

IDENTIFICATION

Species: *Sorghum bicolor*

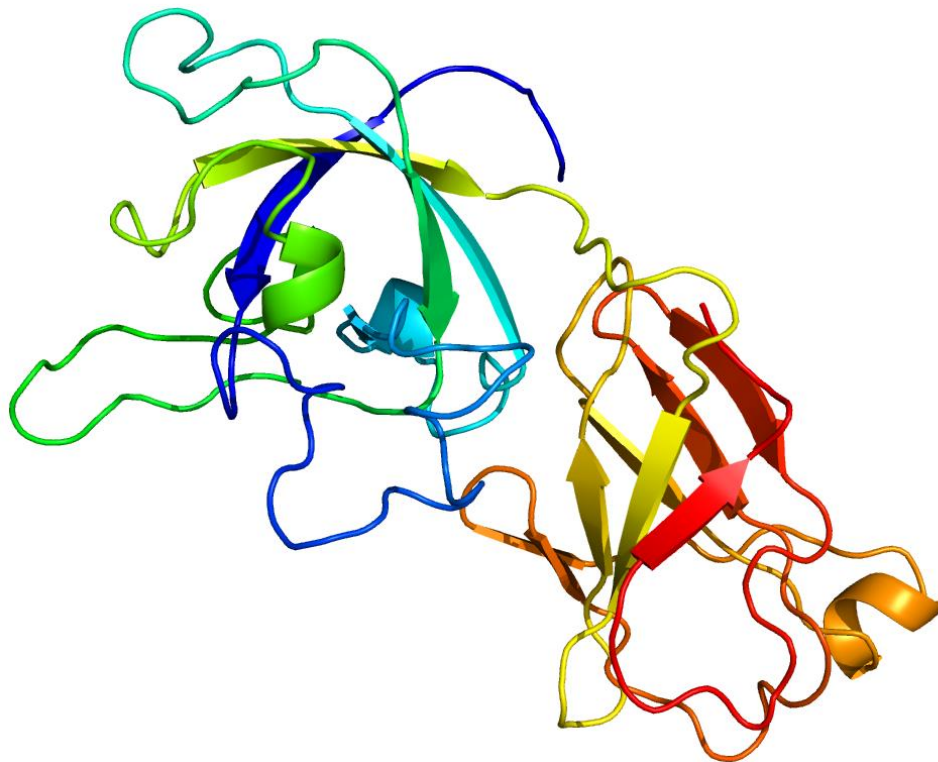
Locus: Sobic.001G356400

Gene Model: Sobic.001G356400.1.p

Description: SbEXPA-11

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

Query seq. Superfamilies

PLN00050

Name	Accession	Description	Interval	E-value
PLN00050 super family	cl31535	expansin A; Provisional	15-260	6.50e-104

SEQUENCES

Peptide

>SbEXPA-11

MASLAVLLLLALLSMTFSSSAQGYGVGRWINAHATFYGGADASGTMGGACGYGDL
 YSQGYGTATTALSTALFSGGQTCGACFELRCAGGGDRGSCVPSSSVVVTATNLCPPN
 YALPSDAGGWCNPPLRHFDLSQPAFLRIARYRAGVVPVAYRRVPCRRRGGIRFTVNG
 HAYFNLVLVANVGGAGDVRALAVGAGGARRRRTRWLAMARNWQNWQSAARLD
 HGQPLSFRVTTSDRRSVVSYNAAPAGWAFGQTFTGAQFP*

CDS (coding sequence)

>SbEXPA-11

ATGGCATCGCTCGCGGTGCTACTCTTGCTTGCCCTGCTCTCCATGACGTTCTCCTC
 TTCAGCGCAAGGCTATGGCGTCGGCCGATGGATCAATGCGCACGCCACCTTCTAC
 GGCGGCGCCGACGCTTCCGGCACCATGGGTGGCGCGTGCGGGTACGGCGACCTG
 TACAGCCAGGGGTACGGCACGGCGACGACGGCGCTGAGCACGGCGCTGTTCAGC
 GGCGGGCAGACCTGCGGCGCGTGCTTCGAGCTGCGGTGCGCCGGCGGCGGCGAC
 CGCGGCTCGTGCGTGCCATCGTCATCCGTCGTGGTGACGGCCACCAACCTGTGCC
 CGCCCAACTACGCGCTCCCGAGCGACGCCGGCGGGTGGTGCAACCCGCCGCTGC
 GGCACTTCGACCTGTGCGAGCCGGCGTTCCTCCGCATCGCCCGTTACCGCGCGGG
 CGTCGTGCCCGTCGCCTACCGCAGGGTGCCGTGCCGGAGGCGGGGCGGCATCCG
 GTTCAACCGTCAACGGCCACGCCTACTTCAACCTGGTTCTGGTTCGCCAACGTGGGC
 GGCGCCGGCGACGTGCGCGCGCTCGCCGTGGGGCGGGCGGCGCCCGGCGGCGG
 AGGACGCGGTGGCTGGCCATGGCGCGGAAGTGGGGACAGAACTGGCAGAGCGCC
 GCGCGCCTCGACCACGGCCAGCCGCTCTCCTTCAGGGTCACCACCAGCGACCGCC
 GCTCCGTCGTGTTACAACGCCGCGCCCGCCGGGTGGGCCTTCGGCCAGACATT
 CACCGGCGCCCAGTTCCCGTAG

Nucleotide

>SbEXPA-11

TAGCGTGCAGTGTCGGTCACTATAGGTCCAAGCATCTGATCTGCATCTCTCTAGCT
 ACTTAAACCCGCACACGCGTCGCTGCTCTTCTCTGCGCCCCCTGCATTGCATTGCA
 TTGCATTGCATACTGACAGGAGATGGCATCGCTCGCGGTGCTACTCTTGCTTGCC
 TGCTCTCCATGACGTTCTCCTCTTCAGCGCAAGGCTATGGCGTCGGCCGATGGATC
 AATGCGCACGCCACCTTCTACGGCGGCGCCGACGCTTCCGGCACCATGGGTACGT
 TACCATGATCGATTTGTTGATCATCAGTTGCTGCTGCCTCCAACCTCCAATACCTAA

ACTAATAATATACTTACTAAGGAGCAATGCATGCACAGGTGGCGCGTGCGGGTAC
GGCGACCTGTACAGCCAGGGGTACGGCACGGCGACGACGGCGCTGAGCACGGCG
CTGTTTCAGCGGCGGGCAGACCTGCGGGCGCGTGCTTCGAGCTGCGGTGCGCCGGCG
GCGGCGACCGCGGCTCGTGCGTGCCATCGTCATCCGTCGTGGTGACGGCCACCAA
CCTGTGCCCGCCAACTACGCGCTCCCGAGCGACGCCGGCGGGTGGTGCAACCCG
CCGCTGCGGCACTTCGACCTGTCGCAGCCGGCGTTCCTCCGCATCGCCCGTTACC
GCGCGGGCGTCGTGCCCGTCGCCTACCGCAGGGTGCCGTGCCGGAGGCGGGGCG
GCATCCGGTTCACCGTCAACGGCCACGCCTACTTCAACCTGGTTCTGGTCGCCAA
CGTGGGCGGGCGCCGGCGACGTGCGCGCGCTCGCCGTGGGGCGGGCGGGCGCCCG
GCGGCGGAGGACGCGGTGGCTGGCCATGGCGCGGAACTGGGGACAGAACTGGCA
GAGCGCCGCGCGCCTCGACCACGGCCAGCCGCTCTCCTTCAGGGTCACCACCAGC
GACCGCCGCTCCGTCGTGTCTTACAACGCCGCGCCCGCCGGGTGGGCCTTCGGCC
AGACATTCACCGGCGCCCAGTTCCCGTAGACAGACAAGTTCAATTTTGGCACGCG
CGTGTACTGGGTGCGGCTTCACTGAATGTGAATCGATCAATCAATGATATA