

IDENTIFICATION

Species: *Brachypodium distachyon*

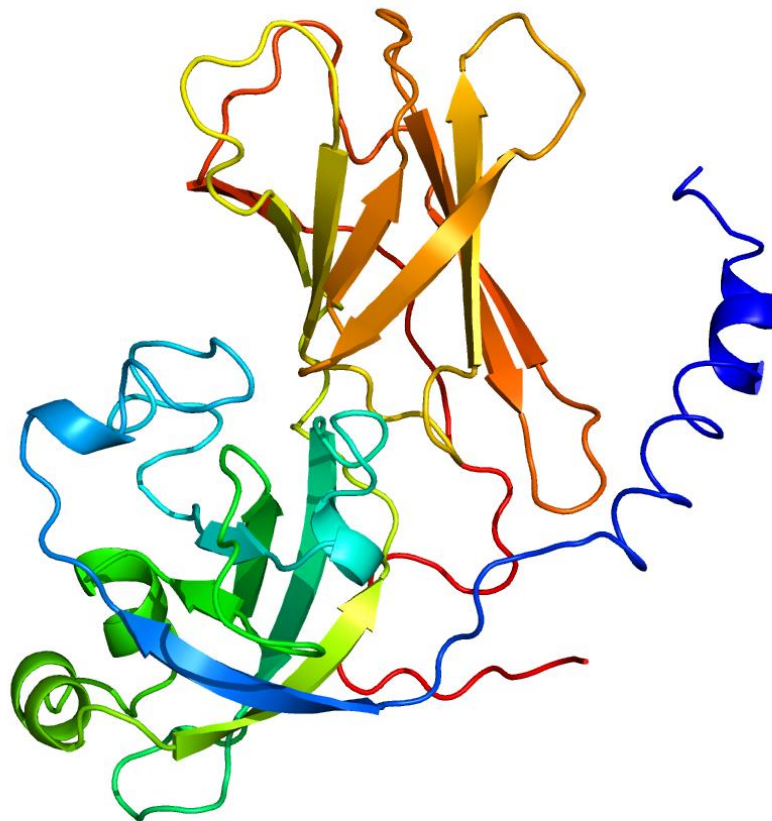
Locus: Bradi1g76260

Gene Model: Bradi1g76260.1.p

Description: BdEXLA-03

Family: Expansin Like Alpha

3D structure:



GENOME DATABASES

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

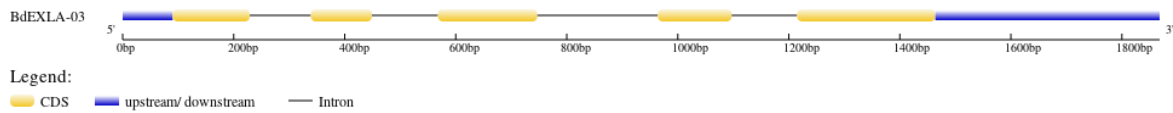
KEGG: <https://www.genome.jp/entry/T01717>

EXTERNAL RESOURCES

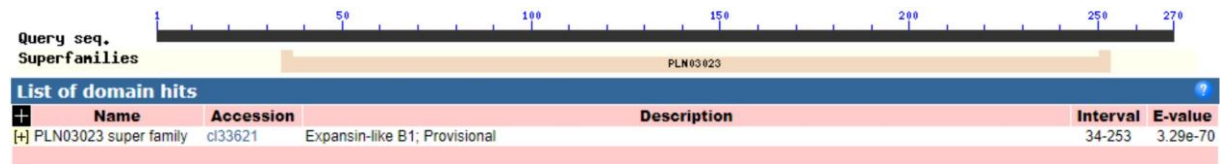
<https://brachypodium.org/>

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

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>BdEXLA-03

MAVSIPSSSTLLL VFLFSFLVSLASACDRCVRTSRAAYYTSSLTLAAGSCGYGTAAASF
NGGLLAAASPALYRDGVGCGACFQVRCKDKKLCGAAGARVVVTDRARTNRTDLVL
SSPAFAAMARPGMAAQLAKFGAVKVEYKRVPCYKGNLSVRVEERSRAPNELAIR
FLFQGGQTDIVAVDVAQVGSNWKFMARDSGPAWSTSQAPPGLQFRVVVTGGYD
GKWVWAEKEVLPRRWRAGEVYDTGVQITDVAQEGCFPCDTQEW*

CDS (coding hits)

>BdEXLA-03

ATGGCCGTCTCCATCCCGTCCTCATCCACTCTGCTCCTCGTCTTCCTCTTCTCCTTC
CTCGTCTCGCTCGCCTCCGCCTGCGACCGCTGCGTGCGCACCTCCAGGGCCGCCT
ACTACACCTCCTCGCTCACCTCGCCGCCGGGTCTTGTGGGTATGGCACGGCGGC
CGCGTCTTCAACGGCGGCCTGCTCGCCGCGGCCAGCCCCGCCCTGTACAGAGAC
GGCGTAGGCTGCGGCGCGTGCTTCCAGGTGAGATGCAAGGACAAGAAGCTGTGC
GGCGCGGCGGGCGCCAGGGTCGTGGTCACGGACCGGGCCAGGACGAACCGCACG
GACCTCGTGCTCAGCAGCCCGGCGTTCGCCGCCATGGCCCGGCCCGGCATGGCCG
CGCAGCTCGCCAAGTTCGGCGCTGTCAAAGTCGAGTACAAGAGGGGTGCCGTGCG
AGTACAAGGGGAAGAACCTCTCGGTGCGTGTCGAAGAGAGGAGCCGCGCGCCCA
ACGAGCTTGCCATCAGGTTCTTCCAGGGCGGCCAGACCGACATCGTCGCCGT
CGACGTGCGACAGGTGGGATCGTCGAATTGGAAGTTCATGGCGCGGGACAGCGG
GCCGGCGTGGAGCACGAGCCAGGCGCCGCCGGGGCCGCTGCAGTTCAGGGTGGT
GGTCACCGGCGGGTACGACGGCAAGTGGGTGTGGGCAGAGAAGGAAGTGCTGCC
GCGCCGGTGGCGCGCCGGCGAGGTCTACGACACGGGCGTCCAGATCACCGACGT
GGCGAAGAAGGCTGCTTCCCTTGCACACGCAGGAGTGGAGGTGA

Nucleotide

>BdEXLA-03

CTCCCCTCCTCTCCTCTTTGAGCTTCTCTCAGCTTCAAGCAATCACACAAACCCAC
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TCATCCACTCTGCTCCTCGTCTTCCTCTTCTCCTTCTCGTCTCGCTCGCCTCCGCC
TGCGACCGCTGCGTGCGCACCTCCAGGGCCGCCTACTACACCTCCTCGCTCACCC

TCGCCGGTAAGTGTACTCCCGGCCGCCGCCATCGATCGATTGGTACAACCTGCGC
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TCGCCGCGGCCAGCCCCGCCCTGTACAGAGACGGCGTAGGCTGCGGCCGCGTGCTT
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TCGGCGATGCAGGTGAGATGCAAGGACAAGAAGCTGTGCGGCCGCGGCCGGGCGCC
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TCCTCTTCCAGGGCGGCCAGACCGACATCGTCGCCGTCGACGTCGCACAGGTACA
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