MASCOT Search Results

Protein View: XP_009410104.1

PREDICTED: alpha-amylase isozyme 3D-like [Musa acuminata subsp. malaccensis]

Database:	NCBIprot
Score:	79
Expect:	0.082
Monoisotopic mass (M_r):	47382
Calculated pI:	5.63
Taxonomy:	Musa acuminata subsp. malaccensis

Sequence similarity is available as an NCBI BLAST search of XP_009410104.1 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:	49
Mass values matched:	12

Protein sequence coverage: 29%

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

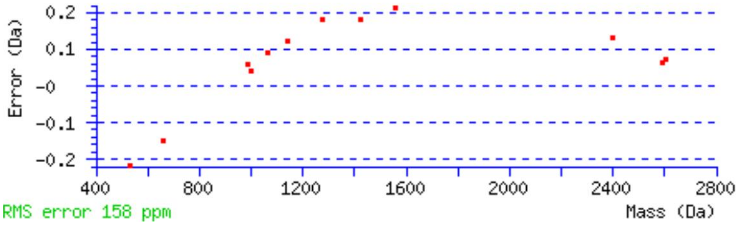
1 MKPLLLAFVF LVVLSLTTAQ SQILFQGFNW ESWRK**QGGWY** **NFLR**SQVPDI
51 AR**AGVTHVWL** **PPPSHSVSEQ** **GYMPGR**LYDL NASKYGTRDE LK**SLIAAFHD**
101 **K**GIKCVADIV INHR**CAERK**D AR**GIYCIFEG** **GTSDSR**LDWG PHMICSDDTQ
151 YSDGTGNRDT GGDFGAAPDI DHLNQQVQQE LTDWLNWLR**T** **DIGFDGWR**LD
201 FARGYSPSIA KIYVSHTSPD FVVAELWSSL TYGGDGKPAY DQDGSR**QELV**
251 **NWVHDVGGPA** **AAFDFTTKGV** **LQAAVQGELW** **R**LRDPQGK**AS** **GMIGWWPEK**A
301 VTFVDNHDTG STQK**LWPFPS** **DK**VMQGYAYI LTHPGVPTIF YDHLFDWGLK
351 DEITGLAAIR TRNGILPGST LRILVADADL YLAVIDEKVM VKIGQRYDVG
401 NLVPANFHVV ASGNGYCIWE KR

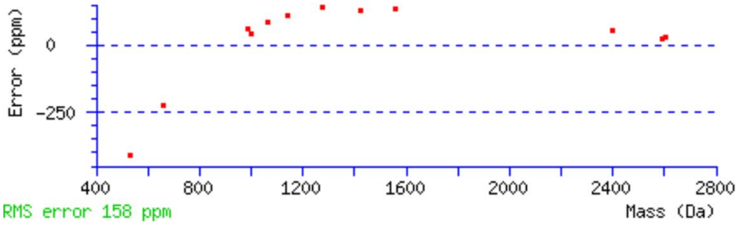
Unformatted sequence string: 422 residues (for pasting into other applications).

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
    36 - 44     1140.6810  1139.6737  1139.5512   0.1225 0  K.QGGWYNFLR.S
    53 - 76     2589.3320  2588.3247  2588.2594   0.0653 0  R.AGVTHVWLPPPSHSVSEQGYMPGR.L
    53 - 76     2605.3340  2604.3267  2604.2544   0.0724 0  R.AGVTHVWLPPPSHSVSEQGYMPGR.L + Oxidation (M)
    93 - 101    1001.5840  1000.5767  1000.5342   0.0426 0  K.SLIAAFHDK.G
   115 - 118     535.0110   534.0037   534.2220  -0.2183 0  R.CAER.K
   115 - 119     663.1750   662.1677   662.3170  -0.1492 1  R.CAERK.D
   123 - 136    1561.9090  1560.9017  1560.6879   0.2139 0  R.GIYCIFEGGTSDSR.L
   190 - 198    1066.5870  1065.5797  1065.4880   0.0917 0  R.TDIGFDGWR.L
   247 - 268    2402.3110  2401.3037  2401.1703   0.1334 0  R.QELVNWVHDVGGPAAAFDFTTK.G
   269 - 281    1426.9630  1425.9557  1425.7728   0.1829 0  K.GVLQAAVQGELWR.L
   289 - 299    1277.7810  1276.7737  1276.5910   0.1827 0  K.ASGMIGWWPEK.A + Oxidation (M)
   315 - 322     989.5700   988.5627   988.5018   0.0609 0  K.LWPFPSDK.V
```

No match to: 526.9750, 531.0360, 532.9870, 536.6040, 537.0070, 584.0910, 625.1920, 647.1760, 698.8790, 714.8610, 724.2350, 735.2500, 825.4080, 842.4460, 856.4560, 870.4870, 1036.5480, 1123.6450, 1383.8480, 1475.9360, 1909.1240, 1941.1340, 2230.3360, 2239.3080, 2385.2580, 2564.2650, 2663.3600, 2678.3490, 2691.3300, 2807.3100, 2810.3730, 2825.3210, 2914.4790, 3337.5540, 3347.4620, 3353.4980, 5572.5650





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LOCUS       XP_009410104             422 aa            linear   PLN 25-OCT-2016
DEFINITION  PREDICTED: alpha-amylase isozyme 3D-like [Musa acuminata subsp.
            malaccensis].
ACCESSION   XP_009410104
VERSION     XP_009410104.1
DBLINK      BioProject: PRJNA262552
DBSOURCE    REFSEQ: accession XM_009411829.2
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_025208.1) 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.
FEATURES             Location/Qualifiers
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                     /chromosome="7"
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                     /calculated_mol_wt=46995
     Region          5..421
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                     /note="alpha-amylase; Provisional"
                     /db_xref="CDD:165762"
     Region          23..365
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                     /note="Alpha amylase catalytic domain found in archaeal,
                     bacterial, and plant Alpha-amylases (also called
                     1,4-alpha-D-glucan-4-glucanohydrolase); cd11314"
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                     /db_xref="CDD:200453"
     Site            order(112,169)
                     /site_type="other"
                     /note="Ca binding site [ion binding]"
                     /db_xref="CDD:200453"
     Site            order(200,225,308)
                     /site_type="active"
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                     /region_name="Alpha-amyl_C2"
                     /note="Alpha-amylase C-terminal beta-sheet domain;
                     smart00810"
                     /db_xref="CDD:129046"
     CDS             1..422
                     /gene="LOC103992212"
                     /coded_by="XM_009411829.2:86..1354"
                     /db_xref="GeneID:103992212"
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Mascot: http://www.matrixscience.com/