MASCOT Search Results

Protein View: IP21_SOLTU

Proteinase inhibitor PTI OS=Solanum tuberosum OX=4113 PE=1 SV=1

Database: SwissProt
Score: 50
Expect: 0.43
Monoisotopic mass (M_r): 6055
Calculated pI: 8.19
Taxonomy: Solanum tuberosum

Sequence similarity is available as an NCBI BLAST search of IP21_SOLTU 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: 54
Mass values matched: 4

Protein sequence coverage: 94%

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

```
 1 RICTNCCAGY KGCNYYSANG AFICEGESDP KNPNVCPRNC DTNIAYSKCL
51 R
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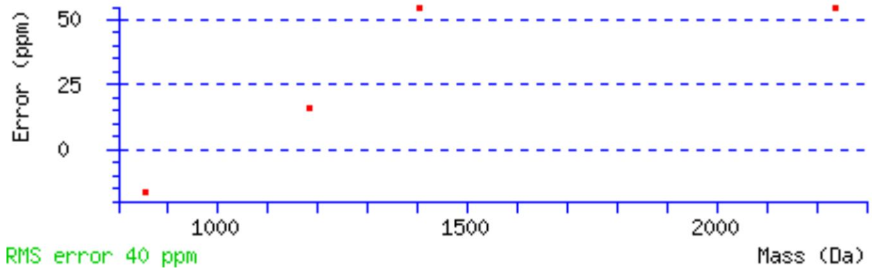
Unformatted sequence string: 51 residues (for pasting into other applications).

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

Start – End	Observed	Mr(expt)	Mr(calc)	ppm	M	Peptide
1 – 11	1402.6790	1401.6717	1401.5952	54.6	1	-.RICTNCCAGYK.G
12 – 31	2239.0290	2238.0217	2237.8994	54.7	0	K.GCNYYSANGAFICEGESDPK.N
32 – 38	856.3950	855.3877	855.4021	-16.8	0	K.NPNVCPR.N
39 – 48	1185.5390	1184.5317	1184.5132	15.7	0	R.NCDTNIAYSK.C

No match to: 532.9310, 536.4780, 614.1060, 625.0920, 647.0950, 663.0940, 685.2030, 698.8030, 714.7960, 777.2940, 842.3720, 870.4010, 871.3630, 877.2880, 894.3150, 935.3750, 961.4960, 1113.6060, 1159.5170, 1175.5160, 1181.5100, 1191.5170, 1216.5490, 1233.5570, 1248.6430, 1251.5580, 1265.5790, 1271.7130, 1293.6520, 1331.6200, 1388.6640, 1404.6570, 1429.7150, 1940.8990, 2230.0840, 2263.0030, 2277.9930, 2303.9630, 2320.9050, 2334.9720, 2342.8430, 2563.9670, 2662.0680, 2690.9960, 2806.9820, 2824.9680, 2914.1110, 3136.0140, 3347.0280, 5571.9170



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ID   IP21_SOLTU              Reviewed;          51 AA.
AC   P01079;
DT   21-JUL-1986, integrated into UniProtKB/Swiss-Prot.
DT   21-JUL-1986, sequence version 1.
DT   31-JUL-2019, entry version 69.
DE   RecName: Full=Proteinase inhibitor PTI;
OS   Solanum tuberosum (Potato).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliopsida; eudicotyledons; Gunneridae;
OC   Pentapetalae; asterids; lamiids; Solanales; Solanaceae; Solanoideae;
OC   Solaneae; Solanum.
OX   NCBI_TaxID=4113;
RN   [1]
RP   PROTEIN SEQUENCE.
RX   PubMed=7074039; DOI=10.1021/bi00533a027;
RA   Hass G.M., Hermodson M.A., Ryan C.A., Gentry L.;
RT   "Primary structures of two low molecular weight proteinase inhibitors
RT   from potatoes.";
RL   Biochemistry 21:752-756(1982).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the protease inhibitor I20 (potato type II
CC       proteinase inhibitor) family. {ECO:0000305}.
DR   PIR; A01318; XKPOT.
DR   SMR; P01079; -.
DR   PRIDE; P01079; -.
DR   Proteomes; UP000011115; Unassembled WGS sequence.
DR   ExpressionAtlas; P01079; baseline.
DR   GO; GO:0005576; C:extracellular region; IEA:UniProtKB-SubCell.
DR   GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA:UniProtKB-KW.
DR   InterPro; IPR003465; Prot_inh_I20.
DR   Pfam; PF02428; Prot_inhib_II; 1.
PE   1: Evidence at protein level;
KW   Complete proteome; Direct protein sequencing; Disulfide bond;
KW   Protease inhibitor; Reference proteome; Secreted;
KW   Serine protease inhibitor.
FT   CHAIN         1     51       Proteinase inhibitor PTI.
FT                                /FTId=PRO_0000217674.
FT   SITE         38     39       Reactive bond for trypsin. {ECO:0000250}.
FT   DISULFID      3     40       {ECO:0000250}.
FT   DISULFID      6     24       {ECO:0000250}.
FT   DISULFID      7     36       {ECO:0000250}.
FT   DISULFID     13     49       {ECO:0000250}.
SQ   SEQUENCE   51 AA;  5602 MW;  CE49F1BF60CD40F5 CRC64;
     RICTNCCAGY KGCNYYSANG AFICEGESDP KNPNVCPRNC DTNIAYSKCL R
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Mascot: http://www.matrixscience.com/