

IDENTIFICATION

Species: *Miscanthus sinensis*

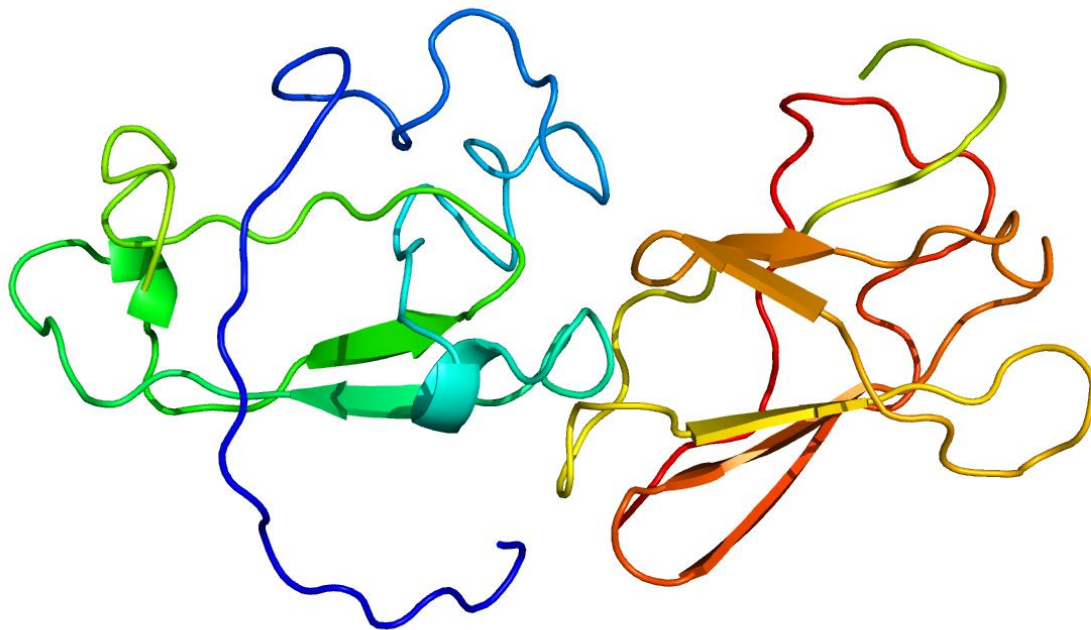
Locus: Misin01G211600

Gene Model: Misin01G211600.1.p

Description: McsEXPA-01

Family: Alpha Expansin

3D structure:



GENOME DATABASES

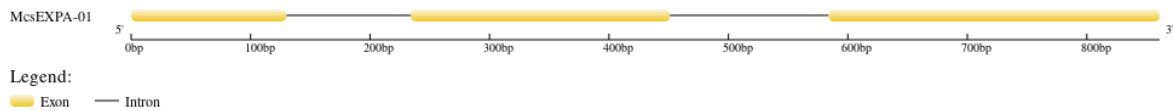
Phytozome: https://phytozome-next.jgi.doe.gov/info/Msinensis_v7_1

KEGG:-

EXTERNAL RESOURCES

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

GENE STRUCTURE



DOMAIN ARCHITECTURE

Query seq. MSTEMAKSLMLFTALAAACPALAAADWSQGTATFYGGPDGSGTMGGACGYENLYNAGYGVNNAALSPVLFNDGASCGQCYVIICDASRPGGQYCRTWVTVTATNLCPSNYALPNGGCMAGNYYFLLVNIQNLAGSGSVAAAWIKGDKTEWIQMSRNWGANWQALAGLVGQGLSFAVTSTGGQYIQFLNVVPGWWQFGMTFNTNQNFNY*

Superfamilies PLN0193

Name	Accession	Description	Interval	E-value
PLN00193 super family	cl33423	expansin-A: Provisional	26-205	1.61e-63

SEQUENCES

Peptide

>McsEXPA-01

MSTEMAKSLMLFTALAAACPALAAADWSQGTATFYGGPDGSGTMGGACGYENLYNAGYGVNNAALSPVLFNDGASCGQCYVIICDASRPGGQYCRTWVTVTATNLCPSNYALPNGGCMAGNYYFLLVNIQNLAGSGSVAAAWIKGDKTEWIQMSRNWGANWQALAGLVGQGLSFAVTSTGGQYIQFLNVVPGWWQFGMTFNTNQNFNY*

CDS (coding sequence)

>McsEXPA-01

ATGTCCACAGAAATGGCCAAGTCCCTGATGCTGTTCACAGCGCTCGCGGGCGTGCC
CCGCGCTTGCCGCCGCGGACTGGTCTCAGGGCACCGCCACGTTCTACGGTGGACC
CGACGGCTCCGGCACGATGGGAGGCGCATGCGGCTACGAGAACCTATAACAACGC
CGGGTACGGCGTCAACAACGCAGCTCTAAGCCCGGTGCTGTTCAACGACGGCGC
GTCGTGCGGGCAGTGCTACGTCATCATCTGCGACGCGTCACGTCCGGGCGGCCAG
TACTGCCGCACGTGGGTACCGTGACGGCCACCAACCTGTGCCCATCCAACACTACG
CGCTGCCAACGGCGGGTGCATGGCCGGCAACTACTACTTCTGCTCGTCAATAT
CCAGAACCTCGCCGGCAGCGGCTCTGTGGCCGCCGCTGGATCAAGGGCGATAA
GACAGAGTGGATCCAGATGTCCAGGAACTGGGGAGCCAACTGGCAGGCGCTCGC
CGGGCTCGTCGGCCAGGGGCTCAGCTTCGCCGTGACCAGCACAGGTGGGCAGTA
CATCCAGTTCCTCAACGTCGTACCAGGATGGTGCCAGTTTGGCATGACCTTCAAC
ACAAACCAGAATTTTAACTACTAA

Nucleotide

>McsEXPA-01

ATGTCCACAGAAATGGCCAAGTCCCTGATGCTGTTCACAGCGCTCGCGGGCGTGCC
CCGCGCTTGCCGCCGCGGACTGGTCTCAGGGCACCGCCACGTTCTACGGTGGACC
CGACGGCTCCGGCACGATGGGTAATTACTTTCGCATGCATGCATTTTCGGTACATG
ATGAGACAGTGTATATATGCTAATCCATGCATGCATGCTCGTATTTCGTATAATGT
ATACATTATTACAGGAGGCGCATGCGGCTACGAGAACCTATAACAACGCCGGGTA
CGGCGTCAACAACGCAGCTCTAAGCCCGGTGCTGTTCAACGACGGCGCGTTCGTGC
GGGCAGTGCTACGTCATCATCTGCGACGCGTCACGTCCGGGCGGCCAGTACTGCC
GCACGTGGGTACCGTGACGGCCACCAACCTGTGCCCATCCAACACTACGCGCTGCC
CAACGGCGGGTGGTGCGGTCCGGGGCGGCCCCCACTTTGACATGTCGCAGCCGGC

GTGGGAGAACATCGGCATCTACAGCGGCGGCATCATCCCGGTGCTGTACCAGCA
GGTCAAGTGCTAGCGCAACGGCGGCGTGCGCTTCAGCATGGCCGGCAACTACTAC
TTCCTGCTCGTCAATATCCAGAACCTCGCCGGCAGCGGCTCTGTGGCCGCCGCCT
GGATCAAGGGCGATAAGACAGAGTGGATCCAGATGTCCAGGA ACTGGGGAGCCA
ACTGGCAGGCGCTCGCCGGGCTCGTCGGCCAGGGGCTCAGCTTCGCCGTGACCAG
CACAGGTGGGCAGTACATCCAGTTCCTCAACGTCGTACCAGGATGGTGGCAGTTT
GGCATGACCTTCAACACAAACCAGAATTTTAACTACTAA