

## IDENTIFICATION

**Species:** *Brachypodium stacei*

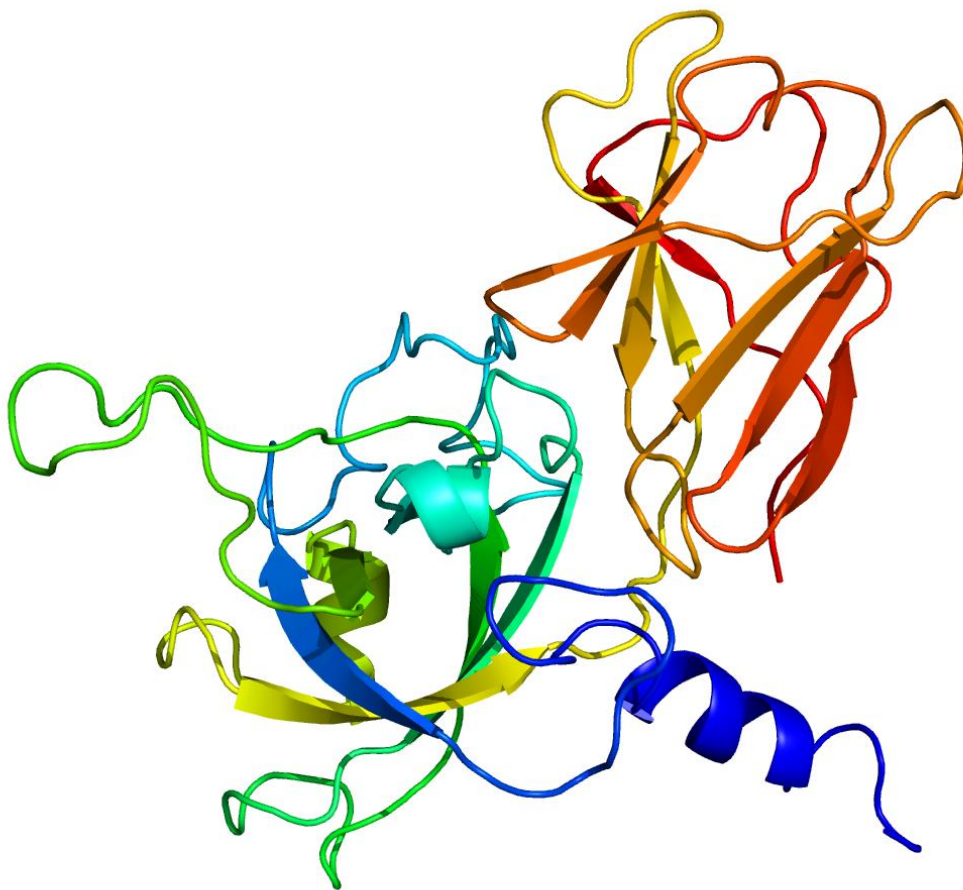
**Locus:** Brast08G167900

**Gene Model:** Brast08G167900.1.p

**Description:** BstEXPA-29

**Family:** Alpha Expansin

**3D structure:**



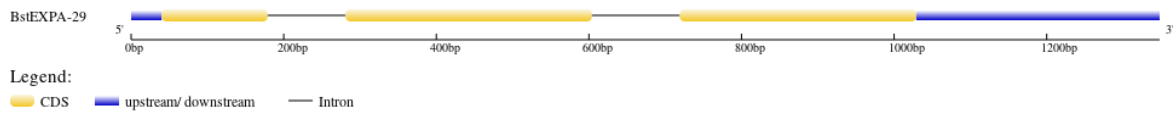
## GENOME DATABASES

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

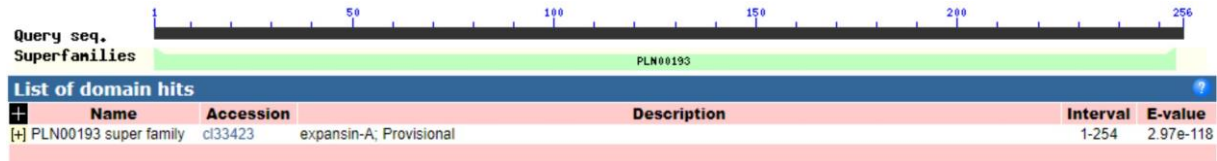
## EXTERNAL RESOURCES

<https://brachypodium.org/>

## GENE STRUCTURE



## DOMAIN ARCHITECTURE



## SEQUENCES

### Peptide

>BstEXPA-29

MAKQIVLLALLTVLCKLASHAVHAQYSWTSATATFYGGSDGSGTLGGACGYGNLY  
NTGYGLNNAALSSALFNDGAMCGACYNIYCDTSKSNWCKPGTSITISATNLCPPNYA  
KPNNDGGWCNPPRLHFDMSQPAWTTIAVYQAGIVPVNYKRVSCQKQNGIRFGINGN  
NYFELVVVTNVGGSGVVAQMWIKGSRTDWMAMSRNWGANWQSNAYLNGQSLSF  
RVKLDDGRQVTATDVAPYYWYFGATYSSGVNFY\*

### CDS (coding sequence)

>BstEXPA-29

ATGGCAAACAATAAGTACTACTGCTGGCGCTTCTGACAGTGCTATGCAAATTAG  
CTTCTCATGCTGTACACGCGCAGTATTCGTGGACGAGCGCTACGGCGACGTTCTA  
CGGCGGCAGCGACGGCTCCGGAACATTGGGAGGAGCGTGTGGGTACGGCAACCT  
GTACAACACCGGGTACGGGCTGAACAACGCGGCGCTGAGCTCGGCGCTGTTCAA  
CGACGGCGCCATGTGCGGGGCGTGCTACAACATCTACTGCGACACGAGCAAGAG  
CAACTGGTGCAAGCCCGGCACGTCCATCACAATCTCGGCCACCAACCTCTGCCCG  
CCCAACTACGCTAAGCCCAACGACAACGGCGGGCTGGTGCAACCCGCCGCGGCTG  
CACTTCGACATGTCGCAGCCCGCCTGGACGACCATCGCCGTCTACCAAGCCGGCA  
TCGTCCCCGTCAACTACAAGAGGGTGTCTGTGCCAGAAGCAGAATGGCATCCGGTT  
CGGGATAAACGGGAATAACTACTTCGAGCTGGTGGTGGTGACCAACGTGGGAGG  
ATCCGGCGTGGTGGCGCAGATGTGGATCAAGGGGTCCAGAACAGACTGGATGGC  
CATGAGCAGGAAGTGGGGGGCCAACTGGCAGAGCAACGCCTACCTCAACGGGCA  
GAGCCTCTTTTCAGGGTGAAGCTCGACGACGGCCGCCAAGTCACGGCCACCGAC  
GTCGCGCCCTACTACTGGTACTTCGGGGCCACCTACTCGTCCGGGGTCAACTTTTA  
CTAG

### Nucleotide

>BstEXPA-29

TACGAGTACTATCGCGCTCCTTATCATCTCTACACGTCAAATGGCAAACAATA  
GTAATACTACTGCTGGCGCTTCTGACAGTGCTATGCAAATTAGCTTCTCATGCTGTACA  
CGCGCAGTATTCGTGGACGAGCGCTACGGCGACGTTCTACGGCGGCAGCGACGG  
CTCCGGAACATTGGGTTTGTTCCTCCGAGCCCTCCATTAATTTACACACGTATAC

CTTGTTTTGTTATTGAGATATAAAGGATTACCTGTGTTTACTCATATTGTGTGCGT  
GCAGGAGGAGCGTGTGGGTACGGCAACCTGTACAACACCGGGTACGGGCTGAAC  
AACGCGGCGCTGAGCTCGGCGCTGTTCAACGACGGCGCCATGTGCGGGGCGTGCT  
ACAACATCTACTGCGACACGAGCAAGAGCAACTGGTGCAAGCCCCGGCACGTCCA  
TCACAATCTCGGCCACCAACCTCTGCCCGCCAACTACGCTAAGCCCAACGACAA  
CGGCGGCTGGTGCAACCCGCCGCGGCTGCACTTCGACATGTCGCAGCCCCGCCTGG  
ACGACCATCGCCGTCTACCAAGCCGGCATCGTCCCCGTCAACTACAAGAGGCAAG  
TACATATGCAACCGGCTAATTTAGGCGTACGTATCAATTGAAAACCTCGATTGCG  
ATCGATGTGTGAGAGTAGTTGTGATGGAGCCTGCCTGGCCTATGATATATATGAT  
GCAGGGTGTGCGTGCCAGAAGCAGAATGGCATCCGGTTCGGGATAAACGGGAATA  
ACTACTTCGAGCTGGTGGTGGTGACCAACGTGGGAGGATCCGGCGTGGTGGCGC  
AGATGTGGATCAAGGGGTCCAGAACAGACTGGATGGCCATGAGCAGGAACTGGG  
GGGCCAACTGGCAGAGCAACGCCTACCTCAACGGGCAGAGCCTCTCTTTCAGGGT  
GAAGCTCGACGACGGCCGCCAAGTCACGGCCACCGACGTCGCGCCCTACTACTG  
GTACTIONCGGGGCCACCTACTCGTCCGGGGTCAACTTTTACTAGCTAGCTAGAGAG  
CTGAATCCATCGGCACGCACGCGCGGCAATAAAAAATCCACCGCTGGATGATCGA  
ACAATTACTTATAATTGATCTTACGGGGGGATTAAAGGTTAATGACGTGCCCACT  
TTGCCTAGCTAGTACATACATCACTGCACCGATGTTGAGAGGCAATCGGAGCAGC  
GCTTGTTAACTGTAAGAATTTTGTCTACTTACTTCTTTCTGCTCGATCCTAGCTGC  
ATGGATTCTTGTAGGAGCTGCTTCGCATTTGTATTGCCTAGTCAGCGGCTTGGTAC  
CCCACAAGCCCCGCTACGCAATCAACTCAGC