

## IDENTIFICATION

**Species:** *Brachypodium distachyon*

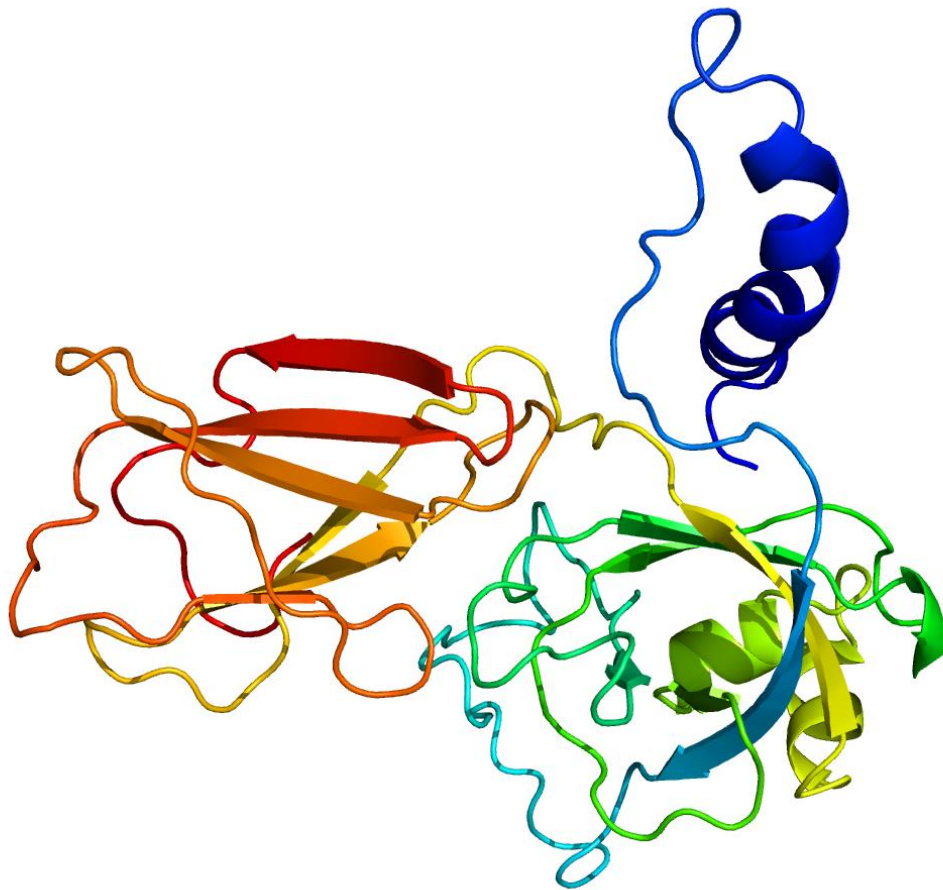
**Locus:** Bradi2g35007

**Gene Model:** Bradi2g35007.1.p

**Description:** BdEXPB-05

**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

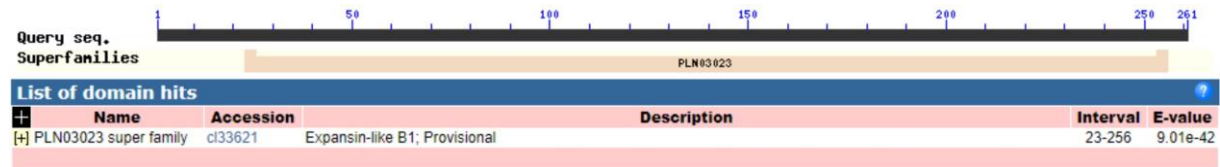
<https://brachypodium.org/>

[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-05

MGSFSGIVAVVAVLAALLAGASCFVVVPPGNITTSYDGHWLHAKATWYGSPTGAG  
PPDNGGSCGIKETNLPPYNSLTSCGNLPIFKDGKGCSCFKIKCGNKVCSKPPVVVFIT  
DMNYYQFAPYHFDLSGTAFGALAMPGRESELRRYGIIDLRFRRVRCCLAPKMKIAFH  
VEEGSNPEYLAVLVKFVAGDGDIVQMDLKQEGWPEWKPMRESWGAIWRMDVDYH  
TPLQGPFSIRLTSESGKVLVAPHVIPADWKPKTV\*

### CDS (coding sequence)

>BdEXPB-05

ATGGGATCCTTCTCGGGCATCGTCGCCGTCGTCGCAGTCTTGGCGGGCGCTCCTGG  
CCGGCGCCTCGTGT TTTGTGGTGGTGCCGCCCGGCCCAACATCACGACCAGCTA  
CGACGGCCATTGGCTCCACGCCAAGGCCACTTGGTATGGCAGCCCCACAGGCGCC  
GGCCCCCTGACAACGGTGGTTCGTGTGGGATCAAGGAGACGAACCTGCCTCCCT  
ACAACAGCTTGACCTCTTGC GGCAACCTCCCCATCTTCAAGGACGGCAAGGGCTG  
CGGCTCCTGCTTCAAGATCAAGTGTGGTAACAAGGTGTGCTCGAAGAAGCCGGTG  
GTCGTGTTTCATCACGGACATGAACTACTACCAGTTCGCCCCGTACCCTTTGACCT  
CTCCGGCACGGCCTTCGGGGCCCTGGCGATGCCGGGGAGGGAGAGCGAGCTGCCG  
GCGCTACGGCATTATCGACCTCCGGTTCAGGAGGGTGCGCTGCAAGCTCGCGCCG  
AAGATGAAGATCGCGTTCACGTCGAGGAAGGGTCCAACCCGGAATACCTGGCG  
GTGTTGGTGAAGTTCGTTCGCGGGAGACGGTGACATCGTGCAGATGGACCTGAAG  
CAGGAGGGCTGGCCGGAGTGGAAGCCGATGAGGGAGTCGTGGGGCGCCATCTGG  
AGGATGGACGTGGACTATCACACGCCGCTCCAGGGCCCATTCTCCATCCGCCTCA  
CCAGCGAGTCCGGCAAGGTGCTCGTCGCCCTCACGTCATCCCGGCTGACTGGAA  
GCCAAAACCTGTCTAA

### Nucleotide

>BdEXPB-05

GACGGAACCTCGTCTGCCCTCTCCAATTGACCAATTCAATTTAGCACAAATTCATT  
CAGCACGATGGGATCCTTCTCGGGCATCGTCGCCGTCGTCGCAGTCTTGGCGGGC  
CTCCTGGCCGGCGCCTCGTGT TTTGTGGTGGTGCCGCCCGGCCCAACATCACGA  
CCAGCTACGACGGCCATTGGCTCCACGCCAAGGCCACTTGGTATGGCAGCCCCAC

AGGCGCCGGCCCCCTGACAACGGTAATCTACCTGGTCTCCGTTTCATAATTCTT  
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TTCGACAAGAATTATGTAACGGAGATAGTACTATATTGAGGATATCATTATATCA  
GTCAACGATTGTGCTTTTGAAAATGTTGTATATAAAGAAATGATGTTCTTGGGGC  
ATATATTGCTTGGCATAACATGGAAGGAAAGAAGTCACCGCATCTTTCAGTTTAAA  
TCTGTTGATCCTGTGGTCTTGGCAGATCTCATTAGAGATGATATTAAGATGCTTGA  
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CCCGCCCCCTCCCCCCCCCCCCACCCACACACACACACACAGAGTATCGGA  
ATTTTTTTTCTTTTCTGTTCCCTTGACTTCGGTCTTGTAATGTTTCTTCTTATAATG  
AAAAAAGGCAGAACACCTGCCATGTTTCGTCAAAAAAAAAAAGAAAAAAAAAATGTGC  
TATATATCCTGCAGGTGGTTCGTGTGGGATCAAGGAGACGAACCTGCCTCCCTAC  
AACAGCTTGACCTCTTGCGGCAACCTCCCATCTTCAAGGACGGCAAGGGCTGCG  
GCTCCTGCTTCAAGGTTTTCATTTTCATCATGCAATAATAATAAAGAAGTTAATTT  
GCACGTGTACCTTTGTTGACATATATCGAAATAAATGTTATTTGCATGCAGATCA  
AGTGTGGTAACAAGGTGTGCTCGAAGAAGCCGGTGGTCGTGTTTCATCACGGACAT  
GAACTACTACCAGTTCGCCCCGTACCACTTTGACCTCTCCGGCACGGCCTTCGGG  
GCCCTGGCGATGCCGGGGAGGGAGAGCGAGCTGCGGCGCTACGGCATTATCGAC  
CTCCGGTTCAGGAGGGTGCGCTGCAAGCTCGCGCCGAAGATGAAGATCGCGTTCC  
ACGTCGAGGAAGGGTCCAACCCGGAATACCTGGCGGTGTTGGTGAAGTTCGTTCGC  
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CACGCCGCTCCAGGGCCCATTCTCCATCCGCCTACCAGCGAGTCCGGCAAGGTG  
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CAAACATTCAGTTCTAAACTTTGCCATTCATTTTCATTCATCGATCCGTGAGTTTA  
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TGCATGTGTTTGAGCCTTTGAGGATGTAACCGTGTAGATCAAACCTCGATCTGCAG  
TATTGCAATAGAGATAAATGTTTTT