

IDENTIFICATION

Species: *Miscanthus sinensis*

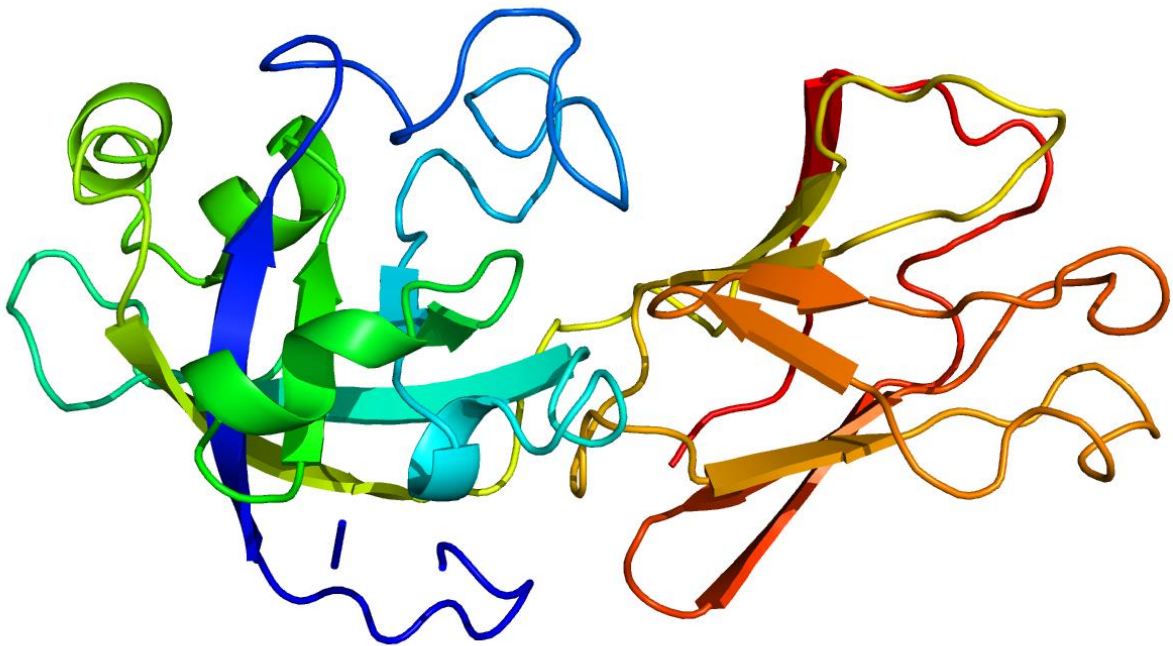
Locus: Misin08G230500

Gene Model: Misin08G230500.1.p

Description: McsEXPB-46

Family: Beta Expansin

3D structure:



GENOME DATABASES

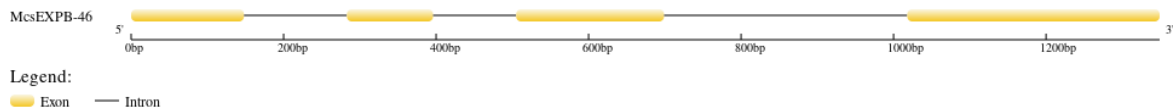
Phytozome: https://phytozome-next.jgi.doe.gov/info/Msinensis_v7_1

KEGG:-

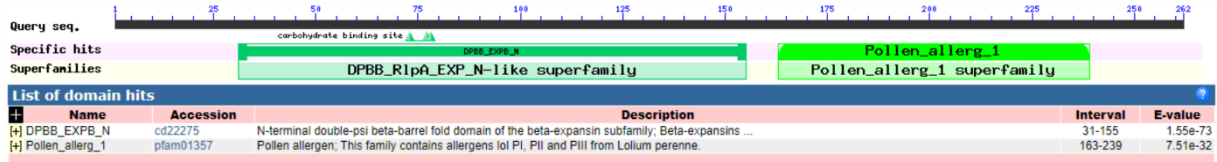
EXTERNAL RESOURCES

<https://grass-genome-hub.southgreen.fr/Genomeassembly/47213>

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>McsEXPB-46

MVLCRFVAFVALACLLRPGAPVELHRKLSGWSGDAGATWYGAATGAGSDGGACG
YQNAVDQPPFASMI AAGSLSIFQNGEGCGSCYQVKCTGHASCSGSPVSVVLTDECPV
GACLAEPVHFDLSGTAFGAMAKPGQADQLRSAGRLNIQYARVPCNWNMGMDIAFKV
DAGSNPNYFAVLIEYESGDGELRSVELMQRGAGAAWAPMQRSWGAVWRYNSGAA
LQAPFSVRLTSDSGRTLVASDVIPAGWTPGATYCSVVNFNN*

CDS (coding sequence)

>McsEXPB-46

ATGGTCCTGTGTCGCTTTGTGGCCTTCGTGGCTCTGGCCTGCCTCCTCCGCCCTGG
CGCGCCCGTCGAGCTCCACCGCAAGCTCTCCGGCTGGTCCGGCGACGCCGGCGCG
ACGTGGTACGGCGCAGCCACCGGTGCCGGGAGCGACGGTGGTGCCTGCCGGGTAC
CAGAACGCCGTCGACCAGCCGCCGTTCCGCGTCCATGATCGCCGCCGGCAGCCTGT
CCATCTTCCAGAACGGCGAGGGCTGCGGCTCCTGCTATCAGGTGAAATGCACCGG
TCACGCGTCGTGCTCCGGCAGCCCGGTGTCGGTGGTCCACCGACGAGTGCCCC
GTCGGCGCGTGCCTGGCCGAGCCCGTGCACCTCGACCTGAGCGGCACGGCGTTCC
GAGCCATGGCGAAGCCCGGCCAGGCCGACCAGCTACGCAGCGCCGGACGCCTCA
ACATCCAGTACGCTCGGGTGCCGTGCAACTGGAACGGGATGGACATCGCGTTCAA
GGTGGACGCCGGCTCGAACCCGAACACTTCGCGGTGCTGATCGAGTACGAGTCC
GGCGACGGCGAGCTGAGGTCCGTGGAGCTCATGCAGCGCGGCCGCCGGCGCGGCG
TGGGCTCCGATGCAGCGGTCTGTTGGGGCGCGGTGTGGAGGTACAACCTCGGGCGCC
GCCCTGCAGGCGCCCTTCTCCGTCCGCCTCACCTCAGACTCCGGCAGGACGCTCG
TCGCCAGCGACGTCATCCCCGCGGGGTGGACGCCCGGCCACGTACTGCTCGGT
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Nucleotide

>McsEXPB-46

ATGGTCCTGTGTCGCTTTGTGGCCTTCGTGGCTCTGGCCTGCCTCCTCCGCCCTGG
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AAACGCCGCGTGACCGTGACGCATGCAGGGTGCACGTACGTACAAACATTCTTGT
GTAGCTAGCTAGCCTTTCCGTCCGTTGGTGTACTAGTGATGATAGACTAGAGTGT
CTGTTCCCTCGCGCTTGTCTTTTGTGCCGCCCATGTCCATGTCCATGTCCATGCAC
CGGTCTCGTCGCGTGC GCGTACATGCAGGGTGCCGTGCAACTGGAACGGGATGG
ACATCGCGTTCAAGGTGGACGCCGGCTCGAACCCGA ACTACTTCGCGGTGCTGAT
CGAGTACGAGTCCGGCGACGGCGAGCTGAGGTCCGTGGAGCTCATGCAGCGCGG
CGCCGGCGCGGCGTGGGCTCCGATGCAGCGGTCGTGGGGCGCGGTGTGGAGGTA
CAACTCGGGCGCCGCCCTGCAGGCGCCCTTCTCCGTCCGCCTCACCTCAGACTCC
GGCAGGACGCTCGTCGCCAGCGACGTCATCCCCGCGGGGTGGACGCCCGGCCGCC
ACGTA CTGCTCGGTGCTCAACTTCAACA ACTAA