

IDENTIFICATION

Species: *Brachypodium stacei*

Locus: Brast04G227500

Gene Model: Brast04G227500.1.p

Description: BstEXPA-21

Family: Alpha Expansin

3D structure:



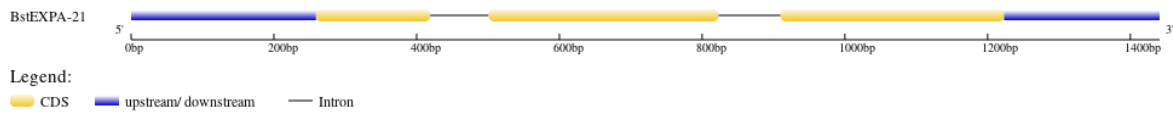
GENOME DATABASES

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

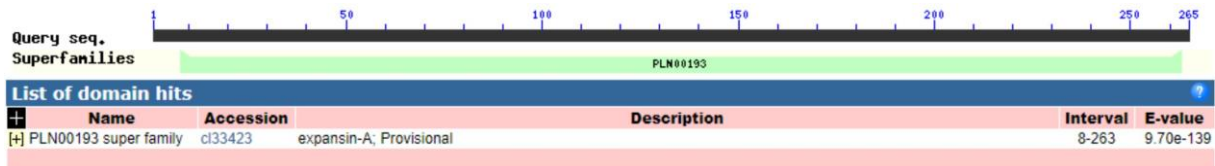
EXTERNAL RESOURCES

<https://brachypodium.org/>

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>BstEXPA-21

MAMPPATAQVISVLLTVGYTAFAVAASSPQAPAVWQRAHATFYGGADASGTMGG
ACGYGNLYSEGYGTRSAALSTVLFNDGVACGQCYKIACDRKVDPRWCKPGITVTVT
ATNLCPPNNA LPNDNGGWCNIPRPHFDMAQPAWEKIGVYRGGIIPVMYQRVPCVKK
GGVRFKINGHDYFNLVLTNVA AIGSIKSMDVKSSVSKDWAPMSRNWGANWHSLA
YLSGKTL SFRLNTDGTLEFNNIVPSGWKFGQTFASKVQFN*

CDS (coding hits sequence)

>BstEXPA-21

ATGGCTATGCCGCCGGCTACAGCTCAAGTAATATCGGTGGTGCTCCTCACAGTGG
GGTATACTGCTTTCGCTGTAGCCGCATCGTCGCCTCAGGCACCGGCCGTTTGGCA
GAGGGCACACGCGACGTTCTACGGTGGAGCTGATGCCTCCGGCACTATGGGTGGT
GCGTGTGGGTACGGCAACCTGTACTCTGAGGGGTACGGGACCCGGTCAGCGGCG
CTGAGTACAGTGTTGTTCAACGACGGCGTAGCATGCGGACAATGTTACAAGATTG
CGTGCGACCGCAAGGTGGACCCACGATGGTGTA AACCTGGTATAACGGTGACGG
TCACGGCCACAAACCTCTGTCCGCCCAACAATGCCCTTCCGAACGACAATGGTGG
TTGGTGCAACATACCGCGGCCGCACTTCGACATGGCGCAGCCAGCCTGGGAGAA
GATCGGTGTCTACAGGGGCGGCATCATCCCGGTCATGTATCAGAGGGTTCCATGC
GTGAAGAAGGGCGGCGTGCGATTTAAGATCAACGGCCATGACTATTTCAATCTTG
TGCTTGTGACCAACGTTGCAGCCATCGGCTCGATAAAATCGATGGATGTGAAGAG
CTCTGTTTCAAAGACTGGGCGCCAATGTCACGCAACTGGGGTGCAA ACTGGCAC
TCGTTGGCCTATCTTAGCGGGAAAACGCTCTCGTTTAGATTAACCAACACTGACG
GGCAAACACTTGAATTCAACAACATTGTGCCAAGTGGATGGAAGTTTGGGCAA
CATTTGCAAGCAAAGTGCAGTTCAACTAA

Nucleotide

>BstEXPA-21

GCCCGTAAGCAATGGTGCAGGCGTGCGGCTGCTACCTGCTTCGTCATTCCTAATG
ACCATGCCAAGAGACCTCCACCTATATATACAGACGCGATCTACATAGGATCATC
ACACAAATTTAATTAAGCCAGCAGAAGCAAATATTCCACATAGCCAAAAGAGAA

CACACCAAAGGAGCAGAGACATCTAGCTTTTGGCCGGGTCTCATCTCAGAAGAT
CGTGTGAATTCTTTTTGTAAGGCCGTCCATCGATACACATATGGCTATGCCGCCGG
CTACAGCTCAAGTAATATCGGTGGTGCTCCTCACAGTGGGGTATACTGCTTTCGCT
GTAGCCGCATCGTCGCCTCAGGCACCGGCCGTTTGGCAGAGGGCACACGCGACGT
TCTACGGTGGAGCTGATGCCTCCGGCACTATGGGTAAGTACTAGCTTATCATAAACTC
TGCGCTGATTAATTCTATGCATGCTTGCCAATTAATTTGTTTTGTTTATTACAAT
ACAGGTGGTGCCTGTGGGTACGGCAACCTGTACTCTGAGGGGTACGGGACCCGG
TCAGCGGCCGCTGAGTACAGTGTTGTTCAACGACGGCGTAGCATGCGGACAATGTT
ACAAGATTGCGTGCAGCCGCAAGGTGGACCCACGATGGTGTAAACCTGGTATAA
CGGTGACGGTCACGGCCACAAACCTCTGTCCGCCAACAAATGCCCTTCCGAACGA
CAATGGTGGTTGGTGCAACATAACCGCGGCCGCACTTCGACATGGCGCAGCCAGCC
TGGGAGAAGATCGGTGTCTACAGGGGCGGCATCATCCCGGTCATGTATCAGAGGT
ACACAAACAATTTTGTGGTAAAATTTTGTGCTTTTGTATTTAATAATGGATCAAAG
TCAATCTAGCTGAAACCAAATCGTTGTAGGGTTCCATGCGTGAAGAAGGGCGGCG
TGCGATTTAAGATCAACGGCCATGACTATTTCAATCTTGTGCTTGTGACCAACGTT
GCAGCCATCGGCTCGATAAAAATCGATGGATGTGAAGAGCTCTGTTTCAAAGACT
GGGCGCCAATGTCACGCAACTGGGGTGCAAACTGGCACTCGTTGGCCTATCTTAG
CGGGAAAACGCTCTCGTTTAGATTAACCAACACTGACGGGCAAACACTTGAATTC
AACAAACATTGTGCCAAGTGGATGGAAGTTTGGGCAAACATTTGCAAGCAAAGTG
CAGTTCAACTAATTGATTTGTCACAGGTTGAATAATTTGTTGGTATTTACTGATAT
TGTGGTGCTTAACTACTTGTATATAACTAAATAGGAATTCTTTGGTTACCGCTGTA
ACTCTAATGTGTGTGTTAAACATGTTTTGGTATGTAGTGTTTGATTCTGTTGATGT
GTTACTTTCAAAGTTTTTGTATTCAAAGCTTTTGGAAATTGACAATGCATGAGTTAG
TCGTTA