

MALDI TOF-TOF MS identification of barley shoots Zadoks stage 07 and 10 TBPs

Spot No.	Calculated		Experimental		ExPASy		Related protein	Organism	Accession No.
	¹ pI	² Mass, kDa	pI	³ Mass, kDa	⁴ Score	Sequence coverage, %			
1	4.8	37	4.4	20	1.08	6	DR100_DNA-damage-repair/toleration protein	<i>Arabidopsis thaliana</i>	Q00874
1	6.8	43	4.4	20	1.03	6	C3H35_Zinc finger CCCH domain-containing protein	<i>Oryza sativa</i>	Q6L4N4
1	6.4	41	4.4	20	0.42	6	C3H2_Zinc finger CCCH domain-containing protein	<i>Oryza sativa</i>	Q9FU27
2	6.4	50	4.4	20	0.67	6	CIPK1_CBL-interacting serine/threonine-protein...	<i>Arabidopsis thaliana</i>	Q8RWC9
2	6.4	41	4.4	20	0.42	5	C3H2_Zinc finger CCCH domain-containing protein	<i>Oryza sativa</i>	Q9FU27
2	6.8	43	4.4	20	1.03	5	C3H35_Zinc finger CCCH domain-containing protein	<i>Oryza sativa</i>	Q6L4N4
2	5.3	26	4.4	20	1.1	11	Probable kinetochore protein SPC25	<i>Kluyveromyces lactis</i> (Yeast)	Q6CUV0
2	5.2	65	4.4	20	0.6	5	Transcriptional activator protein Pur-b	<i>Arabidopsis thaliana</i>	Q6PHK6
3	4.9	26	5.2	24	0.61	12	RBP1A_Ran-binding protein 1 homolog	<i>Arabidopsis thaliana</i>	Q9LMK7
3	4.8	41	5.2	24	1.42	7	PP1R7_Protein phosphatase 1 regulatory subunit.	PONAB	Q5RFS7
4	9.9	17	5.2	24	4.97	27	PP14A_PIG (C_1) Protein phosphatase 1 regulatory	Pig	O18734
4	5.0	80	5.2	24	0.28	3	Serine/threonine-protein kinase WNK1	<i>Arabidopsis thaliana</i>	Q9CAV6
5	5.8	22	5.6	25	2.53	14	ARR15_Two-component response regulator ARR15	<i>Arabidopsis thaliana</i>	Q7G8V2
5	5.3	11	5.6	25	3.52	32	SUMO1_ONCMY (C_1) Ubiquitin-related modifier 1	<i>Oncorhynchus mykiss</i>	Q9PT08
6	6	24	5.6	25	2.97	16	IAA16_Auxin-responsive protein IAA16.	<i>Oryza sativa</i>	P0C127
6	5.8	32	5.6	25	1.72	10	PUR_Transcription factor Pur-alpha 1	<i>Arabidopsis thaliana</i>	Q9SKZ1
6	6.8	21	5.6	25	2.46	19	MED10_Mediator of RNA polymerase II transcription activator	CAEEL	P45966
7	5.6	40	5.9	25	0.59	5	DRL35_Probable disease resistance protein At5g...	<i>Arabidopsis thaliana</i>	Q9FHI7
7	5.2	24	5.9	25	1.18	8	HSPBB_Heat shock protein beta-11	DANRE	A5JV83
7	5.0	40	5.9	25	1.18	8	P2C11_Probable protein phosphatase 2C	<i>Oryza sativa</i>	Q6ETK3
8	5.6	40	5.9	25	0.59	5	DRL35_Probable disease resistance protein At5g	<i>Arabidopsis thaliana</i>	Q9FHI7
9	5.6	44	4.4	20	1.40	9	DRL26_Probable disease resistance protein At4g	<i>Arabidopsis thaliana</i>	Q84WD3
10	6.3	46	4.4	20	2.12	8	Protein ALF	<i>Petunia hybrida</i>	O22621
10	7.1	44	4.4	20	1.1	7	Cyclin-B1-4	<i>Arabidopsis thaliana</i>	O48790
10	5.8	47	4.4	20	0.92	5	P2C75_Probable protein phosphatase 2C 75	<i>Oryza sativa</i>	Q2R637
10	6.3	52	4.4	20	1.50	8	CIPK1_CBL-interacting protein kinase 1	<i>Oryza sativa</i>	Q9LGV5
10	5.5	89	4.4	20	1.85	5	DEAD-box ATP-dependent RNA helicase 28	<i>Arabidopsis thaliana</i>	Q9ZRZ8

11	6.5	49	5.2	24	0.63	6	Transcription factor IWS1	<i>Gibberella zeae</i>	Q4IJ11
11	6.9	50	5.2	24	0.61	8	Nuclear hormone receptor family member	<i>Caenorhabditis briggsae</i>	A8XNK6
11	5.6	44	5.2	24	0.44	5	DRL26_Probable disease resistance protein At4g...	<i>Arabidopsis thaliana</i>	Q84WD3
11	6.1	43	5.2	24	2.11	7	RN150_DANRE (C_1) RING finger protein 150	<i>Danio rerio</i> (Zebrafish)	Q566M8
11	5.9	67	5.2	24	0.56	4	Cell cycle checkpoint protein RAD17	<i>Arabidopsis thaliana</i>	Q9MBA3
12	7	23	5.2	24	1.26	10	PSF1_DNA replication complex GINS protein PSF	Mouse	Q9CZ15
12	5.3	42	5.2	24	0.65	8	ACT1 Actin-1	<i>Oryza sativa</i>	A2XLF2
13	5.6	44	5.6	25	0.44	5	DRL26_Probable disease resistance protein At4g...	<i>Arabidopsis thaliana</i>	Q84WD3
13	6.4	50	5.6	25	0.38	6	CIPK1_CBL-interacting serine/threonine-protein	<i>Arabidopsis thaliana</i>	Q8RWC9
13	5.5	46	5.6	25	0.23	3	FBK46_F-box/Kelch-repeat protein At2g44130	<i>Arabidopsis thaliana</i>	O80582
14	6.4	50	5.6	25	0.38	6	CIPK1_CBL-interacting serine/threonine-protein	<i>Arabidopsis thaliana</i>	Q8RWC9
14	5.5	46	5.6	25	0.23	3	FBK46_F-box/Kelch-repeat protein At2g44130	<i>Arabidopsis thaliana</i>	O80582
15	6.3	36	6.1	25	1.38	13	GAT10_GATA transcription factor 10	<i>Arabidopsis thaliana</i>	Q9SV30
15	5.5	63	6.1	25	0.995	3	Transcription factor ABA-inducible bHLH	<i>Arabidopsis thaliana</i>	Q9ZPY8
15	5.5	85	6.1	25	0.72	3	Homeobox-leucine zipper protein ROC1	<i>Oryza sativa</i>	Q6ZAR0
16	7.9	62	6.1	25	0.71	6	Transcriptional adapter ADA2a	<i>Arabidopsis thaliana</i>	Q9SFD5
16	5.2	17	6.1	25	0.84	17	HMGL_HMG1/2-like protein	<i>Vicia faba</i>	P40620
17	6.7	33	5.9	40	1.32	7	GAT25_GATA transcription factor 25	<i>Arabidopsis thaliana</i>	Q8H1G0
18	6.1	42	5.9	40	0.44	6	Serine/threonine-protein kinase SAPK4	<i>Oryza sativa</i>	Q5N942
19	6.0	46	5.2	70	0.80	13	PUB57_U-box domain-containing protein 57	<i>Arabidopsis thaliana</i>	Q9SGT1
19	6.8	92	5.2	70	0.39	4	Putative AC transposase	<i>Zea mays</i>	P03010
20	6.3	73	5.2	70	0.61	3	C3H45_Zinc fingerCCCH domain-containing protein	<i>Oryza sativa</i>	Q0DA50
20	6.0	42	5.2	70	0.55	6	GTE6_ARATH (C_1) Transcription factor GTE	<i>Arabidopsis thaliana</i>	Q9FT54
21	5.0	47	5.4	70	1.12	7	SPZ5_Putative serpin-Z5	<i>Oryza sativa</i>	Q53MD3
22	5.6	83	5.4	70	1.09	5	RH24_DEAD-box ATP-dependent RNA helicase 24	<i>Arabidopsis thaliana</i>	O22907
22	6.2	56	6.2	70	1.17	7	Transcriptional adapter ADA2b	<i>Arabidopsis thaliana</i>	Q9ATB4
22	5.5	119	6.2	70	0.47	2	FACT complex sub SPT16	<i>Zea mays</i> (maize)	Q8H6B1

23	5.9	96	5.2	39	1.725	6	Serine/threonine-protein phosphatase BSL	<i>Arabidopsis thaliana</i>	Q8L7U5
24	9.3	93	5.2	30	0.174	4	DEAD-box ATP-dependent RNA helicase	<i>Oryza sativa</i>	A2XVF7
26	6.5	100	5.4	50	1.7	6	E3 ubiquitin-protein ligase BRE1-like 1	<i>Arabidopsis thaliana</i>	Q8RXD6
26	6	198	6.0	50	0.22	2	Transposon protein, putative, CACTA, En/Spm sub-class	<i>Oryza sativa</i>	Q109Z8
26	6.9	168	6.0	50	0.084	2	DNA topoisomerase II	<i>Schizosaccharomyces pombe</i>	P08096
28	6.9	79	6.6	37	6.5	13	Cyclin-dependent kinase G-1	<i>Oryza sativa</i>	A2X6X1
29	7.6	83	6.0	37	0.624	3	ATP-dependent RNA helicase MAK5	<i>Eremothecium gossypii</i>	Q75716
30	6.9	168	5.8	50	0.24	2	DNA topoisomerase II	<i>Schizosaccharomyces pombe</i>	P08096
31	9.4	61	5.3	40	0.36	3	Maturase K (Intron maturase)	<i>Pinus pinaster</i>	Q8HQQ6

Note: ¹ pI calculated; ² mass calculated from the amino acid sequence in databases; ³ mass calculated according to their migration in SDS-PAGE; ⁴ MOWSE scores in UniProtKBSwissProt database. Spots of interest were cut from the gels (Fig. 2), digested with trypsin, and analyzed by MALDI TOF-TOF. The related proteins were identified using the GPS Explorer program.

