

## IDENTIFICATION

**Species:** *Sorghum bicolor*

**Locus:** Sobic.001G306200

**Gene Model:** Sobic.001G306200.1.p

**Description:** SbEXPB-13

**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>

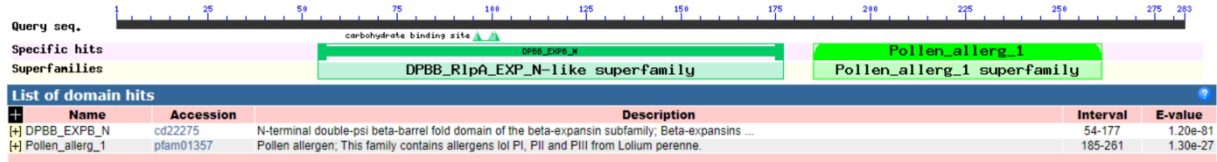
## EXTERNAL RESOURCES

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## GENE STRUCTURE



## DOMAIN ARCHITECTURE



## SEQUENCES

### Peptide

>SbEXPB-13

MATALSFKAAFAVAALLSVVAVTYGAPAQQQPDLHNATDSQSQDRSLLSYSSGWLP  
 AKATWYGAPTGAGPDDNGGACGFKGTNQYFSSMTSCGNEPIFKDGKGCSCYQIR  
 CLKSNHPACSGVPQTVIITDMNYYPVAKYHFDLSGTAFGAMASWGLNDKLRHAGIID  
 MQFRRVPCNFPGLTITFRVQHGSNPMYLAVLIEHENQDGDVVQADIMQNNSGYWEP  
 MHESWGSIWRIDPNRPLRGPFSIRITNESGKQLVAKNIIPANYVADVDYRSYVQYTN\*

### CDS (coding sequence)

>SbEXPB-13

ATGGCCACCGCGCTCTCCTTCAAGGCCGCCTTTGCAGTGGCCGCGCTCCTCTCCGT  
 GGTCGCCGTCACCTATGGCGCTCCCGCCCAGCAGCAGCCCGACCTGCACAACGCC  
 ACCGACTCGCAGTCGCAGGACAGATCCTTGTGTGCCTACAGCAGTGGCTGGCTGC  
 CGGCCAAGGCCACCTGGTACGGAGCGCCACCGGCGCCGGCCCCGACGACAACG  
 GTGGTGCCTGCGGGTTCAAGGGCACGAACCAGTACCCGTTCTCGTCCATGACGTC  
 GTGTGGCAACGAGCCATCTTCAAGGACGGCAAGGGCTGCGGCTCATGCTATCAG  
 ATACGGTGCCTTAAGAGCAACCACCCGGCCTGCTCCGGCGTGCCGCAGACGGTGA  
 TCATCACCGACATGAATACTACCCGGTTGCCAAGTACCACTTCGACCTGAGCGG  
 CACGGCGTTCGGCGCCATGGCGAGCTGGGGCCTCAACGACAAGCTCCGGCACGC  
 CGGGATCATCGACATGCAGTTCAGGAGGGTGCCGTGCAACTTCCCGGGCCTGACC  
 ATCACGTTCCGCGTGCAGCACGGGTCCAACCCCATGTACCTCGCCGTGCTCATCG  
 AGCACGAGAACCAGGACGGCGACGTGGTGCAGGCGGACATCATGCAGAACAACT  
 CCGGCTACTGGGAGCCCATGCACGAGTCCTGGGGATCCATCTGGAGGATCGACCC  
 CAACCGCCCGCTCAGGGGCCCTTCTCCATCCGCATCACCAACGAGTCCGGCAAG  
 CAGCTGGTGGCCAAGAACATTATCCCGGCCAACTATGTCGCCGACGTGCGATTACC  
 GCTCCTACGTCCAGTATACTAATTAA

### Nucleotide

>SbEXPB-13

TCACACCATCGAAACACAAACCAGGCAGCAACGAACTGCCAAGCAAAGCCGAGG  
 TCCCTAGGCCACAGCTACTGCAACAATGGCCACCGCGCTCTCCTTCAAGGCCGCC

TTTGCAGTGGCCGCGCTCCTCTCCGTGGTCGCCGTCACCTATGGCGCTCCCGCCCA  
GCAGCAGCCCGACCTGCACAACGCCACCGACTCGCAGTCGCAGGACAGATCCTT  
GTTGTCCTACAGCAGTGGCTGGCTGCCGGCCAAGGCCACCTGGTACGGAGCGCCC  
ACCGGCGCCGGCCCCGACGACAACGGTAAGGATCCGCGCGCATTCCAAGCCATC  
CATCGATCTCTCCGATCCATGTCTGTATATGTTGTCCTCTGCAATGTGGCCATGCC  
TAAATGTCTTCTTGTGTTTGTCTGAATCTTTGCTAGGTGGTGCCTGCGGGTTCAAGG  
GCACGAACCAGTACCCGTTCTCGTCCATGACGTCGTGTGGCAACGAGCCCATCTT  
CAAGGACGGCAAGGGCTGCGGCTCATGCTATCAGGTGGGTGTGGGTGATAACCG  
TTTTTCACCACGGCCGACGATCGTTTAGTAGTTGGTGCCCAATCATTTTAATTACT  
TGGTTGGTCAAATGAATTGAAGATAGCAGCAGTAGCTAGCGTCCGGCCGTAGCGC  
TCGCCTTGGATTGCTCACATCACATCAGGACCACGTGCATCCGCTGACCTTGTGCT  
TGGCTTTTCCTCCTTCCCAGATACGGTGCCTTAAGAGCAACCACCCGGCCTGCTCC  
GGCGTGCCGCAGACGGTGATCATCACCGACATGAACTACTACCCGGTTGCCAAGT  
ACCACTTCGACCTGAGCGGCACGGCGTTCGGCGCCATGGCGAGCTGGGGCCTCAA  
CGACAAGCTCCGGCACGCCGGGATCATCGACATGCAGTTCAGGAGGGTGCCGTG  
CAACTTCCCGGGCCTGACCATCACGTTCCGCGTGCAGCACGGGTCCAACCCCATG  
TACCTCGCCGTGCTCATCGAGCACGAGAACCAGGACGGCGACGTGGTGCAGGCG  
GACATCATGCAGAACTCCGGCTACTGGGAGCCCATGCACGAGTCCTGGGGA  
TCCATCTGGAGGATCGACCCCAACCGCCCCTCAGGGGGCCCCTTCTCCATCCGCA  
TCACCAACGAGTCCGGCAAGCAGCTGGTGGCCAAGAACATTATCCCGGCCAACT  
ATGTCGCCGACGTCGATTACCGCTCCTACGTCCAGTATACTAATTAATCGACCGA  
CCACACGGTCCATCTTAATTAAGTGTTCTTTTGTGTTAGTGGCTCGGAGACTTGAGG  
ATTTTTCACCTCAATACCGTCGTGGTGTGTGAGCTAGTGTGTCCTGAAGATGCGTG  
GGAAATTAGAGGAGGCAAGCATCAATGTGCTCTCCCGCCCACACTGTCACTCTAC  
CATTACCAGAGTGTGTAACCAGCAAATCATGGTTATATATAATTTATACTACTAT  
ATGGAGTATCTGCTGCTATTTAACT