

IDENTIFICATION

Species: *Musa acuminata*

Locus: GSMUA_Achr11P00090_001

Gene Model: GSMUA_Achr11P00090_001

Description: MacEXLB-02

Family: Expansin Like Beta

3D structure:



GENOME DATABASES

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

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

EXTERNAL RESOURCES

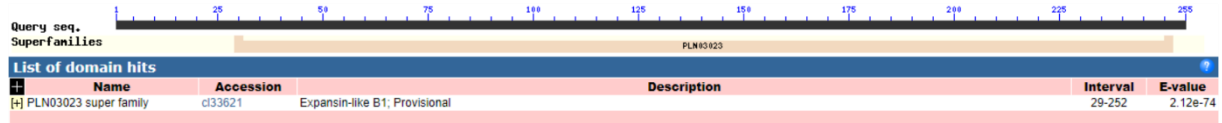
<https://banana-genome-hub.southgreen.fr/>

<https://musabase.org/>

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>MacEXLB-02

MTPSAAQLLLFSLILGSPATAATCSSCFRSRAVHYPDSDRRGTTGACEY GALGAT
LYGGDVSAASKLYRNGV GCGACYLVRCTIRGYCSR DGVVVVITDHGASDSADFILSQ
HFAKMGRSASAGAALLALGVVDVQYRRVPCSYPKKNITFKMDHSSDFPY YFAFQI
WYQQGDRDIVAVQLCETESLTCKLVDRSHGAVWAVAMP PRGPLSARMLLSGDDGD
VTWLVPNDVPEDWRAGAMYDSGIQVYS*

CDS (coding sequence)

>MacEXLB-02

ATGACTCCCTCGGCAGCGCAACTCCTCCTTCTCTTTACTCATCCTCGGGTCTCC
TGCAACTGCAGCCACATGCAGCAGTTGCTTCTCGCGGTCGAGAGCTGTTCACTAT
CCGGACTCCGACAGACGAGGAACAGAAACCGGAGCATGCGAGTATGGTGCCTTG
GGAGCCACACTCTACGGTGGGGATGTCTCTGCAGCATCAAAGCTCTACAGAAACG
GCGTGGGTTGCGGTGCATGTTATCTGGTCAGATGCACGATCAGAGGATACTGTTC
CAGAGATGGGGTTGTCGTCGTCATCACCGACCACGGAGCAAGCGACAGTGCAGA
TTTCATTCTTAGTCAGCACGCTTTTGCGAAGATGGGTCTGAAGCGCCTCCGCTGGC
GCCGCCCTTTTGGCTCTCGGTGTAGTTGACGTCCAGTACCGCAGGGTTCCCTTG
CAGCTACCCGAAGAAGAACATTACATTCAAGATGGATCACAGCAGCGACTTCCC
GTACTTTGCCTTCCAGATATGGTATCAACAAGGAGACCGGGATATAGTCGCCG
TTCAGCTATGCGAGACGGAGAGCTTGACGTGCAAGCTGGTGGATCGGAGCCAT
GGAGCGGTGTGGGCGGTGGCGATGCCACCGAGAGGGCCTCTCTCGGCGAGGAT
GCTGTTGAGTGGAGACGATGGCGATGTAACCTGGCTGGTACCGCCCAACGACGT
ACCGGAGGATTGGAGGGCGGGAGCCATGTACGATTCCGGGATACAAGTGTACTC
CTAA

Nucleotide

>MacEXLB-02

ATGACTCCCTCGGCAGCGCAACTCCTCCTTCTCTTTACTCATCCTCGGGTCTCC
TGCAACTGCAGCCACATGCAGCAGTTGCTTCTCGCGGTCGAGAGCTGTTCACTAT
CCGGACTCCGACAGACGAGGAACAGAAAGTAAGTACATAGAAAGGAAGGCCCTA
CTGCTTGCATTGTTCTTAATTTGCCTTTGCATCTCGTCTGAGCCTTTGAGGCGCA
CCTGTTTCAGCCGGAGCATGCGAGTATGGTGCCTTGGGAGCCACACTCTACGGTG
GGGATGTCTCTGCAGCATCAAAGCTCTACAGAAACGGCGTGGGTTGCGGTGCATG

TTATCTGGTACTTGACAATTCGATTTTAGTCCGAGTTCATGTTCTTTGTGCATTTCT
CTCTAGCCAGCATAACCTTCCAATCCCTTGATCACTACTAGGTCAGATGCACGATC
AGAGGATACTGTTCCAGAGATGGGGTTGTCGTCGTCATCACCGACCACGGAGCAA
GCGACAGTGCAGATTTCAATTCTTAGTCAGCACGCTTTTGCGAAGATGGGTCTGAAG
CGCCTCCGCTGGCGCCGCCCTTTTGGCTCTCGGTGTAGTTGACGTCCAGTACCGCA
GGTGTGTGTTTTCTTACTGCATGGTAATGATCACCGTCACATATAGTCTGGCGGAT
GGTGACCGCAGGCCGGCCATGGGGTTTTTCAGGGTTCCTTGCAGCTACCCGAAGAA
GAACATTACATTCAAGATGGATCACAGCAGCGACTTCCCGTACTACTTTGCCTTC
CAGATATGGTATCAACAAGGAGACCGGGATATAGTCGCCGTTTCAGCTATGCGAG
GTGCTGTATGATAACACAACCTTACCAGTTGATTCGTAGCATAAGAACAAATAG
GTGGTCGGTAAGAAAGCGTCATTTCTGTCTGGCTGCAGACGGAGAGCTTGACGTG
CAAGCTGGTGGATCGGAGCCATGGAGCGGTGTGGGCGGTGGCGATGCCACCGAG
AGGGCCTCTCTCGGCGAGGATGCTGTTGAGTGGAGACGATGGCGATGTAACCTGG
CTGGTACCGCCCAACGACGTACCGGAGGATTGGAGGGCGGGAGCCATGTACGAT
TCCGGGATAACAAGTGTACTCCTAA