

## IDENTIFICATION

**Species:** *Brachypodium distachyon*

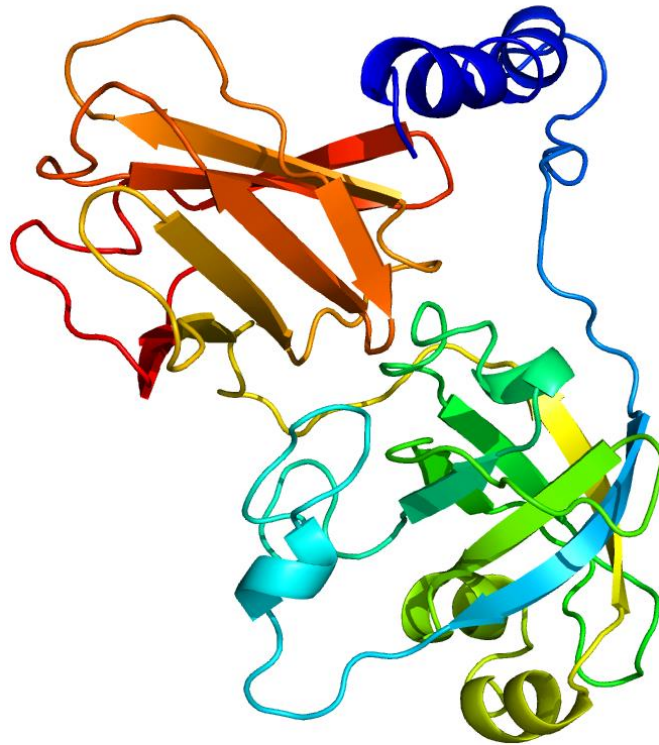
**Locus:** Bradi1g78120

**Gene Model:** Bradi1g78120.1.p

**Description:** BdEXPB-02

**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)

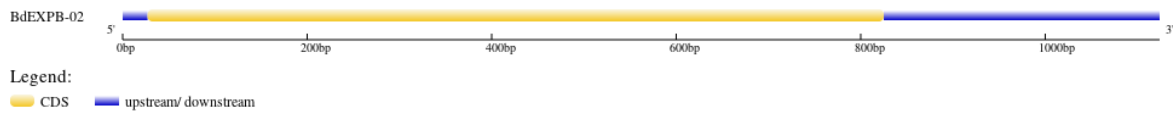
KEGG: <https://www.genome.jp/entry/T01717>

## EXTERNAL RESOURCES

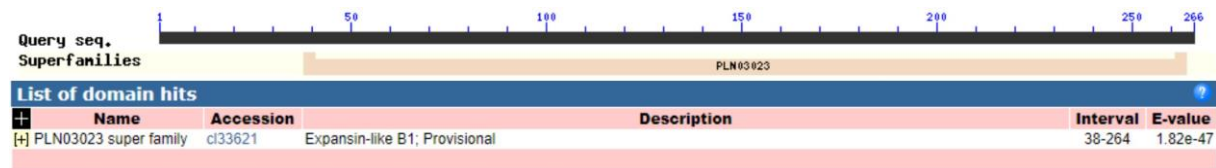
<https://brachypodium.org/>

[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-02

MASSSSSTLLLAASILATLASSAHGIPKVPPGPVNITATYGDKWLDAKSTWYGKPTGAG  
PKDNGGACGYKDVDKEPFGMTSCGNTPIFRDGRGCGSCFEIKCTKPDACSGDPVLV  
HITDDNEEPIAA YHFDLSGHAFGSMAKKGKEQDLRSAGEVEIQFRRVKCKYPEGTKV  
TFHVEKGSSPNYLAILVKYVGGDGDVVAVDVKEKKGKDEWVALKESWGAVWRLDT  
AKPLKGPLTVRYTTDGGTKGESEDEVIPEDWKPD TMYESK\*

### CDS (coding sequence)

>BdEXPB-02

ATGGCGTCTTCTTCTTCTCCTCGACGCTGCTCCTGGCAGCATCGATCCTGGCGCACT  
AGCAAGCTCCGCCACGGCATCCCCAAGGTACCTCCAGGCCCAACATCACGGCC  
ACCTACGGCGACAAATGGCTGGACGCCAAGAGCACCTGGTACGGCAAGCCCACC  
GGCGCCGGCCCCAAGGATAACGGCGGCGCCTGCGGCTACAAGGACGTGGACAAG  
GAGCCCTTCAGCGGCATGACATCCTGCGGCAACACGCCCATCTTCCGCGACGGGC  
GCGGCTGCGGCTCCTGCTTCGAGATCAAGTGCACCAAGCCCGACGCCTGCTCCGG  
CGACCCCGTCTCTGTCACATCACCGACGACAACGAGGAGCCCATCGCCGCCTAC  
CACTTCGACCTTTCGGGCCACGCCTTCGGCTCCATGGCCAAGAAGGGGAAAGAGC  
AGGACCTGCGTAGCGCCGGAAGTGGAGATCCAGTTCCGGAGGGTGAAGTGCA  
AGTACCCTGAGGGCACCAAGGTGACGTTCCATGTGGAGAAGGGGTTCGAGTCCGA  
ATTACTTGGCGATTCTCGTCAAGTATGTGGGTGGCGATGGGGACGTGGTGGCCGT  
TGATGTGAAGGAGAAGGGCAAGGATGAGTGGGTTCGCGCTCAAGGAGTCGTGGGG  
CGCCGTGTGGAGGCTTGATACTGCCAAGCCGCTCAAGGGCCCGCTTACTGTCAGG  
TATACTACTGATGGTGGCACCAAGGGCGAGTCTGAAGATGTCATCCCTGAAGACT  
GGAAACCTGACACCATGTATGAGTCCAAGTGA

### Nucleotide

>BdEXPB-02

GAGAAAACCAAACCACAACCGACCAAGATGGCGTCTTCTTCTTCTCCTCGACGCTGC  
TCCTGGCAGCATCGATCCTGGCGCACTAGCAAGCTCCGCCACGGCATCCCCAA  
GGTACCTCCAGGCCCAACATCACGGCCACCTACGGCGACAAATGGCTGGACGC  
CAAGAGCACCTGGTACGGCAAGCCCACCGGCGCCGGCCCCAAGGATAACGGCGG

CGCCTGCGGCTACAAGGACGTGGACAAGGAGCCCTTCAGCGGCATGACATCCTG  
CGGCAACACGCCCATCTTCCGCGACGGGCGCGGCTGCGGCTCCTGCTTCGAGATC  
AAGTGCACCAAGCCCGACGCCTGCTCCGGCGACCCCGTCCTCGTCCACATCACCG  
ACGACAACGAGGAGCCCATCGCCGCCTACCACTTCGACCTTTCGGGGCCACGCCTT  
CGGCTCCATGGCCAAGAAGGGGAAAGAGCAGGACCTGCGTAGCGCCGGAGAAGT  
GGAGATCCAGTTCCGGAGGGTGAAGTGCAAGTACCCTGAGGGCACCAAGGTGAC  
GTTCCATGTGGAGAAGGGGTCGAGTCCGAATTACTTGGCGATTCTCGTCAAGTAT  
GTGGGTGGCGATGGGGACGTGGTGGCCGTTGATGTGAAGGAGAAGGGCAAGGAT  
GAGTGGGTGCGCGCTCAAGGAGTCGTGGGGCGCCGTGTGGAGGCTTGATACTGCC  
AAGCCGCTCAAGGGCCCGCTTACTGTCAGGTATACTACTGATGGTGGCACCAAGG  
GCGAGTCTGAAGATGTCATCCCTGAAGACTGGAAACCTGACACCATGTATGAGTC  
CAAGTGATTCATTCTTCATCGATCCATCGTCGGCCATGCCTGCAGGTACTACCAT  
ATACTCCTGGCGTGGCCTGCAACTTAACAGAGAATAATCGTCGAGATCGATCTGC  
AGTGAGGCGAATATTGCGTACAAAAGTTTATAGTATGCCGGAGGAAGGCAGGCA  
ACCAAGGATTTGTTTCTGCTTGGTTTGCATCGATCCGGCCAGCCCATTCTCGGTC  
TCGACCGCCTTGTTTTTTTTTTTTTGTACTCAAGCTTGTTTCATGAGATCATTATCAA  
GCAATAAAATGACTCTTTTTTTTTGTATA