

IDENTIFICATION

Species: *Musa acuminata*

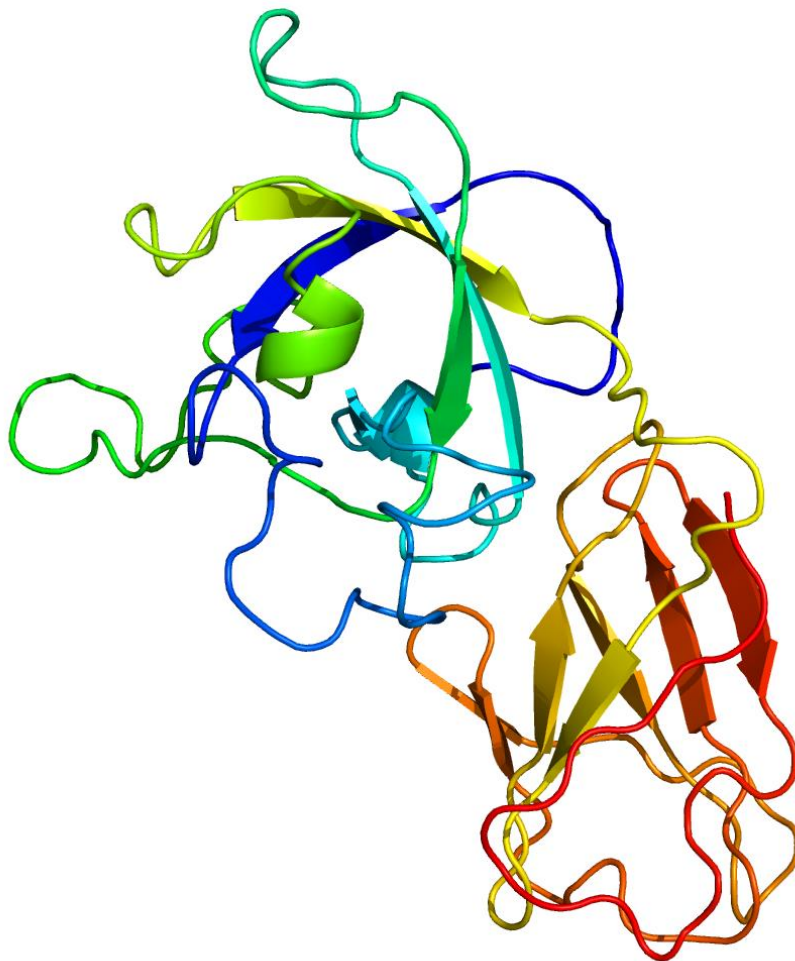
Locus: GSMUA_Achr1P21690_001

Gene Model: GSMUA_Achr1P21690_001

Description: MacEXPA-05

Family: Alpha Expansin

3D structure:



GENOME DATABASES

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

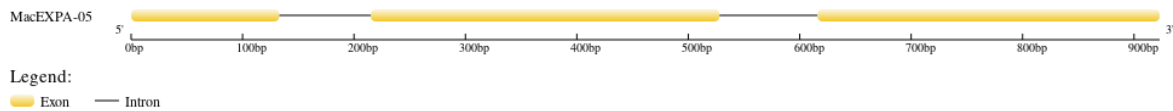
KEGG: <https://www.genome.jp/entry/T03447>

EXTERNAL RESOURCES

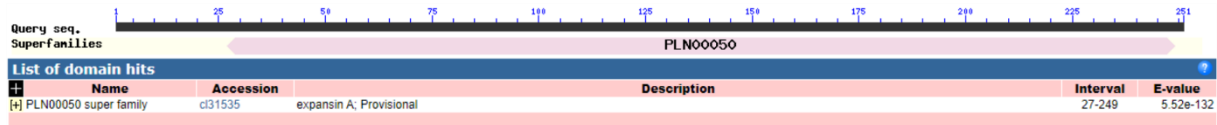
<https://banana-genome-hub.southgreen.fr/>

<https://musabase.org/>

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>MacEXPA-05

MTSLGLVLVAFHSVFSAAAYGYGHGGGWSAAHATFYGGSDASGTMGGACGYGNLYS
QGYGTNTAALSTALFDNGLSCGACYEMKCVNEPQWCLPGSIFVTATNFCPPNDALPN
NNGGWCNPLRHFDLSQPVFLRIARYRAGIVPVA YRRVPCSRRGGIRFTINGHSYFNL
VLITNVGGAGDVHAASVKGSSTGWHPM SRNWGQNWQSNTYLDGQALSFKVTTSDG
VSVVSFNVVPATWSFGQTFSGGQFA*

CDS (coding sequence)

>MacEXPA-05

ATGACTTCTCTTGGTCTGGTTCTGGTTGCCTTTCACTCGGTGTTCTCTGCTGCATAC
GGGTATGGACACGGAGGGGGATGGTCTGCTGCTCATGCTACCTTCTATGGAGGAA
GTGATGCGTCTGGGACAATGGGTGGAGCTTGCGGCTACGGCAACCTGTACAGCCA
GGGCTACGGCACCAATACCGCAGCCCTGAGCACTGCCCTCTTCGACAACGGGCTC
AGCTGCGGCGCCTGCTACGAAATGAAGTGCGTGAATGAGCCGCAGTGGTGCCTG
CCGGGCTCCATTTTGTACAGCCACCAACTTCTGCCACCCAACGATGCCCTCCC
CAACAACAACGGCGGCTGGTGAATCCTCCCCTGCGGCACTTTGACCTCTCCAG
CCCGTCTTCCTGCGCATTGCCCGGTACAGGGCTGGCATTGTGCCCGTTCGCTTACAG
AAGGGTCCCCTGCAGTAGAAGGGGAGGAATCAGGTTACCATCAATGGCCACTC
CTACTTCAACCTCGTGCTCATCACCAATGTGGGAGGAGCCGGAGATGTGCATGCT
GCGTCCGTCAAGGGGTCCAGCACTGGGTGGCACCCCATGTCCAGGAAGTGGGGC
CAGAACTGGCAGAGCAACACCTACCTCGATGGCCAGGCGTTGTCCTTTAAGGTCA
CCACAAGCGATGGCGTGTCTGTGGTCTCCTTCAATGTGGTTCCTGCAACCTGGTCT
TTTGGCCAGACCTTCAGTGGTGGCCAGTTTGCTTGA

Nucleotide

>MacEXPA-05

ATGACTTCTCTTGGTCTGGTTCTGGTTGCCTTTCACTCGGTGTTCTCTGCTGCATAC
GGGTATGGACACGGAGGGGGATGGTCTGCTGCTCATGCTACCTTCTATGGAGGAA
GTGATGCGTCTGGGACAATGGGTGAGTGAGTTCACAGAAGACACCGTTCGTCATT
CGTCATGCAAGAGTAGGCGGCCATTGATGCGTTGAACTTGGTGTGCAGGTGGAGC
TTGCGGCTACGGCAACCTGTACAGCCAGGGCTACGGCACCAATACCGCAGCCCTG

AGCACTGCCCTCTTCGACAACGGGCTCAGCTGCGGGCCTGCTACGAAATGAAGT
GCGTGAATGAGCCGCAGTGGTGCCTGCCGGGCTCCATTTTTGTACAGCCACCAA
CTTCTGCCACCCAACGATGCCCTCCCAACAACAACGGCGGCTGGTGCAATCCT
CCCCTGCGGCACTTTGACCTCTCCAGCCCGTCTTCCTGCGCATTGCCCGGTACAG
GGCTGGCATTGTGCCCGTCGCTTACAGAAGGTTGGTGAGCCAGAATCATACTACT
CTCTTTATGATCCATATGATCAAGTCTCATCTTGTCTTGCTTGGATTGGTTTCGGG
GCGCAGGGTCCCGTGCAGTAGAAGGGGAGGAATCAGGTTACCATCAATGGCCA
CTCCTACTTCAACCTCGTGCTCATCACCAATGTGGGAGGAGCCGGAGATGTGCAT
GCTGCGTCCGTCAAGGGGTCCAGCACTGGGTGGCACCCCATGTCCAGGAACTGGG
GCCAGAACTGGCAGAGCAACACCTACCTCGATGGCCAGGCGTTGTCCTTTAAGGT
CACCACAAGCGATGGCGTGTCTGTGGTCTCCTTCAATGTGGTTCCTGCAACCTGGT
CTTTTGGCCAGACCTTCAGTGGTGGCCAGTTTGCTTGA