

## IDENTIFICATION

**Species:** *Musa acuminata*

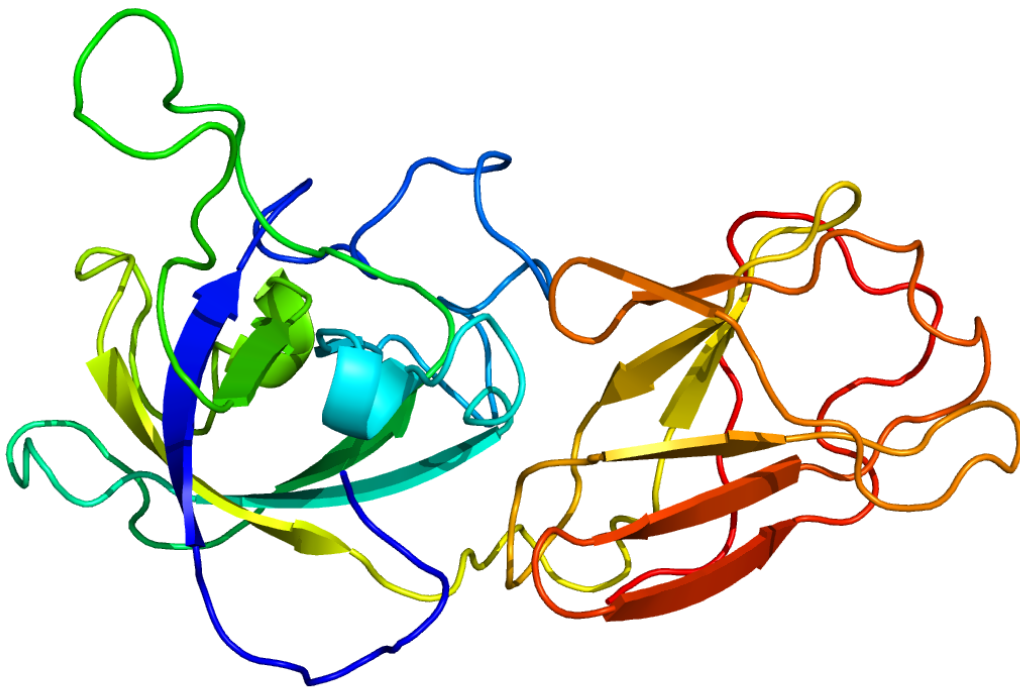
**Locus:** GSMUA\_Achr5P07480\_001

**Gene Model:** GSMUA\_Achr5P07480\_001

**Description:** MacEXPA-18

**Family:** Alpha Expansin

**3D structure:**



## GENOME DATABASES

Phytozome: [https://phytozome-next.jgi.doe.gov/info/Macuminata\\_v1](https://phytozome-next.jgi.doe.gov/info/Macuminata_v1)

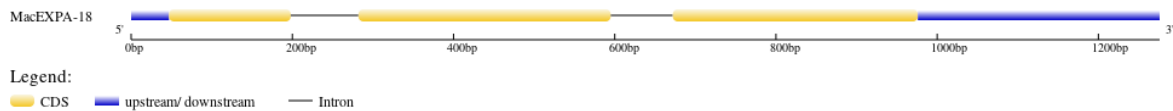
KEGG: <https://www.genome.jp/entry/T03447>

## EXTERNAL RESOURCES

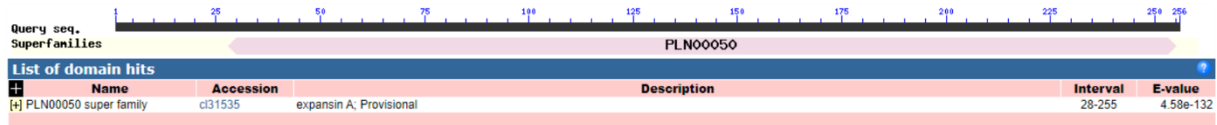
<https://banana-genome-hub.southgreen.fr/>

<https://musabase.org/>

## GENE STRUCTURE



## DOMAIN ARCHITECTURE



## SEQUENCES

### Peptide

>MacEXPA-18

MAKPISSLSDALFFLISSFGFFISGAVGNSYGWQNAHATFYGGGDASGTMGGACGYG  
NLYSQGYGTNTAALSTALFNDGLSCGSCYEMRCADDPRWCLPGSIVVTATNFCPPNN  
ALPNDNGGWCNPPLQHFDLAEPFLQIAQYRAGIVPISFRRVPCVKKGGIRFTINGHS  
YFNLVLITNVGGAGDVHAVSIKGSKTGWQTMSRNWQNWQSNYSYLDGQSLSFQLT  
TSDGRTITSYNVASAGWQFGQTFQGGQF\*

### CDS (coding sequence)

>MacEXPA-18

ATGGCTAAGCCTATCTCCTCCCTCTCCGATGCCCTCTTCTTCCTGATATCGTCCTTC  
GGCTTCTTCATATCAGGAGCCGTGGGAACTCCTACGGGTGGCAGAACGCCCATG  
CCACGTTCTATGGTGGCGGCGACGCCTCCGGCACTATGGGCGGGGCTTGTGGCTA  
TGGCAACCTCTACAGCCAAGGGTACGGGACCAACACCGCGGCCCTCAGTACCGC  
GCTCTTCAACGATGGGCTCAGCTGCGGCTCTTGCTACGAGATGCGGTGCGCCGAT  
GACCCCGGTGGTGCCTCCCGGATCCATCGTCGTCACCGCCACCAACTTCTGTC  
CTCCCAACAACGCCCTCCCAACGACAACGGCGGCTGGTGCAACCCTCCGCTGCA  
ACACTTCGACCTCGCCGAGCCGGCCTTTCTCCAGATAGCGCAGTACCGTGCCGGC  
ATCGTCCCATCTCCTTCCGCAGGGTGCCCTGTGTGAAGAAGGGAGGCATAAGGT  
TCACCATCAATGGTCACTCCTACTTCAACCTGGTGCTGATACCAACGTGGGCGG  
GGCCGGCGACGTGCACGCGGTGTCGATCAAAGGGTGAAGACGGGGTGGCAGAC  
GATGTCGCGCAACTGGGGCCAGAAGTGGCAGAGCAACTCGTACCTGGACGGGCA  
GAGCCTCTCGTTCCAGCTGACGACCAGCGACGGCAGGACGATCACCAGCTACAA  
CGTGGCGTCCGCCGGGTGGCAGTTCGGCCAGACCTTCCAGGGAGGGCAGTTCTAG

### Nucleotide

>MacEXPA-18

CCCAACCAACCACTTCTCCCCTTTCTGCTTGTCAACCCACGGCTCCGATGGCTAAG  
CCTATCTCCTCCCTCTCCGATGCCCTCTTCTTCCTGATATCGTCCTTCGGCTTCTTC  
ATATCAGGAGCCGTGGGAACTCCTACGGGTGGCAGAACGCCCATGCCACGTTCT  
ATGGTGGCGGCGACGCCTCCGGCACTATGGGTAAGTCTGACACATACGACACAA  
ATGATCGTGAAGTCCAGACATCCACCATGTTAATGTGGATGGGCTTATTCTTGT  
GCAGGCGGGGCTTGTGGCTATGGCAACCTCTACAGCCAAGGGTACGGGACCAAC

ACCGCGGCCCTCAGTACCGCGCTCTTCAACGATGGGCTCAGCTGCGGCTCTTGCT  
ACGAGATGCGGTGCGCCGATGACCCCGGTGGTGCCTCCCGGGATCCATCGTCGT  
CACCGCCACCAACTTCTGTCCTCCCAACAACGCCCTCCCAACGACAACGGCGGC  
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TAGCGCAGTACCGTGCCGGCATCGTCCCCATCTCCTTCCGCAGGTGTGAAGCCTT  
TGCCAACCTCCTCATGCTACGCGTGTAAGAAGAAGCTTGTGCGTGACAATATATGACA  
CTCTTGCAAGGTGCCCTGTGTGAAGAAGGGAGGCATAAGGTTACCATCAATGGT  
CACTCCTACTTCAACCTGGTGCTGATCACCAACGTGGGCGGGGCGGGCGACGTGC  
ACGCGGTGTCGATCAAAGGGTTCGAAGACGGGGTGGCAGACGATGTGCGC  
GAACTGGGGCCAGAACTGGCAGAGCAACTCGTACCTGGACGGGCAGAGCCTCTCGTTCC  
AGCTGACGACCAGCGACGGCAGGACGATCACAGCTACAACGTGGCGTCCGCCG  
GGTGGCAGTTCGGCCAGACCTTCCAGGGAGGGCAGTTCTAGGAGCGCCAGCGGC  
CGGGGCTCGTAGCCGCACATTGCCGTTTAAGATCGAGACAGGTATGGAGATACG  
GGAGGACAAGGCTTCTTTAGGCAGAGGCCTTTTTAATCTGGTTGAAGGCAGAGGT  
GGCTTCCTTAGCACCCGCTGAGGCCCAAGTATATGGTTATACATTACAGAGTGAT  
AGTGAGTGATGTACACAATACAAAATCCTCCACAGCCATATGATTTTGCTGGGAG  
ATTGTATCATCTGCATGCAGTGTATCTTATTTCTTCTACTGTTGCATAATTTAAAG  
GTCATGATTTGT