

## IDENTIFICATION

**Species:** *Brachypodium distachyon*

**Locus:** Bradi5g17780

**Gene Model:** Bradi5g17780.1.p

**Description:** BdEXPB-24

**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)

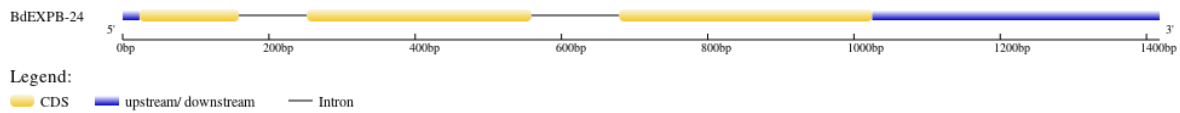
KEGG: <https://www.genome.jp/entry/T01717>

## EXTERNAL RESOURCES

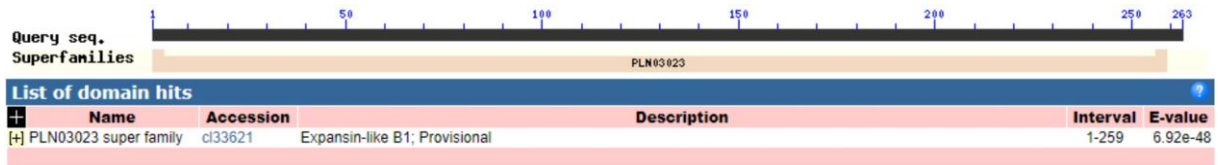
<https://brachypodium.org/>

[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-24

MASSRGTFLFAALGVLSVLSLPDAARSWADGGATWYGGPYGDGSEGGACGYKSDV  
GQDPFSSMIAAGGPSLFKNGKGCYQVRCKEDPACSGKHVTVVITDSCPDGTCQK  
EKAHFDMSGTAFGAMAKPGMADKLRNSGVLKIEFDRVPCKYNGKKISFKMDSGANP  
YYLAMLIEYEAGDGLASVEVMEAGGSKGSAKWMPMRQSWGALWCLDSKSGKPL  
QAPFSFRLTSGSGKVLVANNVVPTGWNAGKAYQANVNYAA\*

### CDS (coding sequence)

>BdEXPB-24

ATGGCTAGCAGCCGAGGCACATTCCTGTTTGCGGCACTCGGCGTTCTGTCCGTCCT  
ATCACTTCCAGACGCAGCGCGCAGCTGGGCGGACGGCGGCGCGACGTGGTACGG  
GGGACCTTACGGTGATGGCAGCGAAGGTGGCGCGTGCGGCTATAAAAGCGATGT  
CGGCCAGGACCCGTTCTCGTCGATGATCGCCGCCGGCGGACCGTCCCTCTTCAAG  
AACGGCAAAGGCTGCGGTGCATGCTACCAGGTTAGGTGCAAAGAAGACCCGGCC  
TGCTCCGGCAAGCATGTGACCGTCGTCATCACCGACTCCTGCCCCGACGGGACAT  
GCCAAAAGGAGAAGGCGCACTTCGACATGAGCGGCACCGCCTTCGGCGCCATGG  
CCAAGCCCAGGATGGCCGATAAGCTCCGTA ACTCCGGAGTCCTCAAGATCGAATT  
CGACAGGGTGCCGTGCAAGTACAACGGCAAGAAGATCAGCTTCAAGATGGACTC  
GGGCGCCAACCCATACTACCTCGCAATGCTGATCGAGTACGAGGCCGGCGACGG  
GGACCTCGCCTCCGTGGAGGTCATGGAGGCCGGCGGCAGCAAGGGCAGCGCCAA  
GTGGATGCCGATGCGGCAGTCGTGGGGCGCCTTGTGGTGTCTCGATTCCAAGAGC  
GGGAAGCCTCTGCAGGCCCGTTCTCGTTCCGGCTCACTTCGGGCTCCGGCAAGG  
TGCTCGTCGGAACAACGTCGTCCCCACCGGGTGGAATGCAGGGAAGGCCTACC  
AAGCCAACGTGAACTACGCCGCCTAA

### Nucleotide

>BdEXPB-24

CATCCTATCAACCAAAGGAAACAATGGCTAGCAGCCGAGGCACATTCCTGTTTGC  
GGCACTCGGCGTTCTGTCCGTCCTATCACTTCCAGACGCAGCGCGCAGCTGGGCG  
GACGGCGGCGCGACGTGGTACGGGGGACCTTACGGTGATGGCAGCGAAGGTAAA  
TTCATATGCACGATATGTAAATTGACCTCTAACTTGTGAGGATGTCACAAAAGAA

ACTCTGTTACGCGAAGGCGACACGCATATGCAGGTGGCGCGTGCGGCTATAAAA  
GCGATGTCGGCCAGGACCCGTTCTCGTCGATGATCGCCGCCGGCGGACCGTCCCT  
CTTCAAGAACGGCAAAGGCTGCGGTGCATGCTACCAGGTTAGGTGCAAAGAAGA  
CCCGGCCTGCTCCGGCAAGCATGTGACCGTCGTCATCACCGACTCCTGCCCCGAC  
GGGACATGCCAAAAGGAGAAGGCGCACTTCGACATGAGCGGCACCGCCTTCGGC  
GCCATGGCCAAGCCCGGGATGGCCGATAAGCTCCGTAACCTCCGGAGTCCTCAAG  
ATCGAATTCGACAGGTGTGCAAACGCATTCCATTGGAGTGATCTGATTAATTTCA  
GAAATCTCTTCAGGTTGACATGGCACACGCCTGCATGTACTACGTGCTGAGATTA  
ATTTGGTGCATTACTTTTCACCAGGGTGCCGTGCAAGTACAACGGCAAGAAGATC  
AGCTTCAAGATGGACTCGGGCGCCAACCCATACTACCTCGCAATGCTGATCGAGT  
ACGAGGCCGGCGACGGGGACCTCGCCTCCGTGGAGGTCATGGAGGCCGGCGGCA  
GCAAGGGCAGCGCCAAGTGGATGCCGATGCGGCAGTCGTGGGGCGCCTTGTGGT  
GTCTCGATTCCAAGAGCGGGAAGCCTCTGCAGGCCCCCGTTCTCGTTCCGGCTCAC  
TTCGGGCTCCGGCAAGGTGCTCGTCGCGAACAACGTCGTCCCACCGGGTGGAAAT  
GCAGGGAAGGCCTACCAAGCCAACGTGAACTACGCCGCCTAAGGGCCTGTTTGA  
GGCCACCGTTGGATGGAGTTTGAATGTTTGATCAAATACAAAGACGGAGCTGGG  
AGCACGGGCACGCTAGCCCCTAGCTAAGTACCGGAATTTGAGAACTGCAATAAG  
TCAATCAGATACCTGATTTGGATATATATTATGGAACTATAAGGAACGTGCTGTT  
TGAAAACCGCAAATTCTCCACAGTTGTGAAGTCAAACAACCGATACAATACACAC  
TTATAAATGTTGATCTGCATTTTACTCCCCTGAACTAATCATGGGATTCGGATTAC  
AACTCTGAATTTTGATTTGCTTCAGGTTACCTCCATCCACAATCCCTCTATCCCTC  
GACTCTCAAACCATTCTAGTACCCTCTCTAGCTAAATTGATTGATTTGGA