

## IDENTIFICATION

**Species:** *Brachypodium distachyon*

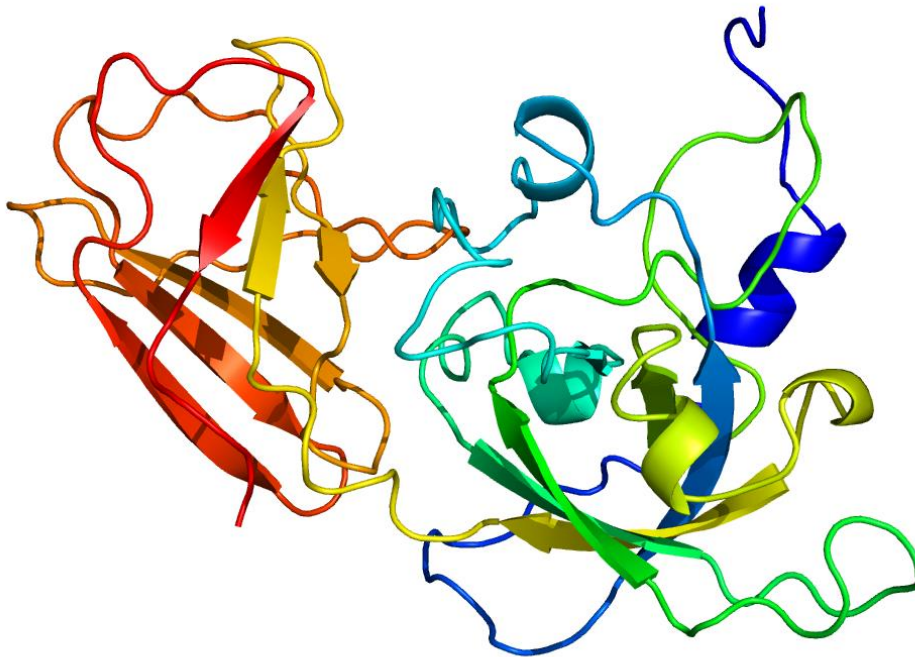
**Locus:** Bradi5g04120

**Gene Model:** Bradi5g04120.1.p

**Description:** BdEXPA-32

**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

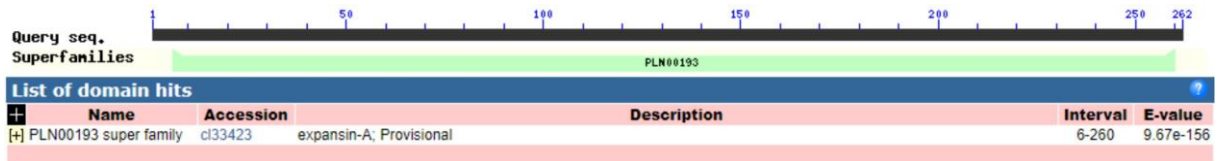
<https://brachypodium.org/>

[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-32

MDISTGSFARFLALLATTCLFWNKASGFRSSGVSRATFYGGSDASGTMGGACGYG  
NLYSTGYGTSTAALSTVLFNDGAACGQCYRISCDHAADPRFCRRGTSVTVTATNLCP  
PNYALPNDGGWCNPPRQHFDMAEPAWLDIGIYSGGIVPVLYQRVACAKKGGVRF  
VSGHDYFELVLSNVGGCGSIQAVSIKGSRTGRWMPMSRNWGVNWQSNALLSGQS  
LSFQVTSTDGQTITFPNVAPAGWGFGQTFQTSRQFS\*

### CDS (coding hits sequence)

>BdEXPA-32

ATGGACATATCAACTGGATCATTGCTCGGTTCTTGCGTTGCTTGCAACAACATG  
CCTCTTTTGAACAAGGCTTCCGGTTTCAGATCGTCCGGCGTCAGCAGAGCCTTC  
GCCACCTTCTATGGCGGCAGTGACGCCTCAGGAACCATGGGTGGGGCATGCGGGT  
ATGGTAACCTGTACTCGACGGGGTACGGGACGAGCACGGCGGGCGCTGAGCACAG  
TGCTGTTCAACGACGGCGCGGCGTGCGGGCAGTGCTACCGGATCTCCTGCGACCA  
CGCGGCGGACCCAGGTTCTGCCGCCGGGGCACGTCGGTGACCGTTACGGCCACA  
AACCTGTGCCCGCCAAACTACGCGCTCCCAACGACGACGGCGGGTGGTGCAAC  
CCGCCGCGGCAGCACTTCGACATGGCGGAGCCGGCGTGGCTCGACATCGGCATCT  
ACAGCGGCGGCATCGTGCCGGTGCTGTACCAGAGGGTGGCCTGCGCCAAGAAGG  
GCGGCGTGAGGTTCCCGTCAGCGGGCACGACTACTTCGAGCTCGTGCTGGTGAG  
CAACGTCGGCGGCTGCGGGTCCATCCAGGCCGTGTCCATCAAGGGGTCCAGGACC  
GGCCGGTGGATGCCCATGTCCAGGAATTGGGGGGTCAACTGGCAGTCCAATGCGT  
TGCTCAGCGGACAGAGCCTGTCGTTTCAGGTCACCAGTACTGATGGACAGACGAT  
CACTTCCCTAACGTCGCTCCGGCTGGATGGGGGTTCGGCCAGACGTTTCAGACC  
TCCAGGCAGTTCTCTTAA

### Nucleotide

>BdEXPA-32

TCGATCTGTAAATTCTCTCTAGCATGGACATATCAACTGGATCATTGCTCGGTT  
CCTTGCGTTGCTTGCAACAACATGCCTCTTTTGAACAAGGCTTCCGGTTTCAGAT  
CGTCCGGCGTCAGCAGAGCCTTCGCCACCTTCTATGGCGGCAGTGACGCCTCAGG  
AACCATGGGTAAATTAAAGAATCATATACAGCTAGTTTGTCTTCTTTTCGACACCT

TTTCAATTGATTCGATCGATTATATGTGTGTACGTAAGGTGGGGCATGCGGGTAT  
GGTAACCTGTACTCGACGGGGTACGGGACGAGCACGGCGGGCGCTGAGCACAGTG  
CTGTTCAACGACGGCGCGGCGTGCGGGCAGTGCTACCGGATCTCCTGCGACCACG  
CGGCGGACCCCAAGTTCTGCCGCCGGGGCACGTCGGTGACCGTTACGGCCACAA  
ACCTGTGCCCGCCAAACTACGCGCTCCCCAACGACGACGGCGGGTGGTGCAACCC  
GCCGCGGCAGCACTTCGACATGGCGGAGCCGGCGTGGCTCGACATCGGCATCTAC  
AGCGGCGGCATCGTGCCGGTGTGTACCAGAGGGTGGCCTGCGCCAAGAAGGGC  
GGCGTGAGGTTCCCGTCAGCGGGCACGACTACTTCGAGCTCGTGCTGGTGAGCA  
ACGTCGGCGGGCTGCGGGTCCATCCAGGCCGTGTCCATCAAGGGGTCCAGGACCG  
GCCGGTGGATGCCCATGTCCAGGAATTGGGGGGTCAACTGGCAGTCCAATGCGTT  
GCTCAGCGGACAGAGCCTGTCGTTTCAGGTCACCAGTACTGATGGACAGACGATC  
ACTTCCCTAACGTCGCTCCGGCTGGATGGGGGTTCGGCCAGACGTTTCAGACCT  
CCAGGCAGTTCTCTTAAGTCTTAACTCCCTAGAGGTCGGATTGTGACTCGTGAGG  
ACCAAGTTATAGGCTTGTGAACGTAATCATCTGATCAGTGTGCGTTGTGTAAAGT  
TCTTTTACCGCTGGTATATATCCCTCAAGAACAGGGAACCAAGTATTTCTTCGAG  
TTAAATCATGTGTCACCAGATCGGCCCCGTCTTTTCGAAGGAAAGTTCACGGGGT  
CGAGCACTCGAGCGCTGGTTGAGTTTGGGGCTGGCGGCTGGGGTCAAATGCCAGC  
CGTA