

IDENTIFICATION

Species: *Brachypodium distachyon*

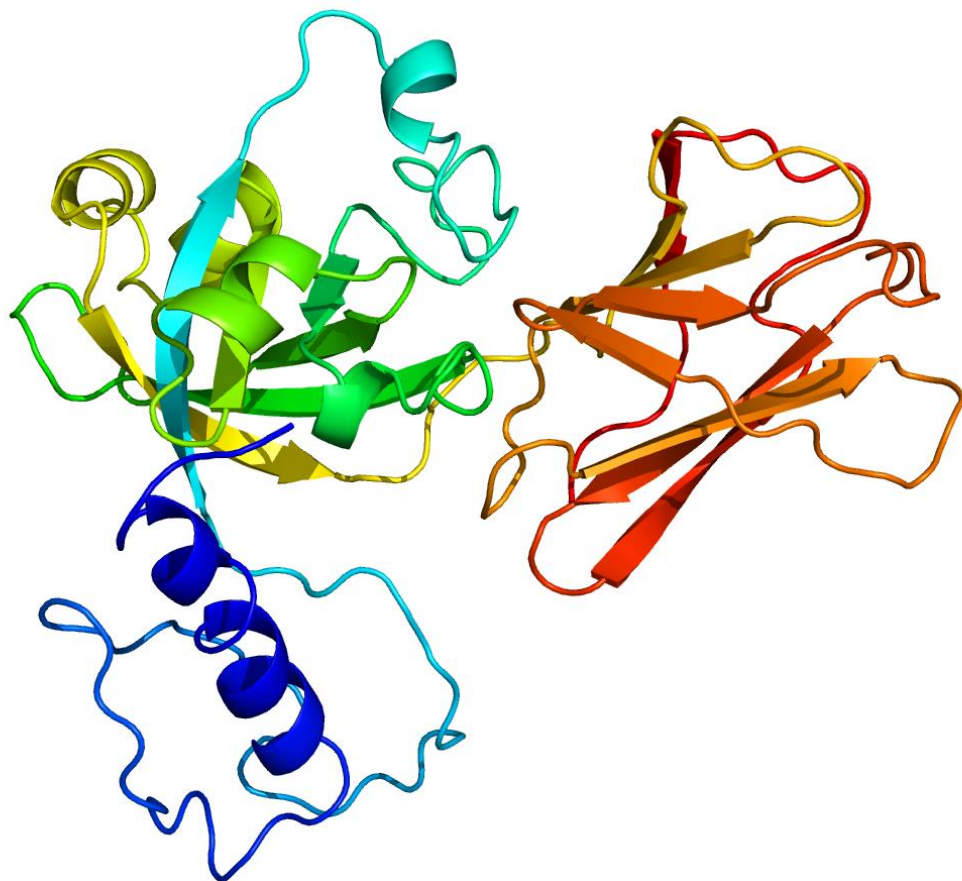
Locus: Bradi3g50750

Gene Model: Bradi3g50750.1.p

Description: BdEXPB-17

Family: Beta Expansin

3D structure:



GENOME DATABASES

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

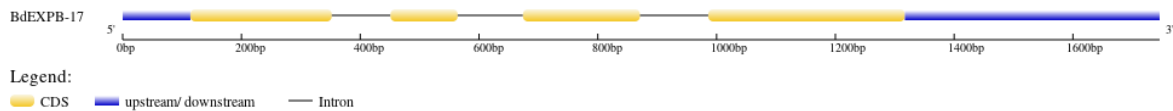
KEGG: <https://www.genome.jp/entry/T01717>

EXTERNAL RESOURCES

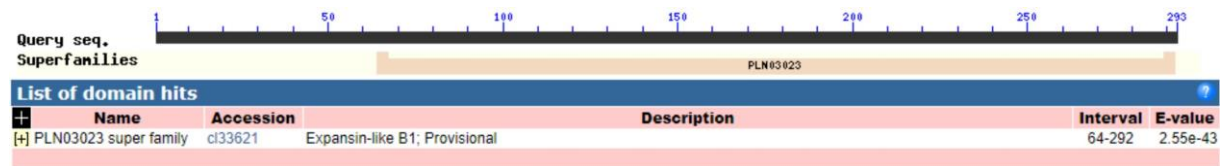
<https://brachypodium.org/>

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

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>BdEXPB-17

MAKTCTLLALIGALVVVSLLVGPAACSRKLSKPLSHKPAIKAPHNNHSTITGPSDAYG
SGGWLYGGATYYGAPNGDGSDDGACGYQSAVGNRPFSSMIAAGNPFLFKGGKGC
ACYEVKCTGNLACSGQPATVVITDECPPGGAACLGEAAHFDMSGTSMGAMAKPGMA
DKLRASGILKIYKRVPCKEYSGVNIAFRVDQGSNPFYLEVLIEFEDDDGDLNAV
DLM EANSGTWTPMVQNW GALWRLNSNTGKPLRGPFSRLTSDSNRKLVVNNVIPATWK
AGQTYRSLVNYP*

CDS (coding sequence)

>BdEXPB-17

ATGGCGAAAACCTTGACACCTTATTAGCGCTAATTGGCGCACTGGTGGTGGTCTCAC
TTCTCGTGGGCCCCGCTGCTTGCTCCCGCAAGCTCTCCAAGCCGCTCAGCCACAA
GCCTGCAATCAAGGCGCCCCACAACAACCATAGTACCATCACTGGCCCCGTCGGAC
GCCTACGGCTCCGGCGGCTGGTTATACGGCGGCGCAACGTATTACGGCGCCCCCA
ACGGCGACGGAAGCGACGGTGGCGCGTGC GGCTACCAAAGCGCTGTCGGGAACC
GGCCATTCTCGTCGATGATCGCCGCCGGGAACCCCAATCTTTTCAAGGGAGGGAA
GGGCTGCGGCGCGTGCTACGAGGTTAAATGTACAGGCAACCTGGCGTGCTCCGGC
CAGCCGGCGACGGTCGTCATCACCGACGAATGCCCGGCGGGGCGGCCTGCCTTG
GCGAGGCGGCCACTTCGACATGAGCGGGACCTCCATGGGGGCCATGGCCAAGC
CTGGCATGGCCGACAAACTGCGTGCCAGTGGCATCCTCAAGATTCAAGTACAAGAG
GGTGCCATGCAAGTACAGCGGCGTGAACATCGCCTTCAGGGTGGACCAGGGGTC
GAACCCGTTCTACCTGGAGGTCCTGATCGAGTTCGAGGACGACGACGGCGACCTC
AACGCCGTGGACCTCATGGAGGCCAACAGCGGCACCTGGACGCCGATGGTGCAG
AACTGGGGCGCGCTGTGGCGCCTCAATTCCAACACCGGCAAGCCGCTGCGCGGG
CCCTTCTCGTCCGGCTCACCTCTGACTCCAACAGGAAGCTCGTCGTAACAACG
TCATCCCCGCCACCTGGAAGGCCGGACAGACGTACCGCTCCTTGGTCAACTACCC
CTAA

Nucleotide

>BdEXPB-17

AACTCACCAAGGCACGCTTGAGCTATAAGCATATCCAATCCATATCCTCTTCCAA
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CCAACGGCGACGGAAGCGACGGTTAGTATACACATTCCACATTGCAATGGACGG
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ACAGCGGGCTGCCTAGCTCCATTACGGTCCTAGCTTTAGCTAAATTAATGTTCTCC
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ACGGTCGTCATCACCGACGAATGCCCCGGCGGGGCGGCCTGCCTTGGCGAGGCG
GCCCACTTCGACATGAGCGGGACCTCCATGGGGGCCATGGCCAAGCCTGGCATG
GCCGACAAACTGCGTGCCAGTGGCATCCTCAAGATTCAGTACAAGAGGTACCACT
ACACTTCAGCCAACATTATCCGCTGGAGCAGCACAAATTAATTGATGGAAGCTGT
GTACTAATTCATTTAATCTTTGTGTTTCTTCATTATTAATCTATCTTTATAGGGTGC
CATGCAAGTACAGCGGCGTGAACATCGCCTTCAGGGTGGACCAGGGGTGCAACC
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