IDENTIFICATION

Species: *Setaria viridis*

Locus: Sevir.9G332200

Gene Model: Sevir.9G332200.1.p

Description: SvEXPB-20

Family: Beta Expansin

3D structure:

GENOME DATABASES

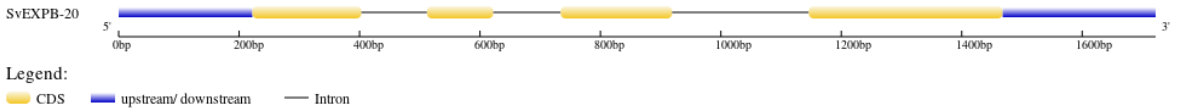
Phytozome: https://phytozome-next.jgi.doe.gov/info/Sviridis_v2_1

KEGG:-

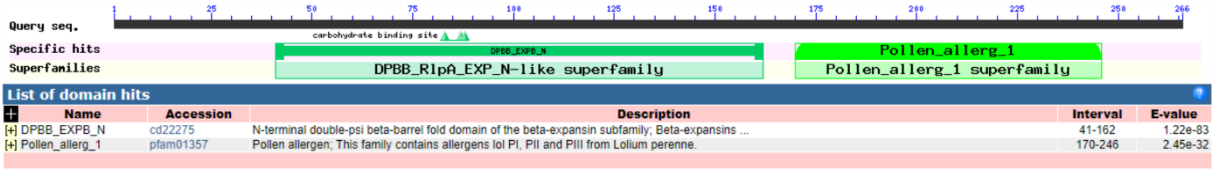
EXTERNAL RESOURCES

-

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>SvEXPB-20

MAFSTKVAALAALIFLLLVTYGSCARPVSFNASDFTADPNWEAARATWYGAPTGAG
PYDDGGACGFKNVNLPPFSSMTSCGNQPLFKDGKGCGSCYQIRCVNNAACSGNPET
VIITDMNYYPVSKYHFDLSGTAFGAMAKPGRNEELRHAGIIDIQFKRVPCNYPGQKVT
FHVEEGSNPVYLAVLVEFEDGDGDVVQVDLMEANSGYWTPMRESWGSIWRMDSNH
RLQAPFSLRITNESGRKLVANRVIPANWAPNTYYRSIIQY*

CDS (coding sequence)

>SvEXPB-20

ATGGCATTCTCCACCAAGGTAGCCGCACTTGCTGCACTGATCTTCTTGCTCCTGGT
CACGTATGGCTCGTGCGCTAGGCCGGTGAGCTTCAACGCCTCCGACTTCACCGCC
GACCCCAACTGGGAGGCCGCCAGGGCCACCTGGTACGGCGCGCCCACCGGCGCC
GGCCCATACGACGACGGTGGTGCCTGTGGATTCAAGAACGTGAACCTGCCGCCGT
TCTCGTCCATGACGTCGTGCGGCAACCAGCCCCTGTTCAAAGACGGCAAGGGCTG
CGGCTCCTGCTACCAGATACGATGCGTCAACAACGCTGCGTGCTCCGGCAACCCG
GAGACGGTGATCATCACTGACATGAACTACTACCCGGTCTCCAAGTACCACTTCG
ACCTCAGCGGCACGGCGTTCGGCGCCATGGCCAAGCCTGGGCGCAACGAAGAGC
TCCGCCACGCCGGCATCATCGACATCCAGTTCAAGAGAGTGCCCTGCAACTACCC
CGGGCAGAAGGTGACGTTCCACGTCGAGGAGGGCTCGAACCCCGTCTACCTTGCT
GTCCTCGTCGAGTTCGAAGACGGCGACGGCGACGTGGTGCAGGTGGACCTCATG
GAGGCCAACTCCGGGTACTGGACGCCGATGCGCGAGTCCTGGGGATCCATCTGG
AGGATGGACTCGAACCACCGGCTGCAGGCGCCCTTCTCGCTGCGCATCACCAACG
AGTCCGGCAGGAAGCTGGTGGCCAACCGGGTCATCCCGGCCAACTGGGCGCCTA
ACACCTACTACCGCTCCATCATCCAATACTAG

Nucleotide

>SvEXPB-20

ATGTGACCCCTACCAAAGCAAGTCGGGGCGCAACGACCGCTGTGATGGCGATCG
CGGCGCACTGCGTTCGATTCCCTTTTCCGGCCTATAAATAACCCGGCAGCGTGCC
CGTTCCAGACCATCCAAGCACACAACTTCTCCTGTCTGCCCAGTGGTAGAACAAA

CTACCCTCCCAAGCTTGCAAGCTTGTCGTTAGTAGCGCTGGTTGCCTAGCTTAGTA
AGATGGCATTCTCCACCAAGGTAGCCGCACTTGCTGCACTGATCTTCTTGCTCCTG
GTCACGTATGGCTCGTGCGCTAGGCCGGTGAGCTTCAACGCCTCCGACTTCACCG
CCGACCCCAACTGGGAGGCCGCCAGGGCCACCTGGTACGGCGCGCCCACCGGCG
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GCATGACGCTAGGCGATCTTGCCGTGCTCATGAACGGTCCATAAACTTGCGTCCA
TTTGTGCGTTCATGCAGGTGGTGCCTGTGGATTCAAGAACGTGAACCTGCCGCCG
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GCGGCTCCTGCTACCAGGTAGATTAATTGGTCAGACAAAGCTAACTCTGGAGCCT
GCGGGTAATGGAAAGGGAAAGCTCCATCACAGGTTCGAGTTTTGACACACTCTGT
TTTGATGCCTTTTTTCCAGATACGATGCGTCAACAACGCTGCGTGCTCCGGCAACC
CGGAGACGGTGATCATCACTGACATGAACTACTACCCGGTCTCCAAGTACCACTT
CGACCTCAGCGGCACGGCGTTCGGCGCCATGGCCAAGCCTGGGCGCAACGAAGA
GCTCCGCCACGCCGGCATCATCGACATCCAGTTCAAGAGGTGGGTAACATGCGCC
GCACGTTGCTCTGAGCCACAAATCCACAATCTGCAGGCCCCACCTGAACAGAATA
TAAGCTCCACTGTCTATCTACTTTGCGCTGCATGTGGAGGAGTGAAACTCCTGTA
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