

IDENTIFICATION

Species: *Setaria italica*

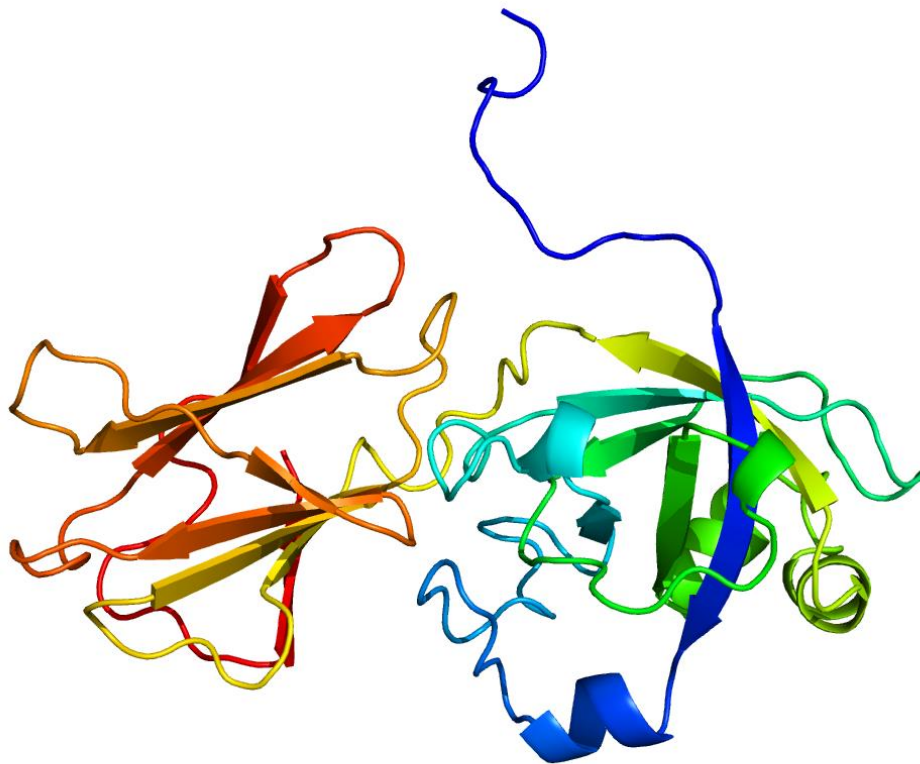
Locus: Seita.9G157100

Gene Model: Seita.9G157100.3.p

Description: SitEXPB-18

Family: Beta Expansin

3D structure:



GENOME DATABASES

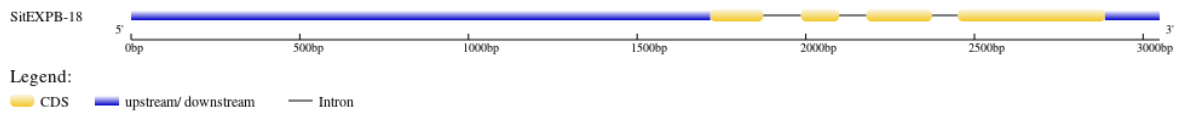
Phytozome: https://phytozome-next.jgi.doe.gov/info/Sitalica_v2_2

KEGG: <https://www.genome.jp/entry/gn:T02818>

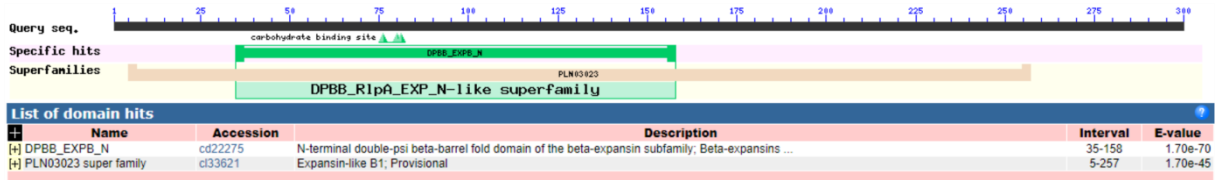
EXTERNAL RESOURCES

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GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>SitEXPB-18

MASKIHPLSFIAITALAFL LHPCASIEFRRELSGWSNGIATWYGTADGAGSDAGACGF
QNDVDQPPFSSMIAAGCSSIYDSGKGCSCYQVVCTGNGGCSGNPVTVVITDECPDC
PCPDDQVHFDMSGTAFGAMAKPGQEGQLRGAGSIQIQYKRVQCEWPGVNATFSVES
GSSPSYLAVLIEYEDGSDLDAVDIMQGGSGQWVPMQQSWGAVWKLNSASPLQGPF
DIRLTFSSGRVLVASNAIPAGWNAGVAYRSGGVAVARARPRSGGCRSHDAAGTLSG
LVYVLLLLVLFLGLEL*

CDS (coding sequence)

>SitEXPB-18

ATGGCTTCCAAGATCCATCCGTTGTCTTTCATTGCCATCACAGCTCTCGCCTTTCTT
CTCCACCCTTGTGCATCCATTGAGTTCCGCCGTGAGCTCTCTGGTTGGTCCAATGG
TATCGCTACATGGTATGGCACAGCTGATGGTGCAGGAAGTGACGCTGGTGCGTGT
GGGTTCCAGAATGATGTTGACCAGCCACCATTCTCCTCCATGATCGCCGCTGGCT
GCTCTTCCATCTACGACTCTGGCAAGGGCTGTGGTTCTTGCTATCAGGTGGTGTGC
ACTGGCAATGGTGGTTGCTCTGGTAACCCGGTGACTGTTGTCATCACCGACGAGT
GCCCTGACTGCCCATGCCCGGATGACCAGGTGCACTTCGACATGAGCGGGACAGC
GTTTGGTGCCATGGCGAAGCCCGGCCAGGAAGGCCAGCTTCGTGGCGCCGGCTCC
ATCCAAATCCAGTACAAACGTGTGCAGTGCAGTGGCCTGGGGTGAACGCCACCT
TCTCCGTGGAGTCCGGGTCCAGCCCGAGCTACCTGGCCGTGCTCATCGAGTACGA
GGACGGCGACAGCGACCTCGACGCCGTGGACATCATGCAGGGCGGGTCGGGGCA
GTGGGTGCCGATGCAGCAGTCGTGGGGCGCCGTGTGGAAGCTGAACTCGGCTTCA
CCCCTCCAGGGCCCCTTCGACATCCGCCTGACGTTTCAGCTCCGGCAGGGTGCTCG
TCGCCAGCAACGCCATACCCGCGGGCTGGAACGCCGGCGTGCGGTACCGGTCCG
GCGGCGTGGCGGTGGCGAGGGCCAGGCCAGGAGCGGTGGCTGCCGGAGCCACG
ACGCTGCTGGGACACTCAGCGGGCTGGTGTATGTCTCCTCCTACTTGTGTTGTTT
CTGGGATTGGAGTTGTGA

Nucleotide

>SitEXPB-18

GCAGTGGGTGCCGATGCAGCAGTCGTGGGGCGCCGTGTGGAAGCTGAACTCGGC
TTCACCCCTCCAGGGCCCCTTCGACATCCGCCTGACGTTTCAGCTCCGGCAGGGTG
CTCGTCGCCAGCAACGCCATAACCGCGGGCTGGAACGCCGGCGTGGCGTACCGGT
CGGGCGGCGTGGCGGTGGCGAGGGCCAGGCCAGGAGCGGTGGCTGCCGGAGCC
ACGACGCTGCTGGGACACTCAGCGGGCTGGTGTATGTCCTCCTCCTACTTGTGTTG
TTTCTGGGATTGGAGTTGTGAAGTGTGGACTGAACTACATTCTCGGAAAAAAGT
GTGGACTGAACTGCGATGCATTTCTGGCGCTACTCTCCGCCCATGTAAATATATA
CAGTATATATGTTTCATGAGAAGGCACATGTTATGTTCTGCTTATGGTTGGTCATAT
TTTCGAAATCATTTTGG