

IDENTIFICATION

Species: *Manihot esculenta*

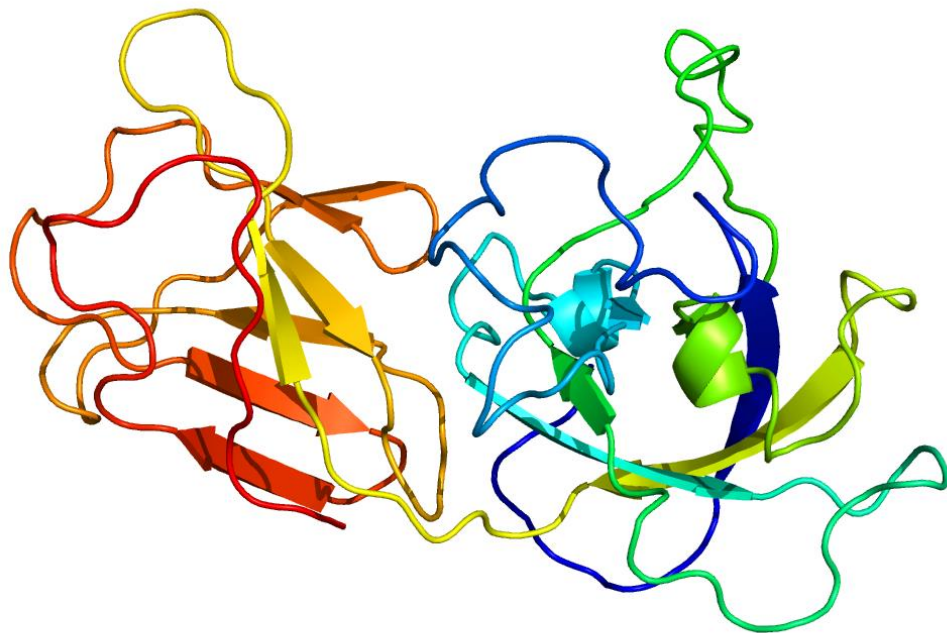
Locus: Manes.15G113800

Gene Model: Manes.15G113800.1

Description: MsEXPA-31

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

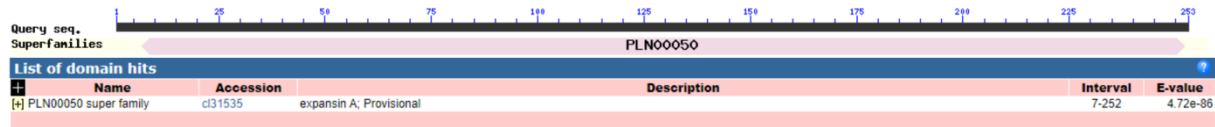
<https://cassavagenome.org/>

<https://cassavabase.org/>

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>MsEXPA-31

MGALKALVHLIMLQTCKIAATNATDEEWKTATATYTKEQFGSITIEGACGYGDIHR
ATYGKYSAGLSSMLFNKGSTCGACFEVRCVDHILWCLQGSPSILTATDFCPPNYGLS
ADYGGWCNFPKEHFEMSEAAFTEIAERKADLIPIQYRRVKCERKGGVRFRTASGSFNFL
QVLITNVGVDGEVVAVKVKGSRTGWIPMARNWQNWQSNVNLVGQPLSFEVTTSS
RTLTAYNVAPANWQFGQTFEGKQF*

CDS (coding sequence)

>MsEXPA-31

ATGGGTGCTCTTAAAGCCTTAGTTCTGCACTTGATCATGTTACAGACATGCAAGA
TTGCTGCCACTAATGCCACTGATGAGGAATGGAAGACGGCCACTGCAACTTACAC
CAAAGAACAATTTGGGTCAATCACTATAGAAGGAGCTTGTGGGTATGGTGATATT
CACAGAGCCACCTATGGTAAGTATAGTGCTGGATTGAGTAGTATGTTGTTCAACA
AAGGGAGTACCTGTGGAGCTTGCTTTGAGGTCAGATGCGTAGATCACATCTTATG
GTGCTGCAAGGTAGCCCCTCTATCATTCTCACTGCCACAGATTTCTGTCTCCAA
ATTATGGGCTTTTACAGCAGATTATGGTGGCTGGTGCAATTTTCCCAAAGAACATTTT
GAGATGTCAGAGGCAGCATTCACTGAAATTGCTGAAAGGAAAGCCGATTTAATTC
CAATCCAGTACAGGAGGGTGAAGTGTGAGAGGAAGGGTGGGGTGAGATTCACAG
CTAGTGGGAGTTTTAACTTCTTACAGGTGCTCATTACCAACGTAGGAGTAGATGG
TGAAGTGGTTGCAGTGAAGGTGAAGGGATCAAGAACAGGATGGATACCTATGGC
AAGAACTGGGGCCAGAAGTGGCAATCCAATGTCAATCTTGTGGACAGCCTCTT
TCTTTTGAAGTCACTACTAGCAGCAGAACTCACAGCTTACAATGTTGCACCAG
CAAAGTGGCAATTCGGTCAGACATTTGAGGGCAAACAATTCTAG

Nucleotide

>MsEXPA-31

ATGGGTGCTCTTAAAGCCTTAGTTCTGCACTTGATCATGTTACAGACATGCAAGA
TTGCTGCCACTAATGCCACTGATGAGGAATGGAAGACGGCCACTGCAACTTACAC
CAAAGAACAATTTGGGTCAATCACTATAGGTAACTTTTCTCATTACTAGTCTACC
ATTTGGGTAAATGTTCCACCATTTCAACTCATACTGGGGCTTCATGTTCCACACAT
CTCGGTTCTAATTGAGAATGCAGAAATACATAAGTATGGTTCGATTTTCAAGATAGGA
TGGGATTAAGTCTCGGCTAAGCTCAGTTGAGTTGAATATATACGGTTTTTGCAAGT
GTGTAATGGCCTTTTTTGGTGTTCAGAAAGGAGCTTGTGGGTATGGTGATATTCAC
AGAGCCACCTATGGTAAGTATAGTGCTGGATTGAGTAGTATGTTGTTCAACAAAG

GGAGTACCTGTGGAGCTTGCTTTGAGGTCAGATGCGTAGATCACATCTTATGGTG
CCTGCAAGGTAGCCCCTCTATCATTCTCACTGCCACAGATTTCTGTCCTCCAAATT
ATGGGCTTTCAGCAGATTATGGTGGCTGGTGCAATTTCCCAAAGAACATTTTGA
GATGTCAGAGGCAGCATTCACTGAAATTGCTGAAAGGAAAGCCGATTTAATTCCA
ATCCAGTACAGGAGGTATAAGAATGAAATTACAAATAATTTGCAAAATAGTTAC
AATTAATAAGCAAACATTATTATTGCAATTTTATGCAGGGTGAAGTGTGAGAGGA
AGGGTGGGGTGAGATTCACAGCTAGTGGGAGTTTTAACTTCTTACAGGTGCTCAT
TACCAACGTAGGAGTAGATGGTGAAGTGGTTGCAGTGAAGGTGAAGGGATCAAG
AACAGGATGGATACCTATGGCAAGAACTGGGGCCAGAACTGGCAATCCAATGT
CAATCTTGTTGGACAGCCTCTTTCTTTTGAAGTCACTACTAGCAGCAGAACACTCA
CAGCTTACAATGTTGCACCAGCAAACCTGGCAATTCGGTCAGACATTTGAGGGCAA
ACAATTCTAG