

## IDENTIFICATION

**Species:** *Miscanthus sinensis*

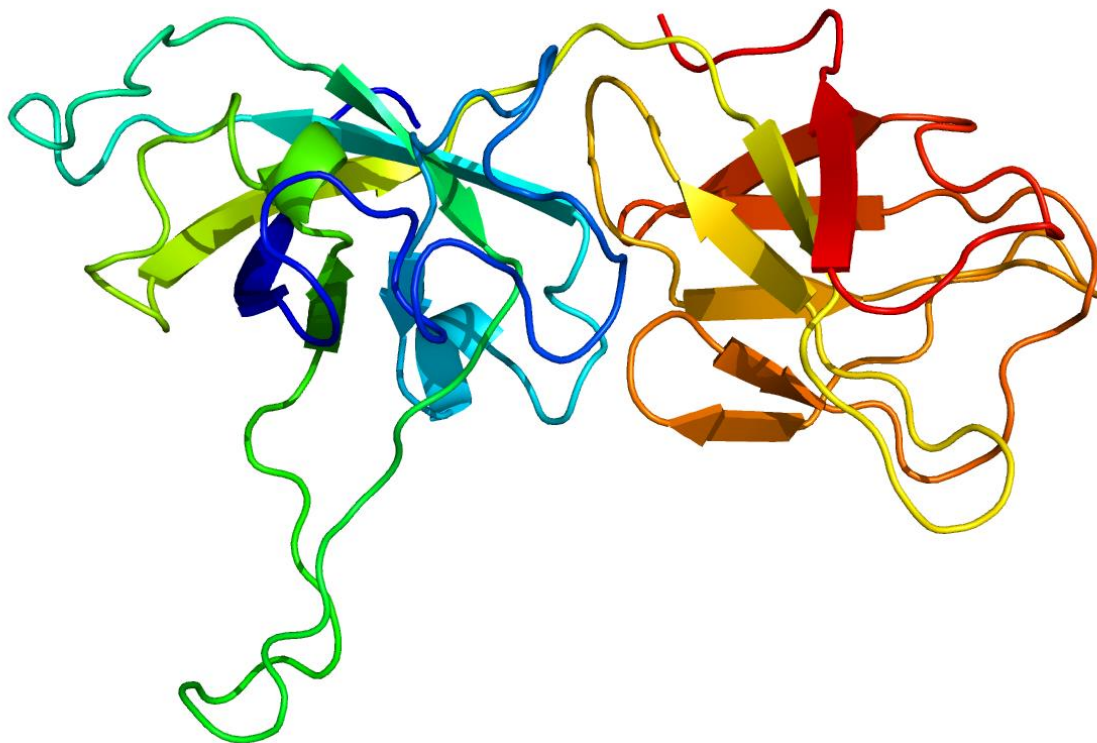
**Locus:** Misin01G478300

**Gene Model:** Misin01G478300.1.p

**Description:** McsEXPA-07

**Family:** Alpha Expansin

**3D structure:**



## GENOME DATABASES

Phytozome: [https://phytozome-next.jgi.doe.gov/info/Msinensis\\_v7\\_1](https://phytozome-next.jgi.doe.gov/info/Msinensis_v7_1)

KEGG:-

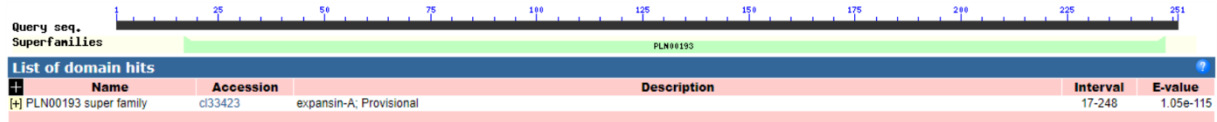
## EXTERNAL RESOURCES

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

## GENE STRUCTURE



## DOMAIN ARCHITECTURE



## SEQUENCES

### Peptide

>McsEXPA-07

MDRVLALLAAVLAATFFAPAQGWN YGTATFYGGRDGS GTMGGACGYGNLYQAGY  
GTNTAALSSVLFNDGAACGQC YLVMCDNSASPWCRRGAAVTVTATNFCPPNWAQP  
SNSGGWCNPPRPHFDMAQPAWERIGVYSAGIIPVLYQQVTCWRQGGMRITIGGSSFF  
QLVQFSNVAGSGSIRS VSVKGTGTGWVALNRNWGANWQCNSPLFGQALSFSVTSTG  
GQTLYMTDVVPSWWQIGMV FASN YNFYY\*

### CDS (coding sequence)

>McsEXPA-07

ATGGACAGAGTCTTGGCATTGCTCGCCGCCGTCCTGGCGGCGACGTTCTTCGCGC  
CGGCGCAGGGCTGGA ACTACGGGACGGCGACGTTCTACGGTGGCCGCGACGGCT  
CCGGCACAATGGGTGGCGCATGCGGGTACGGCAACCTGTACCAGGCCGGGTACG  
GGACGAACACGGCGGGCGCTGAGCTCGGTGCTGTTCAACGACGGTGC GGCGGTGCG  
GGCAGTGCTACCTGGTGATGTGCGACAGCAACGCGTCGCCATGGTGCAGGCGCG  
GCGCCGCGGTGACTGTCACGGCCACCAACTTCTGCCCCGCCAACTGGGCGCAGCC  
CAGCAACAGCGGCGGCTGGTGCAACCCGCCGCGGCCGCATTCGACATGGCGCA  
GCCCCGCTGGGAGCGCATCGGCGTCTACAGCGCCGGCATCATCCCCGTCTCTAC  
CAGCAGGTGACGTGCTGGAGGCAGGGAGGGATGAGGATCACCATCGGAGGGTCC  
AGTTTCTTCCAGCTGGTGCAGTTCTCCAACGTGGCCGGCAGCGGCTCCATCCGGT  
CCGTGTCAGTGAAGGGGACCAAGACCGGGTGGGTCGCTCTGAACCGCAACTGGG  
GCGCCAACTGGCAGTGCAACTCGCCGCTTTCGGCCAGGCGCTCTCCTTCTCCGT  
ACCTCCACCGGCGGCCAGACGCTCTACATGACCGACGTCGTGCCGTCGTGGTGGC  
AAATCGGCATGGTCTTCGCAAGCAACTATAATTCTACTACTGA

### Nucleotide

>McsEXPA-07

GGTTTGGTTTACTGAAACCGACGACTCCCACTACTCGATAATCTGTATCCGTGTTG  
TTCTCTGCGACAGATAGATGGACAGAGTCTTGGCATTGCTCGCCGCCGTCTGGC  
GGCGACGTTCTTCGCGCCGGCGCAGGGCTGGA ACTACGGGACGGCGACGTTCTAC  
GGTGGCCGCGACGGCTCCGGCACAATGGGTAAATAACAACA ACTCCAAAGCCGC  
GTGCAGTGCAGTGTGGATTCCCGAGCTAATCAGCAGCACTCGATCGTACGTGTAG  
GTGGCGCATGCGGGTACGGCAACCTGTACCAGGCCGGGTACGGGACGAACACGG

CGGCGCTGAGCTCGGTGCTGTTCAACGACGGTGCGGCGTGCGGGCAGTGCTACCT  
GGTGATGTGCGACAGCAACGCGTCGCCATGGTGCAGGCGCGGGCGCCGCGGTGAC  
TGTCACGGCCACCAACTTCTGCCCGCCAACTGGGCGCAGCCCAGCAACAGCGGC  
GGCTGGTGCAACCCGCCGCGGGCCGATTTTCGACATGGCGCAGCCCCGCCTGGGAGC  
GCATCGGCGTCTACAGCGCCGGCATCATCCCCGTCCTCTACCAGCAGTAAGTGCA  
GTGTGCAGGTGCAGCGTTGCGTACGTGTATTCTTCTTATGGCCCCGTTTCGCTGGTC  
TGAAACTTAGCTGAAACTGACTGAAAACACTGTTCCGGCTGAATTGTCGTGAGAG  
AAAAACACGGTTCAGCTGAAAAAAGAAGCCGAACAAACCATTTTTAAGACAAGC  
GAACGAATATATATCCTGGCTTCGTTCCCTGCCTTTCTCCGACGAACTCATCGCCGG  
TCCGGTGATGGTGGTGGTGCAGGGTGACGTGCTGGAGGCAGGGAGGGATGAGGA  
TCACCATCGGAGGGTCCAGTTTCTTCCAGCTGGTGCAGTTCTCCAACGTGGCCGG  
CAGCGGCTCCATCCGGTCCGTGTCAGTGAAGGGGACCAAGACCGGGTGGGTTCGC  
TCTGAACCGCAACTGGGGCGCCAACTGGCAGTGCAACTCGCCGCTCTTCGGCCAG  
GCGCTCTCCTTCTCCGTCACCTCCACCGGCGGCCAGACGCTCTACATGACCGACG  
TCGTGCCGTCGTGGTGGCAAATCGGCATGGTCTTCGCAAGCAACTATAATTTCTA  
CTACTGA