

## IDENTIFICATION

**Species:** *Manihot esculenta*

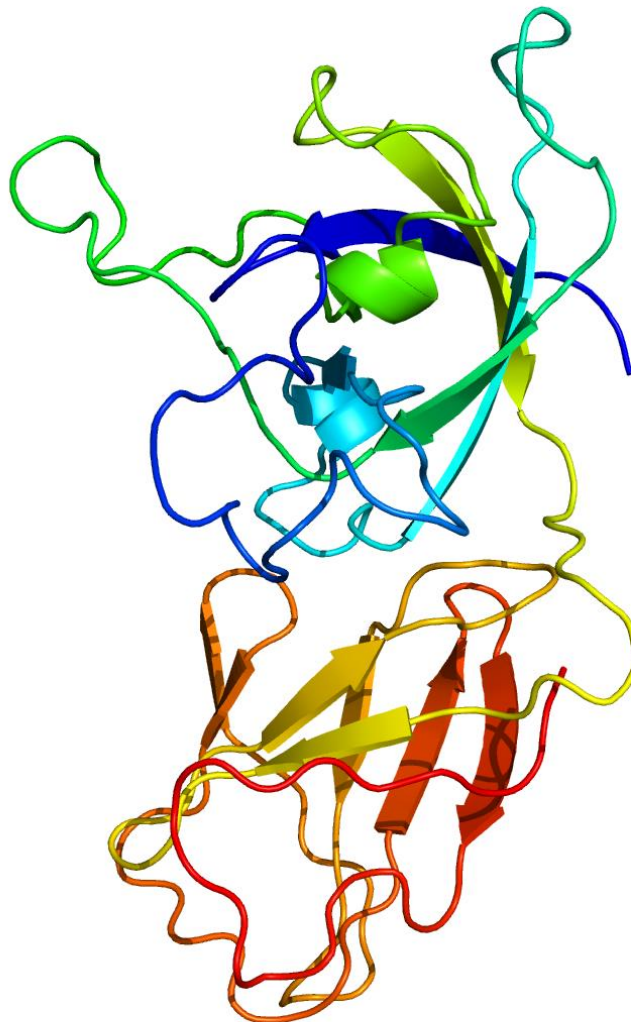
**Locus:** Manes.S055800

**Gene Model:** Manes.S055800.1

**Description:** MsEXPA-33

**Family:** Alpha Expansin

**3D structure:**



## GENOME DATABASES

Phytozome: [https://phytozome-next.jgi.doe.gov/info/Mesculenta\\_v7\\_1](https://phytozome-next.jgi.doe.gov/info/Mesculenta_v7_1)

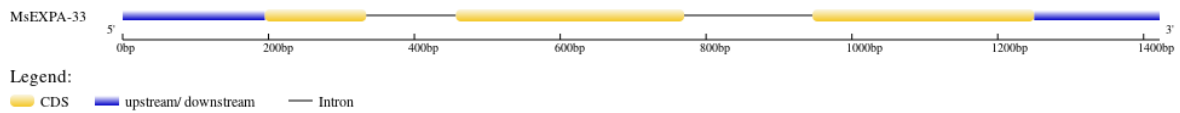
KEGG: <https://www.genome.jp/entry/T05761>

## EXTERNAL RESOURCES

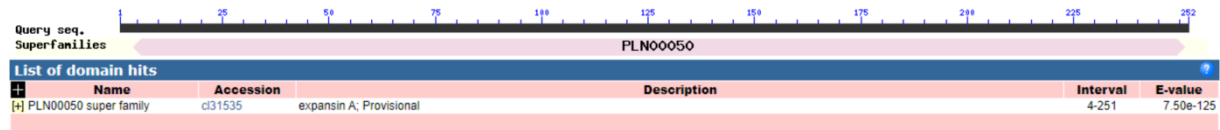
<https://cassavagenome.org/>

<https://cassavabase.org/>

## GENE STRUCTURE



## DOMAIN ARCHITECTURE



## SEQUENCES

### Peptide

>MsEXPA-33

MSAETLSFSLILLCFSLSLREILADYGGWESAHATFYGGGDASGTMGGACGYGNLYG  
QGYGTNTAALSTALFNNGMSCGACYEMRCDDDPWCLPGTLT VTATNFCPPNPSLP  
NNGGWCNPPQLQHFDLAEP AFLQIAQYRAGIVPVAFRRVPCVKKGGTRFTINGHSYF  
NLVLITNVAGAGDVHAVSIKGSRTGWQPMSRNWQNWQSN SYLNGQSLSFQVTTTS  
DGRTVTSYNVVPAGWQFGQTFEGGQF\*

### CDS (coding sequence)

>MsEXPA-33

ATGTCGGCTGAAACACTTTCTTTCTCTCTTATTCTCTTGTGTTTCTCACTCTCTTTA  
CGCGAAATTTTAGCTGATTATGGAGGGTGGGAGAGTGCTCATGCCACCTTCTACG  
GCGGCGGTGATGCTTCAGGAACAATGGGAGGAGCATGCGGGTACGGGAATTTGT  
ATGGGCAAGGGTATGGAACAAACACAGCAGCACTAAGCACAGCGTTGTTCAACA  
ATGGAATGAGCTGTGGAGCATGTTATGAAATGAGATGTGATGATGATCCAAGAT  
GGTGTCTTCCTGGGACCCTCACTGTTACTGCTACTAATTTTTGTCCACCAAATCCT  
TCTCTCCCAACAACAATGGCGGATGGTGTAAATCCTCCTCTCCAGCACTTCGATTT  
GGCTGAGCCTGCTTTCTCCAGATTGCTCAATACCGTGCTGGAATTGTCCCTGTCCG  
CCTTTCGAAGGGTTCATGTGTGAAGAAAGGAGGAACAAGGTTACCATTAATGG  
TCACTCTTACTTCAACCTGGTGTGATCACCAACGTCGCCGGTGCAGGAGATGTT  
ATGCAGTTTCGATCAAAGGATCCAGAACAGGATGGCAACCAATGTCAAGAAATT  
GGGACAAAACACTGGCAAAGTAACTCTTACCTCAACGGTCAAAGCCTATCCTTTCA  
AGTCACCACCAGTGACGGTAGAACTGTGACAAGCTACAACGTGGTGCCTGCTGGT  
TGGCAGTTTGGCCAGACCTTTGAAGGAGGCCAATTTTAA

### Nucleotide

>MsEXPA-33

TGATTTTCCTATACCAGCTTTTTCTAGCTTGTGTTTGGCCTTTTCTTCAATGCTCAA  
ACCCACCTACTGGGTTTTTCTCCTTCCCTCTGCTTATAAATACTCGCTCATATTC  
ATGCCTTTGGACAACAAAACCTTAAATTAGCAAATTTAGTTTTAATTTAGTGTTTT  
CTTCCCTTGGTTTGTCTCAATTGGCAATGTCGGCTGAAACACTTTCTTTCTCTTTAT  
TCTCTTGTGTTTCTCACTCTCTTTACGCGAAATTTAGCTGATTATGGAGGGTGGG  
AGAGTGCTCATGCCACCTTCTACGGCGGGCGGTGATGCTTCAGGAACAATGGGTAA  
GTGTTATATATTTTCTCTAAAGTCGAATTTTATGAAATTTTAAATTTCAATTCAGA  
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ATGTATAGGAGGAGCATGCGGGTACGGGAATTTGTATGGGCAAGGGTATGGAAC  
AAACACAGCAGCACTAAGCACAGCGTTGTTCAACAATGGAATGAGCTGTGGAGC  
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ACTGTTACTGCTACTAATTTTTGTCCACCAAATCCTTCTCTCCCAACAACAATGG  
CGGATGGTGTAAATCCTCCTCTCCAGCACTTCGATTTGGCTGAGCCTGCTTTCCTCC  
AGATTGCTCAATACCGTGCTGGAATTGTCCCTGTCGCCTTTCGAAGGTAACCTTAA  
AAAAATAAAAACATATATTTAAAAGCTTGAGATTCAAAGTATTAACCTAATTAAA  
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AAATATGAAATTTAAAAGAAATTAAGTATGTTTTGTCTATAAATGATGTGGACA  
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CTTCAACCTGGTGTGATCACCAACGTCGCCGGTGCAGGAGATGTTTCATGCAGTT  
TCGATCAAAGGATCCAGAACAGGATGGCAACCAATGTCAAGAAATTGGGGACAA  
AACTGGCAAAGTAACTCTTACCTCAACGGTCAAAGCCTATCCTTTCAGTCACCA  
CCAGTGACGGTAGAACTGTGACAAGCTACAACGTGGTGCCTGCTGGTTGGCAGTT  
TGGCCAGACCTTTGAAGGAGGCCAATTTAAGGCTTATTATTATTTTTTTAAATAT  
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AAGAAATAAAAATAAAAATATATATATGTAATGCAAA