

IDENTIFICATION

Species: *Brachypodium distachyon*

Locus: Bradi1g74750

Gene Model: Bradi1g74750.1.p

Description: BdEXPA-08

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

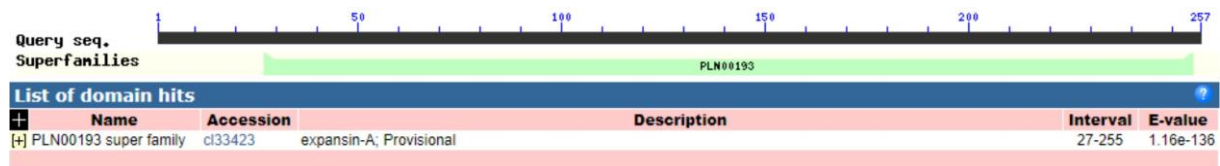
<https://brachypodium.org/>

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

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>BdEXPA-08

MARSRALLYHLAVVVAACLA AATPGGAADWMSGSATFYGGSDASGTMGGACGYG
NLYSTGYGTNTAAMSTALFNDGAACGECYQVQCDSQNSQWCNKGATVTITATNLC
PPDYSKPSNNGGWCNPPRRHLDMAQPAWEKIGVYRAGIVPVMFRRVPCSRRTGGVRF
TINGNDYFELVLITNMGGAGSISVQIKGSRTGWVTMSRNWGANWQCNNYLNQSI
SFTVTATDGKKQVFQD VAPGNWRFQGTFSSAVQFY*

CDS (coding sequence)

>BdEXPA-08

ATGGCGCGCAGCAGAGCCTTGTGTATCACTTGGCCGTCGTTGTCGCGGCTTGCCT
CGCGGCGGCGACGCCCGGAGGCGCTGCCGACTGGATGAGCGGCTCCGCGACCTT
CTACGGCGGGAGCGACGCTCCGGCACCATGGGCGGGGCGTGCGGGTACGGGAA
CCTGTACTCGACGGGGTACGGGACGAACACGGCGGCGATGAGCACGGCGCTGTT
CAACGACGGGGCGGCGTGCGGGGAGTGCTACCAGGTGCAGTGCGACAGCCAGAA
CTCGCAGTGGTGCAACAAGGGCGCCACGGTGACCATCACGGCCACCAACCTCTGC
CCGCCCGACTACTCCAAGCCCAGCAACAACGGCGGCTGGTGCAACCCGCCCGG
AGGCACCTCGACATGGCCCAGCCCGCCTGGGAGAAGATCGGCGTCTACCGCGCC
GGCATCGTGCCCGTCATGTTCCGCCGGGTGCCCTGCTCCAGGACCGGCGGGGTCC
GGTTCACCATCAACGGGAACGACTACTTCGAGCTCGTGCTCATCAACCATGGG
CGGCGCCGGGTCCATCTCGTCCGTGCAGATCAAGGGGTCCAGGACCGGCTGGGTC
ACCATGTCCAGGA ACTGGGGCGCCA ACTGGCAGTGCAACA ACTACCTCAACGGC
CAGTCCATCTCCTTACGGTCACCGCCACCGACGGCAAGAAGCAAGTCTTCCAGG
ACGTCGCGCCCCGGCAACTGGAGGTTCCGGCCAGACCTTCTCCAGCGCCGTCCAGTT
CTACTAG

Nucleotide

>BdEXPA-08

TGAGCCCGCGCCGGGGTTCGCGCGCGCCAAATCGATCAACTCCCGTGCCCTCCGT
CCGCTCAAATCGATCGAATCGCCCGAGCTTCCTATTTAAGCACCGCCGAGCCA
TCGCTTTCCACCTCCTCACTTCAACTCGCACCGTTCCTGTAAATCGGTGATCCCG
TTACGTCCGTGCCCCGTGAGTATAACCCAGGGACTCCGTGCATTGGCCCTGTAC

CTGAAGCCATATTTTCGAGCAATGGCGCGCAGCAGAGCCTTGTTGTATCACTTGGC
CGTCGTTGTCGCGGGCTTGCCTCGCGGGCGGGCAGCCCCGGAGGCGCTGCCGACTGG
ATGAGCGGCTCCGCGACCTTCTACGGCGGGAGCGACGCCTCCGGCACCATGGGTA
TGCACGCAAAAGAACAACCACTATAACCTTTACTCGTTCCTTCTTGTCCGTGCA
GTTTAATCTTGCACCTACTTGGGCGCATTTGCGCGCATGACATGAAGGATATACA
TAACTGATTAATTGATCACCAAGGCGGGGCGTGCGGGTACGGGAACCTGTACTCGA
CGGGGTACGGGACGAACACGGCGGGCGATGAGCACGGCGCTGTTCAACGACGGGG
CGGCGTGCGGGGAGTGCTACCAGGTGCAGTGCGACAGCCAGAACTCGCAGTGGT
GCAACAAGGGGCGCCACGGTGACCATCACGGCCACCAACCTCTGCCCGCCGACT
ACTCCAAGCCCAGCAACAACGGCGGGCTGGTGCAACCCGCCCGGAGGCACCTCG
ACATGGCCCAGCCCGCCTGGGAGAAGATCGGCGTCTACCGCGCCGGCATCGTGCC
CGTCATGTTCCGCCGGGTGCCCTGCTCCAGGACCGGCGGGGTCCGGTTCACCATC
AACGGGAACGACTACTTCGAGCTCGTGCTCATCACCAACATGGGCGGGCGCCGGGT
CCATCTCGTCCGTGCAGATCAAGGGGTCCAGGACCGGCTGGGTACCATGTCCAG
GAACTGGGGCGCCAACTGGCAGTGCAACAACCTCAACGGCCAGTCCATCTCC
TTCACGGTCACCGCCACCGACGGCAAGAAGCAAGTCTTCCAGGACGTCGCGCCCCG
GCAACTGGAGGTTTCGGCCAGACCTTCTCCAGCGCCGTCCAGTTCTACTAGCCACG
CGTGCGCCTTAAATTCATCAGTCTACTCACCCCTTTTCTTTTCTCCTTTTCGCATTT
GGGACTTGCATATGGCAAGGAGACCTTGAAATTAGCTGCATTCTGATGGGAAAC
TACTACTAGTCGCCTGTTAGGTAGTAGGGGAACTATATGTCTACTGGCTAGGCGT
ACACGCACGGTGGTTTGCATGGCTGAGGTGGGTTTCATGGGTTCCGCAATCGCCAT
GCCGCCTGGCCGGCCTCATCAGTTAATTACCCGCCGTGCCTGCCGCCTTGCATAT
GAGATGTTTGCTCAGTATGAGACCATGGAAATTGTTCCAAGAACTATTCATATTT
GATGTGTGGTTTTAACTGGGTGCCATGGTCATTATTGTTTCTCTTCCC