

## IDENTIFICATION

**Species:** *Miscanthus sinensis*

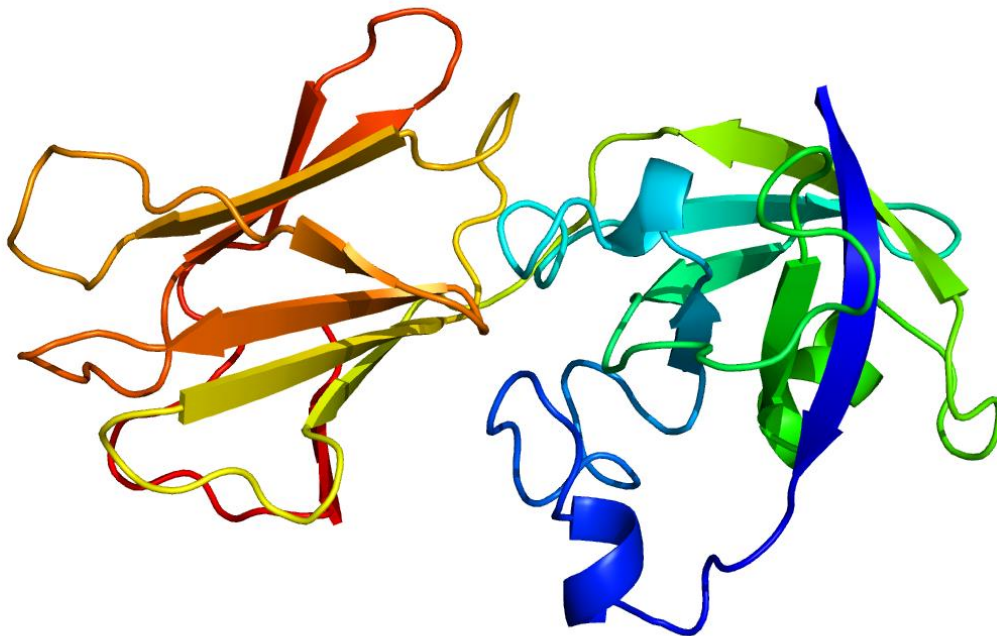
**Locus:** Misin09G151000

**Gene Model:** Misin09G151000.1.p

**Description:** McsEXPA-47

**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

Query seq. `114SRMITGTYGGRDSDTTDGGSCGYKGE L GKDYGALTA AVGPSLYSNGVGC GA  
CYELKGTKGT VVVTATNQAPPPVSGQKGEHFDLTMPTFLKIAEEKAGIVPITYRKVA  
CVRQRDIRYMITGNPHYNMVMVTNVGGVGDVVGLLVKGNKRVKWTLMKRSWGQ  
LWMTEVDLTGESL TFRVMTGDHRKATSWHV VPRDSKFDKMYQATKNF*`

Superfamilies **PLN00050**

Name	Accession	Description	Interval	E-value
PLN00050 super family	c131535	expansin A, Provisional	3-206	1.38e-47

## SEQUENCES

### Peptide

>McsEXPA-47

MAASRWTGTFYGGRDGSDTTDGGSCGYKGE L GKDYGALTA AVGPSLYSNGVGC GA  
CYELKGTKGT VVVTATNQAPPPVSGQKGEHFDLTMPTFLKIAEEKAGIVPITYRKVA  
CVRQRDIRYMITGNPHYNMVMVTNVGGVGDVVGLLVKGNKRVKWTLMKRSWGQ  
LWMTEVDLTGESL TFRVMTGDHRKATSWHV VPRDSKFDKMYQATKNF\*

### CDS (coding sequence)

>McsEXPA-47

ATGGCCGCTCCCGCTGGACGGGGACGTTCTACGGCGGGCGTGACGGGTCCGAC  
ACCACGGACGGCGGCTCGTGCGGGTACAAGGGCGAGCTAGGAAAAGACTACGGC  
GCGCTGACGGCGGCCGTGGGCCCCGTC ACTGTACAGCAACGGGGTTCGGGTGCGGC  
GCGTGCTACGAGCTCAAGGGCACCAAGGGCACCGTGGTGGTGACGGCCACCAAC  
CAGGCCCCGCCGCGGTGAGCGGGCAGAAGGGCGAGCACTTCGACCTACCATG  
CCGACGTTCCCTCAAGATCGCCGAGGAGAAGGCTGGCATCGTGCCCATCACCTACC  
GCAAGGTGGCGTGCGTGAGGCAACGCGACATCCGGTACATGATCACGGGGAACC  
CGACTACAACATGGTGATGGTGACGAACGTCGGCGGCGTCGGGGACGTGGTGG  
GGCTGTTGGTGAAGGGCAACAAGCGCGTCAAGTGGACGCTGATGAAGCGCAGCT  
GGGGCCAGCTCTGGATGACGGAGGTTGACCTACCGGCGAGTCGCTGACGTTCCG  
CGTCATGACCGGCGACCACCGCAAGGCCACCTCCTGGCAGTCGTCGCCCCGCGAC  
TCGAAGTTCGACAAGATGTACCAGGCCACCAAGAACTTCTAG

### Nucleotide

>McsEXPA-47

ATGGCCGCTCCCGCTGTAGCTCGACGGGCGTG GGGCGGTACGGGGATAGGGAC  
GGGGACGTTCTACGGCGGGCGTGACGGGTCCGACACCACGGACGGCGGCTCGTG  
CGGGTACAAGGGCGAGCTAGGAAAAGACTACGGCGCGCTGACGGCGGCCGTGGG  
CCCGTCACTGTACAGCAACGGGGTTCGGGTGCGGCGCGTGCTACGAGCTCAAGGG  
CACCAAGGGCACCGTGGTGGTGACGGCCACCAACCAGGCCCGCCGCGGTGAG  
CGGGCAGAAGGGCGAGCACTTCGACCTACCATGCCGACGTTCCCTCAAGATCGCC  
GAGGAGAAGGCTGGCATCGTGCCCATCACCTACCGCAAGTACGTAGTTGTAGTGC  
AGCACTCCGTATGCATGCGCATCATCTACTGATCTACGTACAAACAATTGACAC

ACGCATATGCAGGGTGGCGTGCGTGAGGCAACGCGACATCCGGTACATGATCAC  
GGGGAACCCGCACTACAACATGGTGATGGTGACGAACGTCGGCGGGCGTCGGGGA  
CGTGGTGGGGCTGTTGGTGAAGGGCAACAAGCGCGTCAAGTGGACGCTGATGAA  
GCGCAGCTGGGGCCAGCTCTGGATGACGGAGGTTGACCTCACCGGGCAGTCGCT  
GACGTTCCGCGTCATGACCGGCGACCACCGCAAGGCCACCTCCTGGCACGTCGTG  
CCCCGCGACTCGAAGTTCGACAAGATGTACCAGGCCACCAAGAACTTCTAG