

IDENTIFICATION

Species: *Brachypodium stacei*

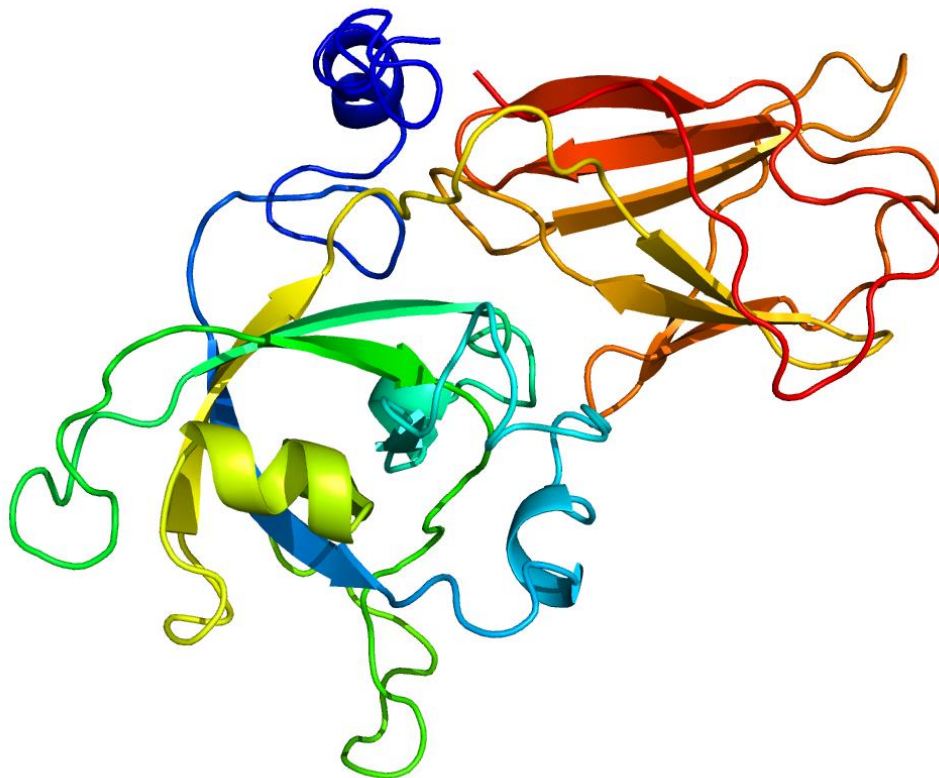
Locus: Brast09G038700

Gene Model: Brast09G038700.1.p

Description: BstEXPA-30

Family: Alpha Expansin

3D structure:



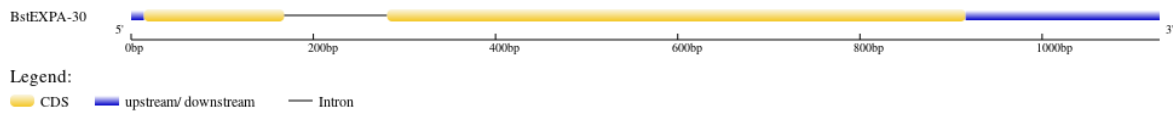
GENOME DATABASES

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

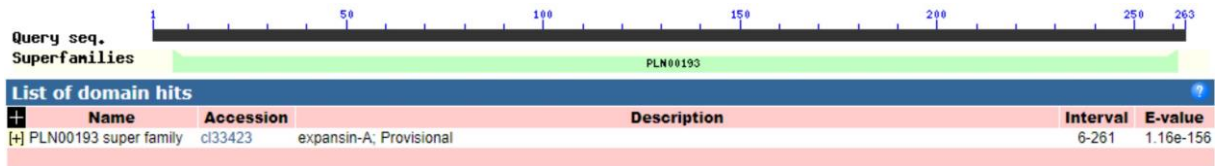
EXTERNAL RESOURCES

<https://brachypodium.org/>

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>BstEXPA-30

MDISTGSLARFLALLATTTCLLNKQASGFRSSGVSRAFATFYGGSDASGTMGGACGY
GNLYSTGYGTSTAALSTVLFNDGAACGQCYSRISCDYAADPRFCRRGTSVTVTATNLC
PPNYALPNDDGGWCNPPRQHFDMAEPAWLSIGVYSGGIVPVLYQRVACA KGGVRF
AVSGHDYFELVLVSNVGGCGSIQAVSVKGSRTGRWMPMSRNWGVNWQSNALLSGQ
SLSFQVTSTDGQTLTFPNVAPAGWGFGQTFQTSRQFS*

CDS (coding sequence)

>BstEXPA-30

ATGGACATATCAACCGGATCGTTAGCTCGGTTCCCTCGCGTTGCTAGCAACAACAA
CATGCCTCCTTAACAAGCAGGCTTCCGGTTTCAGATCGTCCGGCGTCAGCAGAGC
CTTCGCCACCTTCTACGGCGGCAGTGACGCCTCAGGAACCATGGGTGGGGCATGC
GGGTACGGCAACCTGTACTCGACGGGGTACGGGACGAGCACGGCGGGCGCTGAGC
ACGGTGCTGTTCAACGATGGCGCGGCATGCGGGCAGTGCTACCGGATCTCCTGCG
ACTACGCTGCGGACCCCGTTTCTGCCGTCGGGGCACGTCGGTGACAGTCACGGC
CACAAACCTGTGCCCGCCAAACTACGCGCTCCCAACGACGACGGCGGGTGGTG
CAACCCGCCGCGGCAGCACTTCGACATGGCGGAGCCGGCGTGGCTCAGCATCGG
CGTCTACAGCGGGCGGCATCGTGCCGGTGCTCTACCAGAGGGTGGCCTGCGCCAAG
AAGGGCGGCGTGCGGTTTCGCCGTCAGCGGACACGACTACTTCGAGCTCGTCCTGG
TCAGCAACGTCGGCGGGTCCATCCAGGCCGTGTCCTCAAGGGGTCCAG
GACAGGCCGGTGGATGCCCATGTCCAGGAATTGGGGGGTCAACTGGCAGTCCAA
CGCCTTGCTCAGCGGGCAGAGCCTGTCTTTCCAGGTCACCAGTACTGATGGACAG
ACGCTCACTTCCCTAACGTCGCTCCGGCCGGATGGGGCTTCGGCCAGACGTTTC
AGACCTCCAGGCAGTTCTCTTAG

Nucleotide

>BstEXPA-30

AATTTCTCTCTAGCATGGACATATCAACCGGATCGTTAGCTCGGTTCCCTCGCGTTG
CTAGCAACAACAACATGCCTCCTTAACAAGCAGGCTTCCGGTTTCAGATCGTCCG
GCGTCAGCAGAGCCTTCGCCACCTTCTACGGCGGCAGTGACGCCTCAGGAACCAT

GGGTAAGAAACCAAGAATTATATATATGCATAGAGATATATAGCTTCTTCTTTCC
GATTGATTCGATCTGTAATGATCGATGTGAGCATTGCCTGGATGTATATATGTGT
GTAGGTGGGGCATGCGGGTACGGCAACCTGTACTCGACGGGGTACGGGACGAGC
ACGGCGGGCGCTGAGCACGGTGCTGTTCAACGATGGCGCGGCATGCGGGCAGTGC
TACCGGATCTCCTGCGACTACGCTGCGGACCCCGTTTCTGCCGTCGGGGCACGT
CGGTGACAGTCACGGCCACAAACCTGTGCCCGCCAAACTACGCGCTCCCCAACGA
CGACGGCGGGTGGTGCAACCCGCCGCGGCAGCACTTCGACATGGCGGAGCCGGC
GTGGCTCAGCATCGGGCTCTACAGCGGGCGGCATCGTGCCGGTGCTCTACCAGAGG
GTGGCCTGCGCCAAGAAGGGCGGGCTGCGGTTCCCGTCAGCGGACACGACTAC
TTCGAGCTCGTCCTGGTCAGCAACGTCGGCGGCTGCGGGTCCATCCAGGCCGTGT
CCGTCAAGGGGTCCAGGACAGGCCGGTGGATGCCCATGTCCAGGAATTGGGGGG
TCAACTGGCAGTCCAACGCCTTGCTCAGCGGGCAGAGCCTGTCTTTCCAGGTCAC
CAGTACTGATGGACAGACGCTCACTTTCCCTAACGTCGCTCCGGCCGGATGGGGC
TTCGGCCAGACGTTTCAGACCTCCAGGCAGTTCTCTTAGCTAAACTACCTCCAGG
CAGTTCTCTTCAGGCTTCTGAATGTCCTCATCTGATCAGTGTGCGTTGTGTAAAGT
TCTTTTACCGCGTATATATATCCCTCAAAGGACATACAGGGAACCAAGTACATTT
CCTTTGAGTTAACGGTTAAATCACGTGTCACCAGATCGGCCCCCGTCTTTCGAAAC
AAAACCTTGTAATAGAAGACCCGAGAGGGTGA