

## IDENTIFICATION

**Species:** *Setaria viridis*

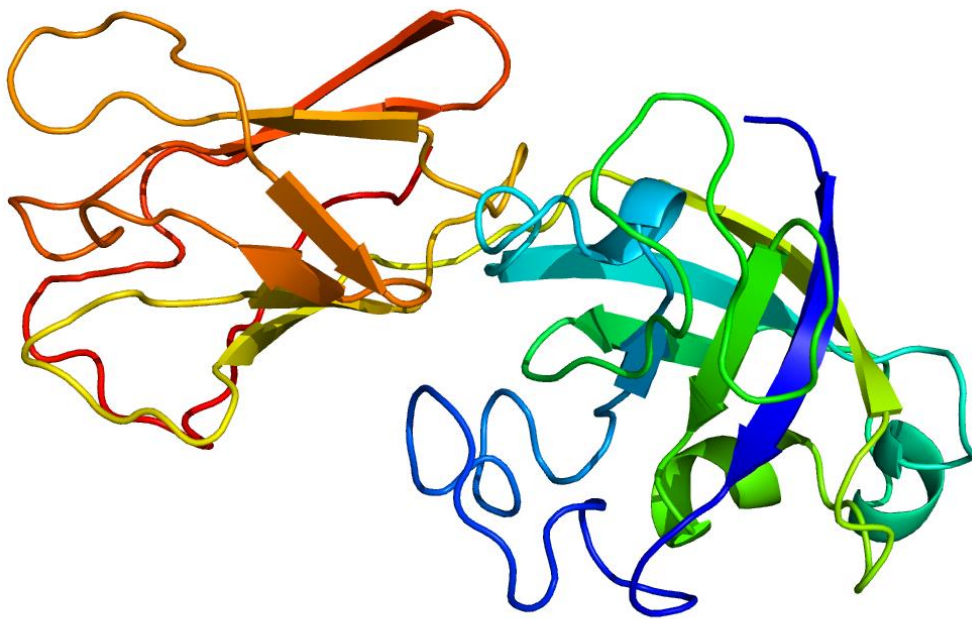
**Locus:** Sevir.9G241600

**Gene Model:** Sevir.9G241600.1.p

**Description:** SvEXPA-26

**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:-

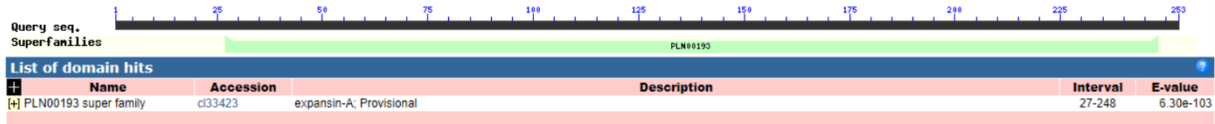
## EXTERNAL RESOURCES

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## GENE STRUCTURE



## DOMAIN ARCHITECTURE



## SEQUENCES

### Peptide

>SvEXPA-26

MDMAKSLILCTVLAACLALAAQGSPGTATFYGGPDGSGTMGGACGYDNLNAGY  
GVLNAALSQTLFNDGASCGQCYTITCDRSRTGGQYCKPGNSITVTATNLCPANYALP  
NGGWCGPGRPHFDMSQPAWENIGIYQAGVIPVLYQQVKCSRSSGGVRFSLAGSNYFLL  
VNIQNLAGSGSVGAAWVKGDKTGWIQMSRNWGANWQALAGLVGQGLSFAVTSTG  
GQYIQFLNIVPAWWQFGQTFSSNNYQNFA Y\*

### CDS (coding sequence)

>SvEXPA-26

ATGGATATGGCCAAGTCCCTGATCTTGTGCACAGTCCTTGCGGCGTGCCCTCGCGC  
TCGCCGCGGCCAGGGCTCTCCCGGCACCGCCACGTTCTACGGTGGACCCGACGG  
TTCCGGCACCATGGGTGGCGCCTGCGGGTACGACAACCTCTACAACGCCGGGTAC  
GGCGTGCTCAATGCGGCGCTGAGCCAGACGCTGTTCAACGACGGCGCGTCAATGCG  
GGCAGTGCTACACCATCACCTGCGACAGATCACGCACCGGCGGACAGTACTGCA  
AGCCCGGCAACAGCATCACCGTCACGGCCACCAACCTGTGCCCGGCCAACTACGC  
CCTGCCAACGGCGGCTGGTGC GGCCCGGGGCGCCCTCACTTCGACATGTCGCAG  
CCGGCGTGGGAGAACATCGGAATCTACCAGGCCGGCGTCAATCCCTGTCTGTACC  
AGCAGGTCAAGTGCTCCCGCAGCGGCGGCGTGCCTTCAGCCTCGCCGGCTCCAA  
CTACTTCTCTCGTCAACATCCAGAACCTCGCCGGAAGTGGCTCCGTGGGAGCC  
GCCTGGGTCAAGGGCGACAAAACGGGGTGGATCCAGATGTCCAGGAACTGGGGC  
GCCAACTGGCAGGCGCTCGCCGGGCTCGTCGGCCAGGGTCTCAGCTTCGCCGTGA  
CCAGCACCGGCGGGCAGTACATTCAGTTCCTCAACATCGTGCCGGCGTGGTGGCA  
GTTCGGCCAGACCTTCTCCAACA ACTACCAGAATTTGCCTACTGA

### Nucleotide

>SvEXPA-26

GCTCAAAAACAATTAGCATCCAACCTCCATTGCCAGCTTCCTCGTCTGCTCCCAT  
TTCCATCTCCTCTGCAGCTCTACCTGTGCATTGGCGTTGGCGTCCATGGATATGGC  
CAAGTCCCTGATCTTGTGCACAGTCCTTGC GGCGTGCTCGCGCTCGCCGCGGCC  
CAGGGCTCTCCCGGCACCGCCACGTTCTACGGTGGACCCGACGGTTCGGCACCA  
TGGGTAAGCTGCCTTGCATGCATCACATTCGCTACAAGAAAGATCTGCATAGAT  
GCACATTTTGCTTACAGTCGGCGCGCACTGATGATCCAATGCATACGTGTGTAGG

TGGCGCCTGCGGGTACGACAACCTCTACAACGCCGGGTACGGCGTGCTCAATGCG  
GCGCTGAGCCAGACGCTGTTCAACGACGGCGCGTCATGCGGGCAGTGCTACACC  
ATCACCTGCGACAGATCACGCACCGGCGGACAGTACTGCAAGCCCGGCAACAGC  
ATCACCGTCACGGCCACCAACCTGTGCCCGGCCAACTACGCCCTGCCAACGGCG  
GCTGGTGCGGCCCGGGGCGCCCTCACTTCGACATGTTCGCAGCCGGCGTGCGGAGA  
ACATCGGAATCTACCAGGCGGCGTCATCCCTGTCCTGTACCAGCAGGTCAAGTG  
CTCCCGCAGCGGCGGCGTGCGCTTCAGCCTCGCCGGCTCCAACACTTTCCTCCTCG  
TCAACATCCAGAACCTCGCCGGAAGTGGCTCCGTGGGAGCCGCCTGGGTCAAGG  
GCGACAAAACGGGGTGGATCCAGATGTCCAGGAACTGGGGCGCCAACACTGGCAGG  
CGCTCGCCGGGCTCGTCGGCCAGGGTCTCAGCTTCGCCGTGACCAGCACCGGCGG  
GCAGTACATTCAGTTCCTCAACATCGTGCCGGCGTGTTGGCAGTTCGGCCAGACC  
TTCTCCAACAACACTACCAGAAATTCGCCTACTGAAACTTTCAAGCAGGAGAGAGCG  
CTTGGTCTCATTGGCCATTTCTTGCAATTCGGTCGTATGGCGAGTACGCTCGTGAT  
TTTGACGGAGCTTGCTCTACTTGCCATTGCATTCTTGTTGATGACCGCCTGGCTCC  
GACTGCACACTGCAGGAGAAAACGGCTGGCATAACGTGGATTATTTACCCTACACT  
GTAGATACAGCATATTATGCTATTGTGTACTTGACATCTTGATATACATACATACT  
AAATTTAAATCTGTTTCCGCACTATAATAGACTTCCAAACTTGAGTAGTACGTGG  
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GTAGGCTCGAATCTCCCGGTTAAATAAGCAAGCCGTTGGTCAGGGTGCAAGGTTC  
CATTGCGTGA