13	Similar to Steroleosin-B.	chlo	0.06	TCA
205	Os04t0574200-01	44679	7	0.13	FAS1 domain domain containing protein.	plas	0.32	misc
206	Os01t0611000-01	40112	14	0.13	Protein of unknown function DUF642 domain containing protein.	chlo	0.04	cell wall
208	Os01t0823300-00	15381	6	0.12	Similar to Ribosomal protein S26.	chlo	0.42	not assitned
209	Os02t0622300-00	15435	3	0.12	Ribosomal protein L14 family protein.	cyto	0.24	protein
207	Os11t0451700-00	31233	11	0.12	Similar to Dehydrin DHN1 (M3) (RAB-17 protein).	nucl	0.22	protein
210	Os03t0101600-01	36833	5	0.12	Similar to Oxidoreductase, zinc-binding dehydrogenase family protein, expressed.	chlo	0.05	not assitned
212	Os01t0834500-01	15765	11	0.12	Similar to 40S ribosomal protein S23 (S12).	cyto	0.23	misc
213	Os04t0394200-01	48310	5	0.12	Similar to 2-oxoglutarate dehydrogenase E2 subunit.	mito	0.45	TCA
211	Os12t0478200-02	15693	10	0.12	GRAM domain containing protein.	nucl	0.22	hormone
214	Os05t0268500-01	54131	17	0.11	Similar to Serine carboxypeptidase 2.	chlo	0.05	metabolism
215	Os06t0167600-01	27180	3	0.11	Similar to Proteasome subunit alpha-3 (Fragment).	chlo	0.15	protein
217	Os02t0257200-01	32543	7	0.11	Conserved hypothetical protein.	plas	0.08	protein
219	Os03t0735300-01	32498	6	0.11	Alba, DNA/RNA-binding protein family protein.	nucl	0.25	not assitned
220	Os04t0404400-01	32258	9	0.11	Similar to H0502B11.4 protein.	extr	0	RNA
216	Os05t0469600-01	66083	22	0.11	Similar to Pyruvate decarboxylase (Fragment).	chlo	0.01	stress
218	Os11t0149200-00	15846	2	0.11	Conserved hypothetical protein.	cyto	0.01	fermentation
221	Os01t0783500-01	27781	5	0.11	Rossmann-like alpha/beta/alpha sandwich fold domain containing protein.	chlo	0.14	not assitned
223	Os08t0545200-01	39990	6	0.11	Alcohol dehydrogenase superfamily, zinc-containing protein.	cyto	0.01	stress
222	Os09t0501850-01	16394	2	0.11	Similar to FK506-binding protein 2-1 precursor (EC 5.2.1.8)	extr	0.09	misc
224	Os04t0605900-01	28401	11	0.11	Similar to 60S ribosomal protein L7-2.	cyto	0.53	cell
225	Os06t0727200-01	57064	9	0.11	Catalase isozyme B (EC 1.11.1.6) (CAT-B).	pero	0.13	not assitned
226	Os11t0455800-01	51812	4	0.11	Similar to Serine hydroxymethyltransferase.	cysk	0.01	redox
230	Os01t0348700-01	17040	6	0.11	Similar to 60S ribosomal protein L23a (L25).	cyto	0.36	C1-
232	Os01t0598600-01	51795	6	0.11	Peptidase A1 domain containing protein.	chlo	0.15	metabolism
231	Os05t0156300-01	40429	7	0.11	Similar to protein disulfide isomerase.	chlo	0.12	amino acid
228	Os05t0584200-01	16706	4	0.11	Similar to Late embryogenesis abundant protein Lea14-A.	nucl	0.01	metabolism
229	Os07t0492000-01	16851	2	0.11	Nucleoside diphosphate kinase I (EC 2.7.4.6)	cyto	0.01	development
227	Os10t0390500-01	34639	3	0.11	Similar to Alanine aminotransferase.	cyto	0.09	nucleotide

233	Os07t0188800-01	57666	6	0.11	Similar to Methylmalonate-semialdehyde dehydrogenase (EC 1.2.1.27).	chlo	0.02	amino acid metabolism
234	Os05t0589600-01	41004	7	0.1	Similar to Nuclear RNA binding protein B (Fragment).	nucl	0.45	RNA
236	Os03t0807700-01	41248	7	0.1	Protein of unknown function DUF642 domain containing protein.	chlo	0.01	not assitned
240	Os03t0851000-01	17275	3	0.1	Similar to Transcription factor homolog BTF3-like protein.	cyto	0.31	RNA
235	Os05t0438800-01	41866	5	0.1	Similar to Actin 1.	cysk	0.01	cell
237	Os06t0507200-01	17405	2	0.1	Bifunctional inhibitor/plant lipid transfer protein/seed storage domain containing protein.	chlo	0.28	not assitned
238	Os09t0278000-00	17324	2	0.1	Hypothetical conserved gene.	cyto	0.06	not assitned
239	Os11t0454300-01	17315	20	0.1	Similar to Water-stress inducible protein RAB21.	nucl	0.25	not assitned
241	Os02t0196800-01	47645	7	0.1	Similar to Fumarylacetoacetase (Fragment).	cyto	0.07	amino acid metabolism
242	Os01t0531500-01	30505	5	0.1	Dienelactone hydrolase domain containing protein.	chlo	0.14	misc
243	Os06t0675700-01	96503	24	0.1	Similar to High pI alpha-glucosidase.	chlo	0.1	misc
246	Os03t0794700-01	17709	6	0.1	Similar to 40S ribosomal protein S18.	cyto	0.24	protein
247	Os04t0613600-00	18053	9	0.1	Similar to 40S ribosomal protein S11.	cyto/nucl	0.09	protein
248	Os05t0157200-01	18163	2	0.1	UspA domain containing protein.	cyto	0.01	stress
244	Os05t0576700-01	18145	2	0.1	Oleosin family protein.	plas	0.04	lipid metabolism
245	Os07t0206500-00	17923	4	0.1	13 kDa prolamin precursor.	extr	0.25	not assitned
249	Os09t0505600-01	24608	3	0.1	Proteasome subunit beta type 1 (EC 3.4.25.1)	chlo	0.09	protein
251	Os01t0860300-01	24837	4	0.1	Similar to Ribosomal protein L1.	cyto	0.16	protein
250	Os02t0797500-01	50547	7	0.1	Similar to Plastidic aspartate aminotransferase.	chlo	0.03	amino acid metabolism
252	Os12t0502200-01	25086	4	0.1	Similar to Low temperature-responsive RNA-binding protein.	nucl	0.22	RNA
253	Os06t0662000-01	68711	5	0.1	Similar to Vacuolar H ⁺ -ATPase subunit A (Fragment).	chlo	0.07	transport
255	Os01t0702500-01	19331	8	0.09	Similar to Dehydrin Rab25.	nucl	0.34	stress
254	Os03t0296400-01	38496	7	0.09	Similar to Eukaryotic translation initiation factor 2 subunit 1	cyto	0.25	protein
256	Os01t0172400-01	85659	14	0.09	Similar to Phospholipase D alpha 1.	chlo	0.25	lipid metabolism
257	Os03t0113700-01	72806	10	0.09	Similar to Heat shock 70 kDa protein, mitochondrial precursor.	mito	0.25	stress
263	Os01t0300200-01	66541	6	0.09	Similar to ATP-citrate lyase subunit B.	chlo	0.11	TCA
258	Os01t0542000-00	33660	4	0.09	Similar to DNA-damage-repair/toleration protein DRT102.	cyto	0.01	DNA
259	Os01t0817700-01	60980	6	0.09	Similar to 2,3-bisphosphoglycerate-independent phosphoglycerate mutase (EC 5.4.2.1)	cyto	0.03	not assitned
260	Os08t0338700-01	33755	4	0.09	Similar to Chaperone GrpE type 2.	chlo	0.63	protein
262	Os11t0579800-01	20050	2	0.09	Gar1 protein RNA-binding region family protein.	nucl	0.15	RNA
261	Os12t0207600-00	53704	10	0.09	Similar to ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit.	cyto	0.16	protein
264	Os03t0189600-01	41305	3	0.09	Similar to Alcohol dehydrogenase.	cyto	0	misc
266	Os05t0302700-01	41122	9	0.09	Similar to ATP/ADP carrier protein.	chlo	0.14	transport
265	Os06t0232000-01	41752	6	0.09	Similar to Pro-resilin.	nucl	0.6	not assitned
267	Os07t0568700-02	36012	8	0.09	Polygalacturonase inhibitor 1 precursor (Polygalacturonase-inhibiting protein) (Floral organ regulator 1).	chlo	0.25	cell wall
268	Os10t0177200-02	42732	3	0.09	EF-HAND 2 domain containing protein.	cyto	0.3	sitnallint
269	Os12t0145700-01	57862	8	0.08	Pyruvate kinase family protein.	cyto	0.04	lipid metabolism
270	Os12t0567700-01	28460	5	0.08	Similar to 60S ribosomal protein L2 (Fragment).	cyto	0.13	protein
273	Os01t0752300-01	21500	5	0.08	Similar to 60S ribosomal protein L18a-1.	nucl	0.38	protein
274	Os01t0829800-01	42046	12	0.08	Similar to Malate dehydrogenase precursor (EC 1.1.1.1.37).	chlo	0.03	TCA
272	Os03t0796000-02	21255	2	0.08	Similar to Ripening-associated protein (Fragment).	chlo	0	hormone metabolism
271	Os06t0264300-01	43107	3	0.08	Similar to RAD23, isoform I.	chlo	0.29	DNA
276	Os03t0212700-01	58829	10	0.08	Similar to Cytochrome C reductase-processing peptidase subunit I, MPP subunit I, P55.	mito	0.29	protein
277	Os09t0482100-01	80435	14	0.08	Similar to Heat shock protein 82.	nucl	0.53	stress
275	Os10t0548100-01	29200	2	0.08	Similar to DM280 protein.	chlo	0.06	not assitned
278	Os08t0345700-01	67910	11	0.08	Similar to Fructose-6-phosphate 1-phosphotransferase (Fragment).	cyto	0.12	not assitned
279	Os01t0328700-01	53009	10	0.08	FAD-dependent pyridine nucleotide-disulphide oxidoreductase domain containing protein.	chlo	0.13	TCA
280	Os04t0677500-01	55875	6	0.07	Pyruvate kinase (EC 2.7.1.40).	cyto	0.01	lipid metabolism
284	Os02t0774300-01	73081	7	0.07	Similar to Heat shock 70 kDa protein, mitochondrial precursor.	mito	0.29	stress
283	Os03t0695600-01	23634	4	0.07	Proteasome subunit beta type 2 (EC 3.4.25.1)	cyto	0.02	protein
281	Os06t0708500-01	24167	10	0.07	Similar to Peptidyl-prolyl cis-trans isomerase.	mito	0.05	cell
282	Os11t0104866-00	64410	8	0.07	Similar to Clathrin heavy chain.	cyto	0.3	not assitned
286	Os05t0304400-01	50074	6	0.07	Similar to GDP dissociation inhibitor protein OsGDI2.	cyto	0.14	sitnallint
285	Os07t0614500-01	24904	3	0.07	Similar to Elongation factor 1 beta 2.	cyto	0.05	protein
287	Os01t0896700-00	34773	14	0.07	Similar to 60S ribosomal protein L5.	mito	0.55	not assitned
290	Os02t0770000-01	26371	7	0.07	Beta 1 subunit of 20S proteasome.	cyto	0.02	protein
291	Os03t0146100-01	25740	2	0.07	Tonoplast intrinsic protein (Tonoplast water channel).	vacu	0	transport
289	Os06t0111500-01	52973	11	0.07	Cytosolic 6-phosphogluconate dehydrogenase.	chlo	0.03	OPP
288	Os07t0609000-01	26540	9	0.07	Stress responsive alpha-beta barrel domain containing protein.	chlo	0.03	not assitned
292	Os04t0650800-01	64153	3	0.06	Similar to Phosphoglycerate dehydrogenase.	mito	0.08	amino acid metabolism
293	Os05t0103200-01	26745	2	0.06	Cyclophilin-like domain containing protein.	chlo	0.04	cell
294	Os10t0492600-01	27496	7	0.06	Similar to Tonoplast membrane integral protein ZmTIP3-1.	mito	0.01	transport
295	Os09t0451500-02	47703	4	0.06	Thioredoxin domain 2 containing protein.	chlo	0.01	redox
296	Os02t0248800-01	56996	32	0.06	Similar to Glutelin type-B 2 precursor.	vacu	0.4	development
299	Os02t0537700-01	28307	5	0.06	Similar to 2-cys peroxiredoxin BAS1, chloroplast precursor (EC 1.11.1.15)	chlo	0.04	redox
300	Os03t0202200-01	29456	15	0.06	Porin-like protein.	cyto	0.01	transport
298	Os03t0851100-01	48564	19	0.06	Similar to Translational elongation factor EF-TuM.	mito	0.03	protein
297	Os04t0610600-01	28848	2	0.06	Similar to Cor14b protein precursor.	chlo	0.28	not assitned
301	Os09t0361400-01	29202	2	0.06	Outer mitochondrial membrane protein porin (Voltage-dependent anion-selective channel protein) (VDAC).	cyto	0.12	transport
303	Os02t0205200-01	39575	5	0.06	Similar to Unidentified precursor.	extr	0.09	not assitned
302	Os10t0155500-01	39620	4	0.06	Similar to Aldose 1-epimerase-like protein.	cyto	0.02	minor CHO metabolism
304	Os07t0410100-01	59248	10	0.06	Similar to Dihydrolipoamide S-acetyltransferase (EC 2.3.1.12).	mito	0.42	TCA
305	Os02t0187100-00	30010	4	0.06	Similar to cyclase.	plas	0	DNA
306	Os02t0669100-01	30904	2	0.06	Dehydrin family protein.	nucl	0.37	not assitned
307	Os04t0386700-01	29660	2	0.06	Similar to OSIGBa0148P16.6 protein.	plas	0.02	RNA

308	Os06t0486800-01	41543	5	0.06	Similar to Formate dehydrogenase, mitochondrial precursor (EC 1.2.1.2)	mito	0.01	C1-metabolism
309	Os12t0620400-01	31548	3	0.05	Methyl-CpG DNA binding domain containing protein.	nucl	0.57	RNA
310	Os01t0711000-01	54360	3	0.05	Similar to Vacuolar ATP synthase subunit B isoform 2 (EC 3.6.3.14)	cysk	0.14	mitochondrial electron transport protein
311	Os01t0937100-01	44500	5	0.05	Similar to Xylanase inhibitor precursor (Xylanase inhibitor TAXI-I).	chlo	0.18	major CHO metabolism
312	Os03t0340500-01	92501	5	0.05	Similar to Sucrose synthase (EC 2.4.1.13).	cyto	0.1	protein
314	Os04t0117900-01	45861	7	0.05	Amidase family protein.	cyto	0	major CHO metabolism
313	Os06t0726400-01	93747	3	0.05	Branching enzyme-I precursor (Starch-branching enzyme I)	chlo	0.17	amino acid metabolism
315	Os02t0817700-02	47370	3	0.05	Similar to 3-ketoacyl-CoA thiolase (Fragment).	chlo	0.05	protein
316	Os05t0155601-00	59100	8	0.05	Importin alpha-1b subunit.	nucl	0.64	protein
317	Os03t0143400-01	61292	7	0.05	Similar to mitochondrial chaperonin-60 [Oryza sativa (japonica cultivar-group)].	mito	0.06	protein
318	Os06t0538000-01	61316	3	0.05	Similar to T-complex protein 1, gamma subunit (TCP-1-gamma)	cyto	0.18	protein
319	Os09t0474300-01	75044	7	0.05	Similar to Heat-shock protein precursor.	chlo	0.49	stress
320	Os02t0575800-01	40366	2	0.04	Aldose-1-epimerase domain containing protein.	chlo	0.03	minor CHO metabolism
322	Os02t0735200-01	39405	4	0.04	Glutamine synthetase shoot isozyme (EC 6.3.1.2)	cyto	0.06	N-metabolism
325	Os02t0767500-01	39333	2	0.04	Mitochondrial phosphate transporter.	extr	0.03	transport
321	Os04t0390800-01	39547	7	0.04	NAD(P)-binding domain containing protein.	chlo	0.01	misc
324	Os06t0716700-02	93044	4	0.04	Similar to Heat shock protein 90.	vacu	0.44	stress
323	Os07t0622000-01	38913	20	0.04	Serine/threonine-protein kinase SAPK2 (EC 2.7.1.37)	cysk	0.1	protein
328	Os01t0118000-01	42253	2	0.04	Similar to Fructose-bisphosphate aldolase (EC 4.1.2.13) (Fragment).	chlo	0.06	PS
326	Os02t0815500-01	41652	4	0.04	Alcohol dehydrogenase class III (EC 1.1.1.1)	extr	0.01	misc
327	Os03t0610650-01	42114	2	0.04	Similar to cDNA clone:002-125-A07, full insert sequence.	plas	0.18	not assitned
329	Os09t0115400-01	71870	2	0.04	Similar to Poly(A)-binding protein.	nucl	0.38	RNA
331	Os01t0180800-01	93904	6	0.04	Heat shock protein Hsp70 family protein.	cyto	0.24	stress
330	Os10t0470900-01	45593	4	0.04	Nucleotide-binding, alpha-beta plait domain containing protein.	nucl	0.19	RNA
332	Os04t0670200-01	50964	7	0.03	Similar to Oryzain beta chain precursor (EC 3.4.22.-).	extr	0.05	protein
333	Os07t0134800-01	69494	3	0.03	Similar to Succinate dehydrogenase [ubiquinone] flavoprotein subunit, (EC 1.3.5.1)	mito	0.1	TCA
334	Os02t0523500-01	108515	5	0.03	Similar to 110 kDa 4SNc-Tudor domain protein (Fragment).	chlo	0.3	RNA
337	Os08t0440800-01	53963	2	0.03	Glyceraldehyde-3-phosphate dehydrogenase.	cyto	0.01	PS
335	Os09t0440300-01	55208	3	0.03	Similar to Aldehyde dehydrogenase family 7 member A1 (EC 1.2.1.3)	chlo	0.07	fermentation
336	Os11t0525600-01	114599	4	0.03	Similar to Alpha-mannosidase.	chlo	0.22	misc
338	Os02t0274100-01	79038	8	0.03	Similar to Peroxisomal fatty acid beta-oxidation multifunctional protein (MFP).	plas	0.06	lipid metabolism
341	Os02t0100100-01	62443	2	0.03	Thioredoxin domain domain containing protein.	E.R.	0.06	redox
343	Os02t0644100-01	65159	3	0.03	Similar to Heat shock protein STI (Stress inducible protein) (GmSTI).	mito	0.59	stress
340	Os04t0164900-01	62247	3	0.03	Similar to Starch debranching enzyme.	chlo/nucl	0.16	not assitned
339	Os07t0447800-01	58553	2	0.03	Alpha-D-phosphohexomutase, alpha/beta/alpha I, II and III domain containing protein.	chlo	0.06	tlycolysis
342	Os08t0192900-01	60472	2	0.03	Nucleotide-binding, alpha-beta plait domain containing protein.	nucl	0.68	sitnallint
344	Os03t0136900-01	106862	8	0.03	Similar to Aconitate hydratase, cytoplasmic (EC 4.2.1.3)	chlo	0.04	TCA
345	Os03t0810600-01	72125	4	0.02	Miro-like domain containing protein.	plas	0.61	sitnallint
346	Os06t0303400-00	90373	10	0.02	Similar to aconitate hydratase, cytoplasmic.	cyto	0.08	TCA
347	Os05t0405000-01	103578	3	0.02	Orthophosphate dikinase precursor (EC 2.7.9.1).	chlo	0.11	not assitned
348	Os01t0226400-01	93590	6	0.02	ATPase, AAA-type, core domain containing protein.	vacu	0.76	protein
349	Os02t0218200-01	98904	7	0.02	Peptidase M1, membrane alanine aminopeptidase family protein.	cyto	0.05	protein

a protein ID is according to The Rice Annotation Project Database, b m.f. means number of matched peptide, the protein with ≥ 2 matched peptides were considered, c mior (%) is the percentate calculated using each emPAI of identified protein to divide the total emPAI of total identified proteins, dWoLFPSORT is protein location prediction software, eNucPred is protein location prediction software, fFunction were obtained using MapMan bin codes. d nucl, nuclear; cyto, cytoplasm; chlo, chloroplast; mito, mitochondria; E.R., endoplasmic reticulum; vacu, vacuole; cysk, cytoskeletal filaments; plas, plasma membrane, Extr, extracellular. For results from NucPred, the consensus score is basically the fraction of predictors which vote "nuclear". For a discrete prediction, the user has to decide on a score threshold (preferably 0.8). Proteins score greater than or equal to this threshold are predicted to spend time in the nucleus. f protein, protein synthesis/detratation/tartetint/others; RNA, RNA processint/retulation of transcription; DNA, DNA synthesis/repair; cell, cell organization/vesicle transport; major CHO metabolism, major carbohydrates metabolism; TCA, tricarboxylic acid cycle; misc, miscellaneous; not assitned, unknown.g genes were identified as aerobic or anaerobic responders in Narsai et al.work.