

IDENTIFICATION

Species: *Sorghum bicolor*

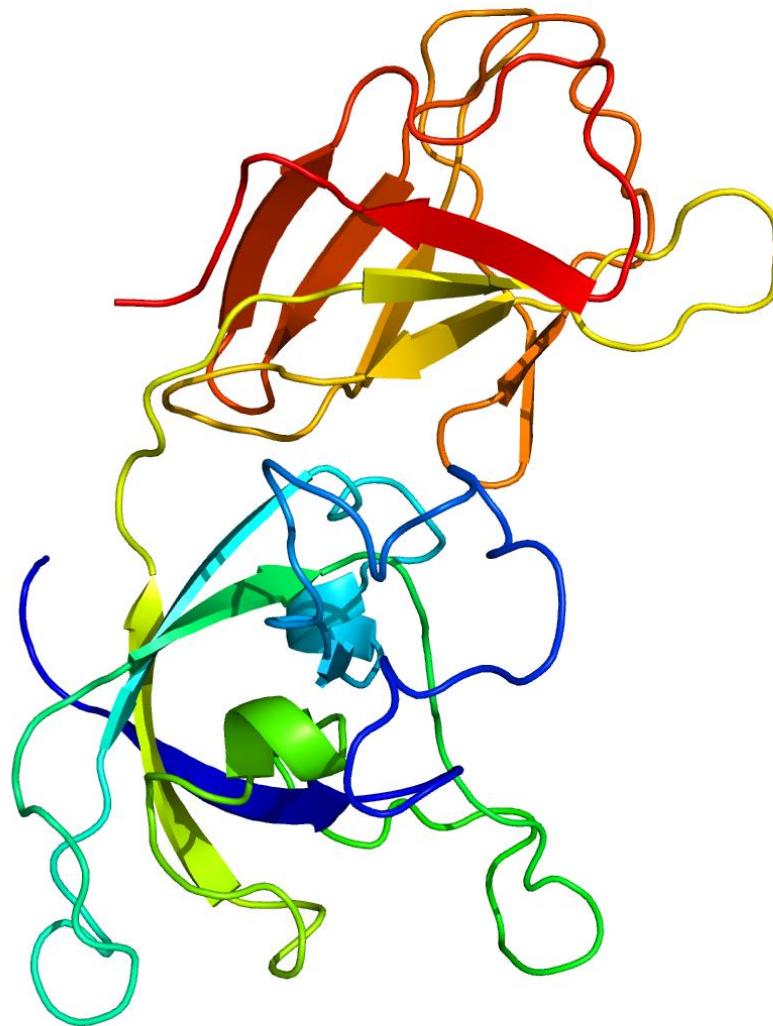
Locus: Sobic.001G499701

Gene Model: Sobic.001G499701.1.p

Description: SbEXPA-12

Family: Alpha Expansin

3D structure:



GENOME DATABASES

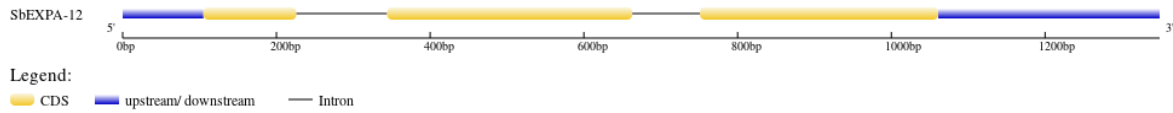
Phytozome: https://phytozome-next.jgi.doe.gov/info/Sbicolor_v3_1_1

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

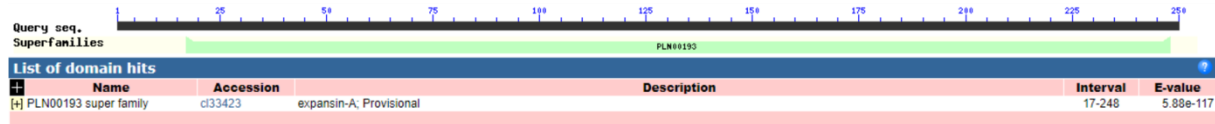
EXTERNAL RESOURCES

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GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>SbEXPA-12

MDRPLALLAVLAATSFFAPAKGWN YGTATFYGGRDGS GTMGGACGYGNLYQAGY
 GTNTAALSSVLFNDGAACGQCYLVMCDNS ASPWCRRGAA VTVTATNFCPPNWAQP
 SNSGGWCNPPRPHFDMAQPAWERIGVYRAGIIPVLYQQVTCWRQGGIRITIGSSFFQ
 LVQFSNVAGSGSIRS SVSVKGTGTGWVALNRNWGANWQCNSALFGQSLSFSTSTGG
 QTLYMTDVVPSWWQIGMAFGSNYFY*

CDS (coding sequence)

>SbEXPA-12

ATGGACAGACCCTCGCATTGCTCGCCGTCCTGGCGGCGACGTCGTTCTTCGCGC
 CGGCGAAGGGCTGGA ACTACGGGACGGCGACGTTCTACGGCGGCCGCGACGGCT
 CCGGCACAATGGGTGGCGCGTGC GGGTATGGCAACCTGTACCAGGCCGGGTACG
 GGACGAACACGGCGGCGCTGAGCTCGGTGCTGTTCAACGACGGCGCGGCGTGCG
 GTCAGTGCTACCTGGTGATGTGCGACAGCAACGCGTCCCCCTGGTGCAGGCGCGG
 CGCCGCGGTGACCGTACGGCCACCAACTTCTGCCCGCCCAACTGGGCGCAGCCC
 AGCAACAGCGGCGGCTGGTGCAACCCGCCGCGGCCGCACTTCGACATGGCGCAG
 CCCGCCTGGGAGCGCATCGGCGTCTACAGAGCCGGCATCATCCCCGTCCTGTACC
 AGCAGGTGACGTGCTGGAGGCAGGGAGGGATCAGGATCACCATCGGAGGGTCCA
 GCTTCTTCCAGCTGGTGAGTTCTCCAACGTGGCCGGCAGCGGCTCCATCCGGTC
 CGTGTCTGTGAAGGGGACCAAGACCGGGTGGGTGCGGCTGAACCGCAACTGGGG
 CGCCA ACTGGCAGTGCAACTCGGCGCTTTCGGCCAGTCGCTCTCCTTCTCCGTCA
 CCTCCACCGGCGGCCAGACGCTCTACATGACCGACGTCGTGCCGTCGTGGTGGCA
 GATCGGCATGGCTTTCGGAAGCAACTATAATTTCTACTAA

Nucleotide

>SbEXPA-12

AGCATCCTACGCATTTGAGCTCCTGGTTTGGTTTACTGAAACCACTACATACTCCT
 CCTCTGTATCTGTATTGTTCACTGAGAGATAGAGATAGACGATATATAGATGGAC
 AGACCCCTCGCATTGCTCGCCGTCCTGGCGGCGACGTCGTTCTTCGCGCCGGCGA
 AGGGCTGGA ACTACGGGACGGCGACGTTCTACGGCGGCCGCGACGGCTCCGGCA
 CAATGGGTAAGTGAAAAGAACA ACTCCAAAGCCACCATAATATATATACATACG
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 GTGAATAATAATAGGTGGCGCGTGC GGGTATGGCAACCTGTACCAGGCCGGGTA

CGGGACGAACACGGCGGGCGCTGAGCTCGGTGCTGTTCAACGACGGCGCGGGCGTG
CGGTCAGTGCTACCTGGTGATGTGCGACAGCAACGCGTCCCCCTGGTGCAAGGCGC
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CCAGCAACAGCGGGCGGCTGGTGCAACCCGCCGCGGGCCGCACTTCGACATGGCGC
AGCCCGCCTGGGAGCGCATCGGCGTCTACAGAGCCGGCATCATCCCCGTCCTGTA
CCAGCAGTAAGAGTGCAGCGTTGCGTTGCGTTTCGTCTTGCCTTGCTTCTCCGGTC
GGTGAAGTACTGATCGACGGCGACGGCGGTGGTGCAGGGTGACGTGCTGGAGG
CAGGGAGGGATCAGGATCACCATCGGAGGGTCCAGCTTCTTCCAGCTGGTGCAGT
TCTCCAACGTGGCCGGCAGCGGCTCCATCCGGTCCGTGTCTGTGAAGGGGACCAA
GACCGGGTGGGTTCGCGCTGAACCGCAACTGGGGCGCCAACCTGGCAGTGCAACTC
GGCGCTCTTCGGCCAGTCGCTCTCCTTCTCCGTCACCTCCACCGGCGGGCCAGACGC
TCTACATGACCGACGTCGTGCCGTCGTGGTGGCAGATCGGCATGGCTTTCGGAAG
CAACTATAATTTCTACTAAATGATACGGATCATTTGCCTAGCTCTAGCTCTAGCTC
GGCCACCACGTACGTTGGGGTTGGGCCAAGTGCAGCTACTCAGCTAGCTAGGGAT
GATGTTTGTCCGCGAACCCGTAAATAGGTTGTAAAAATTAACATGTTTACGGGT
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GTTATTTTTTGGACTGCTCTGTACATTTGTTGTCAGAAAAAAGAAAAATATATTA
ATCATATTTTTCGGACTTAAATGGGTCCA