

## IDENTIFICATION

**Species:** *Sorghum bicolor*

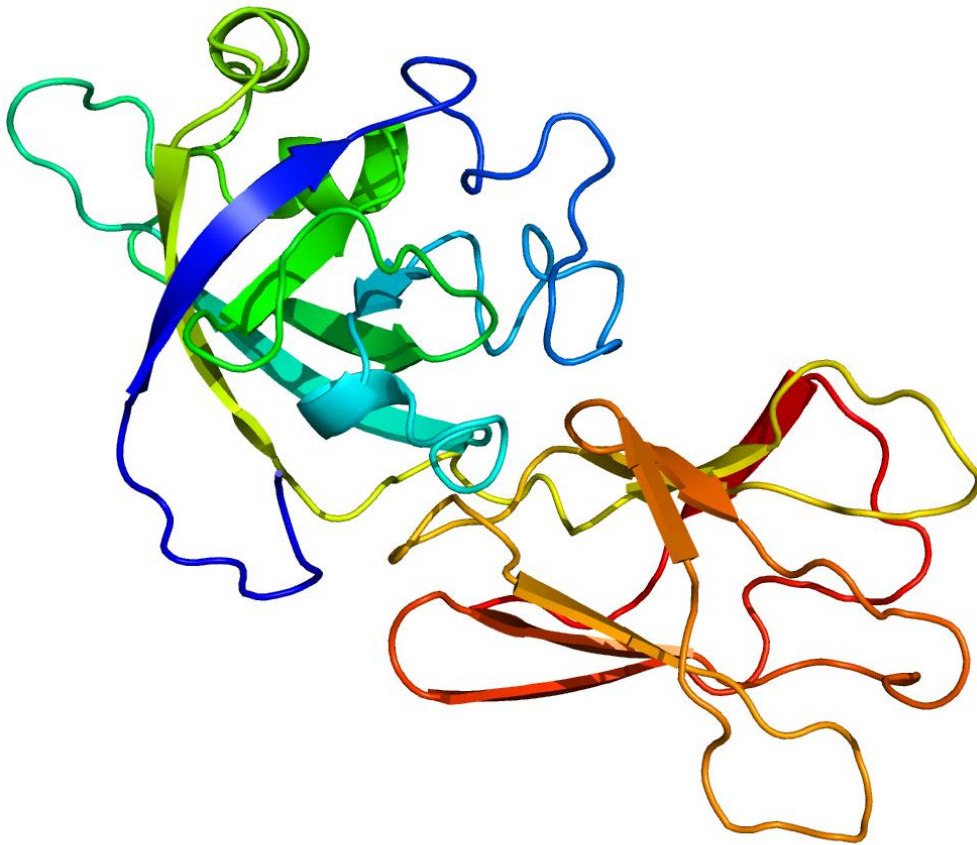
**Locus:** Sobic.001G301500

**Gene Model:** Sobic.001G301500.1.p

**Description:** SbEXPB-11

**Family:** Beta Expansin

**3D structure:**



## GENOME DATABASES

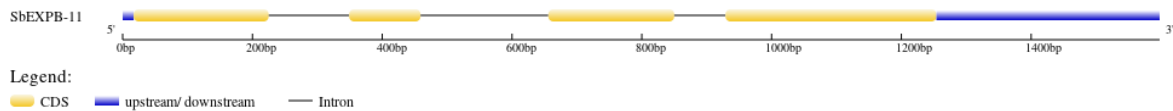
Phytozome: [https://phytozome-next.jgi.doe.gov/info/Sbicolor\\_v3\\_1\\_1](https://phytozome-next.jgi.doe.gov/info/Sbicolor_v3_1_1)

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

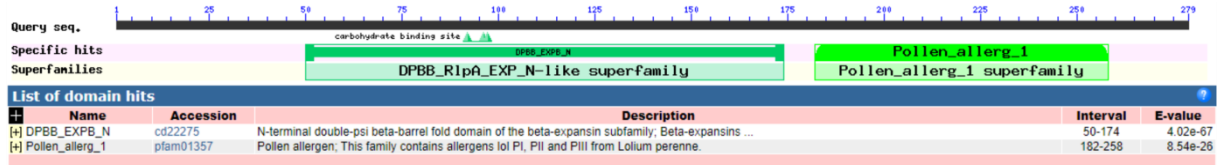
## EXTERNAL RESOURCES

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## GENE STRUCTURE



## DOMAIN ARCHITECTURE



## SEQUENCES

### Peptide

>SbEXPB-11

MAVAISIKVAALVISVFATHGARAQPSYNNASSSSARRELYYSSTTGGSWLPAKATW  
YGRPNGAGPDNNGGGCGYSGTNLYPFNSMTSCGDRNVFRDGKGCSCYQIKCVSSN  
NPACSGVPQTIITDVNYDTSLGPNRFDLSGTAFGAMAKPGLNGKLRNAGALSIQYRR  
VPCNYKGLNVRFHVMGGCNPFYFAVIVYYAGSDGAVVQVELKEANSRTWRPLYES  
WGAVWRIDPGHPLRAPLSLRVRSDDGGKTLVAYDVIPINWRGNADYRTIAQFR\*

### CDS (coding sequence)

>SbEXPB-11

ATGGCCGTCGCGATCTCCATCAAGGTGGCTGCACTCGTCATCTCCGTGTTCCGCCAC  
GCATGGCGCTCGCGCGCAGCCGAGCTACAACAACGCCTCCTCCTCCTCCGCCCGC  
AGAGAGTTGTACTACTCCAGCACCACCGGCGGCAGCTGGCTCCCTGCCAAGGCCA  
CCTGGTACGGCCGGCCCAACGGCGCCGGCCCTGACAACAACGGTGGCGGGTGTG  
GGTACAGCGGCACCAACCTGTACCCTTTCAATTCCATGACGTCCTGTGGCGACAG  
GAACGTGTTACAGGACGGCAAGGGCTGCGGCTCATGCTACCAGATAAAATGCGT  
GAGCAGCAACAACCCTGCCTGCTCCGGCGTGCCCCAGACGATTATCATCACCGAC  
GTGAACTACGACACCAGCCTCGGCCCAACCGTTTCGACCTCAGCGGCACGGCGT  
TCGGCGCCATGGCTAAGCCTGGCCTCAACGGCAAGCTCCGCAATGCCGGCGCCCT  
CAGCATCCAGTACAGGAGGGTGCCCTGCAACTACAAGGGCTTGAACGTGAGGTT  
CCACGTGATGGGAGGCTGCAACCCATTCTACTTCGCGGTGATCGTGTACTACGCG  
GGCAGCGATGGCGCCGTGGTGCAGGTGGAGCTCAAGGAGGCCAACTCGCGGACA  
TGGAGGCCGCTGTACGAGTCGTGGGGCGCCGTCTGGAGGATAGACCCGGGCCAC  
CCGCTGAGGGCGCCCCTCTCGCTGCGCGTCCGCAGCGACGGCGGCAAGACTCTGG  
TGGCTACGACGTCATCCCGATCAACTGGAGGGGCAATGCCGATTACCGTACCAT  
CGCTCAGTTCGCTGA

### Nucleotide

>SbEXPB-11

GACGACCTTGAGCTGAGATGGCCGTCGCGATCTCCATCAAGGTGGCTGCACTCGT  
CATCTCCGTGTTCCGCCACGCATGGCGCTCGCGCGCAGCCGAGCTACAACAACGCC

TCCTCCTCCTCCGCCCCGAGAGAGTTGTACTACTCCAGCACCACCGGCGGCAGCT  
GGCTCCCTGCCAAGGCCACCTGGTACGGCCGGCCCAACGGCGCCGGCCCTGACA  
ACAACGGTGTGTGTGCGCCTGGAATGCTGTTCGTGTTTTTCCTTGTGTTTTAATTTAA  
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CCTGACGCATCGATCGATCGACCTGATGACCCACGCCGACGCCGACGGGTGCCCT  
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