MATRIX SCIENCE MASCOT Search Results

Protein View: DNPEP_RICCO

Probable aspartyl aminopeptidase OS=Ricinus communis OX=3988 GN=RCOM_1506700 PE=2 SV=2

Database:	SwissProt
Score:	59
Expect:	0.047
Monoisotopic mass (M_r):	54329
Calculated pI:	6.36
Taxonomy:	**Ricinus communis**

Sequence similarity is available as **an NCBI BLAST search of DNPEP_RICCO against nr**.

Search parameters

MS data file:	`SPOT_83.mgf`
Enzyme:	Trypsin: cuts C-term side of KR unless next residue is P.
Fixed modifications:	**Carbamidomethyl (C)**
Variable modifications:	**Oxidation (M)**

Protein sequence coverage: 24%

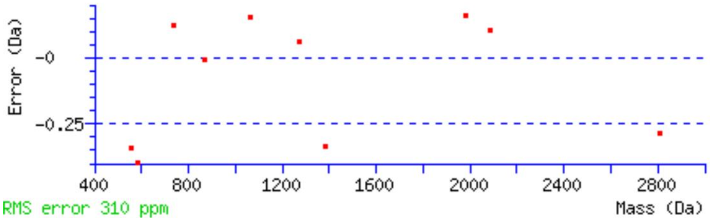
Matched peptides shown in ***bold red***.

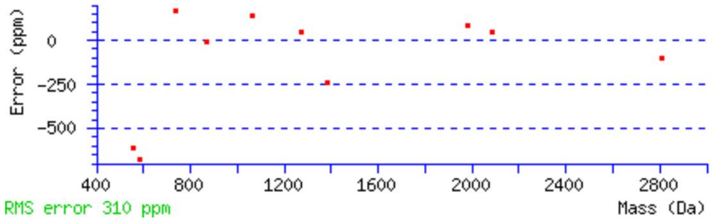
1 MAKQDSQTEG ISIDSDLINF LNASPTAFHA IDEAKKRLKH SGYVQVSERD
51 DWK**LELGK**RY FFTR**NHSTIV** **AFAIGKKYVA** **GNGFYVVGAH** **TDSPCIKLKP**
101 **VSK**VTKSGYL EVGVQPYGGG LWHTWFDRDL AVAGRVIVRE EKHGSVSYSH
151 R**LVRIEEPIM** **R**VPTLAIHLD RNVNTDGFKV NTQSHLLPVL ATSVKAELSK
201 VVAENGTVGN DEETDGMKSS KGTTNANSKH HSLLLQMIAG QIGCNGSDIC
251 DFELQACDTQ PSVIAGAAKE FIFSGRLDNL CMSFCSLK**AL** **IDATASDSHL**
301 **ENESGVR**MVA LFDHEEVGSD SAQGAGSPVM FDALSRITST FNSDSKLLR**K**
351 **AIQKSFLVSA** **DMAHALHPNY** **ADK**HEENHQP R**MHGGLVIKH** **NANQR**YATNS
401 VTSFLFKEIA SKHNLPVQDF VVRNDMPCGS TIGPILASGV GIRTVDVGAP
451 QLSMHSIR**EM** **CAVDDVK**YSY EHFKAFFEDF SHLDSKITVD M

Unformatted sequence string: **491 residues** (for pasting into other applications).

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

Query	Start – End	Observed	Mr(expt)	Mr(calc)	Delta	M	Score	Peptide
6	54 – 58	559.0026	557.9954	558.3377	-0.3423	0		K.LELGK.R
39	65 – 77	1385.4536	1384.4463	1384.7827	-0.3363	1		R.NHSTIVAFAIGKK.Y
48	78 – 103	2807.1724	2806.1651	2806.4476	-0.2825	1		K.YVAGNGFYVVGAHTDSPCIKLKPVSK.V
35	152 – 161	1271.7750	1270.7677	1270.7067	0.0610	1		R.LVRIEEPIMR.V + Oxidation (M)
44	289 – 307	1985.1175	1984.1102	1983.9497	0.1605	0		K.ALIDATASDSHLENESGVR.M
10	350 – 354	586.9919	585.9846	586.3802	-0.3956	1		R.KAIQK.S
45	355 – 373	2087.1030	2086.0958	2085.9942	0.1016	0		K.SFLVSADMAHALHPNYADK.H
22	382 – 389	870.4819	869.4746	869.4793	-0.0047	0		R.MHGGLVIK.H + Oxidation (M)
19	390 – 395	739.4839	738.4766	738.3521	0.1245	0		K.HNANQR.Y
28	459 – 467	1066.6064	1065.5991	1065.4471	0.1520	0		R.EMCAVDDVK.Y





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ID   DNPEP_RICCO             Reviewed;         491 AA.
AC   B9RAJ0;
DT   18-APR-2012, integrated into UniProtKB/Swiss-Prot.
DT   18-APR-2012, sequence version 2.
DT   31-JUL-2019, entry version 43.
DE   RecName: Full=Probable aspartyl aminopeptidase;
DE            EC=3.4.11.21;
GN   ORFNames=RCOM_1506700;
OS   Ricinus communis (Castor bean).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliopsida; eudicotyledons; Gunneridae;
OC   Pentapetalae; rosids; fabids; Malpighiales; Euphorbiaceae;
OC   Acalyphoideae; Acalypheae; Ricinus.
OX   NCBI_TaxID=3988;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=cv. Hale;
RX   PubMed=20729833; DOI=10.1038/nbt.1674;
RA   Chan A.P., Crabtree J., Zhao Q., Lorenzi H., Orvis J., Puiu D.,
RA   Melake-Berhan A., Jones K.M., Redman J., Chen G., Cahoon E.B.,
RA   Gedil M., Stanke M., Haas B.J., Wortman J.R., Fraser-Liggett C.M.,
RA   Ravel J., Rabinowicz P.D.;
RT   "Draft genome sequence of the oilseed species Ricinus communis.";
RL   Nat. Biotechnol. 28:951-956(2010).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 1-283.
RX   PubMed=17672910; DOI=10.1186/1471-2229-7-42;
RA   Lu C., Wallis J.G., Browse J.;
RT   "An analysis of expressed sequence tags of developing castor endosperm
RT   using a full-length cDNA library.";
RL   BMC Plant Biol. 7:42-42(2007).
RN   [3]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 36-302.
RA   Kroon J.T., Kunst L., Slabas A.R., Smith M.A.;
RT   "Genomic Resources for Castor Bean (Ricinus communis); Generation of a
RT   normalized cDNA library from developing castor seed and sequencing of
RT   Expressed Sequence Tags.";
RL   Submitted (NOV-2008) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Likely to play an important role in intracellular
CC       protein and peptide metabolism. {ECO:0000250}.
CC   -!- CATALYTIC ACTIVITY:
CC       Reaction=Release of an N-terminal aspartate or glutamate from a
CC         peptide, with a preference for aspartate.; EC=3.4.11.21;
CC   -!- COFACTOR:
CC       Name=Zn(2+); Xref=ChEBI:CHEBI:29105; Evidence={ECO:0000250};
CC       Note=Binds 2 Zn(2+) ions per subunit. {ECO:0000250};
CC   -!- SUBUNIT: Tetrahedron-shaped homododecamer built from six
CC       homodimers. {ECO:0000250}.
CC   -!- SUBCELLULAR LOCATION: Cytoplasm {ECO:0000250}.
CC   -!- SIMILARITY: Belongs to the peptidase M18 family. {ECO:0000305}.
CC   -!- SEQUENCE CAUTION:
CC       Sequence=EEF51817.1; Type=Erroneous gene model prediction; Evidence={ECO:0000305};
CC       Sequence=EV523896; Type=Frameshift; Positions=271; Evidence={ECO:0000305};
DR   EMBL; EQ973773; EEF51817.1; ALT_SEQ; Genomic_DNA.
DR   EMBL; EV523896; -; NOT_ANNOTATED_CDS; mRNA.
DR   EMBL; GE636502; -; NOT_ANNOTATED_CDS; mRNA.
DR   SMR; B9RAJ0; -.
DR   MEROPS; M18.A01; -.
DR   InParanoid; B9RAJ0; -.
DR   Proteomes; UP000008311; Unassembled WGS sequence.
DR   GO; GO:0005737; C:cytoplasm; IEA:UniProtKB-SubCell.
DR   GO; GO:0004177; F:aminopeptidase activity; IEA:UniProtKB-KW.
DR   GO; GO:0008237; F:metallopeptidase activity; IEA:UniProtKB-KW.
DR   GO; GO:0008270; F:zinc ion binding; IEA:InterPro.
DR   Gene3D; 2.30.250.10; -; 1.
DR   InterPro; IPR001948; Peptidase_M18.
DR   InterPro; IPR023358; Peptidase_M18_dom2.
DR   PANTHER; PTHR28570; PTHR28570; 1.
DR   Pfam; PF02127; Peptidase_M18; 1.
DR   PRINTS; PR00932; AMINO1PTASE.
PE   2: Evidence at transcript level;
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KW   Aminopeptidase; Complete proteome; Cytoplasm; Hydrolase;
KW   Metal-binding; Metalloprotease; Protease; Reference proteome; Zinc.
FT   CHAIN         1    491       Probable aspartyl aminopeptidase.
FT                                /FTId=PRO_0000416986.
FT   METAL        90     90       Zinc 1. {ECO:0000250}.
FT   METAL       278    278       Zinc 1. {ECO:0000250}.
FT   METAL       278    278       Zinc 2. {ECO:0000250}.
FT   METAL       316    316       Zinc 2. {ECO:0000250}.
FT   METAL       361    361       Zinc 1. {ECO:0000250}.
FT   METAL       455    455       Zinc 2. {ECO:0000250}.
FT   BINDING     168    168       Substrate. {ECO:0000250}.
FT   BINDING     315    315       Substrate. {ECO:0000250}.
FT   BINDING     361    361       Substrate. {ECO:0000250}.
FT   BINDING     364    364       Substrate. {ECO:0000250}.
FT   BINDING     389    389       Substrate. {ECO:0000250}.
FT   BINDING     396    396       Substrate. {ECO:0000250}.
SQ   SEQUENCE   491 AA;  53907 MW;  F50A244121BA1A8F CRC64;
     MAKQDSQTEG ISIDSDLINF LNASPTAFHA IDEAKKRLKH SGYVQVSERD DWKLELGKRY
     FFTRNHSTIV AFAIGKKYVA GNGFYVVGAH TDSPCIKLKP VSKVTKSGYL EVGVQPYGGG
     LWHTWFDRDL AVAGRVIVRE EKHGSVSYSH RLVRIEEPIM RVPTLAIHLD RNVNTDGFKV
     NTQSHLLPVL ATSVKAELSK VVAENGTVGN DEETDGMKSS KGTTNANSKH HSLLLQMIAG
     QIGCNGSDIC DFELQACDTQ PSVIAGAAKE FIFSGRLDNL CMSFCSLKAL IDATASDSHL
     ENESGVRMVA LFDHEEVGSD SAQGAGSPVM FDALSRITST FNSDSKLLRK AIQKSFLVSA
     DMAHALHPNY ADKHEENHQP RMHGGLVIKH NANQRYATNS VTSFLFKEIA SKHNLPVQDF
     VVRNDMPCGS TIGPILASGV GIRTVDVGAP QLSMHSIREM CAVDDVKYSY EHFKAFFEDF
     SHLDSKITVD M
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