

IDENTIFICATION

Species: *Sorghum bicolor* Rio

Locus: SbRio.09G183000

Gene Model: SbRio.09G183000.1.p

Description: SbrEXPA-29

Family: Alpha Expansin

3D structure:



GENOME DATABASES

Phytozome: https://phytozome-next.jgi.doe.gov/info/SbicolorRio_v2_1

KEGG:-

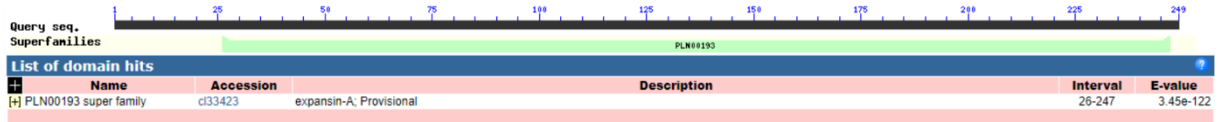
EXTERNAL RESOURCES

<https://www.sorghumbase.org/post/sorghum-bicolor-rio>

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>SbrEXPA-29

MAIAGALFLLLGLLAGEAAAGGYGGWQSAHATFYGGGDASGTMGGACGYGNLYST
GYGTNTAALSTALFNDGAACGSCYELRCDNAGRSCPLPGTITVTATNFCPPNYGLPSD
DGGWCNPPRPHFDMAEPAFLHIAQYRAGIVPVAFRRVPCVKKGGIRFTINGHSYFNL
VLVTNVAGAGDVRSVSIRGSRTGWQPMsrNWGQNWQSNADLDGQALSFQVTASDG
RTVTSNNAAPAGWQFGQTFEGAQF*

CDS (coding sequence)

>SbrEXPA-29

ATGGCCATTGCCGGTGCTCTTTTCTCCTGCTCGGTCTCCTCGCCGGGGAAGCCGC
GGCGGGCGGCTACGGCGGGTGGCAGAGCGCGCACGCCACGTTCTACGGCGGCGG
CGACGCGTCCGGCACAATGGGCGGCGCGTGC GGGTACGGCAACCTGTACAGCAC
CGGGTACGGCACGAACACGGCGGGCGCTGAGCACGGCGCTGTTCAACGACGGCGC
GGCGTGCGGGTCTGCTACGAGCTGCGGTGCGACAACGCCGGGCGGTTCGTGCCTG
CCGGGCACCATCACCGTGACGGCCACCACTTCTGCCCTCCCAACTACGGCCTCC
CCAGCGACGACGGCGGCTGGTGCAACCCGCCGCGGCCGCACTTCGACATGGCCG
AGCCCGCCTTCTCCACATCGCGCAGTACCGCGCCGGCATCGTGCCCGTGCCTT
CAGGAGAGTGCCGTGCGTGAAGAAGGGCGGCATCCGGTTCACCATCAACGGGCA
CTCCTACTTCAACCTGGTGCTGGTGACCAACGTGGCGGGCGCGGGGGACGTGCGG
TCCGTCTCCATCCGGGGCTCGCGGACGGGGTGGCAGCCATGTTCGCGGAACTGGG
GCCAGAACTGGCAGAGCAACGCGGACCTGGACGGGCAGGCGCTGTTCGTTCCAGG
TCACCGCCAGCGACGGCCGCACCGTCAACAGCAACAACGCCGCCCGCCCGGAT
GGCAGTTCGGCCAGACCTTCGAGGGCGCCAGTTCTGA

Nucleotide

>SbrEXPA-29

TTAGCCGCACCAAATCGCAGAGAAATTTTGTATACGCGCACGGCGCGGGGCAC
CGGCACGGCCCGCGAGTCTCGCAACCGCCACCGGCGCCTTTGGTTCGGCTATAAA
TAGTTGGGTGCTGGGAGGGCAAGCTCCTCACTGCCAGCCAGACGTTTCCAAGCCA
TTAGTTGTTGGTAGCACACAAGCTAAGCTTTAGATAACCTTCTTCTTCTCCTGCT
TCTGTCTCGAAGGCAGCTTCGGAGCTCGGAGCGCCAGCCAGCAATGGCCATTGC
CGGTGCTCTTTTCTCCTGCTCGGTCTCCTCGCCGGGGAAGCCGCGGCGGGCGGC

TACGGCGGGTGGCAGAGCGCGCACGCCACGTTCTACGGCGGGCGGCGACGCGTCC
GGCACAATGGGTGAGTCGTCGTCCTACTGCCCTGCCCTCGGCCTGCCGCGGCCGTGC
GTTCCGATCATCGTCGATCGGCTCAGCAGCAAATTAAGAAACTGATGGTTGTT
TTTTGTGACATCCCTTCTTTCTCGTCCAGGCGGGCGCGTGCGGGTACGGCAACCTGT
ACAGCACCGGGTACGGCACGAACACGGCGGGCGCTGAGCACGGCGCTGTTCAACG
ACGGCGCGGCGTGCGGGTCTGCTACGAGCTGCGGTGCGACAACGCCGGGCGGT
CGTGCCTGCCGGGCACCATCACCGTGACGGCCACCAACTTCTGCCCTCCCAACTA
CGGCCTCCCCAGCGACGACGGCGGCTGGTGAACCCGCCGCGGCCGCACTTCGAC
ATGGCCGAGCCCGCCTTCCCTCCACATCGCGCAGTACCGCGCCGGCATCGTGCCCG
TCGCCTTCAGGAGGTAACCCCTCATGCTGGCTCGATCAGTTTGCTCTTGATCAC
ATGCCCCGTGCTGGCTGCCTGCACATGTGTGCTGCTGGCACGGCACGGCGCCGTGG
TCACGCACGCACACATGCACGATATGGGCCCCGAGCTGCTATGCTACGGCTCGCCC
CGCCTTGTGGTGGACCAAATCGACCCAACCGCGTCCGGACGTCGGTTTCAAGGTTG
GTGGACCCGCACCCCAAGTTCGGCCATTAGTTCGGTGGGCCACCCTGCAGATTC
GATACGGGTCTCGTGGGGTCCAGGATGAGCTGCAGGCGACGCGCATGTGCCGTG
CCACCACAACACTCTAGCGTAGTACTCACACGCACTACTGACTACTCCATTGAC
GCCGATCACGAATCGGTCGTCCTACGTATACGTAGTGGCCGTTAGTTGCAAACGC
ATCGATCTGCATGTGAAAATGACATGTGCTACACGTACGATGGCATGCATGCAG
AGTGCCGTGCGTGAAGAAGGGCGGCATCCGGTTCACCATCAACGGGCACTCCTAC
TTCAACCTGGTGCTGGTGACCAACGTGGCGGGCGCGGGGGACGTGCGGTCCGTCT
CCATCCGGGGCTCGCGGACGGGGTGGCAGCCCATGTCGCGGAACTGGGGCCAGA
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CCAGCGACGGCCGCACCGTCACCAGCAACAACGCCGCCCCCGCCGGATGGCAGT
TCGGCCAGACCTTCGAGGGCGCCCAGTTCTGATTTCTGAACGAACTTCTTCTGATC
GTCGATGAAGTGGACGATTAGTCAGTCAGTCAGTCAATTAATTACGGTACTATTT
TTATCGATTTGTTTCTTTTTTTTTTGCCTTTTGC GCGTGATGAGTGTGCAAGAGAGA
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CCTAGTAGTACGTAGTAGACGGTTTTCTTTGCTTTTGGCTCTGGTGGTGGTGGTGG
TGGTGGATTATGGAGTGTGGACCAAAGATTGGAGATCCAGCTCCTAGAAGTACGT
ACTAATAGTACTTGAAGAAATGAATAATAGTTGTAATTTATTTTTGGACCTAGCTT
GTTGTTATTATTATTGTA CTGCGCCGGCCTTGAGTCGAAATTGAAGCTCGCGCAA
GGCCGGCCGGCCAGCCATTGCTCTCATT CATCAGTAGCTTCGTTCTGGTGTGTTTG
TACGTATGGGTGGCGGTGGTGACTTTTGGTGTGTTGTTGGGGGTGTAACGCCAAGT
ACAGTATCTTCTGCTCACATGGGTGGGGGCAAACCATGTCGTGTGCTGCCTTGGA
TTCCGCGGCCGCGAGCGAGCGGTGTCGGTTGCGTCCCTCTGCTGGCTAGCTGCTG
CCTGCGGCTAAGGTCTTGTTAATTCCAAAATTTTTTGCAAACAGACATCGTAGC
ATTTTCGTTTGTATGTGACAAATATTGTCTAATCATGCACTAACTAGGCTCAAAG
ATTCGTCTCGTCAATTTTCGATCAA ACTGTGCAATTAGTTTTTATTTTCTTCTATATT
TAATACTCCATACATGCGTCTAAAA