

M A P I K E F I S K F S D F K N N K L I L S S A A I A L L L L A S I V G I A A	40
T T N Q N K N Q K I T T L S S T S H A I L K S V C S S T L Y P E L C F S A V A	80
A T G G K E L T S Q K E V I E A S L N L T T K A V K H N Y F A V K K L I A K R K	120
G L T P R E V T A L H D C L E T I D E T L D E L H V A V E D L H Q Y P K Q K S L	160
R K H A D D L K T L I S S A I T N Q G T C L D G F S Y D D A D R K V R K A L L K	200
G Q V H V E H M C S N A L A M I K N M T E T D I A N F E L R D K S S T F T N N N	240
N R K L K E V T G D L D S D G W P K W L S V G D R R L L Q G S T I K A D A T V A	280
D D G S G D F T T V A A A V A A A P E K S N K R F V I H I K A G V Y R E N V E V	320
<u>T K K K T N I M F L G D G R G K T I I T G S R N V V D G S T T F H S A T V A A V</u>	360
<u>G E R F L A R D I T F Q N T A G P S K H Q A V A L R V G S D F S A F Y Q C D M F</u>	400
<u>A Y Q D T L Y V H S N R Q F F V K C H I T G T V D F I F G N A A V L Q D C D I</u>	440
<u>N A R R P N S G Q K N M V T A Q G R S D P N Q N T G I V I Q N C R I G G T S D L</u>	480
<u>L A V K G T F P T Y L G R P W K E Y S R T V I M Q S D I S D V I R P E G W H E W</u>	520
<u>S G S F A L D T L T Y R E Y L N R G G G A G T A N R V K W K G Y K V I T S D T E</u>	560
A Q P F T A G Q F I G G G G W L A S T G F P F S L S L	587

Supplementary Figure 2. Cartography of At1g53830 by MALDI-TOF MS

The protein has been identified in the I, J, K, and V CWP fractions obtained by CEC (Irshad et al. 2008). PMF results have been obtained using the ProteinProspector software. Underlined peptides were found by MS. Trypsin cut sites are indicated in bold. Numbering of amino acids is on the right.

Colour code:

Putative signal peptide between amino acids 1 and 40, as predicted by TargetP (<http://www.cbs.dtu.dk/services/TargetP/>)

PMEI domain between amino acids 56 and 215 (PF04043, as predicted by InterProScan, <http://www.ebi.ac.uk/Tools/InterProScan/>)

PME domain between amino acids 276 and 573 (PF01095 as predicted by InterProScan, <http://www.ebi.ac.uk/Tools/InterProScan/>)