

IDENTIFICATION

Species: *Sorghum bicolor*

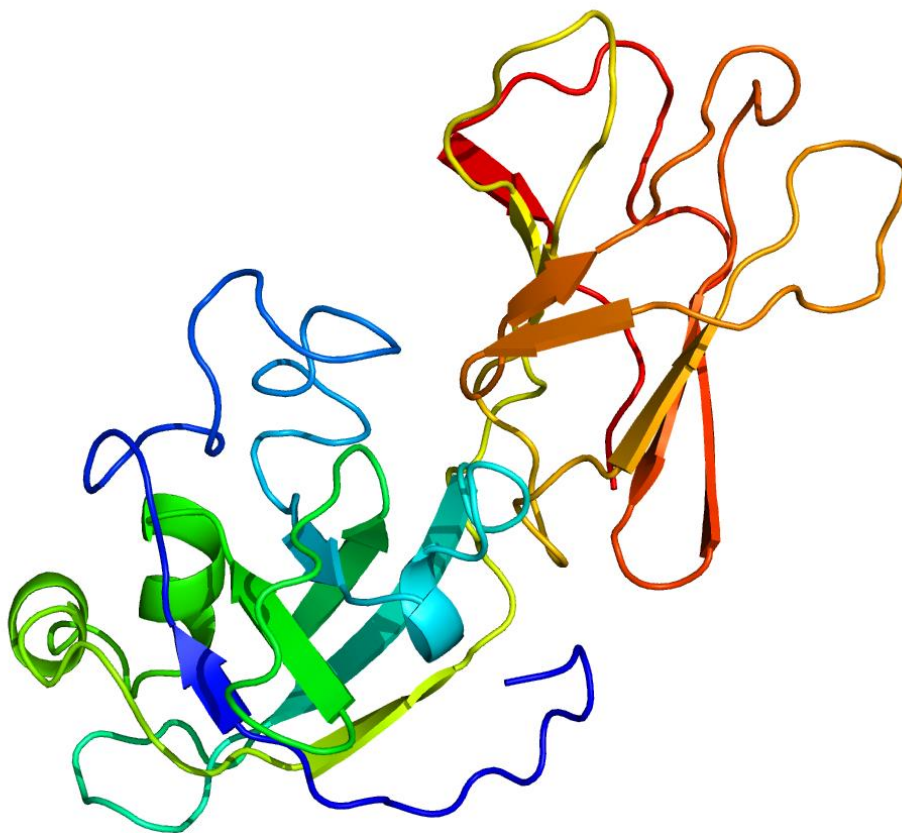
Locus: Sobic.001G306500

Gene Model: Sobic.001G306500.2.p

Description: SbEXPB-18

Family: Beta Expansin

3D structure:



GENOME DATABASES

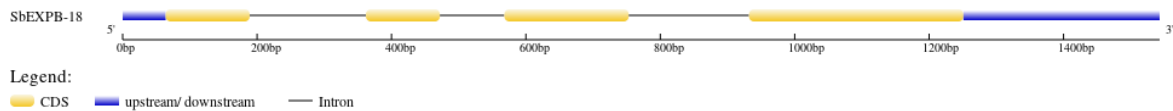
Phytozome: https://phytozome-next.jgi.doe.gov/info/Sbicolor_v3_1_1

KEGG: <https://www.genome.jp/entry/T01086>

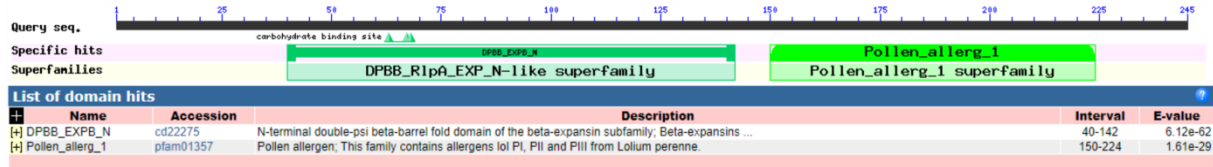
EXTERNAL RESOURCES

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GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>SbEXPB-18

MGSLANKIVAMAAVLAALVTGGSCAPKKFPPGPNITTNYNNGGACGIKNVNLPPYNGF
TACGNVPIFKDGKGCSCYEVRCKEMPECSGNPITVFITDMNYEPIAPYHFDFSGKAF
GSLAKPGLNDKLRHCGIMNVEFRRVRCKLGGKIMFHVEKGSNPNYLAVLVKNVADD
GNIVLMELEDKASPGFKPMKQSWGAVWRFDTPKPKVKGPF SIRLTSESGKKLVAPNVI
PATWKPD TLYNSNIQF*

CDS (coding sequence)

>SbEXPB-18

ATGGGATCCCTCGCCAACAAAATCGTGGCCATGGCGGCTGTCCTTGC GGCGCTCG
TCACCGGCGGCTCGTGC GCGCCCAAGAAGTTCCCGCCTGGCCCCAACATCACAAC
CAACTACAACGGCGGTGCGTGCGGAATCAAGAACGTGAACCTGCCACCCTACAA
TGGCTTCACGGCCTGCGGTAACGTCCCCATCTTCAAGGATGGCAAGGGCTGCGGC
TCATGCTACGAGGTGAGATGCAAGGAAATGCCAGAGTGTTTCGGGCAACCCGATC
ACGGTGTTTCATACCGACATGAACTATGAGCCCATCGCACCTACC ACTTTGACT
TCAGCGGCAAGGCCTTCGGCTCCCTAGCAAAGCCTGGGCTCAACGACAAGCTCCG
CCACTGCGGCATCATGAACGTGGAGTTCAGGAGGGTGCGGTGCAAGCTTGGGGG
CAAGATCATGTTCCACGTTGAGAAGGGGTCCAACCCCAACTACCTGGCCGTGCTG
GTCAAGAACGTGGCGGACGACGGCAACATCGTGCTCATGGA ACTCGAGGACAAG
GCGTCGCCGGGGTTCAAGCCAATGAAGCAATCCTGGGGCGCCGTGTGGAGGTTTG
ACACACCCAAGCCGTCAAGGGCCCCTTCTCCATCCGCCTACCAGCGAGTCCGG
CAAGAAGCTCGTCGCCCCGAACGTCATCCCGGCGACCTGGAAGCCCGACACCCTC
TACAACTCCAACATCCAGTTCTAA

Nucleotide

>SbEXPB-18

AATCACAAACACACAGAGCGACATTCGTTGAATATCACAGTTGAGCGCAAAGAA
GACACCCGCGATGGGATCCCTCGCCAACAAAATCGTGGCCATGGCGGCTGTCCTT
GCGGCGCTCGTACCGGCGGCTCGTGC GCGCCCAAGAAGTTCCCGCCTGGCCCCA
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ACGTGAACCTGCCACCCTACAATGGCTTCACGGCCTGCGGTAACGTCCCCATCTT
CAAGGATGGCAAGGGCTGCGGCTCATGCTACGAGGTATGTACATTATATATATAG
CAACCAAACCAAACAACACATGCATGAGAGAGAGAGAGAGATCATCTCGCTA
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AACCCGATCACGGTGTTTCATCACCGACATGAACTATGAGCCCATCGCACCCTACC
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GGTGCGGTGCAAGCTTGGGGGCAAGATCATGTTCCACGTTGAGAAGGGGTCCAA
CCCCAACTACCTGGCCGTGCTGGTCAAGAACGTGGCGGACGACGGCAACATCGT
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CTGGGGCGCCGTGTGGAGGTTTGACACACCCAAGCCGGTCAAGGGCCCCTTCTCC
ATCCGCCTCACCAGCGAGTCCGGCAAGAAGCTCGTCGCCCCGAACGTCATCCCGG
CGACCTGGAAGCCCGACACCCTCTACAACCTCCAACATCCAGTTCTAATAGACTTT
GCATGCCCTTCATCCGGCCTCTTATGCCTCTTATGTTTATTTGCATGAGAGAATGC
ACCGCTAATAAATAGTAGTACTGAGTCTTCTGCATTCTAGCTAGTATGTGATCCCT
GTTGTTGTTTCGGGCTCATGATCGAATTCCAAACAGTGGAAAATAAAAGGTTGAAT
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ATGGCG