IDENTIFICATION

Species: *Sorghum bicolor*

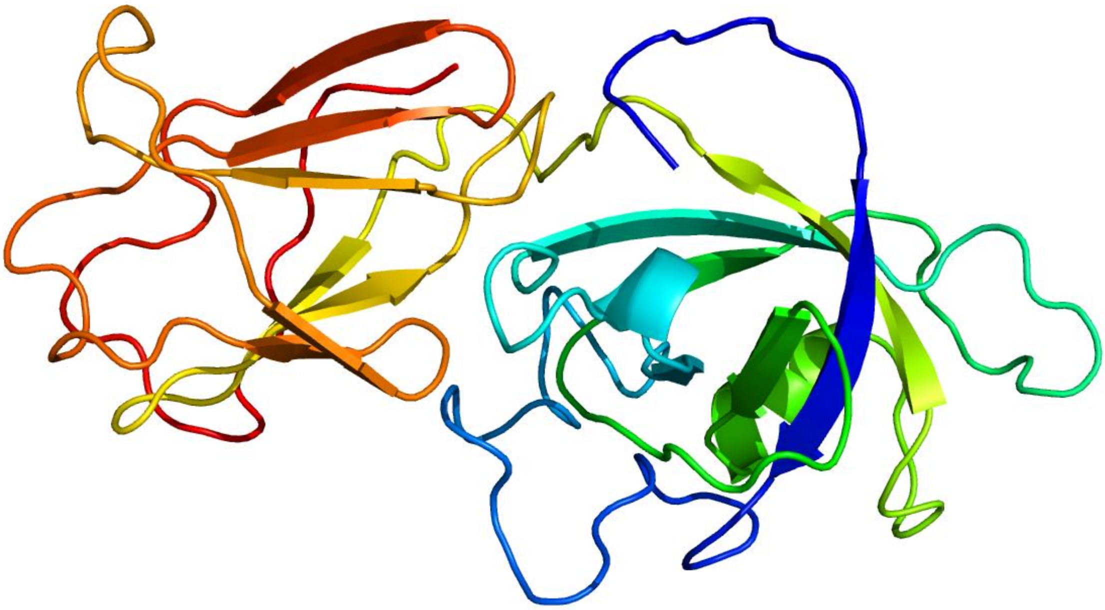
Locus: Sobic.001G237800

Gene Model: Sobic.001G237800.1.p

Description: SbEXPA-03

Family: Alpha Expansin

3D structure:



GENOME DATABASES

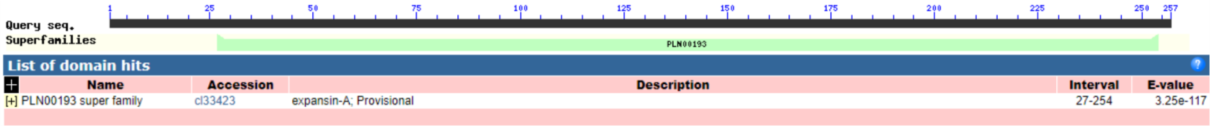
Phytozome: https://phytozome-next.jgi.doe.gov/info/Sbicolor_v3_1_1
KEGG: https://www.genome.jp/entry/T01086

EXTERNAL RESOURCES

-

GENE STRUCTURE

DOMAIN ARCHITECTURE



Name	Accession	Description	Interval	E-value
[+] PLN00193 super family	cl33423	expansin-A; Provisional	27-254	3.25e-117

SEQUENCES

Peptide

>SbEXPA-03

METPKPLAVVFLAVVALAAAPPAVDAWSRGTATFYGGGDASGTMGGACGYGNLY
ATGYGQYTAALSQVLYNDGASCGQCYQISCDPQTDARWCRQGAGPVTVSATNLCPP
NYAYSGSNGGWCNPPRAHFDMSQPAWLKIGIYQGGIIPVLYQRVPCVKQGGVRFTIT
GFNHYELVLISNVAGSGSVASAWVQGANTNRVPMSRNWGANWQSLAGIAGQALTF
GVTSTGGQSIVFPYVVPQNWVFGMSFTSNLQFSY*

CDS (coding sequence)

>SbEXPA-03

ATGGAGACACCCAAACCTCTGGCCGTCGTGTTCCTCGCGGTGGTCGCGCTGGCTG
CCGCGCCGCCGGCCGTCGACGCCTGGTCCAGGGGCACCGCCACGTTCTACGGCGG
CGGCGACGCCTCGGGCACAATGGGCGGGGCGTGCGGGTACGGCAACCTGTACGC
GACGGGCTACGGGCAGTACACGGCGGCCCTGAGCCAGGTCCTGTACAACGACGG
CGCGTCGTGCGGGCAGTGCTACCAGATCTCGTGCGACCCGCAGACGGACGCGCG
GTGGTGCCGGCAGGGCGCCGGCCCCGTCACGGTCTCGGCCACCAACCTGTGCCCG
CCCAACTACGCCTACTCCGGCAGCAACGGCGGCTGGTGCAACCCGCCGCGGGCG
CACTTCGACATGTCCCAGCCGGCGTGGCTCAAGATCGGCATCTACCAGGGCGGCA
TCATCCCGGTGCTGTACCAGCGCGTGCCCTGCGTGAAGCAGGGCGGCGTGCGCTT
CACCATCACCGGGTTCAACCACTACGAGCTGGTGCTCATCTCCAACGTCGCCGGC
AGCGGCTCGGTGGCCAGCGCCTGGGTCCAGGGCGCCAACACCAACCGGGTGCCC
ATGAGCAGGAACTGGGGCGCCAACTGGCAGTCGCTGGCCGGGATCGCCGGCCAG
GCGCTCACCTTCGGCGTCACGTCCACAGGCGGACAGAGCATCGTCTTCCCGTACG
TCGTGCCGCAGAACTGGGTGTTCGGCATGTCATTCACCAGCAACTTGCAGTTCTC
CTACTAA

Nucleotide

>SbEXPA-03

AGCGCACCCACGCCACGCCATGCACTTGCGCTTGCAGCGCCGATCTGAATCTGAT
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TCCTAGCTATTTAAGAACCGATTGTAGCAACCACATCGAAGACCACCACCTTTCG
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CCTCGGGCACAATGGGTATGTACCCACTACCGTCTACCCTACCCATGCGCTAGTA
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TCCTGTACAACGACGGCGCGTCGTGCGGGCAGTGCTACCAGATCTCGTGCGACCC
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AACCCGCCGCGGGCGCACTTCGACATGTCCCAGCCGGCGTGGCTCAAGATCGGCA
TCTACCAGGGCGGCATCATCCCGGTGCTGTACCAGCGCGTGCCCTGCGTGAAGCA
GGGCGGCGTGCGCTTCACCATCACCGGGTTCAACCACTACGAGCTGGTGCTCATC
TCCAACGTCGCCGGCAGCGGCTCGGTGGCCAGCGCCTGGGTCCAGGGCGCCAAC
ACCAACCGGGTGCCCATGAGCAGGAACTGGGGCGCCAACTGGCAGTCGCTGGCC
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