

## IDENTIFICATION

**Species:** *Brachypodium distachyon*

**Locus:** Bradi3g43080

**Gene Model:** Bradi3g43080.1.p

**Description:** BdEXPA-29

**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

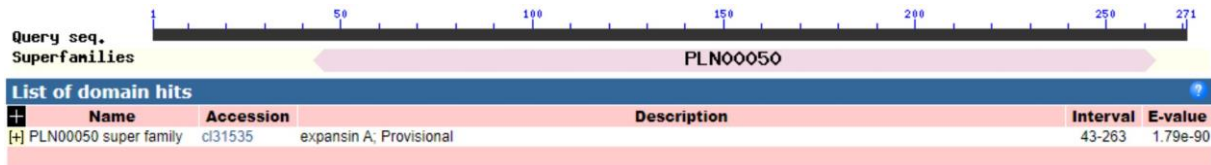
<https://brachypodium.org/>

[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-29

MSGWWAPLLVVVLVLLASAASNVAAPGEARVHHNHGKFMEGPWRPAHATFYGDH  
DGTGTRAGACGYKDTV AEGYGLQTV ALSTAMFNGGATCGACYEVRCTESPKWCKP  
GAPPLVVTATNLCPPNYQQSGDNGGWCNPPREHFDLTMPAFLQIAEEKAGIVPISYRR  
VSCLKQGGIRYTITGNKYFNMVTVTNVGGAGDVVA VTVKGDDRKWTPLTRNWG  
QVWQTGEILVGESLTFRVMTSDHRKATSWHVLPRDWQFGV TYRATKNFH\*

### CDS (coding sequence)

>BdEXPA-29

ATGTCTGGTTGGTGGGCGCCTCTCCTCGTCGTCGTCCTGGTGCTGCTCGCCTCGGC  
GGCGAGCAATGTTGCCGCCCCCGGCGAGGCAAGGGTGCACCACAACCACGGCAA  
GTTCATGGAGGGCCCGTGGCGGCCAGCGCACGCCACCTTCTATGGCGACCACGAT  
GGGACCGGAACGCGGGCCGGCGCGTGCGGGTACAAGGACACGGTGGCGGAAGG  
GTACGGCCTGCAGACGGTGGCGTTGAGCACGGCCATGTTCAACGGCGGGCGCAAC  
GTGCGGGGCGTGCTATGAGGTGAGGTGCACGGAGAGCCCTAAGTGGTGCAAGCC  
CGGGGCGCCGCGTTGGTGGTGACGGCGACGAACCTGTGCCCCCCAAACTACCA  
GCAGTCGGGCGACAACGGCGGGTGGTGCAACCCGCCGCGGAGCACTTTGACCT  
CACCATGCCCCGATTCCTCCAGATCGCCGAGGAGAAGGCCGGCATTGTGCCCATC  
TCCTACCGCCGGGTGAGCTGTTTGAAGCAGGGCGGGATCCGGTACACCATCACGG  
GGAACAAGTACTTCAACATGGTGACGGTGACAAACGTGGGCGGGGCGGGGGACG  
TGGTAGCGGTGACGGTCAAGGGGGACGACCGAGTCAAGTGGACCCCGTTGACGC  
GGA ACTGGGGCCAGGTGTGGCAGACCGGGGAGATCCTCGTCGGCGAGTCACTCA  
CGTTCGCGGTGATGACCAGCGACCACCGCAAGGCCACCTCCTGGCACGTGCTCCC  
CCGCGACTGGCAGTTCGGCGTCACCTACCGGGCAACCAAGA ACTTCCACTAG

### Nucleotide

>BdEXPA-29

AAAATTGATCCCCTGCACGAGTGCATCAGAAA ACTTAGCTAGTAATTAATAAATC  
GTTAGTCTGTATCATTTTAATTAGCTGTTGATTCATTCATTCATGTCTGGTTGGTGG  
GCGCCTCTCCTCGTCGTCGTCCTGGTGCTGCTCGCCTCGGCGGGCGAGCAATGTTGC  
CGCCCCGGCGAGGCAAGGGTGCACCACAACCACGGCAAGTTCATGGAGGGCCC

GTGGCGGCCAGCGCACGCCACCTTCTATGGCGACCACGATGGGACCGGAACGCG  
GGCCGGCGCGTGCGGGTACAAGGACACGGTGGCGGAAGGGTACGGCCTGCAGAC  
GGTGGCGTTGAGCACGGCCATGTTCAACGGCGGCGCAACGTGCGGGGCGTGCTA  
TGAGGTGAGGTGCACGGAGAGCCCTAAGTGGTGCAAGCCCGGGGCGCCGCCGTT  
GGTGGTGACGGCGACGAACCTGTGCCCCCAAACCTACCAGCAGTCGGGCGACAA  
CGGCGGGTGGTGCAACCCGCCGCGGAGCACTTTGACCTCACCATGCCCGCATTC  
CTCCAGATCGCCGAGGAGAAGGCCGGCATTGTGCCCATCTCCTACCGCCGGTAGG  
TGACCAAACATACATATACACGCCTCTTAACCTTGTTGCGGGTGCATGGAACTCGA  
TGAATAAATGTCCTGCATGCAGGGTGAGCTGTTTGAAGCAGGGCGGGATCCGGTA  
CACCATCACGGGGAACAAGTACTTCAACATGGTGACGGTGACAAACGTGGGCGG  
GGCGGGGGACGTGGTAGCGGTGACGGTCAAGGGGGACGACCGAGTCAAGTGGAC  
CCCGTTGACGCGGAACTGGGGCCAGGTGTGGCAGACCGGGGAGATCCTCGTCGG  
CGAGTCACTCACGTTCCGCGTGATGACCAGCGACCACCGCAAGGCCACCTCCTGG  
CACGTGCTCCCCCGCGACTGGCAGTTCGGCGTCACCTACCGGGCAACCAAGAACT  
TCCACTAGCTAACCTAACCTACTATACCCCTTCTTCTGCCGTCGCCGGCCATTG  
ACAACCATTTACCGAGACCGTGTGTAAATTTGATGATGCTTTCATTCTCCACTGCA  
TGTGGTCGATATGATCGATCGAATCATGTTGCAAATCGAACGAGGCGTACAGGAA  
GAAACAAGCTGAATGAAAGCTAGGTGTCATGTTGCCTCCATCTG