**IDENTIFICATION**

**Species:** *Musa acuminata*

**Locus:** GSMUA_Achr6P10730_001

**Gene Model:** GSMUA_Achr6P10730_001

**Description:** MacEXPA-21

**Family:** Alpha Expansin

**3D structure:**

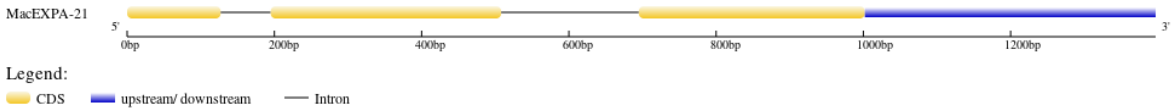
**GENOME DATABASES**

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

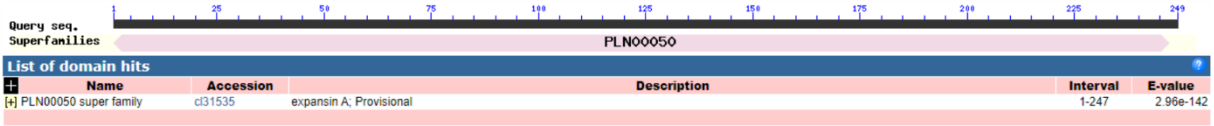
**EXTERNAL RESOURCES**

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

## GENE STRUCTURE




## DOMAIN ARCHITECTURE




## SEQUENCES

### Peptide

>MacEXPA-21

MRLLGLAVIAFVSLLSAAHGYGGGWTRAHATFYGGSDASGTMGGACGYGNLYSQG
YGTNTAALSTALFNNGLSCGACYELMCVNDHQYCLRGTIVVTATNFCPPNSALPND
AGGWCNPPLQHFDLSQPVFLRIAQYRAGIVPVAYRRVPCRKRGGIRFTINGHSYFNLV
LITNVGGAGDVNAVSVKGSRTGWQSMSRNWGQNWQSNSYLNGQALSFKVTTGDG
RSLVSYNVAPASWSFGQTFSGGQFR*

### CDS (coding sequence)

>MacEXPA-21

ATGCGTCTTCTTGGGCTTGCTGTGATTGCTTTCGTCTCGTTGCTCTCTGCTGCACAT
GGGTATGGAGGGGGATGGACCAGAGCTCATGCTACCTTCTATGGTGGAAGCGAT
GCGTCGGGGACAATGGGTGGTGCTTGTGGCTACGGCAACTTGTACAGCCAAGGGT
ATGGGACTAACACAGCTGCCCTGAGCACAGCCCTCTTCAACAATGGCCTCAGCTG
TGGAGCTTGCTATGAGCTGATGTGCGTGAACGACCACCAATACTGCCTGCGGGGA
ACCATCGTGGTCACTGCCACCAACTTCTGCCCGCCCAACAGCGCCCTCCCAAACG
ATGCTGGGGGATGGTGTAACCCTCCCCTGCAGCATTTCGATCTCTCTCAGCCCGTC
TTCCTCCGCATTGCTCAGTACAGGGCTGGAATTGTGCCCGTCGCGTATCGCAGGG
TCCCATGCAGGAAGAGAGGAGGGATCAGGTTCACCATCAATGGCCACTCCTACTT
CAACCTGGTTCTGATCACCAACGTTGGAGGAGCCGGAGATGTGAACGCGGTGTCC
GTCAAAGGGTCCAGGACCGGGTGGCAGTCCATGTCCAGGAACTGGGGCCAGAAC
TGGCAGAGCAACAGCTACCTCAATGGCCAAGCCCTCTCCTTCAAGGTCACCACCG
GCGACGGACGCTCTCTGGTCTCCTACAATGTGGCTCCTGCAAGCTGGTCCTTCGG
ACAAACCTTCAGCGGTGGCCAATTCCGCTAA

### Nucleotide

>MacEXPA-21

ATGCGTCTTCTTGGGCTTGCTGTGATTGCTTTCGTCTCGTTGCTCTCTGCTGCACAT
GGGTATGGAGGGGGATGGACCAGAGCTCATGCTACCTTCTATGGTGGAAGCGAT
GCGTCGGGGACAATGGGTGAGCTAAGGAAACTAAGACTGATATCCACGACTTGG
ATCTCTAATCGGTGAACCTTGGGAATGCAGGTGGTGCTTGTGGCTACGGCAACTT
GTACAGCCAAGGGTATGGGACTAACACAGCTGCCCTGAGCACAGCCCTCTTCAAC
AATGGCCTCAGCTGTGGAGCTTGCTATGAGCTGATGTGCGTGAACGACCACCAAT

ACTGCCTGCGGGGAACCATCGTGGTCACTGCCACCAACTTCTGCCCGCCCAACAG
CGCCCTCCCAAACGATGCTGGGGGATGGTGTAACCCTCCCCTGCAGCATTTCGAT
CTCTCTCAGCCCGTCTTCCTCCGCATTGCTCAGTACAGGGCTGGAATTGTGCCCGT
CGCGTATCGCAGGTTGGTCATCCACATCAGAAACCTTCTTCCTTCCATCACTAAAG
TTTGGTTTGAGAGTTGTGATGCACGACCACAAACCTTTTACCCTCCTTCGGCACAC
GTAGTCTCTTGCTCTCTGTTCTTTGTTCACTTTGGGCTTTGGTCTTGTCTTACTCGC
TGTGATCTTGATCGTGGACTTGGAACGCAGGGTCCCATGCAGGAAGAGAGGAGG
GATCAGGTTCACCATCAATGGCCACTCCTACTTCAACCTGGTTCTGATCACCAAC
GTTGGAGGAGCCGGAGATGTGAACGCGGTGTCCGTCAAAGGGTCCAGGACCGGG
TGGCAGTCCATGTCCAGGAACTGGGGCCAGAACTGGCAGAGCAACAGCTACCTC
AATGGCCAAGCCCTCTCCTTCAAGGTCACCACCGGCGACGGACGCTCTCTGGTCT
CCTACAATGTGGCTCCTGCAAGCTGGTCCTTCGGACAAACCTTCAGCGGTGGCCA
ATTCCGCTAAACCATTTCGGTTCGCGGTAAAGATTACATTGCATGGTATATACTG
GAGTCTCAGTGTACAATTTAGAGATCAGAGGGGCTTGTTTTACTTCGGCCCTTCGT
AGTATTGGTATTGAATTCGTCGTCTAGGCCTTGTATTAGAGGCTTACTACTGCTCT
TGGAGAAGAAAAGTTAAGGGAACTGCTTCTCTCTTCGGGCAGATGCTAGCAGCG
GTGGAATCCTACTACCCGCTCGGTATCAGATAGGATGAGGGACGGGTGTTTTTGG
TGTGGTGTTCTTTTAACTCTGAGAGAAGGAGATTCTGAAGAGAAGGCTCCTTTTT
GCTTGTACTGTTGTTGCATTTGCTGTATTAACCATATAATTTATGCTAAGTGGATC
TATTTGTTTTGGAAGATG