

IDENTIFICATION

Species: *Sorghum bicolor*

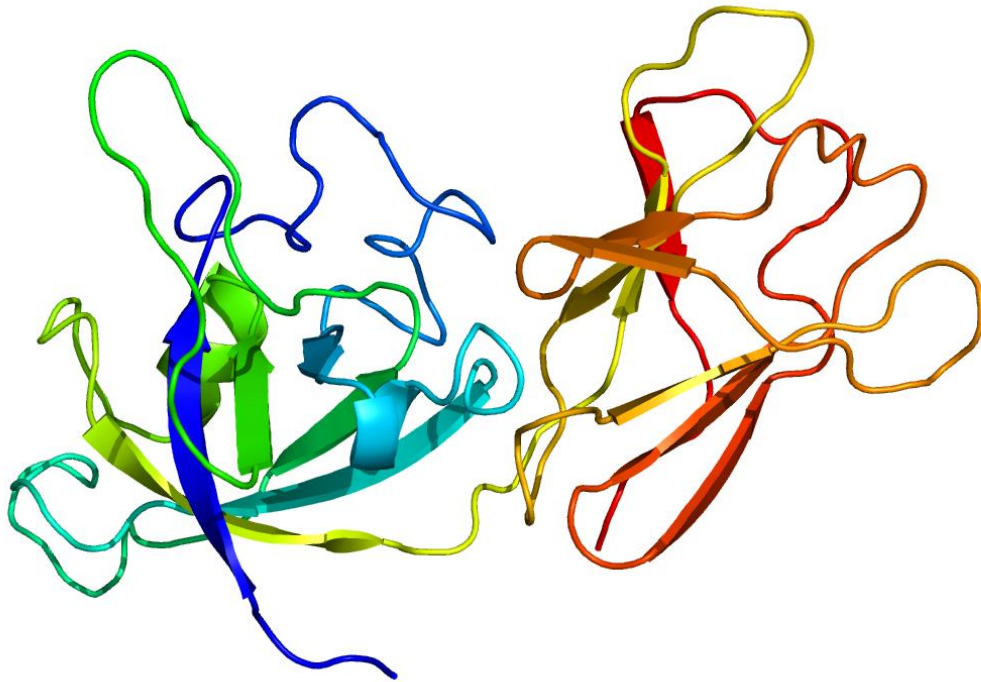
Locus: Sobic.001G238200

Gene Model: Sobic.001G238200.1.p

Description: SbEXPA-07

Family: Alpha Expansin

3D structure:



GENOME DATABASES

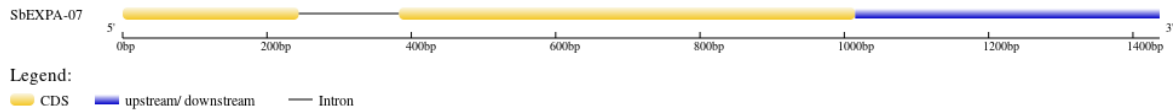
Phytozome: https://phytozome-next.jgi.doe.gov/info/Sbicolor_v3_1_1

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

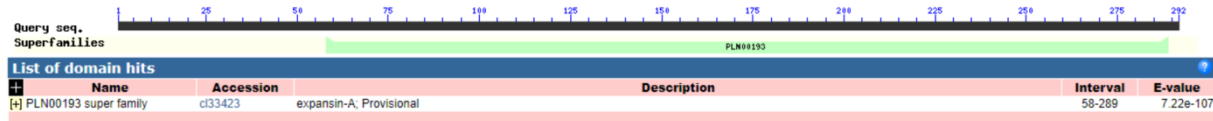
EXTERNAL RESOURCES

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GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>SbEXPA-07

MHQTGLKHLHPHIPCLGTPNTHPRSSILFSICIQLSISNDEMANSFMLCTVVVASCLAV
AAAGWSQGTATFYGGVDASGTMGGACGYDNLNAGYGVNNAALGPTLFNDGASC
GQCYLITCDTSRSGGQWCKPGNSITVSAATNLCPSNYALPNGGWCGPGRPHFDMSQPA
WEHIGIYSAGVVPVLYQQVKCSRTGGVRFSLAGSQYFLLVNIQNLGGSGSVGAAWV
KGDKTGWIQMSRNWGANWQALAGLVGQGLSFAVTTTGGQYIQFNVVPGWWQF
GQTYSTTQNFYY*

CDS (coding sequence)

>SbEXPA-07

ATGCATCAAACCGGCCTGAAACATCTTCATCCTCATATTCCCTGCTTAGGAACAC
CGAACACACACCCTCGATCGTCAATCTTGTCTCTATCTGCATCCAGCTCTCCATT
TCGAACGACGAAATGGCCAATTCCTTTATGCTGTGCACGGTGGTTGTTGCGTCGT
GCCTCGCCGTCGCCGCCGCCGGCTGGTCTCAAGGCACTGCCACTTCTACGGCGG
AGTCGACGCGTCCGGCACGATGGGCGGCGCATGCGGGTACGACAACCTGTACAA
CGCGGGGTACGGCGTGAACAACGCGGCGCTGGGCCCGACCTTGTTCAACGACGG
CGCGTTCGTGTGGGCAGTGCTACCTCATCACCTGCGACACGTCACGGAGCGGCGGG
CAGTGGTGCAAGCCGGGCAACTCCATCACGGTGTCCGCCACCAACCTGTGCCCCT
CCAACCTACGCGCTGCCAACGGCGGGTGGTGCGGCCCGGGGCGCCCCACTTCGA
CATGTTCGCAGCCGGCGTGGGAGCACATCGGCATCTACAGCGCCGGCGTTCGTC
GTCCTGTACCAGCAGGTCAAGTGCTCGCGCACCGGCGGGCGTTCGCTTCAGCCTCG
CCGGCTCCCAGTATTTCTGCTCGTCAACATCCAGAACCCTCGGCGGCAGTGGCTC
TGTGGGCGCTGCGTGGGTGAAGGGTGACAAGACGGGGTGGATCCAGATGTCCAG
GAACTGGGGCGCCAACCTGGCAGGCGCTCGCCGGGCTCGTCCGGCCAGGGGCTCAG
CTTCGCCGTTACCACTACGGCGGGCAGTACATTCAGTTCTGGAACGTGGTGCCT
GGGTGGTGGCAGTTCGGACAGACCTACTCCACAACCCAGAATTTCTACTACTAA

Nucleotide

>SbEXPA-07

ATGCATCAAACCGGCCTGAAACATCTTCATCCTCATATTCCCTGCTTAGGAACAC
CGAACACACACCCTCGATCGTCAATCTTGTCTCTATCTGCATCCAGCTCTCCATT
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GCCTCGCCGTCGCCGCCGCCGGCTGGTCTCAAGGCACTGCCACTTCTACGGCGG

AGTCGACGCGTCCGGCACGATGGGTAAGAATGCATGCATTCATTTCTGTACAGAG
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TTCGTCACACTGATGCATGCATGTTTTTATATATGATATGATACACGTACAGGCGG
CGCATGCGGGTACGACAACCTGTACAACGCGGGGTACGGCGTGAACAACGCGGC
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ACCTGCGACACGTACGGAGCGGGCGGGCAGTGGTGCAAGCCGGGCAACTCCATC
ACGGTGTCCGCCACCAACCTGTGCCCGTCCAACACTACGCGCTGCCCAACGGCGGGT
GGTGCGGCCCGGGGCGCCCCACTTCGACATGTGCGCAGCCGGCGTGGGAGCACA
TCGGCATCTACAGCGCCGGCGTCTGCCGGTCTGTACCAGCAGGTCAAGTGCTC
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AACATCCAGAACCTCGGCGGCAGTGGCTCTGTGGGCGCTGCGTGGGTGAAGGGT
GACAAGACGGGGTGGATCCAGATGTCCAGGAAGTGGGGCGCCAACTGGCAGGGC
CTCGCCGGGCTCGTTCGGCCAGGGGCTCAGCTTCGCCGTTACCACTACCGGCGGGC
AGTACATTCAGTTCTGGAACGTGGTGCCTGGGTGGTGGCAGTTCGGACAGACCTA
CTCCACAACCCAGAATTTCTACTACTAATAAGACCCTACTGCCGACGACGCCGAG
GAAGCTCGATGGATGTCCTCCTTATTTGCCCATTTCTTGAGGTTTAGTCGAGTGG
CGAGTGCATTCTTGTATTCTGACGCAGAGCTAAATGCACTTGTTGCTGTTGTATC
ATATTATATTGCTTCTTTGGCGACCCCCGGATTGACGTCCATCCTACGTGATGCTC
CAGCTCTGCTGGAGGAAATAATGGAAGGGTAGGATGAACAAGAGAAGGGGATCG
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GTTAT