MATRIX SCIENCE MASCOT Search Results

Protein View: XP_013672706.1

iron-sulfur protein NUBPL-like isoform X1 [Brassica napus]

Database:	NCBIprot
Score:	78
Expect:	0.12
Monoisotopic mass (M_r):	41234
Calculated pI:	9.32
Taxonomy:	Brassica napus

Sequence similarity is available as an NCBI BLAST search of XP_013672706.1 against nr.

Search parameters

MS data file:	SPOT_70.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: 42%

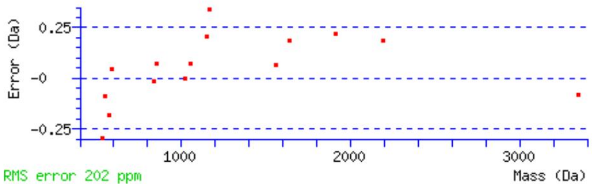
Matched peptides shown in ***bold red***.

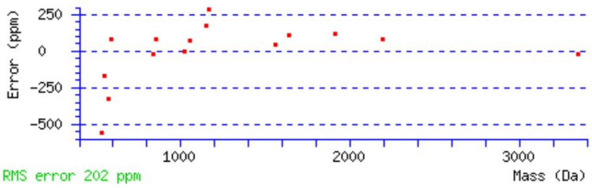
1 MAVSAQKQFS SNTKKKKEPH SEK**ANKCVAS** **SNIAAAPLR**I LRSNHDFKRH
51 RIELR**IDLSL** **SPMATAGLLR** SLRRR**ELHAA** **SVAWAYRFSS** **ASAGGR**TTEL
101 R**LDGVK**DIIA VASGKGGVGK SSTAVNLAVA LANKCELK**IG** **LLDADVYGPS**
151 **VPIMMNISQK** **PQVNQDMKMI** **PVENYGVKCM** **SMGLLVDKDA** **PLVWRGPMVM**
201 **SALAK**MTRGV DWGDLDVLVV DMPPGTGDAQ ITISQNLKLS GAVIVSTPQD
251 VALADANR**GI** **SMFDKVR**VPI LGLVENMSCF ICPHCNEASF IFGK**EGARRM**
301 **AAKK**GLKLIG EIPLEMKIR**E** **GSDEGVPVVV** **SSPGSVVSK**A YEDLAQNVVN
351 ALKELRDNPE NEIQMKLNVP HSSGSSYNKP

Unformatted sequence string: 380 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
58	24 – 39	1643.0543	1642.0471	1641.8620	0.1850	1		K.ANKCVASSNIAAAPLR.I
55	56 – 70	1557.9323	1556.9250	1556.8596	0.0654	0		R.IDLSLSPMATAGLLR.S
75	76 – 96	2194.2631	2193.2558	2193.0715	0.1843	1		R.ELHAASVAWAYRFSSASAGGR.T
22	88 – 96	839.3867	838.3795	838.3933	-0.0139	0		R.FSSASAGGR.T
1	102 – 106	531.0187	530.0115	530.3064	-0.2950	0		R.LDGVK.D
88	139 – 168	3349.5653	3348.5581	3348.6404	-0.0823	0		K.IGLLDADVYGPSVPIMMNISQKPQVNQDMK.M + 3 Oxidation (M)
45	169 – 178	1165.9293	1164.9220	1164.5849	0.3371	0		K.MIPVENYGVK.C + Oxidation (M)
43	179 – 188	1153.7477	1152.7404	1152.5341	0.2063	0		K.CMSMGLLVDK.D
24	189 – 195	856.5395	855.5322	855.4603	0.0719	0		K.DAPLVWR.G
33	196 – 205	1020.5173	1019.5100	1019.5144	-0.0044	0		R.GPMVMSALAK.M + Oxidation (M)
36	259 – 267	1052.6304	1051.6231	1051.5484	0.0746	1		R.GISMFDKVR.V
9	295 – 299	588.3689	587.3617	587.3139	0.0477	1		K.EGARR.M
6	299 – 303	576.1426	575.1353	575.3213	-0.1860	1		R.RMAAK.K
5	300 – 304	548.2305	547.2232	547.3152	-0.0919	1		R.MAAKK.G
66	320 – 339	1915.1863	1914.1790	1913.9582	0.2208	0		R.EGSDEGVPVVVSSPGSVVSK.A





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LOCUS       XP_013672706             380 aa            linear   PLN 04-OCT-2017
DEFINITION  iron-sulfur protein NUBPL-like isoform X1 [Brassica napus].
ACCESSION   XP_013672706
VERSION     XP_013672706.1
DBLINK      BioProject: PRJNA293435
DBSOURCE    REFSEQ: accession XM_013817252.2
KEYWORDS    RefSeq.
SOURCE      Brassica napus (rape)
  ORGANISM  Brassica napus
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; Gunneridae;
            Pentapetalae; rosids; malvids; Brassicales; Brassicaceae;
            Brassiceae; Brassica.
COMMENT     MODEL REFSEQ:  This record is predicted by automated computational
            analysis. This record is derived from a genomic sequence
            (NC_027770.2) annotated using gene prediction method: Gnomon,
            supported by EST evidence.
            Also see:
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                Documentation of NCBI's Annotation Process

            ##Genome-Annotation-Data-START##
            Annotation Provider         :: NCBI
            Annotation Status           :: Full annotation
            Annotation Version          :: Brassica napus Annotation Release
                                           101
            Annotation Pipeline         :: NCBI eukaryotic genome annotation
                                           pipeline
            Annotation Software Version :: 7.4
            Annotation Method           :: Best-placed RefSeq; Gnomon
            Features Annotated          :: Gene; mRNA; CDS; ncRNA
            ##Genome-Annotation-Data-END##
            COMPLETENESS: full length.
FEATURES             Location/Qualifiers
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                     /chromosome="C4"
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                     /db_xref="CDD:287566"
     Region          108..357
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                     /note="Cellulose biosynthesis protein BcsQ [Cell
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                     /note="Walker A motif"
                     /db_xref="CDD:238994"
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                     /db_xref="GeneID:106377090"
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Mascot: http://www.matrixscience.com/