

IDENTIFICATION

Species: *Sorghum bicolor*

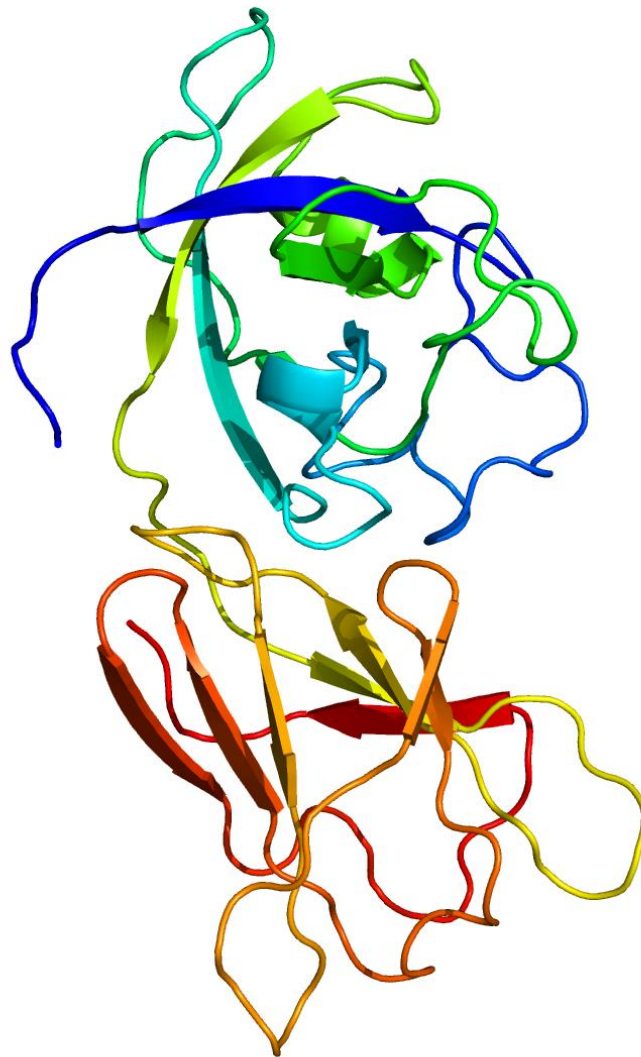
Locus: Sobic.009G173700

Gene Model: Sobic.009G173700.1.p

Description: SbEXPA-36

Family: Alpha Expansin

3D structure:



GENOME DATABASES

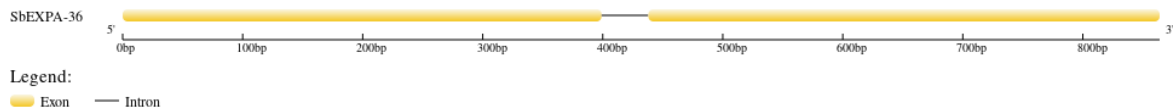
Phytozome: https://phytozome-next.jgi.doe.gov/info/Sbicolor_v3_1_1

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

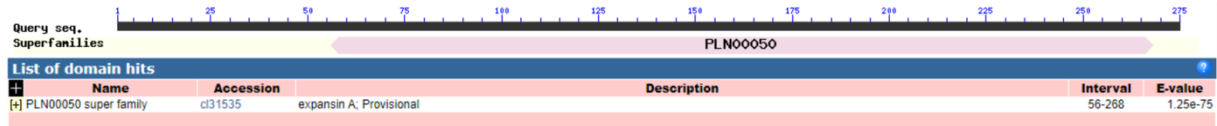
EXTERNAL RESOURCES

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GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>SbEXPA-36

MSGSWMAPRLLVSSLLVAVLAVAAADVANAGGAKPLTPGGRVVHHNHGKFTAGE
WKRAHATFYGGRDGS GTTAGACGYKDTRSEGYGVQTVAVSSVLFNGAACGGCYE
VRCVDSPDGCKPPGAAAAAALVSADSGGWCNPPREHFDLSMPAFLQIAEEKAGIVP
VSYRRVACARQGGIRYAIAGNKYFNMVTVTNVGGAGDVA AVSVKGSKRVKWTELK
RNWGVVWQTGEDLTCESLTFRVMTGDHRKATSWHVLPE DWKFGVTYQASKNF*

CDS (coding sequence)

>SbEXPA-36

ATGTCTGGTTCGTGGATGGCGCCACCGCGTCTCCTGGTGTCGTCGCTGCTGGTCGC
CGTGCTCGCGGTGGCGGCCCGCGATGTTCGCAATGCCGGCGGGCGCCAAGCCCCTG
ACGCCCGGCGGGGCGCGTGGTGCACCACAACCACGGCAAGTTCACCGCCGGCGAG
TGGAAGCGCGCCACGCGACCTTCTACGGCGGCCGGGACGGGTCCGGCACCACG
GCGGGCGCGTGCGGGTACAAGGACACGCGGTCCGAGGGCTACGGCGTGCAGACG
GTGGCCGTGAGCTCGGTGCTGTTTCGGCAATGGCGCGGCCTGCGGCGGTTGCTACG
AGGTGCGGTGCGTGGACAGCCCCGACGGGTGCAAGCCGCCCGGCGCGGCGGCGG
CGGCGGCGGCGCTGGTGTTCGGCGGACAGCGGCGGGTGGTGCAACCCGCCGCGGG
AGCACTTCGACCTGTCCATGCCGGCGTTCCTCCAGATCGCGGAGGAGAAGGCCGG
CATCGTGCCCGTCTCCTACCGGCGGGTGGCGTGC GCGAGGCAGGGCGGCATCCGG
TACGCCATCGCCGGAACAAGTACTTCAACATGGTGACGGTCACCAACGTGGGC
GGCGCCGGCGACGTGGCGGCGGTGTTCGGTGAAGGGGAGCAAGCGCGTCAAGTGG
ACGGAGCTGAAGCGCAACTGGGGGGTAGTGTGGCAGACCGGGGAGGACCTCACC
TGCAGTTCGCTGACGTTTCAGGGTGATGACCGGCGACCACCGCAAGGCCACGTCGT
GGCACGTCTCCCCGAGGACTGGAAGTTCGGCGTCACGTACCAGGCGTCCAAGA
ACTTCTAA

Nucleotide

>SbEXPA-36

ATGTCTGGTTCGTGGATGGCGCCACCGCGTCTCCTGGTGTCGTCGCTGCTGGTCGC
CGTGCTCGCGGTGGCGGCCCGCGATGTTCGCAATGCCGGCGGGCGCCAAGCCCCTG
ACGCCCGGCGGGGCGCGTGGTGCACCACAACCACGGCAAGTTCACCGCCGGCGAG

TGGAAGCGCGCCACGCGACCTTCTACGGCGGCCGGGACGGGTCCGGCACCACG
GCGGGCGCGTGCGGGTACAAGGACACGCGGTCCGAGGGCTACGGCGTGCAGACG
GTGGCCGTGAGCTCGGTGCTGTTCCGGCAATGGCGCGGCCTGCGGCGGTTGCTACG
AGGTGCGGTGCGTGGACAGCCCCGACGGGTGCAAGCCCGCCCGGCGCGGCGGCGG
CGGCGGCGGCGCTGGTGGTGACGGCGACGAACCTGTGCCCGCCCAACGAGCAGT
AGTCGGCGGACAGCGGCGGGTGGTGCAACCCGCCGCGGGAGCACTTCGACCTGT
CCATGCCGGCGTTCCTCCAGATCGCGGAGGAGAAGGCCGGCATCGTGCCCGTCTC
CTACCGGCGGGTGGCGTGCGCGAGGCAGGGCGGCATCCGGTACGCCATCGCCGG
GAACAAGTACTTCAACATGGTGACGGTCACCAACGTGGGCGGCGCCGGCGACGT
GGCGGCGGTGTCGGTGAAGGGGAGCAAGCGCGTCAAGTGGACGGAGCTGAAGCG
CAACTGGGGGGTAGTGTGGCAGACCGGGGAGGACCTCACCTGCGAGTCGCTGAC
GTTCAAGGTGATGACCGGCGACCACCGCAAGGCCACGTCGTGGCACGTCCTCCCC
GAGGACTGGAAGTTCGGCGTCACGTACCAGGCGTCCAAGA ACTTCTAA