MATRIX SCIENCE MASCOT Search Results

Protein View: XP_020586064.1

14-3-3-like protein [Phalaenopsis equestris]

Database:	NCBIprot
Score:	86
Expect:	0.015
Monoisotopic mass (M_r):	29081
Calculated pI:	4.90
Taxonomy:	Phalaenopsis equestris

Sequence similarity is available as an NCBI BLAST search of XP_020586064.1 against nr.

Search parameters

MS data file:	`SPOT_81.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: 44%

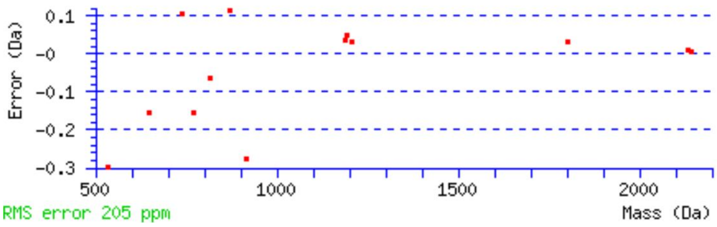
Matched peptides shown in ***bold red***.

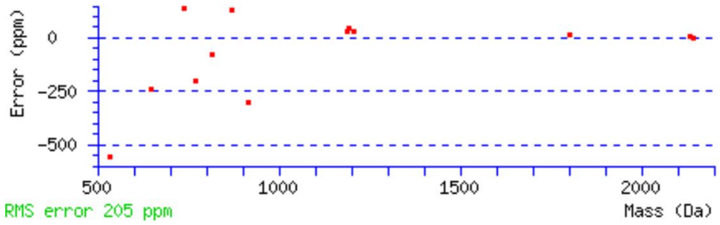
```
  1 MSSSESSRED NVYMAKLAEQ AERYEEMVEF MEKVAKTGSV NELSVEERNL
 51 LSVAYKNVIG ARRASWRIIS SIEQKEEGRG NEDRVTIIKD YRGKIETELS
101 KICDGILKLL DSHLIPSASA AESKVFYLKM KGDYHRYLAE FKTGAERKEA
151 AESTLLAYKS AQDIALAELA PTHPIRLGLA LNFSVFYYEI LNSPDRACNL
201 AKQAFDEAIS ELDTLGEESY KDSTLIMQLL RDNLTLWTSD ITEDAGDEIK
251 ESSKHES
```

Unformatted sequence string: 257 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
21	1 – 8	870.4778	869.4705	869.3549	0.1156	0		-.MSSSESSR.E
15	2 – 8	739.4262	738.4189	738.3144	0.1045	0		M.SSSESSR.E
17	17 – 23	816.3589	815.3516	815.4137	-0.0621	0		K.LAEQAER.Y
23	68 – 75	917.2546	916.2473	916.5229	-0.2756	0		R.IISSIEQK.E
11	132 – 136	647.1349	646.1276	646.2823	-0.1547	0		K.GDYHR.Y
16	137 – 142	770.2512	769.2440	769.4010	-0.1571	0		R.YLAEFK.T
3	143 – 147	532.9702	531.9629	532.2605	-0.2976	0		K.TGAER.K
26	149 – 159	1195.6704	1194.6631	1194.6132	0.0500	0		K.EAAESTLLAYK.S
33	160 – 176	1803.0065	1801.9992	1801.9686	0.0306	0		K.SAQDIALAELAPTHPIR.L
40	203 – 221	2144.9917	2143.9845	2143.9797	0.0048	0		K.QAFDEAISELDTLGEESYK.D
25	222 – 231	1189.6954	1188.6881	1188.6536	0.0345	0		K.DSTLIMQLLR.D
27	222 – 231	1205.6889	1204.6817	1204.6485	0.0331	0		K.DSTLIMQLLR.D + Oxidation (M)
39	232 – 250	2136.0055	2134.9982	2134.9906	0.0076	0		R.DNLTLWTSDITEDAGDEIK.E





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LOCUS       XP_020586064             257 aa            linear   PLN 10-APR-2017
DEFINITION  14-3-3-like protein [Phalaenopsis equestris].
ACCESSION   XP_020586064
VERSION     XP_020586064.1
DBLINK      BioProject: PRJNA382149
DBSOURCE    REFSEQ: accession XM_020730405.1
KEYWORDS    RefSeq.
SOURCE      Phalaenopsis equestris
  ORGANISM  Phalaenopsis equestris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae;
            Epidendroideae; Vandeae; Aeridinae; Phalaenopsis.
COMMENT     MODEL REFSEQ:  This record is predicted by automated computational
            analysis. This record is derived from a genomic sequence
            (NW_018164953.1) annotated using gene prediction method: Gnomon.
            Also see:
                Documentation of NCBI's Annotation Process

            ##Genome-Annotation-Data-START##
            Annotation Provider         :: NCBI
            Annotation Status           :: Full annotation
            Annotation Version          :: Phalaenopsis equestris Annotation
                                           Release 100
            Annotation Pipeline         :: NCBI eukaryotic genome annotation
                                           pipeline
            Annotation Software Version :: 7.3
            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="Unknown"
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                     /calculated_mol_wt=28854
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                     /note="14-3-3 domain; cl02098"
                     /db_xref="CDD:321801"
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                     /note="dimer interface [polypeptide binding]"
                     /db_xref="CDD:206755"
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                     229,232..233)
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                     /note="peptide binding site [polypeptide binding]"
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     CDS             1..257
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                     /coded_by="XM_020730405.1:107..880"
                     /db_xref="GeneID:110028516"
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