

IDENTIFICATION

Species: *Brachypodium sylvaticum*

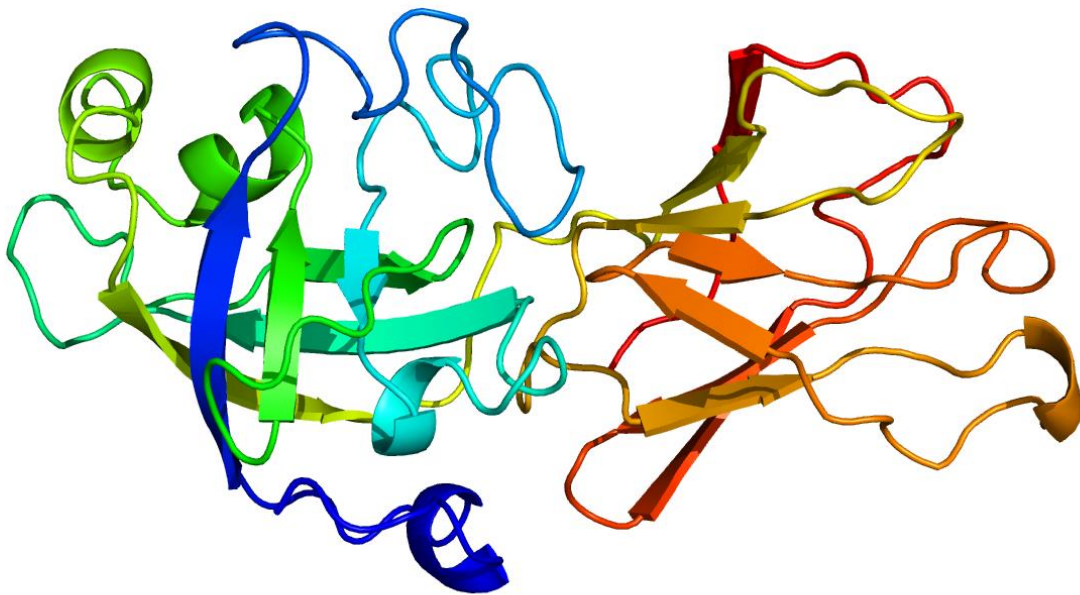
Locus: Brasy3G211800

Gene Model: Brasy3G211800.1.p

Description: BsyEXPB-13

Family: Beta Expansin

3D structure:



GENOME DATABASES

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

KEGG:-

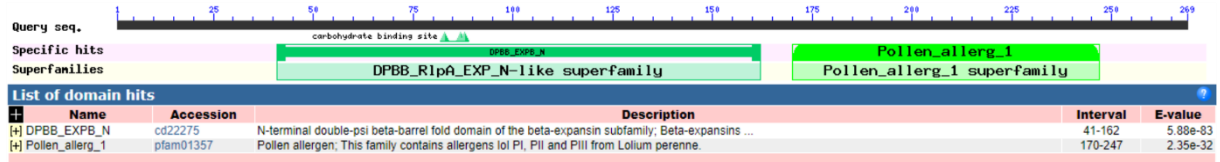
EXTERNAL RESOURCES

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

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>BsyEXPB-13

MAALSSKAVALVALSSLLVITYVAAGPPVNYNASAFATADPNWENARATWYGAPTGA
GPDDDGGACGFKNVNQYPFSAMTSCGNEPLFKDGKGCSCYQIRC VNDQSCSGNPE
TVVITDMNYYPVSKYHFDLSGTAFGAMAKPGLNDKLRHSGIIDIQFKRVPCNFPGLK
VTFHVEQGSNPVYFAVLVEYEDGDGDVQVDLMEANSGGAWTPMRESWGSIWRLD
SGHRLQAPFLRITNESGKTLVADKVIPANWAPSAVYRSFVQYSG*

CDS (coding sequence)

>BsyEXPB-13

ATGGCAGCTCTTTCCTCCAAGGCCGTTGCACTCGTTGCACTCTCCTCCCTCCTTGT
CACCTATGTCGCCGCTGGCCCAGTGAATTACAATGCTTCCGCCTTCACCGCC
GACCCCAACTGGGAGAACGCCAGGGCCACCTGGTATGGCGCGCCACCGGCGCC
GGCCCTGACGACGACGGTGGTGCCTGTGGGTTCAAGAACGTGAACCAGTACCCG
TTCTCGGCCATGACCTCCTGCGGCAACGAGCCCCTGTTCAAAGACGGCAAGGGCT
GCGGCTCCTGCTACCAGATAAGATGCGTCAACGACCAATCCTGTTCCGGCAACCC
GGAGACTGTGGTCATCACCGACATGAACTACTACCCGGTCTCCAAGTACCACTTC
GACCTGAGCGGCACGGCGTTCGGCGCCATGGCCAAGCCGGGCCTCAACGACAAG
CTGCGCCACTCCGGCATCATCGACATCCAGTTCAAGAGGGTGCCCTGCAACTTCC
CGGGGCTGAAGGTGACCTTCCACGTGGAGCAAGGGTCGAACCCGGTGTACTTCGC
GGTGTGGTGGAGTACGAGGACGGCGACGGCGACGTGGTCCAGGTGGACCTGAT
GGAGGCCAACTCGGGCGGCGCGTGGACGCCGATGCGCGAGTCGTGGGGCTCCAT
CTGGCGCCTCGACTCCGGCCACCGCCTCCAGGCGCCCTTCTCCCTCCGCATACCA
ACGAGTCCGGCAAGACGCTCGTCGCCGACAAGGTCATCCCGGCCAACTGGGCGC
CCAGCGCCGTCTACCGCTCCTTCGTCCAGTACAGCGGCTGA

Nucleotide

>BsyEXPB-13

TTTTTCCAGAATATCACTCTCTGCATGCACACAAAACATATTCAGAGTATCAAT
TAACAGGCAGGTAGTCTGGTAGTGTCCAGAGACACCTGCGATAACCGCTAAACA
GCCGTGATTTACATAAATATTCTAGTTTGTAGTGCCTGGTGAACGAACGGAACCTG

ATCGCCCTCCATTCCCTCCCATGATTTCCCTCCCGTAGCCATGTGACCCCTATCACCA
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GCACTGATCGATCTGATCTCTGTGTGCTTGCAGGTGGTGCCTGTGGGTTCAAGAA
CGTGAACCAGTACCCGTTCTCGGCCATGACCTCCTGCGGCAACGAGCCCCTGTTC
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TCTCTCAATGCGTGGTTTTCTTTTTCTTTCTGTCGACGAGTGCTATTTCTGGTGCT
TGCCCCTGCCGTGGTGGAAAAGGAGCTGGTGGACTCTCGGGCACGTTGCTTTGCC
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ACGACCAATCCTGTTCCGGCAACCCGGAGACTGTGGTCATCACCGACATGAACATA
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TCAAGAGGTCTGTCTGTCTGTCTTTGTGGCCCTACCTGAACAGAACTTTCACGATA
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