

IDENTIFICATION

Species: *Sorghum bicolor*

Locus: Sobic.001G542100

Gene Model: Sobic.001G542100.1.p

Description: SbEXPB-24

Family: Beta Expansin

3D structure:



GENOME DATABASES

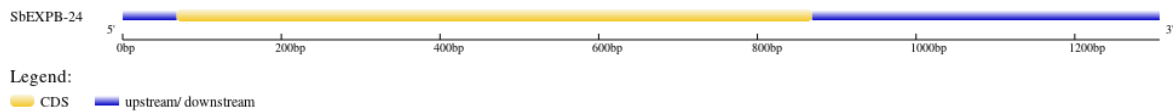
Phytozome: https://phytozome-next.jgi.doe.gov/info/Sbicolor_v3_1_1

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

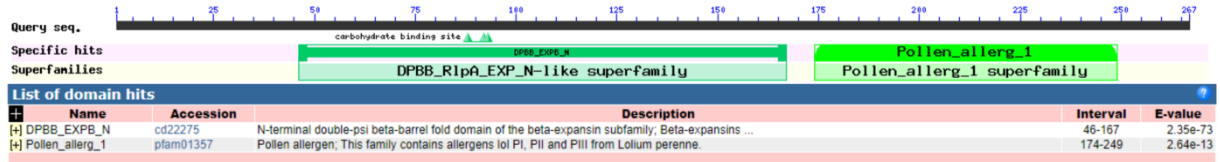
EXTERNAL RESOURCES

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GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>SbEXPB-24

MGVNMMSWSMQVVLVVALAFLVGGAWCGPPKVAPGKNITATYGSDWLEAKATW
YGKPTGAGPDDNNGGACGYKDVNKAPFNSMGACGNLPIFKDGLGCGSCFEIKCDKPA
ECSGEAVVVHITDMNYEQIAAYHFDLAGTAFGAMAKKGEEELRKAGIIDMQFRRV
KCKYGEKVTFHVEKGSNPNYLALLVKYVDGDGDVVGVDIKEKGGDAYQPLKHSWG
AVWRKDSKPIKFPVTVQITTEGGTKTAYEDVIPEGWKADTTYTAK*

CDS (coding sequence)

>SbEXPB-24

ATGGGAGTGAACATGATGTCGTGGTTCGATGCAGGTGGTGTGGTGGTGGCGCTGG
CGTTTTTGGTGGGTGGTGCATGGTGCGGTCCTCCCAAGGTTGCCCGGGCAAGAA
CATCACGGCCACCTACGGCAGCGACTGGCTGGAAGCGAAGGCGACATGGTACGG
CAAGCCGACGGGCGCCGGCCCCGACGACAACGGCGGCGCGTGCGGGTACAAGGA
TGTGAACAAGGCCCCCTTCAACAGCATGGGCGCGTGCGGCAACCTCCCCATCTTC
AAAGACGGCCTCGGCTGTGGCTCCTGCTTTGAGATCAAGTGCGACAAGCCAGCCG
AGTGCTCCGGCGAGGCTGTGGTGGTGCACATCACGGACATGAAGTACGAGCAA
TCGCCGCCTACCACTTCGACCTCGCCGGCACGGCATTTCGGTGCCATGGCCAAGAA
GGGCGAGGAGGAGAAGCTGCGCAAGGCGGGCATCATCGACATGCAATTCCGCCG
GGTCAAGTGCAAGTACGGTGAAAAGGTCACCTTCCACGTGGAGAAGGGGAGCAA
CCCCAACTACCTGGCATTGCTGGTCAAGTATGTTCGATGGCGACGGTGACGTTGTG
GGGGTGGACATCAAGGAGAAGGGTGGCGACGCTTACCAGCCCCTCAAGCACTCC
TGGGGCGCTGTTTGGAGGAAGGACAGCGACAAGCCCATCAAGTTCCCCGTCACTG
TCCAAATCACCACCGAGGGAGGCACCAAGACCGCCTACGAAGACGTCATCCCCG
AAGGATGGAAGGCCGACACCACGTACACCGCCAAATAA

Nucleotide

>SbEXPB-24

ATATTCATCGCCTCACAGTTACATACATTATTACATACCATCCACCGATCAACGAT
CCAAGGAAGAAGATGGGAGTGAACATGATGTCGTGGTTCGATGCAGGTGGTGTG
GTGGTGGCGCTGGCGTTTTTGGTGGGTGGTGCATGGTGCGGTCCTCCCAAGGTTG
CCCCGGGCAAGAACATCACGGCCACCTACGGCAGCGACTGGCTGGAAGCGAAGG

CGACATGGTACGGCAAGCCGACGGGCGCCGGCCCCGACGACAACGGCGGGCGCGT
GCGGGTACAAGGATGTGAACAAGGCCCCCTTCAACAGCATGGGCGCGTGCGGCA
ACCTCCCCATCTTCAAAGACGGCCTCGGCTGTGGCTCCTGCTTTGAGATCAAGTG
CGACAAGCCAGCCGAGTGCTCCGGCGAGGCTGTGGTGGTGCACATCACGGACAT
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GCCATGGCCAAGAAGGGCGAGGAGGAGAAGCTGCGCAAGGCGGGGCATCATCGA
CATGCAATTCCGCCGGGTCAAGTGCAAGTACGGTGAAAAGGTCACCTTCCACGTG
GAGAAGGGGAGCAACCCCAACTACCTGGCATTGCTGGTCAAGTATGTTCGATGGC
GACGGTGACGTTGTGGGGGTGGACATCAAGGAGAAGGGTGGCGACGCTTACCAG
CCCCTCAAGCACTCCTGGGGCGCTGTTTGGAGGAAGGACAGCGACAAGCCCATC
AAGTTCCCCGTCACCTGTCCAAATCACCAACCGAGGGAGGCACCAAGACCGCCTACG
AAGACGTCATCCCCGAAGGATGGAAGGCCGACACCACGTACACCGCCAAATAAG
CTATCCAGCAGACCTACCACAGATCTGGGCTGGGTTGGATTGGATCCAGCTACC
CAAGCAATGCATTACACTTATGCATGCATTGATCCATGCATAATATCTATTTTTTA
CTGCTGCTATTGTGACGAAGACAACGTCCTCCTTCATCCTCTCCATATGTAGCTAG
AGCGAGGCTTCCTTCATCCTTTCCATATATAGCTAGGGCGAGACTCCATCCGCTTT
GTTATTATATTAATAAAGAGAAGGGTGAAGAAACAGAGACCGGATAAATAATA
AGTATCTAACGAGAGATTTGGGAGGCTTTTGTATGTAATAAAAGGAGAGCGAGA
TAAACAACGGTTGTCCATAGATCTCCCATGTAATCTCAATTTTATCATGCCTACAT
TTTAAGTGAATACACATTTTTTTCAAGACTAATTGAAATTTTCAGATACGC