

IDENTIFICATION

Species: *Brachypodium distachyon*

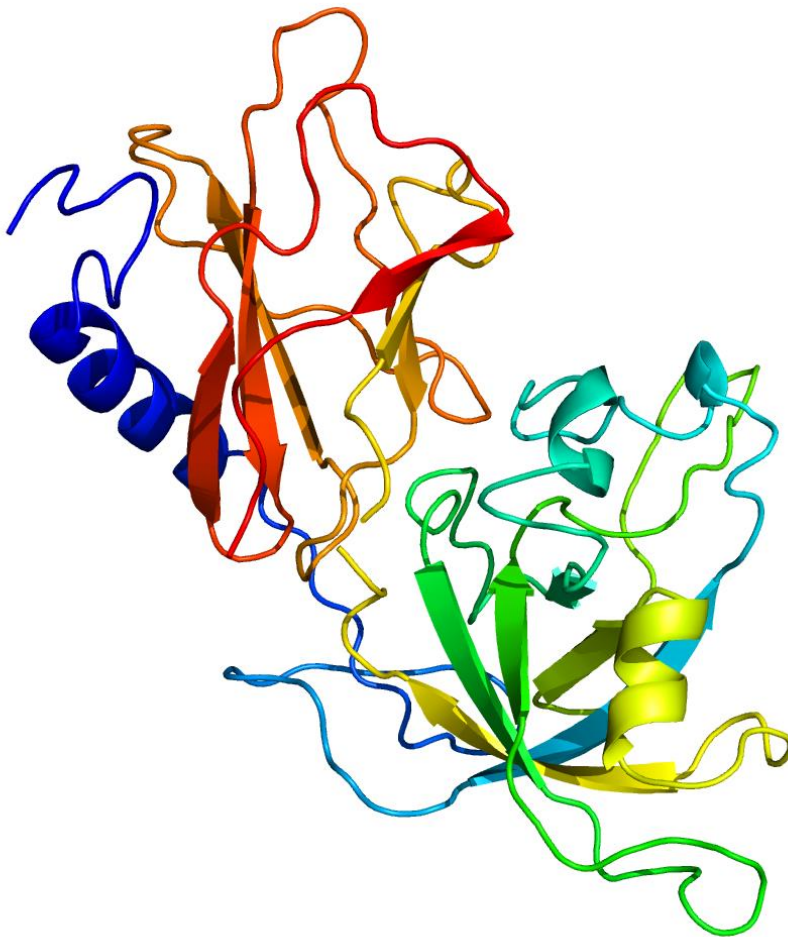
Locus: Bradi1g51990

Gene Model: Bradi1g51990.1.p

Description: BdEXPA-03

Family: Alpha Expansin

3D structure:



GENOME DATABASES

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

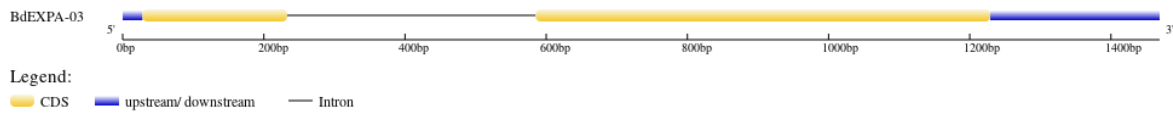
KEGG: <https://www.genome.jp/entry/T01717>

EXTERNAL RESOURCES

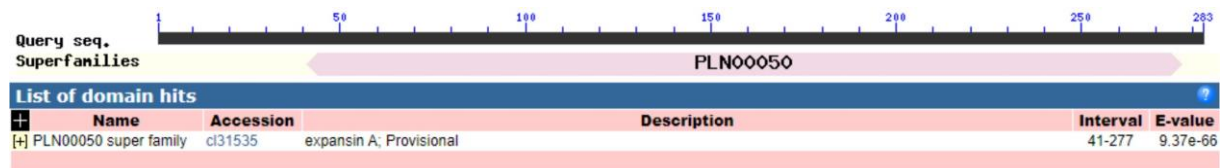
<https://brachypodium.org/>

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

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>BdEXPA-03

MAMSDNPAIAMA AAAAAMMVLMAARLASANIPPSQWSPATTGGYSTSVWIDGSA
TFYGDASGLGADFGGACGFSANDIASLYSTATAALSTPLFADGDGCGRCYELRCVK
PWCNPGSPSITVTGTNLCPPNWYLPNDDGGWCNPPRQHFDLAPPSFLRLAARVAGIV
PVQFRRVPCQRTGGVRFYVTGNPYWLLHIMNVGGAGDVCQVAVRMVGGNGGWI
TTSKNWGSTFQAFSALDKSKGLAVKLTTTCGDPQQSIVVGDAIPSWWSTGLTYQGSNN
FW*

CDS (coding sequence)

>BdEXPA-03

ATGGCGATGTCTGATAATCCGGCGATAGCCATGGCGGCGGCGGCGGCGGCGGCGATG
ATGGTGTGATGGCGGCTCGGCTGGCGAGCGCCAACATACCTCCTTCCCAATGGT
CGCCTCCTGCTACCACCGGCGGCTACTCCACGTCCGTCTGGATAGATGGCAGCGC
CACCTTCTACGGCGACGCCTCTGGACTCGGCGCCGACTTCGGCGGAGCGTGC
TTCAGCGCCAACGACATCGCGTCGCTGTACTCGACGGCGACGGCGGCACTGAGCA
CGCCATTGTTTCGACAGACGGCGACGGGTGCGGGCGGTGCTATGAGCTGCGGTGCGT
CAAGTCCCCCTGGTGCAACCCAGGGTCGCCGTCAATCACCGTCACGGGGACCAAC
CTCTGCCCCGCCAATTGGTACCTCCCCAACGACGACGGTGGCTGGTGCAACCTC
CCCGACAACACTTCGACTTGGCGCCGCGTCTCCTCCTCCGGCTCGCCGCCAGGGT
CGCCGGCATCGTGCCCGTGCAGTTCCGGCGGGTGCCTGCCAGAGGACCGGCGG
CGTCCGGTTCTACGTCACCGGGAACCCCTACTGGCTCCTGCTGCACATCATGAAC
GTTGGCGGCGCTGGTGTGCTGCCAGGTCGCCGTCAGGATGGTCCGGCGGCAATG
GCGGGTGGATCACGACGTCCAAGAATTGGGGCAGCACGTTCCAGGCCTTCTCTGC
GCTGGACAAGAGCAAGGGGCTCGCCGTTAAGCTAACGACTTGCGGCGACCTCA
GCAAAGCATCGTCGTCGGCGACGCCATTCCGTCGTGGTGGTCCACCGGACTCACC
TACCAGGGATCAAACA ACTTCTGGTGA

Nucleotide

>BdEXPA-03

CTTAATTTGAGTTCATCTATCATCGGCCATGGCGATGTCTGATAATCCGGCGATAG
CCATGGCGGCGGCGGCGGCGGCGATGATGGTGTGATGGCGGCTCGGCTGGCGA

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AACCCATGTCTATACATGTACGTAATGCAGGGCGGAGCGTGCGGGTTCAGCGCCAA
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TGGTGCAACCCAGGGTCGCCGTCAATCACCGTCACGGGGACCAACCTCTGCCCGC
CCAATTGGTACCTCCCCAACGACGACGGTGGCTGGTGCAACCCTCCCCGACAACA
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CCTTGGCTTCTAAACATTTTCTAATGGTT