IDENTIFICATION

Species: *Musa acuminata*

Locus: GSMUA_Achr5P11590_001

Gene Model: GSMUA_Achr5P11590_001

Description: MacEXLA-02

Family: Expansin Like Alpha

3D structure:

GENOME DATABASES

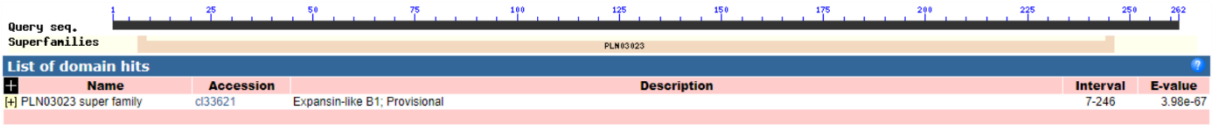
Phytozome: https://phytozome-next.jgi.doe.gov/info/Macuminata_v1
KEGG: https://www.genome.jp/entry/T03447

EXTERNAL RESOURCES

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

GENE STRUCTURE

DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>MacEXLA-02

MGCDSVCLIFVLFLLPCSAMACDRCVHQARAGYSSSSAFSVGACGYGSLALGFSGGY
VAAAGSSLHRGGIGCGACFQVRCKNTKICSSGGVKVILTDLNKISDTDLALNRPAYA
AMARYGMAKELKKLGIVDVEYKRIPCEHNKNLSIRVEEKSQSPNYLAIKVLYQGGQT
DIVAVDVAQVGSSDWQFMSREYGPVWSTNRAPPGPLQLRMVVTGGYDGKWVWSQ
EEVLPVDWKTGSVYDLRVQITDIAQEGCFTCDAKDW*

CDS (coding sequence)

>MacEXLA-02

ATGGGTTGTGACTCTGTCTGCTTGATTTTTGTTCTCTTCCTTCTTCCCTGCTCTGCT
ATGGCTTGTGACAGGTGTGTACATCAAGCCAGGGCTGGCTACTCCTCCTCCTCTG
CTTTCTCTGTCGGAGCTTGCGGATATGGTTCCTTGGCTTTGGGCTTCAGCGGAGGC
TATGTTGCTGCTGCAGGCTCTTCTCTTCACAGAGGTGGTATTGGCTGTGGAGCATG
TTTCCAGGTAAGATGCAAGAACACGAAGATATGCAGCAGCGGAGGTGTCAAAGT
GATCCTTACGGACCTCAACAAGATCAGCGACACCGATTTGGCTCTCAATAGGCCG
GCTTATGCAGCCATGGCACGATATGGGATGGCCAAAGAGCTGAAGAAACTGGGC
ATCGTAGATGTGGAATACAAGAGGATTCCATGTGAGCACAACAAGAACTTATCC
ATTAGAGTGGAAGAGAAAAGCCAAAGCCCGAACTATCTGGCCATCAAGGTCCTG
TATCAGGGAGGTCAGACTGATATAGTAGCAGTGGACGTGGCACAGGTGGGATCG
TCGGATTGGCAATTCATGAGCCGGGAATACGGACCTGTGTGGAGCACGAACCGG
GCGCCTCCGGGGCCGCTACAGCTCAGAATGGTGGTCACCGGCGGCTACGACGGG
AAGTGGGTTTGGTCTCAGGAGGAGGTCCTGCCGGTCGACTGGAAGACCGGGTCG
GTTTACGACTTGCGGGTTCAGATCACTGACATCGCTCAAGAAGGCTGCTTCACCT
GTGACGCAAAAGACTGGTAG

Nucleotide

>MacEXLA-02

ATGGGTTGTGACTCTGTCTGCTTGATTTTTGTTCTCTTCCTTCTTCCCTGCTCTGCT
ATGGCTTGTGACAGGTGTGTACATCAAGCCAGGGCTGGCTACTCCTCCTCCTCTG
CTTTCTCTGGTATGTTGCAGCACTGCAAACTTGTGCTTCTTTAGTTCAGTGCTCCA
AAGCAGAAGAGGTTTTATCCGGTTCGATCGGTTTGTCCTTACAGTCGGAGCTTGC
GGATATGGTTCCTTGGCTTTGGGCTTCAGCGGAGGCTATGTTGCTGCTGCAGGCTC

TTCTCTTCACAGAGGTGGTATTGGCTGTGGAGCATGTTTCCAGGTTAGATTCACAT
GCAATTCCACGTAAAACTTATTGCTCTTGTCAATCATATAATCACTCGTTTTAAGC
AGGTAAGATGCAAGAACACGAAGATATGCAGCAGCGGAGGTGTCAAAGTGATCC
TTACGGACCTCAACAAGATCAGCGACACCGATTTGGCTCTCAATAGGCCGGCTTA
TGCAGCCATGGCACGATATGGGATGGCCAAAGAGCTGAAGAAACTGGGCATCGT
AGATGTGGAATACAAGAGGTAGTGAGTTGAATGTTGGATGTCAGAGTTGTGGTCA
GACATGCATATATTGTTTCTCGCAACATGGTAGCCACTGTTGTTTCTGAATCGGAA
ACTTCTTCTTGTTTGCTGTGATCAGGATTCCATGTGAGCACAACAAGAACTTATCC
ATTAGAGTGGAAGAGAAAAGCCAAAGCCCGAACTATCTGGCCATCAAGGTCCTG
TATCAGGGAGGTCAGACTGATATAGTAGCAGTGGACGTGGCACAGGTAGTAAAA
AGGCTCACAAGAACCAATTGAACCGGAGTACTAATGCTACGCGTTGGGTCCACA
GGTGGGATCGTCGGATTGGCAATTCATGAGCCGGGAATACGGACCTGTGTGGAG
CACGAACCGGGCGCCTCCGGGGCCGCTACAGCTCAGAATGGTGGTCACCGGCGG
CTACGACGGGAAGTGGGTTTGGTCTCAGGAGGAGGTCCTGCCGGTCGACTGGAA
GACCGGGTCGGTTTACGACTTGCGGGTTCAGATCACTGACATCGCTCAAGAAGGC
TGCTTCACCTGTGACGCAAAAGACTGGTAG