

IDENTIFICATION

Species: *Manihot esculenta*

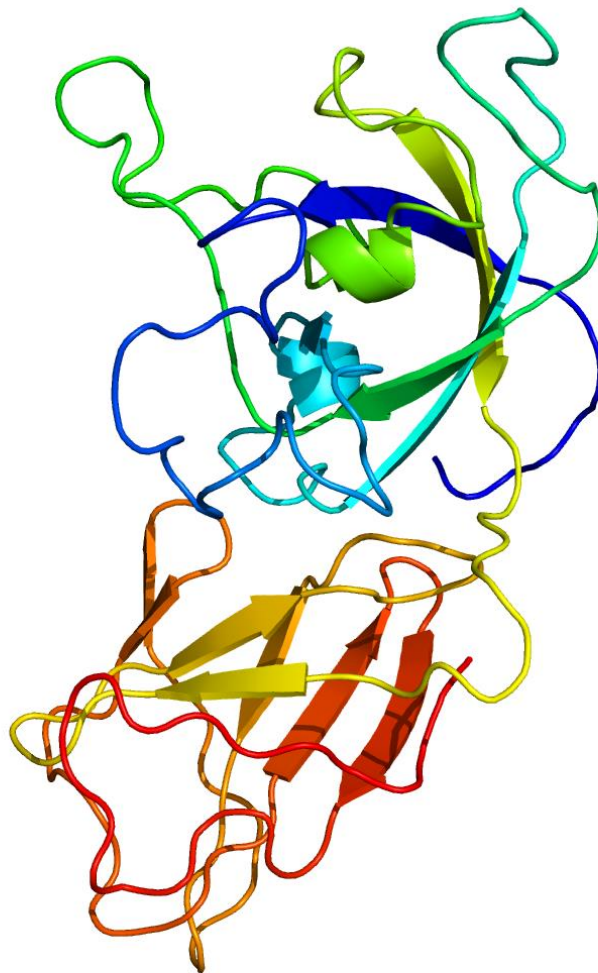
Locus: Manes.05G006600

Gene Model: Manes.05G006600.1

Description: MsEXPA-12

Family: Alpha Expansin

3D structure:



GENOME DATABASES

Phytozome: https://phytozome-next.jgi.doe.gov/info/Mesculenta_v7_1

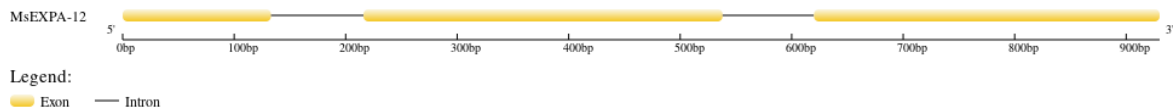
KEGG: <https://www.genome.jp/entry/T05761>

EXTERNAL RESOURCES

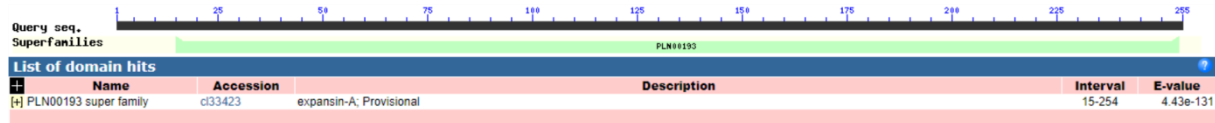
<https://cassavagenome.org/>

<https://cassavabase.org/>

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>MsEXPA-12

MQILTMPFVLLLGLFSSKPYVASAAWLRAHATFYGGNDASGTMGGACGYGNLYTD
GYGVKTAALSTALFNDGKSCGGCYQIVCDGTQVPQWCLKGSSITITATNFCPPNYNL
PNDNGGWCNPPRPHFDMSQPAFETIAKYRAGIVPVFYRRVGCRRSGGIRFTINGRDYF
ELVLISNVGGAGEISSVWIKGSKSNRWETMSRNWGVNWQSLSYLNGQSLSFRVQAS
DGSIVTALNVVPSNWVFGQSFKSNVQF*

CDS (coding sequence)

>MsEXPA-12

ATGCAGATACTGACCATGCCTTTTGTCTTTCTCTTGCTGGGGCTTTTCTCCTCAA
ACCATACGTAGCATCAGCTGCTTGGCTCCGAGCCCATGCAACTTTCTATGGTGGG
AATGATGCTTCTGGTACAATGGGCGGTGCTTGTGGATATGGAAATCTATACACCG
ATGGTTATGGAGTCAAACTGCTGCACTGAGCACAGCTTTGTTCAACGATGGCAA
GTCATGTGGTGGGTGCTATCAGATTGTCTGCGATGGAACCCAGGTCCCCCAATGG
TGCCTTAAGGGCTCATCGATTACTATTACTGCTACAACTTCTGCCACCAAATTA
TAATCTCCCTAATGACAATGGAGGGTGGTGAATCCTCCACGGCCACACTTCGAC
ATGTCTCAACCTGCATTCGAGACCATTGCCAAGTACCGGGCCGGAATTGTACCTG
TTTTCTACCGGAGAGTGGGATGCAGGAGAAGTGGGGGCATAAGATTCACAATCA
ATGGAAGGGACTACTTTGAGCTTGTGCTGATATCAAATGTAGGAGGAGCAGGAG
AGATCTCCAGTGTGTGGATCAAAGGGTCTAAGTCCAACAGATGGGAGACCATGTC
AAGAAATTGGGGTGTGAATTGGCAGAGCCTGAGCTATCTAAATGGGCAGAGCTT
GTCGTTTAGAGTCCAAGCCAGCGACGGAAGTATCGTCACTGCTCTAACGTTGTA
CCTTCCAACCTGGGTGTTTGGGCAGTCCTTCAAAGCAATGTTCAATTCTAG

Nucleotide

>MsEXPA-12

ATGCAGATACTGACCATGCCTTTTGTCTTTCTCTTGCTGGGGCTTTTCTCCTCAA
ACCATACGTAGCATCAGCTGCTTGGCTCCGAGCCCATGCAACTTTCTATGGTGGG
AATGATGCTTCTGGTACAATGGGTAAGTTTCCATTCTATTTCCATGCGAGAATTG
ATCAGCTGTAGCTAATATTTGTGATAATCTCATGTGCTGAATGTTATAGGCGGTGC
TTGTGGATATGGAAATCTATACACCGATGGTTATGGAGTCAAACTGCTGCACTG
AGCACAGCTTTGTTCAACGATGGCAAGTCATGTGGTGGGTGCTATCAGATTGTCT
GCGATGGAACCCAGGTCCCCCAATGGTGCCTTAAGGGCTCATCGATTACTATTAC
TGCTACAACTTCTGCCACCAAATTATAATCTCCCTAATGACAATGGAGGGTGG

TGCAATCCTCCACGGCCACACTTCGACATGTCTCAACCTGCATTCGAGACCATTG
CCAAGTACCGGGCCGGAATTGTACCTGTTTTCTACCGGAGGTAAGTTCTCAACCC
TCATCAATAAACTTAATATTTATGGGAATCTTTTCTAAATATTGAATGACAAGCTG
TGGTGAATCAGAGTGGGATGCAGGAGAAGTGGGGGCATAAGATTCACAATCAAT
GGAAGGGACTACTTTGAGCTTGTGCTGATATCAAATGTAGGAGGAGCAGGAGAG
ATCTCCAGTGTGTGGATCAAAGGGTCTAAGTCCAACAGATGGGAGACCATGTCAA
GAAATTGGGGTGTGAATTGGCAGAGCCTGAGCTATCTAAATGGGCAGAGCTTGTC
GTTTAGAGTCCAAGCCAGCGACGGAAGTATCGTCACTGCTCTTAACGTTGTACCT
TCCAACTGGGTGTTTGGGCAGTCCTTCAAAAGCAATGTTCAATTCTAG