

IDENTIFICATION

Species: *Brachypodium stacei*

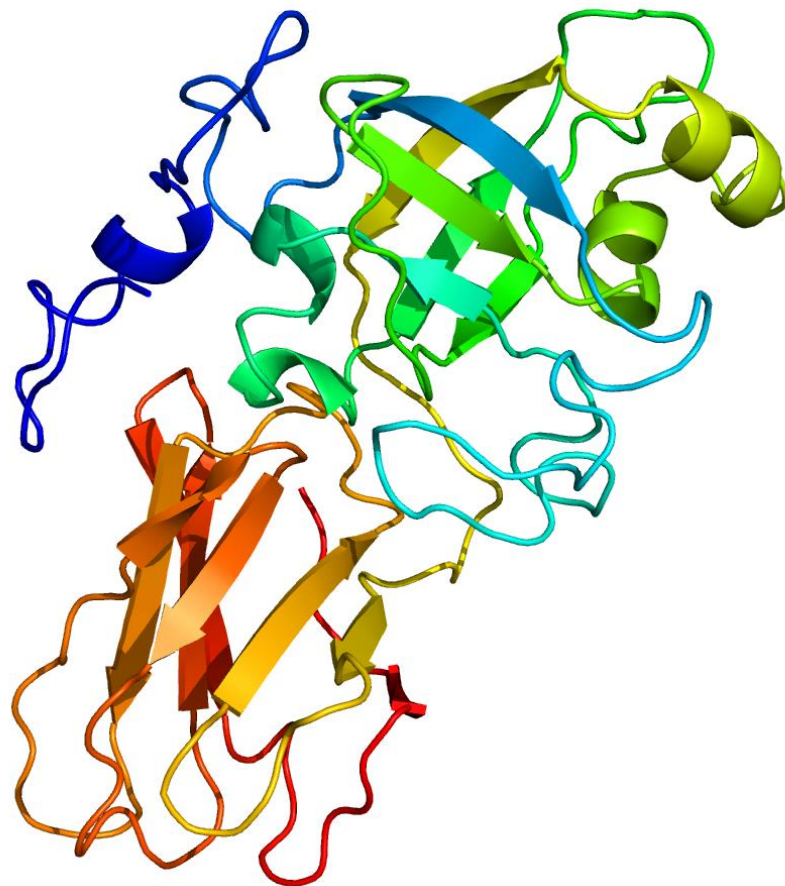
Locus: Brast03G191600

Gene Model: Brast03G191600.1.p

Description: BstEXPB-05

Family: Beta Expansin

3D structure:



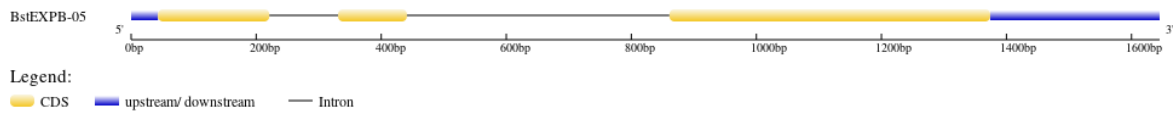
GENOME DATABASES

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

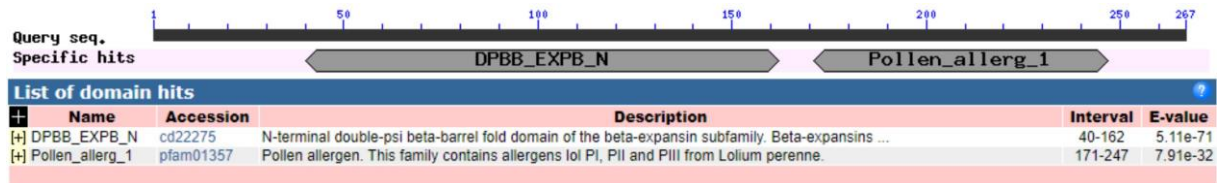
EXTERNAL RESOURCES

<https://brachypodium.org/>

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>BstEXPB-05

MGSLSYVLAGVVLAALVAGGACIPKVPVPPGNVTANYNGLWLNAMATWYGRPQGA
GPKDNGGACGIKDVNLPYSAMIACGNIPFKDGRGCGSCYEVKCQVPAKLCSNKPV
TVIITDMNYEPIAPYHFDLSGTAFLMAQPGKEQLLRNCGELQMQRFRVRCKLPPGT
KITFHIEKGSNPNYLAVLVKFKVSDGDIVQMDLQDHMSPEWKPMKESWGAVWRMD
SIKPLKGPYSIRVTSESGKKLIAKDIPLNWKPDFTFLKSNIQF*

CDS (coding sequence)

>BstEXPB-05

ATGGGTTCCCTCTCGTACGTGCTCGCTGGCGTGGTGCTGGCGGGCGCTGGTGGCCG
GCGGCGCGTGCATCCCCAAGGTGCCGCCGGGGCCCAACGTGACGGCCA ACTACA
ACGGCCTGTGGCTCAACGCCATGGCCACCTGGTACGGCAGGCCCAAGGCGCCG
GGCCCAAAGACAACGGTGGTGCCTGCGGGATCAAGGACGTGAACCTGCCGCCCT
ACAGCGCCATGATCGCCTGCGGCAACATTCCCATCTTCAAGGACGGCAGGGGATG
CGGCTCCTGCTACGAGGTCAAGTGCCAGGTACCGGCGAAGCTGTGCTCGAACAA
GCCCGTAACGGTGATCATCACGGACATGAACTACGAGCCGATCGCGCCGTACCAC
TTCGACCTCTCCGGCACGGCGTTCGGCCTGATGGCTCAGCCCGGGAAGGAGCAGC
TGCTCCGCAACTGCGGGGAGCTGCAGATGCAGTTCAGGAGGGTCCGCTGCAAGTT
ACCGCCGGGCACCAAGATCACCTTCCACATCGAGAAGGGGTCCAACCCAACTA
CCTGGCCGTGCTCGTCAAGTTCGTCTCCGACGACGGCGACATCGTGCAGATGGAC
CTCCAGGACCACATGTCGCCGGAGTGGAAGCCATGAAGGAGTCGTGGGGCGCC
GTCTGGAGGATGGACTCCATCAAGCCGCTCAAGGGCCCTTACTCTATCCGCGTCA
CCAGCGAGTCCGGCAAGAAGCTTATTGCCAAGGATATTATCCCGCTCAACTGGAA
GCCCGACACCTTCTTGAAGTCCAATATCCAGTTCTAG

Nucleotide

>BstEXPB-05

GCCAGCCAGAGGAGCGAGCGTCTCTCTATCTACAGCTCTACACATGGGTTCCCTC
TCGTACGTGCTCGCTGGCGTGGTGCTGGCGGGCGCTGGTGGCCGGGCGGCGCGTGCA
TCCCCAAGGTGCCGCCGGGGCCCAACGTGACGGCCA ACTACAACGGCCTGTGGCT

CAACGCCATGGCCACCTGGTACGGCAGGCCCCCAAGGCGCCGGGCCCAAAGACAA
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GTCACCTCAAATGCGCAGAATTACGTAAATTAGCATCAACAAAAAAGGAAGTG
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GTATATCACAGATCTGATATTCATATTAATTGCAGGTCAAGTGCCAGGTACCGGC
GAAGCTGTGCTCGAACAAGCCCGTAACGGTGATCATCACGGACATGAACTACGA
GCCGATCGCGCCGTACCACTTCGACCTCTCCGGCACGGCGTTCGGCCTGATGGCT
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AGGAGGGTCCGCTGCAAGTTACCGCCGGGCACCAAGATCACCTTCCACATCGAG
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ACTGGGTTTGAGAGAGAAGTGCTTTGGAAAAAGAAAAGTAAACTTATTTGTG