

IDENTIFICATION

Species: *Miscanthus sinensis*

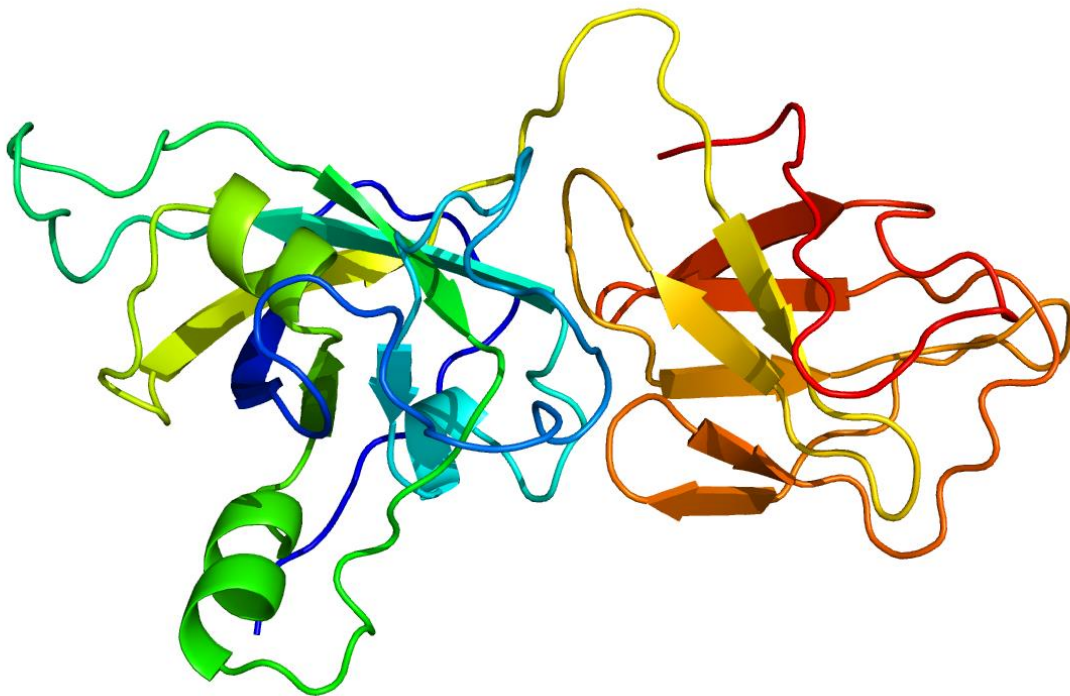
Locus: Misin08G116000

Gene Model: Misin08G116000.1.p

Description: McsEXPA-43

Family: Alpha Expansin

3D structure:



GENOME DATABASES

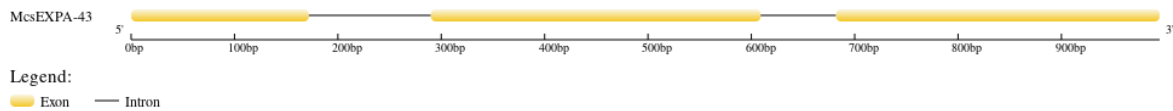
Phytozome: https://phytozome-next.jgi.doe.gov/info/Msinensis_v7_1

KEGG:-

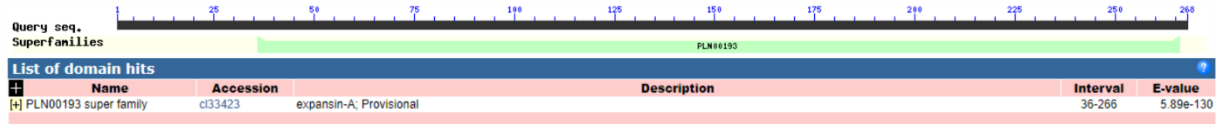
EXTERNAL RESOURCES

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

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>McsEXPA-43

MAPARVFILLLLAAAGWASAMAANDAVPTTSSSPAPTGWLKAHATFYGGADASDT
MGGACGYGNLYSQGYGTRTAALSTVLFQDGASCGQCYKIACDRKRADPRFCKPGVT
VTVTATNFCPPNMALPDGGWCNQQRPHFDMAQPAFEKIGVHTGGIIPVMYQRVPCV
KRGVVRFTINGHDYFNLVLVTNVAAAGSIKSMEVKTSNSSNWTPLARNWGANWHS
LAYLTGQMLSFRVTDTDGQTIEFTNVVPQGWKFGQTFASKLQFK*

CDS (coding sequence)

>McsEXPA-43

ATGGCTCCAGCTCGAGTTTTTCATACTCTTGCTGCTGGCAGCTGCCGGTTGGGCGTC
GGCCATGGCCGCTAATGACGCCGTCACCACCACGTCGTCGTCTCCGGCACCA
ACCGGGTGGCTGAAGGCGCATGCCACCTTCTACGGAGGCGCTGATGCCTCGGACA
CCATGGGCGGCGCGTGCAGGACCGGAACTTACTCCAGGGCTACGGCACGC
GGACGGCGGCCCTGAGCACGGTGCTTTTCAGGATGGGGCCTCATGCGGGCAGTG
CTACAAGATCGCGTGCGACCGCAAGAGAGCCGACCCAAGGTTTTGCAAACCCGG
CGTCACAGTCACCGTCACGGCCACCAACTTCTGCCACCCAACATGGCGCTGCC
GACGGCGGCTGGTGCAATCAGCAGCGCCCGCACTTCGACATGGCACAGCCGGCA
TTTGAGAAGATCGGCGTCCACACCGGCGGCATCATCCCGTCATGTACCAGAGAG
TTCCTTGCGTGAAGCGAGGTGGGGTGCGCTTACCATCAATGGGCATGACTACTT
CAACCTTGCTTGTGACCAACGTTGCGGCTGCTGGCTCCATCAAGTCCATGGAA
GTCAAGACCTCCAATTCGAGTAAGTGGACACCAATTGGCACGCAACTGGGGTGGCA
ACTGGCACTCTCTTGCATATCTTACCGGGCAGATGCTCTCGTTTAGAGTCACAGAC
ACGGATGGACAAACTATTGAATTCACAAACGTGGTGCCACAAGGATGGAAGTTT
GGCCAAACATTTGCATCCAAGTTGCAGTTCAAGTGA

Nucleotide

>McsEXPA-43

ATGGCTCCAGCTCGAGTTTTTCATACTCTTGCTGCTGGCAGCTGCCGGTTGGGCGTC
GGCCATGGCCGCTAATGACGCCGTCACCACCACGTCGTCGTCTCCGGCACCA
ACCGGGTGGCTGAAGGCGCATGCCACCTTCTACGGAGGCGCTGATGCCTCGGACA
CCATGGGTAAGCTAACCGCTCAAGAACCATGCATGGGACAGCTTTCCTATATATG
CCATGAACATATATGATGCACATCTGTCATCGTCTGATCTGATCTAATAATATTTG

TGTCTGGTGGCAGGCGGCGCGTGCGGGTACGGGAACCTCTACTCCCAGGGCTACG
GCACGCGGACGGCGGCCCTGAGCACGGTGCTCTTTCAGGATGGGGCCTCATGCGG
GCAGTGCTACAAGATCGCGTGCGACCGCAAGAGAGCCGACCCAAGGTTTTGCAA
ACCCGGCGTACAGTCACCGTCACGGCCACCAACTTCTGCCCACCCAACATGGCG
CTGCCCCGACGGCGGCTGGTGCAATCAGCAGCGCCCGCACTTCGACATGGCACAGC
CGGCATTTGAGAAGATCGGCGTCCACACCGGCGGCATCATCCCCGTCATGTACCA
GAGGTATTTTTATTTATTTCTACTACTACCTCTTCCTAGCTGAAAAAAAAACAAA
AACTAATTTCTTGCTTGTAGAGTTCCTTGCGTGAAGCGAGGTGGGGTGCCTTCA
CCATCAATGGGCATGACTACTTCAACCTTGTGCTTGTGACCAACGTTGCGGCTGCT
GGCTCCATCAAGTCCATGGAAGTCAAGACCTCCAATTCGAGTAACTGGACACCAT
TGGCACGCAACTGGGGTGCGA ACTGGCACTCTCTTGCATATCTTACCGGGCAGAT
GCTCTCGTTTAGAGTCACAGACACGGATGGACAACTATTGAATTCACAAACGTG
GTGCCACAAGGATGGAAGTTTGGCCAAACATTTGCATCCAAGTTGCAGTTCAAGT
GA