IDENTIFICATION

Species: *Sorghum bicolor*

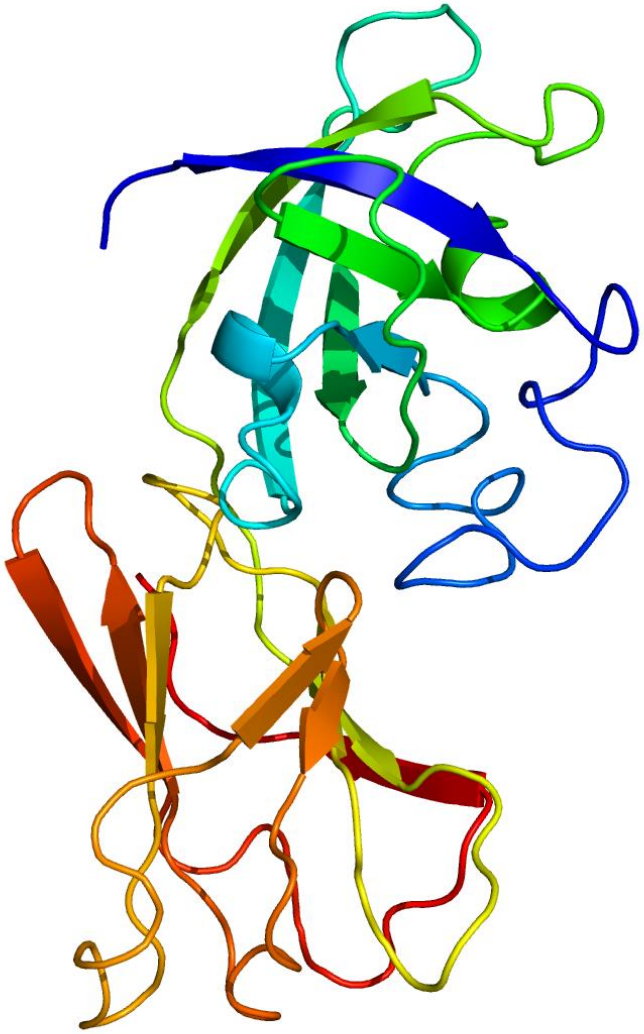
Locus: Sobic.001G314600

Gene Model: Sobic.001G314600.1.p

Description: SbEXPA-10

Family: Alpha Expansin

3D structure:



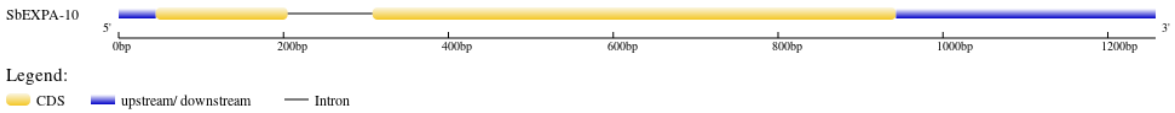
GENOME DATABASES

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

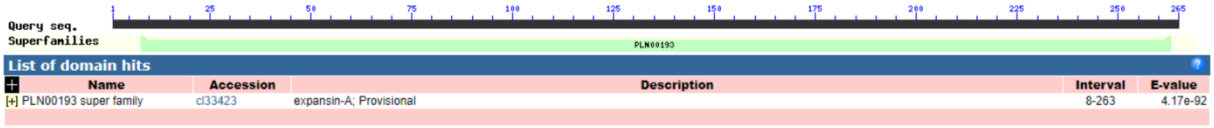
EXTERNAL RESOURCES

-

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>SbEXPA-10

MASPSTGTAFLALVIIFLALLCAATTANARFTAMQWTPAHATFYGDETAAETMGGA
CGYGNLYATGYGTDTAALSTTLFKDGHGCGTCYQIRCTGSPWCYAGSPSITVTATNL
CPPNWAQDTNNGGWCNPPRTHFDLSKPAFMKMAQWRAGIVPVMYRRVPCVRRGG
LRFALQGNPYWLLAYVMNVGGAGDVVEMWVKSGTSSCAWIRMTHNWGAAYQAF
AQLGGKALSFKVTSYTTRQTIVATNVAPANWGLGLTYQARVNFS*

CDS (coding sequence)

>SbEXPA-10

ATGGCTTCTCCCTCCACAGGCACGGCCTTCTTGGCCCTCGTCATCATCTTCTTGGC
TTTGCTATGTGCGGCCACCACGGCGAACGCGAGGTTCACGGCGATGCAGTGGACT
CCGGCGCACGCCACCTTCTACGGCGACGAGACCGCAGCGGAGACCATGGGTGGG
GCGTGCGGATATGGCAACCTGTACGCGACCGGGTACGGCACGGACACGGCGGCG
CTGAGCACGACGCTGTTCAAGGACGGGCACGGTTGCGGGACGTGCTACCAGATC
CGGTGCACGGGTTCCCCGTGGTGCTACGCCGGCTCGCCGTCGATCACGGTGACGG
CCACCAACCTGTGCCCGCCCAACTGGGCGCAGGACACCAACAACGGCGGGTGGT
GCAACCCGCCGCGCACCCACTTCGACCTCTCCAAGCCGGCCTTCATGAAGATGGC
GCAGTGGCGCGCCGGGATCGTGCCCGTCATGTACCGCCGCGTGCCCTGCGTGCGC
AGGGGCGGCCTCCGGTTCGCGCTCCAGGGGAACCCTTACTGGCTGCTGGCGTACG
TGATGAACGTCGGCGGCGCCGGCGACGTCGTCGAGATGTGGGTGAAGAGCGGCA
CGTCGTCCTGCGCGTGGATACGGATGACCCACAACTGGGGCGCCGCGTACCAGGC
GTTCGCGCAGCTCGGCGGCAAGGCGCTCAGCTTCAAGGTCACCTCCTACACCACC
CGGCAGACCATCGTCGCCACCAACGTCGCGCCGGCGAACTGGGGCCTGGGGCTC
ACGTACCAGGCCCGCGTCAACTTCTCCTGA

Nucleotide

>SbEXPA-10

TGCCTTAACCAAAGGTACGAACACCACGAGCGAAAAGTAGCAGCAATGGCTTCT
CCCTCCACAGGCACGGCCTTCTTGGCCCTCGTCATCATCTTCTTGGCTTTGCTATG
TGCGGCCACCACGGCGAACGCGAGGTTCACGGCGATGCAGTGGACTCCGGCGCA
CGCCACCTTCTACGGCGACGAGACCGCAGCGGAGACCATGGGTACGTTGCTCACC
ATCGCCGCCGGCATTGCACTGCCACGCTCGTTCCCTCTTGGCATTTCTCATTTCTC
TTACGGGCAACCCCGTGCGACGTCTTCCTACAGGTGGGGCGTGCGGATATGGCAA

CCTGTACGCGACCGGGTACGGCACGGACACGGCGGCGCTGAGCACGACGCTGTT
CAAGGACGGGCACGGTTGCGGGACGTGCTACCAGATCCGGTGCACGGGTTCCCC
GTGGTGCTACGCCGGCTCGCCGTCGATCACGGTGACGGCCACCAACCTGTGCCCG
CCCAACTGGGCGCAGGACACCAACAACGGCGGGTGGTGCAACCCGCCGCGCACC
CACTTCGACCTCTCCAAGCCGGCCTTCATGAAGATGGCGCAGTGGCGCGCCGGGA
TCGTGCCCGTCATGTACCGCCGCGTGCCCTGCGTGCGCAGGGGCGGCCTCCGGTT
CGCGCTCCAGGGGAACCCTTACTGGCTGCTGGCGTACGTGATGAACGTCGGCGGC
GCCGGCGACGTCGTCGAGATGTGGGTGAAGAGCGGCACGTCGTCCTGCGCGTGG
ATACGGATGACCCACAACTGGGGCGCCGCGTACCAGGCGTTCGCGCAGCTCGGC
GGCAAGGCGCTCAGCTTCAAGGTCACCTCCTACACCACCCGGCAGACCATCGTCG
CCACCAACGTCGCGCCGGCGAACTGGGGCCTGGGGCTCACGTACCAGGCCCGCG
TCAACTTCTCCTGAGAGCGCAGCAGATCACGTCGATTTGCAACTGAAGCTGCAGG
GGCTGCCAACGCTCTGCTCTGCTTTCGTAGTTTTATTTCGACAATCGTAGAGTTAG
CACGTGCTTTCGTTCGTAGTTTCATTACACATTTGCGCTTGAAGAATTAGCACGTG
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TTTTTAATGTCAAAATTTTAAACCCGTCAACTGTCATGGTTGGGCGGTTTAT