

IDENTIFICATION

Species: *Brachypodium distachyon*

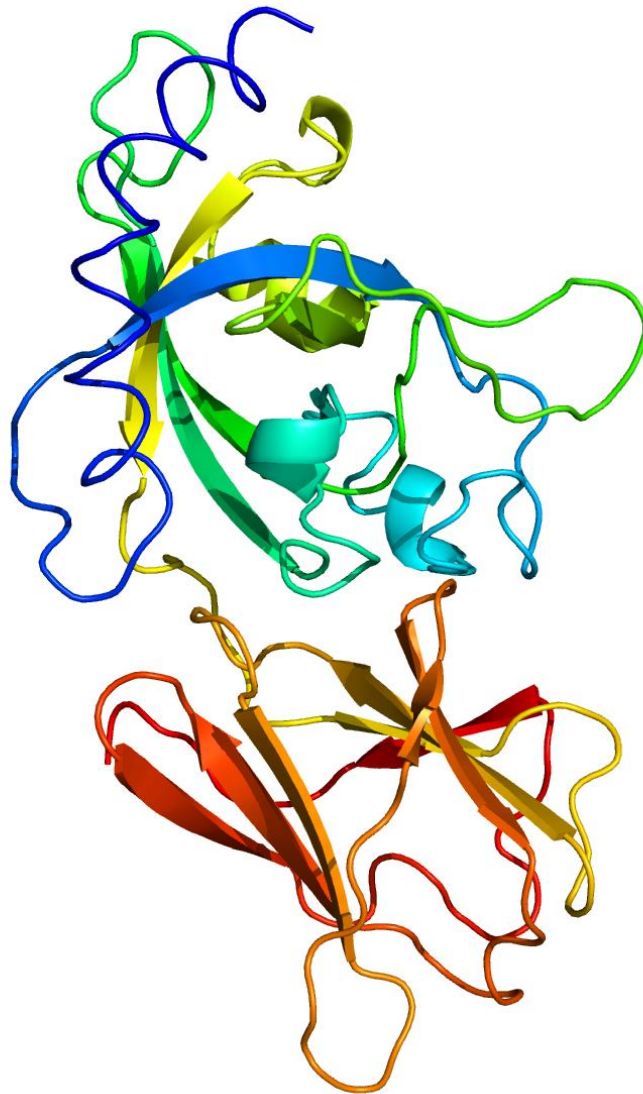
Locus: Bradi3g27470

Gene Model: Bradi3g27470.1.p

Description: BdEXPA-27

Family: Alpha Expansin

3D structure:



GENOME DATABASES

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

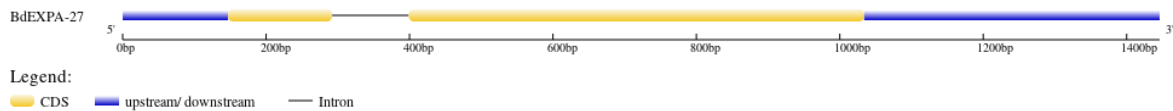
KEGG: <https://www.genome.jp/entry/T01717>

EXTERNAL RESOURCES

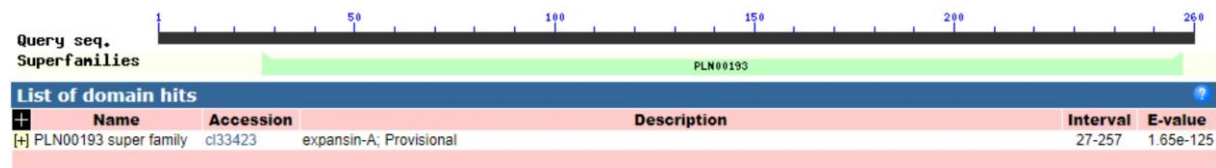
<https://brachypodium.org/>

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

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>BdEXPA-27

MTMEASKSLPAFLALAVAAALMFLAPASAGWSQGSATFYGGSDASGTMGGACGYG
NLYFTGYGKSTAALSVAMFNDGASCQCQYQISCDYQTNPQWCRQGTSVTITATNLC
PANYALPSNNGGWCNPPRAHFDMAEPAWLQIGVYQGGYIPVLYQRVSCVKQGGVR
FTVTGKNYFELVLSNVGGSGSVQAMWAKSANTGQVAMSRNWGANWQCLAGLV
GQAITFGVTTTGGQTIVFQNVVPASWSFGMSFISNLQFTY*

CDS (coding sequence)

>BdEXPA-27

ATGACAATGGAGGCGTCCAAATCTCTACCCGCCTTCCTCGCCCTCGCCGTCGCCG
CCGCGCTGATGTTCCCTCGCGCCGGCCTCCGCTGGCTGGTCCCAGGGCTCGGCCAC
GTTCTACGGAGGCAGCGACGCCTCCGGCACCATGGGCGGCGCGTGCGGGTACGG
CAACCTGTACTTTACGGGGTACGGCAAGAGCACGGCGGCGCTGAGCGTGGCGAT
GTTCAACGACGGCGCGTTCGTGCGGGCAGTGCTACCAGATCAGCTGCGACTACCAG
ACGAACCCGCAGTGGTGCCGGCAGGGCACCAGCGTGACCATCACGGCCACAAAC
CTCTGCCCGGCCAACTACGCGCTCCCCAGCAACAACGGCGGCTGGTGCAACCCGC
CGCGGGCGCACTTCGACATGGCGGAGCCGGCGTGGCTGCAGATCGGGGTGTACC
AGGGCGGCTACATCCCGGTGCTGTACCAGCGGGTGTCTGCGTGAAGCAAGGAG
GGGTGCGCTTACGGTGACGGGGAAGAACTACTTCGAGCTGGTGCTCGTCAGCAA
CGTCGGCGGGAGCGGGTCCGTGCAGGCCATGTGGGCCAAGAGCGCCAACACGGG
GCAGGTGGCCATGAGCAGGAACTGGGGCGCCAACCTGGCAGTGCCTGGCAGGGCT
CGTTGGTCAGGCCATCACCTTCGGCGTCACCACCACCGGCGGCCAGACCATCGTC
TTCCAGAACGTCGTGCCGGCCAGCTGGAGCTTCGGCATGTCTTCATCAGCAACC
TGCAGTTCACATACTGA

Nucleotide

>BdEXPA-27

TTCATCGATCCACACAGTTCCTATTTAAGAACCGCGCCACTAACAAGCTGCAGTA
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GAACTACTTCGAGCTGGTGCTCGTCAGCAACGTCGGCGGGAGCGGGTCCGTGCAG
GCCATGTGGGCCAAGAGCGCCAACACGGGGCAGGTGGCCATGAGCAGGAACTGG
GGCGCCAACTGGCAGTGCCTGGCAGGGCTCGTTGGTCAGGCCATCACCTTCGGCG
TCACCACCACCGGCGGCCAGACCATCGTCTTCCAGAACGTCGTGCCGGCCAGCTG
GAGCTTCGGCATGTCCTTCATCAGCAACCTGCAGTTCACATACTGACCACTGCAC
GACCGTACGTGCTACGGTATATCATCCGTCGGACTTGGTAGTTTGTTAGGGGATC
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ACTTTCTGTGCGTAATTTGACTCGGAATTCTAGCGGGGGCACGTCCCCTGCTCTGT
CTTCTCAAGCGGCCGCTGACTCGCTCGCAGCCTCGCACGCTTCGGATCGATGCGT
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