

**MATRIX SCIENCE MASCOT Search Results**

**Protein View: XP\_009396738.1**

**PREDICTED: late embryogenesis abundant protein D-34-like [Musa acuminata subsp. malaccensis]**

**Database:** NCBIprot  
**Score:** 105  
**Expect:** 0.00021  
**Monoisotopic mass (M<sub>r</sub>):** 29027  
**Calculated pI:** 4.78  
**Taxonomy:** Musa acuminata subsp. malaccensis

Sequence similarity is available as [an NCBI BLAST search of XP\\_009396738.1 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:** 42  
**Mass values matched:** 13

**Protein sequence coverage: 59%**

Matched peptides shown in **bold red**.

1 MSQE**QPR**TD **QGWGAGCDQP** **IKYGDVFPVA** **GDLAQQT**IA**P** RDAAMMHAAE  
 51 NRALGLTPKG GPASVMESAA TRNEQRGLVG HDQFSPIPAN QGVSITQTEI  
 101 HGLPGQR**LVT** **EFVAGQAVGQ** **YVVDAESGDG** **GAPGGR**RGVE **RGQSLGGVSS**  
 151 **WTDKMTIGEA** **LEAAGRAAGD** **EPIEMSDAAA** **VEAAESAATG** **LNTVLRGGIA**  
 201 **AAAQSAATLN** **AR**ITRDEDKT **KLGDVLQDAA** **MRL**LLDDREAT RVDAERVVRA  
 251 EMR**NSPDV**CV **RPGGVADSMV** **SAAR**FNQEP

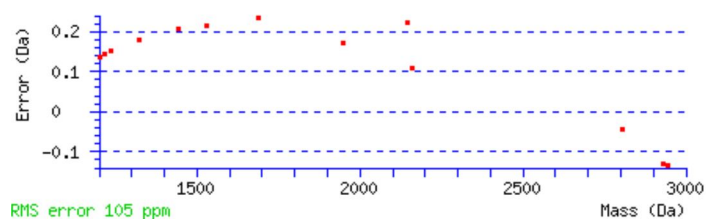
Unformatted sequence string: **279 residues** (for pasting into other applications).

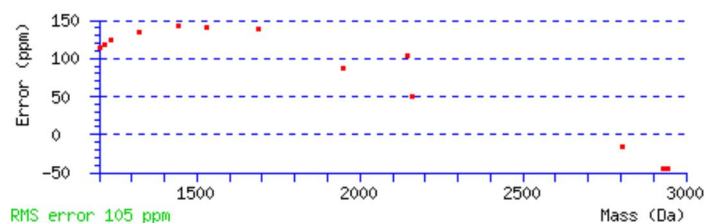
Sort by  residue number  increasing mass  decreasing mass

Show  matched peptides only  predicted peptides also

Start - End	Observed	Mr (expt)	Mr (calc)	Delta M	Peptide
8 - 22	1689.0160	1688.0087	1687.7737	0.2351 1	R.RTD <b>QGWGAGCDQPIK</b> .Y
9 - 22	1532.8950	1531.8877	1531.6726	0.2152 0	R.TD <b>QGWGAGCDQPIK</b> .Y
23 - 41	1947.1680	1946.1607	1945.9898	0.1709 0	K.YGDVFPVAGD <b>LAGQTIAPR</b> .D
108 - 136	2806.3210	2805.3137	2805.3570	-0.0433 0	R.LVTEFVAGQAVGQYVVD <b>EAESGDGGAPGGR</b> .R
142 - 154	1321.8170	1320.8097	1320.6310	0.1787 0	R.Q <b>SLGGVSSWTDK</b> .M
155 - 166	1218.7590	1217.7517	1217.6074	0.1443 0	K.M <b>TIGEALEAAGR</b> .A
155 - 166	1234.7630	1233.7557	1233.6023	0.1534 0	K.M <b>TIGEALEAAGR</b> .A + Oxidation (M)
167 - 196	2930.2740	2929.2667	2929.3974	-0.1307 0	R.AAGDEPIEMSDAA <b>VEAAESAATGLNTVLR</b> .G
167 - 196	2946.2660	2945.2587	2945.3924	-0.1336 0	R.AAGDEPIEMSDAA <b>VEAAESAATGLNTVLR</b> .G + Oxidation (M)
197 - 212	1442.9760	1441.9687	1441.7637	0.2050 0	R.GG <b>IAAAAQSAATLNAR</b> .I
222 - 232	1204.7360	1203.7287	1203.5918	0.1370 0	K.LGDVL <b>QDAAMR</b> .L + Oxidation (M)
254 - 274	2145.2410	2144.2337	2144.0103	0.2234 0	R.NSPDVCVR <b>PGGVADSMVSAAR</b> .F
254 - 274	2161.1220	2160.1147	2160.0052	0.1095 0	R.NSPDVCVR <b>PGGVADSMVSAAR</b> .F + Oxidation (M)

**No match to:** 527.0190, 531.0560, 533.0320, 535.0370, 536.9140, 584.0930, 625.2560, 647.1960, 662.1690, 663.2000, 786.3320, 825.4380, 832.2810, 842.5000, 856.4970, 870.5370, 917.3040, 1122.6650, 1155.7010, 1803.1820, 1941.1540, 2136.1280, 2217.3050, 2239.3270, 2691.2090, 2914.3920, 3213.3520, 3346.1510, 3353.3870





LOCUS XP\_009396738 279 aa linear PLN 25-OCT-2016  
 DEFINITION PREDICTED: late embryogenesis abundant protein D-34-like [Musa acuminata subsp. malaccensis].  
 ACCESSION XP\_009396738  
 VERSION XP\_009396738.1  
 DBLINK BioProject: PRJNA262552  
 DBSOURCE REFSEQ: accession XM\_009398463.2  
 KEYWORDS RefSeq.  
 SOURCE Musa acuminata subsp. malaccensis (wild Malaysian banana)  
 ORGANISM Musa acuminata subsp. malaccensis  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Zingiberales; Musaceae; Musa.  
 COMMENT MODEL REFSEQ: This record is predicted by automated computational analysis. This record is derived from a genomic sequence (NC\_025205.1) 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      :: Musa acuminata Annotation Release
                        101
Annotation Pipeline     :: NCBI eukaryotic genome annotation
                        pipeline
Annotation Software Version :: 7.2
Annotation Method       :: Best-placed RefSeq; Gnomon
Features Annotated      :: Gene; mRNA; CDS; ncRNA
##Genome-Annotation-Data-END##
COMPLETENESS: full length.
```

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                        /db_xref="GeneID:103981724"
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**Mascot: <http://www.matrixscience.com/>**