

IDENTIFICATION

Species: *Brachypodium stacei*

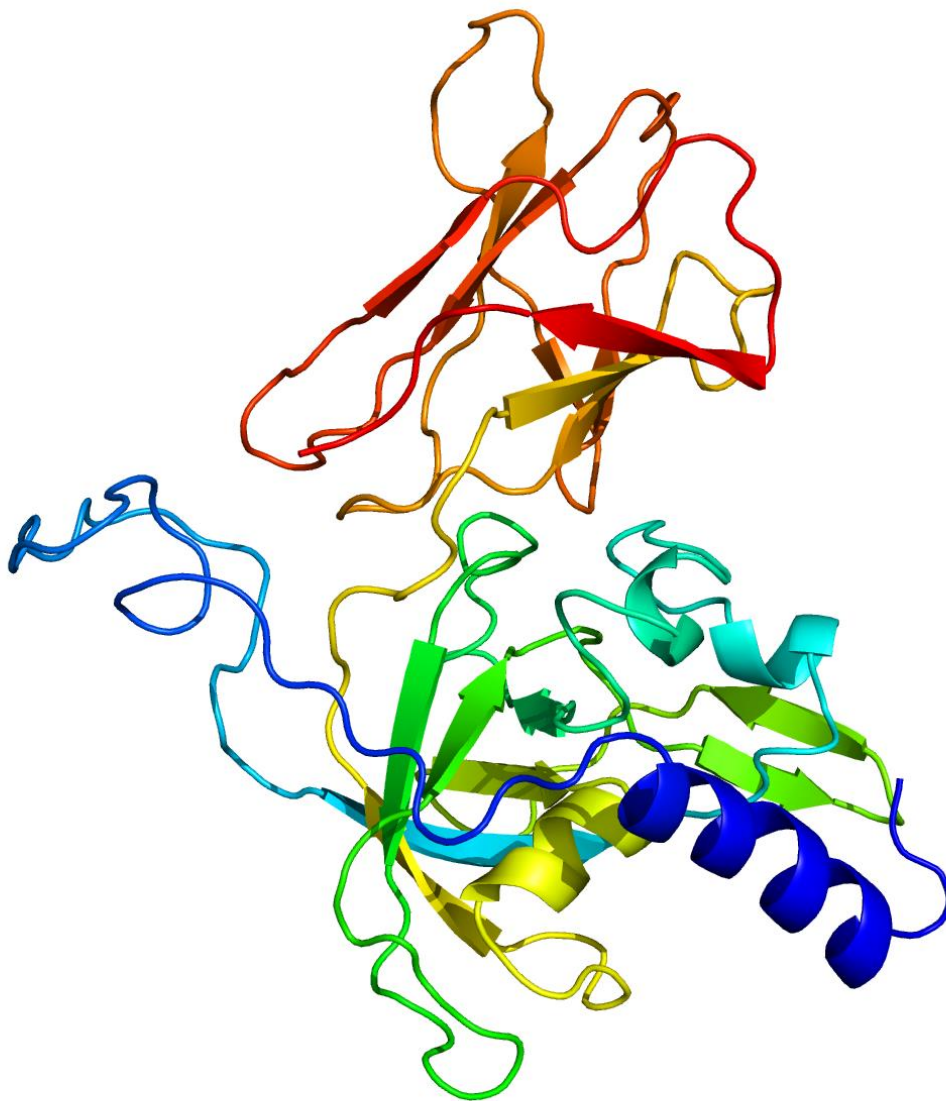
Locus: Brast07G005300

Gene Model: Brast07G005300.1.p

Description: BstEXPA-25

Family: Alpha Expansin

3D structure:



GENOME DATABASES

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

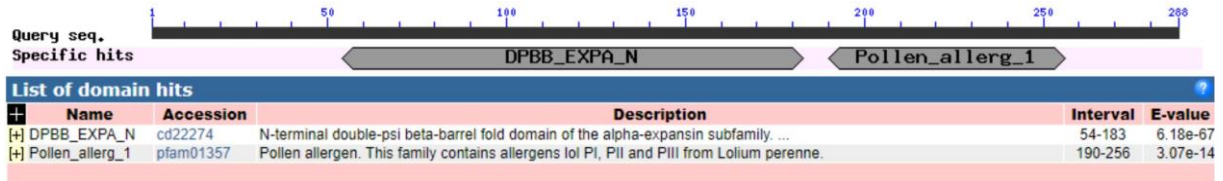
EXTERNAL RESOURCES

<https://brachypodium.org/>

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>BstEXPA-25

MAKSNNPAMAMAAMMMVLMGARLASANIPPSQWSPPPPSSSSYPATTGGYSTSGWI
DGSATFYGDASGLGADFGGACGFSANDIASLYSTATAALSTPLFADGDGCGRCYELR
CVKSPWCNPGSPSITVTGTNLCPNWLNDNGGWCNPPRQHFDLAPPSFLRLAARV
AGIVPVQFRRVPCQRTGGVRFYVTGNPYWLLLHIMNVAGAGDVCQVSVRMVGGNG
GWITTSKNWGSTFQAFSALDKSKGLAVQLTTCGYPKQSVVVGDAIPAWWSTGLTYQ
GSNNFW*

CDS (coding sequence)

>BstEXPA-25

ATGGCGAAGTCTAATAATCCGGCAATGGCCATGGCGGCGATGATGATGGTGTGTTGA
TGGGGGCTCGACTGGCGAGCGCCAACATACCTCCTTCGCAATGGTCACCGCCGCC
GCCACCGTTCGTCGTATCCTGCCACCACCGGCGGCTACTCCACGTCCGGCTGG
ATAGACGGCAGCGCCACCTTCTACGGCGACGCCTCTGGCCTCGGCGCCGACTTCG
GCGGGGCGTGC GGTTTCAGCGCCAACGACATCGCGTCGCTGTACTCGACGGCGA
CGGCGGCGCTGAGCACGCCGCTGTTTCGCGGACGGCGACGGGTGCGGGCGGTGCT
ACGAGCTGCGCTGCGTCAAGTCGCCCTGGTGCAACCCGGGGTCGCCGTCCATCAC
CGTCACGGGGACCAACCTCTGCCCCGCCCAACTGGTACCTCCCCAACGACAACGGC
GGCTGGTGCAACCCTCCTCGGCAGCACTTCGACCTGGCGCCGCCGTCTCTCTCC
GGCTCGCCGCCAGGGTCGCCGGC ATCGTGCCCGTGCAGTTCCGCCGGGTGCCGTG
CCAGAGGACCGGCGGCGTCCGCTTCTACGTCACCGGGAACCCTTACTGGCTTTTG
CTGCACATCATGAACGTTGCCGGCGCTGGTGTCTGCCAGGTGTCCGTCAGGA
TGGTCGGCGGTAATGGCGGGTGGATCACGACGTCCAAGAATTGGGGCAGCACGT
TCCAGGCCTTCTCTGCGCTGGACAAGAGCAAGGGGCTCGCCGTCCAGCTCACCAC
CTGCGGCTACCCTAAGCAGAGCGTCGTCGTCGGCGACGCCATTCCGGCGTGGTGG
TCCACCGGGCTCACCTACCAGGGGTCAAACA ACTTCTGGTGA

Nucleotide

>BstEXPA-25

CAACGATCCACTATCTAGCAGCTTAATTTGTGTTTCATATCGGCCATGGCGAAGTCT
ATAAATCCGGCAATGGCCATGGCGGCGATGATGATGGTGTGATGGGGGCTCGA
CTGGCGAGCGCCAACATAACCTCCTTCGCAATGGTCACCGCCGCCCGCCACCGTCGT
CGTCGTATCCTGCCACCACCGGCGGCTACTCCACGTCCGGCTGGATAGACGGCAG
CGCCACCTTCTACGGCGACGCCTCTGGCCTCGGCGCCGACTTCGGTACATACATT
CATAATAACAGTAAACATGCATCGTATGTACTTGTTCGTTTCTAAATGTAACA
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TTATTTGATATTCCAGATGTTGTATATTTTTCATAACTTGATCAAACCTTTTAGAA
GTTTGACTTAGGACAAAGTTAAACTTCTTATATTTAGGAGCGGAGCCAGTGGAA
TGCAAATTAACCCATGTATGTCTGAATGCAGGCGGGGCGTGCGGGTTCAGCGCCA
ACGACATCGCGTCGCTGTACTCGACGGCGACGGCGGGCGCTGAGCACGCCGCTGTT
CGCGGACGGCGACGGGTGCGGGCGGTGCTACGAGCTGCGCTGCGTCAAGTCGCC
CTGGTGCAACCCGGGGTCGCCGTCATACCGTACCGGGACCAACCTCTGCCCG
CCAACTGGTACCTCCCCAACGACAACGGCGGGCTGGTGCAACCCTCCTCGGCAGC
ACTTCGACCTGGCGCCGCCGTCCTCCTCCGGCTCGCCGCCAGGGTCGCCGGCAT
CGTGCCCGTGCAGTTCCGCCGGGTGCCGTGCCAGAGGACCGGCGGGCGTCCGCTTC
TACGTCACCGGGAACCCTTACTGGCTTTTGCTGCACATCATGAACGTTGCCGGCG
CTGGTGATGTCTGCCAGGTGTCCGTCAGGATGGTCGGCGGTAATGGCGGGTGGAT
CACGACGTCCAAGAATTGGGGCAGCACGTTCCAGGCCTTCTCTGCGCTGGACAAG
AGCAAGGGGCTCGCCGTCCAGCTCACACCTGCGGCTACCCTAAGCAGAGCGTCG
TCGTCGGCGACGCCATTCCGGCGTGGTGGTCCACCGGGCTCACCTACCAGGGGTC
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CAAGATTGAGTTTATGATATTAATTAACCTGGAGTTGTTGTTGTAATCTCTCTGT
GGTCCCGCTTTTAATCCATTTTGTTCCTTAATTTTATACATTTTGGTCCCTAAGAG
TTGTGTGTAGATATATGTATGCTATATGTATATCCTT