

IDENTIFICATION

Species: *Sorghum bicolor*

Locus: Sobic.001G539880

Gene Model: Sobic.001G539880.1.p

Description: SbEXPB-21

Family: Beta Expansin

3D structure:



GENOME DATABASES

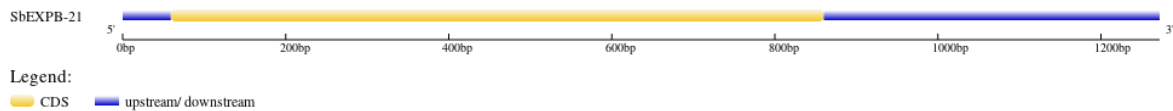
Phytozome: https://phytozome-next.jgi.doe.gov/info/Sbicolor_v3_1_1

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

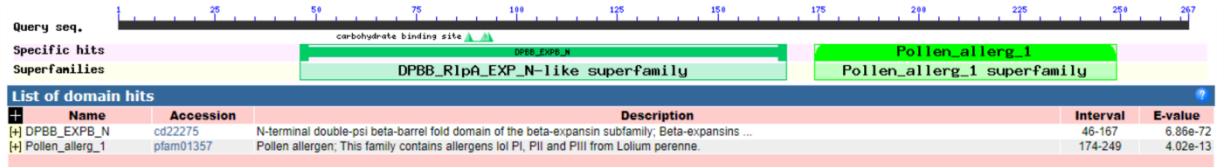
EXTERNAL RESOURCES

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GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>SbEXPB-21

MGANMMSWSMQVALVVALAFLVGGAWCGPPKVAPGKNITATYGSDWLEAKATW
YGKPTGAGPDDNGGACGYKDVNKAPFNSMGACGNLPIFKDGLGCGSCFEIKCDKPA
ECSGEAVVVHITDMNYEQIAAYHFDLAGTAFGAMAKKGEEELRKAGIIDMKFRRV
KCKYGEKVTFHVEKGSNPNYLALLVKYVDGDGDVVGVDIKEKGGDAYQPLKHSWG
AIWRKDSDKPIKFPVTVQITTEGGTKTAYEDVIPEGWKADTTYTAK*

CDS (coding sequence)

>SbEXPB-21

ATGGGAGCGAACATGATGTCGTGGTTCGATGCAGGTGGCGTTGGTGGTGGCGCTG
GCGTTTCTGGTGGGCGGCGCATGGTGCGGTCCCTCCCAAGGTTGCCCGGGCAAGA
ACATCACGGCCACCTACGGCAGCGACTGGCTGGAAGCGAAGGCAACATGGTACG
GTAAGCCAACAGGCGCCGGCCCCGACGACAACGGCGGCGCATGTGGTTACAAGG
ATGTGAACAAGGCCCTTCAACAGCATGGGCGCGTGCGGCAACCTCCCATCTT
CAAGGACGGCCTCGGCTGCGGCTCCTGCTTTGAGATCAAGTGTGACAAGCCGGCC
GAGTGCTCCGGCGAGGCCGTGGTGGTGCACATCACGGACATGAACTACGAGCAA
ATCGCCGCTACCACTTCGACCTGGCCGGCACGGCGTTCGGCGCCATGGCCAAGA
AGGGCGAGGAGGAGAAGCTGCGCAAGGCGGGCATCATCGACATGAAGTTCGGCC
GGGTCAAGTGCAAGTACGGCGAAAAGGTCACCTTCCACGTGGAGAAGGGGAGCA
ACCCAACTACCTGGCGCTGTTGGTCAAGTACGTCGACGGCGACGGTGACGTTGT
GGGGGTGGACATCAAGGAGAAGGGTGGCGACGCGTACCAGCCCCTCAAGCACTC
CTGGGGCGCTATCTGGAGGAAGGACAGCGACAAGCCAATCAAGTTTCCCGTCAC
CGTCCAAATCACCACCGAAGGAGGCACCAAGACCGCCTATGAAGACGTCATCCC
CGAAGGCTGGAAGGCCGACACCACCTACACCGCCAAATAA

Nucleotide

>SbEXPB-21

ATTCATATTCATCGCATCGTAGTTACATTACATAACCATCCACCAAACGATCAAAG
GAAGATGGGAGCGAACATGATGTCGTGGTTCGATGCAGGTGGCGTTGGTGGTGGC
GCTGGCGTTTCTGGTGGGCGGCGCATGGTGCGGTCCCTCCCAAGGTTGCCCGGGC

AAGAACATCACGGCCACCTACGGCAGCGACTGGCTGGAAGCGAAGGCAACATGG
TACGGTAAGCCAACAGGCGCCGGCCCCGACGACAACGGCGGGCGCATGTGGTTAC
AAGGATGTGAACAAGGCCCCCTTCAACAGCATGGGCGCGTGCGGCAACCTCCCC
ATCTTCAAGGACGGCCTCGGCTGCGGCTCCTGCTTTGAGATCAAGTGTGACAAGC
CGGCCGAGTGCTCCGGCGAGGCCGTGGTGGTGCACATCACGGACATGAACTACG
AGCAAATCGCCGCCTACCACTTCGACCTGGCCGGCACGGCGTTCGGCGCCATGGC
CAAGAAGGGCGAGGAGGAGAAGCTGCGCAAGGCGGGCATCATCGACATGAAGTT
CCGCCGGGTCAAGTGCAAGTACGGCGAAAAGGTCACCTTCCACGTGGAGAAGGG
GAGCAACCCCAACTACCTGGCGCTGTTGGTCAAGTACGTCGACGGCGACGGTGAC
GTTGTGGGGGTGGACATCAAGGAGAAGGGTGGCGACGCGTACCAGCCCCTCAAG
CACTCCTGGGGCGCTATCTGGAGGAAGGACAGCGACAAGCCAATCAAGTTTCCC
GTCACCGTCCAAATCACCACCGAAGGAGGCACCAAGACCGCCTATGAAGACGTC
ATCCCCGAAGGCTGGAAGGCCGACACCACCTACACCGCCAAATAAACTGTCCAA
CAGACCTAACGCTGCTCTGGGCTCGGTTGGATTGGATCCCAACTTCCAAGCAAT
GCATTACACTTACGCATGCATGGATCCATGCACAATATCTATTTTTTTACTGCTGC
TACTGCTACGACAATGTCCTCCTTTGTCCTCTCCATATATAGCTAGAGTCAGGCTC
TGCTCTCTTATATTATTATTATATAAGATAAGAAATAGGAGAGAGAGAGGAGAGA
GACCGAGTACATAATAAGTGTCTAATTAAGAGAGATTTGAGAGGCCTTTATTTT
ATATATAATAAGAATCCAAGGAGTGAGGCAAACAGCAACAAAAATGCGTTGTA
CTGTCCATGGATTTCCATGTAATCTCAATTATACCATGTCTACATTTTAATAGAAT
ACACACTTTTTAATGA