

IDENTIFICATION

Species: *Musa acuminata*

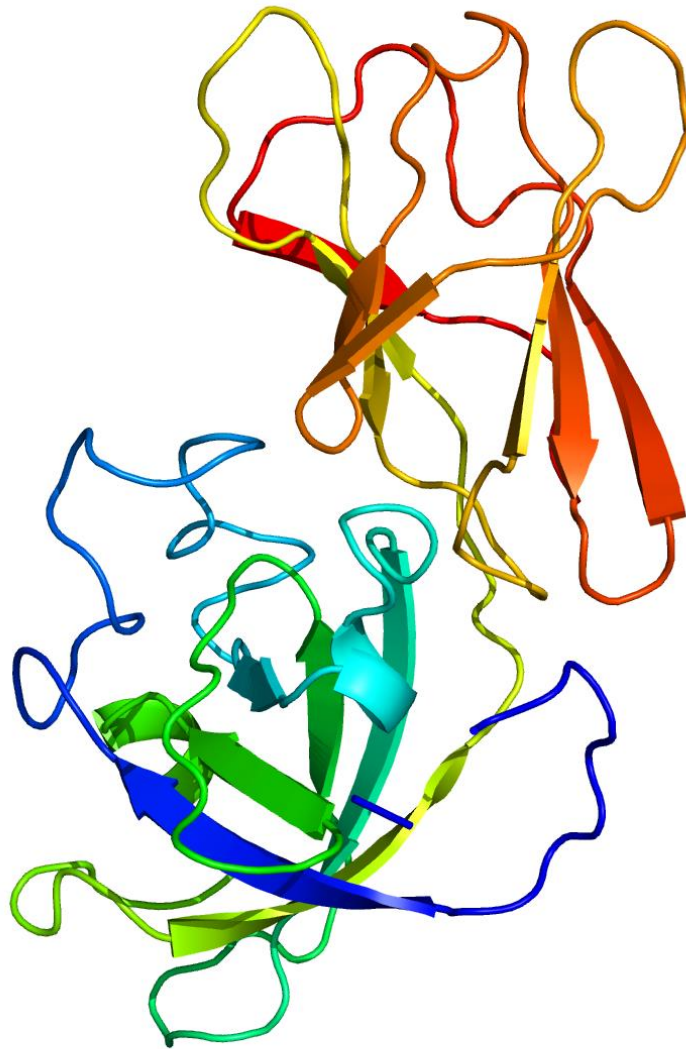
Locus: GSMUA_Achr5P20270_001

Gene Model: GSMUA_Achr5P20270_001

Description: MacEXPA-20

Family: Alpha Expansin

3D structure:



GENOME DATABASES

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

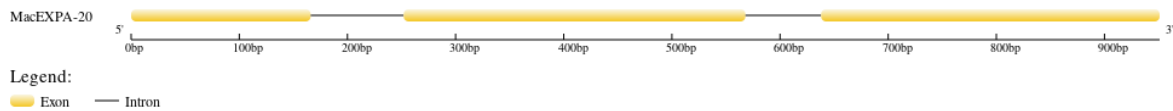
KEGG: <https://www.genome.jp/entry/T03447>

EXTERNAL RESOURCES

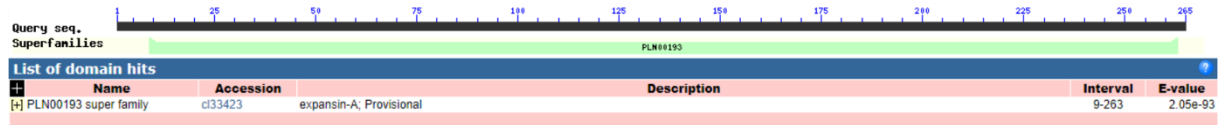
<https://banana-genome-hub.southgreen.fr/>

<https://musabase.org/>

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>MacEXPA-20

MASLLWPCSLVFFLVSTATVSSALSLPIPSLRFPQGPWRYAHATFYGDESASETMGGA
CGYGNLFSSGYGIATAALSSTLFNDGFACGTCYQIRCRGSPHCYGSFPIITVTGTNLCP
PNWAQPSDNGGWCNPPRRHFDLSKPAFMQIAYWRAGIVPVMYRRVPCVRKGGIRFL
LQGNEYWLLAFVMNVGGEGDVGSMWVKGSNTDWMRMSRNW GASFQAFSRLGGQ
SLSFKITSYTTRKTIATDVAPSTWYLGMTYEADV NFA*

CDS (coding sequence)

>MacEXPA-20

ATGGCTTCCTACTGTGGCCGTGCAGCCTTGTCTTCTTCCTCGTTTCTACTGCGAC
GGTGTTCGTTCGGCCCTTTCCTTGCCGATACCAAGTCTCAGGTTTCAGCCGGGTCCAT
GGAGATACGCCACGCTACATTCTACGGCGACGAGTCGGCGTCGGAGACCATGG
GTGGAGCTTTCGGCTACGGGAACCTCTTCAGCTCCGGGTACGGGATCGCGACGGC
GGCGCTCAGCTCGACGCTGTTCAATGACGGATTTCGCTGCGGGACGTGCTACCAG
ATTCGGTGCAGAGGGTCGCCGCATTGCTACGGGAGCTTCCCAATCATCACGGTGA
CCGGCACCAACCTCTGCCC GCCTAACTGGGCCAGCCCTCCGACAACGGCGGGTG
GTGCAACCCCCCAGGAGACACTTCGACCTGTCGAAGCCGGCGTTCATGCAGATC
GCATATTGGAGGGCCGGCATCGTCCCCGTCATGTACCGCAGGGTGCCCTGCGTCA
GGAAGGGAGGGATCCGGTTCTTGCTCCAGGGTAACGAGTACTGGCTGCTGGCCTT
CGTGATGAACGTGGGAGGGGAAGGAGACGTGGGAAGCATGTGGGTGAAGGGGA
GCAACACGGATTGGATGAGGATGAGCCGCAACTGGGGAGCCTCCTTCCAGGCCTT
CTCAAGGCTCGGGGGCCAGTCGCTCTCCTTCAAGATCACCTCCTACACCACCAGG
AAGACCATCATCGCCACCGACGTCGCTCCCTCCACCTGGTACTTGGGAATGACGT
ACGAGGCCGACGTAACTTCGCGTGA

Nucleotide

>MacEXPA-20

ATGGCTTCCTACTGTGGCCGTGCAGCCTTGTCTTCTTCCTCGTTTCTACTGCGAC
GGTGTTCGTTCGGCCCTTTCCTTGCCGATACCAAGTCTCAGGTTTCAGCCGGGTCCAT
GGAGATACGCCACGCTACATTCTACGGCGACGAGTCGGCGTCGGAGACCATGG
GTACGTAGCTACGGATCTACCACGGGGCTGGTCCCTCGGCTTTCGTTGTTCTTCC
ACGTTGCTCACCGGGGTTTCTTCCGCGTAGGTGGAGCTTTCGGCTACGGGAACCT

CTTCAGCTCCGGGTACGGGATCGCGACGGCGGGCGCTCAGCTCGACGCTGTTCAAT
GACGGATTTCGCCTGCGGGACGTGCTACCAGATTTCGGTGCAGAGGGGTCGCCGCATT
GCTACGGGAGCTTCCCAATCATCACGGTGACCGGCACCAACCTCTGCCCGCCTAA
CTGGGCCCAGCCCTCCGACAACGGCGGGTGGTGCAACCCCCCAGGAGACACTTC
GACCTGTCGAAGCCGGCGTTCATGCAGATCGCATATTGGAGGGCCGGCATCGTCC
CCGTCATGTACCGCAGGTACGTACGTAGATGGATCTCGGCCAGCACAGGTGGCGT
CGGTGTTGACGTAGCTTGGGAATCGCTGCAGGGTGCCCTGCGTCAGGAAGGGAG
GGATCCGGTTCTTGCTCCAGGGTAACGAGTACTGGCTGCTGGCCTTCGTGATGAA
CGTGGGAGGGGAAGGAGACGTGGGAAGCATGTGGGTGAAGGGGAGCAACACGG
ATTGGATGAGGATGAGCCGCAACTGGGGAGCCTCCTTCCAGGCCTTCTCAAGGCT
CGGGGGCCAGTCGCTCTCCTTCAAGATCACCTCCTACACCACCAGGAAGACCATC
ATCGCCACCGACGTGCTCCCTCCACCTGGTACTTGGGAATGACGTACGAGGCCG
ACGTAACTTCGCGTGA