

IDENTIFICATION

Species: *Sorghum bicolor*

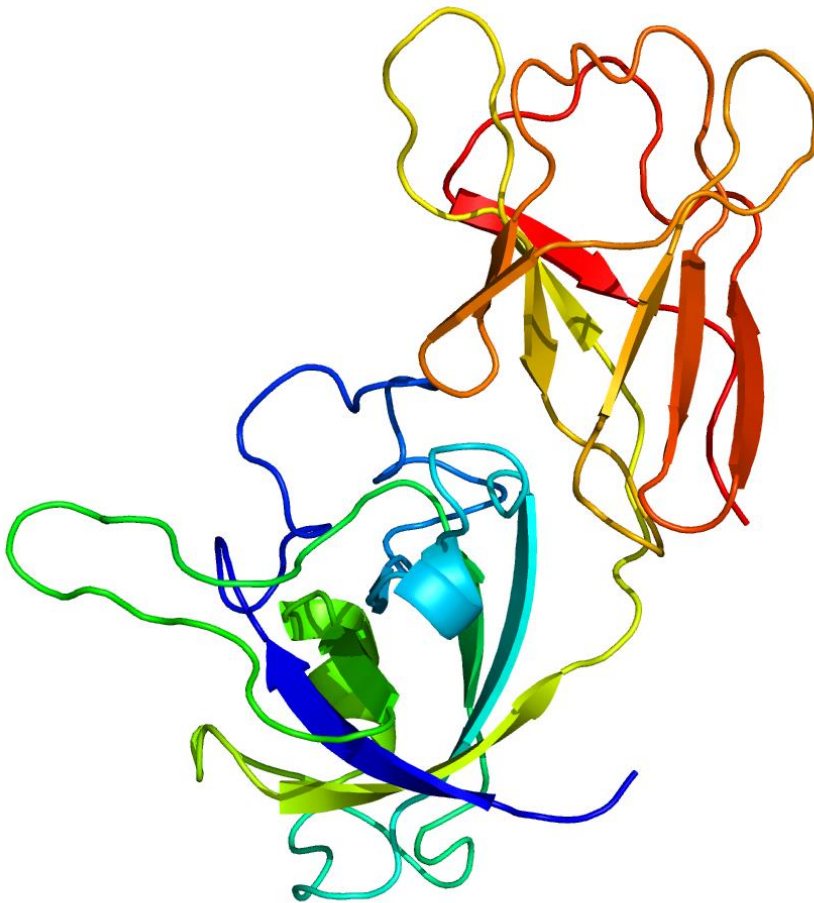
Locus: Sobic.001G238100

Gene Model: Sobic.001G238100.1.p

Description: SbEXPA-06

Family: Alpha Expansin

3D structure:



GENOME DATABASES

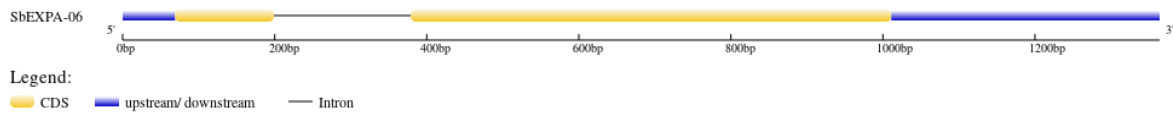
Phytozome: https://phytozome-next.jgi.doe.gov/info/Sbicolor_v3_1_1

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

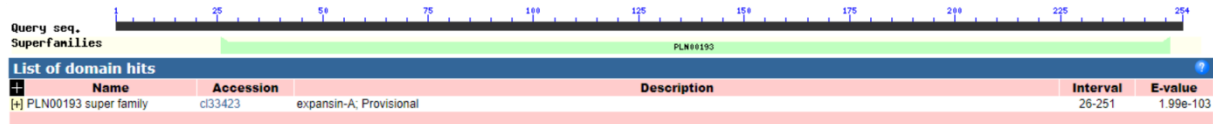
EXTERNAL RESOURCES

-

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>SbEXPA-06

MSTEMAKSLTLLTALAACLALAAADWSQGTATFYGGPDGSGTMGGACGYENLYNA
 GYGVNNAALSPVLFNDGASCGQCYVIICDASRPGGQYCKPGTWITVTATNLCPSNYA
 LPNGGWCGPGRPHFDMSQPAWEKIGIYSGGIIPVQYQQVKCWRNNGGVRFSIAGNYFF
 LLVNIQNLAGSGSVAAAWVKGDKTGWIQMSRNWGANWQAHAGLVGQGLSFAVTS
 TGGHYIQFLNVVPGWWQFGMTFNTNQNFYY*

CDS (coding sequence)

>SbEXPA-06

ATGTCCACAGAAATGGCCAAGTCCCTGACGTTGCTCACAGCGCTCGCGGCGTGCC
 TCGCGCTTGCCGCCGCCGACTGGTCTCAGGGCACCGCCACGTTCTACGGTGGACC
 CGACGGCTCCGGCACGATGGGAGGCGCATGCGGCTACGAGAACCTATAACAACGC
 CGGGTACGGCGTGAACAACGCAGCGCTGAGCCCGGTGCTGTTCAACGACGGCGC
 GTCGTGCGGGCAGTGCTACGTATCATCTGCGACGCATCCCGTCCGGGCGGGCAG
 TACTGCAAGCCCGGCACCTGGATCACCGTGACGGCCACGAACCTATGCCCATCCA
 ACTACGCGCTGCCCAACGGCGGGTGGTGCGGCCCGGGGCGGCCTCACTTCGACAT
 GTCGCAGCCGGCGTGGGAGAAGATCGGCATCTACAGCGGCGGCATCATCCCGGT
 GCAGTACCAGCAGGTCAAGTGCTGGCGCAACGGCGGCGTGCGCTTCAGCATCGC
 CGGCAACTATTACTTCTGCTCGTCAATATCCAGAACCTCGCCGGCAGCGGCTCT
 GTGGCCCGCCGCTGGGTCAAGGGCGATAAGACGGGGTGGATCCAGATGTCCAGG
 AACTGGGGCGCCAACTGGCAGGCGCACGCCGGGCTCGTCCGGCCAGGGGCTTAGC
 TTCGCCGTGACAAGCACAGGAGGGCACTACATCCAGTTCCTCAACGTCGTGCCCG
 GATGGTGGCAGTTCGGCATGACCTTCAACACAAACCAGAATTTTTACTACTAA

Nucleotide

>SbEXPA-06

ACAGCTAAATTAAGCAAACAAAATCCTCATACCATCTCCTCTACACTCTTACC
 CTCTACATGCATTGATGTCCACAGAAATGGCCAAGTCCCTGACGTTGCTCACAGC
 GCTCGCGGCGTGCCCTCGCGCTTGCCGCCGCCGACTGGTCTCAGGGCACCGCCACG
 TTCTACGGTGGACCCGACGGCTCCGGCACGATGGGTACGTAATTTTTTCGCACGT
 ACACATGCATGCATGCATTTCCGGTACATATATCTGCTAATAATCCATGCATGCAT
 GCATGTTTCGGTACATGTTGAGACAAATTAATTAATGTATACGTATATATGCTA
 AAATAATAATCCATGCATATGCATGTTTCGTATTCGTATACATATTGCAGGAGGCG

CATGCGGCTACGAGAACCTATACAACGCCGGGTACGGCGTGAACAACGCAGCGC
TGAGCCCGGTGCTGTTCAACGACGGGCGCGTCGTGCGGGCAGTGCTACGTCATCAT
CTGCGACGCATCCCGTCCGGGCGGGCAGTACTGCAAGCCCGGCACCTGGATCACC
GTGACGGCCACGAACCTATGCCCATCCAACACTACGCGCTGCCCAACGGCGGGTGGT
GCGGCCCGGGGCGGCCTCACTTCGACATGTTCGCAGCCGGCGTGGGAGAAGATCG
GCATCTACAGCGGCGGCATCATCCCGGTGCAGTACCAGCAGGTCAAGTGCTGGCG
CAACGGCGGGCGTGCGCTTCAGCATCGCCGGCAACTATTACTTCCTGCTCGTCAAT
ATCCAGAACCTCGCCGGCAGCGGCTCTGTGGCCGCCGCCTGGGTCAAGGGCGATA
AGACGGGGTGGATCCAGATGTCCAGGAACTGGGGCGCCAACCTGGCAGGGCGCACG
CCGGGCTCGTCGGCCAGGGGCTTAGCTTCGCCGTGACAAGCACAGGAGGGCACT
ACATCCAGTTCCTCAACGTCGTGCCCGGATGGTGGCAGTTCGGCATGACCTTCAA
CACAAACCAGAATTTTTACTACTAAATTTTGCAAGCAGCAGCTAGCGGAGAGTGA
GTGAACCATCTTATATAGCTATATTGCTCATGTGGTTCAGTGGAATGGAGAGTGT
GTTCTCTGTGATCATCTCTGGCTCACTCTCTCCTACGTGATCTCTCCTCCTGAAGT
GTAATGGCAAGGGTTGAATCATGGAAGATGGGCATGCATGCAACACAGACCTG
AAGGCCTAGATACCATGCATGTTTCAACACTATGCATTCTCAACACTGTATATCA
AATTTAATTAATGTTAATCCATGCATGCATGTTCTTACATGGATTTAAGCTTGAGC
TGCACCGCTCAAACATGTACGTAACCTCAAGGGCAGGTTTAGATG