

IDENTIFICATION

Species: *Sorghum bicolor*

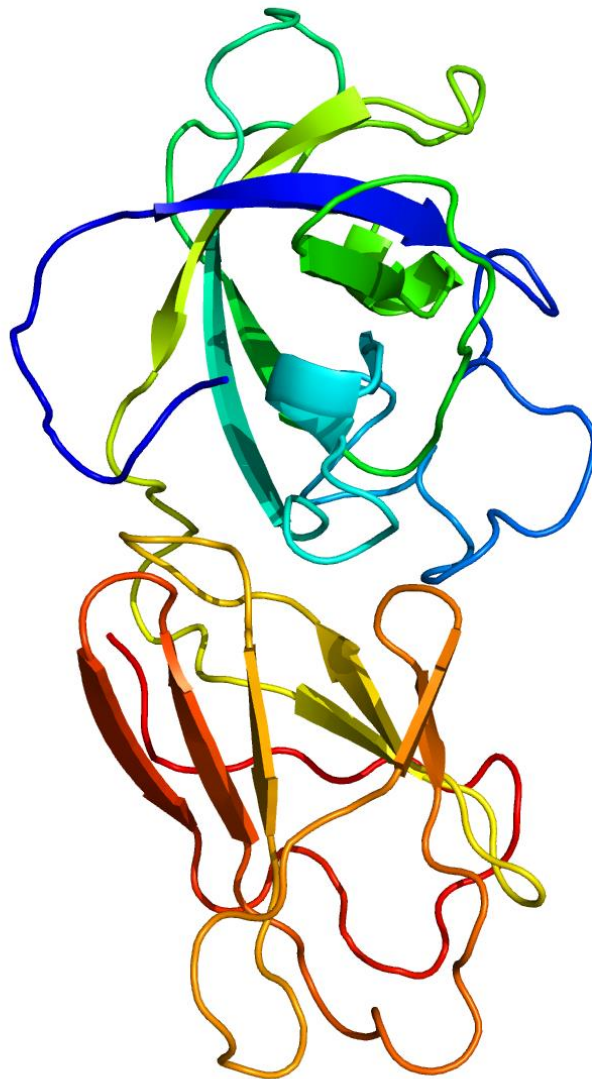
Locus: Sobic.007G020100

Gene Model: Sobic.007G020100.1.p

Description: SbEXPA-33

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>

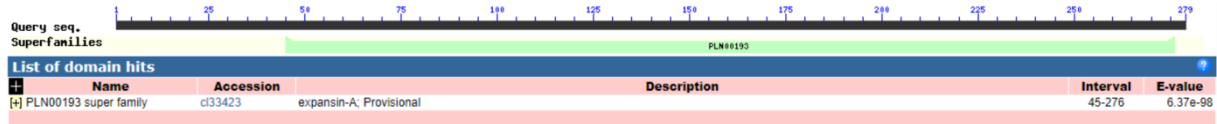
EXTERNAL RESOURCES

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GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>SbEXPA-33

MSTVSTYISSSCSQPFPSKMGKRFLHQLLAVVLALFLSPARSGDWLPATATFYGGAD
GSDTMGGACGYSDLYEQGYGINNAALSTALFNDGASCGQCYVIICDSSKTRWCKPG
NNWVVVSATNFCPPNWDLPAVGDLPAGGWCAPPRPHFDMSQPAWENIGIYSAGVIN
VLYQRVKCWKSGGVRFTMAGFNGFYMVLVTNVAGSGSIQSMVAVKGNSTDWIPMYR
NWGANWHCLSGGLVGQGLSFALVSTGGQNLVFKDVVPAWWQFGQTYTTYQNFY
*

CDS (coding sequence)

>SbEXPA-33

ATGTCTACTGTCTCTACATATATATCTAGTAGCTGCAGCCAGCCGTTTCCGAGCAA
GATGGGGAAACGCTTCCTCCACCAGCTGCTCGCCGTCGTCCTTGCCTTTCTCT
CGCCGGCGAGATCGGGCGACTGGCTTCCGGCCACCGCCACGTTCTACGGTGGCGC
TGACGGCTCCGACACAATGGGTGGCGCGTGTGGGTACAGCGACCTGTACGAGCA
GGGCTACGGCATCAACAACGCAGCGCTGAGCACGGCGCTCTTCAACGACGGCGC
GTCGTGCGGGCAGTGCTACGTCATCATCTGCGACAGCAGCAAGACCCGGTGGTGC
AAGCCCGGCAACAACCTGGGTCGTCGTCCTCCGCTACCAACTTCTGCCCGCCAACT
GGGACCTCCCCGCCGTCGGAGACCTCCCCGCCGGCGGCTGGTGCAGCCCGCCGCG
GCCCCACTTCGACATGTCCCAGCCCGCCTGGGAGAACATCGGCATCTACAGCGCC
GGCGTCATCAACGTCCTCTACCAGCGAGTCAAGTGCTGGAAGAGCGGCGGCGTG
CGCTTACCATGGCCGGCTTCAACGGCTTCTACATGGTGCTCGTCACCAACGTCG
CCGGCAGCGGCTCCATCCAGAGCATGGCGGTGAAGGGCAACAGCACGGATTGGA
TCCCCATGTACAGGAACTGGGGCGCCAACCTGGCACTGCCTCTCCGGCGGGCTCGT
CGGACAGGGCCTCAGCTTCGCGCTCGTCTCCACCGGCGGCCAGAACCTCGTCTTC
AAGGACGTCGTGCCGGCGTGGTGGCAGTTCGGACAAACATACACCACCTACCAG
AATTCGACTACTAA

Nucleotide

>SbEXPA-33

CAAACCTGCATGTCTACTGTCTCTACATATATATCTAGTAGCTGCAGCCAGCCGTT
TCCGAGCAAGATGGGGAAACGCTTCCTCCACCAGCTGCTCGCCGTCGTCCTTGC
CTCTTTCTCTCGCCGGCGAGATCGGGCGACTGGCTTCCGGCCACCGCCACGTTCTA

CGGTGGCGCTGACGGCTCCGACACAATGGGTGGGTAACCTACCTGCCTTTATCTT
TCGTTGGGTGTTTCAGAGTCAGACTTTGATCTGATCAAACGAGCACGCATACACAT
GCAGGTGGCGCGTGTGGGTACAGCGACCTGTACGAGCAGGGCTACGGCATCAAC
AACGCAGCGCTGAGCACGGCGCTCTTCAACGACGGCGCGTCGTGCGGGCAGTGC
TACGTCATCATCTGCGACAGCAGCAAGACCCGGTGGTGCAAGCCCGGCAACAAC
TGGGTCGTCTCCGCTACCAACTTCTGCCCCGCCAACTGGGACCTCCCCGCCGT
CGGAGACCTCCCCGCCGGCGGCTGGTGCGCCCCGCCGCGGCCCCACTTCGACATG
TCCCAGCCCGCCTGGGAGAACATCGGCATCTACAGCGCCGGCGTCATCAACGTCC
TCTACCAGCGAGTCAAGTGCTGGAAGAGCGGCGGCGTGCCTTACCATGGCCG
GCTTCAACGGCTTCTACATGGTGCTCGTCACCAACGTCGCCGGCAGCGGCTCCAT
CCAGAGCATGGCGGTGAAGGGCAACAGCACGGATTGGATCCCCATGTACAGGAA
CTGGGGCGCCAACTGGCACTGCCTCTCCGGCGGGCTCGTCGGACAGGGCCTCAGC
TTCGCGCTCGTCTCCACCGGCGGCCAGAACCTCGTCTTCAAGGACGTCGTGCCGG
CGTGGTGGCAGTTCGGACAAACATACACCACCTACCAGAATTTGACTACTAAAC
TGCACTGCTTCATAATTATATACAGTCCACAACAATATAAACTACACTGGTTTGTC
TTCATTTTCATCTCATTTGTAGTTTGGAAATCACTTTATTATTATTCAACCGCCAACT
GATCATTGTAAACAGAGTACACTGAAAATTTATTGTAAAGTACCCACCTAATCCTG
TGTTTGCGGTTGATTTGATTTGTGGATTTAAAATTTCCACCCACGAATTATTCTTTT
GCTTCATCGTGA