

## IDENTIFICATION

**Species:** *Brachypodium distachyon*

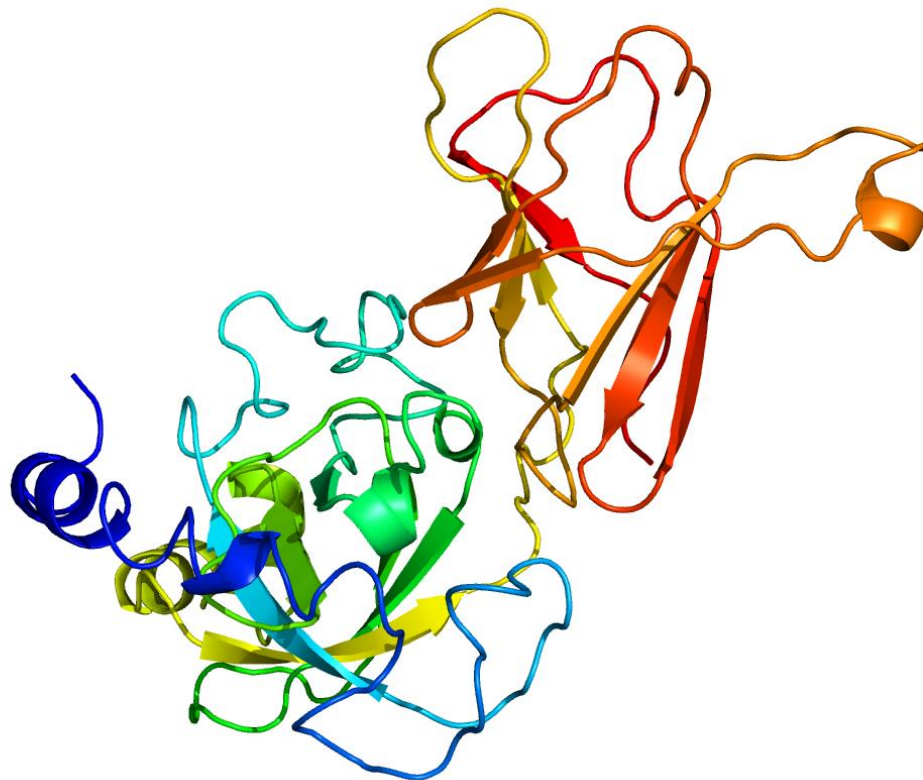
**Locus:** Bradi3g33160

**Gene Model:** Bradi3g33160.1.p

**Description:** BdEXPB-13

**Family:** Beta 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

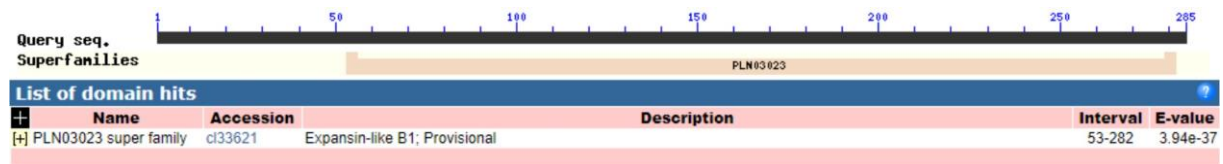
<https://brachypodium.org/>

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

## GENE STRUCTURE



## DOMAIN ARCHITECTURE



## SEQUENCES

### Peptide

>BdEXPB-13

MGTLSSFAALAALLAVLAADAGAVEFNVTDPADYGGAGLNSSEAAVYWGPWTP  
ARATWYGQPNGAGPDDNGGACGFKHTNQYPFASMTSCGNQPLFKDGGKGCSCYKI  
RCRKDQSCSGRTETVIITDMNYYPVAPFHFDLSGTAFGRLAKPGLNDKLRHSGIIDIEF  
TRVPCFPGLKIGFHVVEYSNPVYFAVLVEYEDGDGDVVQVDLMESKTAHGPLTGQ  
WTRMRESWGSIWRLDSNHRLQAPFSIRITNESGKRLIAREVIPANWRPNTFYRSFVQY  
S\*

### CDS (coding sequence)

>BdEXPB-13

ATGGGCACGCTCTCCTCCTTCGCTGCTCTGGCGGCGCTCCTCGCCGTCCTGGCCGC  
CGACGCCGGCGCCGTGGAGTTCAACGTCACCGACGCCACCCCGGCCGACTACGG  
CGGCGCGGGTCTCAACAGCAGCGAGGCCGCGGTGTACTGGGGCCCATGGACCCC  
GGCCAGGGCCACCTGGTACGGCCAGCCAATGGCGCCGGCCCCGACGACAACGG  
TGGCGCCTGCGGCTTCAAGCACACCAACCAGTACCCGTTTCGCGTCCATGACCTCC  
TGCGGCAACCAGCCATTGTTCAAGGACGGCAAGGGATGCGGCTCCTGCTACAAG  
ATCAGATGCCGAAAGGACCAGTCCTGCTCCGGCAGGACGGAGACGGTGATCATC  
ACCGACATGAACTACTACCCCGTGGCGCCGTTCCACTTCGACCTCAGCGGCACGG  
CGTTCGGCAGGCTCGCCAAGCCCGGCCTCAACGACAAGCTCCGTCCTCCGGCAT  
CATCGACATCGAGTTCACCAGGGTGCCGTGTGAGTTCCTCGGGGCTGAAGATCGGG  
TTCCACGTGGAGGAGTACTCAAACCCGGTCTACTTCGCGGTGCTGGTGGAGTACG  
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ACGGGCCGCTAACGGGCCAGTGGACGCGGATGAGGGAGTCGTGGGGGTCCATCT  
GGAGGCTGGACTCCAACCACCGCCTGCAGGCCCGTTCTCCATCCGCATCACCAA  
CGAGTCCGGCAAGAGGCTCATCGCCCGGGAGGTTATCCCGGCCAACTGGAGGCC  
CAACACCTTCTACCGATCCTTCGTCCAGTACAGCTGA

### Nucleotide

>BdEXPB-13

CCCATTGTCTCCACGTTCCCTTTGTGCAGAGCGCAGCTCTCTGAGCTCTGGGCATT  
GGGGGCTGGGGCTTCTCGAAGGCTTAAAGCTAGGTGGCCGTGACCCAGAAAGAA

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CGCTGCGCTCATCACAAATGGCCGGCGGCTCCGCCTGCTCAGGCTCTCCGGCTCC  
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GCGACCCGTATAGTGTGGGTTACGTTTTCTTTCTTTTGAGAATACGCTTCTAGCCG  
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CAGGCTGACACAGCATAAACAGCATGCAGCTAGGAGAAAAAGTAACTGGAGAAA  
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