

IDENTIFICATION

Species: *Manihot esculenta*

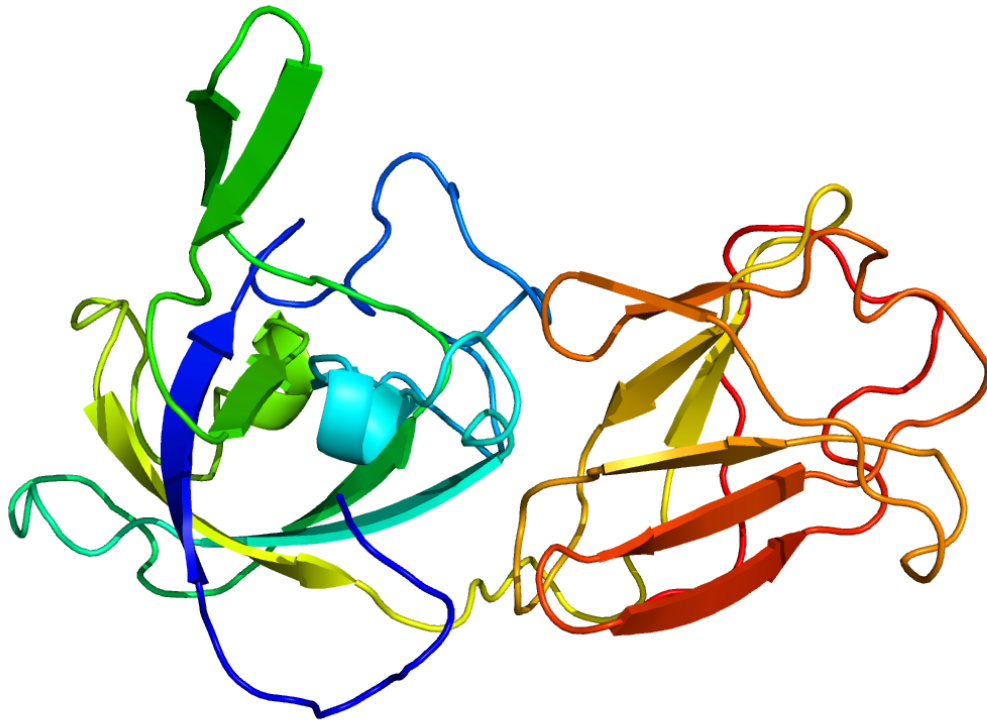
Locus: Manes.08G172000

Gene Model: Manes.08G172000.1

Description: MsEXPA-23

Family: Alpha Expansin

3D structure:



GENOME DATABASES

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

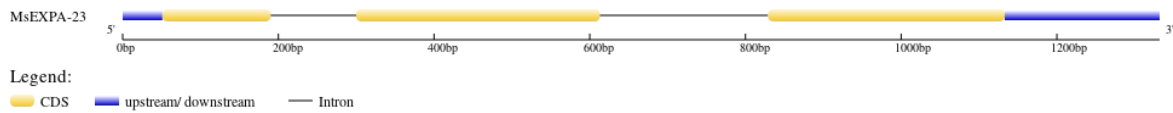
KEGG: <https://www.genome.jp/entry/T05761>

EXTERNAL RESOURCES

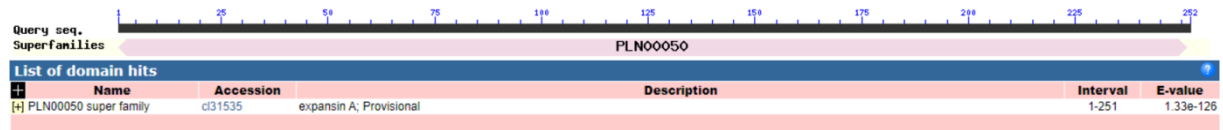
<https://cassavagenome.org/>

<https://cassavabase.org/>

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>MsEXPA-23

MQILSFLRILVVFSLCVHGTYGDNHNLGGWQSAHATFYGGSDASGTMGGACGYGNLY
SQYGTHTAALSTALFNNGFSCGACFQIRCNDPKWCLSRITITVTATNFCPPNYALSN
DNNGWCNPPLQHFDLAEP AFLQIAQYRAGIVPVLFRRVPC LKKGGLRFTINGNSYFNL
VLITNVGGAGDVRAVSVKGSRTGWQTMSRNWQNWQSN SFLSGQSL SFRVTTSDG
RTVSSYNVVPANWQFGQTFEGGQF*

CDS (coding sequence)

>MsEXPA-23

ATGCAAATCTTATCATTCTTCGCATACTAGTTGTGTTTCAGCTTATGTGTTTCATGG
CACTTATGGAGACCACAACCTTGGTGGCTGGCAGAGTGCCCATGCTACATTCTAT
GGAGGCAGTGATGCTTCAGGCACAATGGGTGGTGCTTGTGGATACGGAAACCTGT
ACAGCCAAGGATATGGAACACACACCGCAGCTCTAAGCACTGCCCTTTTAAACAA
TGGCTTCAGCTGTGGTGCCTGCTTCCAGATACGCTGCAACAATGATCCAAAGTGG
TGTCTCTCTCGAACCATCACTGTCACAGCCACCAACTTCTGCCACCAAATTATGC
TTTATCCAATGATAATGGTGGTTGGTGCAATCCCCCTCTCCAACATTTTGATTTGG
CTGAGCCTGCTTTCTTGCAGATTGCTCAATATCGAGCTGGAATTGTTCCCTGTACTC
TTCAGAAGGGTCCCATGTTTGAAAAAAGGGGGATTGAGGTTACCATCAATGGTA
ATTCTTACTTCAACTTGGTCCTGATAACGAATGTGGGTGGAGCAGGGGATGTCCG
GGCAGTGTCCGTCAAGGGGTCCAGAACGGGGTGGCAAACACTATGTCAAGAAATTG
GGGACAAAATTGGCAGAGCAACTCATTCTCAGTGGCCAAAGCCTCTCCTTTAGA
GTTACCACCAGCGACGGCAGGACTGTCTCCAGCTACAATGTAGTGCCTGCCAATT
GGCAATTTGGACAAACTTTCGAGGGGAGGTCAATTCTAG

Nucleotide

>MsEXPA-23

CACCTTCCAACCTTAGTTCCCAATTTCTCTCTTTGCATCAGTAAAGCAAGAATGCA
AATCTTATCATTTCTTCGCATACTAGTTGTGTTTCAGCTTATGTGTTTCATGGCACTTA
TGGAGACCACAACCTTGGTGGCTGGCAGAGTGCCCATGCTACATTCTATGGAGGC
AGTGATGCTTCAGGCACAATGGGTAAAGCAAGAAAGTCTTCAATTACCAATTACCG
CTTCATTTTCTTTTTTCTTTTTTTCTTTTTTAAACAAAAGCCTTACGTGAAGGTG
TACTTGGTGTGCCCCGCAGGTGGTGTGTTGTGGATACGGAAACCTGTACAGCCAA
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TCGAACCATCACTGTCACAGCCACCAACTTCTGCCACCAAATTATGCTTTATCCA
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GCTTTCTTGCAGATTGCTCAATATCGAGCTGGAATTGTTCCCTGTACTCTTCAGAAG
GTAATTTATTTATCATAACAACACTCAATAGAGTCCAGGCAGAACAATCATGGACAT
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CTTTTGCTGTGACTTTTGAAAATCCAAATTATTGAGTTGTTTTCTGACAGGGTCCC
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AGGGGTCCAGAACGGGGTGGCAAACACTATGTCAAGAAATTGGGGACAAAATTGGC
AGAGCAACTCATTCTCAGTGGCCAAAGCCTCTCCTTTAGAGTTACCACCAGCGA
CGGCAGGACTGTCTCCAGCTACAATGTAGTGCCTGCCAATTGGCAATTTGGACAA
ACTTTCGAGGGAGGTCAATTCTAGCAACACTTAAAAGATTGACGAAAATTTGCTT
TTAATTGCAATAGAATAACAAGGATACTTAGTAATATGGCCGGTTATGCAGAGGTC
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TCTTTCGACAACAGAGTGGGATGGAATAAAGCAATTATGGTCCACTTCTTTGGA
GCT