IDENTIFICATION

Species: *Manihot esculenta*

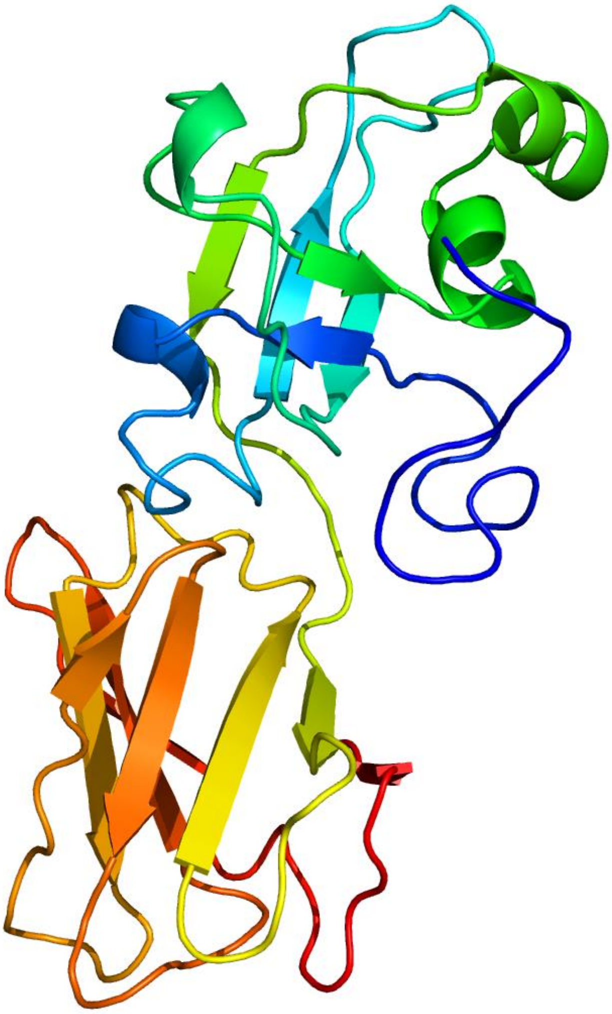
Locus: Manes.06G090900

Gene Model: Manes.06G090900.1

Description: MsEXPA-15

Family: Alpha Expansin

3D structure:



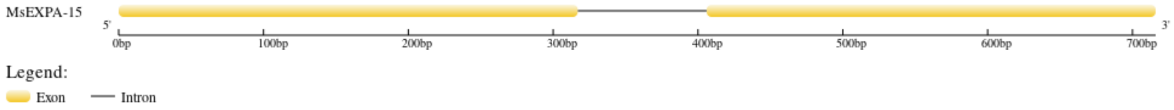
GENOME DATABASES

Phytozome: https://phytozome-next.jgi.doe.gov/info/Mesculenta_v7_1
KEGG: https://www.genome.jp/entry/T05761

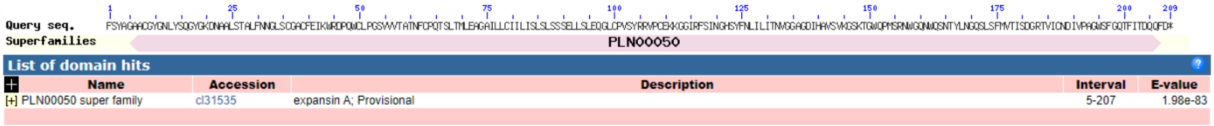
EXTERNAL RESOURCES

https://cassavagenome.org/
https://cassavabase.org/

GENE STRUCTURE



DOMAIN ARCHITECTURE



List of domain hits

Name	Accession	Description	Interval	E-value
[+] PLN00050 super family	cl31535	expansin A; Provisional	5-207	1.98e-83

SEQUENCES

Peptide

>MsEXPA-15

FSYAGAACGYGNLYSQGYGKDNAALSTALFNNGLSCGACFEIKWRDPQWCLPGSVV
VTATNFCPQTSLTMLEAGAILLCIILISLSLSSSELLSLEQGLCPVSYRRVPCEKKGGIRF
SINGHSYFNLILITNVGGAGDIHAVSVKGSKTGWQPMSRNWGQNWQSNTYLNGQSL
SFMVTISDGRTVICNDIVPAGWSFGQTFITDQQFD*

CDS (coding sequence)

>MsEXPA-15

TTCTCTTATGCAGGTGCGGCCTGTGGGTATGGAAACCTATACAGCCAAGGTTACG
GGAAAGACAATGCAGCTTTGAGCACAGCATTGTTCAACAATGGCTTGAGCTGTGG
AGCCTGTTTTGAAATAAAATGGAGGGACCCGCAGTGGTGCCTACCAGGCTCAGTT
GTGGTTACAGCTACCAATTTCTGCCCACAGACCTCACTAACCATGCTGGAGGCTG
GTGCAATCCTCCTCTGCATCATTTTGATCTCGCTCAGCCTGTCTTCTAGCGAATTG
CTAAGTTTAGAGCAGGGATTGTGCCCGGTGTCTTATAGAAGGGTACCATGCGAGA
AGAAAGGAGGAATAAGATTCTCAATCAATGGGCACTCATACTTCAACTTAATACT
GATAACCAACGTTGGAGGTGCTGGCGATATTCATGCAGTTTCAGTAAAAGGGTCA
AAAACTGGATGGCAACCCATGTCAAGAAACTGGGGTCAAAACTGGCAAAGCAAC
ACATACCTCAACGGACAAAGCCTCTCGTTTATGGTGACAATTAGTGATGGACGCA
CTGTGATCTGTAATGATATAGTACCTGCTGGGTGGTCCTTCGGCCAGACCTTCATT
ACCGACCAACAGTTTGATTAA

Nucleotide

>MsEXPA-15

TTCTCTTATGCAGGTGCGGCCTGTGGGTATGGAAACCTATACAGCCAAGGTTACG
GGAAAGACAATGCAGCTTTGAGCACAGCATTGTTCAACAATGGCTTGAGCTGTGG
AGCCTGTTTTGAAATAAAATGGAGGGACCCGCAGTGGTGCCTACCAGGCTCAGTT
GTGGTTACAGCTACCAATTTCTGCCCACAGACCTCACTAACCATGCTGGAGGCTG
GTGCAATCCTCCTCTGCATCATTTTGATCTCGCTCAGCCTGTCTTCTAGCGAATTG
CTAAGTTTAGAGCAGGGATTGTGCCCGGTGTCTTATAGAAGGTATATCATACATG
CACTTGCATGTCTCTCAATATAGATTCAGCGCTGTTTATCAAAAAATTGGGATTTA
TATATGAAATTTATTATAGGGTACCATGCGAGAAGAAAGGAGGAATAAGATTCTC
AATCAATGGGCACTCATACTTCAACTTAATACTGATAACCAACGTTGGAGGTGCT
GGCGATATTCATGCAGTTTCAGTAAAAGGGTCAAAAACTGGATGGCAACCCATGT
CAAGAAACTGGGGTCAAAACTGGCAAAGCAACACATACCTCAACGGACAAAGCC

TCTCGTTTATGGTGACAATTAGTGATGGACGCACTGTGATCTGTAATGATATAGT
ACCTGCTGGGTGGTCCTTCGGCCAGACCTTCATTACCGACCAACAGTTTGATTAA