

IDENTIFICATION

Species: *Setaria viridis*

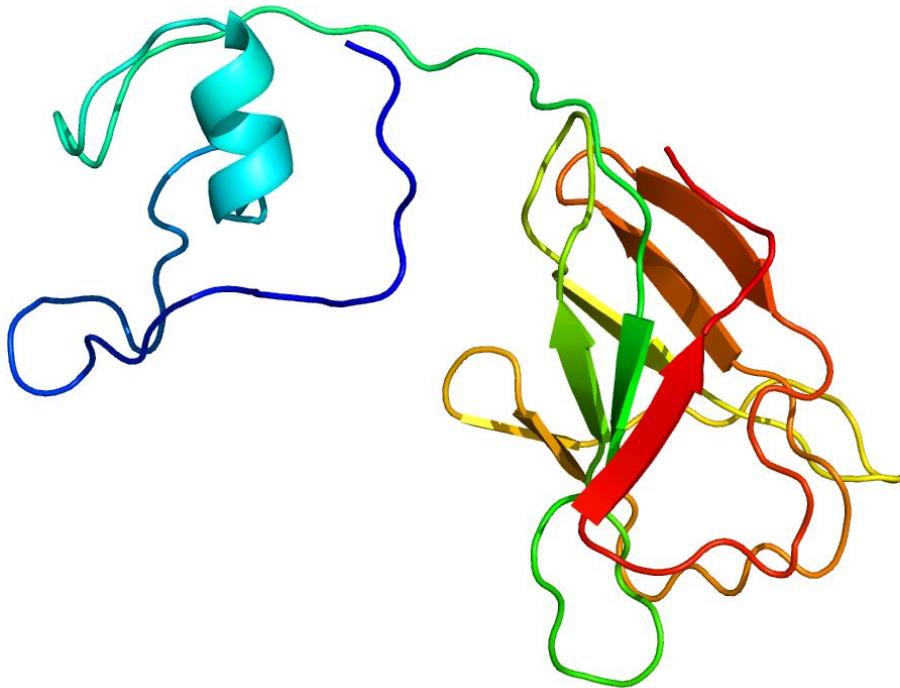
Locus: Sevir.1G010700

Gene Model: Sevir.1G010700.1.p

Description: SvEXPA-06

Family: Alpha Expansin

3D structure:



GENOME DATABASES

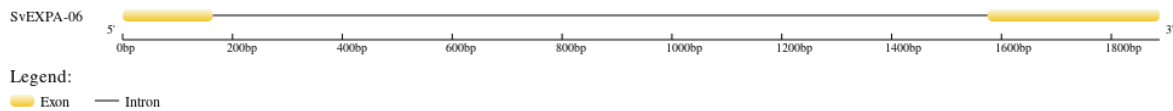
Phytozome: https://phytozome-next.jgi.doe.gov/info/Sviridis_v2_1

KEGG:-

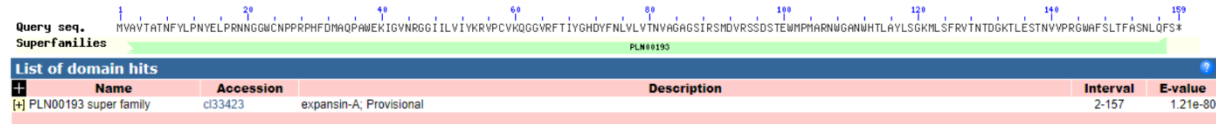
EXTERNAL RESOURCES

-

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>SvEXPA-06

MVAVTATNFYLPNYELPRNNGGWCNPPRPHFDMAQPAWEKIGVNRGGIILVIYKRV
PCVKQGGVRFTIYGHDFNLVLTNVAGAGSIRSMDVRSDDSTEWMPMARNWGAN
WHTLAYLSGKMLSFRVTNTDGKTLESTNVVPRGWAFSLTFASNLQFS*

CDS (coding sequence)

>SvEXPA-06

ATGGTGGCCGTCACGGCCACTAATTTCTACCTGCCTAACTATGAGCTCCCAAGAA
ACAATGGCGGGTGGTGAACCCGCCGCGCCCCACTTCGACATGGCCCAGCCGGC
GTGGGAGAAGATCGGCGTCAATCGCGGCGGCATCATCCTAGTCATTTATAAAAGG
GTTCCGTGCGTCAAGCAAGGTGGGGTGC GGTTACCATCTACGGGCACGACTACT
TCAACCTCGTGCTCGTGACCAACGTCGCAGGAGCCGGCTCCATCAGATCCATGGA
TGTCAGGAGCTCAGATTCCACCGAGTGGATGCCGATGGCGCGCAACTGGGGCGC
GAACTGGCACACTCTGGCATATCTCAGCGGGAAAATGCTCTCGTTCAGGGTGACC
AACACTGATGGAAAACTCTTGAGTCCACAAACGTGGTGCCACGCGGCTGGGCG
TTCAGCTTGACTTTCGCAAGCAACTTGCAGTTCAGTTGA

Nucleotide

>SvEXPA-06

ATGGTGGCCGTCACGGCCACTAATTTCTACCTGCCTAACTATGAGCTCCCAAGAA
ACAATGGCGGGTGGTGAACCCGCCGCGCCCCACTTCGACATGGCCCAGCCGGC
GTGGGAGAAGATCGGCGTCAATCGCGGCGGCATCATCCTAGTCATTTATAAAAGG
TGTGTTGACGCAAAGTCTGGGCTTCAAGCTTCTGTGTCGGCAACACGTGAAGACC
TGGGAGATCTGCTTAACTCCAGTGCAGGCTCCAAATCAGCTCGCGAAAGTGCGTG
GCGTGCCAGTCAATTTGATCTGAAATTGACAAGGTAAATGTCAAATTCTTGAGCT
GATCGGCTGCAAAGTCTTCGAGCTCATCAGTAGCGTTACATCGAAAAACACCAT
TAAATTATGTTTTCAATGTAATCTTATGGTGTGATAAAAAGAAGCATTAAATGGCA
TGTGCCATCAGCTATATGAGCTGACAGGCTAAGATAACAGAGTATTAAGCAGC
AGCCTTTAAATGATAACTTGTCTACCACGTGCATGTTCGATTAACATAACAAATCT
AATTAATATCATGAGCCGATTGATCGGACTTAACCGACACAGTATGGCAGATAGG
GTATTAACCTCGATCTGTAACTACTAAAACGCGGCAACAAGACATCGCACGCAT
AGCCATCGGCTCGATGAAGTCATCCTACTACTGAGAGGGATGGATCAGACCCAAC

CGAAACAGCATCGGCTCAACAGTAGCAGTCTGACGTTAAAGACCGAAAGGCTAG
AGGCAAAGGTAAAGATCTATCGGACCTAGTAAAGATACATCGATTAAGCATGG
AAGATCAAAGTAGTTGATACGATCACATAACTGGTGAACACTTAAACAAGACTA
GGAAGCCGATGAGAATAACCTAATTAGATCTAAGCCGTTTGAGAAGCTATGAGCA
CTTCGAAGACAAACAGATTATTGTACAAAGCCTAGAAAGCTCTATTTGAATCTAT
GCAACTCGATAACTAGACTTACACTAAGAGATTAGAATATTGGACAAATAACGTA
ATGACCGTGTGACGGTACTTACAAGCTCACCTGAGATCAAAACCGATGTAGTCTT
TCGTGCAAGAAGAACTTGTGGTTACTACTCAACTCCTAGGAGCTCCTACTCCT
AGGATTTGGCGGTGTGCCGCCAAAAAAGTAAAGATTGTATTGATTGATTGATGAT
TATTTAATACAAAGCTTATGGGTTTAAATTTATACCTGGAGCGAGCTAAAGTTCT
AATGGTTACAATGTGAACCATTACAATGCATCTAAAAACTATTAAAAATAAATCT
TCACGTTTTTTCTTATTTGGTGGAGTCAATTCCGTTTCGGATCGGATTCCTTCTTGT
CCTCTGTCAACTTCTAGAACCCGGTGTCCGTAGTTGGCCTTAGTCAAAATCTAGCA
TTAACTCTGCAATTTTCATCTGCTATCAGAATCTTGTCTTATATGTCGACTCTG
GTCAAAAACCTTGTGGCAATAGGTAAGTAACTGCCTTGTAACTCTCTTTTTTA
TTGCAGCAATTTAAACGCAGTTATGTTTGACGTAGGGTTCCGTGCGTCAAGCAAG
GTGGGGTGCGGTTACCATCTACGGGCACGACTACTTCAACCTCGTGCTCGTGAC
CAACGTGCGAGGAGCCGGCTCCATCAGATCCATGGATGTCAGGAGCTCAGATTCC
ACCGAGTGGATGCCGATGGCGCGCAACTGGGGCGCGAACTGGCACACTCTGGCA
TATCTCAGCGGGAAAATGCTCTCGTTCAGGGTGACCAACACTGATGGAAAACTC
TTGAGTCCACAAACGTGGTGCCACGCGGCTGGGCGTTCAGCTTGACTTTCGCAAG
CAACTTGCAGTTCAGTTGA