



MASCOT Search Results

Protein View: XP_023922675.1

uncharacterized protein LOC112034124 [Quercus suber]

Database: NCBIprot
Score: 85
Expect: 0.023
Monoisotopic mass (M_r): 29476
Calculated pI: 9.04
Taxonomy: Quercus suber

This protein sequence matches the following other entries:

- POE97701.1 from Quercus suber

Sequence similarity is available as [an NCBI BLAST search of XP_023922675.1 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: 20
Mass values matched: 10

Protein sequence coverage: 44%

Matched peptides shown in **bold red**.

```

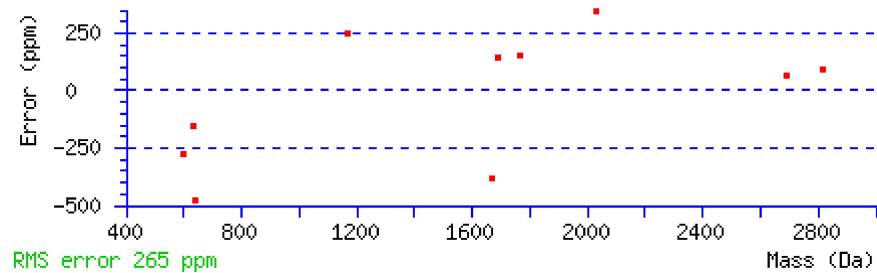
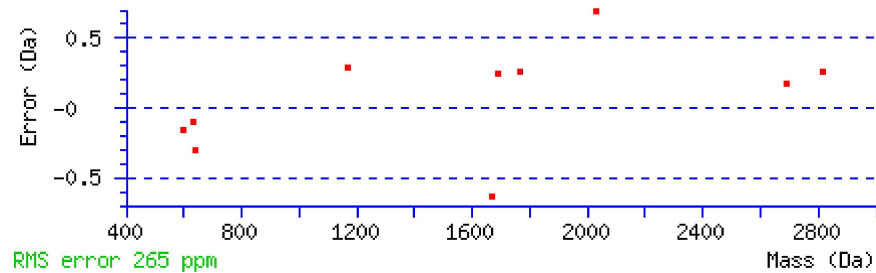
1  MLIQRPRPMI  GKLSELLVAG  NRAGFSDMVT  ISPRGPLELN  KLQSPRGLKN
51  YDLGGVGLGI  VAALEKSREG  CGREILAKYA  VATANLNRSS  PIPVDSSKST
101 STCGRYGNKG  CEELLQGDNC  EEDYTYVTCR  GQGKSITRVF  YEIDDCRTSG
151 QQRNGLQRCN  KRSTVTVKES  RPRYEEDFSA  YPTSIFLSSC  HLCSSKLLHGK
201 DIYMYRGEKA  FCSPECRSRQ  IMMDERKEQQ  CRSEAPRSAD  VSSSSYTRGQ
251 IFSTGIVAI
  
```

Unformatted sequence string: 259 residues (for pasting into other applications).

Sort by residue number increasing mass decreasing massShow matched peptides only predicted peptides also

Start - End	Observed	Mr(expt)	Mr(calc)	Delta M	Peptide
23 - 41	2032.7470	2031.7397	2031.0459	0.6938 1	R.AGFSDMVTISPRGPLELNK.L
42 - 46	600.1810	599.1737	599.3391	-0.1654 0	K.LQSPR.G
50 - 66	1689.1610	1688.1537	1687.9145	0.2392 0	K.NYDLGGVGLGIVAALK.S
89 - 105	1766.1040	1765.0967	1764.8312	0.2655 1	R.SSPIPVDSKSTSTCGR.Y
135 - 147	1673.1630	1672.1557	1672.7879	-0.6322 1	K.SITRVFYEIDDCR.T
163 - 168	634.2810	633.2737	633.3698	-0.0960 0	R.STVTVK.E
169 - 173	644.0400	643.0327	643.3401	-0.3074 0	K.ESRPR.Y
174 - 195	2691.3110	2690.3037	2690.1305	0.1732 0	R.YEEDFSAYPTSYFLSSCHLCSK.K
174 - 196	2819.4960	2818.4887	2818.2254	0.2633 1	R.YEEDFSAYPTSYFLSSCHLCSKK.L
218 - 226	1165.8390	1164.8317	1164.5379	0.2938 1	R.SRQIMMDEK.K

No match to: 650.0690, 666.0640, 1625.1730, 1683.1430, 1697.1850, 1708.1300, 1891.3770, 1994.4150, 2706.1150, 4066.2320



LOCUS XP_023922675 259 aa linear PLN 15-FEB-2018
 DEFINITION uncharacterized protein LOC112034124 [Quercus suber].
 ACCESSION XP_023922675
 VERSION XP_023922675.1
 DBLINK BioProject: PRJNA433227
 DBSOURCE REFSEQ: accession XM_024066907.1
 KEYWORDS RefSeq.
 SOURCE Quercus suber
 ORGANISM Quercus suber
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; Gunneridae;
 Pentapetalae; rosids; fabids; Fagales; Fagaceae; Quercus.
 COMMENT MODEL REFSEQ: This record is predicted by automated computational
 analysis. This record is derived from a genomic sequence
 (NW_019813743.1) annotated using gene prediction method: Gnomon,
 supported by EST evidence.
 Also see:
 Documentation of NCBI's Annotation Process

```
##Genome-Annotation-Data-START##
Annotation Provider      :: NCBI
Annotation Status       :: Full annotation
Annotation Name         :: Quercus suber Annotation Release 100
Annotation Version      :: 100
Annotation Pipeline     :: NCBI eukaryotic genome annotation
                        pipeline
Annotation Software Version :: 8.0
Annotation Method       :: Best-placed RefSeq; Gnomon
Features Annotated     :: Gene; mRNA; CDS; ncRNA
##Genome-Annotation-Data-END##
COMPLETENESS: full length.
```

```
FEATURES
  source      Location/Qualifiers
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              /organism="Quercus suber"
              /isolate="HL8"
              /db_xref="taxon:58331"
              /chromosome="Unknown"
              /tissue_type="leaves"
              /country="Portugal:Montargil"
  Protein     1..259
              /product="uncharacterized protein LOC112034124"
              /calculated_mol_wt=28680
  Region      175..226
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              /note="zinc-finger of the FCS-type, C2-C2; pfam04570"
              /db_xref="CDD:309629"
  CDS         1..259
              /gene="LOC112034124"
              /coded_by="XM_024066907.1:145..924"
              /db_xref="GeneID:112034124"
```

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