

IDENTIFICATION

Species: *Brachypodium distachyon*

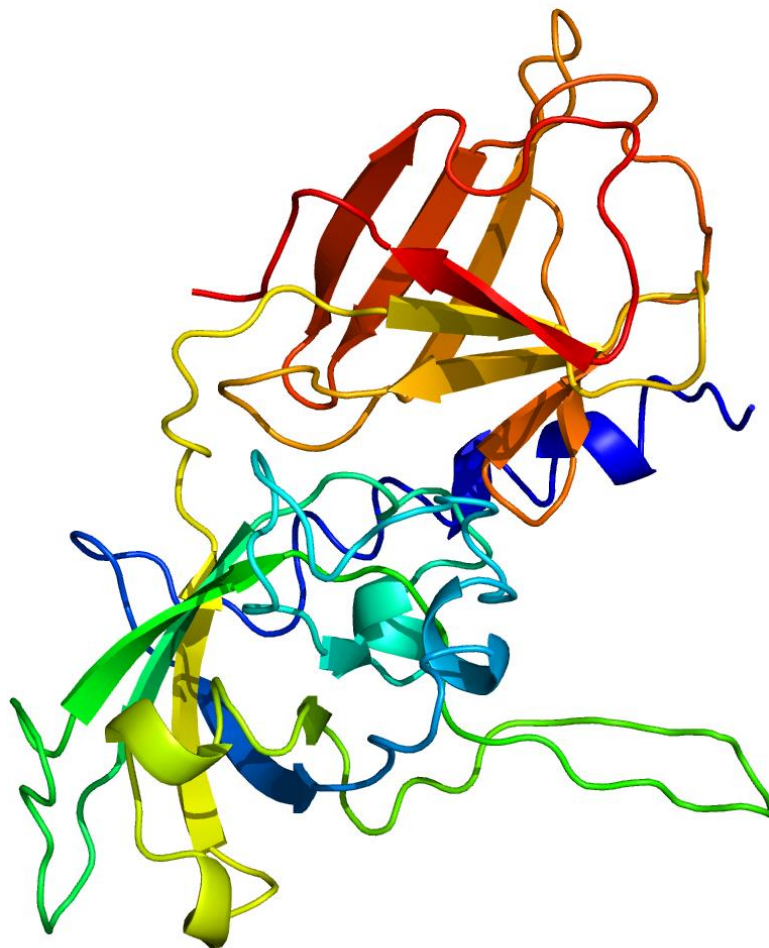
Locus: Bradi3g09967

Gene Model: Bradi3g09967.1.p

Description: BdEXPA-19

Family: Alpha Expansin

3D structure:



GENOME DATABASES

Phytozome: https://phytozome-next.jgi.doe.gov/info/Bdistachyon_v3_1

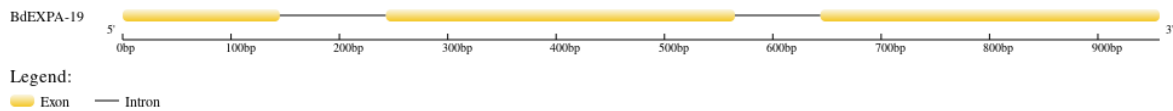
KEGG: <https://www.genome.jp/entry/T01717>

EXTERNAL RESOURCES

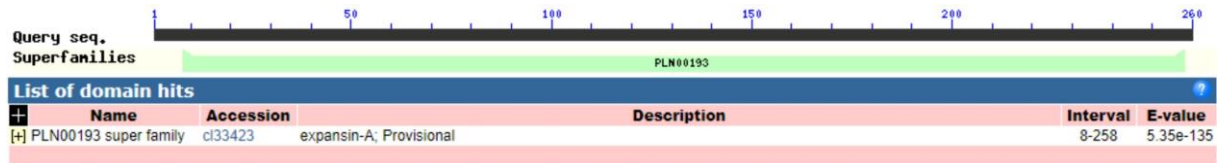
<https://brachypodium.org/>

https://archive.gramene.org/species/brachypodium/brachypodium_intro.html

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>BdEXPA-19

MALAPGQVIAIVLLTAGY TALAGSPSAPFVWQRATATFYGGADASGTMGGACEYGN
LYDEGYGTRSAALSTVLFNDGASCGQCYKIACDRKIDPRWCKPGVTVTITTTNFCPPN
NALPNDNGGWCNTPRAHFDMAQPAWEKIGVHRGGIIPVMYQVRVPCVKKGGVRFKI
NGHDYFNLVLVTNVGAAGSIKSMVMSSDSKDWAPMSRNWGANWYSLAYLSGKQ
LSFRITNTDGQTILFDKIVPSGWKFGQTFASKVQFN*

CDS (coding sequence)

>BdEXPA-19

ATGGCGCTGGCTCCAGGTCAAGTGATTGCGATTGTGCTGCTCACAGCGGGCTATA
CTGCTTTGGCCGGGTCGCCTTCGGCACCGTTCGTTTGGCAGAGGGCGACCGCGAC
GTTCTACGGTGGAGCTGATGCCTCCGGCACCATGGGTGGTGCCTGTGAGTATGGC
AACCTGTACGATGAGGGGTACGGGACCCGGTTCGGCGGCGCTGAGCACGGTGCTG
TTCAACGATGGTGCCTCGTGCAGCAATGCTATAAGATTGCATGTGATCGCAAGA
TTGACCCAAGGTGGTGCAAGCCTGGCGTGACGGTGACAATCACCCTACAACTT
CTGCCACCCAACAATGCCCTTCCGAATGACAACGGCGGATGGTGCAACACACCA
AGGGCACACTTCGACATGGCGCAGCCGGCCTGGGAGAAGATCGGTGTCCACAGA
GGTGGCATCATTCCGGTCATGTATCAGAGGGTTCCATGCGTGAAGAAGGGTGGCG
TACGATTTAAAATCAACGGCCACGACTACTTCAATCTCGTGCTTGTACCAACGT
CGGAGCTGCTGGCTCGATAAAATCGATGGACGTTATGAGCTCCGATTCAAAGAT
TGGGCGCCCATGTCACGCAACTGGGGTGCAAACCTGGTACTCATTGGCATATCTCA
GCGGGAAACAACCTCTCGTTCAGAATAACCAACACAGATGGGCAAACGATTCTGTT
TGACAAGATTGTGCCAAGTGGATGGAAGTTTGGGCAAACATTTGCAAGCAAAGT
ACAGTTCAATTAA

Nucleotide

>BdEXPA-19

ATGGCGCTGGCTCCAGGTCAAGTGATTGCGATTGTGCTGCTCACAGCGGGCTATA
CTGCTTTGGCCGGGTCGCCTTCGGCACCGTTCGTTTGGCAGAGGGCGACCGCGAC
GTTCTACGGTGGAGCTGATGCCTCCGGCACCATGGGTAACCTAATTACAAAC
TCATACGCTAACCTAATTAATGATGCATCTCTCGTGCTAAGAGCACATCGTTAAT

TACCTTCAACGCACACATGCAGGTGGTGCCTGTGAGTATGGCAACCTGTACGATG
AGGGGTACGGGACCCGGTCGGCGGCGCTGAGCACGGTGCTGTTCAACGATGGTG
CGTCGTGCGGACAATGCTATAAGATTGCATGTGATCGCAAGATTGACCCAAGGTG
GTGCAAGCCTGGCGTGACGGTGACAATCACCACTACAACTTCTGCCACCCAAC
AATGCCCTTCCGAATGACAACGGCGGATGGTGCAACACACCAAGGGCACACTTC
GACATGGCGCAGCCGGCCTGGGAGAAGATCGGTGTCCACAGAGGTGGCATCATT
CCGGTCATGTATCAGAGGTACACACATGCAAATTGTATTGTGCTTTTGTAAAGTAA
TATTAGCTCAAAGTCAATCTAAAACCAAATCGTTTAATTAGGGTTCCATGCGTGA
AGAAGGGTGGCGTACGATTTAAAATCAACGGCCACGACTACTTCAATCTCGTGCT
TGTCACCAACGTCGGAGCTGCTGGCTCGATAAAATCGATGGACGTTATGAGCTCC
GATTCAAAAGATTGGGCGCCCATGTCACGCAACTGGGGTGCAAACCTGGTACTCAT
TGGCATATCTCAGCGGGAAACAACCTCTCGTTCAGAATAACCAACACAGATGGGC
AAACGATTCTGTTTGACAAGATTGTGCCAAGTGGATGGAAGTTTGGGCAAACATT
TGCAAGCAAAGTACAGTTCAATTAA