

## IDENTIFICATION

**Species:** *Brachypodium stacei*

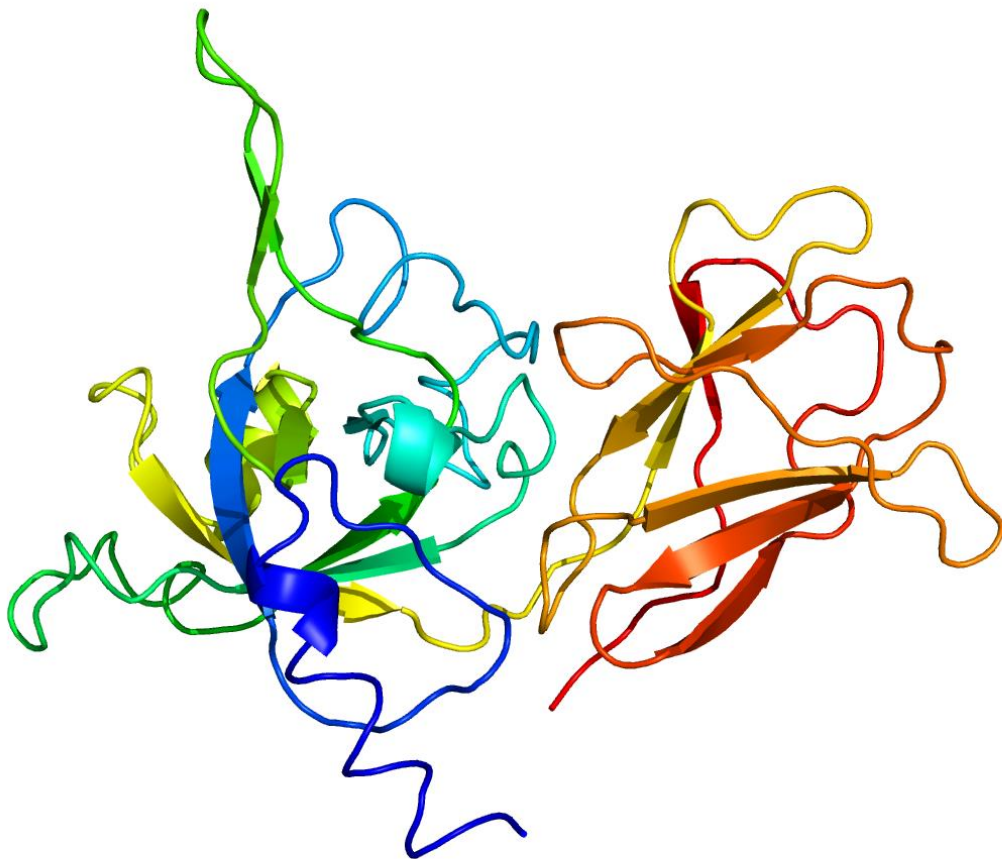
**Locus:** Brast02G046300

**Gene Model:** Brast02G046300.1.p

**Description:** BstEXPA-06

**Family:** Alpha Expansin

**3D structure:**



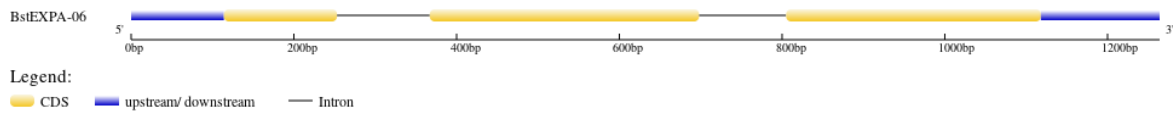
## GENOME DATABASES

Phytozome: [https://phytozome-next.jgi.doe.gov/info/Bstacei\\_v1\\_1](https://phytozome-next.jgi.doe.gov/info/Bstacei_v1_1)

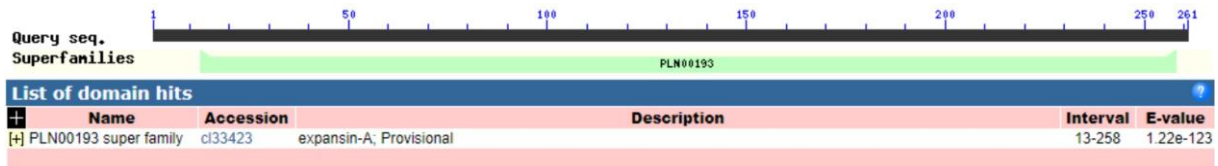
## EXTERNAL RESOURCES

<https://brachypodium.org/>

## GENE STRUCTURE



## DOMAIN ARCHITECTURE



## SEQUENCES

### Peptide

>BstEXPA-06

MEARSKRWSFLQLLVAVAAASPAGEEEEWSKGSATFYGGSDASGTMGGACGYGNL  
YWSGYGTGTAALSPALFNDGASCGQCYRVRCDHESSEPQRCLQPAGKSVAITATNLC  
PPNWALPNDDGGWCNPPRAHFDMSQPSWLRIGVYKAGIIPILYQRVACVKEGGVRF  
MGGFESFELVLISNVGGSGSVKAAWVKGARTERMPMSRNWGANWQSLAALAGQA  
LTFGVTSGGQTLVFQDVVPKWWRFQQAFTSSLQFSY\*

### CDS (coding hits sequence)

>BstEXPA-06

ATGGAGGCGCGGAGTAAGCGATGGAGCTTCCTGCAGCTGTTGGTCGCCGTGGCTG  
CGGCGTCGCCGGCGGGGAGGAGGAGGAATGGTCCAAGGGCTCGGCCACCTTCT  
ACGGCGGCAGCGACGCTTCCGGCACAAATGGGTGGCGCGTGCGGGTACGGGAACC  
TGTA CTGGTCGGGGTACGGGACGGGCACGGCGGCGCTGAGCCC GGCGCTCTTCA  
ACGACGGCGCCTCGTGCGGGCAGTGCTACCGGGTGC GGTGCGACCACGAGTCGT  
CAGAGCCGCAGCGGTGCCTGCAGCCCGCGGGCAAGTCGGTGGCCATCACGGCCA  
CCAACCTCTGCCCGCCCAACTGGGCGCTCCCCAACGACGACGGCGGCTGGTGCAA  
CCCTCCCCGCGCCCACTTCGACATGTCCCAGCCCTCCTGGCTCCGCATCGGCGTCT  
ACAAGGCCGGCATCATCCCCATCCTCTACCAAAGGGTGGCGTGCGTGAAGGAGG  
GAGGGGTGCGGTTACGATGGGAGGGTTCGAGAGCTTCGAGCTGGTGCTCATCTC  
CAACGTGGGCGGGAGCGGGTCGGTGAAGGCGGCGTGGGTGAAGGGGGCCAGGA  
CGGAGAGGATGCCGATGAGCAGGAACTGGGGCGCCA ACTGGCAGTCGCTGGCCG  
CGCTCGCCGGCCAGGCGCTCACCTTCGGGGTCACCTCCAGCGGCGGCCAGACGCT  
CGTCTTCCAGGACGTCGTGCCGAAGTGGTGGCGCTTCGGCCAGGCCTTCACCTCC  
AGCCTCCAGTTCTCCTACTGA

### Nucleotide

>BstEXPA-06

GGAGATTAGTTTCGCTCGATCGATTGTTCACTCAACTATTTAGGAAGTACTGCAC  
ATACTGAAGAACACTGTCACAGCTGGCACTCATTCAGACACTCACGCTCGTGA  
AAAAATGGAGGCGCGGAGTAAGCGATGGAGCTTCCTGCAGCTGTTGGTCGCCGT

GGCTGCGGCGTCGCCGGCGGGGGAGGAGGAGGAATGGTCCAAGGGCTCGGCCAC  
CTTCTACGGCGGCAGCGACGCTTCCGGCACAATGGGTACGCACTACGCACAGAGC  
ACACATCTCAAATCTTGCTTCAGTTCTTCAAAGTCCAGTAGGTACACTGGAGTG  
GTTAATCCCCTGAGCACCAATAATATTTGATGGATGCAGGTGGCGCGTGCGGGTA  
CGGGAACCTGTACTGGTCGGGGTACGGGACGGGCACGGCGGCGCTGAGCCCGGC  
GCTCTTCAACGACGGCGCCTCGTGCGGGCAGTGCTACCGGGTGCGGTGCACCAC  
GAGTCGTCAGAGCCGCAGCGGTGCCTGCAGCCCGCGGGCAAGTCGGTGGCCATC  
ACGGCCACCAACCTCTGCCCCGCCAACTGGGCGCTCCCCAACGACGACGGCGGCT  
GGTGCAACCCTCCCCGCGCCCCTTCGACATGTCCCAGCCCTCCTGGCTCCGCATC  
GGCGTCTACAAGGCCGGCATCATCCCCATCCTCTACCAAAGGTTAAAATTTGCA  
GTTAATAAGTAGTACTCACCACACGCATGTCATTGGACGGTTAATTCGACTTGG  
GTAGATTAAGAAGTTGTGATATGTTTTGTGTGCGTAGGGTGGCGTGCCTGAAGG  
AGGGAGGGGTGCGGTTACGATGGGAGGGTTCGAGAGCTTCGAGCTGGTGCTCA  
TCTCCAACGTGGGCGGGAGCGGGTTCGGTGAAGGCGGCGTGGGTGAAGGGGGCCA  
GGACGGAGAGGATGCCGATGAGCAGGAACTGGGGCGCCAACTGGCAGTCGCTGG  
CCGCGCTCGCCGGCCAGGCGCTCACCTTCGGGGTACCTCCAGCGGCGGCCAGAC  
GCTCGTCTTCCAGGACGTCGTGCCGAAGTGGTGGCGCTTCGGCCAGGCCTTACC  
TCCAGCCTCCAGTTCTCCTACTGATCACTCGTTTGCTTTGCTCGGCCTCCGTGTTA  
GATGCCAAATGTCAAGTTATACTGGTGGGCTGTGAAGTGAGAATCCATCCTTGA  
TGGCAGCCGTTTGTATTCTTGGCCACTCTGAGTGACCAGTCTCAATGTGTAGGAA  
AAGG