IDENTIFICATION

Species: *Setaria viridis*

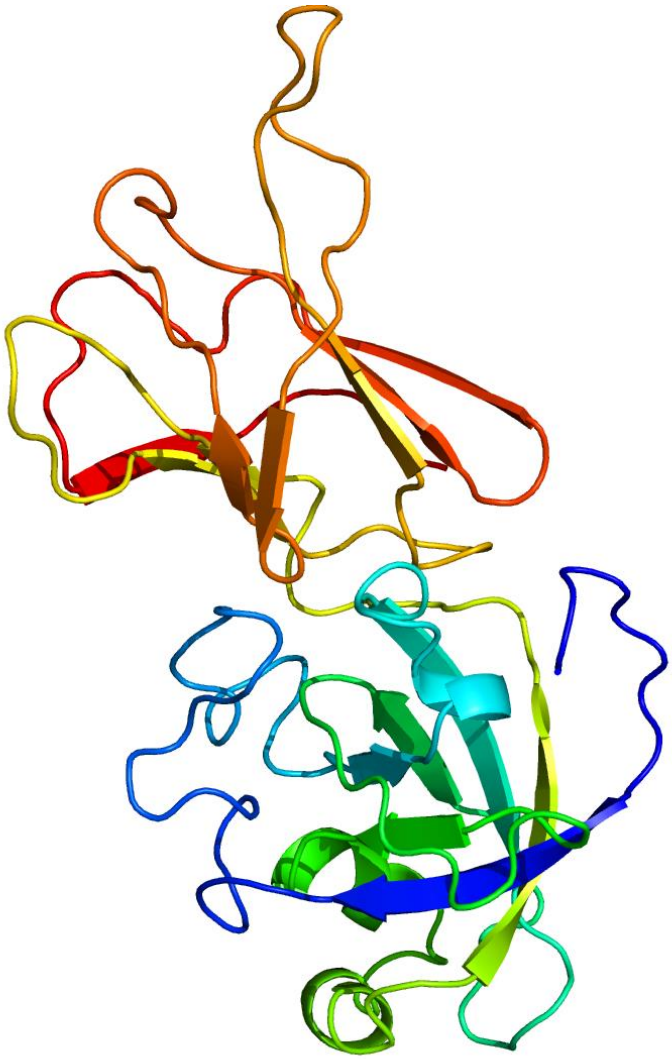
Locus: Sevir.9G581000

Gene Model: Sevir.9G581000.1.p

Description: SvEXPB-30

Family: Beta Expansin

3D structure:



GENOME DATABASES

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

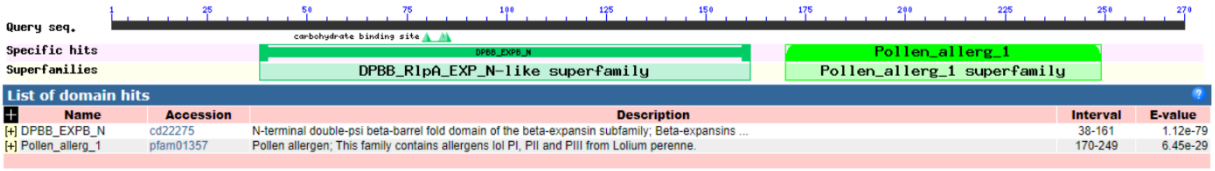
KEGG:-

EXTERNAL RESOURCES

-

GENE STRUCTURE

DOMAIN ARCHITECTURE



List of domain hits

Name	Accession	Description	Interval	E-value
[+] DPBB_EXPB_N	cd22275	N-terminal double-psi beta-barrel fold domain of the beta-expansin subfamily; Beta-expansins ...	38-161	1.12e-79
[+] Pollen_allerg_1	pfam01357	Pollen allergen; This family contains allergens lol PI, PII and PIII from Lolium perenne.	170-249	6.45e-29

SEQUENCES

Peptide

>SvEXPB-30

MGVLSSISLLLLLQAAAAAAASSVSYNDSSSSSLMQMQWGNARATWYGQPNGAGPY
DNGGACGFKKVNEYPFMSMTSCGNQPLFRDGKGCGSCYKIRCSKHPACSGRTETVVI
TDMNYFPVPAAPYHFDLSGTAFGKLAKPGRNEDLRRAGIIDIQFARVPCEFPGLKVGF
HVEEGSTQVYFAVLVEYENGDGDVVQVDLMESSRRGGGGRWTAMRESWGSIWRL
DSNHRLRPPFSIRLRSDSGKTLVARDVIPVNWRPNTFYRSFVQYS*

CDS (coding sequence)

>SvEXPB-30

ATGGGGGTGTTGTCATCAATCTCCCTCCTGCTTCTGCTTCAGGCCGCCGCCGCCGC
CGCCTCCTCCGTGAGCTACAACGACAGCAGCAGCAGCAGCTTGATGCAGATGCA
GTGGGGCAACGCCAGGGCCACCTGGTACGGCCAGCCCAACGGCGCCGGGCCCTA
CGACAACGGCGGCGCTTGCGGTTTCAAGAAGGTGAACGAGTACCCGTTCATGTCG
ATGACGTCCTGCGGCAACCAGCCGCTGTTCCGCGACGGCAAGGGATGCGGGTCCT
GCTACAAGATCAGGTGCTCCAAGCACCCCGCCTGCTCCGGCCGCACCGAGACGGT
GGTCATCACCGACATGAACTACTTCCCCGTGCCGGCGGCGCCATACCACTTCGAC
CTCAGCGGCACCGCCTTCGGCAAGCTGGCCAAGCCCGGCCGCAACGAAGACCTC
CGGCGAGCCGGCATCATCGACATCCAGTTCGCCAGAGTGCCCTGCGAGTTCCCCG
GCCTCAAGGTCGGCTTCCACGTCGAGGAGGGCTCCACACAGGTCTACTTCGCCGT
GCTCGTCGAGTACGAGAACGGCGACGGCGACGTCGTGCAGGTGGACCTCATGGA
ATCATCTCGTCGGGGCGGCGGCGGACGGTGGACGGCGATGCGCGAGTCGTGGGG
CTCCATCTGGCGCCTCGACTCCAACCACCGCCTGCGGCCGCCATTCTCCATCCGCC
TGCGCAGCGACTCCGGCAAGACGCTGGTGGCGCGAGACGTCATCCCCGTCAACTG
GAGGCCAAACACATTCTACAGATCATTCGTCCAGTACTCCTGA

Nucleotide

>SvEXPB-30

AACAAGTAGAGATAGAGAGTAGTTGCTACTAGCTAGCTAGCTCAATCGATCCGAT
CCAAGCAGGCAGCTCTCAGGTCGGTCGTAGCTGGAAACAATGGGGGTGTTGTCAT
CAATCTCCCTCCTGCTTCTGCTTCAGGCCGCCGCCGCCGCCGCCTCCTCCGTGAGC

TACAACGACAGCAGCAGCAGCAGCTTGATGCAGATGCAGTGGGGCAACGCCAGG
GCCACCTGGTACGGCCAGCCCAACGGCGCCGGGCCCTACGACAACGGTAGGTAT
CTCTTGCATTGCACTTGCTGGTTGCATTCATTCCGTTCCATTCCAGTACCACTAGA
GGTTCATCTCTACAAATGAAACATGCAGGCGGCGCTTGCGGTTTCAAGAAGGTGA
ACGAGTACCCGTTCATGTCGATGACGTCCTGCGGCAACCAGCCGCTGTTCCGCGA
CGGCAAGGGATGCGGGTCCTGCTACAAGATCAGGTGCTCCAAGCACCCCGCCTGC
TCCGGCCGCACCGAGACGGTGGTCATCACCGACATGAACTACTTCCCCGTGCCGG
CGGCGCCATACCACTTCGACCTCAGCGGCACCGCCTTCGGCAAGCTGGCCAAGCC
CGGCCGCAACGAAGACCTCCGGCGAGCCGGCATCATCGACATCCAGTTCGCCAG
AGTGCCCTGCGAGTTCCCCGGCCTCAAGGTCGGCTTCCACGTCGAGGAGGGCTCC
ACACAGGTCTACTTCGCCGTGCTCGTCGAGTACGAGAACGGCGACGGCGACGTCG
TGCAGGTGGACCTCATGGAATCATCTCGTCGGGGCGGCGGCGGACGGTGGACGG
CGATGCGCGAGTCGTGGGGCTCCATCTGGCGCCTCGACTCCAACCACCGCCTGCG
GCCGCCATTCTCCATCCGCCTGCGCAGCGACTCCGGCAAGACGCTGGTGGCGCGA
GACGTCATCCCCGTCAACTGGAGGCCAAACACATTCTACAGATCATTCGTCCAGT
ACTCCTGATCGATTCCACGATTAGTTGTTGGATTGCATCTTGCGTTCGTCGATCAT
CTGTACTAATAATTATTACTTACTTATATTACTGCCATGGATGGAGTGTATGTATG
CATGTATGTATCTACAATACTTAAGACTCTATTTAACTACCAATGCAATGGAATG
GATCTGTCCTCAATCGAAAAATACAAAT