

IDENTIFICATION

Species: *Sorghum bicolor*

Locus: Sobic.007G018000

Gene Model: Sobic.007G018000.1.p

Description: SbEXPA-31

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>

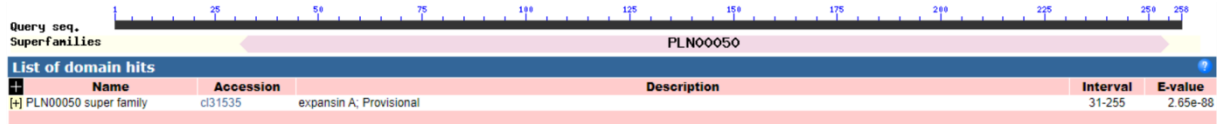
EXTERNAL RESOURCES

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GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>SbEXPA-31

MAPPLLLFLFLLPALAAGHQHPSSYGSSALSEWRPAKASYAAADPEDAIGGACGFGD
LGKHGYGMATVGLSTALFERGAACGGCYEVKCVEDLKYCLPGTSIVVTATNFCAPN
YGLPADAGGHCNPPNHFFLLPIQSFEKIALWKAGIMPIQYRRVKCLREGGVRFSVNG
RHFFFTVLISNVGGAGDVRSVKIKGTELGWLSMGRNWGQVWHINCDMRGQPLSFEL
SSSDGKTLTSFNVVPKDWEYGKTYTGKQFL*

CDS (coding sequence)

>SbEXPA-31

ATGGCTCCGCGCTCCTGCTCTTCCTCTTCCTCCTCCCGGCCCTCGCCGCCGGACA
CCAGCACCCGTCCTCCTATGGTTCGTCGCGCTCTCCGAGTGGCGCCCCGCCAAG
GCATCCTACTACGCCCGCGACCCCGAAGACGCCATCGGTGGGGCGTGCGGGTTCG
GGGATCTGGGGAAGCACGGGTACGGGATGGCGACGGTGGGGCTGAGCACGGCGC
TGTTTCGAGCGCGGCGCGGCGTGCGGCGGCTGCTACGAGGTCAAGTGCGTGCGAGG
ATCTCAAGTACTGCCTCCCCGGCACCTCAATCGTCGTCACGGCCACCAACTTCTGC
GCCCCAACTACGGCCTCCCCGCCGACGCCGGCGGCCACTGCAACCCGCCCAACC
ACCATTTCTCCTCCCATCCAGTCGTTTGAGAAGATTGCGCTCTGGAAGGCCGG
CATCATGCCATCCAGTACCGCCGTGTTAAGTGCCTCCGAGAAGGTGGTGTGTCAGG
TTCTCTGTCAATGGTCGGCACTTCTTCTTTACAGTCCTAATCAGCAATGTTGGTGG
CGCGGGTGATGTTAGATCTGTGAAGATCAAAGGAACAGAGTTAGGATGGCTCTC
GATGGGCCGCAATTGGGGCCAGGTGTGGCACATCAACTGTGACATGAGGGGACA
ACCCCTGTGTTTTGAGCTCAGCTCAAGCGATGGCAAGACACTCACCAGTTTCAAC
GTTGTGCCCAAGGATTGGGAGTATGGCAAGACATACACGGGGAAGCAGTTTCTTC
TGTAG

Nucleotide

>SbEXPA-31

CTGAAAGCACCACTTGCAGCTCCTCAGTCCACACTCCACACTCACTCCTTCCTC
CCCCACTCCCAGCTTACACCGAGGCAGACCATAACCGGCACCGGCAGCGAGCA
GTCGGGAGCCATGGCTCCGCCGCTCCTGCTCTTCCTCTTCCTCCTCCCGGCCCTCG
CCGCCGGACACCAGCACCCGTCCTCCTATGGTTCGTCGCGCTCTCCGAGTGGCG
CCCCGCAAGGCATCCTACTACGCCCGCGACCCCGAAGACGCCATCGGTACGCTT

CCAAACTTGCCTGCCTCATTATTGTTACCCCCATCAACCGCAATTCTGCCAGCC
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GAATTGTGCGTCCGTACGGTCTTGATTGATTCCGGCCGCATGGTGTACCCGTAG
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GCACGGCGCTGTTTCGAGCGCGGCGCGGCGTGCGGCGGCTGCTACGAGGTCAAGT
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GAAGGCCGGCATCATGCCATCCAGTACCGCCGGTACGTGCCACTGCTTATTTTG
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ATAGAGCTTACTTATATGTCACCAGTGATAACAAAATTTGTGGTGCCAGTGGTT
GCCATCCCAAATCCTTCTTCGTTCTTTCATGCTATGTTTCTTGACCAGTTGAGTGGT
CATTAGAACGTAGAATCAGTAGGATGAGTTGCACCAACACACCAAATTCAAAA
CGTAAAACAAATGCTCATAGCTGAGCTAGTCTCTGGGTTTCGCCAAATCTAAGTC
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CCTGTGAATTAGTATTACTGCTGTTCTACTTGTGTTGCCCTTAACCTTGCTTTATGTGT
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TAGAAGGCCGAATTTGGATGTCTCCGTTGTATTACAATATTTTACCTGGCAAGTA
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