

## IDENTIFICATION

**Species:** *Sorghum bicolor*

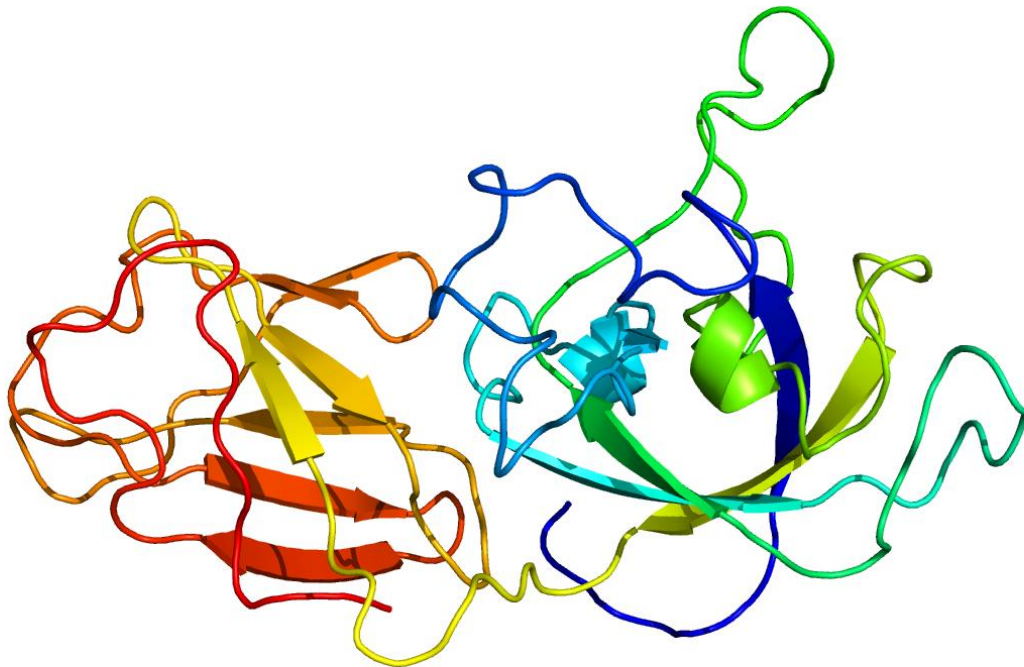
**Locus:** Sobic.006G191700

**Gene Model:** Sobic.006G191700.1.p

**Description:** SbEXPA-30

**Family:** Alpha Expansin

**3D structure:**



## GENOME DATABASES

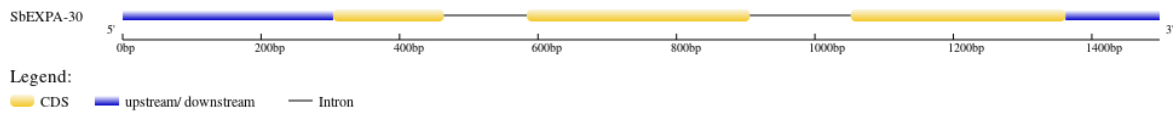
Phytozome: [https://phytozome-next.jgi.doe.gov/info/Sbicolor\\_v3\\_1\\_1](https://phytozome-next.jgi.doe.gov/info/Sbicolor_v3_1_1)

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

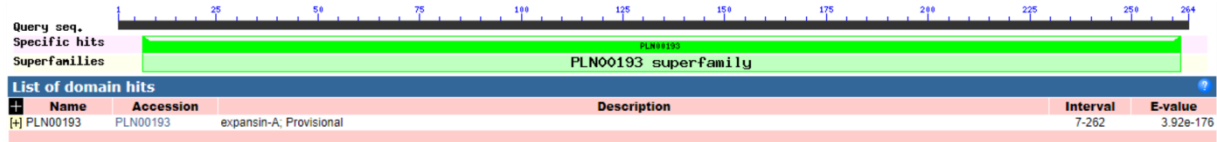
## EXTERNAL RESOURCES

-

## GENE STRUCTURE



## DOMAIN ARCHITECTURE



## SEQUENCES

### Peptide

>SbEXPA-30

MKATTGSSSVARVLVLLATTACLLWKEAACFSASGMNKA FATFYGGSDASGTMGG  
ACGYGNLYSTGYGTNTAALSTALFNDGASCGQCYRISCDYQADPRFCIRGTSVTITAT  
NLCPPNYALPNDDGGWCNPPRQHFDMAEPAWLKIGIYRGGIVPVNYQRVPCVKQGG  
VRFTINGRDYFELVLISNVGGCGSIQSASIKSRTGWMAMSRNWGVNWQSNAYLDG  
QSLSFQVTSSDGQTKTFLNVAPAGWGFGQTFATSQQFS\*

### CDS (coding sequence)

>SbEXPA-30

ATGAAGGCAACA ACTGGGTCATCATCAGTAGCTCGCGTTCCTGTTTTGCTTGCGA  
CGACGGCATGCCTCCTGTGGAAAGAAGCCGCGTGCTTCTCGGCGTCCGGCATGAA  
CAAGGCGTTCGCCACTTTCTACGGCGGTAGCGACGCTTCAGGAACGATGGGTGGA  
GCTTGTGGGTATGGGAACCTGTACTCGACGGGGTACGGCACGAACACGGCGGGC  
CTGAGCACGGCGCTGTTCAACGACGGCGCCTCGTGCGGGCAGTGCTACCGGATCT  
CGTGCGACTACCAGGCGGACCCGCGGTTCTGCATCCGCGGCACGTCGGTGACCAT  
CACGGCCACCAACCTTTGCCCTCCCAACTACGCGCTGCCCAACGACGACGGCGGC  
TGGTGCAACCCGCCCGGCAGCACTTCGACATGGCCGAGCCTGCTTGCTCAAGA  
TCGGCATCTACCGCGGCGGCATTGTTCCCGTCAACTACCAAAGGGTGCCATGTGT  
GAAGCAAGGAGGGGTGAGGTTCAACATCAACGGGCGCGACTACTTCGAGCTGGT  
GCTCATCTCCAACGTCGGCGGCTGCGGCTCCATCCAGTCGGCGTCGATCAAAGGA  
TCGAGGACCGGGTGGATGGCCATGTTCGAGGAAGTGGGGAGTCAACTGGCAGTCT  
AACGCGTACCTCGACGGGCAGAGCCTGTTCGTTCCAGGTCACCAGCAGCGACGGC  
CAGACCAAGACCTTCCTCAACGTCGCGCCCCGCGGCTGGGGGTTCGGCCAAACGT  
TCGCGACCTCGCAGCAGTTCTCTTAG

### Nucleotide

>SbEXPA-30

AGCTCTAGCTCGTGTCAGCGTCAGCTCCCCAGTAGCAGCAGCATGCGCTCCCACA  
TGCACGCACGGCCTCTGCCGGCCGCGCGCGGCGCGATGGATCGATGGTGACGATC  
ACCGCGTGCATGGCCTGTGTCTGATCCAGTCCAGAACGGACGATTGGCACCGTCC  
TCCGGGCGATCGATCACCACCTCGATCGATTCTTAGCTATTTAAACGACGTAGCC

CTGCTCAGACGTTTGGCCATTAGTGCTGTGCTGGTGGTTCATCTCCTAGCTCTCGC  
TACTAGCTTATTGCTGACAGTAACAACAATGAAGGCAACAACCTGGGTTCATCATCA  
GTAGCTCGCGTTCTTGTTTTGCTTGCACGACGGCATGCCTCCTGTGGAAAGAAG  
CCGCGTGCTTCTCGGGCGTCCGGCATGAACAAGGCGTTCGCCACTTTCTACGGCGG  
TAGCGACGCTTCAGGAACGATGGGTAAGTATGTAAGTAAGAAGATCGATCGATG  
ATCGAGACGGCAATAACATATACAGTCCAAAACCTAGCTATAATAGCTGATGCATA  
CAAATCCATGCATGCATCGATACTGTGTGTGCAGGTGGAGCTTGTGGGTATGGGA  
ACCTGTACTCGACGGGGTACGGCACGAACACGGCGGGCGCTGAGCACGGCGCTGT  
TCAACGACGGCGCCTCGTGCGGGCAGTGCTACCGGATCTCGTGCGACTACCAGGC  
GGACCCGCGGTTCTGCATCCGCGGCACGTCGGTGACCATCACGGCCACCAACCTT  
TGCCCTCCCAACTACGCGCTGCCAACGACGACGGCGGCTGGTGCAACCCGCCCC  
GGCAGCACTTCGACATGGCCGAGCCTGCTTGGCTCAAGATCGGCATCTACCGCGG  
CGGCATTGTTCCCGTCAACTACCAAAGGTTTCATATATTTGATATATATATATATTT  
CCAGTAAAAAAAAAAGCTGCATGCATGATCTGAATTCTGAATGTATGTACGTTGT  
TGATCCAATTAATTCAATTAACCTGCTACTATTACTACTGTTTGTGAATATAT  
GAACAGGGTGCCATGTGTGAAGCAAGGAGGGGTGAGGTTACCATCAACGGGCG  
CGACTACTTCGAGCTGGTGCTCATCTCCAACGTCGGCGGCTGCGGCTCCATCCAG  
TCGGCGTCGATCAAAGGATCGAGGACCGGGTGGATGGCCATGTCGAGGAACTGG  
GGAGTCAACTGGCAGTCTAACGCGTACCTCGACGGGCAGAGCCTGTCGTTCCAGG  
TCACCAGCAGCGACGGCCAGACCAAGACCTTCCTCAACGTCGCGCCC GCCGGCTG  
GGGGTTCGGCCAAACGTTTCGCGACCTCGCAGCAGTTCTCTTAGTTATTTATTAGTG  
GACGTTTTTGCTCTCTCTCGCTCGTCTTTTCGTATACATAATATGCCTCAGACTCG  
ACTCGATCGTCAATACCGTGTAAGTTTACCTGCCTTTCTTCACATGTCCCCACCC  
GCCGCGGTCAA