

IDENTIFICATION

Species: *Brachypodium distachyon*

Locus: Bradi3g32070

Gene Model: Bradi3g32070.1.p

Description: BdEXPA-28

Family: Alpha Expansin

3D structure:



GENOME DATABASES

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

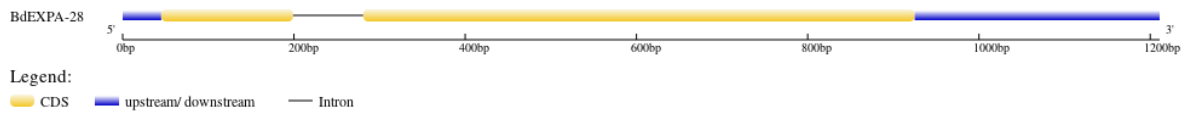
KEGG: <https://www.genome.jp/entry/T01717>

EXTERNAL RESOURCES

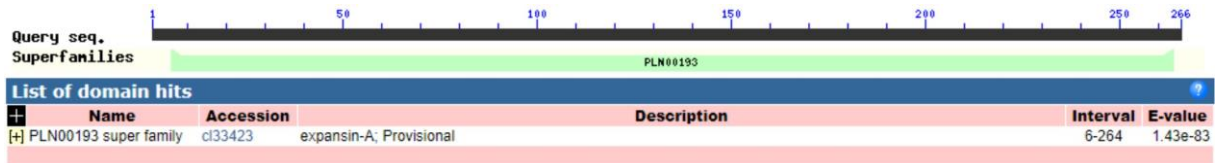
<https://brachypodium.org/>

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

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>BdEXPA-28

MASAPSTATAILALLVSLAGVATTAHGRFTAMQWTPAHATFYGDETA AETMGGAC
GYGNLYATGYGTDTAALSTTLFLDG YGCGTCYQMRCV GAPACYQGSPVITVTATNL
CPPNWEQDSNAGGWCNPPRTHFDLAKPAFMKMAAWRAGIVPVMYRRVPCVRKGG
LRFQGNPHWLLVYVMNVAGAGDVRDMWVKGCDGGGHVQGWVRMSHNWGAA
FQAFGQLGGHALSFKLTSYTTGQTIIAADAAPRTWSVGLTYQARANFS*

CDS (coding sequence)

>BdEXPA-28

ATGGCTTCTGCTCCGTCCACGGCCACGGCCATCTTGGCCCTTCTCGTCTCCCTGGC
CGGCGTGGCCACCACCGCGCACGGCAGGTTACGGCGATGCAGTGGACCCCGC
CCACGCCACCTTCTACGGCGACGAGACCGCGGGCGGAGACCATGGGCGGGGCGTG
CGGGTACGGCAACCTGTACGCGACAGGGTACGGCACGGACACGGCGGGCGCTGAG
CACGACGCTGTTCTGGACGGGTACGGGTGCGGGACGTGCTACCAGATGCGGTGC
GTGGGGGCGCCGGCCTGCTACCAGGGCTCGCCCGTGATCACGGTCACGGCCACCA
ACCTGTGCCCGCCCAACTGGGAGCAGGACTCCAACGCGGGGGGGTGGTGCAACC
CGCCGCGCACCCACTTCGACCTCGCCAAGCCGGCCTTCATGAAGATGGCCGCTG
GCGCGCCGGCATCGTGCCCGTCATGTACCGCAGGGTGCCCTGCGTGCGCAAGGGC
GGACTGCGCTTCGCGTTCAGGGGAACCCTCACTGGCTGCTCGTCTACGTCATGA
ACGTCGCCGGCGCCGGGGACGTCCGGGACATGTGGGTCAAGGGCTGCGACGGCG
GCGGCCACGTCCAGGGGTGGGTGCGGATGAGCCACAACCTGGGGCGCCGCGTTCC
AGGCCTTCGGCCAGCTCGGCGGCCACGCGCTCAGCTTCAAGCTCACCTCCTACAC
CACCGGGCAGACCATCATCGCCGCCGACGCCGCGCCGCGGACCTGGTCCGTCGG
GCTCACGTACCAGGCCCGCGCCAACCTTCTCTTAA

Nucleotide

>BdEXPA-28

GAAAGAAGAGAGCACTACACAACACAAGCAGAGGGAAGGAAAGCAATGGCTTC
TGCTCCGTCCACGGCCACGGCCATCTTGGCCCTTCTCGTCTCCCTGGCCGGCGTGG
CCACCACCGCGCACGGCAGGTTACGGCGATGCAGTGGACCCCGCCACGCCA
CCTTCTACGGCGACGAGACCGCGGGCGGAGACCATGGGTACGTTTACTTGACAAG

CTAGTCCATCGGCAATGGCAATGGCATGCTGCCAGACTCATTTGCTGACACGGTG
ACACGCAGGCGGGGCGTGCGGGTACGGCAACCTGTACGCGACAGGGTACGGCAC
GGACACGGCGGCGCTGAGCACGACGCTGTTCTGACGGGTACGGGTGCGGGAC
GTGCTACCAGATGCGGTGCGTGGGGGCGCCGGCCTGCTACCAGGGCTCGCCCGTG
ATCACGGTCACGGCCACCAACCTGTGCCCGCCAACTGGGAGCAGGACTCCAAC
GCGGGGGGGTGGTGCAACCCGCCGCGCACCCACTTCGACCTCGCCAAGCCGGCCT
TCATGAAGATGGCCGCCTGGCGCGCCGGCATCGTGCCCGTCATGTACCGCAGGGT
GCCCTGCGTGCGCAAGGGCGGACTGCGCTTCGCGTTCCAGGGGAACCCTCACTGG
CTGCTCGTCTACGTCATGAACGTCGCCGGCGCCGGGGACGTCCGGGACATGTGGG
TCAAGGGCTGCGACGGCGGCGGCCACGTCCAGGGGTGGGTGCGGATGAGCCACA
ACTGGGGCGCCGCGTTCCAGGCCTTCGGCCAGCTCGGCGGCCACGCGCTCAGCTT
CAAGCTCACCTCCTACACCACCGGGCAGACCATCATCGCCGCCGACGCCGCGCCG
CGGACCTGGTCCGTGCGGGCTCACGTACCAGGCCCGCGCCAACCTTCTCTTAATCTCT
TAGGGAGGGGGCGGCCGGCCGGCCAAACTGTGAAAGCACATCAAGTAGCAGGAG
CTGACGATGCTCTGCTCGGCTCTGATTTTTTGTCTTCTCTATAACCACATTTTCAGTTC
AGTCTAGAGTATTGTTCTTACACGTTGTCCCCGATCCATTTGTAAACAGCGGGTT
TGACTTTGACGCACACGATGACCATGCAAACCTCTGTACACTTGCATTCAAAAAAT
TGGTGCCACCCAGCTGGAAGTTCGGCCAAACATTTTCTAGCAATGTGCAGTTCAA
GTGA