

IDENTIFICATION

Species: *Manihot esculenta*

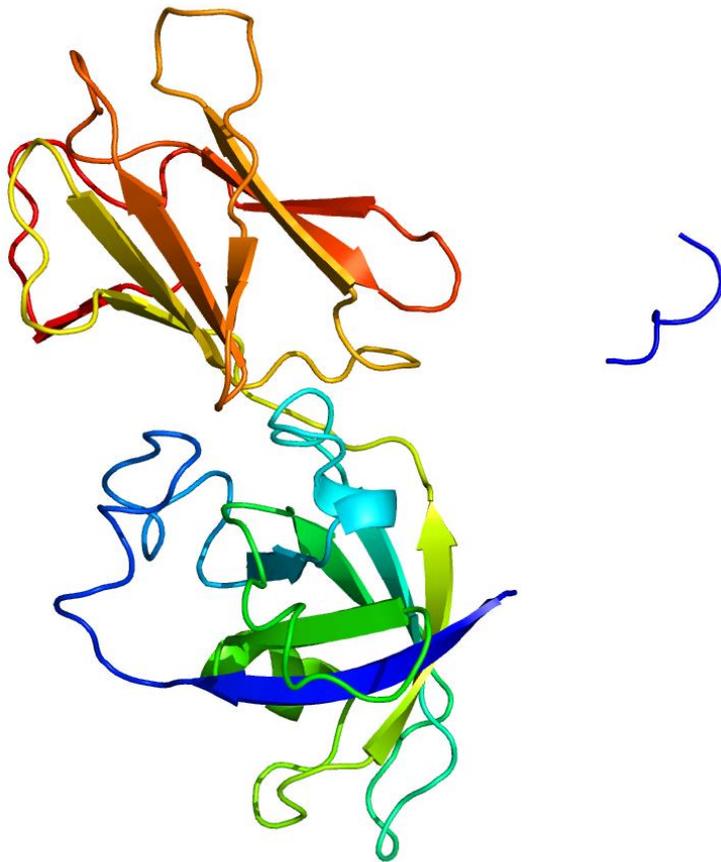
Locus: Manes.S069300

Gene Model: Manes.S069300.1

Description: MsEXPA-35

Family: Alpha Expansin

3D structure:



GENOME DATABASES

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

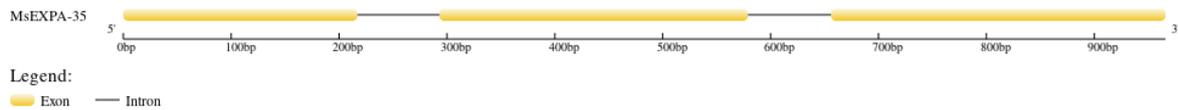
KEGG: <https://www.genome.jp/entry/T05761>

EXTERNAL RESOURCES

<https://cassavagenome.org/>

<https://cassavabase.org/>

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>MsEXPA-35

MASPLGALSAMLLLLVVALAKNCEATAMHSAIHAVRRRHGHKLKPIKQNKSKFKSGP
WRKAHATFYGGGTDSFGGACGYKDVVQQGYTLNTAAISDVLFKKGKCGGCFELK
CVNSPKWCKKGSFLVTATNLCPSNPSLPGKEHFDIAQPVFNKIADYIAGIPIQYRRVP
CNKKGGIRFTIMGNPWFNQVIVWNVGGAGDVVSLQVKGNDNVKWTKLERDWGVT
WKTSTHLVGESLTFRVTTSDGRELTSWHVAPKNWQFGQTYEGKNFK*

CDS (coding sequence)

>MsEXPA-35

ATGGCGTCGCCTTTGGGAGCTCTTTCTGCCATGTTATTGCTTTTAGTTGTTGCACT
GGCTAAAAATTGCGAAGCAACGGCTATGCACTCTGCTATTCATGCTGTTTCGACGA
CATGGCCACAACTTAAACCTATCAAACAAAACAAATCTAAGTTCAAGTCTGGGC
CATGGAGAAAAGCTCATGCCACTTTTTATGGCGGTGGCACCGATTCCCTTTGGAGG
AGCTTGTGGCTATAAAGATGTTGTACAGCAGGGTTACACCTTGAACACAGCAGCT
ATAAGCGACGTTTTATTCAAGAAAGGGAAGGGCTGTGGTGGATGTTTTGAATTAA
AGTGTGTCAATAGCCCTAAATGGTGCAAGAAAGGATCTCTCTTTGTTACAGCAAC
AAATCTCTGCCATCAAATCCATCTCTACCGGGTAAAGAGCATTTCGATATAGCC
CAGCCCGTCTTCAACAAAATCGCTGACTACATTGCTGGGATTATTCCTATCCAATA
CAGAAGGGTTCATGCAACAAGAAAGGAGGGATTCGGTTCACAATAATGGGAAA
CCCATGGTTCACCAAGTGATAGTGTGGAATGTTGGTGGAGCCGGAGATGTTGTG
TCCCTTCAAGTGAAGGGCAATGACAACGTTAAGTGGACCAAATTGGAAAGAGAC
TGGGGTGTACCTGGAAAAGTACCCATTTGGTTGGAGAATCACTAACCTTCA
GAGTTACGACGAGTGATGGCAGAGAATTAACCTCATGGCATGTTGCCCTAAAAA
CTGGCAATTTGGTCAGACTTACGAGGGCAAGAACTTCAAGTAG

Nucleotide

>MsEXPA-35

ATGGCGTCGCCTTTGGGAGCTCTTTCTGCCATGTTATTGCTTTTAGTTGTTGCACT
GGCTAAAAATTGCGAAGCAACGGCTATGCACTCTGCTATTCATGCTGTTTCGACGA
CATGGCCACAACTTAAACCTATCAAACAAAACAAATCTAAGTTCAAGTCTGGGC
CATGGAGAAAAGCTCATGCCACTTTTTATGGCGGTGGCACCGATTCCCTTTGGTAA
AAATTTTATTCTAATGAATCTCTTATATATATTTAAAGAAATGGGAAATAAATA
AGCATAAAAATTTGCAGGAGGAGCTTGTGGCTATAAAGATGTTGTACAGCAGGG
TTACACCTTGAACACAGCAGCTATAAGCGACGTTTTATTCAAGAAAGGGAAGGGC

TGTGGTGGATGTTTTGAATTAAGTGTGTCAATAGCCCTAAATGGTGCAAGAAAG
GATCTCTCTTTGTTACAGCAACAAATCTCTGCCCATCAAATCCATCTCTACCGGGT
AAAGAGCATTTCGATATAGCCCAGCCCGTCTTCAACAAAATCGCTGACTACATTG
CTGGGATTATTCCTATCCAATACAGAAGGTTAGATGATAATGTCCATTCCTTACA
GTCTTAACATGTGCAGGTTTTACATTTAAATGAGTTGTGTTCTTTGCAGGGTTCCA
TGCAACAAGAAAGGAGGGATTCGGTTCACAATAATGGGAAACCCATGGTTCAAC
CAAGTGATAGTGTGGAATGTTGGTGGAGCCGGAGATGTTGTGTCCCTTCAAGTGA
AGGGCAATGACAACGTTAAGTGGACCAAATTGGAAAGAGACTGGGGTGTACCT
GGAAAAGTACCCATTTGGTTGGAGAATCACTAACCTTCAGAGTTACGACGAG
TGATGGCAGAGAATTAACCTTCATGGCATGTTGCCCTAAAACTGGCAATTTGGT
CAGACTTACGAGGGCAAGAAGTCAAGTAG