

Protein View: ABI54569.1

dimeric alpha-amylase inhibitor, partial [Aegilops sharonensis]

Database: NCBIprot  
Score: 87  
Expect: 0.012  
Monoisotopic mass (M<sub>r</sub>): 13891  
Calculated pI: 5.25  
Taxonomy: [Aegilops sharonensis](#)

This protein sequence matches the following other entries:

- ABI54595.1 from [Aegilops longissima](#)
- ABI54596.1 from [Aegilops longissima](#)
- ABI54602.1 from [Aegilops longissima](#)

Sequence similarity is available as [an NCBI BLAST search of ABI54569.1 against nr.](#)

Search parameters

Enzyme: Trypsin: cuts C-term side of KR unless next residue is P.  
Fixed modifications: [Carbamidomethyl \(C\)](#)  
Variable modifications: [Oxidation \(M\)](#)  
Mass values searched: 11  
Mass values matched: 5

Protein sequence coverage: 55%

Matched peptides shown in **bold red**.

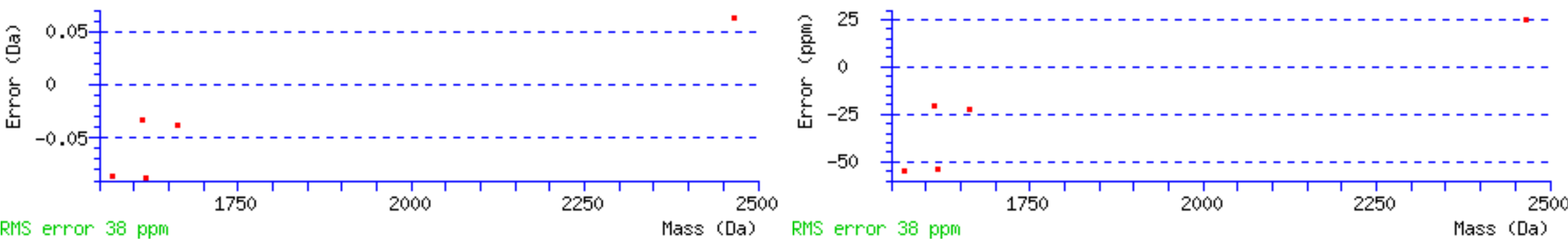
1 SGPWMCYPGQ AFQVPALPGC RPLLR**LQCNG SQVPEAVLR**D CCQQLADISE  
51 WCRCGALYSM LDDMYK**EHGA QEGQAGTGAF** PRCRRE**EVVKL TAASITAVCR**  
101 **LPIIVVDASGD GAYVCKDVAA YPDA**

Unformatted sequence string: [124 residues](#) (for pasting into other applications).

Sort by ☒ residue number ☐ increasing mass ☐ decreasing mass  
Show ☒ matched peptides only ☐ predicted peptides also

Start – End	Observed	Mr (expt)	Mr (calc)	Delta M	Peptide
26 – 39	1570.7140	1569.7068	1569.7933	-0.0866 0	<b>R.LQCNGSQVPEAVLR.D</b>
67 – 82	1612.7131	1611.7059	1611.7390	-0.0331 0	<b>K.EHGAQEGQAGTGAFPR.C</b>
86 – 100	1617.8114	1616.8042	1616.8920	-0.0878 1	<b>R.EVVKLTAASITAVCR.L</b>
101 – 116	1663.7980	1662.7907	1662.8287	-0.0380 0	<b>R.LPIIVVDASGDGAYVCK.D</b>
101 – 124	2466.2482	2465.2409	2465.1785	0.0625 1	<b>R.LPIIVVDASGDGAYVCKDVAAYPDA.-</b>

No match to: 1350.6466, 1372.6162, 1667.7974, 1698.8978, 1715.9218, 2211.1040



LOCUS	ABI54569	124 aa	linear	PLN 14-JUL-2016
DEFINITION	dimeric alpha-amylase inhibitor, partial [Aegilops sharonensis].			
ACCESSION	ABI54569			
VERSION	ABI54569.1			
DBSOURCE	accession DQ856415.1			
KEYWORDS	.			
SOURCE	Aegilops sharonensis			
ORGANISM	Aegilops sharonensis			
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BOP clade; Pooideae; Triticodae; Triticeae; Triticinae; Aegilops.			
REFERENCE	1 (residues 1 to 124)			
AUTHORS	Wang,J.R., Zhang,L., Wei,Y.M., Yan,Z.H., Baum,B.R., Nevo,E. and Zheng,Y.L.			
TITLE	Sequence polymorphisms and relationships of dimeric alpha-amylase inhibitor genes in the B genomes of Triticum and S genomes of Aegilops			
JOURNAL	Plant Sci. 173 (1), 1-11 (2007)			
REFERENCE	2 (residues 1 to 124)			
AUTHORS	Wang,J., Wei,Y., Yan,Z. and Zheng,Y.			
TITLE	Direct Submission			
JOURNAL	Submitted (17-JUL-2006) Sichuan Agricultural University, Triticeae Research Institute, Yaan Sichuan China, Yaan, Sichuan 625014, China			
COMMENT	Method: conceptual translation.			
FEATURES	Location/Qualifiers			
source	1..124 /organism="Aegilops sharonensis" /cultivar="PI584394" /db_xref="taxon:58530" /clone="5"			
Protein	<1..124 /product="dimeric alpha-amylase inhibitor"			
Region	3..103 /region_name="AAI_SS" /note="AAI_SS: Alpha-Amylase Inhibitors (AAIs) and Seed Storage (SS) Protein subfamily; composed of cereal-type AAIs and SS proteins. They are mainly present in the seeds of a variety of plants. AAIs play an important role in the natural defenses of plants...; cd00261" /db_xref="CDD:238163"			
Site	order(4,49..51,58) /site_type="other" /note="alpha-amylase binding site [polypeptide binding]" /db_xref="CDD:238163"			
Site	order(38,90,94,100) /site_type="other" /note="dimer interface [polypeptide binding]" /db_xref="CDD:238163"			
CDS	1..124 /coded_by="DQ856415.1:<1..375"			