

## IDENTIFICATION

**Species:** *Brachypodium distachyon*

**Locus:** Bradi4g41117

**Gene Model:** Bradi4g41117.1.p

**Description:** BdEXPA-31

**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

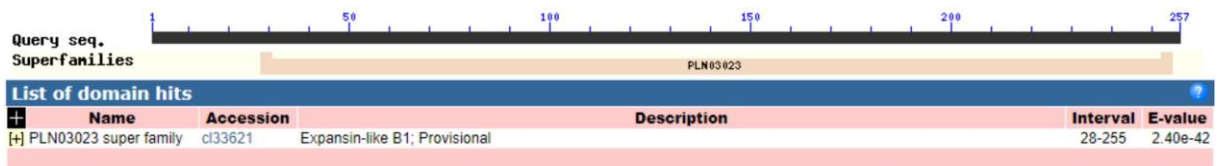
<https://brachypodium.org/>

[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-31

MTTTLGHKSFIVLSPFLKACLLLLLRPCSSWSDAGATWYGPANGAGTDGGACGYQR  
DVELPPFSAMVTAGGPSIYQDGKGCYQVKCMDNPACSGNPVTVVVDQCPGGP  
CAADRVHFDLSGKAFGALAKPGLAGSLRNVGNIKVQFNRVACNWHGVNVAFRVDA  
GSNPNYLA VLVEDEAGDGNLSAVELQQRGGAGGWAPMQRSWGATWKYNGAVKA  
PVSIRLTSSSGKKLVAANVIPVGWQPGRTYRSLVNY\*

### CDS (coding sequence)

>BdEXPA-31

ATGACCACCACCTCGGCCACAAAAGCTTTATAGTACTCTCTCCATTTCTCAAAGC  
CTGCCTCCTCCTCCTGCTCCGCCCGTGTAGCAGTTGGTCCGACGCCGGCGCCACGT  
GGTACGGCCCCGCTAACGGCGCCGGCACCGACGGTGGTGCCTGCGGGTACCAGC  
GCGACGTGGAGCTGCCGCCGTTCTCCGCCATGGTGACCGCCGGCGGCCCTCCAT  
CTACCAGGACGGCAAGGGCTGCGGCGCATGCTACCAGGTGAAATGCATGGACAA  
CCCGGCTTGCTCCGGCAACCCGGTGACAGTCGTGGTGACAGACCAGTGCCCGGGC  
GGGCCGTGCGCCGCGGACCGCGTCCACTTCGACCTCAGCGGCAAGGCCTTCGGCG  
CCCTGGCCAAGCCCGGACTAGCCGGCAGCCTCCGCAACGTTGGCAACATCAAAGT  
CCAATTCAACCGGGTGGCGTGCAACTGGCACGGGGTGAACGTGGCCTTCAGGGT  
GGACGCCGGGTGCAACCCGAACCTACCTGGCGGTGCTGGTGGAGGACGAGGCCGG  
CGACGGCAACCTGTGCGCGGTGGAGCTCCAGCAGCGCGGCGGCGCTGGCGGGTG  
GGCCCCGATGCAGCGCTCCTGGGGCGCCACGTGGAAGTACAACGGCGCGGTGAA  
GGCGCCCGTGTCCATCCGGCTCACGTCGAGCTCCGGCAAGAAGCTCGTCGCCGCC  
AACGTCATCCCCGTGCGCTGGCAGCCCCGGCCGCACCTACCGCTCTCTCGTTAACT  
ACTGA

### Nucleotide

>BdEXPA-31

ATGACCACCACCTCGGCCACAAAAGCTTTATAGTACTCTCTCCATTTCTCAAAG  
GTTGGCGTATTTTGATTTCGTTAAGACAAGGCTTTAACCAATGAAAACCTCTATTAAT  
ATGTGTTTTTTTCATACATGCAATTTATATCAATGGATTCATTTTTAAAAGTTCTTGC  
TAATGATCATGGTTTCGTATCATATAACTTACATATTAATAAGAATAATTTGGTC

AAATGCTTGTCTTAACGAAAGAAAATACGCCAACCTTTGTGAAATGGATCGAGGA  
GTATGATCTAACCCATTAGTAGCCTGCAGCCTCATGCCGCTCTGCACTTGCAGCTG  
TAGCGCGTCGCCGTCGACCGTTAATATAATATTACACATAATATATAGATCATGA  
CAATAAAGTCGCTTTCAAAGTATTATACGTACTTATGAATGTAATTCCAAATCAC  
ATTAACCACGATTAGCCGCTAGACACAAAAGTCTTTTATATATTTAAAATCATTCT  
AAAGTATTACACCTGCATGTGTACGTCGCTTATGAAATACTCCTACCAGCTAAAG  
TTAGAACGAATTTGATCCCCTCCAAGCTACAATCCTATATACGGAGTAGGAAATC  
ATCCCGAAATTATCAGCCTCAATGCAGAAAATCCCCACGAAATCACAAAATCAAT  
ACAGTATTTCTATAATCGGATTGACGATCACAAAATAATCTGCGCCCGTGCGCT  
CCACTAGTCCATTCTGCCGCACGTACAGCATGCCTATAAATCCACGGCAAGGATG  
ATAGGCTTGCTACCACATCATCTCTCCAAGCTGCCTTGCTCTTCTTAATTCCTCCT  
ACGATCGATCGAGAGAGCTAGTTGCGAGGAGCTTAGCTAGCATGGCTTCTTGTT  
ATCTTCCGTGTTGGTGGCGGCTCTAGCCTGCCTCCTCCTCCTGCTCCGCCCGTGTA  
GCAGTTGGTCCGACGCCGGCGCCACGTGGTACGGCCCCGCTAACGGCGCCGGCA  
CCGACGGTACGTACATATATGCATATATGCATACATATACGGAATATATATTTAG  
TGGTTGCTCGGAGATCAGCTAGCTATCCAGTTTTGTTGAGTACTGAGTTGCT  
GACACGGCGACACCTGCATGTATGTACGTAGGTGGTGCCTGCGGGTACCAGCGC  
GACGTGGAGCTGCCGCCGTTCTCCGCCATGGTGACCGCCGGCGGCCCTCCATCT  
ACCAGGACGGCAAGGGCTGCGGGCGCATGCTACCAGGTACCGTTACCACTTATCTA  
ACGTAGTACTAAATCAGCGATGCTTACACTTATTATGGGTCCGATAGGGAGTATT  
AGTTATGTGAGAATTCGCTTGATACTGTGTCCAGGTGAAATGCATGGACAACCCG  
GCTTGCTCCGGCAACCCGGTGACAGTCGTGGTGACAGACCAGTGCCCGGGCGGG  
CCGTGCGCCGCGGACCGCGTCCACTTCGACCTCAGCGGCAAGGCCTTCGGCGCCC  
TGGCCAAGCCCGGACTAGCCGGCAGCCTCCGCAACGTTGGCAACATCAAAGTCC  
AATCAACCGGTAATCAACCAGGAGTAACTAACTAACTATACCTAGCCATCATCT  
CCTTCAACTCGGCATGAATTATACAAATCCGCCTCACTTATTTTCGGACGGAGCG  
AGGATCAAACATGCGCGTGTGTGCGTGTATACGCAGGGTGGCGTGCAACTGGCA  
CGGGGTGAACGTGGCCTTCAGGGTGGACGCCGGGTGCAACCCGAACTACCTGGC  
GGTGTGGTGGAGGACGAGGCCGGCGACGGCAACCTGTTCGGCGGTGGAGCTCCA  
GCAGCGCGGCGGCGCTGGCGGGTGGGCCCCGATGCAGCGCTCCTGGGGCGCCAC  
GTGGAAGTACAACGGCGCGGTGAAGGCGCCCGTGTCCATCCGGCTCACGTGAG  
CTCCGGCAAGAAGCTCGTCGCCGCAACGTCATCCCCGTCGGCTGGCAGCCCGGC  
CGCACCTACCGCTCTCTCGTTAACTACTGA