

IDENTIFICATION

Species: *Sorghum bicolor*

Locus: Sobic.007G019900

Gene Model: Sobic.007G019900.1.p

Description: SbEXPA-32

Family: Alpha Expansin

3D structure:



GENOME DATABASES

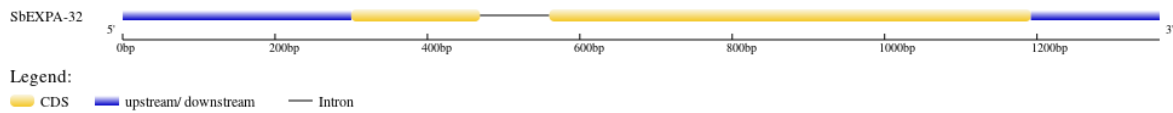
Phytozome: https://phytozome-next.jgi.doe.gov/info/Sbicolor_v3_1_1

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

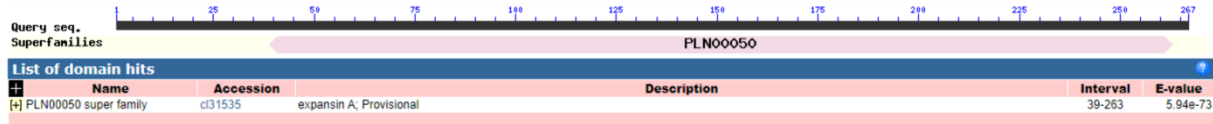
EXTERNAL RESOURCES

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GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>SbEXPA-32

MDPSSSSSRFPAAA VVAALLLLLPALSSAGDDDWQQWQAAHATFYGDESGADT
MQGACGYGDLLQQGYGLETTALSVALFNWWSGGCYEIRCQGSTFCPRGGAPVTV
TATNLCPANYSKPNENWCNPLRHFDSLKPMFLRLVTDHFVGIIPVEYRRVACANKR
GGVRFEMKGNRWVAVLVFNVAGAGDVKAVAAGKSRDGGQWVDLSRSWGQVW
TNGDGRSVGEGLSFRVVAGDGRAVVLDDAVPPGWAFGQSFEGRGQF*

CDS (coding sequence)

>SbEXPA-32

ATGGACCCTAGTTCGTCGTCGTCGCTTCCGGCGGGCGGCCGCGGTGGTGGCGG
CAGCACTGCTGCTGCTTCTGCCGGCGTTGTCGTCGGCCGGCGACGACGACTGGCA
GCAGTGGCAAGCGGCGCACGCCACGTTCTACGGCGACGAAAGCGGCGCCGACAC
CATGCAGGGTGCCTGTGGCTACGGCGACCTGTTGCAGCAGGGGTACGGGCTGGA
GACGACGGCGCTGAGCGTGGCGCTTCAACGAGGGCTGGTCCTGCGGCGGCTGC
TACGAGATACGGTGCCAGGGGAGCACGTTCTGCCCGCGGGCGGCGCGCCGGTG
ACGGTGACGGCGACGAACCTGTGCCCGGCGAACTACTCGAAGCCGAACGAGAAC
TGGTGCAACCCGCGCTGCGGCACTTCGACCTGTCCAAGCCATGTTCTGCGCC
TCGTCACCGACTTCCACGTCGGGATCATCCCCGTGGAGTACCGCCGCGTGGCGTG
CGCCAACAAGCGCGGGCGGCGTCCGGTTCGAGATGAAGGGCAACCGGTGGTGGGT
CGCCGTGCTCGTCTTCAACGTCGCCGGCGCTGGCGACGTCAAGGCCGTGCGCGG
AAGGGGTCCCGCGACGGCGGGCAGTGGGTGCGACTTGTCGCGCAGCTGGGGACAG
GTGTGGACGAACGGCGATGGACGGAGCGTCCGGGAGGGCCTCTCGTTCGCGGTC
GTCGCCGGCGATGGACGCGCCGTCGTGCTCGACGACGCCGTGCCGCTGGGTGGG
CGTTCGGCCAGAGCTTCGAGGGCAGGGGCCAGTTCTGA

Nucleotide

>SbEXPA-32

ATCTCCAGCAACAAATATATACTTCCAAACTGAAATTCATATACACAGTGATTAA
TGCAAAATCTTCCCCTGGGATTTACCGCTGACTGTATATATGCAGGTTGTCAATT
AGCAAAATCCCAACAAATCTTGCTAATTTTCGTC AACGCGCAAAAAAGAAAAAGA
CCATTTTTTTTAAAAAAAAGACTGTCATTGGCTGCTCGCCAGCTCTATATATA
CCTGGCTTTTGCAATGATCTGAACCAGCACACGGCTGCACACTACACCAGTCCAA

AAGCCCGTTTCGTCAGTGGCTTACATGGACCCTAGTTCGTCGTCGTCGCTCGCTTCC
GGCGGCGGCCGCGGTGGTGGCGGCAGCACTGCTGCTGCTTCTGCCGGCGTTGTCC
TCGGCCGGCGACGACGACTGGCAGCAGTGGCAAGCGGCGCACGCCACGTTCTAC
GGCGACGAAAGCGGCGCCGACACCATGCGTGAGTCTCTTGCATGCTCTGCTGTTC
GTCGTCACGCACGTTCTAACCTTTTTTTTTTCCCAATCGGTGACGGTGCGTCCAT
GCATGCAGAGGGTGCGTGTGGCTACGGCGACCTGTTGCAGCAGGGGTACGGGCT
GGAGACGACGGCGCTGAGCGTGGCGCTCTTCAACGAGGGCTGGTCCTGCGGCGG
CTGCTACGAGATACGGTGCCAGGGGAGCACGTTCTGCCCCGCGGGCGGCGGCC
GGTGACGGTGACGGCGACGAACCTGTGCCCGGCGAACTACTCGAAGCCGAACGA
GAACTGGTGCAACCCGCCGCTGCGGCACTTCGACCTGTCCAAGCCCATGTTCTG
CGCCTCGTCACCGACTTCCACGTCGGGATCATCCCCGTGGAGTACCGCCGCGTGG
CGTGCGCCAACAAGCGCGGCGGCGTCCGGTTCGAGATGAAGGGCAACCGGTGGT
GGGTCGCCGTGCTCGTCTTCAACGTCGCCGGCGCTGGCGACGTCAAGGCCGTCGC
CGCGAAGGGGTCCCGCGACGGCGGGCAGTGGGTCGACTTGTGCGCGCAGCTGGGG
ACAGGTGTGGACGAACGGCGATGGACGGAGCGTCGGGGAGGGCCTCTCGTTCCG
CGTCGTCGCCGGCGATGGACGCGCCGTCGTGCTCGACGACGCCGTGCCGCCTGGG
TGGGCGTTCGGCCAGAGCTTCGAGGGCAGGGGCCAGTTCTGACACACCTGTACGC
AAGGGATGTTTGCAATTGCTAGCGTCCGTCCATGCTTTGTATTACCGGCGCCTGT
TCTTTAGTTTTCAAATTGCCAAGATGTCGTTTATGGAAAACCTGTGTTTTTTTTAT
TATCAATCATCATCAAACCTGAGAAATGCAAAAGGTTTTGATTA