IDENTIFICATION

Species: *Brachypodium distachyon*

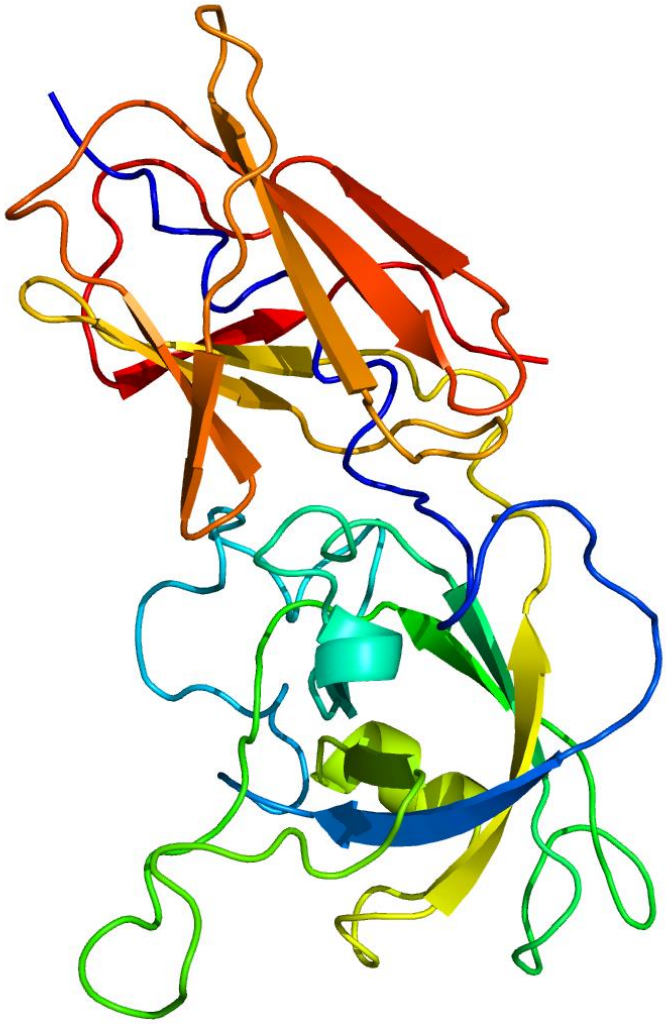
Locus: Bradi3g19500

Gene Model: Bradi3g19500.1.p

Description: BdEXPA-23

Family: Alpha Expansin

3D structure:



GENOME DATABASES

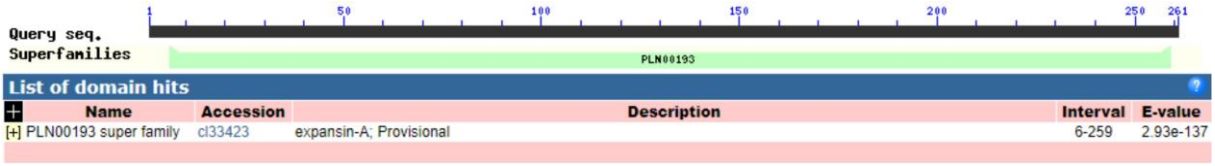
Phytozome: https://phytozome-next.jgi.doe.gov/info/Bdistachyon_v3_1
KEGG: https://www.genome.jp/entry/T01717

EXTERNAL RESOURCES

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

GENE STRUCTURE

DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>BdEXPA-23

MAPAPAQVIAVVLLTAGYTALAAGSPPAPIVWQRATATFYGGADASGTMGGACGY
GNLYDEGYGTRSAALSTVLFNDGASCGQCYKIACDRKIDPRWCKPGVTVTITATNFC
PPNNALPNDNGGWCNTPRPHFDMAQPAWEKIGVYRGGIIPVMYQRVPCVKKGGLRF
KINGHDYFNLVLVTNVATAGSIKSMDVMSSDSKDWVPMSRNWGANWHSLAYLSGK
QLSFRITNTDGQTLVFDKIVPSGWKFGQTFASKVQFN*

CDS (coding sequence)

>BdEXPA-23

ATGGCGCCGGCTCCAGCTCAAGTGATTGCGGTGGTGCTGCTCACAGCGGGCTATA
CTGCTTTGGCCGCTGGGTCGCCTCCGGCGCCGATCGTTTGGCAGAGGGCGACCGC
CACGTTCTACGGTGGAGCTGACGCCTCCGGCACCATGGGTGGTGCGTGTGGGTAT
GGCAACCTGTACGACGAGGGGTACGGGACCCGGTCGGCGGCGCTGAGCACGGTG
CTGTTCAACGACGGCGCGTCGTGTGGACAGTGCTATAAGATTGCATGTGATCGCA
AGATAGACCCGAGGTGGTGCAAACCTGGCGTGACGGTGACAATCACCGCTACAA
ACTTCTGCCCGCCCAACAATGCCCTTCCGAACGACAACGGAGGCTGGTGCAACAC
GCCACGGCCACATTTCGACATGGCGCAGCCGGCCTGGGAGAAGATCGGTGTCTAT
AGAGGTGGCATCATTCCGGTCATGTATCAGAGGGTTCCGTGCGTGAAGAAGGGTG
GCCTACGGTTTAAAATCAACGGCCACGACTACTTCAATCTCGTGCTTGTCACCAA
CGTTGCAACTGCTGGCTCGATAAAATCCATGGACGTCATGAGCTCCGATTCAAAA
GATTGGGTCCCCATGTCACGCAACTGGGGTGCCAACTGGCACTCGTTGGCATACC
TCAGCGGGAAACAACTCTCGTTCAGAATAACCAACACAGATGGGCAAACACTTG
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Nucleotide

>BdEXPA-23

GCCAGCAGAAGCAACTATTCCACTTTCCACATAGGCAGAAGAAGAAACAAACGA
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GAGCACGGTGCTGTTCAACGACGGCGCGTCGTGTGGACAGTGCTATAAGATTGCA
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TCGGTGTCTATAGAGGTGGCATCATTCCGGTCATGTATCAGAGGTACACACATGC
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AACGGCCACGACTACTTCAATCTCGTGCTTGTCACCAACGTTGCAACTGCTGGCT
CGATAAAATCCATGGACGTCATGAGCTCCGATTCAAAAGATTGGGTCCCCATGTC
ACGCAACTGGGGTGCCAACTGGCACTCGTTGGCATACCTCAGCGGGAAACAACTC
TCGTTCAGAATAACCAACACAGATGGGCAAACACTTGTGTTCGACAAGATTGTGC
CAAGTGGATGGAAGTTTGGGCAAACATTTGCAAGCAAAGTACAGTTCAATTAATC
ATTCCCATCAGATCAAAATATAAGGTGGTTGATTCGATGCAGTACTTGTATATAG
ATGCCGAATGGGTCATGTCATGTACATATACAATATTAATATTGTGTTGTGTTATG
TATTGTTTGTGTTTATAACTCATGGGGTGTATAATTTTAAGATTGCTTGATTTAAT
CTCAGACAGAAAACTGTTTGTACAAAT