

IDENTIFICATION

Species: *Musa acuminata*

Locus: GSMUA_Achr7P22100_001

Gene Model: GSMUA_Achr7P22100_001

Description: MacEXPA-25

Family: Alpha Expansin

3D structure:



GENOME DATABASES

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

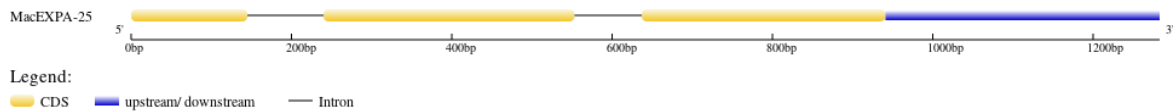
KEGG: <https://www.genome.jp/entry/T03447>

EXTERNAL RESOURCES

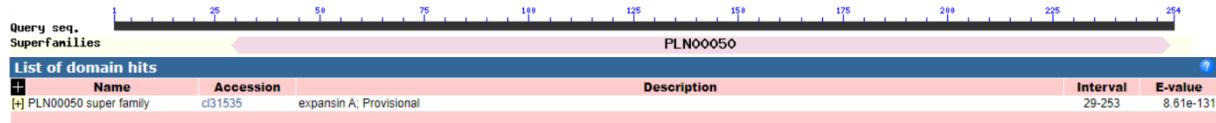
<https://banana-genome-hub.southgreen.fr/>

<https://musabase.org/>

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>MacEXPA-25

MASPNSSLSNAVFLFSSLGFLVAGASGYSGWESAHATFYGGGDASGTMGGACGYGN
LYSQYGTNTAALSTALFNDGLSCGSCYELKCDDDPRWCLPGSIVVTATNFCPPNNA
LPSDNGGWCNPPRPHFDMAQPAFLQIAQYRAGIVPVAFRRVPCVKKGGVRFTHINGHS
YFNLVLITNVAGAGDVHSVSIKGSKSGWQVMSRNWQONWQSNYSYLDGQSLFRITA
SDGRTITSFNVAPAGWQFGQTFEGGQF*

CDS (coding sequence)

>MacEXPA-25

ATGGCATCACCAAACCTCCTCCCTCTCCAATGCCGTCTTCCTCTTCTCTTCCCTCGG
CTTTCTCGTCGCCGGGGCCTCCGGGTACTCCGGGTGGGAGAGCGCCACGCCACG
TTCTACGGCGGGGGCGACGCTTCCGGCACCATGGGTGGAGCGTGTGGGTATGGCA
ACCTTTATAGCCAAGGCTATGGCACGAACACGGCGGGCGCTGAGCACGGCGCTGTT
CAACGACGGGCTCAGCTGCGGATCCTGCTACGAGCTGAAGTGCGACGACGACCC
GCGGTGGTGCCTCCCGGGGTCGATCGTGGTACCGCCACCAACTTCTGCCCGCCC
AACAACGCGCTCCCGAGCGACAATGGCGGGTGGTGAACCCGCCTCGGCCCCAC
TTCGACATGGCCCAGCCGGCCTTCCCTCCAGATCGCGCAGTACCGCGCCGGGATCG
TGCCGGTGGCCTTCAGAAGGGTGCCGTGCGTGAAGAAGGGCGGGGTGAGTTCA
CCATCAACGGCCACTCCTACTTCAACCTGGTGTGATACCAACGTCGCGGGGCGC
CGGCGACGTGCACTCCGTGTCCATCAAGGGCTCCAAGAGCGGGTGGCAGGTGAT
GTCCCGCAACTGGGGCCAGAACTGGCAGAGCAACTCCTACCTCGACGGCCAGAG
CCTCTCCTTCCGCATCACCGCCAGCGACGGCCGACCATCACAGCTTCAACGTC
GCGCCCGCCGGCTGGCAGTTCGGCCAGACCTTCGAGGGCGGGCCAGTTCTGA

Nucleotide

>MacEXPA-25

ATGGCATCACCAAACCTCCTCCCTCTCCAATGCCGTCTTCCTCTTCTCTTCCCTCGG
CTTTCTCGTCGCCGGGGCCTCCGGGTACTCCGGGTGGGAGAGCGCCACGCCACG
TTCTACGGCGGGGGCGACGCTTCCGGCACCATGGGTAACTAGCTGCCCTTTATGT
CTCTCTCTCTCTCCGTCAGTACGTATGGCGAGTGCTGTGGTTATATTGCTGCTG
CCTTTGTGTGAATGGCAGGTGGAGCGTGTGGGTATGGCAACCTTTATAGCCAAGG
CTATGGCACGAACACGGCGGGCGCTGAGCACGGCGCTGTTCAACGACGGGCTCAG

CTGCGGATCCTGCTACGAGCTGAAGTGCGACGACGACCCGCGGTGGTGCCTCCCG
GGGTCGATCGTGGTCACCGCCACCAACTTCTGCCCGCCCAACAACGCGCTCCCGA
GCGACAATGGCGGGTGGTGAACCCGCCTCGGCCCACTTCGACATGGCCCAGCC
GGCCTTCTCCAGATCGCGCAGTACCGCGCCGGGATCGTGCCGGTGGCCTTCAGA
AGGTGAGCTCCTTTCTCCCGAGACCCACGCGGGCGCCACCACGTCCGCGACATC
TCTCACTGATGTGCCTGCGATGCCGCTGCAGGGTGCCGTGCGTGAAGAAGGGCGG
GGTCAGGTTACCATCAACGGCCACTCCTACTTCAACCTGGTGCTGATCACCAAC
GTCGCGGGCGCCGGCGACGTGCACTCCGTGTCCATCAAGGGCTCCAAGAGCGGG
TGGCAGGTGATGTCCCCTCAACTGGGGCCAGAAGTGGCAGAGCAACTCCTACCTCG
ACGGCCAGAGCCTCTCCTTCCGCATCACCGCCAGCGACGGCCGCACCATCACCAG
CTTCAACGTCGCGCCCCGCCGGCTGGCAGTTCGGCCAGACCTTCGAGGGCGGCCAG
TTCTGACCTCCATCACTCCCATTCTTCCACCCACCAACCATCGCAGCAGGAAGAG
AGAGAAGAAACCTCTTCAAACACTATATATACATACATATTATGGGTGTGTGAGA
GAGAGATGATGCCAAGGCCGAGGTTGCTTGATGAGCACCCGCCAATGCCTTCTCT
TACAAGTAGAGACGTATCATATGATGCTGGTCTTAATTAGCTTATAAGGATTGCA
GGCAGTAGTACTACTCTATTATTCCTCATCAAATGGATGAGAGATGGCTGTGGGG
AGAGGCAACTGTACTCGTGTGTTGTGGCAAGACACTCATGAAATATATGAAACAT
GCATTGCTTGTTCGTTTGG