

IDENTIFICATION

Species: *Miscanthus sinensis*

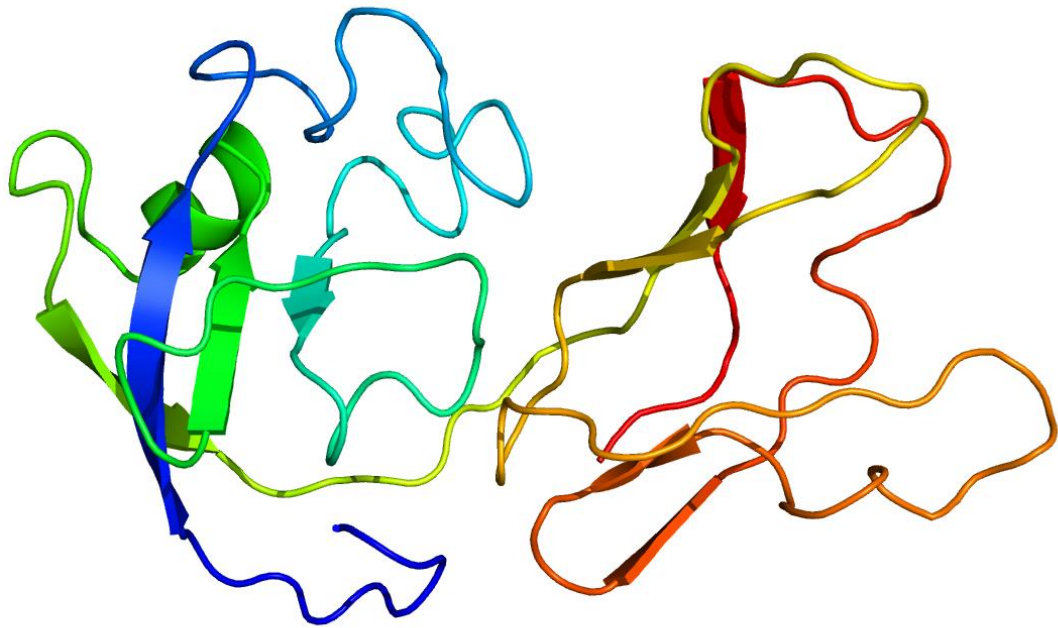
Locus: Misin08G115600

Gene Model: Misin08G115600.1.p

Description: McsEXPA-42

Family: Alpha Expansin

3D structure:



GENOME DATABASES

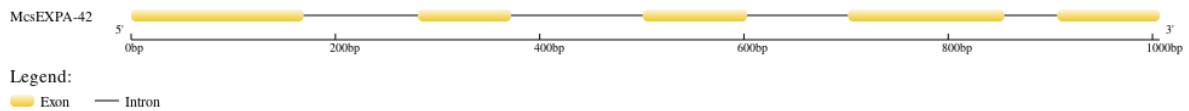
Phytozome: https://phytozome-next.jgi.doe.gov/info/Msinensis_v7_1

KEGG:-

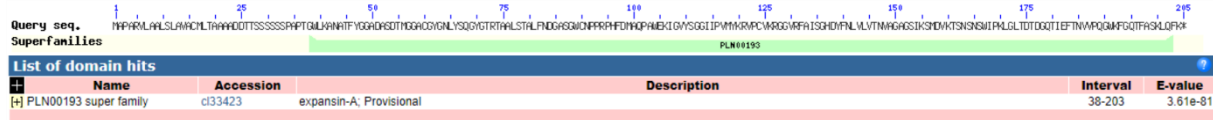
EXTERNAL RESOURCES

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

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>McsEXPA-42

MAPARVLAALSLAVACMLTAAAADDTTSSSSSSPAPTGWLKANATFYGGADASDT
MGGACGYGNLYSQGYGTRTAALSTALFNDGASGWCNPPRPHFDMAQPAWEKIGVY
SGGIIPVMYKRVPVCVKRGGVRFASIGHDYFNLVLTNVAGAGSIKSMDVKTSNSNSW
IPKLGLTDTDGQTIEFTNVVPQGWKFGQTFASKLQFK*

CDS (coding sequence)

>McsEXPA-42

ATGGCTCCAGCTCGAGTTCTTGCAGCCCTGTCGCTCGCAGTTGCCTGCATGCTGAC
CGCAGCCGCCGCTGATGACACCACCAGCAGCAGTTCATCGTCTCCGGCACCGACC
GGATGGCTCAAGGCGAATGCCACGTTCTACGGCGGCGCCGATGCCTCTGACACCA
TGGGAGGTGCGTGTGGGTACGGCAACCTGTACTCACAGGGCTACGGCACAAGAA
CGGCTGCGCTGAGCACTGCGCTCTTCAACGACGGTGCCTCCGGCTGGTGCAATCC
TCCTCGGCCGCACTTCGACATGGCGCAGCCGGCCTGGGAGAAGATCGGCGTCTAC
AGCGGTGGCATCATCCCCGTCATGTACAAAAGGGTTCCTTGTGTGAAGCGAGGTG
GGGTGCGGTTGCAATCAGCGGTCACGACTACTTCAATCTCGTGCTTGTGACCAA
TGTTGCAGGTGCTGGCTCCATCAAGTCAATGGATGTCAAGACCTCCAATCCAAT
AGCTGGATACAAAACCTGGGATTGACTGACACTGATGGGCAAACCTATTGAATTCA
CGAACGTGGTGCCACAAGGATGGAAGTTTGGCCAAACATTTGCATCCAAGTTACA
GTTCAAGTGA

Nucleotide

>McsEXPA-42

ATGGCTCCAGCTCGAGTTCTTGCAGCCCTGTCGCTCGCAGTTGCCTGCATGCTGAC
CGCAGCCGCCGCTGATGACACCACCAGCAGCAGTTCATCGTCTCCGGCACCGACC
GGATGGCTCAAGGCGAATGCCACGTTCTACGGCGGCGCCGATGCCTCTGACACCA
TGGGTAATTATGTTGCTCCCTGATTTCTTATTTTCCATGCAGCTAGCAAGGGAAA
AAGAAGAGAGAAAACCTGTATAACCTGATGTGTCCATATATACATCCTTATGTGTC
GCAGGAGGTGCGTGTGGGTACGGCAACCTGTACTCACAGGGCTACGGCACAAGA
ACGGCTGCGCTGAGCACTGCGCTCTTCAACGACGGTGCCTCGTGCGGGGGCAGTG
CTACAAGATCGCGTCTGACCGCAAGAGGGCCAACCCGATGTTTTGCAAACCTGGC
GTCACGGTGACCGTCACGGCCACCAACTTCTGCCCGCCCAACTATGCGCTGCCTG

GCAAGCGGCTGGTGCAATCCTCCTCGGCCGCACTTCGACATGGCGCAGCCGGCCT
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AGCGAGGTGGGGTGCGGTTCGCAATCAGCGGTCACGACTACTTCAATCTCGTGCT
TGTGACCAATGTTGCAGGTGCTGGCTCCATCAAGTCAATGGATGTCAAGACCTCC
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CTTACAGGGCAGATGCTCTCGTTTAGATTGACTGACACTGATGGGCAAACCTATTG
AATTCACGAACGTGGTGCCACAAGGATGGAAGTTTGGCCAAACATTTGCATCCAA
GTTACAGTTCAAGTGA