

## IDENTIFICATION

**Species:** *Brachypodium distachyon*

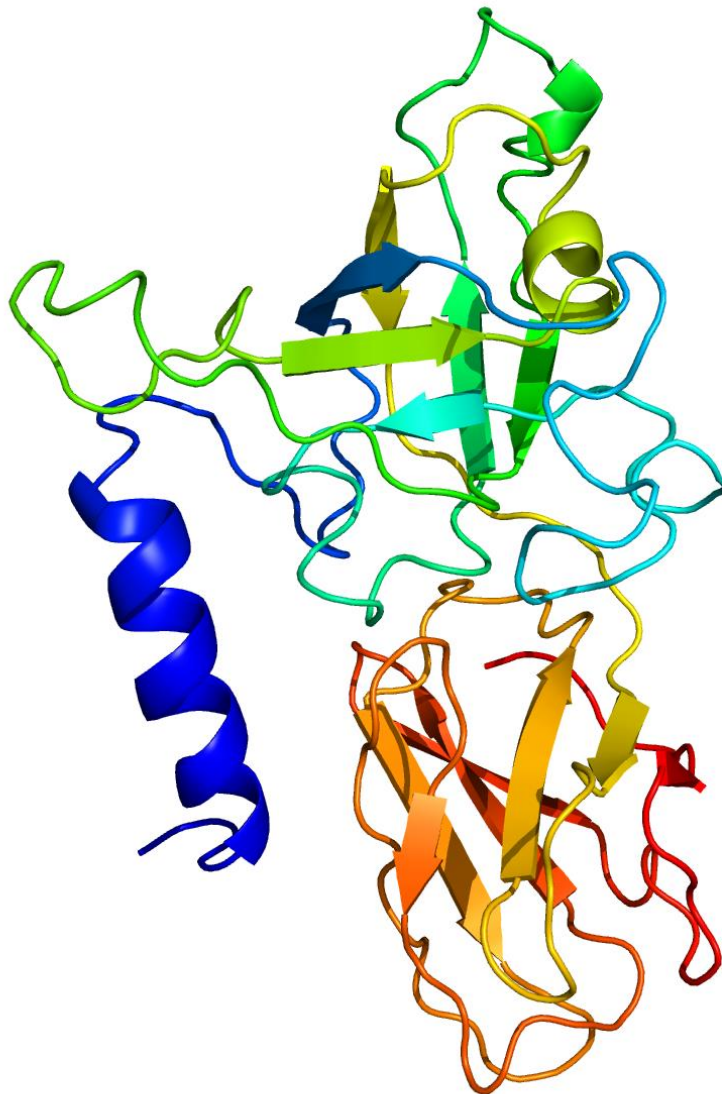
**Locus:** Bradi3g10100

**Gene Model:** Bradi3g10100.1.p

**Description:** BdEXPA-21

**Family:** Alpha Expansin

**3D structure:**



## GENOME DATABASES

Phytozome: [https://phytozome-next.jgi.doe.gov/info/Bdistachyon\\_v3\\_1](https://phytozome-next.jgi.doe.gov/info/Bdistachyon_v3_1)

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

## EXTERNAL RESOURCES

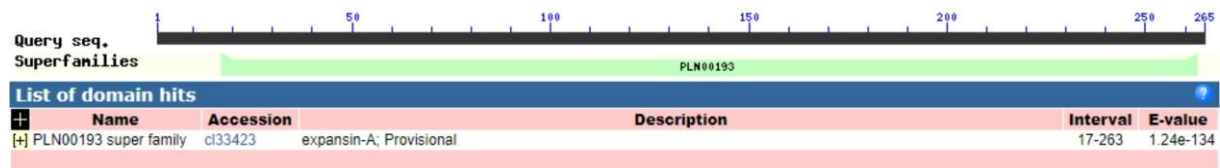
<https://brachypodium.org/>

[https://archive.gramene.org/species/brachypodium/brachypodium\\_intro.html](https://archive.gramene.org/species/brachypodium/brachypodium_intro.html)

## GENE STRUCTURE



## DOMAIN ARCHITECTURE



## SEQUENCES

### Peptide

>BdEXPA-21

MAQARVLAPLVLALLGCALAVTADDVDAPASGGGLLKAHATFYGGADGAGTMGG  
ACGYGNLYSTGYGTNTAALSTALFNDGASCGQCYKIACDSKLVDPGWCKVGETVTI  
TATNFCPPNYDLPSDNNGWCNPPRPHFDMAQPAWEKIGVYRAGIIPVVYRRVPCVRR  
GGVRFTINGHDYFQLVLVTNVGGIGSIKSM DVRGANSSDWMPMARNWGANWHS  
LALYLTGQSLSFRVTNNNGQTLAFKKLVPPSWKFGQTFSSNVQFK\*

### CDS (coding sequence)

>BdEXPA-21

ATGGCTCAAGCAAGGGTGTAGCACCGCTGGTCCTCGCACTACTGGGCTGCGCGT  
TGGCCGTCACCGCCGACGACGTCGACGCACCTGCATCTGGTGGAGGATTACTGAA  
GGCGCATGCGACATTTTACGGGGGCGCGGACGGTGCCGGCACCATGGGTGGTGC  
ATGCGGGTATGGCAACCTGTACTCGACGGGGTACGGCACAAACACGGCAGCGCT  
GAGCACGGCGCTCTTCAATGACGGGGCATCTTGCGGGCAGTGTTACAAGATTGCG  
TGTGACAGCAAGCTGGTGGACCCAGGGTGGTGTAAAGTCGGTGAGACGGTGACC  
ATCACGGCCACAAATTTCTGCCCCGCCAACTACGATTTGCCGAGCGACAATGGTG  
GCTGGTGAACCCACCACGACCACACTTTGACATGGCGCAGCCGGCCTGGGAGA  
AGATCGGTGTTTATCGAGCCGGCATCATCCAGTTGTGTACCGAAGGGTTCCATG  
TGTGAGGCGAGGCGGTGTGCGGTTACGATCAACGGACATGACTACTTCCAGCTT  
GTTCTTGTGACCAATGTCGGAGGTATTGGTTCGATCAAGTCAATGGACGTTAGGG  
GCGCCAATTCATCCGATTGGATGCCCATGGCACGCAACTGGGGTGCAAATTGGCA  
CTCTCTGGCGTACCTCACTGGTCAGAGCCTCTCATTTCAGAGTGACCAACAATAAT  
GGCCAAACACTTGCATTCAAAAAATTGGTGCCACCCAGCTGGAAGTTCGGCCAAA  
CATTTTCTAGCAATGTGCAGTTCAAGTGA

### Nucleotide

>BdEXPA-21

ATGGCTCAAGCAAGGGTGTAGCACCGCTGGTCCTCGCACTACTGGGCTGCGCGT  
TGGCCGTCACCGCCGACGACGTCGACGCACCTGCATCTGGTGGAGGATTACTGAA  
GGCGCATGCGACATTTTACGGGGGCGCGGACGGTGCCGGCACCATGGGTAAACT  
AGCCCTTGCTAACACATCATAGTTACTCTTTCTGCTGGAAAGATATATATCATGTT

AAGAATAAGTCTGATCCAGAAACCCTTTGAAACTAATCTTGGCATGGTCATGGTG  
AATGTTTGCATACGGCAGGTGGTGCATGCGGGTATGGCAACCTGTACTCGACGGG  
GTACGGCACAACACGGCAGCGCTGAGCACGGCGCTCTTCAATGACGGGGCATC  
TTGCGGGCAGTGTTACAAGATTGCGTGTGACAGCAAGCTGGTGGACCCAGGGTG  
GTGTAAAGTCGGTGAGACGGTGACCATCACGGCCACAAATTTCTGCCCGCCAAC  
TACGATTTGCCGAGCGACAATGGTGGCTGGTGCAACCCACCACGACCACACTTTG  
ACATGGCGCAGCCGGCCTGGGAGAAGATCGGTGTTTATCGAGCCGGCATCATCCC  
AGTTGTGTACCGAAGGTACCTAATAAAAAGAAGAACAAAATCGAGAAAAAAAAAGC  
AAGCTGCAAAGAGTAATTTTTTTTTTCCGAAAATGGTAGTTTTTATTGATCTCAAAG  
TTTATATCGAACGATACAAGCAAAGAGTATCACACACCAGTCTCTGTGCCGAAG  
CACACACGGCCACACACCCGCAAAGAGTAAATATGTCACAAAATCTTGACGAAGT  
CACTTGTAGCGGTTGTCTTCGACTAATGATGCCTAACTGCAGGGTTCCATGTGTGA  
GGCGAGGCGGTGTGCGGTTACGATCAACGGACATGACTACTTCCAGCTTGTCT  
TGTGACCAATGTCGGAGGTATTGGTTCGATCAAGTCAATGGACGTTAGGGGCGCC  
AATTCATCCGATTGGATGCCCATGGCACGCAACTGGGGTGCAAATTGGCACTCTC  
TGGCGTACCTCACTGGTCAGAGCCTCTCATTAGAGTGACCAACAATAATGGCCA  
AA