

IDENTIFICATION

Species: *Sorghum bicolor*

Locus: Sobic.004G121900

Gene Model: Sobic.004G121900.1.p

Description: SbEXPA-28

Family: Alpha Expansin

3D structure:



GENOME DATABASES

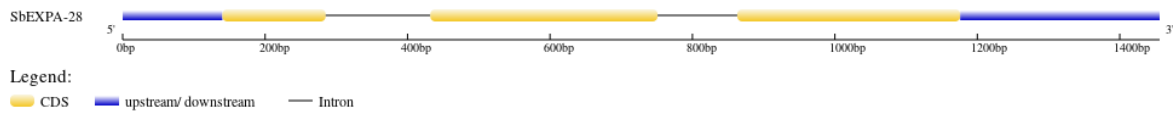
Phytozome: https://phytozome-next.jgi.doe.gov/info/Sbicolor_v3_1_1

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

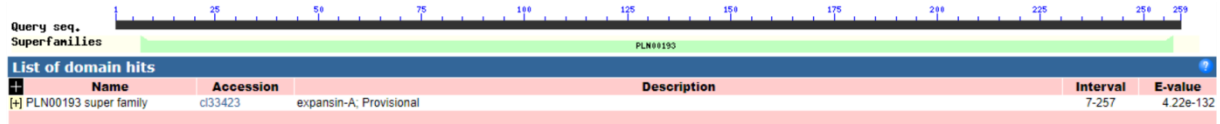
EXTERNAL RESOURCES

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GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>SbEXPA-28

MAQARVFTLLVLAAGWVSAMAANAPAPTGWLKAHATFYGGADASDTMGGACG
YGNLFSQYGTRTAALSTVLFNDGASCGQCYKIACDRKRADPMFCKPGVTVTITATN
FCPPNMALPEGGWCNQQRPHFDMAQPAFEKIGVYSGGIIPVMYKRVPVCRGGVRF
TINGHDYFNLVLVTNVAAAGSIKSMDVKSSNSTEWTPMARNWGANWHSLAYLTGQ
LLSFRVTDTDGQTIEFTNVVPQGWKFGQTFASKLQFK*

CDS (coding sequence)

>SbEXPA-28

ATGGCTCAAGCTCGAGTCTTCACGCTCTTGGTGCTCGCAGCTGCCGGTTGGGTGTC
GGCCATGGCAGCTAATGCTCCGGCACCAACCGGGTGGCTGAAGGCACATGCCAC
CTTCTACGGAGGCGCTGATGCCTCCGACACCATGGGCGGCGCGTGCGGGTACGGC
AACCTCTTCTCACAGGGCTACGGCACGCGGACGGCGGCGCTGAGCACGGTGCTCT
TCAACGACGGCGCCTCATGCGGGCAGTGCTACAAGATCGCGTGTGACCGCAAGA
GAGCCGACCCCATGTTCTGTAAACCTGGTGTCACGGTGACCATCACGGCCACCAA
CTTCTGCCC GCCTAACATGGCGCTGCCTGAGGGCGGCTGGTGCAATCAGCAGCGC
CCGCACTTTGACATGGCGCAGCCGGCGTTTGAGAAAATCGGCGTCTACAGCGGCG
GCATCATCCCCGTCATGTACAAGAGAGTTCCTTGCGTGAAGCGAGGTGGAGTCAG
GTTACAATCAATGGGCATGACTACTTCAATCTTGCTTGTGACCAATGTTGCGG
CTGCCGGCTCCATCAAGTCCATGGATGTCAAGAGCTCGAATTCGACCGAATGGAC
CCCAATGGCACGAACTGGGGCGCAAACCTGGCACTCTTGGCCTATCTCACAGGG
CAACTGCTCTCGTTCAGAGTCACCGACACGGATGGACAAACTATTGAATTCACAA
ACGTGGTGCCACAGGGATGGAAGTTTGGCCAAACATTTGCATCCAAGTTGCAGTT
CAAGTGA

Nucleotide

>SbEXPA-28

CCATACCCATACTTACATATATATACACACACACACCAACAATTTATTTCAGGCAA
CACGATCTCCACTTTCTGAGCTACATATATACAGTAGTACTCCAGATTCTTCTCGA
TCGTACGGTTCATAGAGGTGGTATCTATTATGGCTCAAGCTCGAGTCTTCACGCTC
TTGGTGCTCGCAGCTGCCGGTTGGGTGTCGGCCATGGCAGCTAATGCTCCGGCAC
CAACCGGGTGGCTGAAGGCACATGCCACCTTCTACGGAGGCGCTGATGCCTCCGA

CACCATGGGTAAGCTAGCTAGCCGCTCAAGAACCTGCATTGTATAGCTTTCCTAT
GCCACGAAAATGATGCACGCACTGTGCCGACCGATATCACACATATGTCGTCGTC
TAATCTGTTCTAAGAATATATATGTGTGTGTATGCATGGTGGCAGGCGGCGTG
CGGGTACGGCAACCTCTTCTCACAGGGCTACGGCACGCGGACGGCGGCGCTGAG
CACGGTGCTCTTCAACGACGGCGCCTCATGCGGGCAGTGCTACAAGATCGCGTGT
GACCGCAAGAGAGCCGACCCCATGTTCTGTAAACCTGGTGTCACGGTGACCATCA
CGGCCACCAACTTCTGCCCCCCTAACATGGCGCTGCCTGAGGGCGGCTGGTGCAA
TCAGCAGCGCCCGCACTTTGACATGGCGCAGCCGGCGTTTGAGAAAATCGGGCGTC
TACAGCGGCGGCATCATCCCCGTCATGTACAAGAGGTCTCTTTAATTTAATTTCCA
ACATGTTCCCTAGTCCGCCTCGACCTATCATCATAAAAAAAAAAAGACAAACAAATTG
GGATGCAATATCTTACGATGACTTTCTTGCTTGTAGAGTTCCTTGCGTGAAGCGAG
GTGGAGTCAGGTTCACAATCAATGGGCATGACTACTTCAATCTTGTGCTTGTGAC
CAATGTTGCGGCTGCCGGCTCCATCAAGTCCATGGATGTCAAGAGCTCGAATTCG
ACCGAATGGACCCCAATGGCACGAACTGGGGCGCAAACCTGGCACTCTCTGGCC
TATCTCACAGGGCAACTGCTCTCGTTCAGAGTCACCGACACGGATGGACAAACTA
TTGAATTCACAAACGTGGTGCCACAGGGATGGAAGTTTGGCCAAACATTTGCATC
CAAGTTGCAGTTC AAGTGACGATGAGAGCTCCATCATCCAGGATTATTTCCGGTG
ACTCGTCACTAGTCACAGGAGTATGATTCAAAAAAGTTGCTGGTCAAATGCATG
ATAATGGAGTTGCTTGTGCTAGCTGTACGCTATATATGTGCATGACTTGTATATA
CCGCCTATTCATCAGAGCGACGGCTATATATGACTTGTACCTCTCACTCTTTTTAT
TTATATTGTAATAATAATAGTCATGTCTAAATTCAATTTATATGGTGTATATAAAT
ATGTTCTTAATTTTATATCTT