

MASSSSSLAFSLSLLLALILCFSP	QSY	<b>K</b> TIG <b>K</b> GY <b>R</b> LVSI	40
<u>EESPDGGFIGYLQV</u>	<b>KQ</b> <b>K</b> <b>N</b> KIYGS	<u>DITTL</u> <b>R</b> LFV <b>K</b> HETDS <b>R</b> L	80
<b>R</b> VHITDA <b>K</b> QQ <b>R</b> WEVPYNLL <b>P</b>	<b>R</b> EQPPQVG <b>K</b> VIGKS <b>R</b> KSPIT		120
VQEISGSELIFS	YTTDPFTFAV <b>KRR</b>	SNHETL <b>F</b> <b>N</b> <b>T</b> <b>T</b> SSLVF	160
<b>K</b> DQYLEISTSLPKEASLYGLGENSQANGI	<b>K</b> LVPNEPYTLY		200
TEDVSAINLNTDLYGSHPMYMDLRNVGG	<b>K</b> AYAHAVLLNS		240
NGMDVFY <b>R</b> GDSLTY <b>K</b> VIGGVDFDYFIAGPSPLNVVDQYTQ			280
LIG <b>R</b> PAPMPYWSLGFHQCRWGYH <b>N</b> L <b>S</b> VVEDVVDNY <b>K</b> KAKI	<b>I</b>		320
<u>PLDVIWNDDDHMDGH</u>	<b>K</b> DFTLNPVAY <b>P</b> RAKLLAFLD <b>K</b> IHKI		360
<u>GM</u> <b>K</b> YIVINDPGIGV <b>N</b> ASYGTF <b>R</b> AMAADVFIKYEG <b>K</b> PFLA			400
QVWPGPVYFPDFLNP <b>K</b> TVSWWGDEI <b>K</b> RFHDLVPIDGLWID			440
MNEVSNFC	SGLCTIPEG <b>K</b> QCPSGEGPGWVCCLDCK <b>N</b> IT <b>K</b> T		480
<b>R</b> WDDPPY <b>K</b> IN <b>A</b> T <b>G</b> VVAPVGF <b>K</b> T	<b>I</b> ATSATHYNGV <b>R</b> EYDAHS		520
<u>IYGFSETIATH</u>	<b>K</b> GLLN <b>V</b> Q <b>G</b> K <b>R</b> PFIL <b>S</b> RSTFVGSQYAAHW		560
TGDNQGTWQSLQVSI	STMLNFGIFGVPMVGS	DICGFYPQP	640
TEELCN <b>R</b> WIEVGAFY <b>P</b> FS <b>R</b> DHANYSP <b>R</b> QELYQWDTVADS			680
<u>AR</u> NALGM <b>R</b> Y <b>K</b> ILPFLYTLN	YEAHMTGAPIAR <b>P</b> LFFSFPEY		720
TECYGNS <b>R</b> QFLLGSSFMISPVLEQ <b>G</b> KTEVEALFPPGSWYH			760
MFDMTQAVVS <b>K</b> NG <b>K</b> RVTLPAPLN	FVNVHLYQNTILPTQQG		800
GLIS <b>K</b> DAR <b>T</b> TPFSLVIAFPAGASEGYAT <b>G</b> KLYLDEDELPE			840
<u>M</u> <b>K</b> LGN <b>G</b> QSTYVDFYASV <b>G</b> <b>N</b> GT <b>M</b> <b>K</b> MW <b>S</b> QV <b>K</b> EG <b>K</b> FALS <b>K</b> GWV			880
IE <b>K</b> VSVLGL <b>R</b> GAGQVSEI <b>Q</b> INGSPMT <b>K</b> KIEVSS <b>K</b> EHTYVI			915
GLEDEEEN <b>K</b> S <b>V</b> MVEV <b>R</b> GLEMLVG <b>K</b> DF <b>N</b> MS <b>V</b> KMGIN			

### Supplementary Figure 3. Cartography of At1g68560 by MALDI-TOF MS

The protein has been identified in the G, H, I, and T CWP fractions obtained by CEC (Irshad et al. 2008). PMF results have been obtained using the ProteinProspector software. Underlined peptides were found by MS. Numbering of amino acids is on the right. At the C-terminus of the protein, the GAGQVSEIQINGSPMTK between amino acids 851 and 867 peptide was found 3 times in 18 independent identifications.

Colour code:

Expected signal peptide between amino acids 1 and 27, as predicted by TargetP (<http://www.cbs.dtu.dk/services/TargetP/>)

GH31 domain between amino acids 123 and 882 (PF01055, as predicted by InterProScan, <http://www.ebi.ac.uk/Tools/InterProScan/>)

Putative *N*-glycosylation sites as predicted by Prosite (<http://www.expasy.org/prosite/>) are in bold green letters.

Trypsin cut sites are in bold.