# MASCOT Search Results

## Protein View: XP_009410104.1

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

| | |
|---|---|
| **Database:** | NCBIprot |
| **Score:** | 74 |
| **Expect:** | 0.3 |
| **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

| | |
|---|---|
| **MS data file:** | SPOT_87.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: 35%

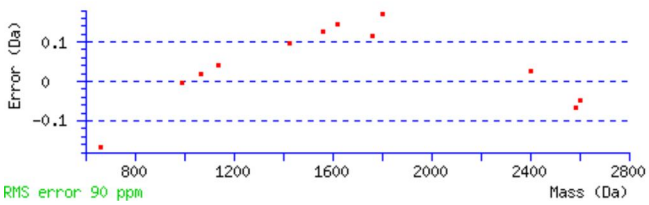
Matched peptides shown in ***bold red***.

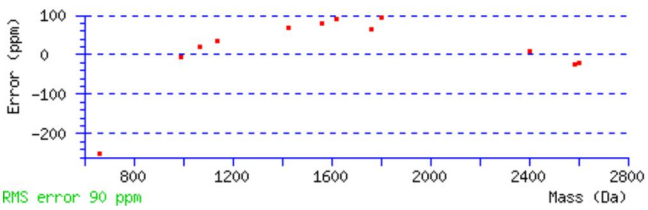
```
  1 MKPLLLAFVF LVVLSLTTAQ SQILFQGFNW ESWRKQGGWY NFLRSQVPDI
 51 ARAGVTHVWL PPPSHSVSEQ GYMPGRLYDL NASKYGTRDE LKSLIAAFHD
101 KGIKCVADIV INHRCAERKD ARGIYCIFEG GTSDSRLDWG PHMICSDDTQ
151 YSDGTGNRDT GGDFGAAPDI DHLNQQVQQE LTDWLNWLRT DIGFDGWRLD
201 FARGYSPSIA KIYVSHTSPD FVVAELWSSL TYGGDGKPAY DQDGSRQELV
251 NWVHDVGGPA AAFDFTTKGV LQAAVQGELW RLRDPQGKAS GMIGWWPEKA
301 VTFVDNHDTG STQKLWPFPS DKVMQGYAYI 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

| Query | Start – End | Observed | Mr(expt) | Mr(calc) | Delta | M | Score | Peptide |
|---|---|---|---|---|---|---|---|---|
| 23 | 36 – 44 | 1140.5979 | 1139.5907 | 1139.5512 | 0.0394 | 0 | | K.QGGWYNFLR.S |
| 42 | 53 – 76 | 2589.1999 | 2588.1926 | 2588.2594 | -0.0668 | 0 | | R.AGVTHVWLPPPSHSVSEQGYMPGR.L |
| 43 | 53 – 76 | 2605.2124 | 2604.2051 | 2604.2544 | -0.0493 | 0 | | R.AGVTHVWLPPPSHSVSEQGYMPGR.L + Oxidation (M) |
| 9 | 115 – 119 | 663.1586 | 662.1514 | 662.3170 | -0.1656 | 1 | | R.CAERK.D |
| 29 | 123 – 136 | 1561.8221 | 1560.8148 | 1560.6879 | 0.1269 | 0 | | R.GIYCIFEGGTSDSR.L |
| 21 | 190 – 198 | 1066.5150 | 1065.5077 | 1065.4880 | 0.0197 | 0 | | R.TDIGFDGWR.L |
| 40 | 247 – 268 | 2402.2021 | 2401.1949 | 2401.1703 | 0.0246 | 0 | | R.QELVNWVHDVGGPAAAFDFTTK.G |
| 28 | 269 – 281 | 1426.8771 | 1425.8698 | 1425.7728 | 0.0970 | 0 | | K.GVLQAAVQGELWR.L |
| 34 | 284 – 299 | 1803.0255 | 1802.0182 | 1801.8457 | 0.1725 | 1 | | R.DPQGKASGMIGWWPEK.A + Oxidation (M) |
| 30 | 300 – 314 | 1619.9120 | 1618.9047 | 1618.7587 | 0.1460 | 0 | | K.AVTFVDNHDTGSTQK.L |
| 19 | 315 – 322 | 989.5039 | 988.4966 | 988.5018 | -0.0052 | 0 | | K.LWPFPSDK.V |
| 32 | 373 – 388 | 1761.0842 | 1760.0769 | 1759.9607 | 0.1161 | 0 | | R.ILVADADLYLAVIDEK.V |




```
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
     source          1..422
                     /organism="Musa acuminata subsp. malaccensis"
                     /sub_species="malaccensis"
                     /db_xref="taxon:214687"
                     /chromosome="7"
     Protein         1..422
                     /product="alpha-amylase isozyme 3D-like"
                     /calculated_mol_wt=46995
     Region          5..421
                     /region_name="PLN00196"
                     /note="alpha-amylase; Provisional"
                     /db_xref="CDD:165762"
     Region          23..365
                     /region_name="AmyAc_arch_bac_plant_AmyA"
                     /note="Alpha amylase catalytic domain found in archaeal,
                     bacterial, and plant Alpha-amylases (also called
                     1,4-alpha-D-glucan-4-glucanohydrolase); cd11314"
                     /db_xref="CDD:200453"
     Site            order(30,72,113,164,198,200..201,203,225,227..228,
                     307..308)
                     /site_type="active"
                     /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"
                     /note="catalytic site [active]"
                     /db_xref="CDD:200453"
     Region          361..421
                     /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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