

## IDENTIFICATION

**Species:** *Setaria viridis*

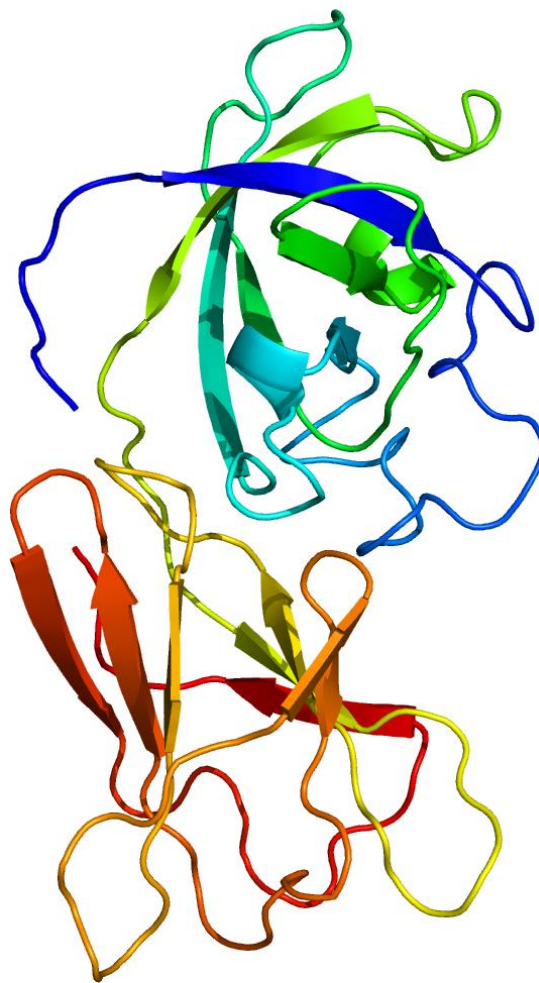
**Locus:** Sevir.9G347600

**Gene Model:** Sevir.9G347600.1.p

**Description:** SvEXPA-32

**Family:** Alpha Expansin

**3D structure:**



## GENOME DATABASES

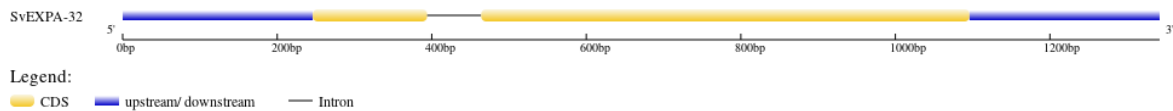
Phytozome: [https://phytozome-next.jgi.doe.gov/info/Sviridis\\_v2\\_1](https://phytozome-next.jgi.doe.gov/info/Sviridis_v2_1)

KEGG:-

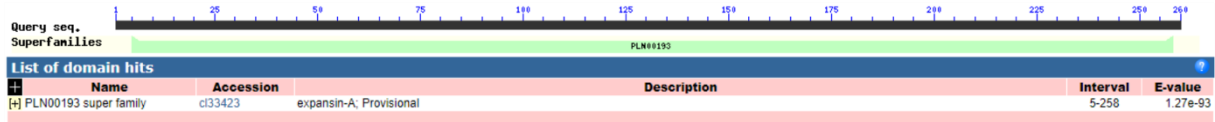
## EXTERNAL RESOURCES

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## GENE STRUCTURE



## DOMAIN ARCHITECTURE



## SEQUENCES

### Peptide

>SvEXPA-32

MASPSTAILLALVIALACAATTADARFTAMQWTPAHATFYGDETA AETMGGACGYG  
NLYATGYGTDTAALSTTLFKDGYGCGTCYQIRCAGSRWCYWGSPVITVTATNLCPP  
NWAQDTNNGGWCNPPRTHFDLSKPAFMKMAQWRAGIVPVMYRRVPCVRRGGLRF  
ALQGNPYWLLAYVMNVAGAGDVAEMWVRSARGAWVRMSHNWGASYQAFACL  
GGRSLSFKVTSYTTRQTVVATDVAPANWCLGLTYQARVNFS\*

### CDS (coding sequence)

>SvEXPA-32

ATGGCTTCTCCATCCACAGCCATCTTGTGGCCCTCGTCATCGCATTGGCCTGTGC  
GGCCACCACGGCGGACGCGAGGTTACGGCGATGCAGTGGACTCCGGCGCACGC  
CACGTTCTACGGCGACGAGACCGCGGCTGAGACCATGGGTGGGGCGTGCGGGTA  
CGGCAACCTGTACGCGACCGGGTACGGCACGGACACGGCGGGCGCTGAGCACGAC  
GCTGTTCAAGGACGGGTACGGGTGCGGGACGTGCTACCAGATCCGGTGC GCGGG  
CTCCCGCTGGTGCTACTGGGGCTCCCGGTGATCACGGTGACGGCCACCAACCTG  
TGCCCGCCCAACTGGGCGCAGGACACCAACAACGGCGGGTGGTGCAACCCGCCG  
CGCACCCACTTCGACCTCTCCAAGCCGGCCTTCATGAAGATGGCGCAGTGGCGCG  
CCGGCATCGTGCCGGTGATGTACCGCCGGGTGCCGTGCGTGAGGCGGGGCGGCCT  
CCGGTTCGCGCTCCAGGGGAACCCCTACTGGCTGCTGGCGTACGTCATGAACGTC  
GCCGGCGCCGGCGACGTCGCGGAGATGTGGGTGAGGAGCGGCGCACGCGGCGCA  
TGGGTGCGCATGAGCCAACTGGGGCGCGTTCGTACCAGGCGTTCGCGCAGCTCG  
GTGGACGGTCGCTCAGCTTCAAGGTGACGTCCTACACCACGCGGCAGACCGTCGT  
AGCCACCGACGTCGCGCCGGCCAACTGGTGCCTCGGGCTCACGTACCAGGCCCGC  
GTCAACTTCTCCTGA

### Nucleotide

>SvEXPA-32

GGTTTCTTGCCCGCACGTATGCCTAGCGAGCCGTACCAATGTCCACGGCCCGCCG  
GTGTGCGCGCACGTCGTCGCGTGAAGTCGTGAACGATGTGTTCTGCCAATCATC  
ACCAACTACCTCTTCGGTTGATCCGACGCAAGCTATAAATACACAGCAGTAGCCC  
TTGGCCATTGCATCGCCTGCAGAGTTCAGCTGCTCAAGCAAGTTACGGTAGAACG  
CCACGAGCAGAAACAAAACAGAGCCATGGCTTCTCCATCCACAGCCATCTTGT

GGCCCTCGTCATCGCATTGGCCTGTGCGGCCACCACGGCGGACGCGAGGTTACG  
GCGATGCAGTGGACTCCGGGCGCACGCCACGTTCTACGGCGACGAGACCGCGGCT  
GAGACCATGGGTACGCTGCTATCTGCCACGCTCGTTTTCTCTTGGCATTGTTGGTGT  
TTTGCTTACGGGTTTCTCCACAGGTGGGGCGTGCGGGTACGGCAACCTGTACGC  
GACCGGGTACGGCACGGACACGGCGGGCGCTGAGCACGACGCTGTTCAAGGACGG  
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TGGGGCTCCCCGGTGATCACGGTGACGGCCACCAACCTGTGCCCCGCCAACTGGG  
CGCAGGACACCAACAACGGCGGGTGGTGCAACCCGCCGCGCACCCACTTCGACC  
TCTCCAAGCCGGCCTTCATGAAGATGGCGCAGTGGCGCGCCGGCATCGTGCCGGT  
GATGTACCGCCGGGTGCCGTGCGTGAGGGCGGGGCGGCCTCCGGTTCGCGCTCCAG  
GGGAACCCCTACTGGCTGCTGGCGTACGTCATGAACGTCGCCGGCGCCGGCGACG  
TCGCGGAGATGTGGGTGAGGAGCGGCGCACGCGGCATGGGTGCGCATGAGCC  
ACAACTGGGGCGCGTTCGTACCAGGCGTTTCGCGCAGCTCGGTGGACGGTCGCTCAG  
CTTCAAGGTGACGTCCTACACCACGCGGCAGACCGTCGTAGCCACCGACGTCGCG  
CCGGCCAACTGGTGCCTCGGGCTCACGTACCAGGCCCGCGTCAACTTCTCCTGAA  
TTGAGAGGCCGGCGGGGCACGACGTTCCGTAGCAGAAGTTTGCAGGAGCTGTGA  
TACTGAGAGCGCTCTGCCCTGCTATGATGTTTCGTTGTTTTCTCTGTTTCTCGTAG  
TTCAAGTTCATTCAGATTTTCAGAGTTGGGACCGTGTGCGCGGTTGCCCCCGTCCAT  
GAGCGGTGGGTTTGACGCCAGCATTATTGATGTAAACTTTCCTTAAATTCAAATG  
CAACACTGAAATTTACTAGAGTC