IDENTIFICATION

Species: *Musa acuminata*

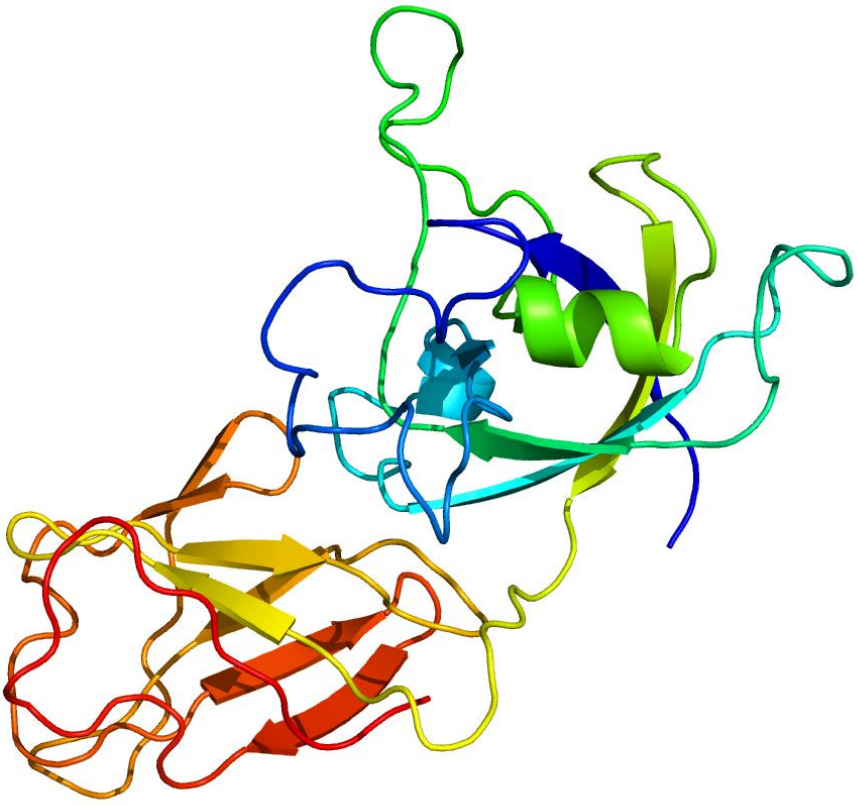
Locus: GSMUA_Achr2P18840_001

Gene Model: GSMUA_Achr2P18840_001

Description: MacEXPA-09

Family: Alpha Expansin

3D structure:



GENOME DATABASES

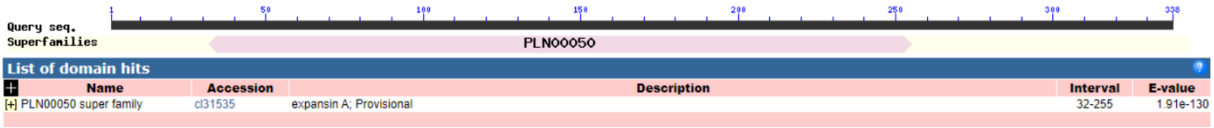
Phytozome: https://phytozome-next.jgi.doe.gov/info/Macuminata_v1
KEGG: https://www.genome.jp/entry/T03447

EXTERNAL RESOURCES

https://banana-genome-hub.southgreen.fr/
https://musabase.org/

GENE STRUCTURE

DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>MacEXPA-09

MAMPNCSLYHVLFFLLPSSCFFLSGALAESYGWRNAHATFYGGGDASGTMGGACGY
GNLYGQGYGTNTAALSTALFENGLSCGACYEMRCADDPRWCLPGSIVVTATNFCPP
NYALPNDNGGWCNPPLQHLDLAEPAFLQIAQYRAGIVPVSFRRVPCVRKGGIRFTING
RSYFNLVLITNVGGAGDVHAVSIKGSKTGWQSMSRNWGQNWQSNSYLDGQSLSFQ
VTTGDGRTVTGYNVAPAGWQFGQTFEGGQLGTKHERRAFRCLSAMCPTWAHGAFR
WGLRLMTNGSAESRVWYLGQDTGVPPAIAYNYKIAGSDGTESLLRKIISQNNAEHNK
*

CDS (coding sequence)

>MacEXPA-09

ATGGCTATGCCAAACTGCTCCCTCTACCATGTTCTCTTCTTCTTACTTCCTTCCTCG
TGCTTCTTCCTATCGGGAGCCCTCGCGGAGTCCTACGGATGGCGGAACGCCCATG
CCACGTTCTACGGCGGTGGCGACGCCTCCGGCACTATGGGAGGGGCTTGTGGCTA
CGGCAACCTCTACGGCCAGGGCTACGGGACCAACACCGCCGCCCTCAGCACCGC
GCTCTTCGAAAACGGGCTCAGCTGCGGCGCCTGCTACGAGATGCGGTGCGCCGAC
GATCCCCGGTGGTGCCTCCCGGGCTCCATCGTCGTCACCGCCACCAACTTCTGCCC
CCCAAACTACGCCCTCCCCAACGACAACGGCGGCTGGTGCAACCCTCCCCTGCAG
CACTTGGACCTCGCCGAGCCCGCCTTCCTCCAGATCGCTCAGTACCGCGCCGGAA
TCGTCCCCGTCTCCTTCCGCAGGGTGCCCTGCGTGAGGAAGGGAGGCATAAGGTT
CACCATCAACGGCCGCTCCTACTTCAACCTGGTGCTGATCACCAACGTCGGCGGG
GCCGGCGACGTGCACGCGGTGTCGATCAAGGGGTCCAAGACCGGGTGGCAGAGC
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GTCGCGCCCGCCGGGTGGCAGTTCGGGCAGACCTTCGAGGGAGGGCAGTTAGGG
ACCAAACACGAGAGGAGAGCCTTCCGTTGCTTGTCAGCCATGTGCCCCACCTGGG
CCCACGGTGCTTTTCGTTGGGGCCTGCGGCTGATGACCAATGGTAGTGCCGAGTC
CCGTGTTTGGTATCTCGGTCAAGACACAGGTGTCCCGCCCGCAATCGCATACAAT
TACAAAATCGCTGGTTCAGATGGAACAGAAAGTCTGTTGAGGAAAATAATATCA
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Nucleotide

>MacEXPA-09

ATGGCTATGCCAAACTGCTCCCTCTACCATGTTCTCTTCTTCTTACTTCCTTCCTCG
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CAATATCTCTCCATTATGTTTGCTGGAATTACCTCGAATATCTCTCGTGCATCTTA
AGGTCGCTCGGTTGGTTGATGCCGCAGGAGGGGCTTGTGGCTACGGCAACCTCTA
CGGCCAGGGCTACGGGACCAACACCGCCGCCCTCAGCACCGCGCTCTTCGAAAA
CGGGCTCAGCTGCGGCGCCTGCTACGAGATGCGGTGCGCCGACGATCCCCGGTGG
TGCCTCCCGGGCTCCATCGTCGTCACCGCCACCAACTTCTGCCCCCCAAACTACGC
CCTCCCCAACGACAACGGCGGCTGGTGCAACCCTCCCCTGCAGCACTTGGACCTC
GCCGAGCCCGCCTTCCTCCAGATCGCTCAGTACCGCGCCGGAATCGTCCCCGTCT
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GCTTCTCATGGCACAACGTTGCTGCTGTCTCACAGGGTGCCCTGCGTGAGGAAGG
GAGGCATAAGGTTCACCATCAACGGCCGCTCCTACTTCAACCTGGTGCTGATCAC
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CCTCGACGGGCAGAGCCTCTCCTTCCAGGTGACGACCGGCGACGGGAGGACGGT
CACCGGCTACAACGTCGCGCCCGCCGGGTGGCAGTTCGGGCAGACCTTCGAGGG
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TATCACAAAACAACGCCGAACACAATAAATAA