

IDENTIFICATION

Species: *Amborella trichopoda*

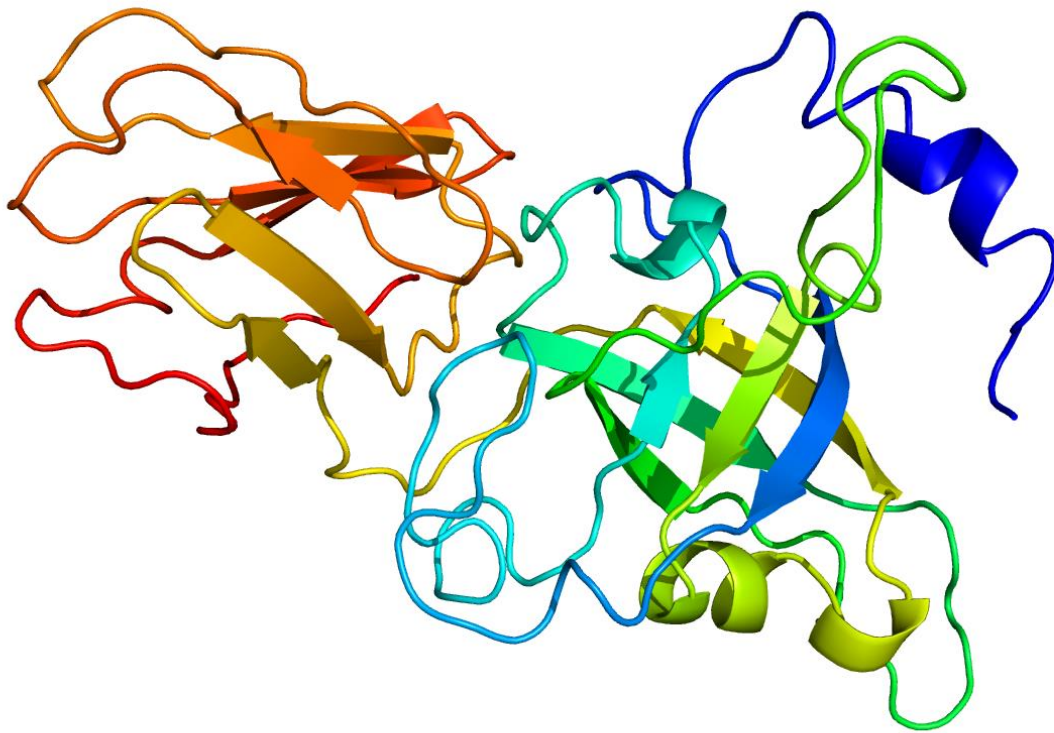
Locus: evm_27.model.AmTr_v1.0_scaffold00001

Gene Model: evm_27.model.AmTr_v1.0_scaffold00001.467

Description: AtrEXPA-02

Family: Alpha Expansin

3D structure:



GENOME DATABASES

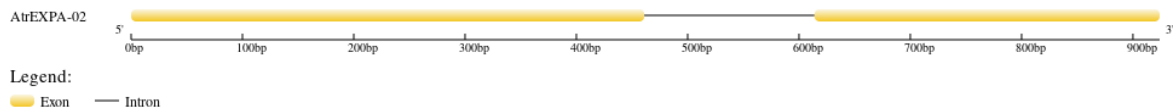
Phytozome: https://phytozome-next.jgi.doe.gov/info/Atrichopoda_v1_0

KEGG: <https://www.genome.jp/entry/gn:T02990>

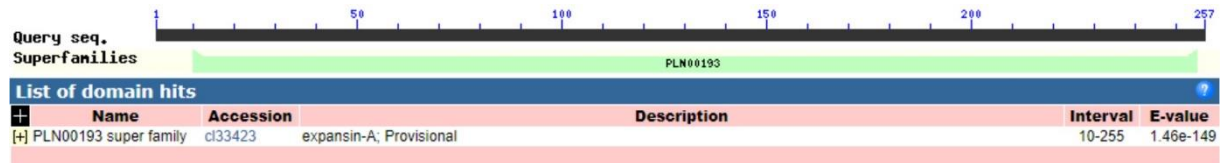
EXTERNAL RESOURCES

https://plants.ensembl.org/Amborella_trichopoda/Info/Index?db=core

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>AtrEXPA-02

MIMASPMVGLLIFLAASGLYTEAMSVGPWTSAHATFYGGSDASGTMGGACGYGNL
YSTGYGTRTAALSTALFNDGASCGQCYQIVCDTKTDPRWCLPGKSVTITATNFCPPNF
ALPNDDGGWCNPPLQHFDMAQPAWEKIGIYRGGIIPILYRSVPCRKHGGIRFTINGRS
YFELVLISNVGGGGSISAVWIKGSEGDWQRMSRNWGANWQSNLSQGLSFRIAN
TDGTTVEFPDVAPPDWQFGQTFSTSLQFS*

CDS (coding sequence)

>AtrEXPA-02

ATGATAATGGCTTCTCCCATGGTTGGTCTGTTGATCTTCCTTGCTGCTTCGGGTTT
GTACACAGAGGCCATGAGTGTGGGCCCATGGACATCAGCCCACGCCACATTCTAC
GGTGGGAGTGACGCGTCGGGAACATGGGCGGTGCGTGCGGCTATGGGAACCTC
TACTCGACCGGCTATGGCACCAGA AACTGCTGCTCTTAGCACTGCTCTTTTCAACGA
CGGGGCGTCCTGCGGTCAAGTGTACCAGATTGTCTGTGATACCAAGACCGACCCC
AGATGGTGCCTGCCCGGAAGTCCGTGACCATCACTGCCACCAATTTCTGCCCTC
CGAACTTTGCTCTCCCAACGACGACGGTGGGTGGTGCAACCCCTCTCCAGCA
CTTTGACATGGCGCAGCCTGCATGGGAGAAGATTGGTATCTACCGAGGAGGCATC
ATTCTATTCTCTACAGAAGTGTCCCTTGTAGGAAGCACGGGGGCATCCGGTTCA
CGATAAATGGGAGGTCTACTTTGAACTGGTTCTGATCAGCAATGTGGGTGGCGG
TGGATCCATTTCTGCGGTGTGGATCAAGGGAAGCGAGGGCGACTGGCAGAGGAT
GTCGAGGA AACTGGGGAGCGAACTGGCAGAGCAATTCATATCTCAACAGCCAGGG
CCTCTCATTCCGCATAGCCAACACCGACGGAACCACCGTCGAATTCCTCCGATGTT
GCACCACCTGACTGGCAGTTTGGCCAAACCTTCTCAACTTCACTCCAATTTTCGTA
G

Nucleotide

>AtrEXPA-02

ATGATAATGGCTTCTCCCATGGTTGGTCTGTTGATCTTCCTTGCTGCTTCGGGTTT
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CGGGGCGTCCTGCGGGTCAGTGTTACCAGATTGTCTGTGATACCAAGACCGACCCC
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CTTTGACATGGCGCAGCCTGCATGGGAGAAGATTGGTATCTACCGAGGAGGCATC
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GTAGGCAGCCAATATAAAAATTCGTTAAACTTATCACAGATCCAATTTTCGTCTG
GTGCAGTGTCCCTTGTAGGAAGCACGGGGGCATCCGGTTCACGATAAATGGGAG
GTCCTACTTTGAACTGGTTCTGATCAGCAATGTGGGTGGCGGTGGATCCATTTCTG
CGGTGTGGATCAAGGGAAGCGAGGGCGACTGGCAGAGGATGTTCGAGGAACTGGG
GAGCGAACTGGCAGAGCAATTCATATCTCAACAGCCAGGGCCTCTCATTCCGCAT
AGCCAACACCGACGGAACCACCGTCGAATTCCCCGATGTTGCACCACCTGACTGG
CAGTTTGGCCAAACCTTCTCAACTTCACTCCAATTTTCGTAG