

## IDENTIFICATION

**Species:** *Brachypodium distachyon*

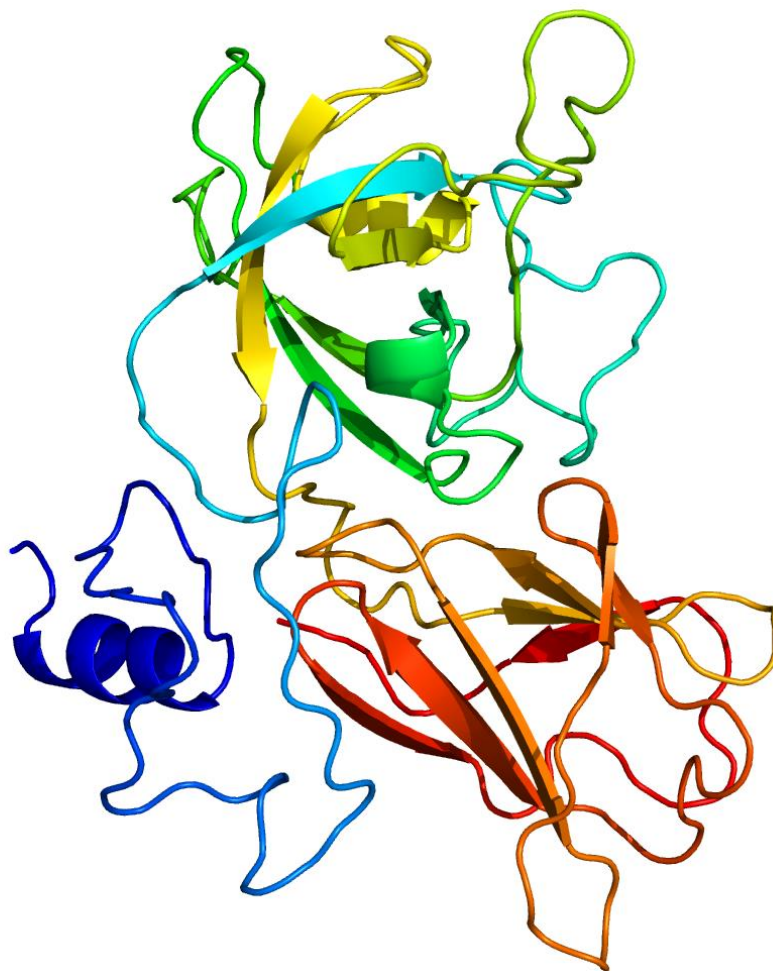
**Locus:** Bradi3g59460

**Gene Model:** Bradi3g59460.1.p

**Description:** BdEXPA-30

**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)

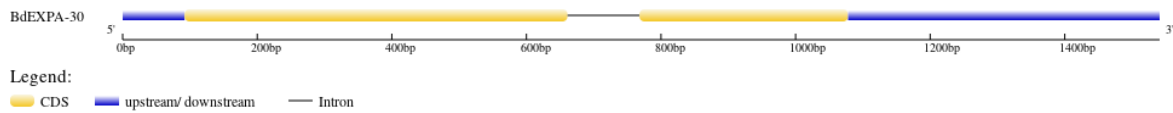
KEGG: <https://www.genome.jp/entry/T01717>

## EXTERNAL RESOURCES

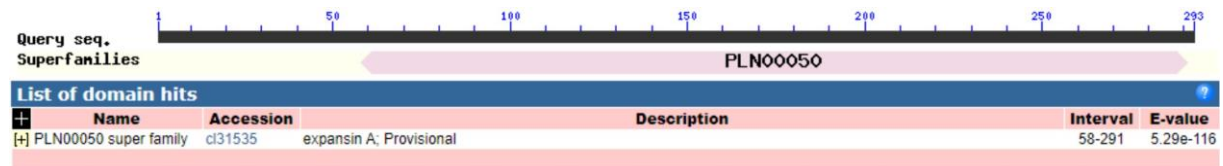
<https://brachypodium.org/>

[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-30

MAPVLRALLLAFLVAAQSPSSALSLGQGHGHHLPGHGLVHRHGNVHGGHGHHAHAP  
 LGGGAWSSAHATFYGGGDASGTMGGACGYGNLYSTGYGSNTAALSTALYNDGLSC  
 GACFEVRCDPAGTEAGAAHACLPGTSVVITATNLCPPNNALPNDDGGWCNPPRAHF  
 DMSQPVFQRIAIYKAGIVPVSYRRVACQKKGGIRFTINGHSYFNLVLSNVGGPGDV  
 HAVAVKSERSPSWQALSRNWQNWQSNALLDRQCLFRVTAGDGSSVVSSNAVPR  
 GWAFGQTFSGAQFT\*

### CDS (coding sequence)

>BdEXPA-30

ATGGCGCCCGTCCTCCGAGCCCTGCTCCTCGCCTTCCTCGTGGCCGCGCAGTCCCC  
 GTCGTCCGCCCTCTCACTCGGGCAGGGGCACGGCCATCATTTGCCCGGCCACGGC  
 CTGGTCCACCGGCATGGGAACGTCCACGGAGGCCACGGCCATGCGCACGCCCCG  
 CTCGGCGGGCGGCGCCTGGTCTCGGCGCACGCGACCTTCTACGGCGGGCGGCGACG  
 CCTCGGGCACCATGGGCGGGGCGTGCGGGTACGGGAACCTCTACAGCACGGGCT  
 ACGGCTCCAACACGGCGGCGCTGAGCACGGCGCTTACAACGACGGCCTCAGCT  
 GCGGGGCTGCTTCGAGGTCCGCTGCGACCCGGCGGGGACGGAAGCCGGCGCGG  
 CGCACGCTGCCTCCCGGGGACCTCCGTCGTCATTACGGCCACCAACCTCTGCCC  
 GCCAACAACGCGCTCCCCAACGACGACGGCGGCTGGTGC AACCTCCCCGCGC  
 AACTTCGACATGTCCAGCCCGTCTTCCAGCGCATCGCGATCTACAAGGCCGGG  
 ATCGTCCCCGTCTCCTACCGCAGGGTGGCGTGCCAGAAGAAGGGCGGAATCAGG  
 TTCACCATCAACGGCCACTCCTACTTCAACCTGGTCTCGTCTCAAACGTTGGCGG  
 GCCGGGCGACGTGCACGCGGTGGCCGTGAAGTCGGAGCGCTCGCCTTCTGGCA  
 GGCCCTGTGCGGCAACTGGGGCCAGAACTGGCAGAGCAACGCGCTGCTAGACCG  
 CCAGTGCTCTCCTTCCGCGTCACCGCCGGCGACGGCAGCTCCGTCGCTCCAGC  
 AACGCCGTGCCCCGCGGCTGGGCCTTCGGCCAGACCTTCAGCGGCGCCCAGTTCA  
 CCTGA

## Nucleotide

>BdEXPA-30

TTTATCCCCGGCCCAACCCCAGTTCACAAACCCCTCAGACCACATTCCCCTTCTCT  
CCGCAGGCCGCTCTGTTCCACGCCCGTCACGCGGCAATGGCGCCCGTCCTCCGAG  
CCCTGCTCCTCGCCTTCTCGTGGCCGCGCAGTCCCCGTCGTCCGCCCTCTCACTC  
GGGCAGGGGCACGGCCATCATTTGCCCGGCCACGGCCTGGTCCACCGGCATGGG  
AACGTCCACGGAGGCCACGGCCATGCGCACGCCCCGCTCGGGCGGCGGGCGCCTGG  
TCCTCGGCGCACGCGACCTTCTACGGCGGGCGGCGACGCCTCGGGCACCATGGGCG  
GGGCGTGCGGGTACGGGAACCTCTACAGCACGGGCTACGGCTCCAACACGGCGG  
CGCTGAGCACGGCGCTCTACAACGACGGCCTCAGCTGCGGGGCCTGCTTCGAGGT  
CCGCTGCGACCCGGCGGGGACGGAAGCCGGCGCGGGCGCACGCCTGCCTCCCGGG  
GACCTCCGTCGTCATTACGGCCACCAACCTCTGCCCGCCCAACAACGCGCTCCCC  
AACGACGACGGCGGCTGGTGCAACCCTCCCCGCGCACACTTCGACATGTCCCAGC  
CCGTCTTCCAGCGCATCGCGATCTACAAGGCCGGGATCGTCCCCGTCTCCTACCG  
CAGGTTAATTCGAGCTCTCTTGTTCTTTGTTACCTCTGAAATCTGAATCTGGAGTA  
ACACACTGACTGACAGTGGCTTTGTTCTTCTTCTTCTTCTTGTGTCTTCAGGGT  
GGCGTGCCAGAAGAAGGGCGGAATCAGGTTACCATCAACGGCCACTCCTACTTC  
AACCTGGTCCTCGTCTCCAACGTTGGCGGGCCGGGCGACGTGCACGCGGTGGCCG  
TGAAGTCGGAGCGCTCGCCTTCTGGCAGGCCCTGTGCGGCAACTGGGGCCAGAA  
CTGGCAGAGCAACGCGCTGCTAGACCGCCAGTGCCTCTCCTTCCGCGTCACCGCC  
GGCGACGGCAGCTCCGTCGTCTCCAGCAACGCCGTGCCCCGCGGCTGGGCCTTCG  
GCCAGACCTTCAGCGGCGCCCAGTTCACCTGAAAAAGTCTCCTTTTCTAGCTCATT  
TTACCCCAAGATTATGCCTTAGTAGTGCTATCCAGTAGCGAGTAGTAGTAGCTTC  
GATTGGAGCGTGCTGGGAGGAGCCATGGTTTTATGGGTGGTTCTTCTTGAAGCAT  
TACTGTACGTTCTTCGGAAGCAGTCAGTAGTAGTATCAGCAGGTAGTTTAGGCC  
TGGTATTAGCATGGGCTTTTAATTGTCCTGGTGTCCAGTGTGTCAGTGTAGCAAGAG  
TGGAGTGGTAGTTTGAGCGAGCTTTTGGCTAAGGATGGCAGCGGTGGTAAAGGCT  
GGGTGGTTAACTGAAGCCGCTTGTATCACCCGCCAATTAGCGATTAGGCCTAT  
TTGGATGATGGCCTTGTCTCGACGGTAATCTGCGTTGGCTTGTACTGATCCTCATT  
CTGGGGTTAACTAATTTATGCATTTGGGGCTTCAGCCTCTTTCGTTCTGTC