

IDENTIFICATION

Species: *Brachypodium distachyon*

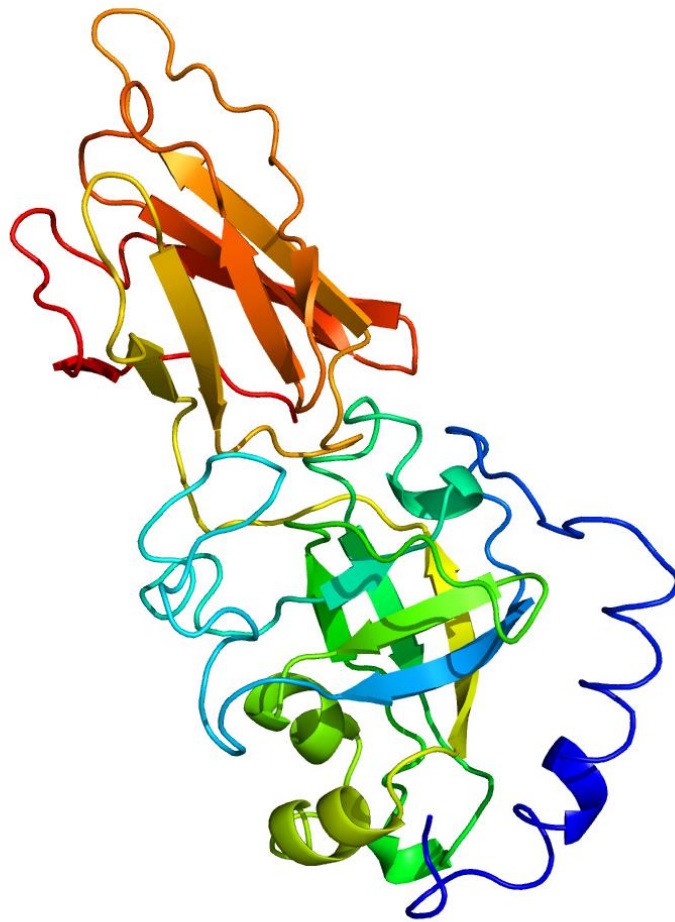
Locus: Bradi3g33112

Gene Model: Bradi3g33112.1.p

Description: BdEXPB-08

Family: Beta Expansin

3D structure:



GENOME DATABASES

Phytozome: https://phytozome-next.jgi.doe.gov/info/Bdistachyon_v3_1

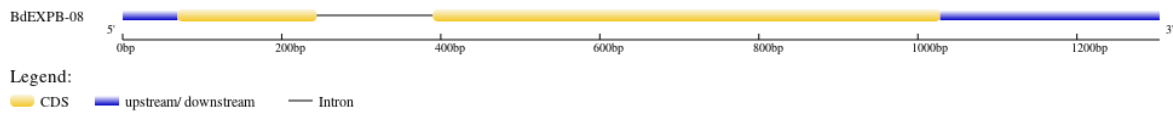
KEGG: <https://www.genome.jp/entry/T01717>

EXTERNAL RESOURCES

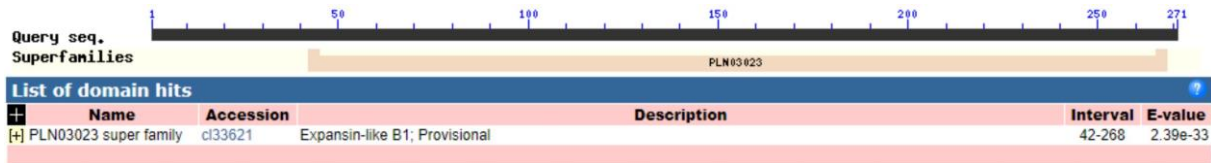
<https://brachypodium.org/>

https://archive.gramene.org/species/brachypodium/brachypodium_intro.html

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>BdEXPB-08

MGRVSAIAIALVALFSAVLVTSGHSQSYDAARSYNSGAWLPAKATWYGAPTGAGP
DDNGGACGYKFTNLYPFSSMTSCGNEPLFMDGAGCGTCYQIKCTSVNNPACSGQPKI
VMITDMNYYPVARYHFDSLGTAFGAMANYGQNDQLRHAGIIDMQFRRVPCNYPGIN
VIFHVEAGSNPMYLAVLVLFANRDGNVVQMDVMESRYGGPTGYWMPMRRSWGAI
WRLDSGHPLQGPFSLRIRSEFGATLVAHQAIADWKPDTNYWSNIQYY*

CDS (coding sequence)

>BdEXPB-08

ATGGGTCGTGTCTCCGCCAATGCCATTGCCCTTGTGGCACTATTCTCGGCCGTGCT
CGTCACCTCCGGGCATTCGCAGAGCTACGACGCCGCTAGATCCTACAACCTCCGGC
GCCTGGCTCCCCGCCAAGGCCACCTGGTACGGCGCCCCTACGGCGCCGGCCCCG
ACGACAACGGTGGTGCATGCGGCTACAAGTTCACCAATCTGTACCCGTTCTCGTC
CATGACCTCCTGCGGCAACGAGCCTCTGTTCATGGATGGCGCGGGCTGCGGCACC
TGCTACCAGATCAAATGCACCAGCGTCAACAACCCTGCCTGCTCCGGCCAGCCGA
AGATCGTCATGATCACCGACATGAACTACTACCCGGTCGCCAGGTACCACTTCGA
CCTGAGCGGGACGGCGTTTCGGCGCCATGGCGAACTACGGCCAGAACGACCAGCT
CCGGCACGCGGGCATCATCGACATGCAGTTCAGGAGGGTGCCGTGCAACTACCC
GGGGATAAACGTGATCTTCCACGTGGAGGCCGGGTTCGAACCCGATGTACCTGGC
GGTGCTCGTCCTGTTCGCGAACCAGGGACGGGAACGTGGTGCAGATGGACGTCATG
GAGTCCAGGTACGGCGGGCCGACCGGGTACTGGATGCCGATGAGGCGGTCTGTTG
GGCGCCATCTGGAGGCTGGACTCGGGCCACCCGCTGCAGGGGCCCTTCTCCCTCC
GCATCCGCAGCGAGTTCGGCGCCACGCTGGTTCGCACACCAGGCCATCCCGGCCGA
CTGGAAGCCCGACACCAACTACTGGTCCAACATCCAGTACTACTAG

Nucleotide

>BdEXPB-08

ACAAACAGGAATTTGGAGTAGCACTACTCCAGCAATTAGAAGGTTTCTATTTTG
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CCGGCGCCGGCCCCGACGACAACGGTAATTAAGCGCGCACGTACGTGCATATAT
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ACGCGGGCATCATCGACATGCAGTTCAGGAGGGTGCCGTGCAACTACCCGGGGA
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CGTCCTGTTTCGCGAACCCGGGACGGGAACGTGGTGCAGATGGACGTCATGGAGTC
CAGGTACGGCGGGCCGACCGGGTACTGGATGCCGATGAGGCGGTTCGTGGGGCGC
CATCTGGAGGCTGGACTCGGGCCACCCGCTGCAGGGGCCCTTCTCCCTCCGCATC
CGCAGCGAGTTCGGCGCCACGCTGGTCGCACACCAGGCCATCCCGGCCGACTGG
AAGCCCGACACCAACTACTGGTCCAACATCCAGTACTACTAGCTCGATCAACCGC
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