

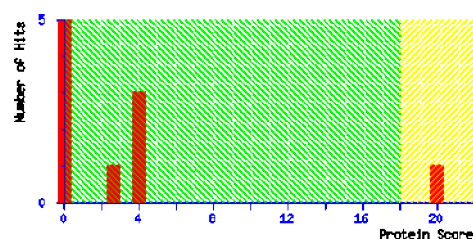
# Mascot Search Results

User : Monica Kannan  
 Email : monica\_kannan2001@yahoo.co.in  
 Search title :  
 MS data file : DATA.TXT  
 Database : SwissProt 57.15 (515203 sequences; 181334896 residues)  
 Taxonomy : Other green plants (16973 sequences)  
 Timestamp : 31 Dec 2019 at 06:44:11 GMT  
 Protein hits :
 

- [IBB1 ARAHY](#) Bowman-Birk type proteinase inhibitor A-II OS=Arachis hypogaea PE=1 SV=1
- [RPOB PINKO](#) DNA-directed RNA polymerase subunit beta OS=Pinus koraiensis GN=rpoB PE=3 SV=1
- [NU5C NEPOL](#) NAD(P)H-quinone oxidoreductase subunit 5, chloroplastic OS=Nephroselmis olivacea GN=ndhF PE=3 SV=1
- [RPOB HELSJ](#) DNA-directed RNA polymerase subunit beta OS=Helicosporidium sp. subsp. Simulium jonesii GN=rpoB PE=3 SV=1
- [DRTS SOYBN](#) Bifunctional dihydrofolate reductase-thymidylate synthase OS=Glycine max PE=1 SV=1
- [NU2C1 ANGEV](#) NAD(P)H-quinone oxidoreductase subunit 2 A, chloroplastic OS=Angiopteris evecta GN=ndhB1 PE=3 SV=1
- [MBB1 CHLRE](#) PsbB mRNA maturation factor Mbb1, chloroplastic OS=Chlamydomonas reinhardtii GN=MBB1 PE=2 SV=1
- [LEC1 DOLBI](#) Seed lectin subunit I OS=Dolichos biflorus PE=1 SV=2
- [DYHG CHLRE](#) Dynein gamma chain, flagellar outer arm OS=Chlamydomonas reinhardtii GN=ODA2 PE=1 SV=1
- [1433X MAIZE](#) 14-3-3-like protein (Fragment) OS=Zea mays PE=3 SV=1

## Mascot Score Histogram

Ions score is  $-10 \cdot \log(P)$ , where P is the probability that the observed match is a random event.  
 Individual ions scores > 18 indicate peptides with significant homology.  
 Individual ions scores > 24 indicate identity or extensive homology ( $p < 0.05$ ).  
 Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



## Peptide Summary Report

Format As Peptide Summary [Help](#)  
 Significance threshold  $p < 0.05$  Max. number of hits 10  
 Standard scoring ☒ MudPIT scoring ☐ Ions score or expect cut-off 0 Show sub-sets 0  
 Show pop-ups ☒ Suppress pop-ups ☐ Sort unassigned Decreasing Score ☒ Require bold red ☐

## Overview Table

Click on column header to jump to entry in results list.  
 Move mouse over any indicator to highlight identical peptides.  
 Click on an indicator to see details of individual match.  
 Use check boxes to select sub-set of queries for new search.

Mouse over: -Query-  
-Accession- -Sequence-

| Hit:                                                               | 1                                   | 2                                   | 3                                   | 4                                   | 5                                   | 6                                   | 7                                   | 8                                   | 9                                   | 10                                  |
|--------------------------------------------------------------------|-------------------------------------|-------------------------------------|-------------------------------------|-------------------------------------|-------------------------------------|-------------------------------------|-------------------------------------|-------------------------------------|-------------------------------------|-------------------------------------|
| <input checked="" type="checkbox"/> <a href="#">3313.8630</a> (1+) | <input checked="" type="checkbox"/> | <input checked="" type="checkbox"/> | <input checked="" type="checkbox"/> | <input checked="" type="checkbox"/> | <input checked="" type="checkbox"/> | <input checked="" type="checkbox"/> | <input checked="" type="checkbox"/> | <input checked="" type="checkbox"/> | <input checked="" type="checkbox"/> | <input checked="" type="checkbox"/> |

Select All ☐ Select None ☐ Search Selected ☐ Error tolerant ☐ Archive Report ☐

1. [IBB1 ARAHY](#) Mass: 8426 Score: 20 Matches: 1(0) Sequences: 1(0)

Bowman-Birk type proteinase inhibitor A-II OS=Arachis hypogaea PE=1 SV=1

☐ Check to include this hit in error tolerant search or archive report

| Query             | Observed  | Mr(expt)  | Mr(calc)  | ppm  | Miss | Score | Expect | Rank | Unique | Peptide                          |
|-------------------|-----------|-----------|-----------|------|------|-------|--------|------|--------|----------------------------------|
| <a href="#">1</a> | 3313.8630 | 3312.8557 | 3308.2913 | 1380 | 0    | 20    | 0.13   | 1    | U      | R.APPYFECVCVDTFDHCPASCNSVCVCTR.S |

2. [RPOB PINKO](#) Score: 5 Matches: 1(0) Sequences: 1(0)

DNA-directed RNA polymerase subunit beta OS=Pinus koraiensis GN=rpoB PE=3 SV=1

☐ Check to include this hit in error tolerant search or archive report

| Query             | Observed  | Mr(expt)  | Mr(calc)  | ppm      | Miss | Score | Expect | Rank | Unique | Peptide                           |
|-------------------|-----------|-----------|-----------|----------|------|-------|--------|------|--------|-----------------------------------|
| <a href="#">1</a> | 3313.8630 | 3312.8557 | 3316.5902 | -1125.99 | 0    | 5     | 4.4    | 2    | U      | K.NTFQDFFGSHPLSQFLDQTNPLTEIAHGR.K |

Proteins matching the same set of peptides:

[RPOB PINTH](#) Score: 5 Matches: 1(0) Sequences: 1(0)

3. [NU5C NEPOL](#) Mass: 71741 Score: 4 Matches: 1(0) Sequences: 1(0)

NAD(P)H-quinone oxidoreductase subunit 5, chloroplastic OS=Nephroselmis olivacea GN=ndhF PE=3 SV=1

☐ Check to include this hit in error tolerant search or archive report

| Query             | Observed  | Mr(expt)  | Mr(calc)  | ppm | Miss | Score | Expect | Rank | Unique | Peptide                              |
|-------------------|-----------|-----------|-----------|-----|------|-------|--------|------|--------|--------------------------------------|
| <a href="#">1</a> | 3313.8630 | 3312.8557 | 3309.8536 | 907 | 0    | 4     | 4.7    | 3    | U      | R.LHGALAIGAMALSFVVSLGVLWNQLHGIAFVR.W |

4. [RPOB\\_HELISJ](#) Score: 3 Matches: 1(0) Sequences: 1(0)  
DNA-directed RNA polymerase subunit beta OS=Helicospiridium sp. subsp. Simulium jonesii GN=rpoB PE=3 SV=1  
☐ Check to include this hit in error tolerant search or archive report

| Query             | Observed  | Mr(expt)  | Mr(calc)  | ppm      | Miss | Score | Expect | Rank | Unique | Peptide                                                    |
|-------------------|-----------|-----------|-----------|----------|------|-------|--------|------|--------|------------------------------------------------------------|
| <a href="#">1</a> | 3313.8630 | 3312.8557 | 3316.6550 | -1145.52 | 0    | 3     | 5.8    | 4    | U      | K.ISFQSLSPYH <b>M</b> ISLATSLIPFLEHNDANR.A + Oxidation (M) |

5. [DRTS\\_SOYBN](#) Score: 2 Matches: 1(0) Sequences: 1(0)  
Bifunctional dihydrofolate reductase-thymidylate synthase OS=Glycine max PE=1 SV=1  
☐ Check to include this hit in error tolerant search or archive report

| Query             | Observed  | Mr(expt)  | Mr(calc)  | ppm      | Miss | Score | Expect | Rank | Unique | Peptide                                                             |
|-------------------|-----------|-----------|-----------|----------|------|-------|--------|------|--------|---------------------------------------------------------------------|
| <a href="#">1</a> | 3313.8630 | 3312.8557 | 3316.4749 | -1091.26 | 0    | 2     | 7.4    | 6    | U      | K.LMALPPCH <b>M</b> FQAQFYVAHGLSCQ <b>M</b> YQR.S + 2 Oxidation (M) |

6. [NU2C1\\_ANGEV](#) Score: 1 Matches: 1(0) Sequences: 1(0)  
NAD(P)H-quinone oxidoreductase subunit 2 A, chloroplastic OS=Angiopteris evecta GN=ndhB1 PE=3 SV=1  
☐ Check to include this hit in error tolerant search or archive report

| Query             | Observed  | Mr(expt)  | Mr(calc)  | ppm | Miss | Score | Expect | Rank | Unique | Peptide                                                     |
|-------------------|-----------|-----------|-----------|-----|------|-------|--------|------|--------|-------------------------------------------------------------|
| <a href="#">1</a> | 3313.8630 | 3312.8557 | 3309.7216 | 947 | 0    | 1     | 11     | 8    | U      | R.IVNGLLTTQ <b>M</b> YNSTGMFISMIFLLVGVGFK.L + Oxidation (M) |

Proteins matching the same set of peptides:

| <a href="#">NU2C2_ANGEV</a> | Score: 1 | Matches: 1(0) | Sequences: 1(0) |
|-----------------------------|----------|---------------|-----------------|
|-----------------------------|----------|---------------|-----------------|

7. [MBB1\\_CHLRE](#) Score: 1 Matches: 1(0) Sequences: 1(0)  
PsbB mRNA maturation factor Mbb1, chloroplastic OS=Chlamydomonas reinhardtii GN=MBB1 PE=2 SV=1  
☐ Check to include this hit in error tolerant search or archive report

| Query             | Observed  | Mr(expt)  | Mr(calc)  | ppm  | Miss | Score | Expect | Rank | Unique | Peptide                               |
|-------------------|-----------|-----------|-----------|------|------|-------|--------|------|--------|---------------------------------------|
| <a href="#">1</a> | 3313.8630 | 3312.8557 | 3312.6110 | 73.9 | 0    | 1     | 11     | 9    | U      | R.LVESNDLSALPDFLSSDDDDVEASLRPPGAAGR.R |

8. [LEC1\\_DOLBI](#) Mass: 29388 Score: 0 Matches: 1(0) Sequences: 1(0)  
Seed lectin subunit I OS=Dolichos biflorus PE=1 SV=2  
☐ Check to include this hit in error tolerant search or archive report

| Query             | Observed  | Mr(expt)  | Mr(calc)  | ppm     | Miss | Score | Expect | Rank | Unique | Peptide |                                   |
|-------------------|-----------|-----------|-----------|---------|------|-------|--------|------|--------|---------|-----------------------------------|
| <a href="#">1</a> | 3313.8630 | 3312.8557 | 3315.7788 | -881.58 | 0    | 0     |        | 13   | 10     | U       | -MASSTVSVVLSLFLLLLQANSANIQSFSFK.N |

9. [DYHG\\_CHLRE](#) Score: 0 Matches: 1(0) Sequences: 1(0)  
Dynein gamma chain, flagellar outer arm OS=Chlamydomonas reinhardtii GN=ODA2 PE=1 SV=1  
☐ Check to include this hit in error tolerant search or archive report

| Query             | Observed  | Mr(expt)  | Mr(calc)  | ppm  | Miss | Score | Expect | Rank | Unique | Peptide                                                    |
|-------------------|-----------|-----------|-----------|------|------|-------|--------|------|--------|------------------------------------------------------------|
| <a href="#">1</a> | 3313.8630 | 3312.8557 | 3309.5257 | 1006 | 0    | 2     | 7.5    | 7    | U      | K.QMCIEFVDDIS <b>M</b> YPYINewGHQVTNEIVR.Q + Oxidation (M) |

10. [1433X\\_MAIZE](#) Mass: 6812 Score: 0 Matches: 1(0) Sequences: 1(0)  
14-3-3-like protein (Fragment) OS=Zea mays PE=3 SV=1  
☐ Check to include this hit in error tolerant search or archive report

| Query             | Observed  | Mr(expt)  | Mr(calc)  | ppm     | Miss | Score | Expect | Rank | Unique | Peptide                                                    |
|-------------------|-----------|-----------|-----------|---------|------|-------|--------|------|--------|------------------------------------------------------------|
| <a href="#">1</a> | 3313.8630 | 3312.8557 | 3315.5340 | -807.81 | 0    | 3     | 6.5    | 5    | U      | K.DSTLI <b>M</b> QLLYDNLTLWTSDTNEDGGDEIK.- + Oxidation (M) |

## Search Parameters

Type of search : MS/MS Ion Search  
 Enzyme : Trypsin  
 Fixed modifications : [Carbamidomethyl \(C\)](#)  
 Variable modifications : [Oxidation \(M\)](#)  
 Mass values : Monoisotopic  
 Protein Mass : Unrestricted  
 Peptide Mass Tolerance :  $\pm 1379.9$  ppm  
 Fragment Mass Tolerance :  $\pm 1.2$  Da  
 Max Missed Cleavages : 0  
 Instrument type : MALDI-TOF-TOF  
 Number of queries : 1

Mascot: <http://www.matrixscience.com/>

# Mascot Search Results

## Protein View

Match to: **IBB1\_ARAHY** Score: **20**

**Bowman-Birk type proteinase inhibitor A-II** OS=Arachis hypogaea PE=1 SV=1  
Found in search of DATA.TXT

Nominal mass ( $M_r$ ): **8426**; Calculated pI value: **5.08**

NCBI BLAST search of [IBB1\\_ARAHY](#) against nr

Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Arachis hypogaea](#)

Fixed modifications: Carbamidomethyl (C)

Variable modifications: Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P

Sequence Coverage: **38%**

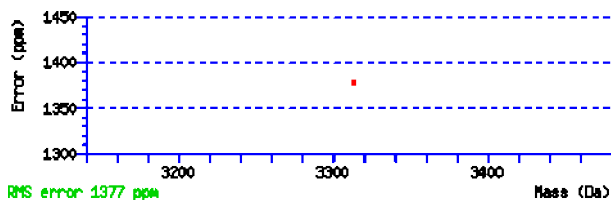
Matched peptides shown in **Bold Red**

**1** EASSSSDDNV CCNGCLCDRR **APPYFECVCV DTFDHCPCASC NSCVCTR**SNP  
**51** PQCRCTDKTQ GRCPVTECRS

Show predicted peptides also

Sort Peptides By ☒ Residue Number ☐ Increasing Mass ☐ Decreasing Mass

| Start - End    | Observed         | Mr (expt)        | Mr (calc)        | ppm         | Miss     | Sequence                                                                  |
|----------------|------------------|------------------|------------------|-------------|----------|---------------------------------------------------------------------------|
| <b>21 - 47</b> | <b>3313.8630</b> | <b>3312.8557</b> | <b>3308.2913</b> | <b>1380</b> | <b>0</b> | <b>R.APPYFECVCVDTFDHCPCASCNSCVCTR.S</b> ( <a href="#">Ions score 20</a> ) |



ID IBB1\_ARAHY Reviewed; 70 AA.  
AC P01066;  
DT 21-JUL-1986, integrated into UniProtKB/Swiss-Prot.  
DT 21-JUL-1986, sequence version 1.  
DT 02-MAR-2010, entry version 58.  
DE RecName: Full=Bowman-Birk type proteinase inhibitor A-II;  
DE Contains:  
DE RecName: Full=Bowman-Birk type proteinase inhibitor A-I;  
DE Contains:  
DE RecName: Full=Bowman-Birk type proteinase inhibitor B-I;  
DE Contains:  
DE RecName: Full=Bowman-Birk type proteinase inhibitor B-III;  
OS Arachis hypogaea (Peanut).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
OC rosids; fabids; Fabales; Fabaceae; Papilionoideae; Dalbergieae;  
OC Arachis.  
OX NCBI\_TaxID=3818;  
RN [1]  
RP PROTEIN SEQUENCE OF 1-19.  
RX MEDLINE=84032360; PubMed=6630176;  
RA Norioka S., Ikenaka T.;  
RT "Amino acid sequences of trypsin-chymotrypsin inhibitors (A-I, A-II,  
RT B-I, and B-II) from peanut (Arachis hypogaea): a discussion on the  
RT molecular evolution of legume Bowman-Birk type inhibitors.";  
RL J. Biochem. 94:589-599(1983).  
RN [2]  
RP PROTEIN SEQUENCE OF 10-70.  
RX MEDLINE=83186120; PubMed=6841347;  
RA Norioka S., Ikenaka T.;  
RT "Amino acid sequence of a trypsin-chymotrypsin inhibitor, B-III, of  
RT peanut (Arachis hypogaea).";  
RL J. Biochem. 93:479-485(1983).  
RN [3]  
RP X-RAY CRYSTALLOGRAPHY (3.3 ANGSTROMS).  
RX MEDLINE=87194702; PubMed=3571206;  
RA Suzuki A., Tsunogae Y., Tanaka I., Yamane T., Ashida T., Norioka S.,  
RA Hara S., Ikenaka T.;  
RT "The structure of Bowman-Birk type protease inhibitor A-II from peanut  
RT (Arachis hypogaea) at 3.3-A resolution.";  
RL J. Biochem. 101:267-274(1987).  
RN [4]  
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).  
RX MEDLINE=94076346; PubMed=8254669; DOI=10.1006/jmbi.1993.1622;

RA Suzuki A., Yamane T., Ashida T., Norioka S., Hara S., Ikenaka T.;  
RT "Crystallographic refinement of Bowman-Birk type protease inhibitor A-  
RT II from peanut (Arachis hypogaea) at 2.3-A resolution.";  
RL J. Mol. Biol. 234:722-734(1993).  
CC -!- FUNCTION: These proteins inhibit trypsin and chymotrypsin, having  
CC 2 sites of interaction with trypsin. The site of interaction with  
CC chymotrypsin has not been determined but is not independent of the  
CC trypsin-reactive sites.  
CC -!- MISCELLANEOUS: Four inhibitors were found that are identical  
CC except at their amino ends and that probably arise by proteolytic  
CC degradation of a single gene product.  
CC -!- SIMILARITY: Belongs to the Bowman-Birk serine protease inhibitor  
CC family.  
CC -----  
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
CC Distributed under the Creative Commons Attribution-NoDerivs License  
CC -----  
DR PIR; A91975; TINPA2.  
DR SMR; P01066; 9-60.  
DR MEROPS; I12.006; -.  
DR MEROPS; I12.017; -.  
DR GO; GO:0005576; C:extracellular region; IEA:InterPro.  
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA:UniProtKB-KW.  
DR InterPro; IPR000877; Prot\_inh\_BBI.  
DR Gene3D; G3DSA:2.10.69.10; Prot\_inh\_BBI; 1.  
DR Pfam; PF00228; Bowman-Birk\_leg; 1.  
DR SMART; SM00269; BowB; 1.  
DR SUPFAM; SSF57247; Prot\_inh\_BBI; 1.  
DR PROSITE; PS00281; BOWMAN\_BIRK; 1.  
PE 1: Evidence at protein level;  
KW Direct protein sequencing; Disulfide bond; Protease inhibitor;  
KW Serine protease inhibitor.  
FT CHAIN 1 70 Bowman-Birk type proteinase inhibitor A-  
FT II.  
FT /FTId=PRO\_0000003260.  
FT CHAIN 4 70 Bowman-Birk type proteinase inhibitor A-  
FT I.  
FT /FTId=PRO\_0000003261.  
FT CHAIN 8 70 Bowman-Birk type proteinase inhibitor B-  
FT I.  
FT /FTId=PRO\_0000003262.  
FT CHAIN 10 70 Bowman-Birk type proteinase inhibitor B-  
FT III.  
FT /FTId=PRO\_0000003263.  
FT SITE 19 20 Reactive bond for trypsin.  
FT SITE 47 48 Reactive bond for trypsin.  
FT DISULFID 11 68  
FT DISULFID 12 29  
FT DISULFID 15 63  
FT DISULFID 17 27  
FT DISULFID 36 43  
FT DISULFID 40 55  
FT DISULFID 45 53  
SQ SEQUENCE 70 AA; 7633 MW; 56CE31B690015CD5 CRC64;  
EASSSSDDNV CCNGCLCDRR APPYFECVCV DTFDHCPASC NSCVCTRSNP PQCRCTDKTQ  
GRCPVTECRS

Mascot: <http://www.matrixscience.com/>