

IDENTIFICATION

Species: *Sorghum bicolor*

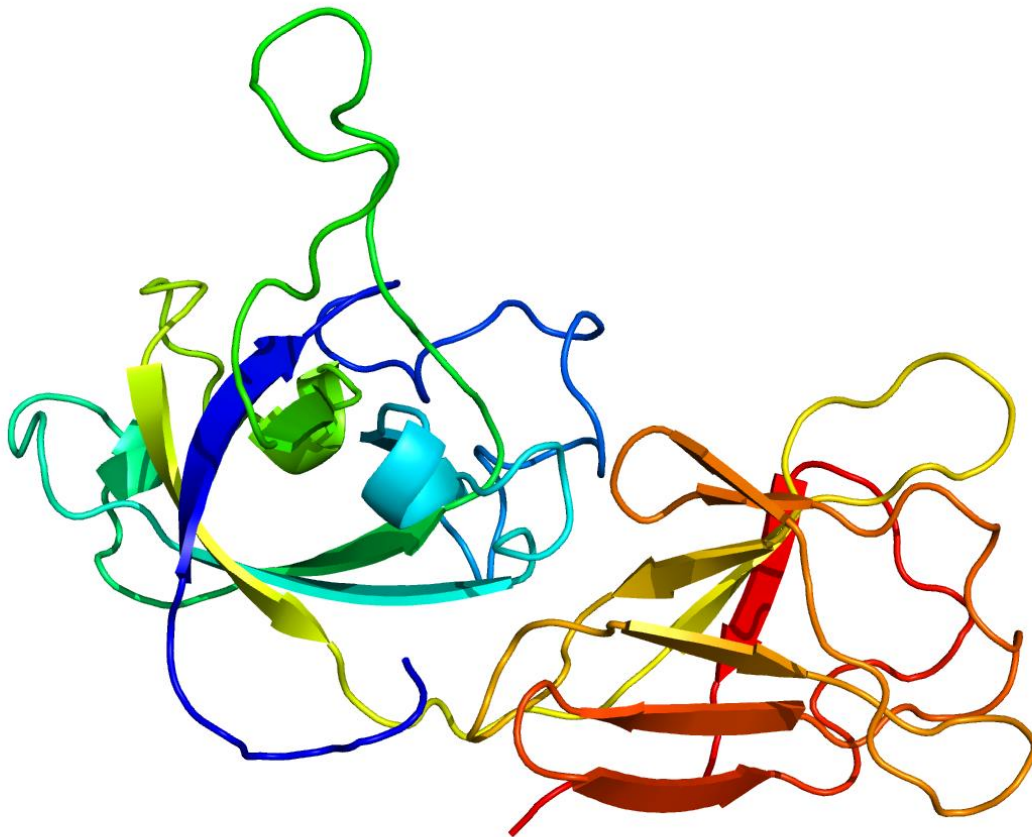
Locus: Sobic.001G499900

Gene Model: Sobic.001G499900.1.p

Description: SbEXPA-14

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>

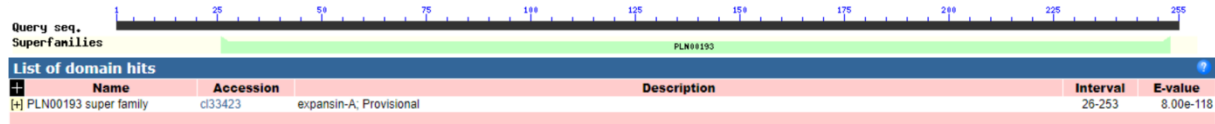
EXTERNAL RESOURCES

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GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>SbEXPA-14

MARKVDLCRLLVAAVAACLAATTVRAGWQRGSATFYGGANAAGTMGGACGYGN
LYSAGYGTDTAALSLAMFNNGAACGECYQVKCDQQNSRWCKPGVTVTVTATNLCP
ADYSQPSNDGGWCNPPRQHFDMSQPSWEKIGVYSSGGIVPVFYQRVSCSRTGGVRFTI
NGNRYFKLVLFNVAGPGSISAVQIKGSSTGWITMSRNWGANWQANSDLTRQISISFR
VTATNGRFLEFYNVAGSNWQLGQTFNGQNFY*

CDS (coding sequence)

>SbEXPA-14

ATGGCGCGCAAGGTCGACCTGTGCCGCTGCTCGTGGCTGCCGTAGCAGCCTGCC
TCGCCGCGACGACGGTCCGGGCCGGGTGGCAGAGAGGCTCGGCGACGTTCTACG
GCGGGGCCAACGCCGCCGACCAATGGGTGGCGCGTGCAGGATGGCAACCTGT
ACTCGGCGGGGTACGGCACGGACACGGCGGGCGCTGAGCTTGGCGATGTTCAACG
GCGGCGCGGCGTGCAGGGAGTGCTACCAGGTGAAGTGCAGACCAGCAGAACAGCC
GGTGGTGCAAGCCGGGCGTGACGGTGACCGTCACCGCCACCAACCTGTGCCCGG
CCGACTACTCCCAGCCCAGCAACGACGGCGGGTGGTGCAACCCGCCGCGGCAGC
ACTTCGACATGTCCCAGCCGTCGTGGGAGAAGATCGGCGTCTACAGCGGCGGCAT
CGTCCCGGTCTTCTACCAGAGGGTGTCTGCTCCAGGACCGGCGGCGTGCCTTC
ACCATCAACGGCAACAGGTAATTCAAGCTCGTGCTCATCTTCAACGTCGCCGGGC
CGGGGTCCATCAGCGCGGTGCAGATCAAGGGCTCGTCCACGGGGTGGATACCA
TGTCCCGGAAGTGGGGCGCCAAGTGGCAGGCCAACAGCGACCTCACCAGGCAGA
GCATCTCCTTCCGTGTCACCGCCACCAACGGCAGGTTCTCGAGTTCTACAACGTC
GCCGGATCCAAGTGGCAGCTGGGCCAGACCTTACCAACGGCCAAAATTTCTACT
AG

Nucleotide

>SbEXPA-14

CGCACGGCGCTGCGTCTGGGTGCGGCATGCATGATGAGCATGTGAGTGAGCCCGC
GCGCGCGTCCGGGTTCCGCGCGCGTGGTGTGATGAGCTCCGCCTCCGCCTCCCCCG
TCGGCCCGCGCGCTCCTATTTAAGCACCGCCGCGATCACCGCCCTCTCTCCCTCAC
TCATCACTCATCACCTCCACTGCGGGCACGTTGCATCGTCCAGCTCGCTCACTCCC
CCACTATCCATTGTCAACTGATCGACATGGCGCGCAAGGTCGACCTGTGCCGCT

GCTCGTGGCTGCCGTAGCAGCCTGCCTCGCCGCGACGACGGTCCGGGCCGGGTGG
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AACCCGCCGCGGCAGCACTTCGACATGTCCCAGCCGTCGTGGGAGAAGATCGGC
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CCGGCGGGCGTGCGCTTACCATCAACGGCAACAGGTACTTCAAGCTCGTGCTCAT
CTTCAACGTCGCCGGGCGGGGTCCATCAGCGCGGTGCAGATCAAGGGCTCGTCC
ACGGGGTGGATCACCATGTCCCAGAACTGGGGCGCCAACTGGCAGGCCAACAGC
GACCTCACAGGCAGAGCATCTCCTTCCGTGTCACCGCCACCAACGGCAGGTTC
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GAAGAAACAGACCACATGTGAGTTTAGTGTCGGCA