

Table S1. Sequences of tryptic fragments obtained by LC-MS/MS analysis

Molecular mass (kDa)	Code SwissProt/AGI	Name	Score	Sequence coverage (%)	Aa position ^c	Peptide sequences ^d
35 ^a	Q9LUL7/At3g14310	AtPME3	180	9	294 - 309	TVAAAVAAAPENSNKR
					342 - 348	TIITGSR
					349 - 368	NVVDGSTTFHSATVAAVGER
					479 - 489	IGATSDLQSVK
22 ^a	Q9LUV1/At3g17220	AtPMEI2	105	14	80 - 85	IQSLVK
					105 - 114	SAISSLNDAK
					105 - 123	SAISSLNDAKQSLASGDGK
35 ^b	Q9LUL7/AT3g14310	AtPME3	571	21	280 - 293	ADATVAADGSGTFFK
					310 - 315	YVIHIK
					316 - 327	AGVYRENVEVAK
					321 - 327	ENVEVAK
					331 - 339	NIMFMGDGR
					342 - 348	TIITGSR
					373 - 384	DITFQNTAGPSK
					385 - 391	HQAVALLR
					456 - 463	NMVTAQGR
					464 - 476	TDPNQNTGIVIQK
479 - 489	IGATSDLQSVK					
490 - 501	GSFPTYLGRPWK					
538 - 551	EYSNTGAGAGTANR					
17 ^b	Q9LNF2/ At1g48020	AtPMEI1	159	21	47 - 51	FLNTK
					52 - 62	FASPNLQALAK
					63 - 71	TTL DSTQAR
					79 - 90	LQSIIDGGVDPR
34 ^{a,b}	Q9SKX2/At2g43050	AtPME	49	1	389 - 396	NFVTAQGR

^aProteins obtained from *AtPMEI-2* transformed plants. ^bProteins obtained from *AtPMEI-1* transformed plants. ^cAmino acid position of fragment in the sequence. ^dPeptide sequence obtained after tryptic digestion