IDENTIFICATION

Species: *Sorghum bicolor Rio*

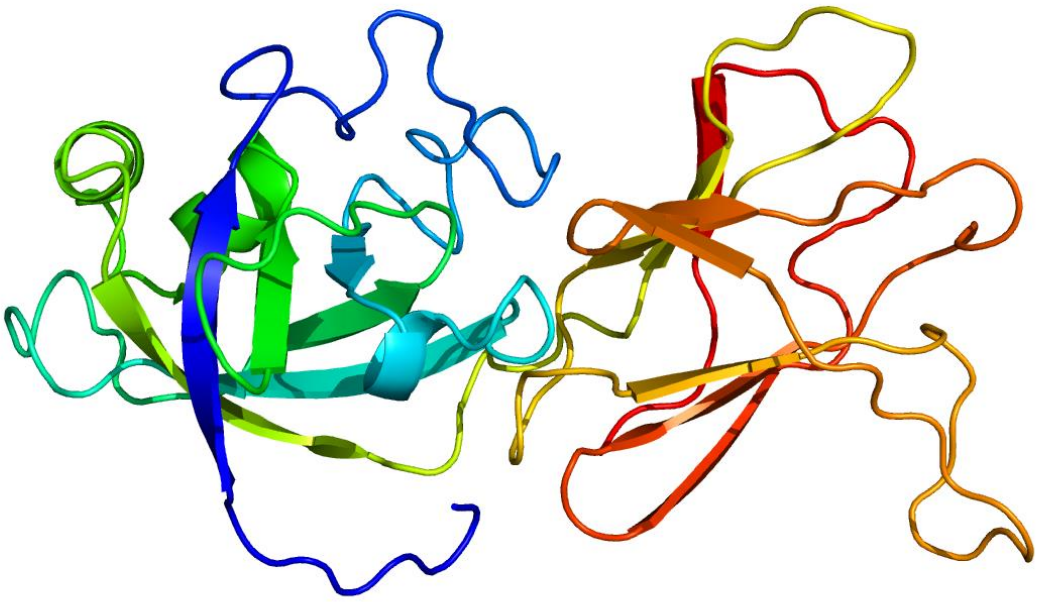
Locus: SbRio.01G293400

Gene Model: SbRio.01G293400.1.p

Description: SbrEXPB-07

Family: Beta Expansin

3D structure:



GENOME DATABASES

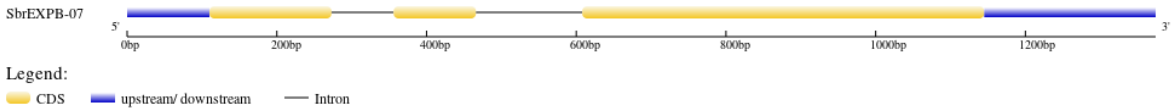
Phytozome: https://phytozome-next.jgi.doe.gov/info/SbicolorRio_v2_1

KEGG:-

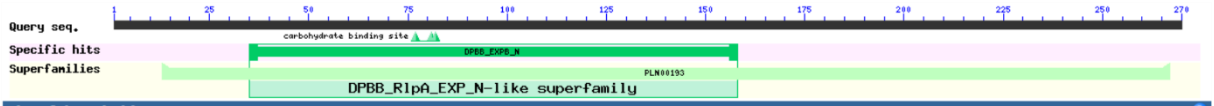
EXTERNAL RESOURCES

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

GENE STRUCTURE



DOMAIN ARCHITECTURE



List of domain hits

Name	Accession	Description	Interval	E-value
[+] DPBB_EXPB_N	cd22275	N-terminal double-psi beta-barrel fold domain of the beta-expansin subfamily; Beta-expansins ...	35-158	1.59e-79
[+] PLN00193 super family	cl33423	expansin-A; Provisional	13-267	5.34e-25

SEQUENCES

Peptide

>SbrEXPB-07

MAAAVISISSKVPALAALFVVLAMSAEAASPNGGWLAAKATWYGAPNGAGPDDNG
GACGFKNTNQYPYMSMTSCGNEPLFKDGKGCGACYQIRCLNSTHDACSGRAKRVIIT
DMNYYPVSKYHFDLSGTAFGAMAKTGLNDKLRHAGIIDIQFRRVPCNYKGLNVNFR
VQVGSNPNYFAVLVQYAGKDGAVVQLDLMETSKATGKPTGVWTPMRVSWGAVW
RLDTKRPLQPPFSLRVRNGSGKTLVASNVIPANWKPMTDYPSNVQFPN*

CDS (coding sequence)

>SbrEXPB-07

ATGGCCGCCGCCGTGATCTCCATCTCCTCAAAGGTGCCTGCACTCGCTGCACTGTT
CGTGGTGCTCGCCATGTCCGCCGAGGCGGCGAGCCCCAACGGCGGCTGGCTGGC
AGCCAAGGCCACATGGTACGGCGCGCCCAACGGCGCAGGCCCTGACGACAATGG
TGGCGCGTGTGGGTTCAAGAACACCAACCAGTACCCGTACATGTCCATGACGTCG
TGCGGCAACGAGCCGCTGTTCAAGGACGGCAAGGGCTGCGGCGCATGCTACCAG
ATACGGTGCCTGAATAGCACCCACGACGCTTGCTCCGGCAGAGCGAAGCGTGTG
ATCATCACGGACATGAACTACTACCCGGTGTCCAAGTACCACTTCGACCTGAGCG
GCACGGCGTTCGGCGCCATGGCCAAGACCGGGCTGAACGACAAGCTCCGGCACG
CGGGCATCATCGACATCCAGTTCAGGCGGGTGCCCTGCAACTACAAGGGCCTGAA
CGTCAACTTCCGCGTCCAGGTGGGTTCCAACCCCAACTACTTCGCGGTGCTGGTG
CAGTACGCGGGCAAGGACGGCGCCGTGGTGCAGCTGGACCTGATGGAGACCAGC
AAGGCCACCGGCAAGCCGACGGGGGTGTGGACGCCGATGCGCGTGTCGTGGGGC
GCCGTCTGGCGCCTCGACACCAAGCGGCCCCTGCAGCCGCCCTTCTCGCTGCGCG
TTCGGAACGGCTCCGGCAAGACGCTGGTGGCCAGCAACGTCATCCCGGCCAACTG
GAAGCCGATGACCGACTACCCCTCCAACGTCCAGTTCCCTAATTAG

Nucleotide

>SbrEXPB-07

CCGATCGACCAAGAAAAACACCGACCGAACATCCAAGTACAAGTACACTCGCTG
TTCTTGAAAATTGTAGGTGATCGACTATAGCTGGTTCGATCGATCGAGCTGAGAC
GATGGCCGCCGCCGTGATCTCCATCTCCTCAAAGGTGCCTGCACTCGCTGCACTG

TTCGTGGTGCTCGCCATGTCCGCCGAGGCGGCGAGCCCCAACGGCGGCTGGCTGG
CAGCCAAGGCCACATGGTACGGCGCGCCCAACGGCGCAGGCCCTGACGACAATG
GTACGTGCGTGCCTGCGTCCCACGCACACGGTGGGTGTCACTACCAATGCCCGTG
TGCATGTCTGACGTTGTTGTGTCTGCAGGTGGCGCGTGTGGGTTCAAGAACACCA
ACCAGTACCCGTACATGTCCATGACGTCGTGCGGCAACGAGCCGCTGTTCAAGGA
CGGCAAGGGCTGCGGCGCATGCTACCAGGTAGTAGAGTCTACTCTTCTACAAATA
AATTAGTTAACCTAGACATAGTTAACTTGCAGTCCCTGGTCAGTTAATTTGATCAT
CGCGGTCAACCGTAGCAGTAACCCCTTTAATATTCTCGTACCAATTGAAAATCCA
TCAGATACGGTGCCTGAATAGCACCCACGACGCTTGCTCCGGCAGAGCGAAGCGT
GTGATCATCACGGACATGAACTACTACCCGGTGTCCAAGTACCACTTCGACCTGA
GCGGCACGGCGTTCGGCGCCATGGCCAAGACCGGGCTGAACGACAAGCTCCGGC
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GAACGTCAACTTCCGCGTCCAGGTGGGTTCCAACCCCAACTACTTCGCGGTGCTG
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GCGTTCGGAACGGCTCCGGCAAGACGCTGGTGGCCAGCAACGTCATCCCGGCCA
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CGCGCTGCAATCGCCCAGATCATTGTTATTCGATCGTCCCATTATTAGTTATATTG
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CT