

IDENTIFICATION

Species: *Brachypodium distachyon*

Locus: Bradi1g30050

Gene Model: Bradi1g30050.1.p

Description: BdEXLA-02

Family: Expansin Like Alpha

3D structure:



GENOME DATABASES

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

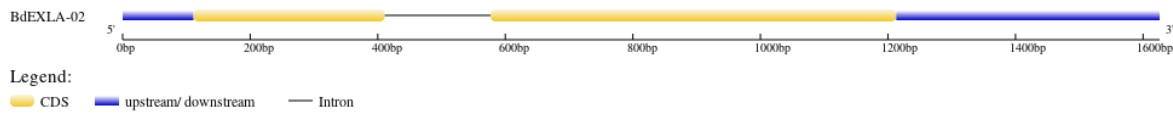
KEGG: <https://www.genome.jp/entry/T01717>

EXTERNAL RESOURCES

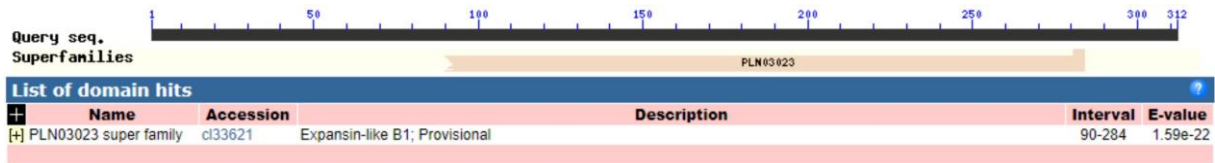
<https://brachypodium.org/>

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

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>BdEXLA-02

MAAAVAQQLLLVLTLLCLTVATASASSSAPSSSYRCGWCRRRRSRGTSATASILPPDA
ATGAACGYGTAISSAAASGGFFFAAASAEFFRRGQAACGVYQLRCRDRASCGQQG
VKVVITDEIKTNRTATASGGWFMLPREALAAMAAPAVHGDLLQQQAVEVDFRRIPC
DLHKDRTLAVRVEETSRKDSGRLALRFLYLGQTDIAAVEVAPAASATLSSSSFSWR
YLTRRDGVWSTTRAPAGPLRLRVVVTAGSGGKWL RADREVLP AERMPGRVYDTGL
RVDEFAVSTCSCSAGDEDDDDKEVHKEEEFR*

CDS (coding sequence)

>BdEXLA-02

ATGGCCGCCGCGTCGCGCAGCAGCTGCTTCTAGTTCTAACCCCTCCTCTGCCTCAC
GGTGGCCACCGCGAGCGCTTCTTCATCCGCTCCGTCCTCGTCGTACCGCTGCGGCT
GGTGCCGCCGCGCCGCTCCGGTACTAGTGCTACCGCCTCCATCCTCCCTCCTGAC
GCGGCCACCGGCGCCGCTGCGGTTACGGGACTGCGATCTCATCAGCTGCTGCCA
GCGGCGGCTTCTTCTTCGCCGCCGCCAGCGCCGAGTTCTTCCGGCGCGGCCAAGC
TGCCTGCGGCGTCTGCTACCGAGTTGAGGTGCAGGGACCGGGCCTCGTGCGGACAA
CAGGGCGTTAAGGTCGTCATCACCGACGAGATCAAGACGAACAGAACAGCCACC
GCCAGCGGCGGGTGGTTCATGCTTCCCAGGGAGGCCTTGCCGCCATGGCTGCCC
CTGCCGTTTCATGGCGATCTGCTGCAGCAGCAGGCAGTGGAGGTGGATTTTCAGGAG
GATCCCCTGCGACCTGCACAAGGACAGGACCCTCGCGGTTTCGTGTGGAGGAGAC
GAGCAGAAAAGACAGTGGCCGCTCGCGCTCCGGTTCCTGTACCTGGGCGGCCA
GACCGACATCGCCGCCGTCGAGGTCGCGCCTGCAGCCTCCGCCACGCTGTCCTCT
TCTTCATTTTCATGGCGTTACTTGACGCGGCGGGATGGGGTGTGGAGCACGACAC
GGGCGCCGGCGGGCCCGCTGCGGCTGCGGGTGGTGGTACGGCGGGGTCCGGCG
GCAAGTGGCTGCGGGCCGACCGGGAGGTGCTCCCCGCCGAGCGGATGCCCGGCA
GGGTGTACGATACCGGGCTCAGGGTGGACGAATTCGCCGTGAGCACTTGCTCTTG
CTCCGCCGGAGACGAAGACGACGACAAAGAAGTCCACAAGGAAGAGGAGTTCA
GATGA

Nucleotide

>BdEXLA-02

GTCCCCAGCGCGCCATTTCCCTTAAACTCGCACGCTAGCTAGCTCACCGGATCAAT
CCATGTACCCATAAAGCGATCTCTTATCTGTCTCCATCGACGACTTGGTTTGACGCC
ATGGCCCGCCGCGTCGCGCAGCAGCTGCTTCTAGTTCTAACCCCTCCTCTGCCTCAC
GGTGGCCACCGCGAGCGCTTCTTCATCCGCTCCGTCCTCGTCGTACCGCTGCGGCT
GGTGCCCGCCGCGCCGCTCCGGTACTAGTGCTACCGCCTCCATCCTCCCTCCTGAC
GCGGCCACCGGCGCCGCCTGCGGTTACGGGACTGCGATCTCATCAGCTGCTGCCA
GCGGCGGCTTCTTCTTCGCCGCCGCCAGCGCCGAGTTCTTCCGGCGCGGCCAAGC
TGCCTGCGGCGTCTGCTACCAGGTGCGCATCATGTCTCGACAAAAGCTCTGTCAA
TCCTTCTTCTGGGCTAGCCAATTTCAATTCTTCAGAGTTGCAGAGAATAAATTGA
CCTGTATTAATCATATTGGAATGTCTGTCAATTCTCGTACTAGTTAACTGAATTTGT
TCCATCTTGCTGCTGTTGCAGTTGAGGTGCAGGGACCGGGCCTCGTGCGGACAAC
AGGGCGTTAAGGTCGTCATCACCGACGAGATCAAGACGAACAGAACAGCCACCG
CCAGCGGCGGGTGGTTCATGCTTCCCAGGGAGGCCTTGGCCGCCATGGCTGCCCC
TGCCGTTTCATGGCGATCTGCTGCAGCAGCAGGCAGTGGAGGTGGATTTTCAGGAGG
ATCCCCTGCGACCTGCACAAGGACAGGACCCTCGCGGTTTCGTGTGGAGGAGACG
AGCAGAAAAGACAGTGGCCGCCTCGCGCTCCGGTTCCTGTACCTGGGCGGCCAG
ACCGACATCGCCGCGTCGAGGTCGCGCCTGCAGCCTCCGCCACGCTGTCTCTT
CTTCATTTTCATGGCGTTACTTGACGCGGCGGGATGGGGTGTGGAGCACGACACG
GGCGCCGCGGGCCCGCTGCGGCTGCGGGTGGTGGTGACGGCGGGGTCCGGCGG
CAAGTGGCTGCGGGCCGACCGGGAGGTGCTCCCCGCCGAGCGGATGCCCGGCAG
GGTGTACGATACCGGGCTCAGGGTGGACGAATTCGCCGTGAGCACTTGCTCTTGC
TCCGCCGGAGACGAAGACGACGACAAAAGAAGTCCACAAGGAAGAGGAGTTCAG
ATGACTTGACGTGCTTCCAGTTCATCCACCACGGAGCTGCGTACACAGATTTAT
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TCTGCATGTACTGTACAGTGCGGCTGTACATTACGTGTCTGAATGATGACGCGAG
ATTGGGGTTAGGACAAGAAGAGCAAAGCCTGTCTGACTGCTCTGTGGATCGATCG
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GATCACATGACAATGTTACTGTTTTTTCGGGCTC