

## IDENTIFICATION

**Species:** *Sorghum bicolor* Rio

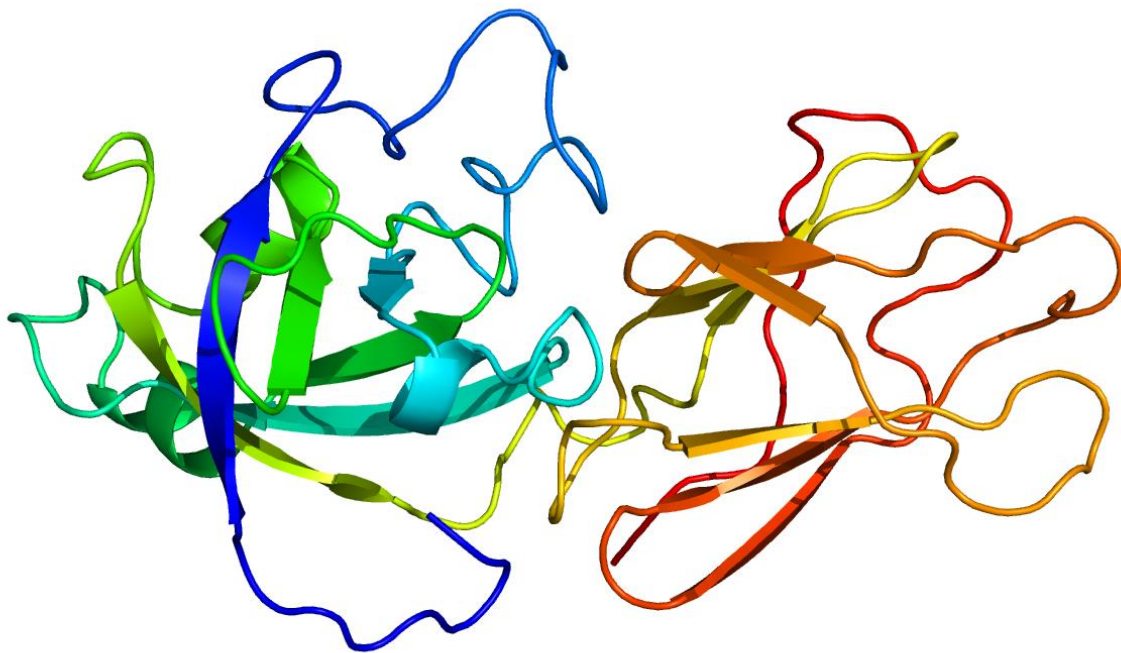
**Locus:** SbRio.07G021300

**Gene Model:** SbRio.07G021300.1.p

**Description:** SbrEXPA-27

**Family:** Alpha Expansin

**3D structure:**



## GENOME DATABASES

Phytozome: [https://phytozome-next.jgi.doe.gov/info/SbicolorRio\\_v2\\_1](https://phytozome-next.jgi.doe.gov/info/SbicolorRio_v2_1)

KEGG:-

## EXTERNAL RESOURCES

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

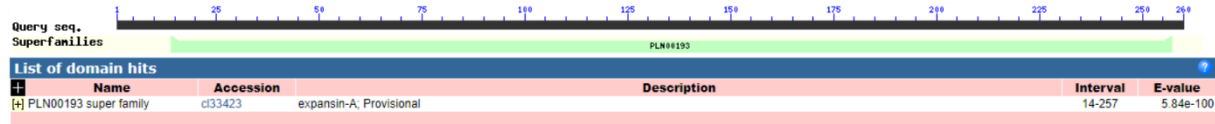
## GENE STRUCTURE



Legend:

Exon — Intron

## DOMAIN ARCHITECTURE



## SEQUENCES

### Peptide

>SbrEXPA-27

MGKRFLHQLLAVVLALFVSPARSGDWLPATATFYGGADGSDTMGGACGYSDLYEQ  
GYGINNAALSTALFNDGASCGQCYVIICDSSKTQWCKPGNNWVVSATNFCPPNWD  
LPAVGDLPAGGWCAPPRPHFDMSQPAWENIGIYSAGVINVLYQRVKCWKSGGVRFTI  
AGFNGFYMVLITNVAGSGSIQSMVVKGNSTDWIPMYRNWGANWHCLSGGLVGQGL  
SFALVSTGGQNLVFKDVVPAWWQFGQTYTTYQNFDY\*

### CDS (coding sequence)

>SbrEXPA-27

ATGGGCAAACGTTTCCTCCACCAACTGCTCGCTGTCGTCCTTGC ACTCTTCGTCTC  
GCCGGCGAGATCGGGCGACTGGCTTCCGGCCACCGCCACGTTCTATGGTGGCGCT  
GACGGCTCCGACACAATGGGTGGCGCGTGTGGGTACAGCGACCTGTACGAGCAG  
GGCTACGGCATCAACAACGCAGCGCTGAGCACGGCGCTCTTCAACGACGGCGCG  
TCGTGCGGGCAGTGCTACGTCATCATCTGCGACAGCAGCAAGACCCAGTGGTGCA  
AGCCCGGCAACA ACTGGGTTGTCGTCTCTGCCACCAACTTCTGCCCGCCTAACTG  
GGACCTCCCCGCCGTCGGAGACCTCCCCGCCGGCGGCTGGTGCGCCCGCCGCGG  
CCCCACTTCGACATGTCCCAGCCCGCCTGGGAGAACATCGGCATCTACAGCGCCG  
GCGTCATCAACGTCCTCTACCAGCGAGTCAAGTGCTGGAAGAGCGGCGGCGTGC  
GCTTACCATCGCCGGCTTCAACGGCTTCTACATGGTGCTCATACCAACGTCGCC  
GGCAGCGGCTCCATTCAGAGCATGGCGGTGAAGGGCAACAGCACGGATTGGATC  
CCCATGTACAGGAACTGGGGCGCCA ACTGGCACTGCCTCTCCGGCGGGCTCGTCC  
GACAGGGCCTTAGCTTCGCGCTCGTCTCCACCGGCGGCCAGAACCTCGTCTTCAA  
GGACGTCGTGCCGGCGTGGTGGCAGTTCGGACAAACTTACACCACCTACCAGAAT  
TTCGACTACTAA

### Nucleotide

>SbrEXPA-27

ATGGGCAAACGTTTCCTCCACCAACTGCTCGCTGTCGTCCTTGC ACTCTTCGTCTC  
GCCGGCGAGATCGGGCGACTGGCTTCCGGCCACCGCCACGTTCTATGGTGGCGCT  
GACGGCTCCGACACAATGGGTAATAACCTAGCTATATATAACCGTTGTCTTTGCGT  
TGTT CAGTATAGATTTCCATCTGACACGCACTAACATGATTGACCGGTCCGAGCA  
CGACACTAAA AAGCATGGTTCAAGCACGGTATAGCCCGGTGGTAGTATCATACT

GGGCCATAACTTCGGCCCCGAGTGCCGGCACGGACACAACACATCTAATAGGCT  
GGCACCACGTCGGCCTGATTATTTCCACCGTTTAGATGCTTTGAGGATACATCATG  
ACCATTAGATGTATTCTGAGTCACATATATAAACATCACGCAACCTTTTCAAACCTC  
TAACTCCCTAGCCAGCGGAGCAGACACATCCTTGCTCCTTCTCCGACATTTGAAC  
AGCCGAACACCTCTGTCTCTCGCTCGCTTGACCAGTGGCCATGCAGATCCTAAGC  
CACTCCCTTCATTGCTCCCTACGTCTTGTACTACCCTTGAGACATGGCTGCGACGA  
CACGGTGGCCTAGCGCAAGGCATAGCTGCTGCGGTGGTGGCTCGGTGGCCTAGCG  
CAAGGCATAGCTGCAAGATGTGGCTGCTGCTACGGCCACTCTCTCTCTCCCCG  
ATGGCTATACGACAGCGGTGACGCCTGTCTTCTCCTTGAGACAGGGCGCAACGAG  
CTTCTCGACTCCTCCTGAAGCCATGGGCCAGCACAGGGCACGATGGGCCACCGTG  
CTTATCTACACGGCACGACACAACCTAAGGAGTCATAATGTCGTGCCTGAGTCGAT  
AGGTTGGCACGATGGTCCGAGACGACACGGCACAGTAGAACATAGTGTGCATA  
ATGCCAGAACCGGCCATCCGTTTGGCCAAGTATATAATGTTTCAGGGTCCGCATGC  
ATGCATGCATGCATTGCAACACATACTGATCTGATGGATGAGCACGCATACACAT  
GCAGGTGGCGCGTGTGGGTACAGCGACCTGTACGAGCAGGGCTACGGCATCAAC  
AACGCAGCGCTGAGCACGGCGCTCTTCAACGACGGCGCGTCGTGCGGGCAGTGC  
TACGTCATCATCTGCGACAGCAGCAAGACCCAGTGGTGCAAGCCCCGGCAACAAC  
TGGGTTGTCGTCTCTGCCACCAACTTCTGCCCCGCTAACTGGGACCTCCCCGCCGT  
CGGAGACCTCCCCGCCGGCGGCTGGTGGCGCCCCGCCGCGGCCCCACTTCGACATG  
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TCTACCAGCGAGTCAAGTGCTGGAAGAGCGGCGGCGTGCGCTTACCATCGCCGG  
CTTCAACGGCTTCTACATGGTGCTCATCACCAACGTCGCCGGCAGCGGCTCCATT  
CAGAGCATGGCGGTGAAGGGCAACAGCACGGATTGGATCCCCATGTACAGGAAC  
TGGGGCGCCAACTGGCACTGCCTCTCCGGCGGGCTCGTCGGACAGGGCCTTAGCT  
TCGCGCTCGTCTCCACCGGCGGCCAGAACCCTCGTCTTCAAGGACGTCGTGCCGGC  
GTGGTGGCAGTTCGGACAAACTTACACCACCTACCAGAATTTGACTACTAA