IDENTIFICATION

Species: *Setaria viridis*

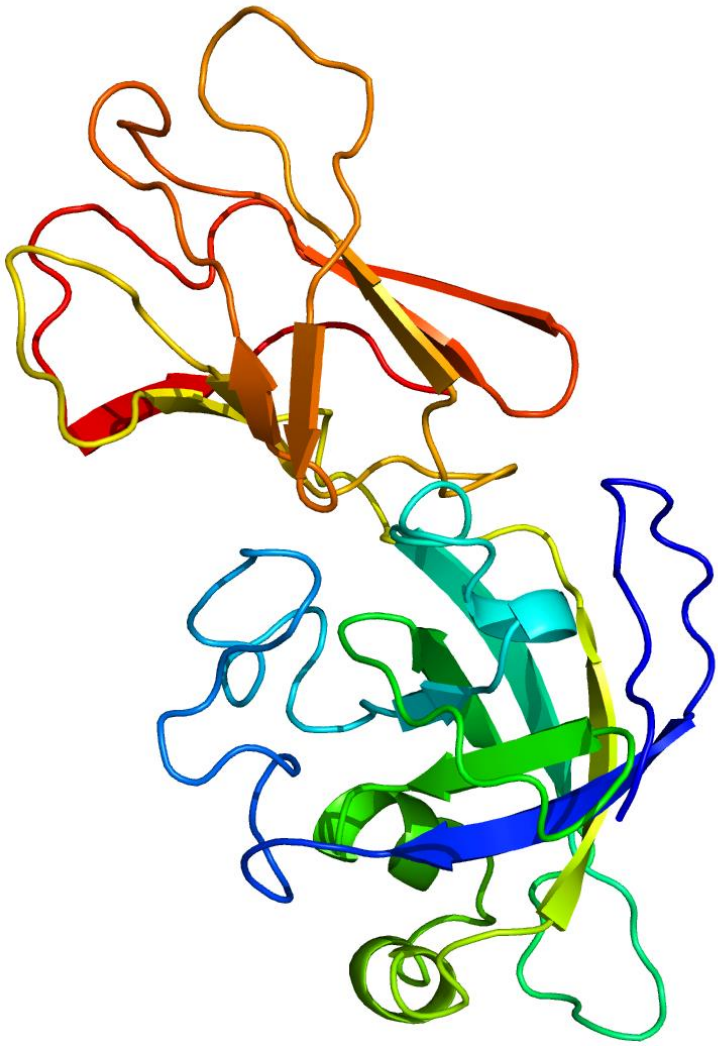
Locus: Sevir.9G332700

Gene Model: Sevir.9G332700.1.p

Description: SvEXPB-23

Family: Beta Expansin

3D structure:



GENOME DATABASES

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

KEGG:-

EXTERNAL RESOURCES

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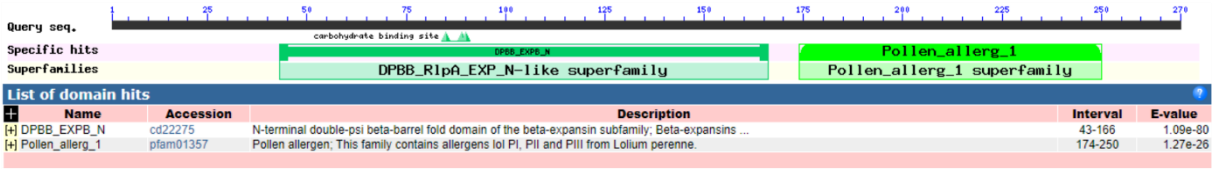
GENE STRUCTURE

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 ...	43-166	1.09e-80
[+] Pollen_allerg_1	pfam01357	Pollen allergen; This family contains allergens lol PI, PII and PIII from Lolium perenne.	174-250	1.27e-26

SEQUENCES

Peptide

>SvEXPB-23

MAARAAALVVALLAVLVAHGVRAHPELNHTSSAARQLRGSGGWLPAKATWYGAP
NGAGPDDNGGACGFKHTNQYPFMSMTSCGNQPLFKDGQGCGACYQIKCTNKNNPA
CSGQPKTVMITDMNYYPVAKYHFDLSGTAFGALARPGLNDLLRHAGIIDIEFRRVSC
DNRGLTINFHVEQGSNPVYLAVLVQYANKEGTVSQMDLLESGSRYWTPMRRSWGS
VWRLDSNHPLRAPFSLRIRGESRRTLVAYNVIPANWRPNTDYRSYVQY*

CDS (coding sequence)

>SvEXPB-23

ATGGCCGCCCGGGCAGCTGCACTCGTCGTCGCCCTCCTCGCCGTGCTTGTCGCCC
ATGGCGTCCGAGCACACCCGGAGTTGAACCACACCTCCTCCGCCGCCCGCCAACT
CCGCGGCTCCGGAGGCTGGCTCCCGGCCAAGGCCACATGGTACGGCGCGCCCAA
CGGCGCCGGCCCCGACGACAACGGTGGCGCGTGCGGGTTCAAGCACACGAACCA
GTACCCGTTCATGTCCATGACGTCGTGCGGCAACCAGCCCCTGTTCAAGGACGGC
CAGGGCTGCGGAGCATGCTACCAGATAAAGTGCACCAACAAGAACAACCCCGCC
TGCTCCGGCCAGCCCAAGACGGTGATGATCACGGACATGAACTACTACCCGGTGG
CCAAGTACCACTTCGACCTGAGCGGCACTGCGTTCGGCGCGCTGGCGCGGCCGGG
CCTGAACGACCTGCTCCGGCACGCCGGCATCATCGACATCGAGTTCCGGCGGGTG
TCCTGCGACAACCGGGGCCTGACCATCAACTTCCACGTGGAGCAGGGGTCCAACC
CCGTGTACCTCGCCGTGCTGGTCCAGTACGCCAACAAGGAAGGCACCGTGTCGCA
GATGGACCTCCTCGAGTCCGGCTCCCGCTACTGGACGCCGATGCGCCGCTCCTGG
GGCTCCGTCTGGCGCCTCGACTCCAACCACCCGCTGCGCGCGCCCTTTTCCCTGCG
CATCCGCGGCGAGTCACGCAGGACGCTCGTCGCCTACAACGTCATCCCGGCCAAC
TGGAGGCCCAACACCGACTACCGCTCCTACGTCCAGTACTAA

Nucleotide

>SvEXPB-23

CGATGTGGCGACGACCACCGATGCCCAACTGCTCGAGCTCCTTTGCCTACCTACT
TGTTGTCCGTCTATAAGTACACCGGCAGTCTCGCCCCTTACACCATCACCAAACTA
CAACACATAAGCCAACAAGTACACAGACAGAAGGTTCTTCTTGGCTTACAAGCTG

AGATAGATGGCCGCCCGGGCAGCTGCACTCGTCGTCGCCCTCCTCGCCGTGCTTG
TCGCCCATGGCGTCCGAGCACACCCGGAGTTGAACCACACCTCCTCCGCCGCCCG
CCAACTCCGCGGCTCCGGAGGCTGGCTCCCGGCCAAGGCCACATGGTACGGCGC
GCCCAACGGCGCCGGCCCCGACGACAACGGTATGTATGCGTTCGTTGCCGCTAAT
TAGCGCTGTCGTGTTAACATGATGTTGCATTGGTTTCGCATGCCGTGTGCCGTGGT
GGCTGACATTGTGTCGTGCATCCCCCGATGGTTTCTGCAGGTGGCGCGTGCGGGT
TCAAGCACACGAACCAGTACCCGTTCATGTCCATGACGTCGTGCGGCAACCAGCC
CCTGTTCAAGGACGGCCAGGGCTGCGGAGCATGCTACCAGGTATCTCCGTTTTAA
ATTATAAATTATTTTAATTTTTTTGAAAGTCAAATCATTTTATATTTGACTTAAATC
ATATGGCATCAAATAGATATACTATAAAAATATATTTAATGAAGAAACTAATAGT
ATTTATTTGGTATCTTAATATTTTATTATATAAATTTAGTCAAAGATGATATTTTG
GTTGAGGAGTAGCGGTTAAATTACCCGGATCATTTAATTCATAAGATCGCTCGGT
CAAATGTACAGACCTACACTGCCAGAGTAGTAGGAGTAGTATATTTTTTCCTCGA
AGTTAACGACATTTTTTAGTAGCCACTAGACTGAGGACTACTAGAATTAATTCTC
GAAGTCAAACTAAAACATGCAAAGCGCATCTTTTCACGTTCTCTGCTAACTTAAT
TACTAAACTCCAGATAAAGTGCACCAACAAGAACAACCCCGCCTGCTCCGGCCA
GCCCAAGACGGTGATGATCACGGACATGAACTACTACCCGGTGGCCAAGTACCA
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CGCCGTGCTGGTCCAGTACGCCAACAAGGAAGGCACCGTGTCGCAGATGGACCT
CCTCGAGTCCGGCTCCCGCTACTGGACGCCGATGCGCCGCTCCTGGGGCTCCGTC
TGGCGCCTCGACTCCAACCACCCGCTGCGCGCGCCCTTTTCCCTGCGCATCCGCG
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AGCACACTTTATTATGAGCTTTTCAGATCAGAGATCACCGTAGAAACCGCATTGC
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ACGTGTATTCATGTTTTTTGTTT