

## IDENTIFICATION

**Species:** *Brachypodium distachyon*

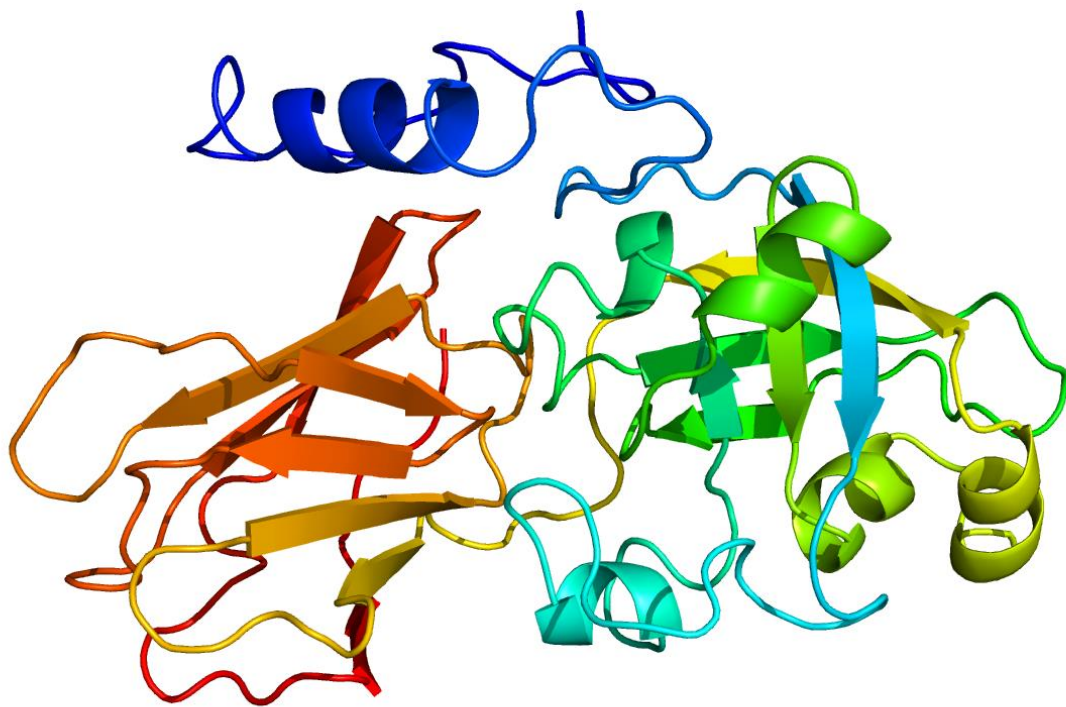
**Locus:** Bradi3g49850

**Gene Model:** Bradi3g49850.1.p

**Description:** BdEXPB-14

**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)

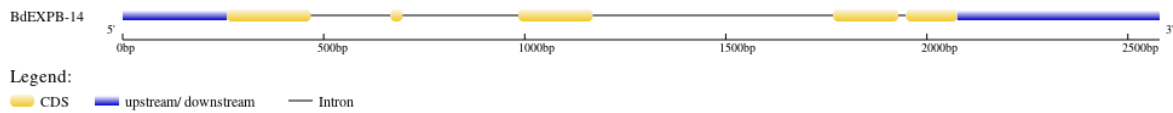
KEGG: <https://www.genome.jp/entry/T01717>

## EXTERNAL RESOURCES

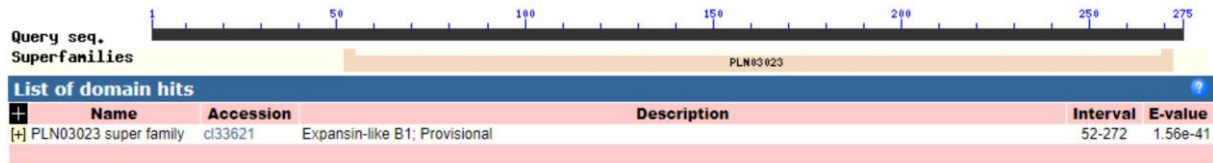
<https://brachypodium.org/>

[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-14

MAGGSACSGSPAPLSTSFARLASLLSAASIFVAAEAGAAHKVVDPPQWHQATATWYG  
SADGDGSDGGACGYGTLVDVAPMKARVGA VSPVLFKGGEGCGACYKVRCLDAGIC  
SRRAVTVIVTDECPGGYCSSGRTHFDLSGAAFRLAVAGHGGQLRNRGEISVFRRT  
PCKYRGKNIAFRVVEGSTSFWLSLLVEFEDGDGDIGSMQLKQAKSAQWQDMKHIWG  
ATWSLTPGPLIGPFSVRLTTLTTKKTLA QDVIPRNWTPKATYTSRLNFI\*

### CDS (coding sequence)

>BdEXPB-14

ATGGCCGGCGGCTCCGCCTGCTCAGGCTCTCCGGCTCCCTTATCGACCAGCTTTGC  
TCGGCTCGCTTCTCTCCTTTCTGCGGGGTCCATCTTCGTTGCCGCGGAGGCCGGGG  
CGGCGCACAAAGGTGGTCGACCCTCAGTGGCATCAGGCCACCGCGACCTGGTACG  
GCAGCGCCGACGGCGACGGCAGCGATGGCGGCGCGTGTGGGTACGGGACGCTGG  
TGGACGTGGCGCCGATGAAGGCCCGCGTGGGCGCGGTGAGCCCGGTGCTGTTCA  
AGGGCGGCGAGGGCTGCGGGCGCGTGTACAAGGTCAGGTGCCTCGACCGCGCA  
TCTGCTCGCGCCGCGCCGTCACCGTCATCGTCACCGACGAGTGCCCCGGCGGCTA  
CTGCTCCTCGGGCCGCACGCACTTCGACCTCAGCGGGCGCCGCTTCGGCAGGCTC  
GCCGTGCGCCGTCACGGCGGGCAGCTGCGCAACCGAGGAGAGATCTCGGTGGTG  
TTCCGCAGGACGCCGTGCAAGTACCGGGGGAAGAACATCGCCTTCCGCGTGGTGC  
AGGGATCGACGAGCTTCTGGCTCTCGCTTCTGGTGGAGTTCGAGGACGGCGACGG  
CGACATTGGATCCATGCAGCTAAAGCAGGCAAAGTCGGCACAGTGGCAAGACAT  
GAAGCACATCTGGGGTGCCACCTGGAGCCTCACGCCAGGCCCACTCATTGGACCA  
TTTTCTGTTAGGTTGACAACCCTGACTACCAAGAAGACCCTCTCCGCTCAGGACG  
TCATCCCAAGGAATTGGACTCCAAGGCTACCTATACGTCTCGCCTCAACTTCAT  
ATAA

### Nucleotide

>BdEXPB-14

TGCATTCGAGCCAGGCCATGTGCCACCCAACATGGCACGTTGCCCCCTCCTC  
TGCTTCTGCTCTGCTCTCGCGCATCACACAGCGCCTCCCCGGCTCGTTACCGGCG  
TACCCGACCCGGCTTATAAATAGCCCCACCGCACACGGCCACCTCCCCACTTAC

AACAAGAACCAAACAAGCCCATCACTCCTCTCACACTACACTCCCCACAGCTCAG  
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TTCAAGGACGGCAAGGGATGCGGCTCCTGCTACAAGGTAATAAAAACCAAACA  
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CGTCGGTCCCTGGAGCGTCTGCGAGTGGACCCACATGCATGTGCGTTCGTGTGTGT  
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TGCCGTTGCCGCGCATTGATTGGCGCTCTCTCTCTTCTACAGCATCTCTGAGGTGC  
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