

IDENTIFICATION

Species: *Brachypodium sylvaticum*

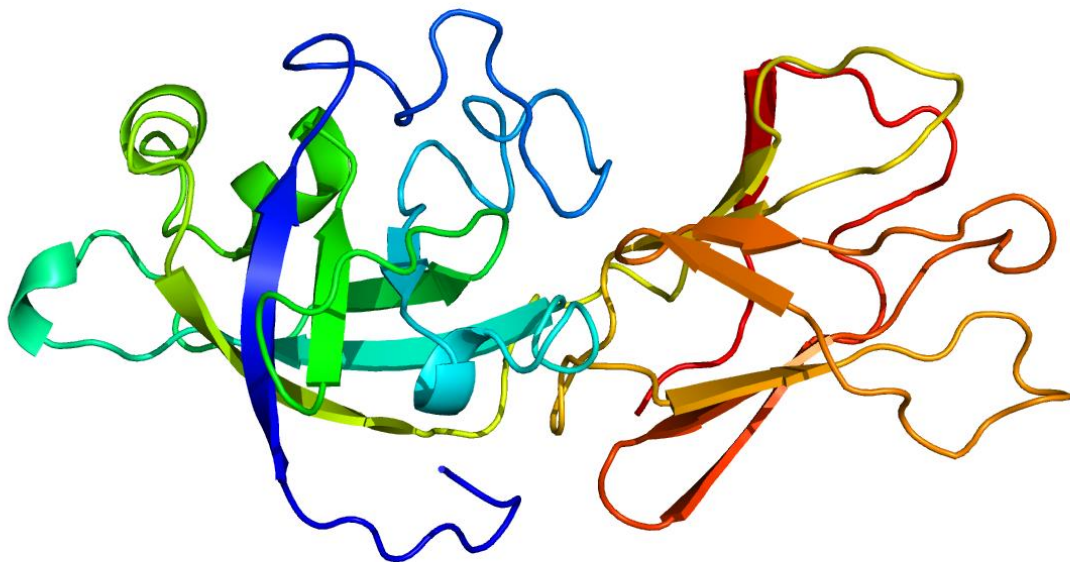
Locus: Brasy3G211600

Gene Model: Brasy3G211600.1.p

Description: BsyEXPB-11

Family: Beta Expansin

3D structure:



GENOME DATABASES

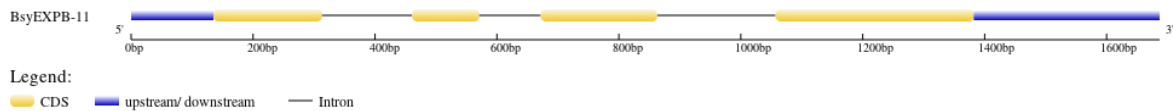
Phytozome: https://phytozome-next.jgi.doe.gov/info/Bsylvaticum_v1_1

KEGG:-

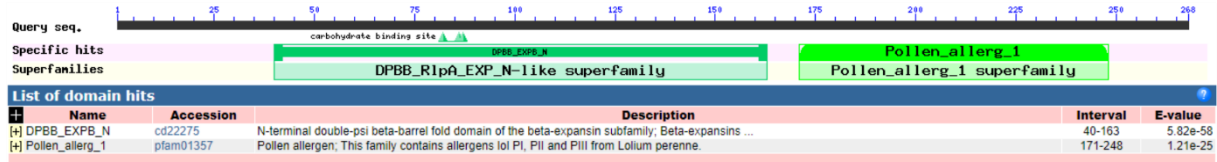
EXTERNAL RESOURCES

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

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>BsyEXPB-11

MAGVFTGAVALVAILFSMLVNRSAAAGYYAASPARAYSSAWLPKATWYGAPTGAG
PANGGGACAYSNNNLYPILSMNACGNQPLFMDGAGCGTCYEIKCDYKNNRACSGQP
KRVTITDMNYNNIAQYYFDLSGTAFGAMAKYGQENLRRAGILDIQFRRVPCNYQG
MNINFRVERGSNPNYLAVLVQHANKDGNVVQMDLKDSGSYGSWTPMKRSWGAIW
RMDTGRPLKAPFSFRMRSEIGATKVAYQVIPVNWKGGNNYWSNVQY*

CDS (coding sequence)

>BsyEXPB-11

ATGGCTGGGGTCTTCACCGGCGCCGTTGCCCTCGTGGCAATCCTCTTCTCCATGCT
CGTCAACCGTTCGGCGGCCGTTACTACGCCGTTCCCCCGCTAGAGCTTACAGC
TCTGCCTGGCTCCCCGCAAAGGCCACCTGGTACGGCGCCCCTACCGGCGCCGGCC
CCGCAAACGGCGGTGGTGCATGCGCCTACTCGAACAATAATCTGTACCCGATTTT
GTCGATGAACGCGTGCGGCAACCAGCCCCTGTTCATGGACGGCGCTGGCTGCGGC
ACCTGCTACGAGATAAAATGCGATTACAAGAACAACCGTGCCTGCTCCGGCCAGC
CGAAGAGGGTGACGATCACTGACATGAACTACAACAACATCGCCCAGTACTACTT
TGACCTCAGCGGCACGGCGTTCGGCGCCATGGCAAAGTACGGCCAGAACGAAAA
CCTCCGCCGCGCCGGCATCCTCGACATCCAGTTCAGGAGGGGTGCCATGCAACTAC
CAGGGGATGAACATCAACTTCCGGGTGGAGCGTGGCTCGAACCCGAACCTACCTG
GCGGTGCTCGTCCAGCACGCGAACAAGGACGGGAACGTGGTGCAGATGGACCTC
AAGGACTCCGGGTCGTATGGCTCCTGGACGCCGATGAAACGGTTCGTGGGGTGCC
ATCTGGAGGATGGACACGGGGCGCCCGCTGAAGGCCCCCTTCTCCTTCCGCATGC
GCAGCGAGATCGGGGCCACGAAGGTGGCCTACCAGGTCATTCCGGTCAACTGGA
AGGGCGGCAACAACACTACTGGTCCAACGTCCAGTACTAA

Nucleotide

>BsyEXPB-11

GCCTATTGGCCCTGCAGCCTATAAATGCACCGGCAATGCCATCTCATGCCGCCAT
CAGAACACAGACAGGAGAAGTACTCCAGCAAGTACATAGCCTAATTAAGGTTTCG
ATCGTGTAGCATATTGTAGTGCCAACATGGCTGGGGTCTTACCGGCGCCGTTGC

CCTCGTGGCAATCCTCTTCTCCATGCTCGTCAACCGTTCGGCGGCCGGTTACTACG
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AGAGGGTGACGATCACTGACATGAACTACAACAACATCGCCCAGTACTACTTTGA
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CCGCCGCGCCGGCATCCTCGACATCCAGTTCAGGAGGTCATTTTCAGTTGACATAA
ATCAATCAATTAATTAAGCGAAGTACTTCCTCGCTGAACCTGATATGACCGCAAT
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CGTGTGCTCGCAATCGATCTGACGCGTACGTCGGCTGCCATGCCATGCCGCTCA
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