

## IDENTIFICATION

**Species:** *Brachypodium distachyon*

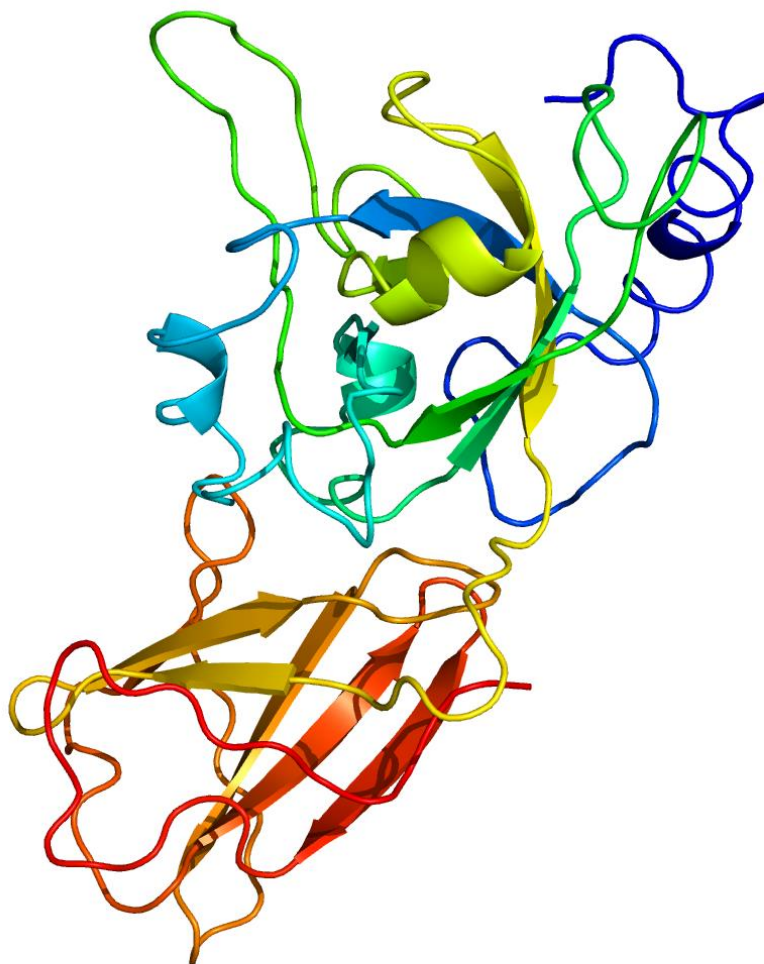
**Locus:** Bradi3g09950

**Gene Model:** Bradi3g09950.1.p

**Description:** BdEXPA-17

**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)

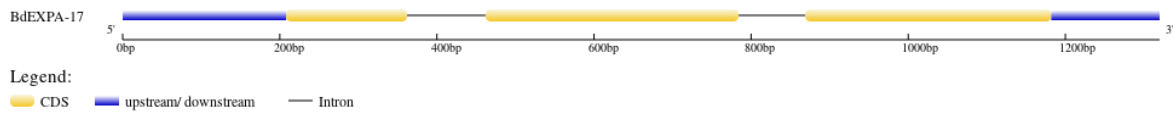
KEGG: <https://www.genome.jp/entry/T01717>

## EXTERNAL RESOURCES

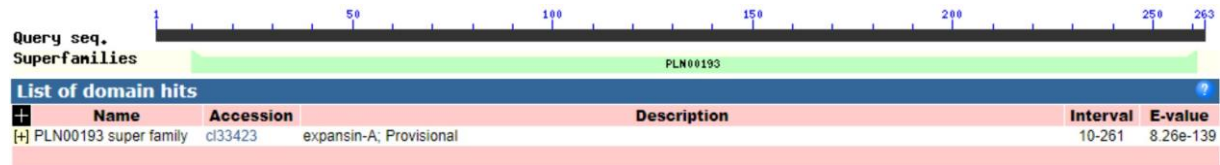
<https://brachypodium.org/>

[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-17

MAPTPAQVTAVVLLTVGCTALAVVASSPQAPVVWQRAHATFYGGADASGTMGGAC  
GYGNLYSEGYGTRTAALSTVLFNDGAACGQCYKIACDRKVDPRWCKPGVTVTVTA  
TNLCPNNAALPNDNGGWCNIPRPHFDMAQPAWEKIGVYRGGIIPVMYQRVPCVKKG  
GVRFKINGHDYFNLVLVTNVAAGSIKSMDVKSSDSKDWAPMARNWGANWHSLAY  
LSGKMLSFRILTNTDGQTLFNNIVPSGWKFGQTFASKLQFN\*

### CDS (coding sequence)

>BdEXPA-17

ATGGCACCGACTCCAGCTCAAGTACTGCGGTGGTTCTGCTCACCGTGGGCTGTA  
CGGCCTTGGCTGTAGTCGCATCGTCGCCCAAGCACCGGTCGTCTGGCAGAGGGC  
GCACGCGACGTTCTACGGTGGAGCTGATGCCTCCGGCACCATGGGCGGCGCGTGT  
GGGTACGGCAACCTGTACTCTGAGGGGTATGGAACCCGGACGGCGGGCGCTGAGC  
ACGGTGCTCTTCAACGACGGCGCGGCATGCGGACAATGCTATAAAATTGCATGCG  
ACCGCAAGGTGGACCCAAGGTGGTGTAAACCGGGTGTGACGGTGACAGTCACGG  
CCACAAACCTCTGCCACCCAACAATGCCCTTCAAATGACAATGGTGGTTGGTG  
CAACATAACCACGACCGCACTTCGACATGGCGCAACCGGCCTGGGAGAAGATCGG  
CGTCTATAGGGGCGGCATCATTCTGTATGTATCAGAGGGTTCCATGTGTGAAG  
AAGGGTGGCGTGCGGTTTAAGATCAACGGCCACGACTATTTCAATCTTGTACTTG  
TGACCAATGTTGCAGCCATCGGCTCGATAAAATCTATGGATGTCAAGAGCTCCGA  
TTCAAAGATTGGGCGCCTATGGCACGCAACTGGGGTGGCAACTGGCACTCGTTG  
GCGTATCTTAGCGGGAAAATGCTCTCGTTCAGACTAACCAACACTGATGGGCAAA  
CACTTGAGTTCAATAACATTGTGCCAAGTGGATGGAAGTTTGGGCAAACATTTGC  
GAGCAAATTGCAGTTCAACTGA

### Nucleotide

>BdEXPA-17

ACGCTAGCTGCTTCTTCATCCCTCCTGCAACGTATTGATCACAAGCGAAGGCTAT  
ATACACACACACGCACAGAATCATCACAAGATCACCAAAGGCAGCAGAAGCAAA  
TCCACATTGACAAAAGAACAACACATTAGCGAGCAAGGACTTCTAGCTTTTCGTC  
AGATTAGTTTTCAAGGCCATCGATCTAGCTTTCCAGCGCCAGATATGGCACCGAC

TCCAGCTCAAGTTACTGCGGTGGTTCTGCTCACCGTGGGCTGTACGGCCTTGGCTG  
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CTACGGTGGAGCTGATGCCTCCGGCACCATGGGTAATTAGCTTATTAAGTAGGAG  
TATAAACTCATGGTCAATTCAATTATACGTCTGCGCCAAAAGCATGTTGTCAATT  
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CGGCATGCGGACAATGCTATAAAATTGCATGCGACCGCAAGGTGGACCCAAGGT  
GGTGTAACCGGGTGTGACGGTGACAGTCACGGCCACAAACCTCTGCCACCCA  
ACAATGCCCTTCCAAATGACAATGGTGGTTGGTGCAACATACCACGACCGCACTT  
CGACATGGCGCAACCGGCCTGGGAGAAGATCGGGCGTCTATAGGGGCGGCATCAT  
TCCTGTCATGTATCAGAGGTACATCACAAATTTATCATCAATTTTGTGCTTTTTTA  
ACTAATAAATAATGGCTCAATGTCAATCTAAAACCAAATCGTTGCAGGGTTCCAT  
GTGTGAAGAAGGGTGGCGTGCGGTTTAAGATCAACGGCCACGACTATTTCAATCT  
TGTACTIONTGACCAATGTTGCAGCCATCGGCTCGATAAAAATCTATGGATGTCAAG  
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CACTCGTTGGCGTATCTTAGCGGGAAAATGCTCTCGTTCAGACTAACCAACACTG  
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