IDENTIFICATION

Species: *Miscanthus sinensis*

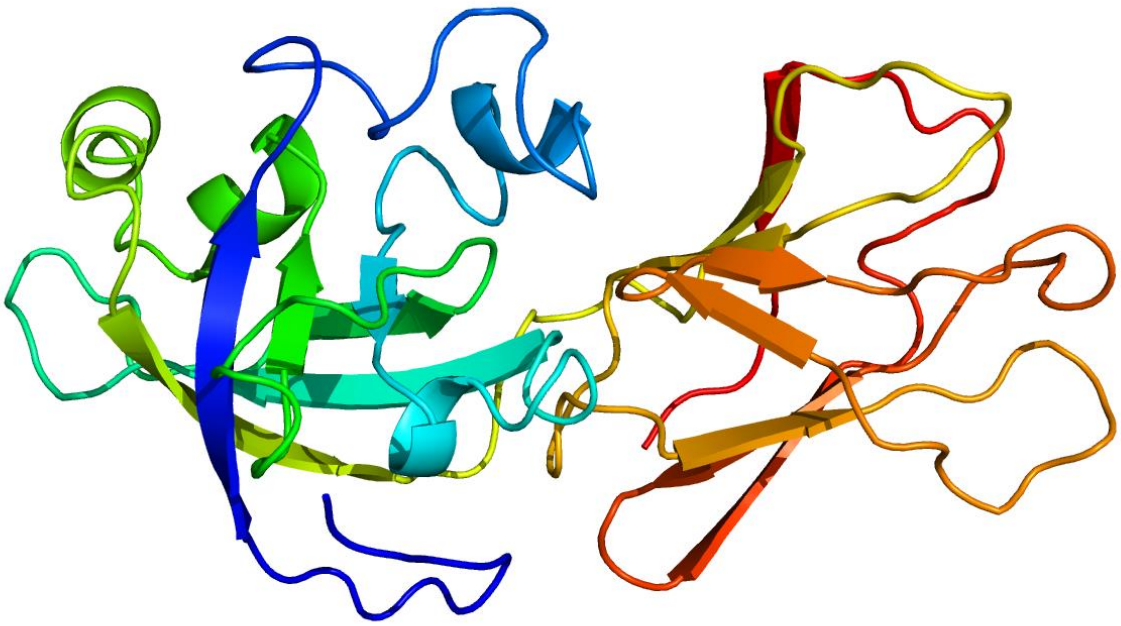
Locus: Misin18G135400

Gene Model: Misin18G135400.1.p

Description: McsEXPB-55

Family: Beta Expansin

3D structure:



GENOME DATABASES

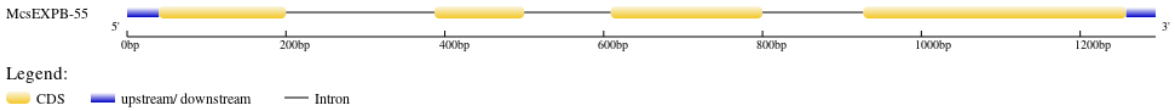
Phytozome: https://phytozome-next.jgi.doe.gov/info/Msinensis_v7_1

KEGG:-

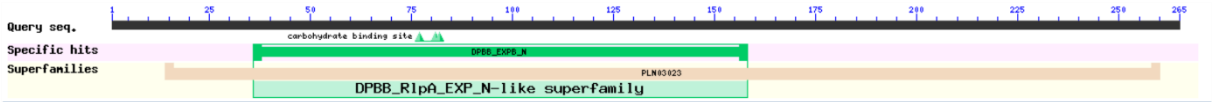
EXTERNAL RESOURCES

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

GENE STRUCTURE



DOMAIN ARCHITECTURE



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 ...	36-158	2.74e-76
[+] PLN03023 super family	cl33621	Expansin-like B1; Provisional	14-260	9.41e-39

SEQUENCES

Peptide

>McsEXPB-55

MASKQIGRVVVLSCFIAIMALAFRPCASVEPMDGGWSDAGATWYGPANGAGSDGG
ACGYQGAVDQPPFSSMITAGSNSIYQDGKGCGTCYQVKCTGHESCSGSPVTVVLTDQ
CPGACQSEPVHFDLSGTTFGAMAKPGQADQLRNAGRLPVQYTRVPCNWNGVDVAF
RVDAGSNANYLAMAIEYESGDGDLGAVELQMQSGAAWAPMERSWGAVWRYQSGS
SLQGPLSVRLTSGSGKTLVASNVIPAGWQPGNTYRSVVNFGQN*

CDS (coding sequence)

>McsEXPB-55

ATGGCTTCCAAGCAGATCGGCCGGGTCGTCGTCTTGTCCTGCTTCATTGCCATCAT
GGCTCTGGCCTTCCGTCCCTGCGCATCCGTCGAGCCCATGGACGGCGGCTGGTCG
GACGCCGGCGCCACCTGGTACGGCCCTGCCAACGGCGCTGGGAGCGACGGTGGT
GCGTGTGGGTACCAGGGCGCCGTCGACCAGCCGCCCTTCTCGTCAATGATCACCG
CCGGCAGCAATTCCATCTACCAGGACGGCAAGGGCTGCGGCACCTGCTACCAGGT
GAAGTGCACCGGACACGAGTCGTGCTCCGGCAGCCCGGTGACAGTGGTCCTCACT
GACCAGTGCCCCGGCGCGTGCCAGTCCGAGCCCGTTCACTTCGACCTGAGCGGGA
CGACGTTCGGTGCCATGGCGAAACCCGGCCAGGCCGACCAGCTCCGAAACGCCG
GCCGCCTCCCAGTCCAGTACACTCGGGTGCCGTGCAACTGGAACGGCGTGGACGT
CGCCTTCAGGGTGGACGCCGGCTCAAACGCCAACTACCTGGCCATGGCCATCGAG
TACGAATCCGGGGACGGGGACCTGGGCGCTGTGGAGCTGCAGATGCAGAGTGGC
GCGGCGTGGGCGCCCATGGAGCGCTCCTGGGGCGCAGTGTGGCGCTACCAGTCC
GGCTCCAGTCTGCAGGGCCCCCTGTCTGTCCGCCTCACCTCTGGCTCCGGCAAGA
CCCTCGTCGCCAGCAACGTCATCCCCGCCGGATGGCAGCCCGGCAACACCTACCG
CTCCGTCGTCAACTTCGGACAAAACTGA

Nucleotide

>McsEXPB-55

TCTAGCTAAGCTAGCGCGCTCGTGTAACCCGGCTTCCGGCATGGCTTCCAAGCAG
ATCGGCCGGGTCGTCGTCTTGTCCTGCTTCATTGCCATCATGGCTCTGGCCTTCCG
TCCCTGCGCATCCGTCGAGCCCATGGACGGCGGCTGGTCGGACGCCGGCGCCACC

TGGTACGGCCCTGCCAACGGCGCTGGGAGCGACGGTACGTTACGTGTGCATTACC
ATGCATGCATGTGTTGTACGTTTTCATTGCGAATGCAGCATGCCTTGATATGATAG
ACGTACATACATAATATATGTGCGTACACAATGCATGGTTTACTGATGCCAGCCC
GCGCTCATCATCTACTAGATATACTAGTTTAATCTTTGTGTTGGTATATATATAGG
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ACCGCCGGCAGCAATTCCATCTACCAGGACGGCAAGGGCTGCGGCACCTGCTACC
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CTGACCAGTGCCCCGGCGCGTGCCAGTCCGAGCCCGTTCACTTCGACCTGAGCGG
GACGACGTTCGGTGCCATGGCGAAACCCGGCCAGGCCGACCAGCTCCGAAACGC
CGGCCGCCTCCCAGTCCAGTACACTCGGTACATACCTCACTGCTAGCTAGCTGCA
TCATGATCTGCATGAGGAAGATGATTATTAGCTCCGTCGTCGTCCGTCGTCATCGC
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CTGGAACGGCGTGGACGTCGCCTTCAGGGTGGACGCCGGCTCAAACGCCAACTA
CCTGGCCATGGCCATCGAGTACGAATCCGGGGACGGGGACCTGGGCGCTGTGGA
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