

IDENTIFICATION

Species: *Musa acuminata*

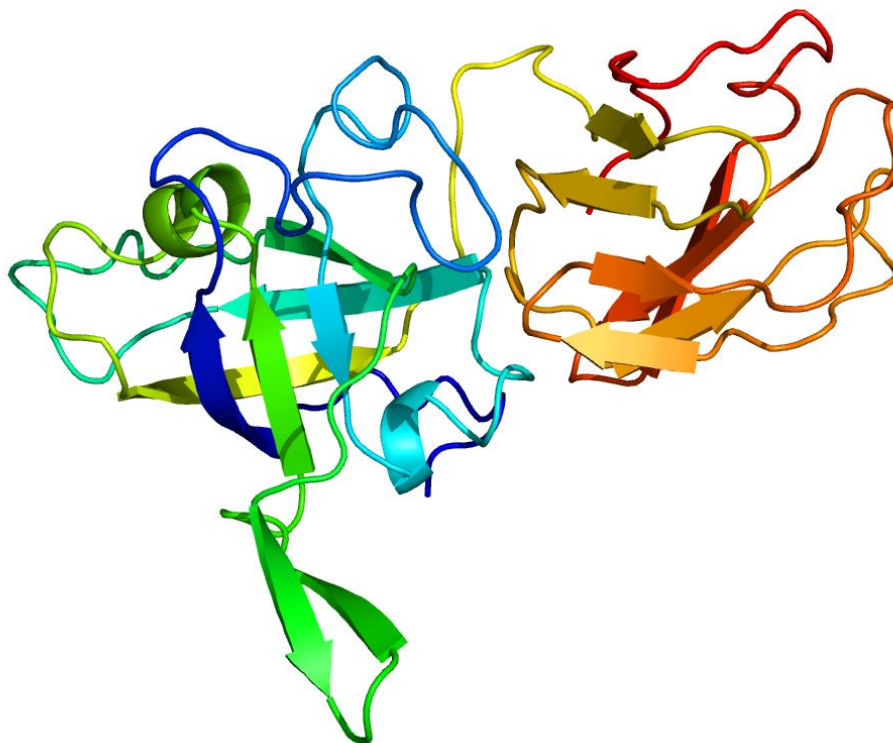
Locus: GSMUA_Achr9P04790_001

Gene Model: GSMUA_Achr9P04790_001

Description: MacEXPA-26

Family: Alpha Expansin

3D structure:



GENOME DATABASES

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

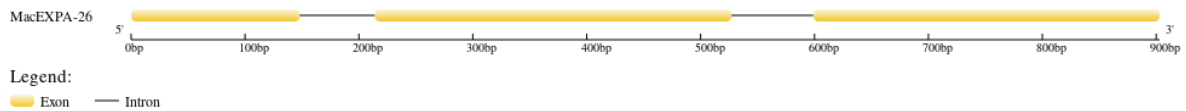
KEGG: <https://www.genome.jp/entry/T03447>

EXTERNAL RESOURCES

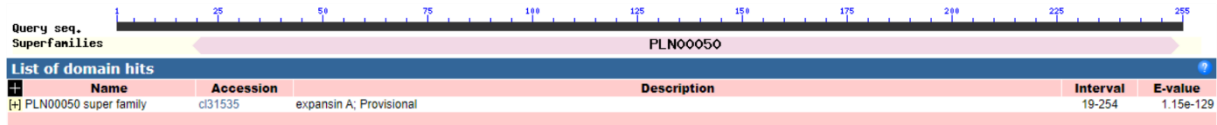
<https://banana-genome-hub.southgreen.fr/>

<https://musabase.org/>

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>MacEXPA-26

MANPKFSLYSALVLCFFSLSVFASTAFADSAWENAHATFYGGGDASGTMGGACGYG
NLYSQGYGTSTAALSTALFNDGLICGACYELRCADDPRWCLPGSIIVTATNFCPPNYA
LANDNGGWCNPPLPFDLAQPAFLRIARYRAGIVPVSFRRVACEKKGGMRFTIDGHS
YFNLVLITNVGGAGDVHAVSIKVSNTGWQAMSRNWGQNWQSNGYLDGHSLSFQVT
TSDGRTVSSIDVAPAGWQFGQTFEGGQF*

CDS (coding sequence)

>MacEXPA-26

ATGGCAAACCCAAAGTTCTCTCTCTACAGTGCTCTCGTCCTCTGCTTCTTCTCCCTT
AGCGTCTTCGCGTCCACGGCCTTCGCAGACTCTGCATGGGAGAACGCCACGCCA
CTTTCTACGGCGGCGGCGACGCCTCCGGCACCATGGGCGGGGCTTGCGGGTACGG
CAACCTCTACAGCCAGGGCTACGGGACGAGCACGGCGGGGCTCAGCACCGCGCT
CTTTAACGACGGCCTCATTGCGGGCGCCTGCTACGAGCTGCGGTGCGCCGACGAC
CCCCGCTGGTGCCTCCCCGGTTCATCATCGTGACCGCCACCAACTTCTGCCCTCC
CAACTACGCCCTCGCCAACGACAACGGCGGCTGGTGCAACCCTCCCCTGCCGCAC
TTCGACCTCGCCAGCCCGCCTTCCCTGCGGATCGCGCGGTACCGTGCCGGCATTG
TCCCCGTCTCCTTCCGCAGGGTGGCTTGCGAGAAGAAGGGAGGGATGCGGTTTAC
CATCGACGGCCACTCCTACTTCAACCTGGTGCTGATACCAACGTGGGCGGGCGCC
GGGACGTGCACGCTGTGTCGATCAAGGTGTGGAACACCGGGTGGCAGGCCATG
TCGCGCAACTGGGGCCAGAACTGGCAGAGTAACGGCTACCTCGACGGGCATAGC
CTCTCCTTTCAGGTCACCACCAGCGACGGCAGGACCGTCAGCAGCATCGACGTGG
CGCCCGCGGGTGGCAGTTCGGGCAGACCTTCGAGGGAGGGCAGTTCTGA

Nucleotide

>MacEXPA-26

ATGGCAAACCCAAAGTTCTCTCTCTACAGTGCTCTCGTCCTCTGCTTCTTCTCCCTT
AGCGTCTTCGCGTCCACGGCCTTCGCAGACTCTGCATGGGAGAACGCCACGCCA
CTTTCTACGGCGGCGGCGACGCCTCCGGCACCATGGGTGAGTTTGGCCCCCATA
AACGACGCAAATGACCGATACTGACATATGAACGTACGTGTTTGCAGGCGGGG
TTGCGGGTACGGCAACCTCTACAGCCAGGGCTACGGGACGAGCACGGCGGGGCT
CAGCACCGCGCTCTTTAACGACGGCCTCATTGCGGGCGCCTGCTACGAGCTGCGG

TGCGCCGACGACCCCCGCTGGTGCCTCCCCGGTTCATCATCGTGACCGCCACCA
ACTTCTGCCCTCCCAACTACGCCCTCGCCAACGACAACGGCGGGCTGGTGCAACCC
TCCCCTGCCGCACTTCGACCTCGCCCAGCCCGCCTTCCTGCGGATCGCGCGGTACC
GTGCCGGCATTGTCCCCGTCTCCTTCGCGAGGTGAGCAGTGACACAAGGCGCCCG
AGTCCACTGTGGTGATGCTGATCCGTGCATAACGTAATCCTCCTGCAGGGTGGCT
TGCGAGAAGAAGGGAGGGATGCGGTTACCATCGACGGCCACTCCTACTTCAAC
CTGGTGCTGATCACCAACGTGGGCGGCGCCGGGGACGTGCACGCTGTGTCGATCA
AGGTGTCGAACACCGGGTGGCAGGCCATGTCGCGCAACTGGGGCCAGAACTGGC
AGAGTAACGGCTACCTCGACGGGCATAGCCTCTCCTTTCAGGTCACCACCAGCGA
CGGCAGGACCGTCAGCAGCATCGACGTGGCGCCCCGCCGGGTGGCAGTTCGGGCA
GACCTTCGAGGGAGGGCAGTTCTGA