

IDENTIFICATION

Species: *Brachypodium distachyon*

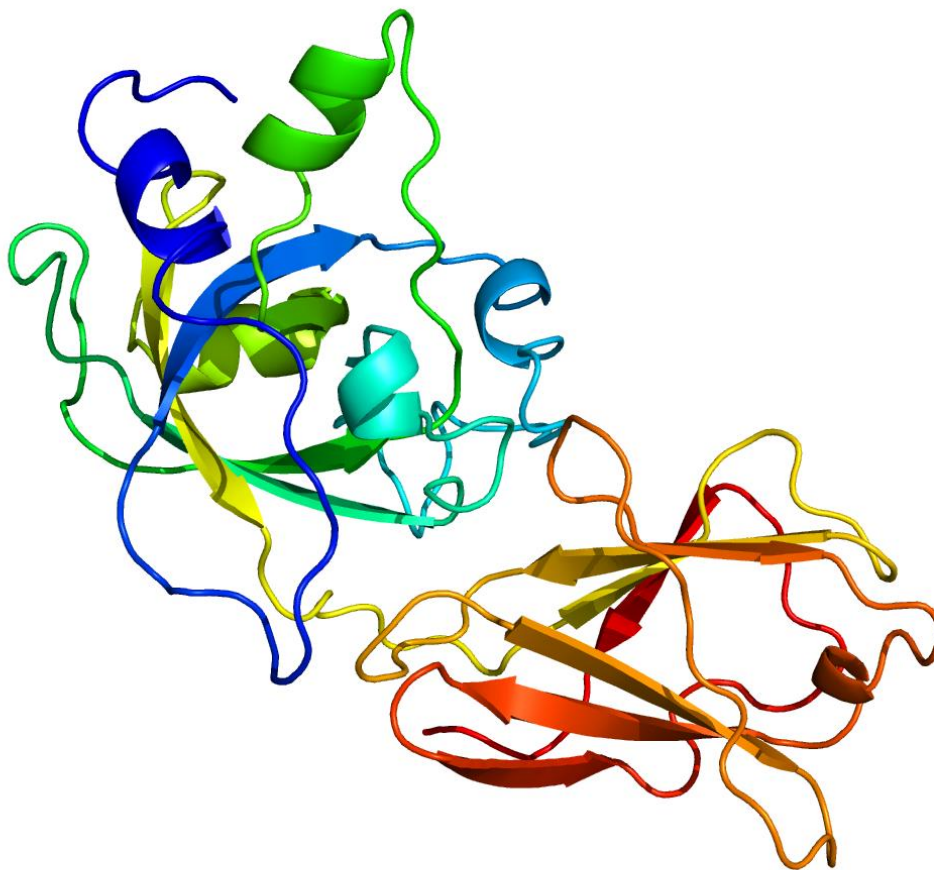
Locus: Bradi3g13720

Gene Model: Bradi3g13720.1.p

Description: BdEXPA-22

Family: Alpha Expansin

3D structure:



GENOME DATABASES

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

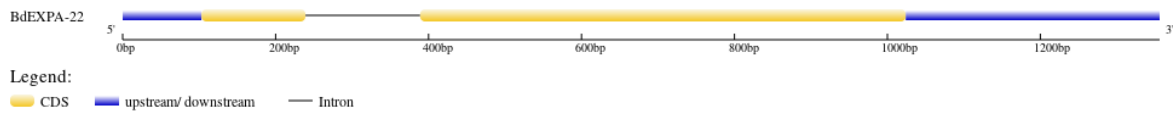
KEGG: <https://www.genome.jp/entry/T01717>

EXTERNAL RESOURCES

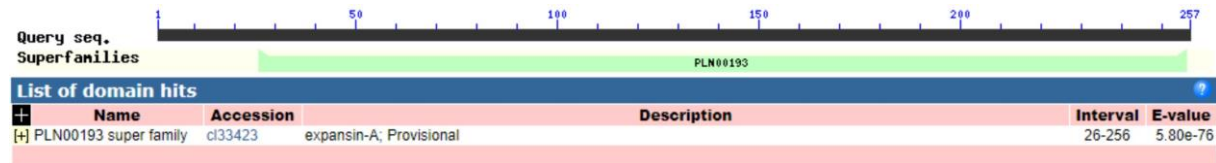
<https://brachypodium.org/>

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

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>BdEXPA-22

MAAAAALLVLAALSSPAPVAAGRRRSGWIDAHATFYGDETGAETMQGACGYGDLF
QQGYGLDTAALSVALFNAGASCGGCYELHCASSTYCRPKGGPITITATNLCPANYSK
PNENWCNPLHHFDLSKPAFLRLVTFHVGIIIPVKYRRVKCGNKRGGVRFQMTGDSR
YWVGVVVFENVAGAGEVKGLAVKGGRDGVWREMKNRWGAVWDGGDVHRLVGGQ
LSFRVVAGDGRMLELEGVAPGNWAVGQSFEGKGF*

CDS (coding sequence)

>BdEXPA-22

ATGGCGGCCGCGGCGGCGCTCCTCGTGCTGGCGGCCTTGTCTTCTCCGGCGCCGG
TAGCAGCCGGCCGCCGCCGAGCGGATGGATCGACGCGCACGCCACGTTCTACG
GCGACGAGACCGGGGCCGAAACCATGCAGGGCGCGTGCGGATACGGTGACCTGT
TCCAGCAAGGATACGGGCTGGACACGGCGGCGCTAAGCGTGGCCCTCTTCAACG
CCGGCGCATCCTGCGGCGGCTGCTACGAGCTCCACTGCGCGTCAAGCACATACTG
CAGGCCCAAGGGCGGCCCAATAACAATCACGGCCACGAACCTCTGCCCGGCCAA
CTACTCCAAGCCAACGAGAAGTGGTGCAACCCGCCATTGCACCCTTCGACCTC
TCGAAACCGGCCTTCTCCGCCTCGTCACCGACTTCCACGTCGGCATCATCCCCGT
CAAGTACCGCCGCGTGAAGTGCGGCAACAAGCGCGGGGGTCCGGTTCAGAT
GACCGGGGACAGCCGGTATTGGGTCGGCGTCGTCGTCCTTCAACGTCGCCGGTGCC
GGAGAAGTGAAAGGGTTGGCCGTGAAAGGGGGGAGAGATGGGGTTTGGAGGGA
GATGAAGAGGAATTGGGGCGCTGTTTGGGATGGTGGCGACGTTTCATCGGCTTGT
GGGCAAGGGCTGTCGTTTAGGGTTGTTGCTGGGGATGGGAGGATGCTTGAGCTTG
AAGGTGTGGCGCCGGGGAAGTGGGCTGTTGGACAGAGCTTCGAAGGCAAGGGAC
AGTTCTGA

Nucleotide

>BdEXPA-22

GCAAAGAGCAGCAGTCATATCGATCCCATTCTCGTCTGACAGACGACACAACAG
ATAAATTCGTATACTAGTAAAAGTAACGGAGAAGAGCCGAGGACTAGCCATGGC
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GCCGGCCGCCGCCGAGCGGATGGATCGACGCGCACGCCACGTTCTACGGCGAC

GAGACCGGGGCCGAAACCATGCGTAAGCTCGATCGATTGCACATTGTCGTGGTTC
TAGTTCAAATCAACCGAGATAGCTAGCATCCCCTAAATTAATTTACTCACCTTTAT
AACATAATCGGCACGTGTCAATCAATATTTATATATACTATCTCTAACATTTCTTA
CGCAGAGGGGCGCGTGC GGATACGGTGACCTGTTCCAGCAAGGATACGGGCTGGA
CACGGCGGCGCTAAGCGTGGCCCTCTTCAACGCCGGCGCATCCTGCGGGCGGCTGC
TACGAGCTCCACTGCGCGTCAAGCACATACTGCAGGCCCAAGGGCGGCCCAATA
ACAATCACGGCCACGAACCTCTGCCCCGGCCA ACTACTCCAAGCCCAACGAGA ACT
GGTGAACCCGCCATTGCACC ACTTCGACCTCTCGAAACCGGCCTTCCTCCGCCTC
GTCACCGACTTCCACGTGCGCATCATCCCCGTCAAGTACCGCCGCGTGAAGTGCG
GCAACAAGCGCGGGCGGGGTCCGGTTCAGATGACCGGGGACAGCCGGTATTGGG
TCGGCGTCGTCGTCTTCAACGTGCCCCGGTGCCGGAGAAGTGAAAGGGTTGGCCGT
GAAAGGGGGGAGAGATGGGGTTTGGAGGGAGATGAAGAGGAATTGGGGCGCTG
TTTGGGATGGTGGCGACGTTTCATCGGCTTGTTGGGCAAGGGCTGTCGTTTAGGGT
TGTTGCTGGGGATGGGAGGATGCTTGAGCTTGAAGGTGTGGCGCCGGGGA ACTG
GGCTGTTGGACAGAGCTTCGAAGGCAAGGGACAGTTCTGAAGTTTCTGCATGTGC
ATCGATCAGCTAGTTCTAGCCTAGCCTAGCTAGAATCCATTGGTAGTTAGTTTTT
GTGATCAAATTAATGTAACGTTGCAGCATTTTGTGGATGGGCTGATTTGTGGTA
ATAAATCTTCAGTAATCGCAGACTCATCATGTAAGATTTGGGGATTTTCTTCTTTG
TTGATGGCTGGTCATTTATGATCGATCCA ACTATCCAAGGATTTATATAATTTAGA
TTGGAAACCACCGTGTGAGATAGGAGTAGGATACAAAGTTGTGACGAACAGATT
AAATTCAGTTTTGTTTCTTCTGAGAAACAACAAAAGATT