

## IDENTIFICATION

**Species:** *Sorghum bicolor*

**Locus:** Sobic.001G033300

**Gene Model:** Sobic.001G033300.1.p

**Description:** SbEXPA-01

**Family:** Alpha Expansin

**3D structure:**



## GENOME DATABASES

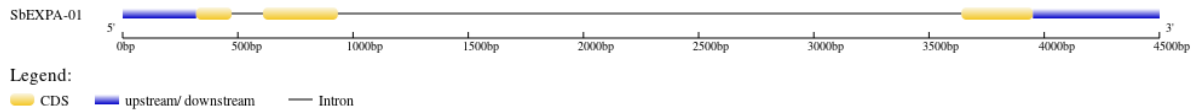
Phytozome: [https://phytozome-next.jgi.doe.gov/info/Sbicolor\\_v3\\_1\\_1](https://phytozome-next.jgi.doe.gov/info/Sbicolor_v3_1_1)

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

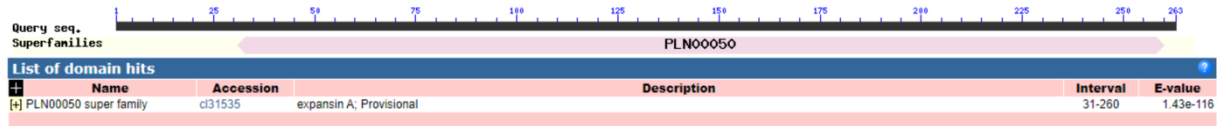
## EXTERNAL RESOURCES

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## GENE STRUCTURE



## DOMAIN ARCHITECTURE



## SEQUENCES

### Peptide

>SbEXPA-01

MAAMPALLLLLVAAMMLSPASARIPGVYGGGGWQSAHATFYGGSDASGTMGGA  
 CGYGNLYSQGYGVNNAALSTALFNEGLSCGACFELKCENQPGWRWCRPGSPSILVT  
 ATNFCPPNYALPSDDGGWCNPPRPHFDLAMPFLHIAEYRAGIVPVSYRRVPCRKSG  
 GVRFTINGFRYFNLVLITNVAGAGDIVRASVKASSTGWLTM SRNWGQNWQSNAILV  
 GQALSFRVTGSDRRTSTSWNAAPRNWQFGQTFEGKNFRV\*

### CDS (coding sequence)

>SbEXPA-01

ATGGCGGCGATGCCGGCGCTCCTGCTGCTGCTGGTGGCCGCGGCGATGATGCTCT  
 CCCAGCGTCCGCCCGCATTCGCCGGGTGTACGGCGGCGGCGGCTGGCAGAGCGC  
 GCACGCCACGTTCTACGGCGGCAGTGACGCCTCGGGCACCATGGGCGGCGCGTG  
 CGGCTATGGCAACCTGTACAGCCAGGGGTACGGCGTGAACAACGCGGCGCTGAG  
 CACGGCGCTGTTCAACGAGGGTCTGAGCTGCGGCGCGTGCTTCGAGCTCAAGTGC  
 GAGAACCAGCCC GGGTGGCGGTGGTGCCGCCCGGGAGCCCCTCCATCCTGGTG  
 ACGGCCACCAACTTCTGCCC GCCAACTACGCGCTCCCCTCCGACGACGGCGGCT  
 GGTGCAACCCGCCACGCCCGCACTTCGACCTCGCCATGCCATGTTCTCCACAT  
 CGCCGAGTACCGCGCCGGCATCGTCCCCGTCTCTACC GCCGGGTGCCATGCCGG  
 AAGTCAGGCGGCGTGCGGTTACCATCAACGGCTTCCGGTACTTCAACCTGGTGC  
 TGATCACGAACGTGGCCGGCGCGGGTGACATCGTGCGCGGAGCGTGAAGGCGT  
 CCAGCACCGGGTGGCTGACCATGTCCCGGAACTGGGGCCAGAACTGGCAGTCCA  
 ACGCCATCCTCGTCGGCCAGGCGCTCTCCTTCCGCGTCACCGGCAGCGATCGCCG  
 CACTCCACATCCTGGAACGCCGCCCGCGCAACTGGCAGTTCGGCCAGACCTTC  
 GAGGGCAAGAACTTCAGGGTCTGA

### Nucleotide

>SbEXPA-01

CAGCAGCTCACCGTCCCGGCATCAGCCGCTGAATCCGGGCAATCAATCGCGCATT  
 CCCCTCAAATCCTCCCCGGCCCGCGGCTGCTCGGCTTCTCCTTTCACCGCGCGCT  
 GTGGGCGGCATTGCCTAGTAGACGCGTAGACTACCCCTCACAAGCAGAGGCC  
 GCGCCCTGGTCTGCCTCGTGCTTCATAAATACGACCCCGCCCTTCGCCATTCCCA  
 GTCGCGCTCCACCGTCCACTCCCTGTGCCGCCGCTGCTGTTGCCACTCGCCTG  
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CCGGCGCTCCTGCTGCTGCTGGTGGCCGCGGCGATGATGCTCTCCCCAGCGTCCG  
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GACGACGGCGGCTGGTGCAACCCGCCACGCCCGCACTTCGACCTCGCCATGCCCA  
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