

IDENTIFICATION

Species: *Musa acuminata*

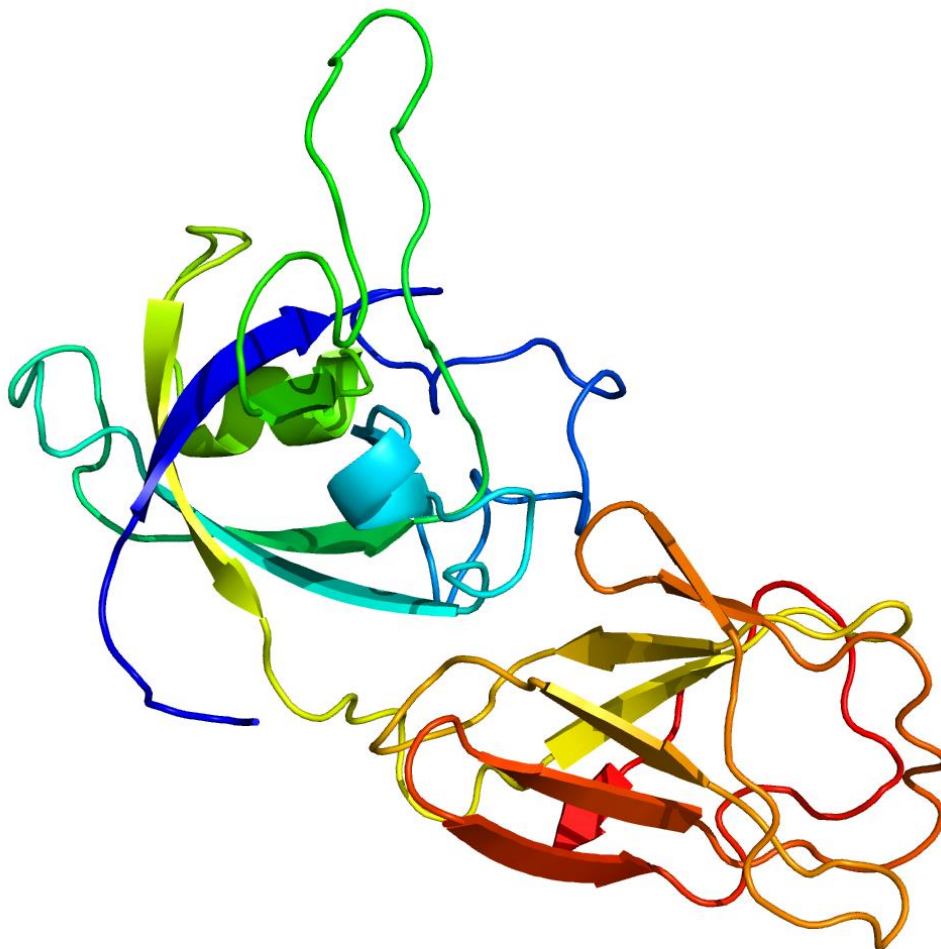
Locus: GSMUA_Achr2P07340_001

Gene Model: GSMUA_Achr2P07340_001

Description: MacEXPA-07

Family: Alpha Expansin

3D structure:



GENOME DATABASES

Phytozome: https://phytozome-next.jgi.doe.gov/info/Macuminata_v1

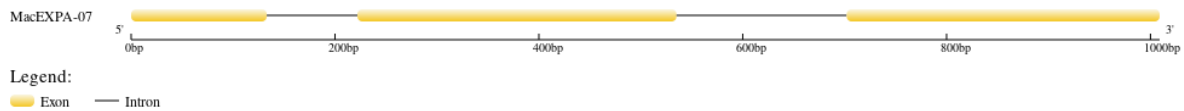
KEGG: <https://www.genome.jp/entry/T03447>

EXTERNAL RESOURCES

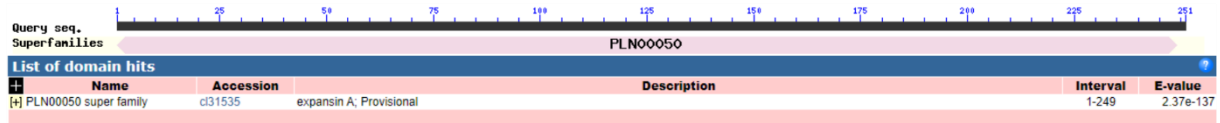
<https://banana-genome-hub.southgreen.fr/>

<https://musabase.org/>

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>MacEXPA-07

MALLGLALVAFPSLFSVAVGYGYGGGWSGAHATFYGGSDASGTMGGACGYGNLYS
QYGTNTAALSTALFNGLSCGSCYELRCVDDPQWCLPGSIVVTATNYCPPNYALPN
NAGGWCNPPLQHFDLSQPVFLHIAQYRAGIVPVA YRRVPCRRRGGIRFTINGHSYFNL
VLITNVGGAGDVHAVSIKGSSTGWQAMSRNWGQNWQSNTYLNQALSFKVTTSDG
RSVVAYNVAPSAWSFGQTFSGGQFA*

CDS (coding sequence)

>MacEXPA-07

ATGGCTCTTCTTGGTCTTGGCTCTGGTTGCCTTTCCTCGCTGTTCTCTGTTGCAGTT
GGGTATGGTTATGGAGGGGGGTGGTCTGGCGCTCATGCTACCTTCTATGGAGGAA
GTGATGCCTCCGGCACGATGGGTGGGGCTTGTGGCTACGGCAACCTGTACAGCCA
GGGCTACGGGACGAACACCGCGGCTCTGAGCACCGCCCTCTTCAACAATGGCCTC
AGCTGCGGCTCTTGGTACGAGCTCAGATGCGTGGACGATCCACAGTGGTGCCTTC
CAGGATCCATTGTTGTGACCGCCACCAACTACTGCCACCCAACTACGCCCTCCC
CAACAATGCGGGGGTGGTGCAACCCTCCTCTGCAGCATTTTGACCTCTCCCAG
CCTGTCTTCCTGCACATTGCTCAGTACAGGGCTGGAATCGTGCCAGTTGCTTACAG
AAGAGTGCCATGCAGGAGAAGAGGGGAATCAGGTTACCATCAATGGCCACTC
CTACTTCAACCTGGTGCTCATAACCAACGTGGGGGGAGCAGGAGATGTGCATGCC
GTGTCCATCAAAGGGTCCAGCACTGGGTGGCAGGCCATGTCCAGGAACTGGGGC
CAGAACTGGCAGAGCAACACCTACCTCAATGGCCAGGCCCTCTCCTTCAAGGTCA
CCACCAGTGATGGTCGCTCTGTGGTCGCCTACAATGTGGCTCCTTCTGCTTGGTCT
TTTGGCCAAACCTTCAAGTGGTGGTCAGTTTGCTTAA

Nucleotide

>MacEXPA-07

ATGGCTCTTCTTGGTCTTGGCTCTGGTTGCCTTTCCTCGCTGTTCTCTGTTGCAGTT
GGGTATGGTTATGGAGGGGGGTGGTCTGGCGCTCATGCTACCTTCTATGGAGGAA
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ATTTGTCATGCGAGAGTAGTGTGCTCACTGAGCTGCTGAGTTCTTTGGCGTGCAG
GTGGGGCTTGTGGCTACGGCAACCTGTACAGCCAGGGCTACGGGACGAACACCG
CGGCTCTGAGCACCGCCCTCTTCAACAATGGCCTCAGCTGCGGCTCTTGGTACGA

GCTCAGATGCGTGGACGATCCACAGTGGTGCCTTCCAGGATCCATTGTTGTGACC
GCCACCAACTACTGCCCACTACGCCCTCCCAACAATGCGGGGGGTTGGT
GCAACCCTCCTCTGCAGCATTGACCTCTCCAGCCTGTCTCCTGCACATTGCT
CAGTACAGGGCTGGAATCGTGCCAGTTGCTTACAGAAGGTTGGTGTTCAGATTC
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AGGGGAATCAGGTTCAACATCAATGGCCACTCCTACTTCAACCTGGTGCTCATA
ACCAACGTGGGGGGAGCAGGAGATGTGCATGCCGTGTCCATCAAAGGGTCCAGC
ACTGGGTGGCAGGCCATGTCCAGGAAGTGGGGCCAGAAGTGGCAGAGCAACACC
TACCTCAATGGCCAGGCCCTCTCCTTCAAGGTCACCACCAGTGATGGTCGCTCTGT
GGTCGCCTACAATGTGGCTCCTTCTGCTTGGTCTTTTGGCCAAACCTTCAGTGGTG
GTCAGTTTGCTTAA