

IDENTIFICATION

Species: *Musa acuminata*

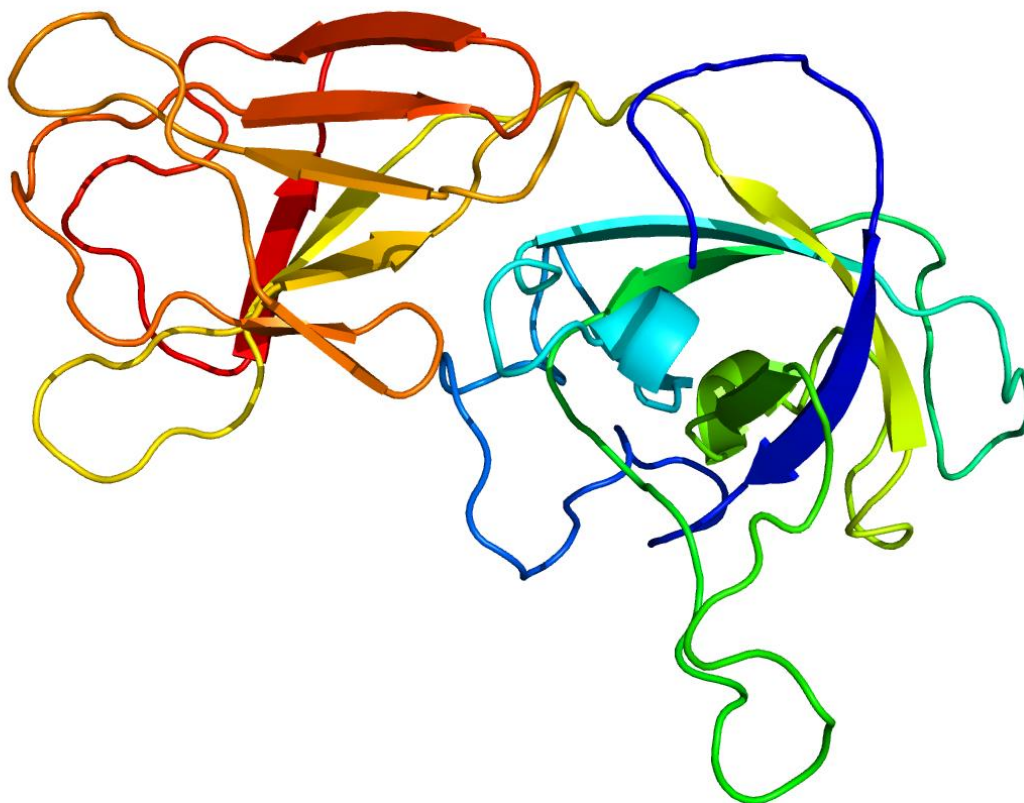
Locus: GSMUA_Achr1P02650_001

Gene Model: GSMUA_Achr1P02650_001

Description: MacEXPA-02

Family: Alpha Expansin

3D structure:



GENOME DATABASES

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

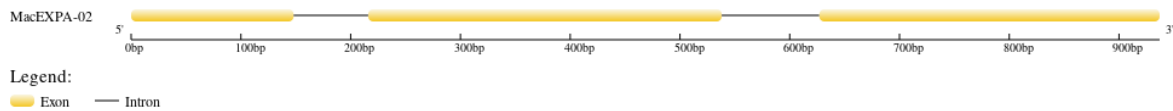
KEGG: <https://www.genome.jp/entry/T03447>

EXTERNAL RESOURCES

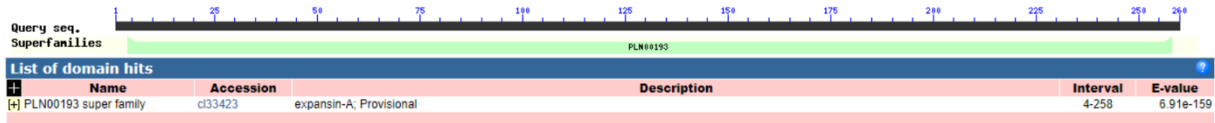
<https://banana-genome-hub.southgreen.fr/>

<https://musabase.org/>

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>MacEXPA-02

METSAFCAGLLVLLVSSFFMSADVEGSASPGWTAASATFYGGSDASGTMGGACGYG
NLYSTGYGTDTAALSTALFDDGDACGQCYRIMCDYQTDPRWCLQGTSVTISATNFCP
PNYALPNDGGWCNPPRQHFDMAQPAWEKIGIYRGGIVPVLYQRVPCVKQGGVRF
INGRDYFELVLVTNVGGGSIQSMSIKGSNTGWMAMSRNWGANWQSNAYLNSQSL
SFRVTTGDGQILVFPDAAPPNWAFFGQFTFTSSLQFS*

CDS (coding sequence)

>MacEXPA-02

ATGGAGACGTCGGCTTTCTGCGCAGGACTGTTGGTCTTGCTGGTCTCGTCCTTCTT
CATGTCCGCCGACGTCGAGGGTTCTGCATCGCCTGGGTGGACTGCAGCTTCCGCG
ACATTTTATGGAGGGAGTGACGCCTCTGGGACCATGGGTGGGGCTTGCGGCTATG
GCAATTTATACTCCACCGGCTACGGGACGGACACTGCAGCGCTGAGCACGGCGCT
CTTCGACGACGGGGATGCGTGCGGGCAGTGTTACAGGATCATGTGCGACTACCAG
ACGGATCCCCGGTGGTGTCTGCAAGGCACTTCGGTGACCATCAGCGCCACCAACT
TCTGCCCCGCAAACACTACGCCCTCCCAACGACGACGGCGGGTGGTGCAACCCCC
GCGGCAGCACTTCGATATGGCGCAGCCGGCGTGGGAGAAGATCGGCATCTACCG
CGGCGGAATCGTCCCGGTGCTGTACCAGAGGGTTCCATGCGTGAAGCAGGGAGG
AGTGAGGTTCAACATCAACGGGCGCGACTACTTCGAGCTCGTCCTGGTAACAAAC
GTGGGCGGCGGCGGGTTCGATCCAGTCCATGTCCATCAAAGGGTCAAACACCGGG
TGGATGGCCATGTCGAGGAACTGGGGAGCAAACCTGGCAGTCGAATGCCTATCTA
AACAGCCAATCCCTCTCCTTCCGCGTCACCACCGGCGACGGGCAGATCCTCGTCT
TCCCGGACGCCGCCACCGAACCTGGGCCTTCGGCCAAACCTTCACCAGCTCTCT
GCAGTTCTCTTAG

Nucleotide

>MacEXPA-02

ATGGAGACGTCGGCTTTCTGCGCAGGACTGTTGGTCTTGCTGGTCTCGTCCTTCTT
CATGTCCGCCGACGTCGAGGGTTCTGCATCGCCTGGGTGGACTGCAGCTTCCGCG
ACATTTTATGGAGGGAGTGACGCCTCTGGGACCATGGGTAAAGCTTTAAGCATCCT
GCTGCTTCGTTGTTTCTCTGTTGGATCTCAATGGGTGGTCTGCTTCAGGTGGGG
CTTGCGGCTATGGCAATTTATACTCCACCGGCTACGGGACGGACACTGCAGCGCT

GAGCACGGCGCTCTTCGACGACGGGGATGCGTGCGGGCAGTGTTACAGGATCAT
GTGCGACTACCAGACGGATCCCCGGTGGTGTCTGCAAGGCACTTCGGTGACCATC
AGCGCCACCAACTTCTGCCCCGCAAACACTACGCCCTCCCCAACGACGACGGCGGGT
GGTGCAACCCCCCGCGGCAGCACTTCGATATGGCGCAGCCGGCGTGGGAGAAGA
TCGGCATCTACCGCGGGCGGAATCGTCCCGGTGCTGTACCAGAGGTAGTGCAGCAA
AAGCCTCATTGCTGCTGCTTCTTGCCGTATCCTTTTTGCTTGTCTATGTTTCGCTGA
CGGAATGCGGTGATCCGTAGGGTTCATGCGTGAAGCAGGGAGGAGTGAGGTTC
ACCATCAACGGGCGCGACTACTTCGAGCTCGTCCTGGTAACAAACGTGGGCGGGC
GCGGGTCGATCCAGTCCATGTCCATCAAAGGGTCAAACACCGGGTGGATGGCCAT
GTCGAGGAACTGGGGAGCAAACACTGGCAGTCGAATGCCTATCTAAACAGCCAATC
CCTCTCCTTCCGCGTCACCACCGGCGACGGGCAGATCCTCGTCTTCCCGGACGCC
GCCCCACCGAACTGGGCCTTCGGCCAAACCTTCACCAGCTCTCTGCAGTTCTCTTA
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