

IDENTIFICATION

Species: *Brachypodium stacei*

Locus: Brast06G131000

Gene Model: Brast06G131000.1.p

Description: BstEXLA-04

Family: Expansin Like Alpha

3D structure:



GENOME DATABASES

Phytozome: https://phytozome-next.jgi.doe.gov/info/Bstacei_v1_1

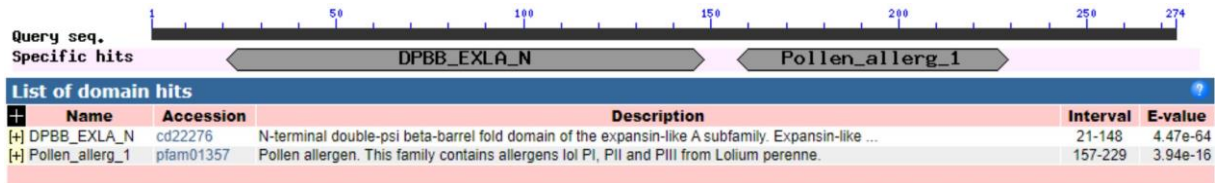
EXTERNAL RESOURCES

<https://brachypodium.org/>

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>BstEXLA-04

MAVLLSAFSSCLLLLLVSSFAAACERCVRQGKAAYSPSPSTQLPAGGGVCGYGAMA
MEINGGFLAAGGPRQHRAGLGCGRCFQMRCRDAKVCSSRGVRVVLDFHRSNRTDF
LLGGPAFVGLAKPGMAQQLRRLDALISIEYKRIPCDYNDKNLSILVEEQSKKPSKLVIK
FLYQGGQTDILAVDVAQVGSDDWRFMSRVHGPVWSTDRAPTGPLQFRAVVTGGYD
GKWVWADKEVLPADWQAGQVYDTGARIADVARESCIGCARPDWEMKVA*

CDS (coding sequence)

>BstEXLA-04

ATGGCTGTCTTGCTCTCCGCCTTCTCCTCCTGCCTCCTGCTCCTCCTGGTCTCTTCC
TTCGCGGCCCGCCTGCGAGAGGTGCGTGCGTCAGGGCAAGGCTGCCTACTCGCCCT
CCCCCTCCACCCAGCTCCCTGCCGGTGGCGGAGTGTGTGGTTATGGGGCCATGGC
CATGGAGATCAATGGGGGATTCCCTCGCCGCTGGGGGACCAAGGCAGCACAGAGC
AGGGCTTGGCTGTGGGAGATGCTTTCAGATGAGATGCAGAGATGCAAAGGTGTG
TAGCAGCAGGGGCGTCCGGGTTGTGCTCACCGACTTCCACAGGAGCAATCGTACA
GATTCCTGCTCGGTGGGCCCGCATTTGTGGGCCTTGCTAAGCCCAGGATGGCCC
AGCAGCTGAGGAGGCTGGACGCTCTGTCCATAGAGTACAAAAGAATTCCCTGCG
ACTACAATGACAAGAACCTGTCCATATTAGTGGAAGAACAGAGCAAGAAGCCAA
GCAAATTGGTCATCAAGTTCCTTTACCAAGGTGGTCAAACCTGATATCTTAGCGGT
GGATGTTGCTCAGGTGGGGTTCGTCAGACTGGCGGTTTCATGAGCCGGGTTACGGG
CCCGTTTGGAGCACCGACCGAGCCCCACCGGGCCGCTGCAGTTCCGGGGCGGTGG
TGACTGGTGGGTACGACGGCAAGTGGGTGTGGGCTGATAAAGAGGTCCCTCCCGG
CTGACTGGCAGGCTGGCCAGGTCTATGACACCGGTGCCCGGATCGCTGACGTGGC
GAGGGAGAGCTGCATTGGCTGTGCCAGGCCGACTGGGAAATGAAAGTGGCTTA
A

Nucleotide

>BstEXLA-04

AGCAGCAGCATGTGCTAGGGAAAAGGCTATTCTTCCCCCTTCCATACTCCTCTTCT
TCTCTCTCTCTCACACGCACTCTCTACTGCTTGGCATCGATCGATTGCCAATCG

CCATGGCTGTCTTGCTCTCCGCCTTCTCCTCCTGCCTCCTGCTCCTCCTGGTCTCTT
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GTCAAGGGTTCCAATTTTGTCTCTTTTTAGCATGATTTTGAGTGGTGCCTGTGGT
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TTGGCTGTGGGAGATGCTTTCAGGTACCAAATTGTTACTACCGACTAGTTCCCCGT
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AACTAGAGAAAACGTTGGAAATGAAAATGTAGCTAGGAAAAGTTTACTGGTTCGT
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TGGTTGGTGCACATTATTATTGGCTTGTAGTACAGTTTCGATGTACATGTGAGAAT
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CTTGAGATGCAGTTACCACACGGTACCACACCAAGTCATTAGAGGGCGTGAGGG
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TATGTA AAAACAAATGTAGCTGGTAGCTAGCTATCTAGCTTCCGCCCCTGCTAATT
GATAGAATAATTAGTGAACATATTGCAATGTTCTCCCTT