

IDENTIFICATION

Species: *Musa acuminata*

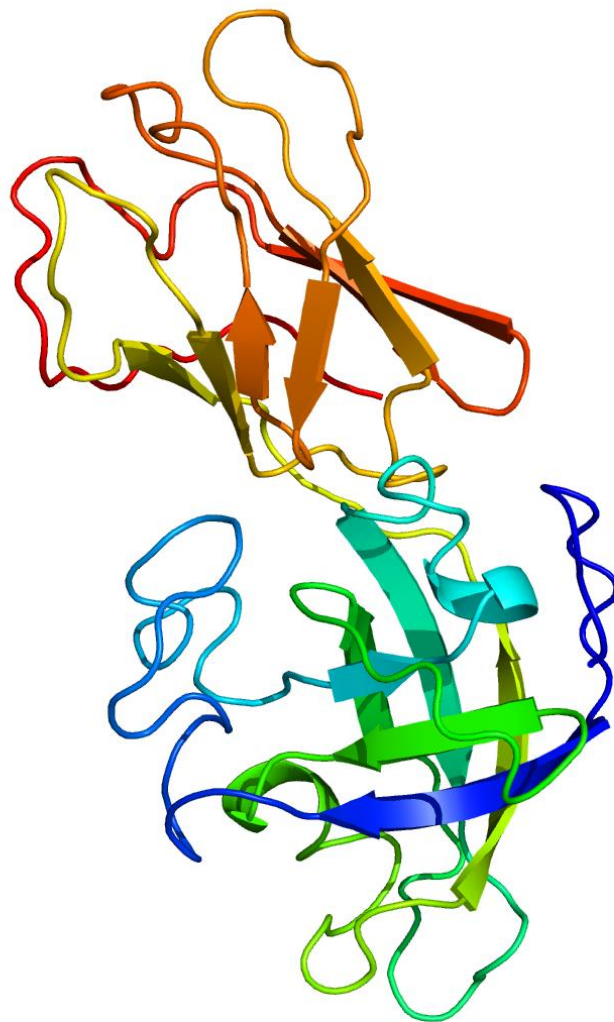
Locus: GSMUA_Achr11P21930_001

Gene Model: GSMUA_Achr11P21930_001

Description: MacEXPA-33

Family: Alpha Expansin

3D structure:



GENOME DATABASES

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

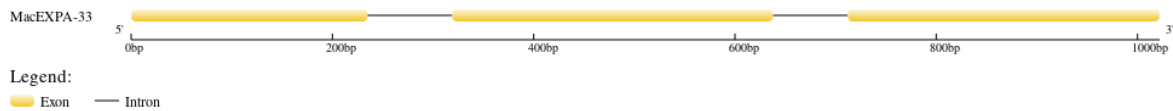
KEGG: <https://www.genome.jp/entry/T03447>

EXTERNAL RESOURCES

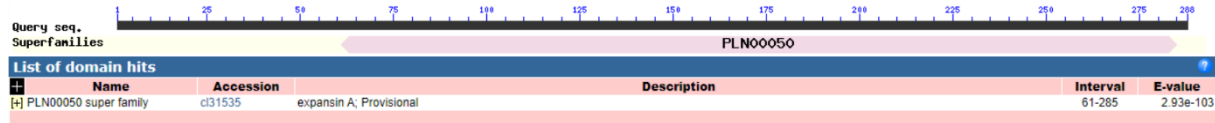
<https://banana-genome-hub.southgreen.fr/>

<https://musabase.org/>

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>MacEXPA-33

MSTLLRALLVAAALLLVFPFRAGAGADAKAEDDHHGKIRYKNHVVHGDHLKGGHGT
FKSGKWEFAHATFYGGSDGSQTREGACGYEDTVTEGYGLQTAAMSTALFNDGLTCG
ACFEIKCVNDKEWCKPGHPSIFVTGTNLCPPNYYQSSDNGGWCNPPRVHFDLTQPAY
LQIAQYKAGIVPVAYRRVPCKKRGIRFTTSGNPYFLLVLVWNVAGAGDVHNMQIK
GNKVGWTAMSRNWGQRWQTNVDLTGQSLFRVTASDGRRSTSWHITPRNWQFGQT
YEGKNFKF*

CDS (coding sequence)

>MacEXPA-33

ATGTCTACTCTCTTGC GCGCCCTCCTTGTAGCTGCAGCGCTGCTGCTGCTTGTGTT
CCCCGCGCCGGCGCCGGCGCCGATGCCAAAGCTGAGGATGACCACCATGGGAA
AATTAGATACAAAACCACGTCCATGGCGATCATCTGAAGGGCCACCACGGGAC
CTTCAAGTCCGGCAAGTGGGAATTCGCGCACGCCACCTTCTACGGAGGCAGTGAT
GGCTCCCAACAAGAGAGGGCGCATGCGGCTACGAGGACACGGTGACCGAAGGG
TACGGGCTGCAGACGGCCGCCATGAGCACGGCTCTGTTCAACGACGGCCTCACAT
GCGGCGCCTGCTTCGAGATCAAGTGCGTAAATGACAAGGAGTGGTGCAAGCCGG
GCCACCCTTCCATCTTCGTCACCGGCACCAACCTTTGCCACCCA ACTACTACCAG
TCCAGCGACAACGGAGGCTGGTGCAACCCTCCCCGTGTGCACTTCGATCTCACGC
AGCCAGCCTACCTCCAGATCGCCAGTACAAGGCCGGAATCGTGCCGGTGGCCTA
CCG CAGGGTCCCGTGCAAGAAGCGGGGAGGCATCAGGTTCACCACCTCAGGGAA
CCCCTACTTCTCCTCGTCCTGGTGTGGAACGTGGCCGGCGCCGGGGACGTCCAC
AACATGCAGATCAAGGGGAACAAGGTGGGGTGGACTGCCATGTCCAGGAACTGG
GGCAGCGCTGGCAGACCAACGTAGACTTAACGGGGCAGTCGTTGTCGTTCCGG
GTCACCGCCAGCGACGGCCGCCGCTCCACCTTTGGCACATCACCCCCGCAACT
GGCAGTTCGGGCAAACCTACGAAGGCAAGA ACTTTAAGTTCTGA

Nucleotide

>MacEXPA-33

ATGTCTACTCTCTTGC GCGCCCTCCTTGTAGCTGCAGCGCTGCTGCTGCTTGTGTT
CCCCGCGCCGGCGCCGGCGCCGATGCCAAAGCTGAGGATGACCACCATGGGAA
AATTAGATACAAAACCACGTCCATGGCGATCATCTGAAGGGCCACCACGGGAC

CTTCAAGTCCGGCAAGTGGGAATTCGCGCACGCCACCTTCTACGGAGGCAGTGAT
GGCTCCCAAACAAGAGGTCTGCCCTTCTCTCCCATGCCTTCTACATGTTGCCTGTG
TTTGCCTTCACGTACGTACGCGCCGAAACTCTACCCTTGCAGAGGGCGCATGC
GGCTACGAGGACACGGTGACCGAAGGGTACGGGCTGCAGACGGCCGCCATGAGC
ACGGCTCTGTTCAACGACGGCCTCACATGCGGCGCCTGCTTCGAGATCAAGTGCG
TAAATGACAAGGAGTGGTGCAAGCCGGGCCACCCTTCCATCTTCGTCACCGGCAC
CAACCTTTGCCACCCA ACTACTACCAGTCCAGCGACAACGGAGGCTGGTGCAAC
CCTCCCCGTGTGCACTTCGATCTCACGCAGCCAGCCTACCTCCAGATCGCCCAGT
ACAAGGCCGGAATCGTGCCGGTGGCCTACCGCAGGTACTCGTCTTCTCGAACCCC
AACATCTCGTCAGAATCCTAACACCAGGACATGAATCACAATGCTGCATGCAGGG
TCCCGTGCAAGAAGCGGGGAGGCATCAGGTTACCACCTCAGGGAACCCCTACTT
CCTCCTCGTCCTGGTGTGGAACGTGGCCGGCGCCGGGGACGTCCACAACATGCAG
ATCAAGGGGAACAAGGTGGGGTGGACTGCCATGTCCAGGAACTGGGGGCAGCGC
TGGCAGACCAACGTAGACTTAACGGGGCAGTCGTTGTCGTTCCGGGTACCGCCA
GCGACGGCCCGCTCCACCTCTTGGCACATCACCCCCGCAACTGGCAGTTCGG
GCAAACCTACGAAGGCAAGAACTTTAAGTTCTGA