

IDENTIFICATION

Species: *Manihot esculenta*

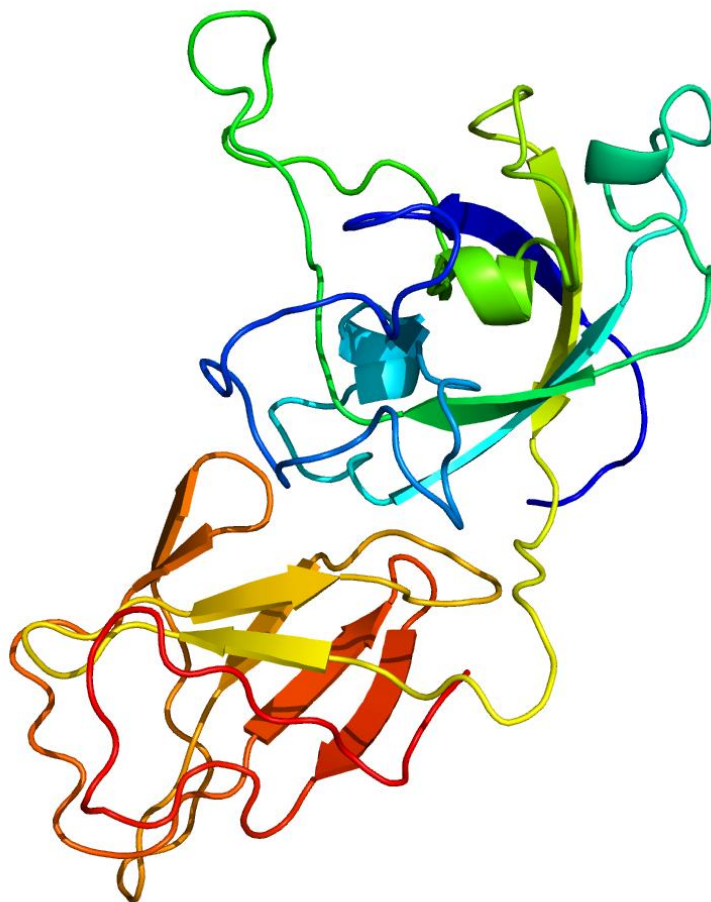
Locus: Manes.01G236600

Gene Model: Manes.01G236600.1

Description: MsEXPA-04

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

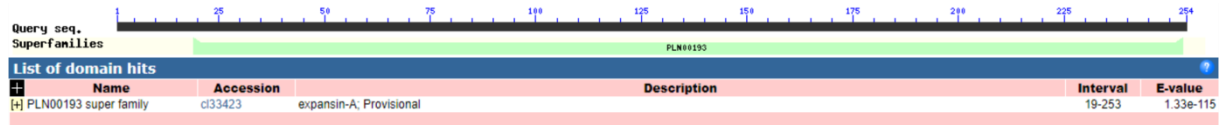
<https://cassavagenome.org/>

<https://cassavabase.org/>

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>MsEXPA-04

MVLMPFVFLLLGLFFTQRYVASGDWLQAHATFYGGDGSMTMGGACGYGNLYTDG
YGIKTAALSTALFNDGNGCGGCYQIACDATQVPQWCLNGTSSITITATNFCPPNYNLP
NDNGGWCNPPRSHFDMSQPAFESIAKYEAGIVPIFYRKVRCEKSGGIRFTIHGNDYFE
LVLISNVGGAGEISNVWIKGSRSKIWEAMSRNWGENWQSLSYLNQSLSFKVQASD
GSTLTALDVVPSNWTFTGQSFTSNIQF*

CDS (coding sequence)

>MsEXPA-04

ATGGTACTGATGCCTTTTGTGTTCCCTATTGCTTGGGCTCTTCTTCACACAACGATA
TGTCGCATCAGGCGATTGGCTGCAAGCCCATGCAACTTTCTACGGTGGAGGTGAC
GGTTCTGGTACGATGGGCGGTGCCTGTGGATATGGAAATCTCTACACAGATGGCT
ATGGAATCAAACACTGCTGCACTGAGCACAGCTCTGTTCAACGATGGCAACGGATG
CGGTGGCTGTTATCAGATTGCTTGCGATGCCACTCAGGTTCCCTCAATGGTGCCTTA
ACGGTACATCATCCATTACGATCACTGCTACAACTTCTGTCCACCGAATTATAAT
CTTCTAACGACAATGGTGGGTGGTGCACCCCAAGATCACACTTCGACATGT
CTCAACCTGCCTTCGAGTCTATTGCCAAGTACGAAGCTGGAATTGTACCTATTTTC
TACAGAAAGGTCAGATGCGAGAAAAGTGGGGGCATAAGATTTACCATCCATGGA
AACGACTACTTTGAGCTTGTGCTCATATCAAATGTAGGAGGAGCAGGAGAGATCT
CCAATGTGTGGATCAAAGGATCTAGATCCAAGATATGGGAAGCCATGTCAAGGA
ATTGGGGTGAAAATTGGCAGAGCCTAAGCTATCTGAATGGCCAGAGCTTGTCTT
CAAAGTCCAAGCAAGCGACGGGAGTACCCTCACTGCTCTTGACGTGGTTCCTTCC
AACTGGACGTTTGGCCAATCCTTACAAGCAATATTCAGTTCTAG

Nucleotide

>MsEXPA-04

ATGGTACTGATGCCTTTTGTGTTCCCTATTGCTTGGGCTCTTCTTCACACAACGATA
TGTCGCATCAGGCGATTGGCTGCAAGCCCATGCAACTTTCTACGGTGGAGGTGAC
GGTTCTGGTACGATGGGTAAGTGTCCATTCTCCTTTTCTTATTTCCCATCTTTTGC
TTGGTACAAAAAATCTATAATCTGCTTAGTTTCAATGCAAGAATTAGCTCG
ATAATGGTTGTATATTTGGTGACCTCTCATAGGCGGTGCCTGTGGATATGGAAAT
CTCTACACAGATGGCTATGGAATCAAACACTGCTGCACTGAGCACAGCTCTGTTCA
ACGATGGCAACGGATGCGGTGGCTGTTATCAGATTGCTTGCGATGCCACTCAGGT
TCCTCAATGGTGCCTTAACGGTACATCATCCATTACGATCACTGCTACAACTTCT

GTCCACCGAATTATAATCTTCCTAACGACAATGGTGGGTGGTGCAACCCCCCAAG
ATCACACTTCGACATGTCTCAACCTGCCTTCGAGTCTATTGCCAAGTACGAAGCT
GGAATTGTACCTATTTTCTACAGAAAGTATGTTCTCAATCCTCGTCCATTATCTTA
ACATTTATGGGAAACTTTTCAGGATACGATCATTACTAGAATATTATTTTAAAAA
TGAATGAAAGATTCTGTTTTGTTTTATCAGGGTCAGATGCGAGAAAAGTGGGGGC
ATAAGATTTACCATCCATGGAAACGACTACTTTGAGCTTGTGCTCATATCAAATG
TAGGAGGAGCAGGAGAGATCTCCAATGTGTGGATCAAAGGATCTAGATCCAAGA
TATGGGAAGCCATGTCAAGGAATTGGGGTGAAAATTGGCAGAGCCTAAGCTATC
TGAATGGCCAGAGCTTGTCTTCAAAGTCCAAGCAAGCGACGGGAGTACCCTCAC
TGCTCTTGACGTGGTTCCTTCCAACCTGGACGTTTGGCCAATCCTTCACAAGCAATA
TTCAGTTCTAG