

## IDENTIFICATION

**Species:** *Brachypodium sylvaticum*

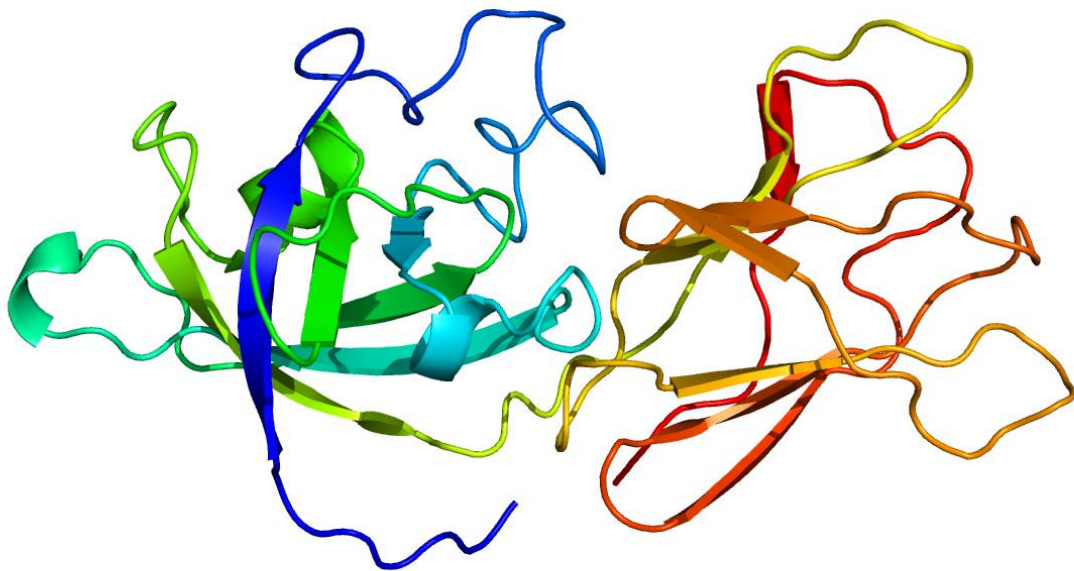
**Locus:** Brasy1G412800

**Gene Model:** Brasy1G412800.1.p

**Description:** BsyEXPA-04

**Family:** Alpha Expansin

**3D structure:**



## GENOME DATABASES

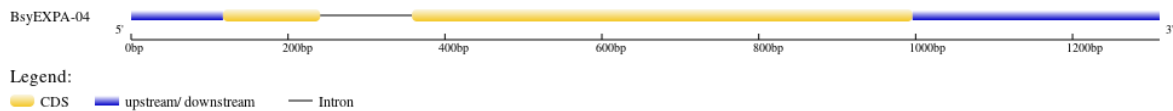
Phytozome: [https://phytozome-next.jgi.doe.gov/info/Bsylvaticum\\_v1\\_1](https://phytozome-next.jgi.doe.gov/info/Bsylvaticum_v1_1)

KEGG:-

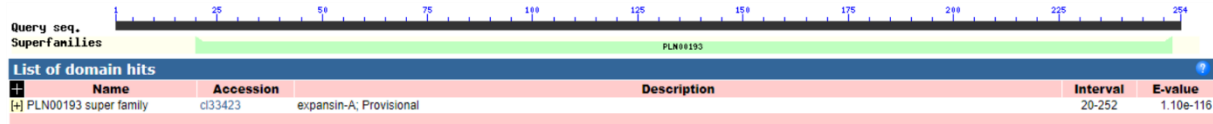
## EXTERNAL RESOURCES

<http://jaiswallab.cgrb.oregonstate.edu/genomics/brasy>

## GENE STRUCTURE



## DOMAIN ARCHITECTURE



## SEQUENCES

### Peptide

>BsyEXPA-04

MALIRMLMLLALFAFLLRASAAQWTPATATFYGGADASGTMGGACGYGNLYGAGY  
GTQTTALSTALFNNGASCGACFTIACDARRSRWCKPGAPPITVTATNFCPPNYALPSD  
NGGWCNPPRRHFDMSQPAWERIGVYRGGIVPVNYRRVRCGGRSGGVRFTVNGHSYF  
ELVLVTNVGGSGVVAQMWVKGSGSTGWMAMARNWGANWQSNAYLNGKSLSFRL  
RSDDGRVVT AENVAPAGWWFGGTYTSGAQFY\*

### CDS (coding sequence)

>BsyEXPA-04

ATGGCGCTCATCAGGATGCTCATGCTCCTGGCGCTGTTTCGCCTTCTGCTCAGAGC  
ATCGGCGGCTCAATGGACACCCGCCACGGCAACGTTCTACGGCGGGCGCCGACGC  
CTCGGGCACCATGGGCGGGGCTGCGGGTACGGCAACCTGTACGGCGCAGGGTA  
CGGCACGCAGACGACGGCGCTGAGCACGGCGCTCTTCAACAACGGCGCCTCGTG  
CGGCGCCTGCTTACCATCGCGTGCGACGCCCGGAGGTCCCGGTGGTGCAAGCCG  
GGGGCGCCCCCATCACGGTCACGGCCACAACTTCTGCCCGCCAACTACGCGC  
TCCCAGCGACAACGGCGGGTGGTGCAACCCGCCGCGGCGGCACTTCGACATGTC  
GCAGCCGGCGTGGGAGCGCATCGGCGTGTACCGTGGCGGCATCGTGCCCGTGAA  
CTACCGGCGGGTGCGGTGCGGCGGCCGACGCGGGGGCGTCCGGTTCACCGTCAA  
CGGGCACAGCTACTTCGAGCTGGTGGTGGTACCAACGTGGGCGGCAGCGGCGT  
GGTGGCGCAGATGTGGGTGAAAGGGTCCGGCAGCACGGGGTGGATGGCGATGGC  
CAGGA ACTGGGGCGGAACTGGCAGAGCAACGCGTACCTCAACGGGAAGAGCCT  
CTCGTTCGCGCTCAGGTCCGATGATGGGCGTGTGTCACGGCGGAGAACGTCGCG  
CCGGCCGGGTGGTGGTTCGGCGGCACCTACACGTCCGGGGCTCAGTTCTACTGA

### Nucleotide

>BsyEXPA-04

ACACACAGTTAAGCCAGCAGCGACATTCCTGGCTAGCTAGCAGCTGTGTAGCAGA  
GTACAATCTTGTAGTACTGGCCCGTACTGTGCCTCAGGTTGTCAGCAGGATCGAG  
CACCGATATGGCGCTCATCAGGATGCTCATGCTCCTGGCGCTGTTTCGCCTTCTGCT  
TCAGAGCATCGGCGGCTCAATGGACACCCGCCACGGCAACGTTCTACGGCGGGCG  
CCGACGCCTCGGGCACCATGGGTACGTTAGTCAACTTAACTAGCTTCCCAGATCG  
TCCTTTTTTGGCAGACTACTCTTGCTACATATAGTCGATGCTAACATGGACATGCA

CTACGGGGTGTTTGTGGATCTTACCAGGCGGGGCCTGCGGGTACGGCAACCTGTA  
CGGCGCAGGGTACGGCACGCAGACGACGGCGCTGAGCACGGCGCTCTTCAACAA  
CGGCGCCTCGTGCGGCGCCTGCTTACCATCGCGTGCGACGCCCGGAGGTCCCGG  
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CCAACCTACGCGCTCCCCAGCGACAACGGCGGGTGGTGCAACCCGCCGCGGGCGG  
ACTTCGACATGTCGCAGCCGGCGTGGGAGCGCATCGGCGTGTACCGTGGCGGCAT  
CGTGCCCGTGAACCTACCGGCGGGTGCGGTGCGGCGGCCGCAGCGGGGGCGTCCG  
GTTACCGTCAACGGGCACAGCTACTTCGAGCTGGTGCTGGTGACCAACGTGGGC  
GGCAGCGGCGTGGTGGCGCAGATGTGGGTGAAAGGGTCCGGCAGCACGGGGTGG  
ATGGCGATGGCCAGGAACTGGGGCGCGAACTGGCAGAGCAACGCGTACCTCAAC  
GGGAAGAGCCTCTCGTTCCGCCTCAGGTCCGATGATGGGCGTGTTCGTCACGGCGG  
AGAACGTCGCGCCGGCCGGGTGGTGGTTCGGCGGCACCTACACGTCCGGGGCTC  
AGTTCTACTGAAGTCATGTACTGATCGATCATTCCGCTGCCGTGCTCTTTCTCGTG  
TGGCTATTTACGTGCGTCGTTTCGCGATTGGTCTCGATCTTTTTGTATGTACACCGT  
GTTCTGCATTTCGACGATGTGAACTGTCTATTTTGCATAGGGCCGAACTGAAGGCC  
GCCACGAGGCAGGCAGGCACGCTACTCTTTGCCGATGTTGGACTTGCTTGCCCTC  
AAAATACAAATATTTGTGTGCAAATTAAGGGAAAAAAAGTGTATTTCTATGTTC  
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