

IDENTIFICATION

Species: *Miscanthus sinensis*

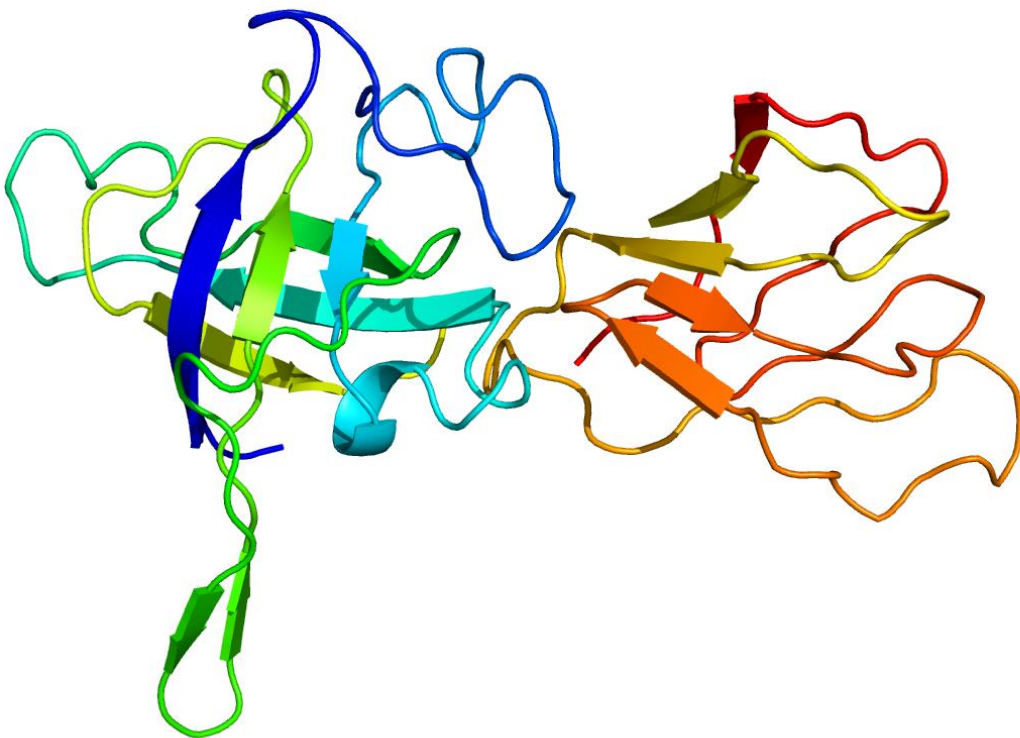
Locus: Misin07G114900

Gene Model: Misin07G114900.1.p

Description: McsEXPA-35

Family: Alpha Expansin

3D structure:



GENOME DATABASES

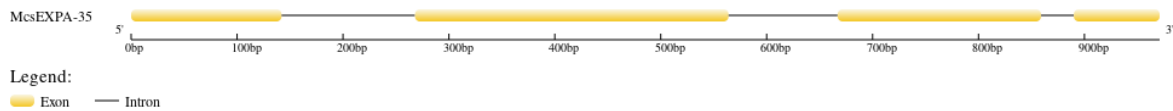
Phytozome: https://phytozome-next.jgi.doe.gov/info/Msinensis_v7_1

KEGG:-

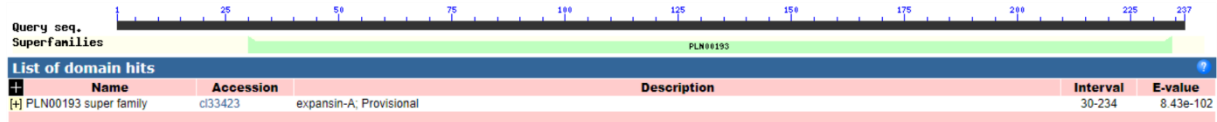
EXTERNAL RESOURCES

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

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>McsEXPA-35

MSGAPYARAAHALALAMVAAAAAVEAQTEWLRAHATFYGGADASGTMGGACGY
GNLFAQGYGTRTTALSTALFSGGASCGQCYKLVCDRKTDATWCKPGVSVTVTATNF
CPPNWKLDPDGGWCNAVVRPHFDMAQPAWEKIPVIYKRHKGGVRFVTVNGHDYFNLVL
LTVNAGPGSIRAMDVKGSPPAEDWMHMERNWGANWHSLAYLTGQATIVFTDVVP
PKWRFGQSFASLQFKL*

CDS (coding sequence)

>McsEXPA-35

ATGTCCGGAGCTCCTTACGCCCGCGCGGGCGCACGCGTTAGCGCTGGCCATGGTGG
CCGCCGCCGACGCGGTCGAGGCGCAGACGGAGTGGCTCAGGGCGCATGCCACGT
TCTACGGCGGCGCGGACGCCTCCGGCACCATGGGGGGCGCGTGCGGGTACGGCA
ACCTGTTTCGCGCAGGGGTACGGCACGCGGACGACGGCGCTGAGCACGGCGCTCT
TCTCCGGCGGCGCCTCCTGCGGGCAGTGCTACAAGCTGGTGTGCGACCGCAAGAC
GGACGCGACGTGGTGCAAGCCC GGCGTGTCCGTCACCGTCACGGCCACCAACTTC
TGCCCGCCCAACTGGAAGCTGCCCCGACGGCGGGTGGTGCAACGCGGTGCGGCC
CACTTCGACATGGCGCAGCCC GCGTGGGAGAAGATCCCCGTCATCTACAAAAGG
CACAAGGGTGGGGTGC GTTTCACCGTTAATGGCCACGACTACTTCAACCTGGTGC
TGCTACCAACGTCGCGGGGCCGGGATCCATCAGGGCCATGGACGTCAAGGGCT
CGCAGCCCCCGGCGGAGGACTGGATGCACATGGAGCGCAACTGGGGCGCCAACT
GGCACTCCCTCGCCTACCTACCGGCCAGGCTACCATCGTCTTACCGACGTCGT
GCCGCCAAGTGGAGGTTGCGCCAGTCTTTCGCCAGCACCCCTGCAGTTCAAGCTG
TGA

Nucleotide

>McsEXPA-35

ATGTCCGGAGCTCCTTACGCCCGCGCGGGCGCACGCGTTAGCGCTGGCCATGGTGG
CCGCCGCCGACGCGGTCGAGGCGCAGACGGAGTGGCTCAGGGCGCATGCCACGT
TCTACGGCGGCGCGGACGCCTCCGGCACCATGGGTAAGCTAAGCTAAGCTAAGCT
AAGCAGCCTCTTATTGCTAACTGCATGCGAGCTGACGACGAACGGCACCATATGC
ATGCCACTGGAATCACTCTTCTGCCGTATCGTATGCATGCATGAGCAGGGGGCG
CGTGCGGGTACGGCAACCTGTTTCGCGCAGGGGTACGGCACGCGGACGACGGCGC

TGAGCACGGCGCTCTTCTCCGGCGGGCGCCTCCTGCGGGCAGTGCTACAAGCTGGT
GTGCGACCGCAAGACGGACGCGACGTGGTGCAAGCCCGGCGTGTCCGTCACCGT
CACGGCCACCAACTTCTGCCCCGCCAACTGGAAGCTGCCCCGACGGCGGGTGGTGC
AACGCGGTGCGGGCCCCACTTCGACATGGCGCAGCCCCGCGTGGGAGAAGATCCCC
GTCATCTACAAAAGGCACGTAATTAACCACATGGGGATCGATCGATGCAGGAAC
TACTTCAACCCGATCTGCAGATGATTAACACATTTGCCTGCTGCATGCAGAGTC
TCTTGCGTGAAGAAGGGTGGGGTGCCTTTCACCGTTAATGGCCACGACTACTTCA
ACCTGGTGCTGCTCACCAACGTCGCGGGGCGGGATCCATCAGGGCCATGGACGT
CAAGGGCTCGCAGCCCCCGGCGGAGGACTGGATGCACATGGAGCGCAACTGGGG
CGCCAACCTGGCACTCCCTCGCCTACCTACCGGCCAGGCTGTTCTTCAGGGTCAC
CGTCACCGACGGCCAGACCATCGTCTTCACCGACGTCGTGCCGCCCAAGTGGAGG
TTCGGCCAGTCCTTCGCCAGCACCCCTGCAGTTCAAGCTGTGA