

IDENTIFICATION

Species: *Sorghum bicolor*

Locus: Sobic.003G444400

Gene Model: Sobic.003G444400.1.p

Description: SbEXPA-20

Family: Alpha Expansin

3D structure:



GENOME DATABASES

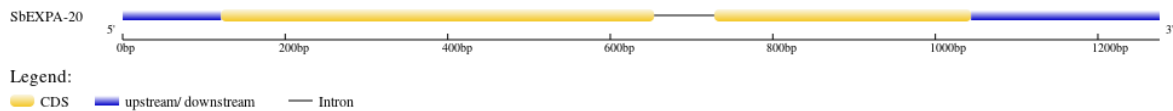
Phytozome: https://phytozome-next.jgi.doe.gov/info/Sbicolor_v3_1_1

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

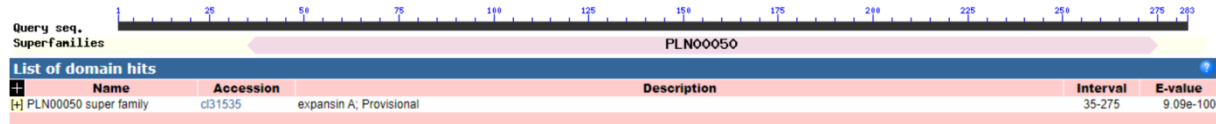
EXTERNAL RESOURCES

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GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>SbEXPA-20

MPGCVSHPSSPRRLHPLLRRSSSNNNNDLLLAGIVILLLLARASAGPWQKSAHATMT
MYGGSDASGTMGGACGYGNLYIAGYGVATGALSTPLFNGLTCGACFEIKCSCRSG
CQCQCHPSVSSVVITATNFCPPNYGLPSDAGGWCNPPRHFDLSMPAFLRIADYRASI
VPVTYRRVACRKSGGIRFSVNGFRYFNLVLISNVGGAGDVVRAAVKASHTEWLPLA
RNWGQNWQCSSILVGGALSFRVTTSDRRTLTSWNVAGPAWRFGQTFTAANKNFRDP*

CDS (coding sequence)

>SbEXPA-20

ATGCCTGGCTGTGTTTCTCATCCCTCATCACCACGGCGGCTACATCCGCTCCTGCG
CCGCAGCAGCAGCAACAACAACAATGATCTCCTGCTTGCCGGCATTGTCATC
CTCCTCCTTGCCCGGGCATCAGCTGGGCCGTGGCAGAAGAGCGCGCACGCCACCA
TGACCATGTATGGTGGCAGCGACGCGTCGGGCACCATGGGCGGCGCCTGCGGGT
ACGGCAACCTCTACATCGCGGGGTACGGCGTGGCGACGGGGGCGCTCAGCACGC
CGCTCTTCAACAACGGACTCACCTGCGGGCGCCTGCTTCGAGATCAAGTGCAGTTG
CAGGAGCGGCTGCCAGTGCCAGTGCCACCCCTCCGTGTCGTCGGTGGTGATCACG
GCCACCAACTTCTGCCCGCCAACTACGGGCTGCCCTCGGACGCCGGCGGGTGGT
GCAACCCGCCGCGCCACCACTTCGACCTTCCATGCCGGCCTTCCTCCGCATCGC
AGACTACCGCGCCAGCATCGTGCCCGTCACATACCGGAGGGTGGCGTGCCGCAA
GTCCGGCGGCATCCGGTTCAGCGTCAACGGCTTCCGCTACTTCAACCTGGTGCTC
ATCAGCAACGTGGGTGGCGCCGGCGACGTGGTCCGCGCCCGCTCAAGGCCTCG
CACACGGAGTGGCTGCCCTGGCGCGCAACTGGGGACAGAACTGGCAGTGCAGC
TCCATCCTCGTGGGCGGGGCGCTCTCCTTCCGCGTCACCACCAGCGACCGCCGCA
CCCTCACCTCCTGGAACGTCGCCGGACCAGCCTGGCGCTTTGGACAGACATTCAC
CGCCGCCAAAACCTTCAGGGACCCCTAG

Nucleotide

>SbEXPA-20

AGCTTTTCTTTTAATTCAGCTGAGATGAGATGAGCTTGGCTTGTGTCCACGGTCC
ACGCCTCACCTCGATGACTAGCTAGCATATATCGATGAGAAGACACAGACACAA
GGAATGCAAAGATGCCTGGCTGTGTTTCTCATCCCTCATCACCACGGCGGCTACA
TCCGCTCCTGCGCCGACGAGCAGCAACAACAACAATGATCTCCTGCTTGCC

GGCATTGTCATCCTCCTCCTTGCCCGGGCATCAGCTGGGCCGTGGCAGAAGAGCG
CGCACGCCACCATGACCATGTATGGTGGCAGCGACGCGTCGGGCACCATGGGCG
GCGCCTGCGGGTACGGCAACCTCTACATCGCGGGGTACGGCGTGGCGACGGGGG
CGCTCAGCACGCCGCTCTTCAACAACGGACTCACCTGCGGGCGCCTGCTTCGAGAT
CAAGTGCAGTTGCAGGAGCGGCTGCCAGTGCCAGTGCCACCCCTCCGTGTGTCGTCG
GTGGTGATCACGGCCACCAACTTCTGCCCGCCCAACTACGGGCTGCCCTCGGACG
CCGGCGGGTGGTGCAACCCGCCGCGCCACCACTTCGACCTCTCCATGCCGGCCTT
CCTCCGCATCGCAGACTACCGCGCCAGCATCGTGCCCGTACATACCGGAGGTAC
AGTACAGTAGACAGACACCTCCAGGCAGAGGCAGGCTTAATTAAGTGGTGTTTGC
ATTATATTATTGCAGGGTGGCGTGCCGCAAGTCCGGCGGCATCCGGTTCAGCGTC
AACGGCTTCCGCTACTTCAACCTGGTGCTCATCAGCAACGTGGGTGGCGCCGGCG
ACGTGGTCCGCGCCCGTCAAGGCCTCGCACACGGAGTGGCTGCCCTGGCGCG
CAACTGGGGACAGAACTGGCAGTGCAGCTCCATCCTCGTGGGCGGGGCGCTCTCC
TTCCGCGTCACCACCAGCGACCGCCGCACCCTCACCTCCTGGAACGTCGCCGGAC
CAGCCTGGCGCTTTGGACAGACATTCACCGCCGCCAAAACTTCAGGGACCCCTA
GGCTCCTCTGGCTAGCATAGCAGCCTGCTGCATCAGCACACTAGCTAGTCATCCA
TGCATCATCATCATTATATAAATTAGCTTGTTGGTTGGTTCTGCTTTTGTGTTA
ATAATCAAATGCAAATCATATTTAGAGGAAGGAAAAAGGCTTAGCCAACATATC
AAAAATCGAGAGGGGGCAACCAGCTGCTACCTTGCCCGTACGCGGTACGTGCTGT
GACTGTTGAA