

## IDENTIFICATION

**Species:** *Sorghum bicolor* Rio

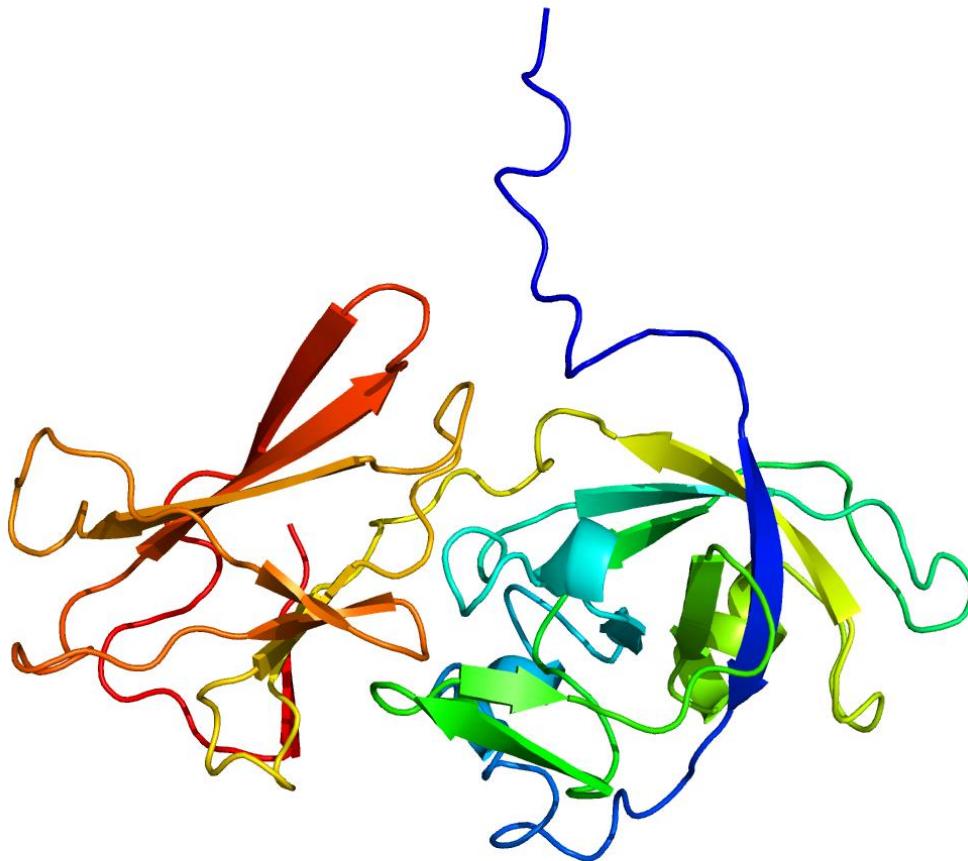
**Locus:** SbRio.10G006800

**Gene Model:** SbRio.10G006800.1.p

**Description:** SbrEXPA-30

**Family:** Alpha Expansin

**3D structure:**



## GENOME DATABASES

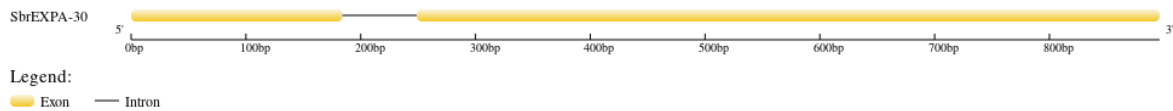
Phytozome: [https://phytozome-next.jgi.doe.gov/info/SbicolorRio\\_v2\\_1](https://phytozome-next.jgi.doe.gov/info/SbicolorRio_v2_1)

KEGG:-

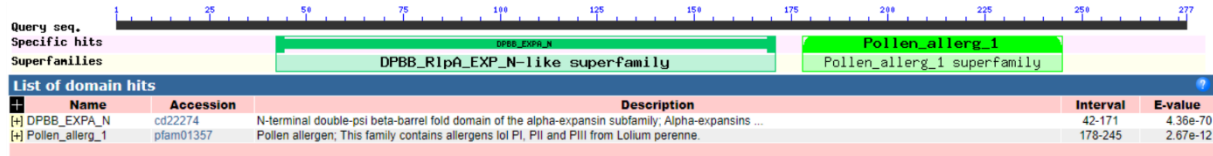
## EXTERNAL RESOURCES

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

## GENE STRUCTURE



## DOMAIN ARCHITECTURE



## SEQUENCES

### Peptide

>SbrEXPA-30

MASSSRAPAMMVVVA AVIMAAHLASGSGYDSAAAAPFTKSDWQDGSATFYGQDS  
GLGADFGGACGYGANDILSLYSTRTAALSTPLFASGAGCGQCYELRCVSSRWCPGS  
PSVVVTGNTLCPNWNLPDNGGWCNPPRRHFDMAPPSFLILAQRVAGIVPVQFRRV  
PCQRSGGVRFYVQGNYYWLLLYVMNVGGSGDVGD LAVKRAGEPDCNYVPASRNW  
GITYQVFAALGNSKGLVVRMTTYS LPRKIIVDDAITAGWCTGLSYQGSNNFY\*

### CDS (coding sequence)

>SbrEXPA-30

ATGGCGTCGTCGTCAGGGCTCCGGCGATGATGGTGGTCGTCGCGGCCGTGATCA  
TGGCGGCGGCACACCTCGCGAGCGGCAGCGGCTATGACAGTGCTGCGGCGGCGC  
CTTTCACCAAGTCGGACTGGCAAGACGGCAGCGCCACCTTCTACGGCCAAGACTC  
CGGCCTTGGCGCAGACTTCGGCGGCGCGTGGCGGCTACGGCGCCAACGACATCCTG  
TCGCTCTACTCGACGCGCACGGCGGCGCTGAGCACGCCGCTGTTTCGCGAGCGGCG  
CCGGGTGCGGGCAGTGCTACGAGCTGCGGTGCGTCAGCTCCCAGTGGTGCAACCC  
GGGTTTCGCCGTCGTCGTCACCGGCACCAACCTCTGCCCGCCAACTGGAAC  
CTCCCAGCGACAACGGCGGCTGGTGCAACCCGCCGCGGAGGCACTTCGACATG  
GCGCCGCCGTCCTTCTCCTCCTCGCGCAGCGCGTGGCGGGCATCGTCCCCGTGC  
AGTTCGCCCGCGTCCCGTGCCAGCGCTCCGGCGGGGTCAGGTTCTACGTGCAGGG  
CAACTACTACTGGCTCCTGCTCTACGTCATGAACGTCGGCGGCAGCGGCGACGTC  
GGCGACCTCGCCGTC AAGAGGGCCGGCGAGCCGGACTGCAACTACGTGCCCGCG  
TCGCGCAACTGGGGCATCACGTACCAGGTGTTTCGCCGCGCTCGGCAACAGCAAG  
GGCCTCGTCGTCAGGATGACCACCTACAGCTTGCCGCGGAAGATCATCGTCGTCG  
ACGACGCCATCACCGCCGGGTGGTGCACTGGACTCTCCTACCAGGGATCCAACAA  
CTTCTATTGA

### Nucleotide

>SbrEXPA-30

ATGGCGTCGTCGTCAGGGCTCCGGCGATGATGGTGGTCGTCGCGGCCGTGATCA  
TGGCGGCGGCACACCTCGCGAGCGGCAGCGGCTATGACAGTGCTGCGGCGGCGC  
CTTTCACCAAGTCGGACTGGCAAGACGGCAGCGCCACCTTCTACGGCCAAGACTC

CGGCCTTGGCGCAGACTTCGGTACGTAGCATGCGTTCATTTGAACTAATGCTGGA  
GGGAGTCAAATGCTCATCATTGGAATGCAGGCGGCGCGTGC GGCTACGGCGCCA  
ACGACATCCTGTCGCTCTACTCGACGCGCACGGCGGCGCTGAGCACGCCGCTGTT  
CGCGAGCGGCGCCGGGTGCGGGCAGTGCTACGAGCTGCGGTGCGTCAGCTCCCG  
GTGGTGCAACCCGGGTTCGCCGTCCGTTCGTCGTCACCGGCACCAACCTCTGCCCG  
CCCAACTGGAACCTCCCCAGCGACAACGGCGGCTGGTGCAACCCGCCGCGGAGG  
CACTTCGACATGGCGCCGCGTCCTTCCTCATCCTCGCGCAGCGCGTGGCGGGCA  
TCGTCCCCGTGCAGTTCGCGCCGCGTCCCGTGCCAGCGCTCCGGCGGGGTGAGGTT  
CTACGTGCAGGGCAACTACTACTGGCTCCTGCTCTACGTTCATGAACGTCGGCGGC  
AGCGGCGACGTCGGCGACCTCGCCGTCAAGAGGGCCGGCGAGCCGGACTGCAAC  
TACGTGCCCCGCGTCGCGCAACTGGGGCATCACGTACCAGGTGTTGCGCCGCGCTCG  
GCAACAGCAAGGGCCTCGTCGTCAGGATGACCACCTACAGCTTGCCGCGGAAGA  
TCATCGTCGTCGACGACGCCATCACCGCCGGGTGGTGCACTGGACTCTCCTACCA  
GGGATCCAACAACCTTCTATTGA