

## IDENTIFICATION

**Species:** *Sorghum bicolor*

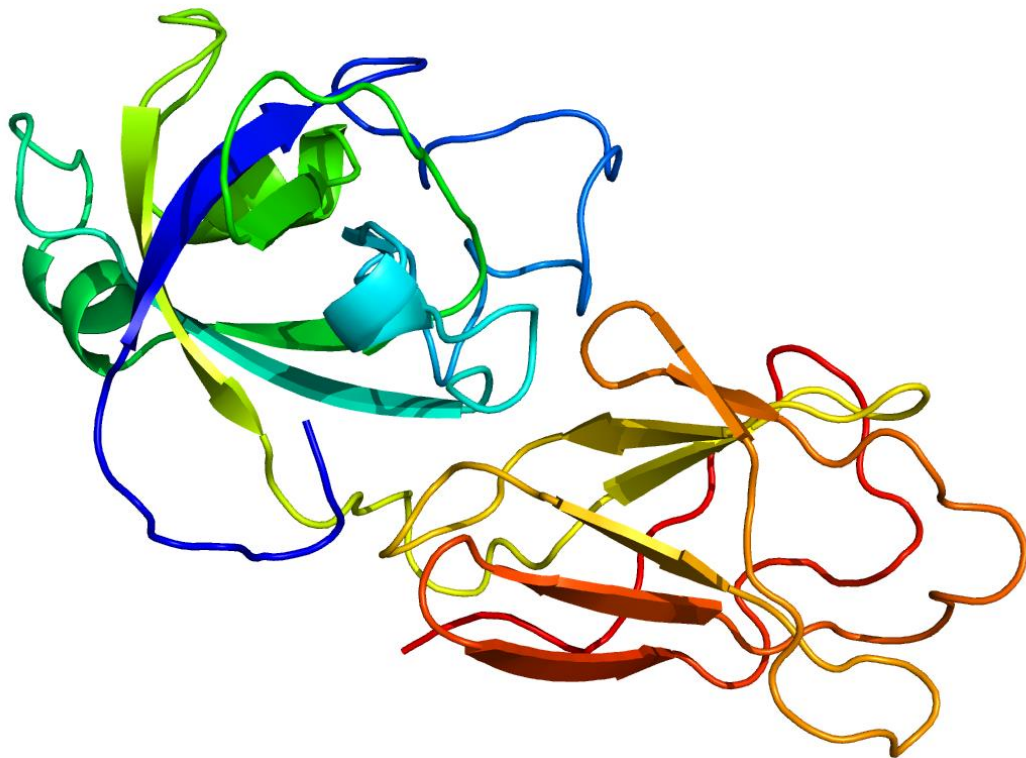
**Locus:** Sobic.007G166500

**Gene Model:** Sobic.007G166500.1.p

**Description:** SbEXPA-35

**Family:** Alpha Expansin

**3D structure:**



## GENOME DATABASES

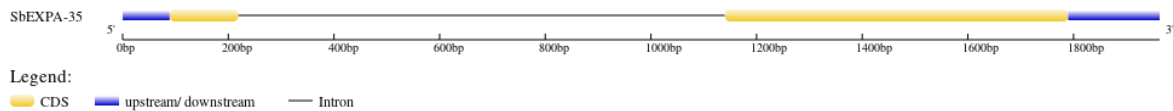
Phytozome: [https://phytozome-next.jgi.doe.gov/info/Sbicolor\\_v3\\_1\\_1](https://phytozome-next.jgi.doe.gov/info/Sbicolor_v3_1_1)

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

## EXTERNAL RESOURCES

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## GENE STRUCTURE



## DOMAIN ARCHITECTURE

Query seq. Superfamilies

List of domain hits

Name	Accession	Description	Interval	E-value
PLN00193 super family	cl33423	expansin-A; Provisional	14-257	5.84e-100

## SEQUENCES

### Peptide

>SbEXPA-35

MGKRFLHQLLAVVLALFVSPARSGDWLPATATFYGGADGSDTMGGACGYSDLYEQ  
GYGINNAALSTALFNDGASCGQCYVIIICDSSKTQWCKPGNNWVVVSATNFCPPNWD  
LPAVGDLPAGGWCAPPRPHFDMSQPAWENIGIYSAGVINVLYQRVKCWKSGGVRFTI  
AGFNGFYMVLITNVAGSGSIQSMVKGNSTDWIPMYRNWGANWHCLSGGLVGQGL  
SFALVSTGGQNLVFKDVVPAWWQFGQTYTTYQNFY\*

### CDS (coding sequence)

>SbEXPA-35

ATGGGCAAACGTTTCCTCCACCAACTGCTCGCTGTCGTCCTTGCACCTTTCGTCTC  
GCCGGCGAGATCGGGCGACTGGCTTCCGGCCACCGCCACGTTCTATGGTGGCGCT  
GACGGCTCCGACACAATGGGTGGCGCGTGTGGGTACAGCGACCTGTACGAGCAG  
GGCTACGGCATCAACAACGCAGCGCTGAGCACGGCGCTCTTCAACGACGGCGCG  
TCGTGCGGGCAGTGCTACGTCATCATCTGCGACAGCAGCAAGACCCAGTGGTGCA  
AGCCCGGCAACAACACTGGGTTGTCGTCTCTGCCACCAACTTCTGCCCGCCTAACTG  
GGACCTCCCCGCCGTCGGAGACCTCCCCGCCGGCGGCTGGTGCGCCCGCCGCGG  
CCCCACTTCGACATGTCCCAGCCCGCCTGGGAGAACATCGGCATCTACAGCGCCG  
GCGTCATCAACGTCCTCTACCAGCGAGTCAAGTGCTGGAAGAGCGGCGGCGTGC  
GCTTACCATCGCCGGCTTCAACGGCTTCTACATGGTGCTCATACCAACGTCGCG  
GGCAGCGGCTCCATTCAGAGCATGGCGGTGAAGGGCAACAGCACGGATTGGATC  
CCATGTACAGGAAC TGGGGCGCCA ACTGGCACTGCCTCTCCGGCGGGCTCGTCCG  
GACAGGGCCTTAGCTTCGCGCTCGTCTCCACCGGGCGGCCAGAACCTCGTCTTCAA  
GGACGTCGTGCCGGCGTGGTGGCAGTTCGGACAAACTTACACCACCTACCAGAAT  
TTCGACTACTAA

### Nucleotide

>SbEXPA-35

AAACCTGTCTACTGTCTCTCTAGTACCTAGCCGCAGCATCTGGGAGATCGGGACG  
GGGATCGATTGCCGGCCATTTCTGAGCGAGCAAGATGGGCAAACGTTTCCTCCAC  
CAACTGCTCGCTGTCGTCTTGCACCTTTCGTCTCGCCGGCGAGATCGGGCGACTG  
GCTTCCGGCCACCGCCACGTTCTATGGTGGCGCTGACGGCTCCGACACAATGGGT  
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GACACGCACTAACATGATTGACCGGTCCGAGCACGACACTAAAAAGCATGGTTC  
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TCTTGTACTACCCTTGAGACATGGCTGCGACGACACGGTGGCCTAGCGCAAGGCA  
TAGCTGCTGCGGTGGTGGCTCGGTGGCCTAGCGCAAGGCATAGCTGCAAGATGTG  
GCTGTGCTACGGCCACTCTCTCTCTCTCCCGCATGGCTATACGACAGCGGTGAC  
GCCTGTCTTCTCCTTGAGACAGGGCGCAACGAGCTTCTCGACTCCTCCTGAAGCC  
ATGGGCCAGCACAGGGCACGATGGGCCACCGTGCTTATCTACACGGCACGACAC  
AACTAAGGAGTCATAATGTCGTGCCTGAGTCGATAGGTTGGCACGATGGTCCGAG  
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