

IDENTIFICATION

Species: *Manihot esculenta*

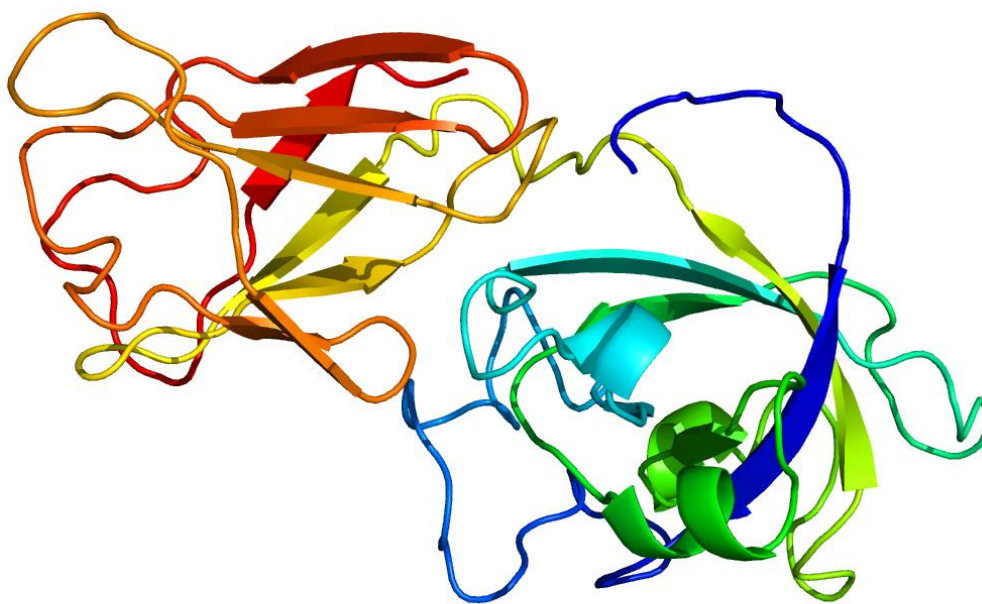
Locus: Manes.02G053000

Gene Model: Manes.02G053000.2

Description: MsEXPA-07

Family: Alpha Expansin

3D structure:



GENOME DATABASES

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

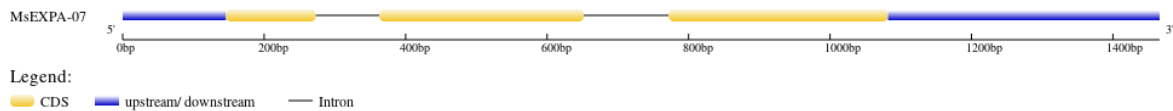
KEGG: <https://www.genome.jp/entry/T05761>

EXTERNAL RESOURCES

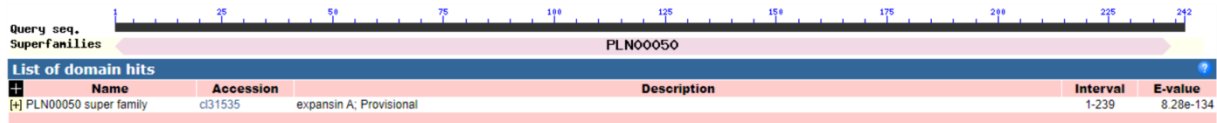
<https://cassavagenome.org/>

<https://cassavabase.org/>

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>MsEXPA-07

MALLGFLAVGFLSLVSSAHGYGGWINAHATFYGGDASGTMGGACGYGNLYSQG
YGINTAALSTALFDNGLSCGACFELRCVNDPQWCLPGSIVVTATNFCPPGGWCDPPN
HHFDLSQPIFQHIAQYRAGIVPVSYRRVSKRSGGIRFTINGHSYFNLVLVTNVGGAG
DVHAVAIAKGSRTRWQPMSRNWQNWQSN SYLNGQSL SFLVTTSDSRSVLSYNVAPA
GWSFGQTYTGSQFRY*

CDS (coding sequence)

>MsEXPA-07

ATGGCTCTTCTTGGATTTCTTGCAGTTGGATTTCTCTCACTTGTCTCATCTGCTCAT
GGATACTATGGAGGTTGGATTAATGCCCATGCCACCTTCTATGGAGGTGGTGACG
CTTCTGGCACAATGGGTGGAGCTTGC GGTTATGGTAACCTCTACAGCCAAGGTTA
TGGAATTAACACAGCAGCACTAAGCACTGCATTATTTGACAATGGCTTGAGCTGC
GGAGCTTGCTTTGAGCTCAGGTGTGTGAATGATCCACAATGGTGCCCTCCCTGGCT
CCATTGTTGTCACTGCCACTAATTTCTGCCACCAGGAGGCTGGTGTGACCCTCCC
AACCATCACTTTGATCTCTCTCAACCAATCTTCCAACACATTGCCCAGTACAGAGC
TGGTATTGTCCAGTAAGTTACAGAAGGGTAAGCTGCAAGAGAAGTGGAGGCAT
TAGGTTACGATCAATGGACATTCCTACTTCAATTTAGTACTGGTAACCAATGTA
GGTGGAGCAGGCGATGTACATGCAGTAGCCATAAAGGGTTCAAGA ACTAGATGG
CAACCAATGTCAAGAACTGGGGCCAAA ACTGGCAGAGTAACTCTTACCTGAAT
GGACAGAGTCTCTTTTCTAGTCACCACCAGTGACAGCCGTAGTGTGCTCTCTTA
CAATGTTGCCCTGCTGGCTGGTCCTTTGGCCAGACATACTGGAAGCCAATTT
CGATATTAA

Nucleotide

>MsEXPA-07

CTCATTTCACCCCTCACAGCAACTCCTTCAAGCTTCCTTTTCTTGTATTAATCTTT
TCCTTATCTTCTTGTCTTCTTACCCATTTTGAATTATAAATTTAAAGCATGTGCT
CAAGTGTCCACATGGTTAATTTGTGCAGGAAAATGGCTCTTCTTGGATTTCTTGCA
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AACTGGTTATCTTTTTTTTTTCTAGGTGGAGCTTGC GGTTATGGTAACCTCTACA
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AGTACAGAGCTGGTATTGTCCCAGTAAGTTACAGAAGGTAGGCCAATTA AAAAC
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AGTACTGGTAACCAATGTAGGTGGAGCAGGCGATGTACATGCAGTAGCCATAAA
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GAGTAACTCTTACCTGAATGGACAGAGTCTCTCTTTTCTAGTCACCACCAGTGAC
AGCCGTAGTGTGCTCTCTTACAATGTTGCCCTGCTGGCTGGTCCTTTGGCCAGAC
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GATGCATTATTAAGCTACAGTATGGATTGAGCAACTACTAATTAGTGCACCTTTG
GTAAAATAGAGTGCACCTTAGAAGAGATCTTGGGGGGTCAAGATTTCTCATGAAT
TGGCCCTTTTTGATTTCTCCCATAGTATTGAGTTTTTGCAGTTGAAGAATTGGCC
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AAGTCAGTTTTTTCATTGCTGTTACTGTATCAACTTATAGACGCAAGTCCTTCTGA
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