

## IDENTIFICATION

**Species:** *Brachypodium sylvaticum*

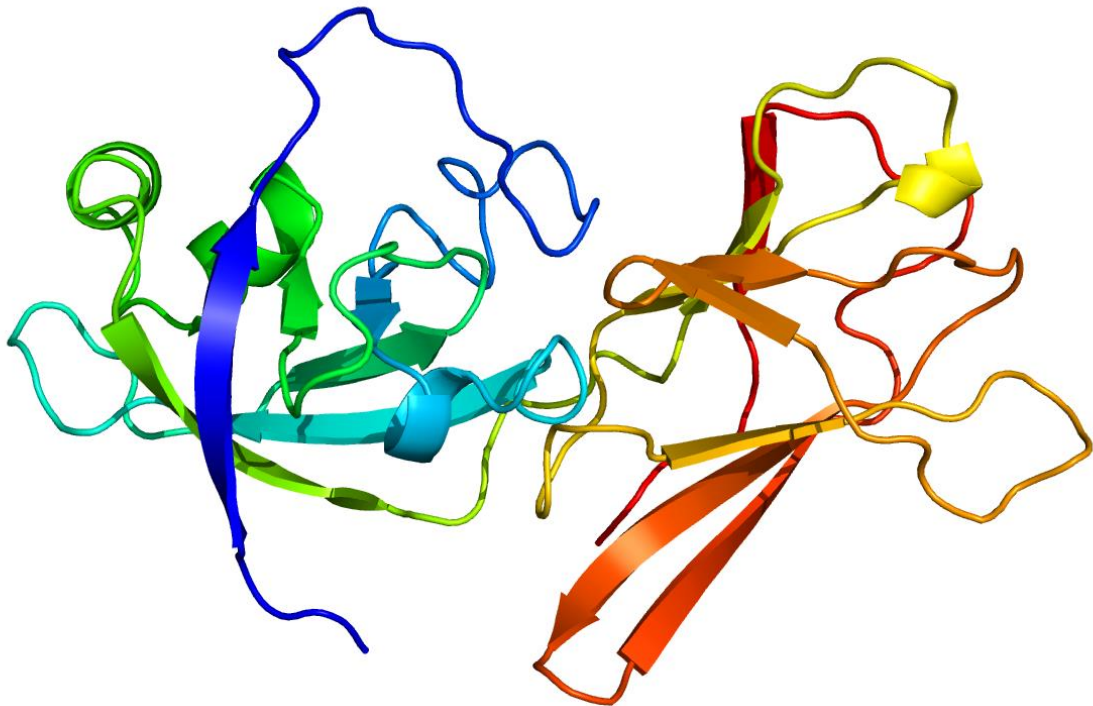
**Locus:** Brasy2G047100

**Gene Model:** Brasy2G047100.1.p

**Description:** BsyEXLA-01

**Family:** Expansin Like Alpha

**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:-

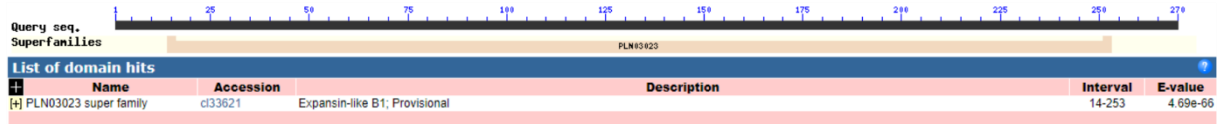
## EXTERNAL RESOURCES

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

## GENE STRUCTURE



## DOMAIN ARCHITECTURE



## SEQUENCES

### Peptide

>BsyEXLA-01

MMAAVSVSFSSTALLALLFLVSAASACDRCLHQSRASFYTSSLTLSAGSCGYGNAAA  
SFNGGMLAAAGPALYRGGVGCACFQVRCKDKELCSAAGAGVIVTDSAKTNRTEL  
VLSSPAFNAMARPGMADRLAKLGEVDVEYKRVPCEYKGNLSVRVEEKSHAPSDLA  
IRFFYQGGQTDIVA VDIAQVGSSNWKFMAREHGPAWSTSQAPPGPLQLRVVVTAGY  
DGKWLWAEKEVLPSAWRAGELYDTGLQITDIAQEGCSPCDTQDWK\*

### CDS (coding sequence)

>BsyEXLA-01

ATGATGGCCGCCGTCTCTGTTCAGTTTCTCCTCGACGGCTCTGCTCGCGCTACTCTT  
CCTCGTGTCCGGCCGCTCCGCCTGCGACCGCTGCCTGCACCAGTCCAGAGCCTCC  
TTCTACACCTCCTCGCTACCCTCTCCGCCGTTCTTGCGGGTACGGCAACGCGGC  
CGCGTCTTCAACGGCGGCATGCTCGCCGCGGCCCGGCCCGCTCTTACCGCGGA  
GGCGTCCGCTGCGGCGCGTGTTCAGGTGCGGTGCAAGGACAAGGAGCTGTGC  
AGCGCTGCCGGCGCCGGGGTTCATCGTACGGACAGCGCCAAGACGAACCGCACG  
GAGCTCGTGTCTCAGCAGCCCGGCCTTCAACGCCATGGCGCGCCCCGGCATGGCCG  
ACCGGCTCGCCAAGCTCGGCGAGGTTCGACGTTCGAGTACAAGAGGGTGCCGTGCG  
AGTACAAGGGGAAGAACCTCTCGGTGAGGGTGGAGGAGAAGAGCCACGCGCCCA  
GCGACCTGGCCATCAGGTTCTTCTACCAGGGCGGCCAGACCGACATCGTCGCCGT  
CGACATCGCACAGGTAGGGTCGTGGAAGTTCATGGCGCGGGAGCACGG  
GCCGGCGTGGAGCACGAGCCAGGCGCCGCGGGACCGCTGCAGCTCAGGGTCTG  
GGTGACCGCCGGGTACGACGGGAAATGGCTGTGGGCGGAGAAGGAAGTGTGCC  
GAGCGCGTGGCGCGCCGGCGAGCTTACGACACCGGGCTCCAGATCACCGACAT  
CGCCCAGGAAGGCTGCTCTCCGTGCGACACGCAGGACTGGAAGTGA

### Nucleotide

>BsyEXLA-01

ACCCCCATCACTGTTTTGTACACAGTCGCCTGTAGTAGTTCAGTTAATAGCACGC  
CGAGGTAGCTGCGCCTCTCTGCGTGCCTGCGCGCCAGTGTGTTGTTGGACC  
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CGGCTCGCCAAGCTCGGCGAGGTCGACGTCGAGTACAAGAGGTAATAAAAACTT  
AAAAAGTCTAAAAAGCATTCTGTTTCCATTTTTACCACCAACCGCGCCATGTGC  
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AAAGAAAGAAAGAAAGTAGCGCCGGGCCCGCCGAGCCCGAACGTGGCATCATAA  
ATACAGAGACCAAGAATTTGGACTTTGGATTGGAAGGGGCTCAAATTTGTCAGCG  
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GAACAACAAAGAACAATAGTACTCCTTCCGTCCCATAAAGATTGGCATGGATTTG  
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