

IDENTIFICATION

Species: *Brachypodium sylvaticum*

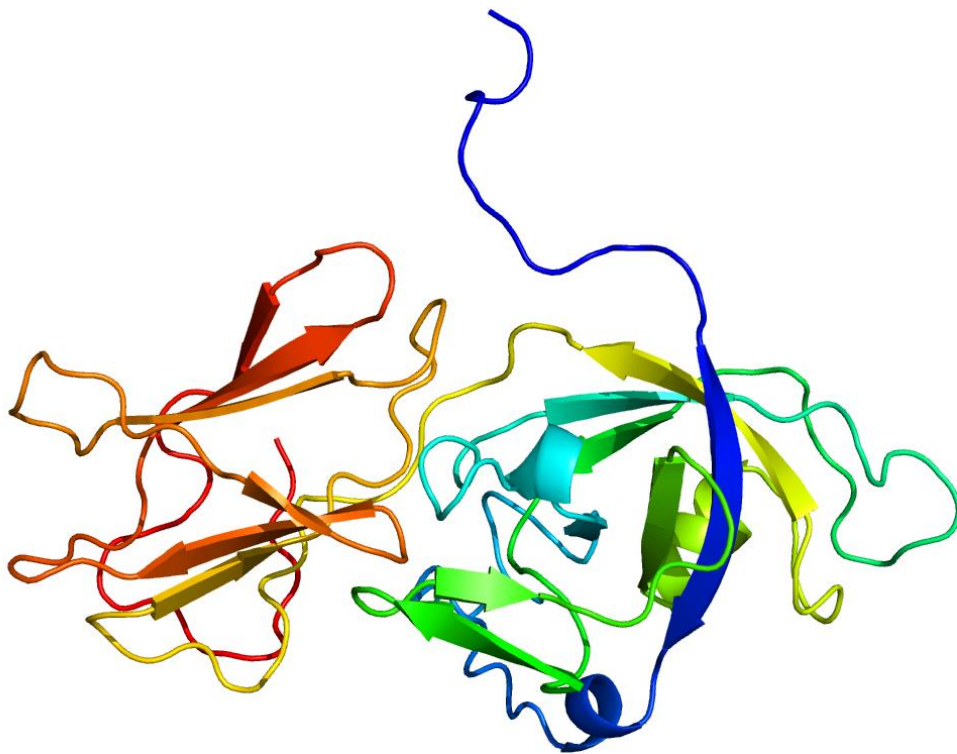
Locus: Brasy3G347300

Gene Model: Brasy3G347300.1.p

Description: BsyEXPA-14

Family: Alpha Expansin

3D structure:



GENOME DATABASES

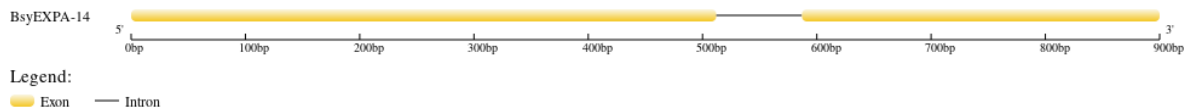
Phytozome: https://phytozome-next.jgi.doe.gov/info/Bsylvaticum_v1_1

KEGG:-

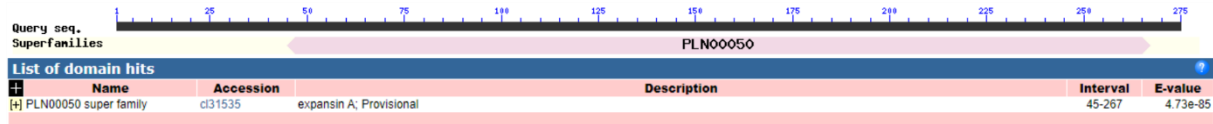
EXTERNAL RESOURCES

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

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>BsyEXPA-14

MSGSWAPLLLLVVVVLVLLAADVVAGTGEARVHHHNHGKFMEGPWRPAHATFYG
EHDGTGTRAGACGYKDTV AEGYGLQTV ALSAAMFKGGATCGACYEVRCTEMSPK
WCKPPGAPPLVVTATNLCPPNYQQPGDNGGWCNPPREHFDLTMPAFLQMAEEKAGI
VPISYRRVSCLKQGGIRYTITGNKYFNMVTVTNVGGAGDVAAVTVKGD DRVKWTP L
TRNWGQVWQTGEILVGESLTFR VMTGDHRKATSWHVLPRDWQFGV TYQATNNFH*

CDS (coding sequence)

>BsyEXPA-14

ATGTCTGGTTCGTGGGCGCCTCTCCTCCTCGTCGTCGTCGTCCTGGTGCTGCT
CGCCGCCGATGTCGTCGCTGGCACCGGCGAGGCGAGGGTGCACCACCACAACCA
CGGCAAGTTCATGGAGGGCCCGTGGCGGCCGGCGCACGCCACCTTCTACGGCGA
GCACGACGGGACCGGGACGCGGGGCCGGCGCGTGCGGGTACAAGGACACGGTGGC
GGAAGGGTACGGCCTGCAGACGGTGGCGTTGAGCGCGGCCATGTTCAAGGGCGG
CGCGACGTGCGGGGCGTGCTATGAGGTGAGGTGCACGGAGATGAGCCCAAAGTG
GTGCAAGCCGCCCGGGCGCCGCGTTGGTGGTGACGGCGACGAACCTGTGCC
CCCAA ACTACCAGCAGCCGGGCGACAACGGCGGGTGGTGCAACCCGCCGCGCGA
GCACTTTGACCTCACCATGCCGGCATTCTCCAGATGGCCGAGGAGAAGGCCGGC
ATTGTGCCCATCTCCTACCGCCGGGTGAGCTGTTTGAAGCAGGGCGGGATCCGTT
ACACGATCACGGGGAACAAGTACTTCAACATGGTGACGGTGACAAACGTGGGCG
GGGCGGGGACGTGGCGGCCGGTGACGGTCAAGGGGGACGACCGAGTCAAGTGG
ACCCCGTTGACGCGGAACTGGGGCCAGGTGTGGCAGACCGGGGAGATCCTCGTC
GGCGAGTCGCTGACGTTCCGCGTCATGACCGGCGACCACCGCAAGGCCACCTCCT
GGCACGTGCTCCCCGCGACTGGCAGTTCGGCGTCACCTACCAGGCAACCAACAA
CTTCCACTAG

Nucleotide

>BsyEXPA-14

ATGTCTGGTTCGTGGGCGCCTCTCCTCCTCGTCGTCGTCGTCCTGGTGCTGCT
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GCACGACGGGACCGGGACGCGGGGCCGGCGCGTGCGGGTACAAGGACACGGTGGC

GGAAGGGTACGGCCTGCAGACGGTGGCGTTGAGCGCGGCCATGTTCAAGGGCGG
CGCGACGTGCGGGGCGTGCTATGAGGTGAGGTGCACGGAGATGAGCCCAAAGTG
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GCACTTTGACCTCACCATGCCGGCATTCCCTCCAGATGGCCGAGGAGAAGGCCGGC
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GACGGTGACAAACGTGGGGCGGGGCGGGGGACGTGGCGGGCGGTGACGGTCAAGG
GGGACGACCGAGTCAAGTGGACCCCGTTGACGCGGAACTGGGGCCAGGTGTGGC
AGACCGGGGAGATCCTCGTCGGCGAGTCGCTGACGTTCCGCGTCATGACCGGCGA
CCACCGCAAGGCCACCTCCTGGCACGTGCTCCCCCGCGACTGGCAGTTCGGCGTC
ACCTACCAGGCAACCAACAACCTTCCACTAG