

IDENTIFICATION

Species: *Musa acuminata*

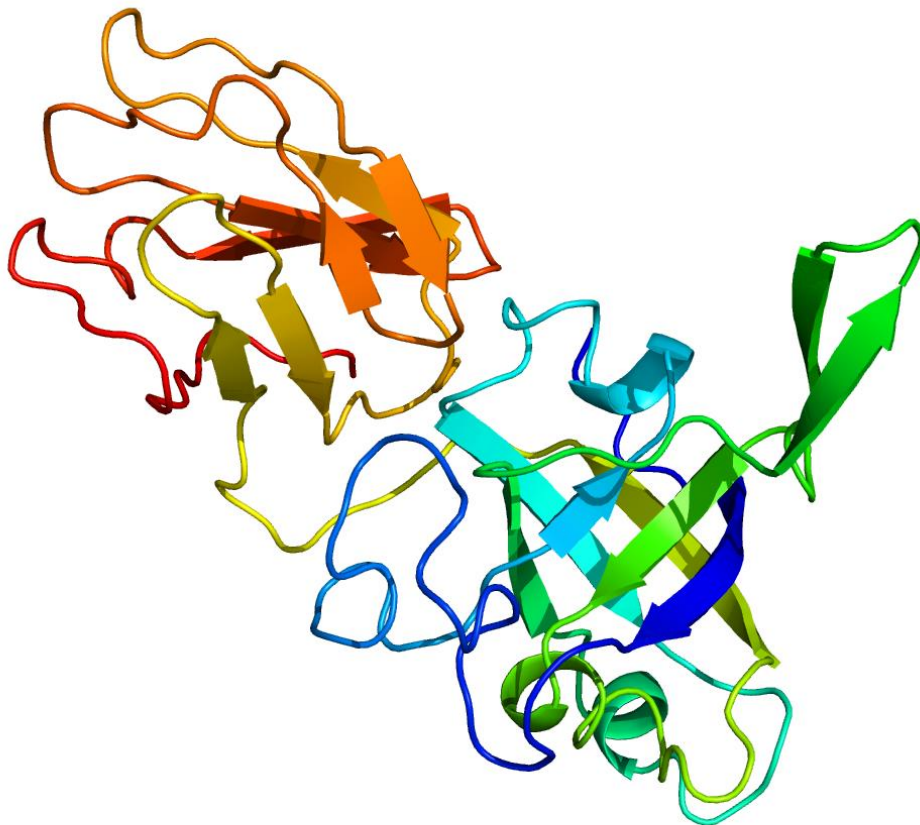
Locus: GSMUA_Achr10P26620_001

Gene Model: GSMUA_Achr10P26620_001

Description: MacEXPA-31

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

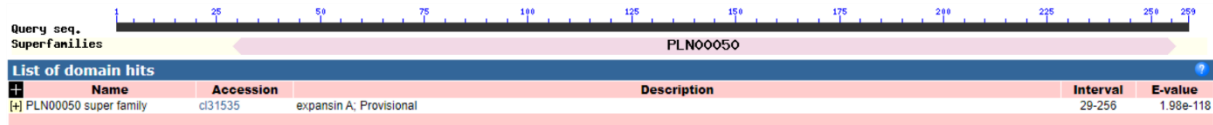
<https://banana-genome-hub.southgreen.fr/>

<https://musabase.org/>

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>MacEXPA-31

MALAAFISVASLLALLAPAAARIPGVYTTGGQWQSAHATFYGGSDASGTMGGACGYG
NLYSQGYGVETAALSTALFDEGQSCGACFEIKCADDPRWCHPGSPSIFITATNFCPPN
YALAPDNGGWCNPPRPHFDLSMPMFLKIAEYRAGIVPVS YRRVPCRRS GGIRFTINGF
QYFNLVLITNVAGAGDIVRASVKGSRTGWMPMSRNWQNWQSNVAVLVGQPLSFRV
TGSDRRTSTSWNIVPSNWQFGQTFEGKNYRA*

CDS (coding sequence)

>MacEXPA-31

ATGGCGTTGGCCGCCTTCATCTCTGTTGCCTCCCTACTGGCCCTTCTTGCCCCGGC
GGCTGCGCGCATTCTGGCGTCTACACTGGGGGCCAGTGGCAGAGCGCCCATGCC
ACATTCTACGGCGGCAGCGACGCGTCCGGGACCATGGGAGGAGCGTGTGGGTAC
GGGAACCTGTACAGCCAGGGGTACGGGGTGGAGACGGCGGGCGCTGAGCACGGCG
CTGTTTCGACGAGGGGCAGAGCTGCGGGGCGTGCTTCGAGATCAAGTGCGCGGAT
GATCCGCGGTGGTGCCACCCCGGGAGCCCCTCCATCTTCATCACGGCTACCAACT
TCTGCCCCGCAAACACTACGCGCTCGCCCCGATAACGGTGGGTGGTGCAACCCGCC
TCGCCCCCACTTCGACCTCTCCATGCCCATGTTCTCAAGATCGCCGAGTACCGCG
CCGGCATCGTCCCCGTCTCATAACGAAGGGTGCCGTGCAGGAGGTCCGGAGGGA
TCCGGTTCACCATCAACGGGTTCAGTACTTCAACCTGGTGCTGATCACCACCGT
GGCGGGCGCCGGTGACATAGTCCGCGCCAGCGTCAAGGGCTCCCGCACCGGGTG
GATGCCCATGTCCCGGAACTGGGGTCAGAACTGGCAGTCGAACGCTGTCTCTCGTC
GGCCAGCCGCTCTCCTTCCGCGTCACCGGCAGCGACCGCCGCACCTCCACCTCCT
GGAACATCGTCCCCTCCAACCTGGCAGTTCGGCCAGACCTTCGAGGGCAAGAACTA
CCGAGCCTGA

Nucleotide

>MacEXPA-31

ATGGCGTTGGCCGCCTTCATCTCTGTTGCCTCCCTACTGGCCCTTCTTGCCCCGGC
GGCTGCGCGCATTCTGGCGTCTACACTGGGGGCCAGTGGCAGAGCGCCCATGCC
ACATTCTACGGCGGCAGCGACGCGTCCGGGACCATGGGTAAGCCGCATTCTCTA
CCGGTGGCCGATCCGTCGCGTTCACCTCGGAGGAGGCGGAATTTGATGGGATTT
GGTGATTTGCAGGAGGAGCGTGTGGGTACGGGAACCTGTACAGCCAGGGGTACG

GGGTGGAGACGGCGGCGCTGAGCACGGCGCTGTTCGACGAGGGGCAGAGCTGCG
GGGCGTGCTTCGAGATCAAGTGCGCGGATGATCCGCGGTGGTGCCACCCCGGGA
GCCCCTCCATCTTCATCACGGCTACCAACTTCTGCCCGCCAAACTACGCGCTCGCC
CCCGATAACGGTGGGTGGTGCAACCCGCCTCGCCCCACTTCGACCTCTCCATGC
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AAGGTATGTACCCCGACGGCCCTCCTCTCCACGATCTCAGATCGGCGTTTGTCGC
GCTTTGAGATGAGCACGAAGACGCGATCAGCGTCATCGACATCCGCGCTTTTGTG
GATCTCTGAGACTGTCAGTTATACCATGCGTTTTTAGTGATCGGTCATCCGTTTAT
GATGTCTTCGAAATCGCTTTAATCGCATAACGTTTCGTGTGATCCATCTTGGCTTCT
CTCTCTTGCTCCGTTTTCTTGATCTATCTAAATTTTTGTACTCAAATAGCGACAAT
CCGGAATTGGTCGCCATGTGTTTGCTGATATGTCCGGGGCCGCAGGGTGCCGTGC
AGGAGGTCGGGAGGGATCCGGTTCACCATCAACGGGTTCAGTACTTCAACCTGG
TGCTGATCACCAACGTGGCGGGCGCCGGTGACATAGTCCGCGCCAGCGTCAAGG
GCTCCCGCACCGGGTGGATGCCCATGTCCCGGAACTGGGGTCAGAACTGGCAGTC
GAACGCTGTCCTCGTCGGCCAGCCGCTCTCCTTCCGCGTCACCGGCAGCGACCGC
CGCACCTCCACCTCCTGGAACATCGTCCCCTCCAACCTGGCAGTTCGGCCAGACCT
TCGAGGGCAAGAACTACCGAGCCTGA