MASCOT Search Results

Protein View: IBB2_PEA

Seed trypsin/chymotrypsin inhibitor TI5-72 OS=Pisum sativum OX=3888 GN=TI572 PE=2 SV=1

Database:	SwissProt
Score:	51
Expect:	0.34
Monoisotopic mass (M_r):	13387
Calculated pI:	5.47
Taxonomy:	**Pisum sativum**

Sequence similarity is available as **an NCBI BLAST search of IBB2_PEA 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:	40
Mass values matched:	5

Protein sequence coverage: 39%

Matched peptides shown in ***bold red***.

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  1 MELMNKKVMM KLALMVFLLS FAANVVNARF DSTSFITQVL SNGDDVKSAC
 51 CDTCLCTKSD PPTCRCVDVG ETCHSACDSC ICALSYPPQC QCFDTHKFCY
101 KACHNSEVEE VIKN
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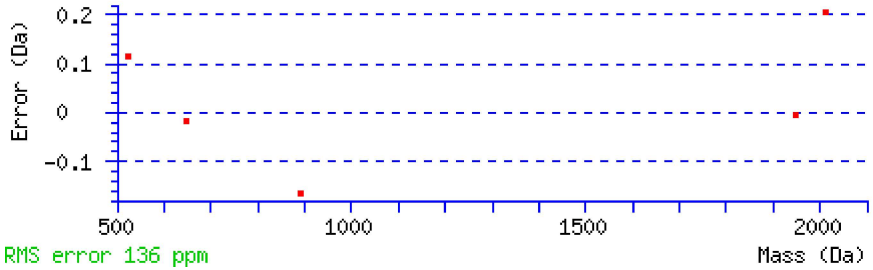
Unformatted sequence string: **114 residues** (for pasting into other applications).

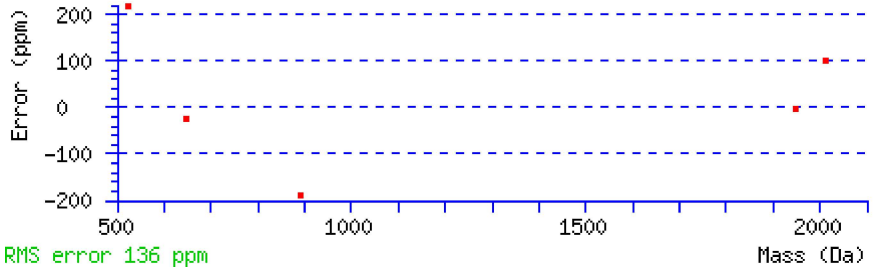
Sort by ◉ residue number ○ increasing mass ○ decreasing mass
Show ◉ matched peptides only ○ predicted peptides also

Start – End	Observed	Mr(expt)	Mr(calc)	Delta	M	Peptide
1 – 7	893.2910	892.2837	892.4510	-0.1673	1	-.MELMNKK.V
2 – 6	650.3020	649.2947	649.3105	-0.0158	0	M.ELMNK.K + Oxidation (M)

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	M	Peptide
8 - 11	524.3710	523.3637	523.2498	0.1139	0	K.VMMK.L + Oxidation (M)
12 - 29	1949.0990	1948.0917	1948.0968	-0.0051	0	K.LALMVFLLSFAANVVNAR.F
98 - 113	2013.1250	2012.1177	2011.9132	0.2046	1	K.FCYKACHNSEVEEVIK.N

No match to: 500.2270, 525.3940, 526.4190, 543.3950, 550.3880, 568.4010, 587.3800, 666.2730, 725.5920, 767.6570, 842.7660, 855.3180, 861.3420, 877.3180, 1325.8090, 1390.8800, 1413.0090, 1428.9940, 1520.1900, 1547.0140, 1688.4190, 1762.3910, 1804.0550, 1950.2320, 1958.7720, 1960.6960, 1980.4220, 1997.1140, 1999.1070, 2000.4750, 2029.1230, 2239.6140, 2384.2290, 2564.4880, 2807.6450



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ID   IBB2_PEA                Reviewed;         114 AA.
AC   Q41066;
DT   15-JUL-1999, integrated into UniProtKB/Swiss-Prot.
DT   01-NOV-1996, sequence version 1.
DT   12-SEP-2018, entry version 74.
DE   RecName: Full=Seed trypsin/chymotrypsin inhibitor TI5-72;
DE   Flags: Precursor;
GN   Name=TI572;
OS   Pisum sativum (Garden pea).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; Gunneridae;
OC   Pentapetalae; rosids; fabids; Fabales; Fabaceae; Papilionoideae;
OC   50 kb inversion clade; NPAAA clade; Hologalegina; IRL clade; Fabeae;
OC   Pisum.
OX   NCBI_TaxID=3888;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RC   STRAIN=cv. Birte;
RX   PubMed=7875292; DOI=10.1016/0014-5793(95)00070-P;
RA   Domoney C., Welham T., Sidebottom C., Firmin J.-L.;
RT   "Multiple isoforms of Pisum trypsin inhibitors result from
RT   modification of two primary gene products.";
RL   FEBS Lett. 360:15-20(1995).
CC   -!- FUNCTION: Inhibitor of trypsin and of chymotrypsin. May function
CC       as a natural phytochemical defense against predators.
CC   -!- TISSUE SPECIFICITY: Seed.
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CC   -!- SIMILARITY: Belongs to the Bowman-Birk serine protease inhibitor
CC       family. {ECO:0000305}.
DR   EMBL; X83210; CAA58212.1; -; mRNA.
DR   PIR; S69006; S69006.
DR   ProteinModelPortal; Q41066; -.
DR   SMR; Q41066; -.
DR   MEROPS; I12.018; -.
DR   GO; GO:0005576; C:extracellular region; IEA:InterPro.
DR   GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA:UniProtKB-KW.
DR   CDD; cd00023; BBI; 1.
DR   InterPro; IPR035995; Bowman-Birk_prot_inh.
DR   InterPro; IPR000877; Prot_inh_BBI.
DR   Pfam; PF00228; Bowman-Birk_leg; 2.
DR   SMART; SM00269; BowB; 1.
DR   SUPFAM; SSF57247; SSF57247; 1.
DR   PROSITE; PS00281; BOWMAN_BIRK; 1.
PE   2: Evidence at transcript level;
KW   Disulfide bond; Protease inhibitor; Serine protease inhibitor; Signal.
FT   SIGNAL        1     28       {ECO:0000255}.
FT   PROPEP       29     42       {ECO:0000255}.
FT                                /FTId=PRO_0000003278.
FT   CHAIN        43    114       Seed trypsin/chymotrypsin inhibitor TI5-
FT                                72.
FT                                /FTId=PRO_0000003279.
FT   SITE         58     59       Reactive bond for trypsin. {ECO:0000250}.
FT   SITE         84     85       Reactive bond for chymotrypsin.
FT                                {ECO:0000250}.
FT   DISULFID     50    103       {ECO:0000250|UniProtKB:P80321}.
FT   DISULFID     51     66       {ECO:0000250|UniProtKB:P80321}.
FT   DISULFID     54     99       {ECO:0000250|UniProtKB:P80321}.
FT   DISULFID     56     64       {ECO:0000250|UniProtKB:P80321}.
FT   DISULFID     73     80       {ECO:0000250|UniProtKB:P80321}.
FT   DISULFID     77     92       {ECO:0000250|UniProtKB:P80321}.
FT   DISULFID     82     90       {ECO:0000250|UniProtKB:P80321}.
SQ   SEQUENCE   114 AA;  12598 MW;  B60FC0768E8AB2A3 CRC64;
     MELMNKKVMM KLALMVFLLS FAANVVNARF DSTSFITQVL SNGDDVKSAC CDTCLCTKSD
     PPTCRCVDVG ETCHSACDSC ICALSYPPQC QCFDTHKFCY KACHNSEVEE VIKN
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Mascot: http://www.matrixscience.com/