

## IDENTIFICATION

**Species:** *Setaria viridis*

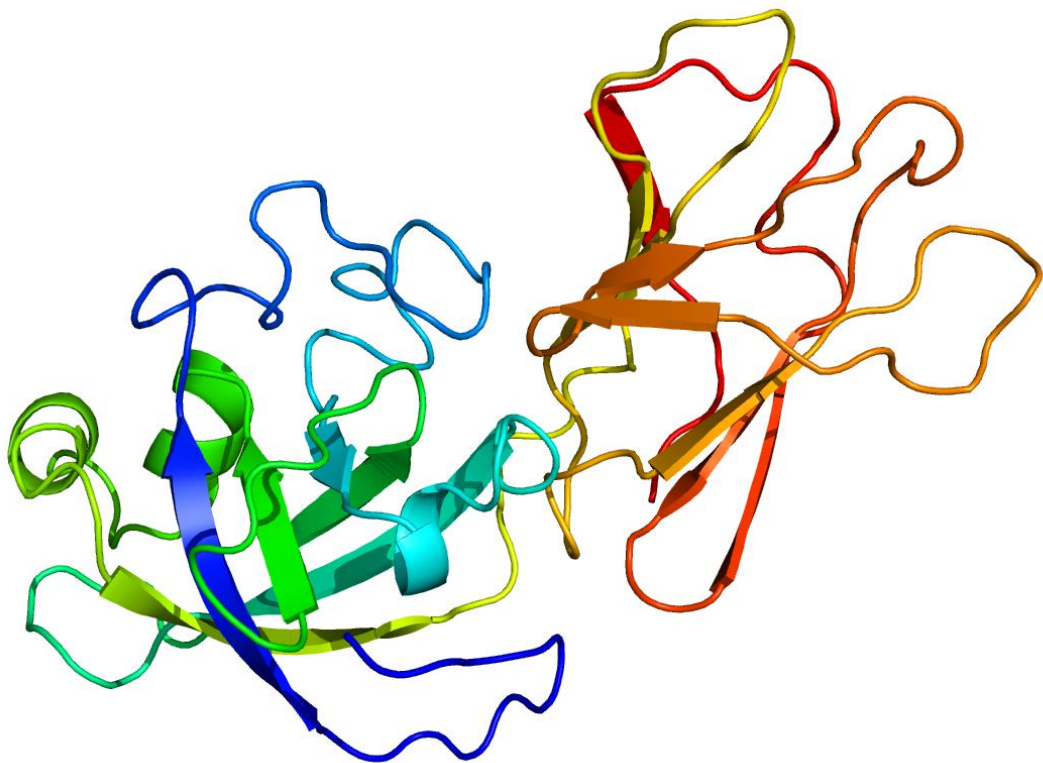
**Locus:** Sevir.9G332600

**Gene Model:** Sevir.9G332600.1.p

**Description:** SvEXPB-22

**Family:** Beta Expansin

**3D structure:**



## GENOME DATABASES

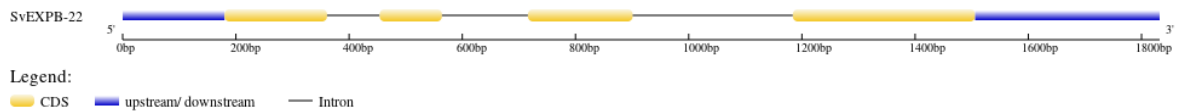
Phytozome: [https://phytozome-next.jgi.doe.gov/info/Sviridis\\_v2\\_1](https://phytozome-next.jgi.doe.gov/info/Sviridis_v2_1)

KEGG:-

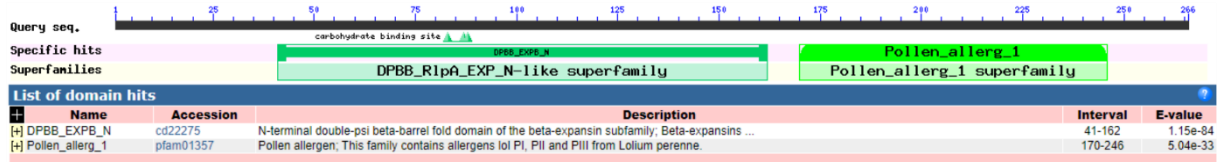
## EXTERNAL RESOURCES

-

## GENE STRUCTURE



## DOMAIN ARCHITECTURE



## SEQUENCES

### Peptide

>SvEXPB-22

MIASFKVVVALGALVFSLLVSYGSCARPVSNASAFATADPNWEAARATWYGAPTGAG  
PDDDDGGACGFKVNLPPFSAMTSCGNEPLFKDGGKGCSCYQIRCVNNPACSGNPETV  
IITDMNYYPVAKYHFDLSGTAFGAMAKPGRNDEL RHAGIIDIQFQRPVPCNYPGQKVT  
FHVEEGSNPVYLA VLVEFEDGDGDVVQVDLMEANSGSWTPMRESWGSIWRLDSNH  
RLQAPFSLRITNESGKTLVANQVIPANWVPNTYYRSIVQY\*

### CDS (coding sequence)

>SvEXPB-22

ATGATCGCCTCGTTCAAGGTGGTTGCACTTGGTGCCTGCTTCTCCCTCCTTGT  
CTCGTACGGCTCGTGCCTAGGCCGGTGAGCTTTAACGCTCTGCCTTCACCGCC  
GACCCCAACTGGGAGGCTGCCAGGGCCACCTGGTACGGCGCGCCACCGGCGCC  
GGCCCCGACGACGACGGTGGCGCCTGCGGGTTCAAGAACGTGAACCTGCCGCCG  
TTCTCGGCCATGACGTCGTGCGCAACGAGCCGCTGTTCAAGGACGGCAAGGGTT  
GCGGCTCCTGCTATCAGATACGATGCGTCAACAACCCTGCGTGCTCCGGCAACCC  
GGAGACGGTGATAATCACCGACATGAACTACTACCCGGTCGCCAAGTACCACTTC  
GACCTGAGCGGCACGGCGTTCGGCGCCATGGCCAAGCCCGGCCGCAACGACGAG  
CTCCGTCACGCCGGCATCATCGACATCCAGTTCAGAGGGTGCCCTGCAACTACC  
CGGGCCAGAAGGTGACGTTCCACGTCGAGGAGGGTCCAACCCCGTCTACCTCGC  
GGTGCTCGTCGAGTTCGAAGACGGCGACGGCGACGTGGTGCAGGTGGACCTCAT  
GGAGGCCAACTCCGGCTCGTGGACTCCGATGCGCGAGTCCTGGGGTTCCATCTGG  
AGGCTGGACTCCAACCACCGGCTGCAGGCGCCCTTCTCGCTGCGCATACCAACG  
AGTCCGGCAAGACGCTGGTGGCAAACCAGGTCATCCCGGCAAACCTGGGTGCCCA  
ACACCTACTACCGCTCCATCGTCCAGTACTAG

### Nucleotide

>SvEXPB-22

ATGTGACCCCTACCAAAGGGCGTCGGGTGCAACGGCCGTTGATGGCGATCGCGG  
CGCACTGCGTTTCGTTTCGATTCTTTTCCCGCCTATAAATACCCCGGCAATGTGCT  
TCTCCCGACCATCGAAACACAGAGCTTCTGTCTGCCAGTACTAGCAACTAACG

AGCTAGGCATCGACGATGATCGCCTCGTTCAAGGTGGTTGCACTTGGTGCACTGG  
TCTTCTCCCTCCTTGTCTCGTACGGCTCGTGCGCTAGGCCGGTGAGCTTTAACGCC  
TCTGCCTTACCGCCGACCCCAACTGGGAGGCTGCCAGGGCCACCTGGTACGGCG  
CGCCCACCGGCGCCGGCCCCGACGACGACGGTACGTCTATGAACGCCGGTGCA  
GGCGTCGCCAGATCGTATATGCTGCGTGTAATGGTGTGGACGAGATCTGTAAGC  
TTTCGTGCATGCAGGTGGCGCCTGCGGGTTCAAGAACGTGAACCTGCCGCCGTT  
TCGGCCATGACGTCGTGCGGCAACGAGCCGCTGTTCAAGGACGGCAAGGGTTGC  
GGCTCCTGCTATCAGGTAGTGCGTTACTTGGTCAGAGATCCTATTTCCAGGACGA  
CACGTGTCGTTTGCCCTCGTGGAACGGAAATGGAGATGGACCGAGAGAAAAAC  
TAGATTATTAGGCACAGTTTTTGCCTAACCATGCATCCTTGTGCTGACCTTTTTTC  
AGATACGATGCGTCAACAACCCTGCGTGCTCCGGCAACCCGGAGACGGTGATAA  
TCACCGACATGAACTACTACCCGGTCGCCAAGTACCACTTCGACCTGAGCGGCAC  
GGCGTTCGGCGCCATGGCCAAGCCCCGGCCGCAACGACGAGCTCCGTCACGCCGG  
CATCATCGACATCCAGTTCCAGAGGTCGGTAAACATTTGCACCGCTCGTTGCAAC  
ACAGAACCCTGACCGACCAATAATCTGAAGGCCCTACACACACGAACAGAAT  
CATATCTTGACCGTCTAGCTACTTTTGTGTTGGAGCCTTTGTACTTTTGTCAATCA  
ACATTTAACGACAACGACCGGTTTAAAGTAGATTTCGCACAAATATTAGTAGCGTAC  
TTCCACTTTACAATTTGGCGTTTTTTGTCATGCCTGGCGACAAATCCTTAACCCAAA  
TTAAACATAACCACATGGCATGTTTCATGTAGGGTGCCCTGCAACTACCCGGGCCAG  
AAGGTGACGTTCCACGTCGAGGAGGGCTCCAACCCCGTCTACCTCGCGGTGCTCG  
TCGAGTTCGAAGACGGCGACGGCGACGTGGTGCAGGTGGACCTCATGGAGGCCA  
ACTCCGGCTCGTGGACTCCGATGCGCGAGTCCTGGGGTTCCATCTGGAGGCTGGA  
CTCCAACCACCGGCTGCAGGCGCCCTTCTCGCTGCGCATCACCAACGAGTCCGGC  
AAGACGCTGGTGGCAAACCAGGTCATCCCGCAAACCTGGGTGCCAACACCTAC  
TACCGCTCCATCGTCCAGTACTAGCAACCAATGGTCTCTGCTGCTGGACACGGCA  
GTGGACACGATAATTCGGCATCATTGGCTCGATTAGCTTGGTACTGCATCGTTTCC  
ATGGGATTGAGGTGCCTTATTAGTTACTACTGATTAATTAGCCGGTGAATATGCC  
GGGTGTCCTTGTATGCTTTAGGTGGTGTGTGTACGTGTCTTCGGAGATTTGACGA  
CTGGGAAATGGAGGAGGCAAAGTTTGCATGTGCTTTCCCGCCCATCATTGTCGAT  
ACGCTTGTACCAGTGTGATCAAGATTATAAATTATTAACAGTATTTTGTGTGCTAC  
ATAGTATAAGTATGCTT