

IDENTIFICATION

Species: *Manihot esculenta*

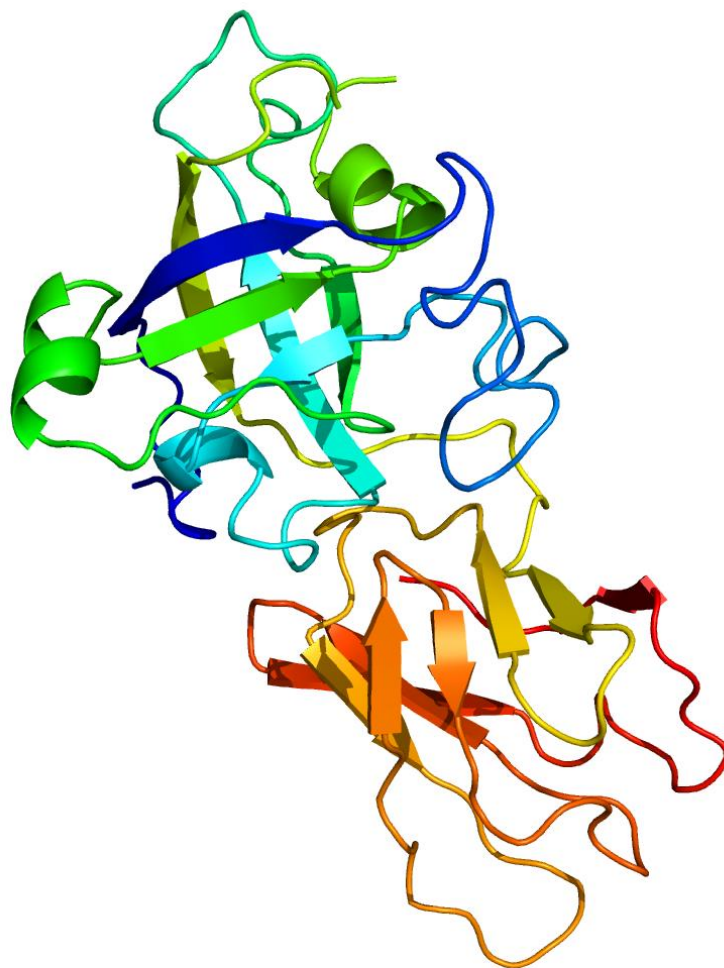
Locus: Manes.03G111500

Gene Model: Manes.03G111500.1

Description: MsEXPA-11

Family: Alpha Expansin

3D structure:



GENOME DATABASES

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

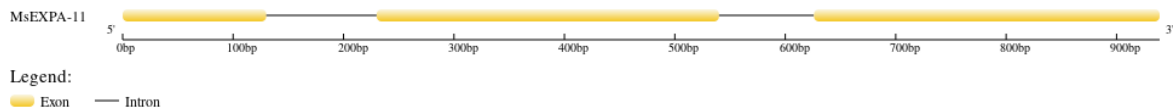
KEGG: <https://www.genome.jp/entry/T05761>

EXTERNAL RESOURCES

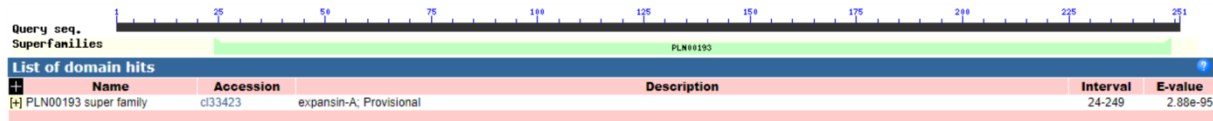
<https://cassavagenome.org/>

<https://cassavabase.org/>

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>MsEXPA-11

MGPIKTL CFLILGLFLEGINQQLNGWIHAHATFYGANQNPSTLGGACGYDNTFFHAGF
GVHTAAVSGALFRNGEACGACYQVMCDFKADPKWCFRRVAVVTVTNFCPANNG
GWCDDPRHHFDMSPAFLRIARQGNIGVPIYRRVACKRRGGVHFTLRGQSNFNLI
MISNVGGSGDIKAAWVRGSRTRTWVPMNRNWGANWQSSVDLRSQTL SFKLT LVDG
KTLAFFNVVPSTWSIGQTYSSRNQFS*

CDS (coding sequence)

>MsEXPA-11

ATGGGGCCTATCAAAACTTTGTGTTTTCTCATTTTAGGTTTGT TTTTGGAGGGCAT
TAATGGTCAACTTAACGGTTGGATTCATGCTCATGCCACTTTCTATGGTGCCAATC
AAAATCCCAGCACTCTTGGAGGAGCTTGTGGATATGATAATACGTTCCATGCTGG
ATTTGGAGTGCACACAGCAGCAGTCAGCGGTGCACTTTTTAGAAACGGAGAAGCT
TGTGGGGCTTGCTACCAAGTCATGTGCGACTTCAAGGCTGACCCTAAGTGGTGTT
TCCGACGAGCTGTTGTGACGGTAACCACCACAAATTTCTGCCCAGCAAACAATAA
TGGAGGATGGTGTGATCCTCCTCGCCACCCTTCGATATGTCCATGCCTGCTTTTC
TTCGCATCGCTAGACAAGGCAATGAAGGCATTGTTCCAGTAATCTACAGAAGGGT
GGCATGCAAGAGAAGGGGAGGTGTTTCATTTACATTAAGAGGACAATCGAATTT
CAATTTGATAATGATATCCAACGTTGGAGGAAGTGGTGATATTAAGGCTGCATGG
GTTAGAGGATCTAGGACAAGAACATGGGTGCCAATGAACAGAACTGGGGTGCA
AATTGGCAAAGCAGTGTGACCTTAGAAGCCAAACGCTGTCGTTAAACTCACTT
TGGTTGATGGAAAAACACTTGCGTTCCTCAATGTTGTCCCTTCAACATGGAGTATT
GGACAGACATATTCTTCACGAAATCAGTTCTCTTAG

Nucleotide

>MsEXPA-11

ATGGGGCCTATCAAAACTTTGTGTTTTCTCATTTTAGGTTTGT TTTTGGAGGGCAT
TAATGGTCAACTTAACGGTTGGATTCATGCTCATGCCACTTTCTATGGTGCCAATC
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AAAATTATCTTTTTTTTTCCCTCTGTGATAAAATCGCTGGAGAATGTGTTGACTAT
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CACAGCAGCAGTCAGCGGTGCACTTTTTAGAAACGGAGAAGCTTGTGGGGCTTGC
TACCAAGTCATGTGCGACTTCAAGGCTGACCCTAAGTGGTGTTTCCGACGAGCTG
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TGATCCTCCTCGCCACCACTTCGATATGTCCATGCCTGCTTTTCTTCGCATCGCTA
GACAAGGCAATGAAGGCATTGTTCCAGTAATCTACAGAAGGTAACAGAAAGTCG
CTAGAGAAATTGACGTTTCTATTGAATTTTTTTATATATGTTTGTTAAAATTGATT
ATTATGAATATTGAAGGGTGGCATGCAAGAGAAGGGGAGGTGTTCAATTCACATT
AAGAGGACAATCGAATTTCAATTTGATAATGATATCCAACGTTGGAGGAAGTGGT
GATATTAAGGCTGCATGGGTTAGAGGATCTAGGACAAGAACATGGGTGCCAATG
AACAGAAACTGGGGTGCAAATTGGCAAAGCAGTGTTGACCTTAGAAGCCAAACG
CTGTCGTTTAAACTCACTTTGGTTGATGGAAAAACACTTGCGTTCTTCAATGTTGT
CCCTTCAACATGGAGTATTGGACAGACATATTCTTCACGAAATCAGTTCTCTTAG