IDENTIFICATION

Species: *Setaria viridis*

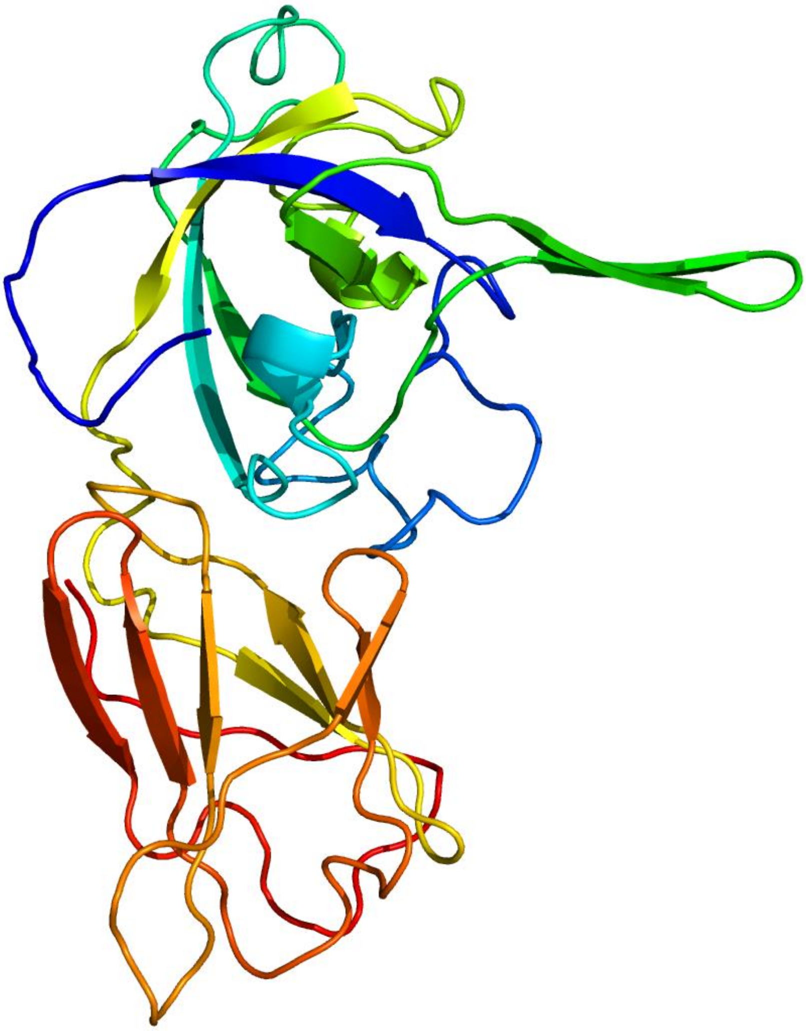
Locus: Sevir.9G389900

Gene Model: Sevir.9G389900.1.p

Description: SvEXPA-33

Family: Alpha Expansin

3D structure:



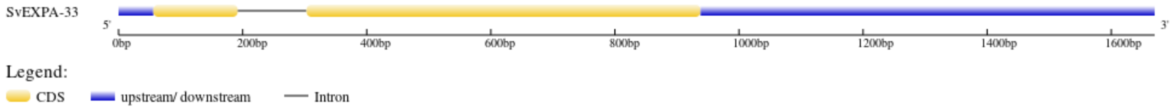
GENOME DATABASES

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

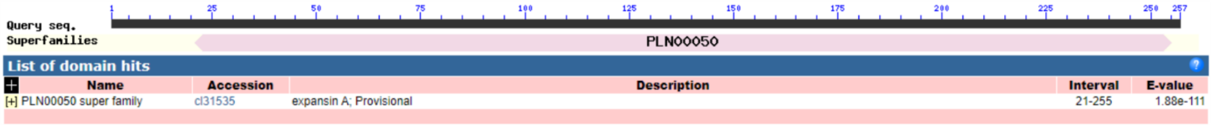
EXTERNAL RESOURCES

-

GENE STRUCTURE



DOMAIN ARCHITECTURE



List of domain hits

Name	Accession	Description	Interval	E-value
[+] PLN00050 super family	cl31535	expansin A; Provisional	21-255	1.88e-111

SEQUENCES

Peptide

>SvEXPA-33

MPSLPFLLLSLALLSLSSPAQGYGVGRWMNARATFYGGADASGTMGGACGYGDLYS
QGYGTETTALSTALFSGGLSCGACFELRCAGGGRGSSSCVPGASVVVTATNFCPPNY
ALPGGAGGWCNPPLRHFDLSQPAFLRIARYRAGVVPVAYRRVPCRRRGGIRFTVNGH
AYFALVLVANVGGAGDVRAVAVRGGARGRWRAMARNWGQNWQSGAPLDGKPLS
FRVTTSDHRSVVSYNVAPAGWAFGQTFTGGQFP*

CDS (coding sequence)

>SvEXPA-33

ATGCCATCGCTCCCGTTCCTTCTGCTCTCGCTGGCCCTGCTCTCGCTGTCCTCTCCA
GCTCAAGGCTATGGCGTCGGGCGCTGGATGAATGCGCGCGCCACCTTCTACGGCG
GCGCCGACGCCTCCGGCACGATGGGCGGCGCGTGCGGGTACGGCGACCTGTACA
GCCAGGGGTACGGCACGGAGACGACGGCGCTGAGCACGGCGCTCTTCAGCGGCG
GGCTGAGCTGCGGCGCGTGCTTCGAGCTCCGGTGCGCCGGCGGCGGCCGTGGGTC
GTCGTCGTGCGTGCCGGGGGCCTCCGTCGTGGTGACGGCCACCAACTTCTGCCCG
CCCAACTACGCGCTCCCCGGCGGCGCCGGCGGGTGGTGCAACCCGCCGCTGCGCC
ACTTCGACCTCTCGCAGCCGGCGTTCCTCCGCATCGCCCGGTACCGCGCCGGCGT
CGTCCCCGTCGCCTACCGCAGGGTGCCGTGCAGGCGGCGCGGCGGCATCCGGTTC
ACCGTCAACGGGCACGCCTACTTCGCCCTGGTGCTGGTCGCCAACGTGGGCGGCG
CTGGCGACGTGCGCGCCGTGGCCGTGAGGGGCGGCGCCCGGGGGCGGTGGCGGG
CCATGGCACGGAACTGGGGCCAGAACTGGCAGAGTGGCGCGCCCCTCGACGGGA
AGCCGCTCTCGTTCAGGGTCACCACCAGCGACCACCGCTCCGTCGTTTCCTACAA
CGTCGCGCCCGCCGGATGGGCCTTCGGCCAGACATTCACCGGGGGCCAGTTCCCG
TAA

Nucleotide

>SvEXPA-33

CGTCTCGCTAGCTTCGCTTGCTTTTGCGCCCGCTGCATTGCACGCTGACAGAGAAG
ATGCCATCGCTCCCGTTCCTTCTGCTCTCGCTGGCCCTGCTCTCGCTGTCCTCTCCA
GCTCAAGGCTATGGCGTCGGGCGCTGGATGAATGCGCGCGCCACCTTCTACGGCG
GCGCCGACGCCTCCGGCACGATGGGTGCGTCGTACAATATGGTCGTCGATCATTT
GGGCCAGATCGAGCTTAGTTTACAACCAATGTGGCTGATCAATTGTTACTGACTC

GGATTAATTAATGTTCATCTACCAGGCGGCGCGTGCGGGTACGGCGACCTGTACA
GCCAGGGGTACGGCACGGAGACGACGGCGCTGAGCACGGCGCTCTTCAGCGGCG
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CCCAACTACGCGCTCCCCGGCGGCGCCGGCGGGTGGTGCAACCCGCCGCTGCGCC
ACTTCGACCTCTCGCAGCCGGCGTTCCTCCGCATCGCCCGGTACCGCGCCGGCGT
CGTCCCCGTCGCCTACCGCAGGGTGCCGTGCAGGCGGCGCGGCGGCATCCGGTTC
ACCGTCAACGGGCACGCCTACTTCGCCCTGGTGCTGGTCGCCAACGTGGGCGGCG
CTGGCGACGTGCGCGCCGTGGCCGTGAGGGGCGGCGCCCGGGGGCGGTGGCGGG
CCATGGCACGGAACTGGGGCCAGAACTGGCAGAGTGGCGCGCCCCTCGACGGGA
AGCCGCTCTCGTTCAGGGTCACCACCAGCGACCACCGCTCCGTCGTTTCCTACAA
CGTCGCGCCCGCCGGATGGGCCTTCGGCCAGACATTCACCGGGGGCCAGTTCCCG
TAAGAAAGATCGGGCACAAGCATGACTGAATGGGATACATGCGTAAGCATGGCA
TGACTGAATGGGTTCATCTTTTACATTTGTATGAAACCTTATACGATTCGTGTATT
CCATACAAAGCTTGAAACTTCGTGACTGAGTCTGAGAGTGATAGAAGTTGTGCAG
CCTTACCTCCGGCGGTGACCACATGTCTGATGTCTCAGCAGTCAGTACAATGGCG
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CATGCAAACACACATCAGAAAGCAGTATACTGTACCAACACCAACATGACATTG
CATTTTGCAGGTACGTAGATTTGCATTCCACTAATGCACAGATCATGATCATGCTT
TGATCGGTGGTCAGGATTACGC