

IDENTIFICATION

Species: *Musa acuminata*

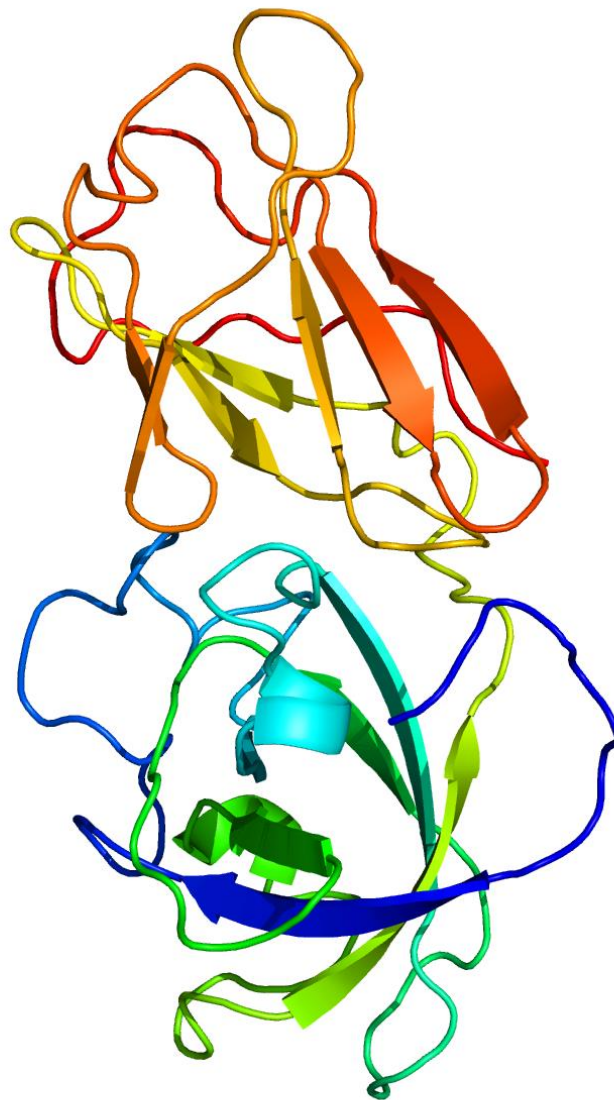
Locus: GSMUA_Achr10P06590_001

Gene Model: GSMUA_Achr10P06590_001

Description: MacEXPA-29

Family: Alpha Expansin

3D structure:



GENOME DATABASES

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

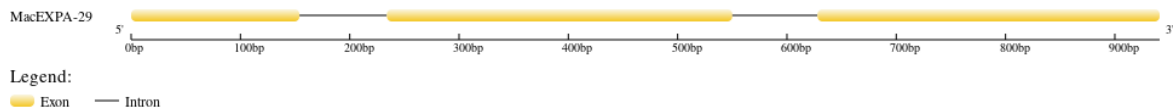
KEGG: <https://www.genome.jp/entry/T03447>

EXTERNAL RESOURCES

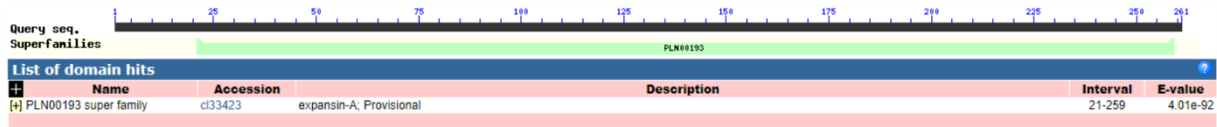
<https://banana-genome-hub.southgreen.fr/>

<https://musabase.org/>

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>MacEXPA-29

MASSSSSSLLCNLGLLVLAMAIARAGAVFRPTPWSMAHATFYGDESASETMGGACG
YGNLFSTGYGTNTAALSSVLFKDFGFCGSCYQIRCSGASACYRGSPIITVTATNLCPPN
WAQPSDNGGWCNPPRVHFDMSKPAFMKIADWHAGIVPVMYRRVPCPVRGGIRFLL
QGNGYWLLAFVTNVGGGGDVARMWVKGSTGWISMSQNWGASYQAFSSLGGQSL
SFKIMSYTTRNTIIASEVAPSNWNVGLTYEATVNFH*

CDS (coding sequence)

>MacEXPA-29

ATGGCTTCGTCGTCGTCGTCGTCGTCCTGTGCAATCTCGGGTTACTGGTGCTGGC
AATGGCGATAGCCAGAGCTGGCGCCGTGTTTCGCCCCACGCCGTGGTTCGATGGCC
CACGCCACCTTCTACGGCGACGAGTCTGCGTCAGAAACCATGGGTGGAGCTTGCG
GATATGGCAACCTGTTCAGCACGGGATACGGCACGAACACCGCGGCACTGAGCT
CGGTGCTGTTCAAGGACGGATTTGGCTGCGGAAGCTGCTACCAGATACGCTGCTC
CGGCGCCTCCGCGTGCTACAGGGGTTCCCCGATCATCACCGTGACAGCCACCAAC
CTCTGCCCCCAACTGGGCTCAGCCCTCCGACAACGGTGGGTGGTGCAACCCCC
CGAGAGTGCCTTCGACATGTCTGAAGCCGGCGTTCATGAAGATCGCCGACTGGCA
TGCCGGTATCGTGCCGGTCATGTACCGCAGGGTTCCTTGCCCGGTTTCGCGGTGGA
ATCCGGTTCCTGCTGCAGGGGAACGGGTAAGGCTGCTGGCCTTCGTGACGAACG
TGGGAGGCGGAGGAGACGTCGCCAGGATGTGGGTGAAGGGAAGCAACACGGGG
TGGATCAGCATGAGCCAGAACTGGGGTGCTTCCTACCAGGCCTTCTCGAGCCTGG
GAGGGCAATCCCTTTCCTTCAAGATCATGTCCTACACCACGAGAAATACCATCAT
CGCGTCCGAGGTCGTCCTTTCGAACTGGAACGTGGGGTTAACCTACGAGGCAACC
GTAACCTCCATTGA

Nucleotide

>MacEXPA-29

ATGGCTTCGTCGTCGTCGTCGTCGTCCTGTGCAATCTCGGGTTACTGGTGCTGGC
AATGGCGATAGCCAGAGCTGGCGCCGTGTTTCGCCCCACGCCGTGGTTCGATGGCC
CACGCCACCTTCTACGGCGACGAGTCTGCGTCAGAAACCATGGGTTCGTCTCATC
TCAACATCGCTTAATGCATCTGTGGAACAGATCTAACGTTGTGAATGGCATCTTT
ACGTATCTCTCAGGTGGAGCTTGCAGGATATGGCAACCTGTTCAGCACGGGATACG

GCACGAACACCGCGGCACTGAGCTCGGTGCTGTTCAAGGACGGATTTGGCTGCGG
AAGCTGCTACCAGATACGCTGCTCCGGCGCCTCCGCGTGCTACAGGGGTTCCCCG
ATCATCACCGTGACAGCCACCAACCTCTGCCCCCCTAACTGGGCTCAGCCCTCCG
ACAACGGTGGGTGGTGCACCCCCGAGAGTGCACCTTCGACATGTCGAAGCCGG
CGTTCATGAAGATCGCCGACTGGCATGCCGGTATCGTGCCGGTCATGTACCGCAG
GTAATCAAAACCATCCATCCTTCCGTTCTCACTGCCGCCATGAAGAGTGCTGAAA
CACCATGGCATGCATGGTTGCAGGGTTCCTTGCCCGGTTTCGCGGTGGAATCCGGT
TCCTGCTGCAGGGGAACGGGTACTGGCTGCTGGCCTTCGTGACGAACGTGGGAGG
CGGAGGAGACGTCGCCAGGATGTGGGTGAAGGGAAGCAACACGGGGTGGATCA
GCATGAGCCAGAACTGGGGTGCTTCCCTACCAGGCCTTCTCGAGCCTGGGAGGGCA
ATCCCTTTCCTTCAAGATCATGTCCTACACCACGAGAAATACCATCATCGCGTCCG
AGGTCGCTCCTTCGAACTGGAACGTGGGGTTAACCTACGAGGCAACCGTAAACTT
CCATTGA