

## IDENTIFICATION

**Species:** *Setaria viridis*

**Locus:** Sevir.1G008200

**Gene Model:** Sevir.1G008200.1.p

**Description:** SvEXPA-02

**Family:** Alpha Expansin

**3D structure:**



## GENOME DATABASES

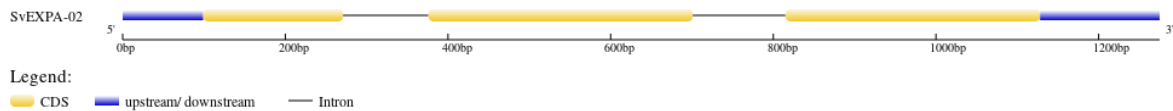
Phytozome: [https://phytozome-next.jgi.doe.gov/info/Sviridis\\_v2\\_1](https://phytozome-next.jgi.doe.gov/info/Sviridis_v2_1)

KEGG:-

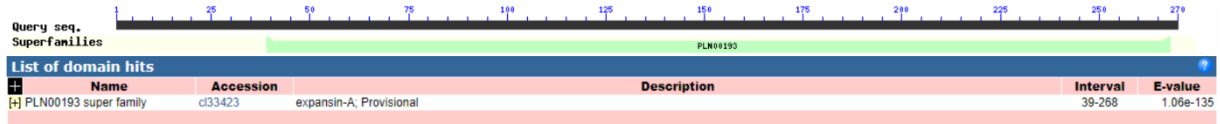
## EXTERNAL RESOURCES

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## GENE STRUCTURE



## DOMAIN ARCHITECTURE



## SEQUENCES

### Peptide

>SvEXPA-02

MAPARVLA VVLLAVVSLSAAAAADDAATGTSSSPAPVGGWLKAHATFYGGADASG  
TMGGACGYGNLYSQGYGTRTAALSAALFNDGASCGQCYKIACDRKRANPLFCCKPG  
VTVTVTATNFCPPNYGLPSDNGGWCNPPRPHFDMAQPAWEKIGVYRGGIIPVMYRR  
VPCVKRGGVRFTHDGFNLVLANVAAAGSIKSMDVKASNSNNWIPMARNWGA  
NWSLAYLTGQMLSFRVTDTDGQTLFNTNVPKGWKFGQTFASKLQFK\*

### CDS (coding sequence)

>SvEXPA-02

ATGGCTCCAGCTCGAGTTCCTTGCAGTCGTGTTGCTCGCAGTCGTCTCGTTGTCGGC  
CGCGGCCGCTGCTGATGACGCTGCCACCGGCACTTCATCGTCTCCGGCGCCGGTC  
GGAGGATGGCTGAAGGCGCATGCCACGTTCTACGGCGGCGCTGACGCCTCCGGC  
ACCATGGGCGGGCGCTTGCGGGTACGGGAATCTCTACTCGCAGGGCTACGGCACGC  
GCACGGCGGCGCTCAGTGCAGCTCTGTTCAACGATGGTGCTTCGTGCGGGCAGTG  
CTACAAGATCGCCTGCGACCGCAAGAGGGGCGAACCCGTTGTTCTGCAAGCCCGGC  
GTCACGGTCACCGTCACCGCCACCAACTTCTGCCCGCCCAACTACGGGCTGCCCA  
GCGACAACGGCGGCTGGTGCAACCCGCCGCGCCCCACTTCGACATGGCGCAGC  
CGGCGTGGGAGAAGATCGGCGTCTACCGCGGCGGCATCATCCCCGTCATGTACAG  
AAGAGTACCCTGCGTGAAGCGAGGTGGAGTGCAGTTCACGATCAACGGGCATGA  
CTACTTCAATCTTGTGCTTGTGGCCAATGTCGCAGCTGCCGGCTCCATCAAGTCCA  
TGGATGTCAAGGCCTCCA ACTCAAATAATTGGATTCCAATGGCGCGCAACTGGGG  
TGCCA ACTGGCACTCTCTTGCATACCTCACGGGACAAATGCTCTCGTTTAGGGTC  
ACTGACACTGATGGACAGACTCTTGAATTCACAAACGTGGTGCCAAAAGGATGG  
AAGTTTGGCCAAACATTTGCATCCAAGTTACAGTTCAAGTGA

### Nucleotide

>SvEXPA-02

CCTTAGTTCCATACATCCAAACAAACCAGTTCCTTGCAGTGTCCAGAAAAATCTTG  
GCTTGAGAGATATAGCTTACTTCCGTGCGGTTTCGAGCCACAGGTATGGCTCCAGC  
TCGAGTTCCTTGCAGTCGTGTTGCTCGCAGTCGTCTCGTTGTTCGGCCGCGCCGCTG  
CTGATGACGCTGCCACCGGCACTTCATCGTCTCCGGCGCCGGTTCGGAGGATGGCT  
GAAGGCGCATGCCACGTTCTACGGCGGCGCTGACGCCTCCGGCACCATGGGTAA

GTATAGCCTTTCTCTTATGCCATGACGAAAACCTGCAGTTACTGAACACCCTAGCT  
AGCTGATCGAGAGATAACGTGATGTCCGCATCATTGTATTTGGCAGGGCGGCGCTT  
GCGGGTACGGGAATCTCTACTCGCAGGGCTACGGCACGCGCACGGCGGCGCTCA  
GTGCAGCTCTGTTCAACGATGGTGCTTCGTGCGGGCAGTGCTACAAGATCGCCTG  
CGACCGCAAGAGGGCGAACCCGTTGTTCTGCAAGCCCGGCGTCACGGTCACCGTC  
ACCGCCACCAACTTCTGCCCCGCCAACTACGGGCTGCCAGCGACAACGGCGGCT  
GGTGCAACCCGCCGCGCCCCACTTCGACATGGCGCAGCCGGCGTGGGAGAAGA  
TCGGCGTCTACCGCGGCGGCATCATCCCCGTCATGTACAGAAGGTGTGTGCAGAT  
TAAAATTCCTCCTCTACTCTGATATCTCCTAATTAGGCAGCAATTGTCCAAAGAAA  
AATATCACCTGCAACAGTATCTTAATTACAAAGTTCTTGCGTGCAGAGTACCCTG  
CGTGAAGCGAGGTGGAGTGCGGTTACGATCAACGGGCATGACTACTTCAATCTT  
GTGCTTGTGGCCAATGTCGCAGCTGCCGGCTCCATCAAGTCCATGGATGTCAAGG  
CCTCCAACCTCAAATAATTGGATTCCAATGGCGCGCAACTGGGGTGCCAACCTGGCA  
CTCTCTTGCATACCTCACGGGACAAATGCTCTCGTTTAGGGTCACTGACACTGATG  
GACAGACTCTTGAATTCACAAACGTGGTGCCAAAAGGATGGAAGTTTGGCCAAA  
CATTTCATCCAAGTTACAGTTCAAGTGAGAGCTCCATACGTGATTGATATGTGA  
TATGGTCAAATACTGCTTGAATTGCATGTGTTGTATGCGTGTGTGTGTGTGTTCT  
TAGCAGATATGCCTCTTATTCTTTCTATTGTACATAAAGATATTTAAATTATTTGT  
GCATTGCTC