

IDENTIFICATION

Species: *Musa acuminata*

Locus: GSMUA_Achr11P19780_001

Gene Model: GSMUA_Achr11P19780_001

Description: MacEXPA-32

Family: Alpha Expansin

3D structure:



GENOME DATABASES

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

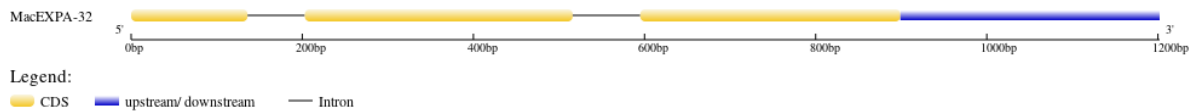
KEGG: <https://www.genome.jp/entry/T03447>

EXTERNAL RESOURCES

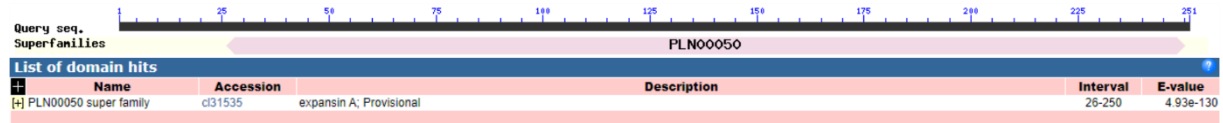
<https://banana-genome-hub.southgreen.fr/>

<https://musabase.org/>

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>MacEXPA-32

MAFPGFSLFLFSSIGLLAAGTSGDSGWQNAHATFYGGGDASGTMGGACGYGDLYS
QYGTNTAALSTALFGDGASCGACYELRCDDDPQWCLSGSIVVTATNFCPPNNALPN
DNGGWCNPLQHFDMAEPAFLQIAQYRAGIVPVAFRRVPCVKKGGIRFTINGHSYFN
LVLITNVGGAGDVHAVAIGKSSTGWQTMSRNWQNWQSNAYLNGQSLSFQVTTSD
GRTVISNDVAPAGWQFGQTFEGGQF*

CDS (coding sequence)

>MacEXPA-32

ATGGCATTCCCTGGCTTCTCCCTCCTCTTCCTCTTCTCTTCCATCGGCCTTCTCGCC
GCTGGCACTTCCGGGGACTCCGGCTGGCAGAACGCGCATGCCACCTTCTACGGCG
GCGGGGATGCCTCCGGCACCATGGGAGGGGCGTGTGGATACGGCGACCTCTACA
GCCAGGGGTACGGCACCAACACCGCCGCCCTCAGCACGGCGCTGTTCGGCGACG
GGCCAGCTGCGGGGCCTGCTACGAGCTGAGGTGCGACGACGACCCGCAGTGGT
GCCTCTCGGGGTGATCGTCGTCACCGCCACCAACTTCTGCCCGCCCAACAACGC
GCTCCCAACGACAACGGCGGATGGTGCAACCTCCCTCTCCAGCACTTCGACATG
GCCGAGCCGGCCTTCCCTTCAGATCGCTCAGTACCGTGCCGGGATCGTGCCGGTGG
CCTTCAGAAGGGTGCCGTGCGTGAAGAAGGGCGGGATCAGGTTCACCATCAACG
GCCACTCCTACTTCAACCTGGTGCTGATCACCAACGTGGGGGGCGCCGGCGACGT
GCATGCGGTGGCCATCAAGGGCTCAAGCACGGGATGGCAGACGATGTCGCGGAA
CTGGGGGCAGAACTGGCAGAGCAACGCGTACCTCAATGGCCAGTCTCTCTTTC
CAGGTCACCACCAGCGACGGCCGACCGTCATCAGTAACGACGTGCGGCCGGCC
GGGTGGCAGTTTGGCCAAACCTTCGAGGGAGGCCAATTCTAG

Nucleotide

>MacEXPA-32

ATGGCATTCCCTGGCTTCTCCCTCCTCTTCCTCTTCTCTTCCATCGGCCTTCTCGCC
GCTGGCACTTCCGGGGACTCCGGCTGGCAGAACGCGCATGCCACCTTCTACGGCG
GCGGGGATGCCTCCGGCACCATGGGTGAGTCCTTGTTTCGCATGTGAATTGCAGGA
GGTGCAGATATAGCTGATGACGGACGTGAATTGCAGGAGGGGCGTGTGGATACG
GCGACCTTACAGCCAGGGGTACGGCACCAACACCGCCGCCCTCAGCACGGCGC
TGTTTCGGCGACGGGGCCAGCTGCGGGGCCTGCTACGAGCTGAGGTGCGACGACG

ACCCGCAGTGGTGCCTCTCGGGGTCGATCGTCGTCACCGCCACCAACTTCTGCCC
GCCAACAACGCGCTCCCCAACGACAACGGCGGATGGTGCAACCTCCCTCTCCAG
CACTTCGACATGGCCGAGCCGGCCTTCCTTCAGATCGCTCAGTACCGTGCCGGGA
TCGTGCCGGTGGCCTTCAGAAGGTGAGCTCGGCTAGCTGCAACATGCAAACGAAC
TGCGCGCTACTCGATGGATCGATCGCTCATCGTGTGTGGGGTGCAGGGTGCCGTG
CGTGAAGAAGGGCGGGATCAGGTTACCATCAACGGCCACTCCTACTTCAACCTG
GTGCTGATCACCAACGTGGGGGGCGCCGGCGACGTGCATGCGGTGGCCATCAAG
GGCTCAAGCACGGGATGGCAGACGATGTGCGGGAAGTGGGGGCAGAACTGGCAG
AGCAACGCGTACCTCAATGGCCAGTCTCTCTCTTTCCAGGTCACCACCAGCGACG
GCCGGACCGTCATCAGTAACGACGTCGCGCCGGCCGGGTGGCAGTTTGGCCAAA
CCTTCGAGGGAGGCCAATTCTAGTTAACCTCGTCAACCCTACTCATCAAGGAGGG
AGAGGCTTTGTGCCAAAGCTGAGGTTGCTTGCCTAGCACCCGCTCATGGCTCTCT
TGGAATATAGGTATATATTTAAGATTGGATTGGCTATGCGTGATGTTACATGGA
TTATTTGCCTTGTGGAGGGATGGCAAGGTTTGAGATGCATGGTGGACAAGACAGA
GTGAAGCATATATGTGTACTTTTGTGGGGAATAGGGTGTGTTGTTGTTGGGATGT
GGGCAAATGTATTTGTTGTGGCCTCATATTTATAACAAGTATATTATTTGG