

IDENTIFICATION

Species: *Brachypodium sylvaticum*

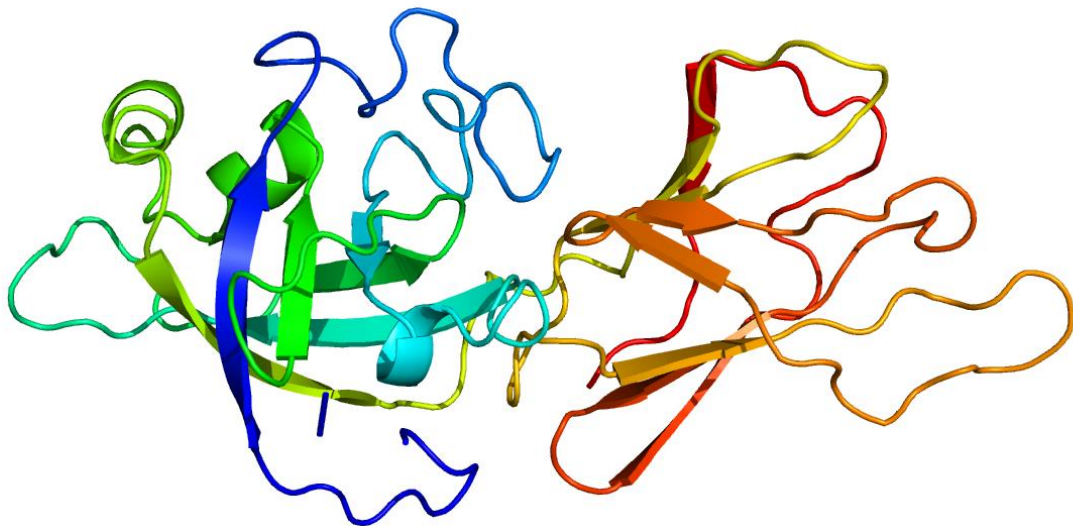
Locus: Brasy3G211500

Gene Model: Brasy3G211500.1.p

Description: BsyEXPB-10

Family: Beta Expansin

3D structure:



GENOME DATABASES

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

KEGG:-

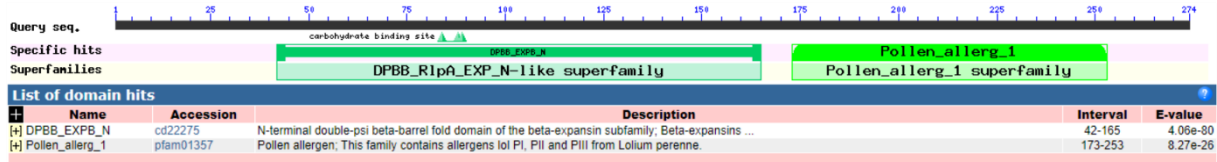
EXTERNAL RESOURCES

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

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>BsyEXPB-10

MAGVSTDAVALVALLSAVLVSTGHSQQVNYD TSAARSYNSGWLPKATWYGAPTG
AGPDDNGGACGYKDTNQYPYSSMISCGNEPLFMGGAGCGTCYQIRCNYANNPACSG
QPRVTITDMNYYPVAKYHFDLSGTAFGAMANNGQNDQLRHAGIIDMQFRRVPCNY
PGMNVNFHVERGSNPNYLAVLVQHNRDGNVVLMEIMESRYGRPTGQWTAMTRS
WGAIWRRD TNRPMQGPFSLRVRSSEGSTLVANQAIPADWKPNARYWSNIQYR*

CDS (coding sequence)

>BsyEXPB-10

ATGGCTGGCGTCTCCACCGATGCCGTTGCCCTTGTGGCACTCCTCTCGGGCGGTGCT
CGTCTCCACCGCCATTCGCAACAGGTCAACTACGACACCTCTGCCGCAAGATCC
TACAACTCAGGTTGGCTCCCCGCCAAGGCCACCTGGTACGGCGCCCCTACCGGCG
CCGGCCCCGACGACAACGGTGGTGCATGCGGCTACAAGGACACGAATCAGTACC
CGTACTCTTCCATGATTTCGTGCGGCAACGAGCCCCTGTTCATGGGCGGCGCGGG
CTGCGGCACCTGCTACCAGATACGATGCAATTACGCCAACAACCCTGCCTGCTCC
GGCCAGCCGAGGACGGTGACGATCACCGACATGAACTACTACCCGGTGGCCAAG
TACCACTTCGACCTCAGCGGCACGGCCTTCGGCGCCATGGCGAACAACGGGCAG
AACGACCAGCTCCGCCACGCCGGCATCATCGACATGCAGTTCAGGAGGGTGCCGT
GCAACTACCCGGGGATGAACGTGAACTTCCACGTGGAGCGCGGCTCGAACCCGA
ACTACCTGGCGGTGCTGGTGCAGCACGCGAACC GGGACGGGAACGTGGTGCTGA
TGGAGATCATGGAGTCCAGGTACGGCCGCCGACCGGGCAGTGGACGGCGATGA
CGCGCTCCTGGGGCGCCATCTGGAGGAGGGACACCAACCGCCCGATGCAGGGGC
CATTCTCCCTCCGCGTCCGCAGCGAGTCCGGCAGCACGCTGGTGGCCAACCAGGC
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TGA

Nucleotide

>BsyEXPB-10

AAAAGGAGTCTGTGGGCTTAGGCGGGGGAGTACTACTACTCCAGCGAGTACTCTG
CCGCAAGAGTAGTATCTTAAGGTTTCGCATAGCTACACTACTTGTACGTAGTGCG

CCGGTATGGCTGGCGTCTCCACCGATGCCGTTGCCCTTGTGGCACTCCTCTCGGCG
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ACATGAACTACTACCCGGTGGCCAAGTACCACTTCGACCTCAGCGGCACGGCCTT
CGGCGCCATGGCGAACAAACGGGCAGAACGACCAGCTCCGCCACGCCGGCATCAT
CGACATGCAGTTCAGGAGGGTGCCGTGCAACTACCCGGGGATGAACGTGAACTT
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GAACCGGGACGGGAACGTGGTGCTGATGGAGATCATGGAGTCCAGGTACGGCCG
CCCGACCGGGCAGTGGACGGCGATGACGCGCTCCTGGGGCGCCATCTGGAGGAG
GGACACCAACCGCCCGATGCAGGGGCCATTCTCCCTCCGCGTCCGCAGCGAGTCC
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TCCTATGCTTGTTAAGTGTGCGTCGTTAATTGTGTGTCCTAGAAGATCTTTGTGTG
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