IDENTIFICATION

Species: *Musa acuminata*

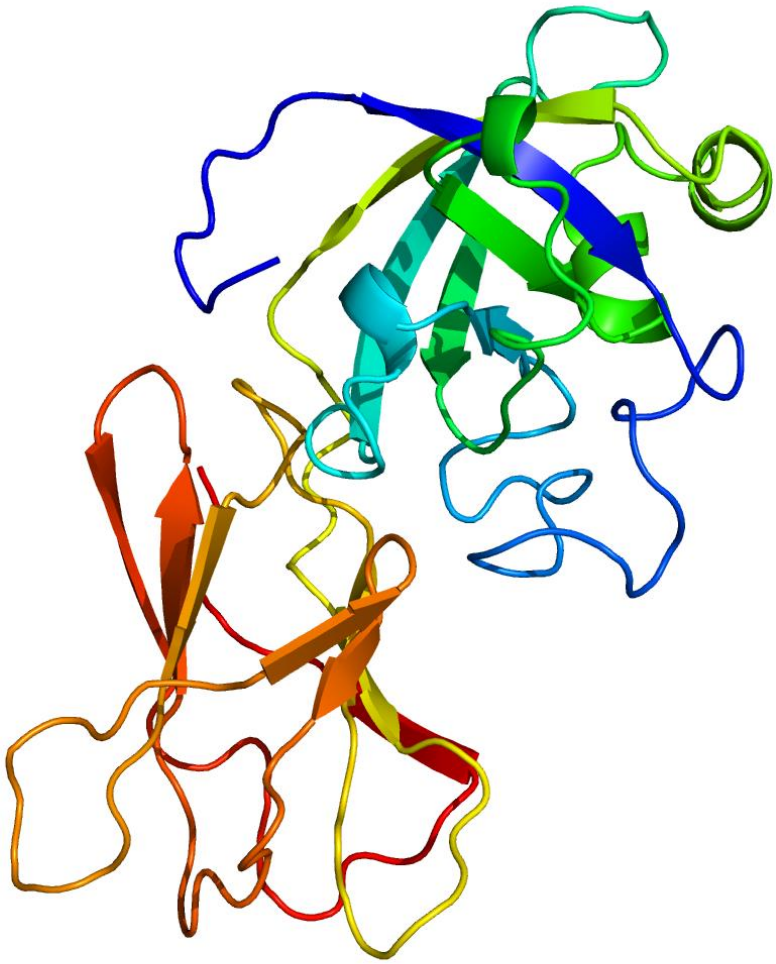
Locus: GSMUA_Achr1P00120_001

Gene Model: GSMUA_Achr1P00120_001

Description: MacEXPB-01

Family: Beta Expansin

3D structure:



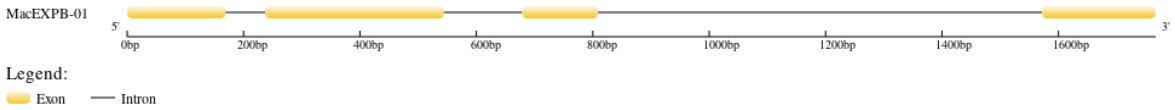
GENOME DATABASES

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

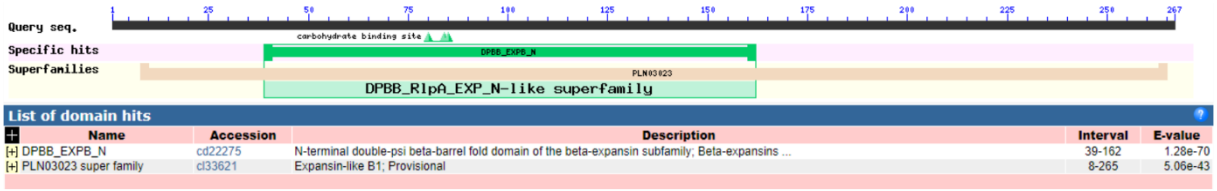
EXTERNAL RESOURCES

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

GENE STRUCTURE



DOMAIN ARCHITECTURE



List of domain hits

Name	Accession	Description	Interval	E-value
[+] DPBB_EXPB_N	cd22275	N-terminal double-psi beta-barrel fold domain of the beta-expansin subfamily; Beta-expansins ...	39-162	1.28e-70
[+] PLN03023 super family	cl33621	Expansin-like B1; Provisional	8-265	5.06e-43

SEQUENCES

Peptide

>MacEXPB-01

MASCFFSPFSFYYSFLLLSVFALFCFDTSEPHPVVDPHWHPATATWYGSPNGDGSDG
GACGYGSLVDVRPLRARVGAVSPVLFKGGEGCGACYKVRCLDPVVCARRPVTVIVT
DECPGGYCAFGRTHFDLSGAAFGRMAVPGKASRLRDRGEMPVVFRRTPCKYPGKSI
AFHVNEGSTNFWLSLLVEFEDDDGDIGSMHIKQANSVEWLEMKHIWGANWCIIGGP
LHGPFSVKLATLTTRKTFSARDVIPRNWSPKATYTSRLNLR*

CDS (coding sequence)

>MacEXPB-01

ATGGCTTCTTGCTTCTTCTCTCCCTTCTCCTTTTATTACTCCTTTCTTCTCTTGTCCG
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TGGCACCCGGCGACCGCGACCTGGTACGGCAGCCCCAACGGCGACGGCAGCGAC
GGTGGGGCGTGCGGGTACGGGTCGCTGGTGGACGTGCGGCCGCTGCGGGCGCGG
GTGGGGGCGGTGAGCCCCGTGTTGTTCAAGGGCGGGGAGGGGTGCGGCGCCTGC
TACAAGGTGCGCTGCCTGGACCCGGTCGTCTGCGCCCGCCGTCCCGTCACCGTCA
TCGTCACCGATGAGTGCCCCGGCGGGTACTGCGCCTTCGGCCGCACCCACTTCGA
CCTCAGCGGCGCCGCGTTCGGCCGCATGGCCGTCCCCGGCAAGGCCAGCCGGCTA
CGTGATCGTGGCGAGATGCCCGTCGTGTTCCGCAGGACTCCATGCAAATACCCAG
GTAAGAGTATCGCTTTTCATGTAAATGAAGGTTCCACAAACTTTTGGCTGTCACTT
CTTGTGGAGTTTGAGGACGATGATGGAGACATCGGATCCATGCATATAAAACAA
GCAAATTCTGTAGAGTGGCTAGAGATGAAGCACATATGGGGAGCAAATTGGTGT
ATCATTGGGGGGCCTCTGCACGGTCCCTTCTCAGTAAAGCTTGCTACGTTAACCA
CCCGGAAGACCTTCTCAGCTCGGGATGTGATTCCCAGGAACTGGTCTCCCAAAGC
CACCTACACCTCTCGGCTCAACTTACGTTAG

Nucleotide

>MacEXPB-01

ATGGCTTCTTGCTTCTTCTCTCCCTTCTCCTTTTATTACTCCTTTCTTCTCTTGTCCG
TGTTTGCCTTGTTCTGTTTCGATACCAGCGAACCACACCCCGTCGTCGACCCGCAT
TGGCACCCGGCGACCGCGACCTGGTACGGCAGCCCCAACGGCGACGGCAGCGAC

GGTGAGTAAGGTGTGGCCAGTAAAGTGTTACGTACAATGTGAATTGGTTGAGCGT
TCCGTGGTTGGCAGGTGGGGCGTGCGGGTACGGGTCGCTGGTGGACGTGCGGCC
GCTGCGGGCGCGGGTGGGGGCGGTGAGCCCCGTGTTGTTCAAGGGCGGGGAGGG
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TCAGAAGTATCTTTTCAGGACTCCATGCAAATACCCAGGTAAGAGTATCGCTTTT
CATGTAAATGAAGGTTCCACAAACTTTTGGCTGTCACTTCTTGTGGAGTTTGAGG
ACGATGATGGAGACATCGGATCCATGCATATAAAACAAGTACGTTTTTCTTACCT
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CATCTACTAGGTGTTTATAGACAGAACTGTTAGATGAAAGCTTATATTATGCTAT
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GCACATATGGGGAGCAAATTGGTGTATCATTGGGGGGCCTCTGCACGGTCCCTTC
TCAGTAAAGCTTGCTACGTTAACCACCCGGAAGACCTTCTCAGCTCGGGATGTGA
TTCCCAGGAACTGGTCTCCCAAAGCCACCTACACCTCTCGGCTCAACTTACGTTA
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