

IDENTIFICATION

Species: *Sorghum bicolor*

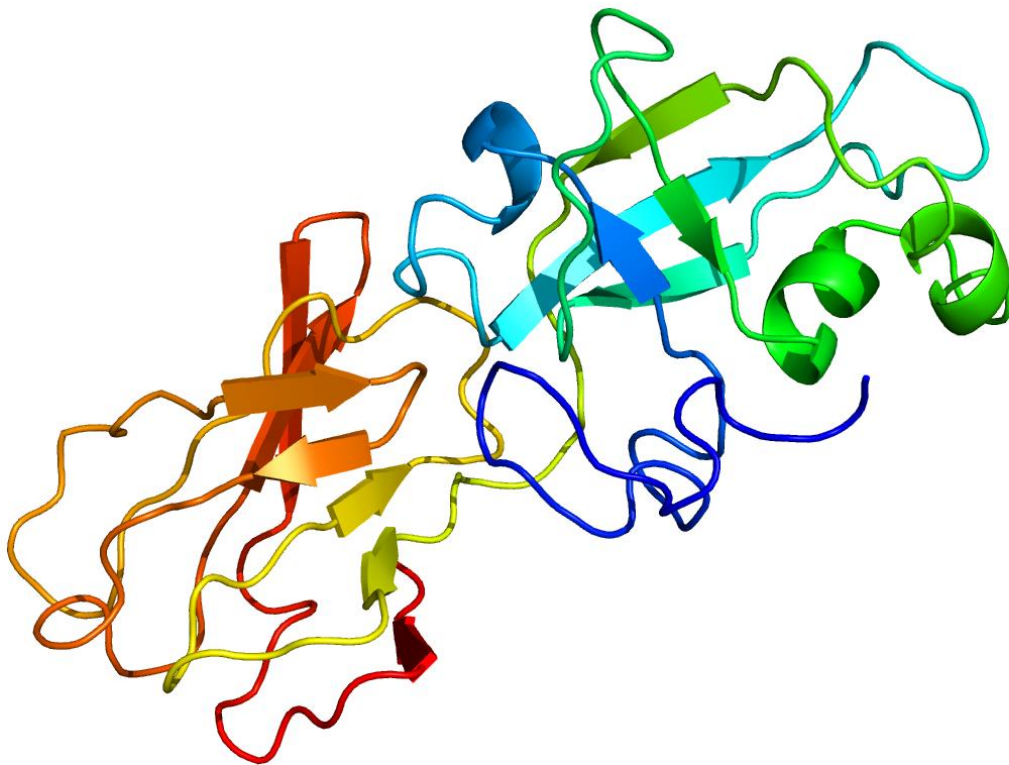
Locus: Sobic.001G539940

Gene Model: Sobic.001G539940.1.p

Description: SbEXPB-22

Family: Beta Expansin

3D structure:



GENOME DATABASES

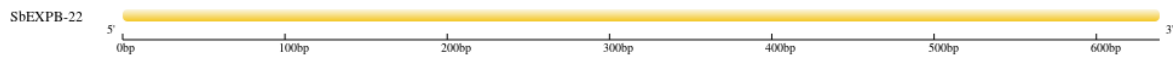
Phytozome: https://phytozome-next.jgi.doe.gov/info/Sbicolor_v3_1_1

KEGG: <https://www.genome.jp/entry/T01086>

EXTERNAL RESOURCES

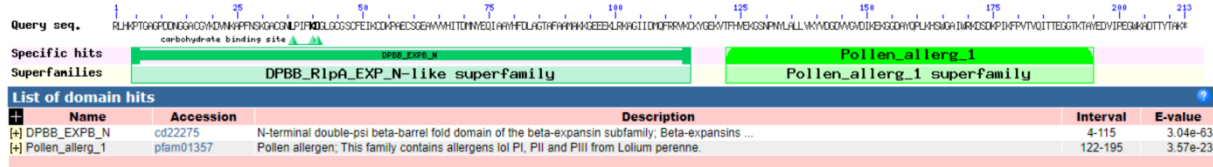
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GENE STRUCTURE



Legend:
 Exon

DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>SbEXPB-22

RLHKPTGAGPDDNGGACGYKDVNKAPFNSKGACGNLPIFKDGLGCGSCFEIKCDKP
 AECSGEAVVVHITDMNYEQIAAYHFDLAGTAFAMAkkGEEKLRKAGIIDMQFRR
 VKCKYGEKVTFHVEKGSNPNYLALLVKYVDGDVVGVDIKEKGGDAYQPLKHSWGA
 IWRKDSKPIKFPVTVQITTEGGTKTAYEDVIPEGWKADTTYTAK*

CDS (coding sequence)

>SbEXPB-22

CGATTGCACAAGCCGACGGGCGCCGGCCCCGACGACAACGGTGGTGC GTGCGGG
 TACAAGGATGTGAACAAGGCCCCCTTCAACAGCAAGGGTGC GTGCGGCAACCTC
 CCCATCTTCAAGGATGGCCTCGGCTGCGGCTCCTGCTTTGAGATCAAGTGTGACA
 AGCCAGCCGAGTGCTCCGGCGAGGCCGTGGTGGTGCACATCACGGACATGAACT
 ACGAGCAAATCGCCGCCTACCACTTCGACCTAGCCGGCACGGCGTTCGCCGCCAT
 GGCCAAGAAGGGCGAGGAGGAGAAGCTGCGGAAGGCGGGCATCATCGACATGC
 AGTTTCGTTCGGGTCAAGTGCAAGTATGGCGAAAAGGTCACCTTCCATGTGGAGAA
 GGGGAGCAACCCCAACTACCTGGCGCTGCTGGTCAAGTACGTCGACGGCGACGTT
 GTGGGGGTGGACATCAAGGAGAAGGGTGGCGACGCTTACCAGCCCCTCAAGCAC
 TCCTGGGGCGCTATCTGGAGGAAGGACAGCGACAAGCCAATCAAGTTCCCCGTC
 ACCGTCCAAATCACCACGGAGGGAGGCACCAAGACCGCCTACGAAGACGTCATC
 CCCGAAGGTTGGAAGGCCGACACCACCTACACCGCCAAATAA

Nucleotide

>SbEXPB-22

CGATTGCACAAGCCGACGGGCGCCGGCCCCGACGACAACGGTGGTGC GTGCGGG
 TACAAGGATGTGAACAAGGCCCCCTTCAACAGCAAGGGTGC GTGCGGCAACCTC
 CCCATCTTCAAGGATGGCCTCGGCTGCGGCTCCTGCTTTGAGATCAAGTGTGACA
 AGCCAGCCGAGTGCTCCGGCGAGGCCGTGGTGGTGCACATCACGGACATGAACT
 ACGAGCAAATCGCCGCCTACCACTTCGACCTAGCCGGCACGGCGTTCGCCGCCAT
 GGCCAAGAAGGGCGAGGAGGAGAAGCTGCGGAAGGCGGGCATCATCGACATGC
 AGTTTCGTTCGGGTCAAGTGCAAGTATGGCGAAAAGGTCACCTTCCATGTGGAGAA

GGGGAGCAACCCCAACTACCTGGCGCTGCTGGTCAAGTACGTCGACGGCGACGTT
GTGGGGGTGGACATCAAGGAGAAGGGTGGCGACGCTTACCAGCCCCTCAAGCAC
TCCTGGGGCGCTATCTGGAGGAAGGACAGCGACAAGCCAATCAAGTTCCCGTC
ACCGTCAAATCACCACGGAGGGAGGCACCAAGACCGCCTACGAAGACGTCATC
CCCGAAGGTTGGAAGGCCGACACCACCTACACCGCCAAATAA