

IDENTIFICATION

Species: *Sorghum bicolor*

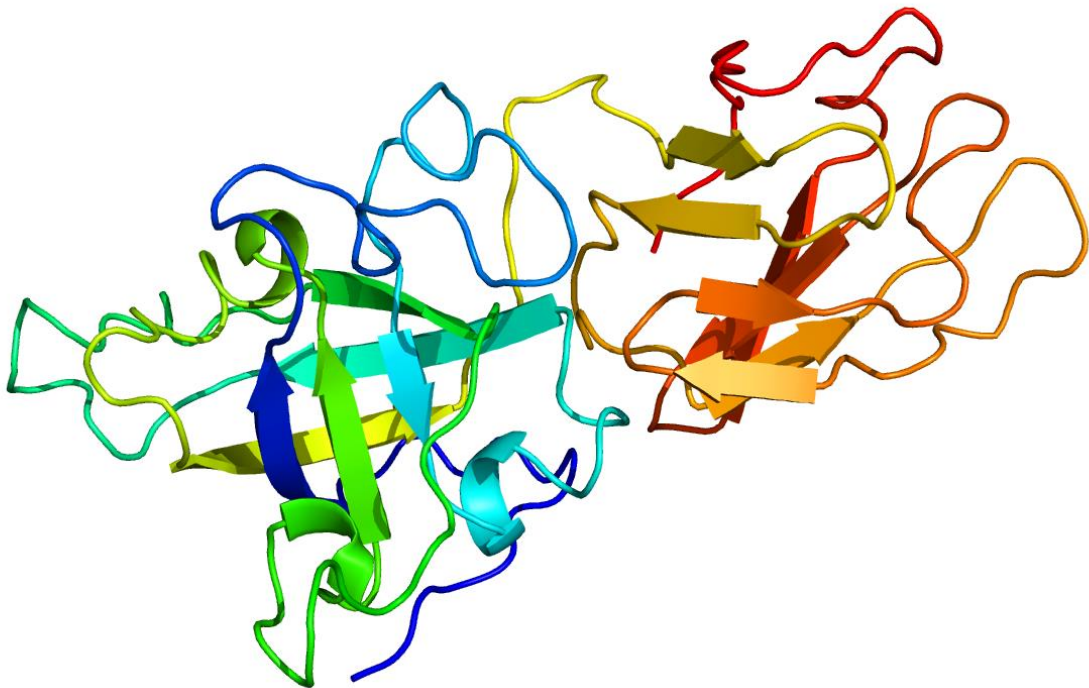
Locus: Sobic.004G121800

Gene Model: Sobic.004G121800.1.p

Description: SbEXPA-27

Family: Alpha Expansin

3D structure:



GENOME DATABASES

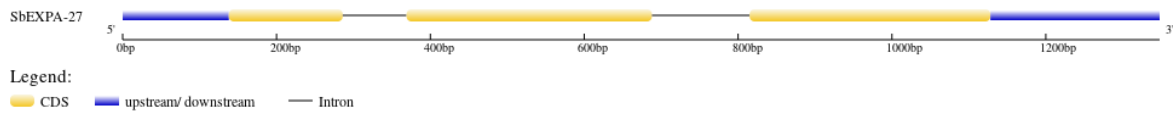
Phytozome: https://phytozome-next.jgi.doe.gov/info/Sbicolor_v3_1_1

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

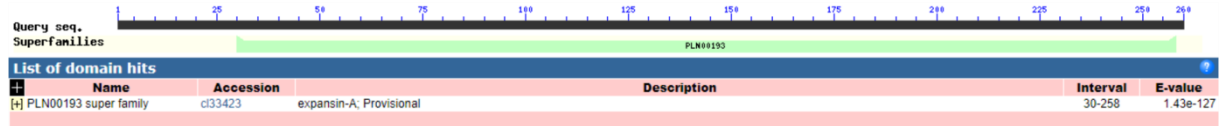
EXTERNAL RESOURCES

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GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>SbEXPA-27

MAVSARVFTLLLLAAAGWVPAMAANAPPTGWLKAHATFYGGADASDTMGGACG
YGNLYSQGYGTRTAALSTVLFNDGASCGQCYKIACDRKRADPMFCKPGVTVTAT
NFCPPNMALPEGGWCNQHRPHFDMAQPAFEKIGVYSGGIIPVMYKRVPCKRGGVR
FSVNGHDYFNLVLVTNVAAAGSIKSMEVKTSNSSNWSPMARNWGANWHSLAYLTG
QMLSFRLTDTDGQTIEFTDVVPQGWKFGQTFASKLQFM*

CDS (coding sequence)

>SbEXPA-27

ATGGCCGTTTCAGCTCGAGTCTTCACGCTCTTGCTGCTCGCAGCTGCCGGTTGGGT
GCCGGCCATGGCAGCTAATGCTCCTGCACCAACCGGGTGGCTGAAGGCGCATGCC
ACCTTCTACGGAGGCGCTGATGCCTCCGACACCATGGGCGGCGCGTGCCGGGTATG
GGAACCTCTACTCCCAGGGCTATGGTACGCGGACGGCGGGCGCTGAGCACGGTCTT
CTTCAACGACGGCGCCTCGTGCGGGCAGTGCTACAAGATCGCTTGTGACCGCAAG
AGAGCTGATCCGATGTTCTGTAAACCTGGTGTACGCGTGACCGTCACGGCCACAA
ACTTCTGCCACCCAACATGGCGCTGCCCGAGGGGGTGGTGCAATCAGCATCG
CCCGCACTTCGACATGGCGCAGCCGGCATTGAGAAGATCGGCGTGTACAGCGGC
GGTATTATCCCCGTCATGTACAAGAGAGTTCTTGCCTGAAGCGAGGTGGCGTCA
GGTTCAGCGTCAACGGCCATGACTACTTCAATCTTGTGCTTGTAAACCAATGTTGCG
GCTGCCGGCTCCATCAAGTCCATGGAAGTCAAGACGTCCAATTCAAGTAACTGGT
CTCCAATGGCACGTAACCTGGGGTGCAAACCTGGCACTCTCTTGCATATCTTACAGG
GCAGATGCTCTCATTTAGGCTCACAGACACGGATGGGCAAACCTATTGAATTCACA
GATGTGGTGCCACAAGGATGGAAGTTTGGCCAAACATTTGCATCCAAGTTGCAGT
TCATGTGA

Nucleotide

>SbEXPA-27

TCCGTCCATACCCATACTTACATATATCTACAGACTGCACCCACCAACAATTTATT
CAGGCTACACGATCTCCAATTTCTGAGCTACATATATACAGTAGTACTCCAGATT
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CTTGTGCTCGCAGCTGCCGGTTGGGTGCCGGCCATGGCAGCTAATGCTCCTGCA

CCAACCGGGTGGCTGAAGGCGCATGCCACCTTCTACGGAGGGCGCTGATGCCTCCG
ACACCATGGGTAAGCTAGCTGTGTGCTGGCCGACGATATCACATCCGTCATCGTC
TGATCTAATAATGTATATATGTATGTATTGATGGCAGGCGGCGCGTGCGGGTATG
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CTTCAACGACGGCGCCTCGTGCGGGCAGTGCTACAAGATCGCTTGTGACCGCAAG
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GGTATTATCCCCGTCATGTACAAGAGGTATATATTTTTATGTCATTTCTACATAC
CTCTTCCAAGCTAGCTTCAATCTATCATAAATAAAACAGAAAAATTAATGGGATG
CAATGCAATATCCTAATACTACAACCTAATTCCTTGCTTGTAGAGTTCCTTGCGTGA
AGCGAGGTGGCGTCAGGTTCAAGCGTCAACGGCCATGACTACTTCAATCTTGTGCT
TGTAACCAATGTTGCGGCTGCCGGCTCCATCAAGTCCATGGAAGTCAAGACGTCC
AATCAAGTAACTGGTCTCCAATGGCACGTAAGTGGGGTGCAAACCTGGCACTCTC
TTGCATATCTTACAGGGCAGATGCTCTCATTTAGGCTCACAGACACGGATGGGCA
AACTATTGAATTCACAGATGTGGTGCCACAAGGATGGAAGTTTGGCCAAACATTT
GCATCCAAGTTGCAGTTCATGTGATGATGAGAGCTCCATCATCCAGGATTATTAT
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CTCTCATTCTTCTATTGTACAGTCCTATGTTTTATTTTTATGGTGTATATAAATA
TGTTCAGTTTATGTCTTCAGT