

IDENTIFICATION

Species: *Musa acuminata*

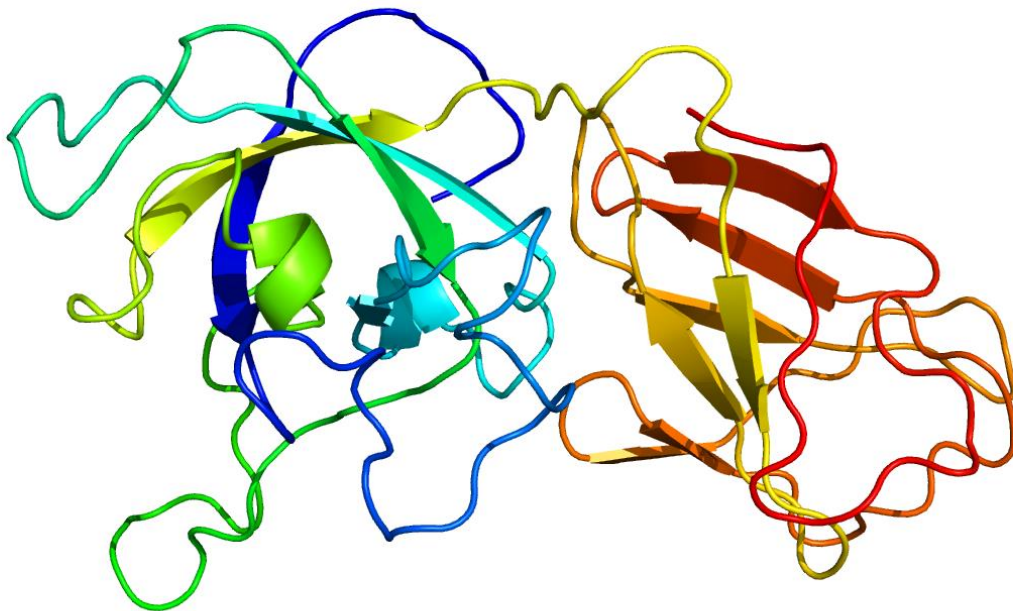
Locus: GSMUA_Achr9P24100_001

Gene Model: GSMUA_Achr9P24100_001

Description: MacEXPA-27

Family: Alpha Expansin

3D structure:



GENOME DATABASES

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

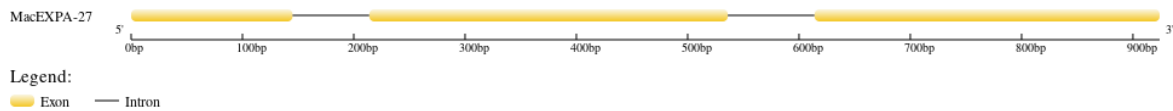
KEGG: <https://www.genome.jp/entry/T03447>

EXTERNAL RESOURCES

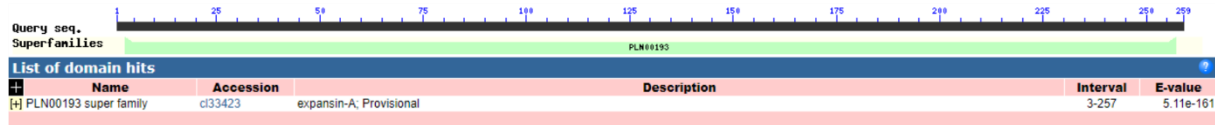
<https://banana-genome-hub.southgreen.fr/>

<https://musabase.org/>

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>MacEXPA-27

MEMGVNFGLFALLILSCCSFTTIEGLARSGWTKGSATFYGGSDASGTMGGACGYGDL
YSAGYGTRTAALSTALFNDGAACGQCYKIVCDFKTDPRWCVRGVSVTVTATNFCPP
NNALPNDNGGWCNTPRQHFDMAQPAWEKIGIYRGGIVPVLFRVPCCKKHGGVRFTI
NGRDYFELVLVTNVAAGSIQSMSIKGSNTGWQPMsrNWGANWQSTAYLNGQSISF
KVTTS DGQTLVFPDIVPSNWGFGQTFSSRLQFK*

CDS (coding sequence)

>MacEXPA-27

ATGGAGATGGGCGTCAACTTTGGCCTCTTCGCTCTGCTAATCCTGAGCTGCTGCTC
GTTACACGATCGAAGGCCTTGCACGATCAGGGTGGACCAAGGGCTCCGCCAC
GTTTTACGGTGGCAGTGATGCGTTCGGGAACAATGGGTGGAGCTTGTGGCTACGGC
GACCTGTACTCGGCGGGGTACGGCACCAGGACCGCCGCCCTGAGCACGGCGCTG
TTCAACGACGGCGCGGCGTGCAGGGCAATGCTACAAGATCGTCTGCGACTTCAAGA
CGGATCCGCGGTGGTGCCTCAGGGGCGTGCAGTACCGGTCACCGCCACCAACTT
CTGCCCCCAACAACGCGCTCCCAACGACAACGGCGGGTGGTGCAACACCCCT
CGCCAGCACTTCGACATGGCCCAGCCGGCGTGGGAGAAGATCGGCATCTACCGC
GGCGGGATCGTGCCGGTGTGTTCCAGAGGGTTCATGCAAGAAGCATGGAGGG
GTGAGGTTACCATCAACGGGCGGGACTACTTCGAGCTGGTGTCTCGTCACCAACG
TCGCAGCAGCCGGATCGATCCAGTCCATGTCCATCAAGGGATCCAATACGGGGTG
GCAGCCGATGTCAAGGAAGTGGGGAGCCAACTGGCAGTCCACCGCCTACCTCAA
TGGACAGTCCATCTCCTTCAAGGTGACAACCAGCGACGGCCAGACGTTGGTCTTC
CCTGACATCGTCCCTTCCAAGTGGGGTTTTGGCCAGACCTTCTCCAGCCGCCTGCA
GTTCAAGTAG

Nucleotide

>MacEXPA-27

ATGGAGATGGGCGTCAACTTTGGCCTCTTCGCTCTGCTAATCCTGAGCTGCTGCTC
GTTACACGATCGAAGGCCTTGCACGATCAGGGTGGACCAAGGGCTCCGCCAC
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TGCTGCGGCCATGTGATTCGAGGTCTCAGTGGATTGTTTGGTGTGCAGGTGGAG
CTTGTGGCTACGGCGACCTGTACTCGGCGGGGTACGGCACCAGGACCGCCGCCCT

GAGCACGGCGCTGTTCAACGACGGCGCGGGCGTGCGGGCAATGCTACAAGATCGT
CTGCGACTTCAAGACGGATCCGCGGTGGTGCATCAGGGGCGTGTCCGGTGACCGTC
ACCGCCACCAACTTCTGCCCCCAACAACGCGCTCCCCAACGACAACGGCGGGT
GGTGCAACACCCCTCGCCAGCACTTCGACATGGCCCAGCCGGCGTGGGAGAAGA
TCGGCATCTACCGCGGGCGGGATCGTGCCGGTGCTGTTCCAGAGGTGGTTCTCCCC
TCTTACTTCTCTCACGAATCCATGAGCATGCTCGACCTGGACCAACCATGTCTCCT
TGCCACGCAGGGTTCCATGCAAGAAGCATGGAGGGGTGAGGTTACCATCAACG
GGCGGGACTACTTCGAGCTGGTGCTCGTCACCAACGTCGCAGCAGCCGGATCGAT
CCAGTCCATGTCCATCAAGGGATCCAATACGGGGTGGCAGCCGATGTCAAGGAA
CTGGGGAGCCAACCTGGCAGTCCACCGCCTACCTCAATGGACAGTCCATCTCCTTC
AAGGTGACAACCAGCGACGGCCAGACGTTGGTCTTCCCTGACATCGTCCCTTCCA
ACTGGGGTTTTGGCCAGACCTTCTCCAGCCGCCTGCAGTTCAAGTAG