

IDENTIFICATION

Species: *Sorghum bicolor*

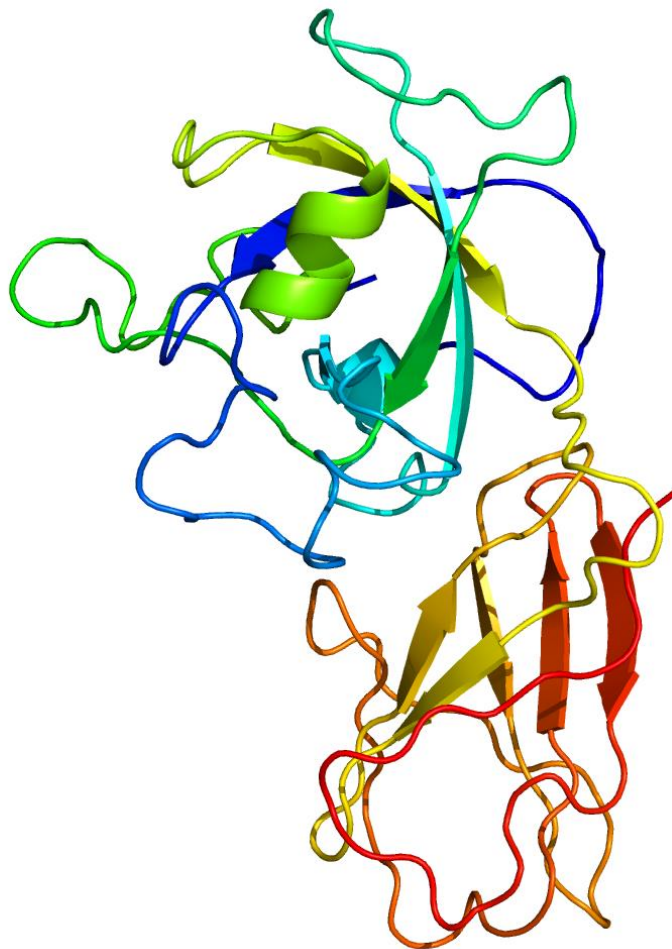
Locus: Sobic.004G238801

Gene Model: Sobic.004G238801.1.p

Description: SbEXPA-29

Family: Alpha Expansin

3D structure:



GENOME DATABASES

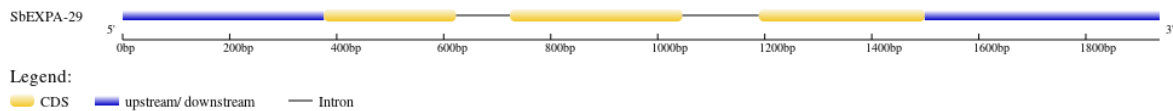
Phytozome: https://phytozome-next.jgi.doe.gov/info/Sbicolor_v3_1_1

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

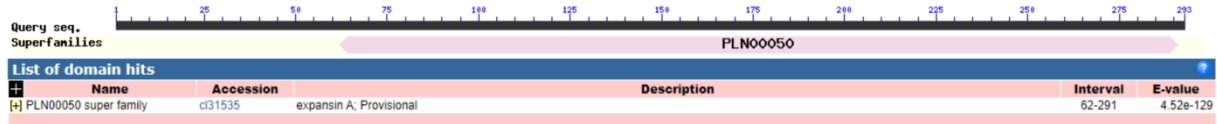
EXTERNAL RESOURCES

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GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>SbEXPA-29

MAPRQAVLAAVVLAALFPLALSRGLGLVHGHVRPHAHGLGLGHHHPRPHPQQQPH
GHAPLGGGAWSSAHATFYGGGDASGTMGGACGYGNLYSQGYGTNTAALSTALFNS
GLSCGACFEVRCDAAGGGSHSCLPGSVVVTATNFCPPNNALPSDDGGWCNPPRAHF
DMSQPVFQRIALYRAGIVPVSYRRVACNKKGGIRFTINGHSYFNLVLVTNVGGAGDV
HAVAVKGERAGWQALSRNWGQNWQSNLLDQALSFRVTTSDGRSVVSNNAAPR
GWAFGQTFSGAQFN*

CDS (coding sequence)

>SbEXPA-29

ATGGCGCCTCGCCAAGCCGTCCTGGCGGCCGTGGTCCTCGCCGCGCTGTTCCC
TCGCCCTCTCTCGCGGGCTGGGCTGGTGCACGGGCATGTGCGGCCGCACGCGCA
CGGGCTGGGGCTTGGCCACCACCACCCAGGCCGCACCCCCAGCAGCAGCCGCA
CGGCCACGCACCGCTCGGAGGTGGCGCGTGGTCCTCGGCTCACGCCACCTTCTAC
GGCGGCGGCGACGCGTCCGGCACCATGGGCGGGGCGTGTGGGTACGGCAACCTC
TACAGCCAGGGGTACGGCACCAACACGGCGGCGCTGAGCACGGCGCTCTTCAAC
AGCGGCCTCAGCTGCGGCGCCTGCTTCGAGGTGCGCTGCGACGCGGCGGGCGGC
GGGAGCCACTCGTGCCTGCCGGGCTCCGTCGTGGTGACGGCCACCAACTTCTGCC
CTCCCAACAACGCGCTCCCCTCCGACGACGGCGGCTGGTGCAACCCGCCCGCGC
CCACTTCGACATGTGCGAGCCCGTGTTCAGCGCATCGCGCTCTACAGGGCCGGC
ATTGTCCCCGTCTCCTACCGCAGGGTCGCGTGCAACAAGAAGGGCGGCATCCGGT
TCACAATCAACGGCCATTCTACTTCAACCTGGTGCTGGTGACCAACGTGGGCGG
CGCCGGCGACGTGCACGCGGTGGCCGTGAAGGGCGAGCGCTCCGCGGGGTGGCA
GGCGCTGTCGCGCAACTGGGGCCAGAACTGGCAGAGCAACACGCTCCTGGACGG
GCAAGCGCTCTCGTTCCGCGTCACCACCAGCGACGGCCGCTCCGTGGTCTCCAAC
AACGCCGCCCCCGCGGCTGGGCCTTCGGCCAGACCTTCAGCGGCGCCAGTTCA
ACTGA

Nucleotide

>SbEXPA-29

CCCTCCCGCCCGCCACGCCTTCCAATGGTGCCCGCCAGAAATCCCGTGTCCCTAC
GCGGGTAGCTGGGCGACTTTTCCAGGGCATGGCCTGACCCACGCCACTCCTCCG

TCCCGCAGGCCGCGCGCGCCGCAAGTGCACACACCCGCAACCACCGTCCATCCC
CCGTCCCGCCCACGCCCTGCGCGCCCCGGCACCATGCGCACCGCGCGCGGGCGGTT
TGAAACCCTTCCGCGCCTCCCCCTCTATTTATCCCCGCACAGCCCCCACCCCA
CATCACCTCACTACACTTCACTCCCTAGCCGCCCTGCGCTGCGCCGCACCGTGCG
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CCAAGCCGTCCTGGCGGCCGTGGTTCCTCGCCGCGCTGTTCCCGCTCGCCCTCTCTC
GCGGGCTGGGCCTGGTGCACGGGCATGTGCGGCCGCACGCGCACGGGCTGGGGC
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CTACTTGTAGATTTCCGTCCCGTGCTGAGATATTTGGGACTGAATTTTACATCTG
AATGCAGGCGGGGCGTGTGGGTACGGCAACCTCTACAGCCAGGGGTACGGCACC
AACACGGCGGGCGCTGAGCACGGCGCTCTTCAACAGCGGCCTCAGCTGCGGGCGCT
GCTTCGAGGTGCGCTGCGACGCGGGCGGGCGGGAGCCACTCGTGCTGCCGG
GCTCCGTCTGTGGTGACGGCCACCAACTTCTGCCCTCCCAACAACGCGCTCCCCTC
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CTGTTATCCTTT