

## IDENTIFICATION

**Species:** *Miscanthus sinensis*

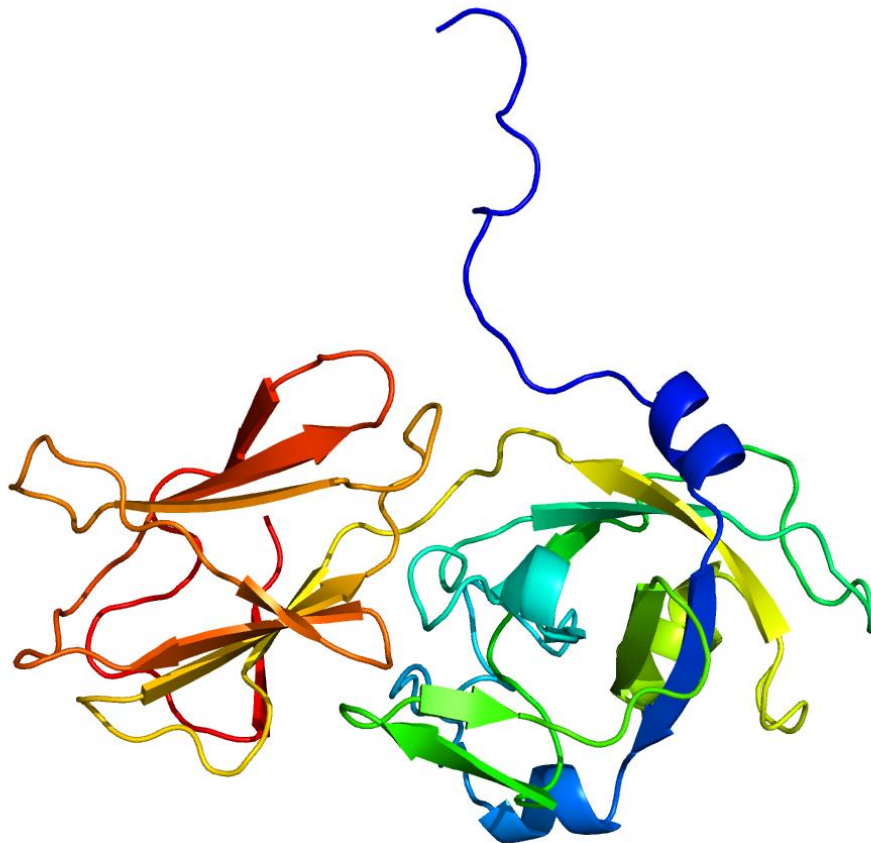
**Locus:** Misin07G271800

**Gene Model:** Misin07G271800.1.p

**Description:** McsEXPA-37

**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

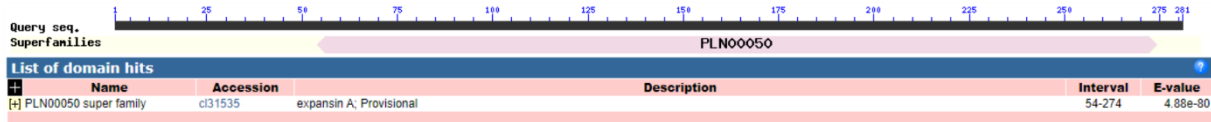
<https://grass-genome-hub.southgreen.fr/Genomeassembly/47213>

## GENE STRUCTURE



Legend:  
Exon

## DOMAIN ARCHITECTURE



## SEQUENCES

### Peptide

>McsEXPA-37

MSGSWMAPPLLVSLLVALVAVAADVANAGGANPLTPGGRVVHGHGKFTAGPW  
KPAHATFYGGRDGS GTTAGACGYKDTRSEGYGVQTVAVSSVLFGGGAACGGCYEV  
RCVDS PDGCKPGAAALVVTATNL CPPNDQQSGDSGGWCNPPREHFDLTPAFLQIA  
QEKAGIVPISYRRVACARQGGIRYTITGNKYFNMVTVTNVGGAGDVAVVSVKGSKR  
VKWTELKRNWGIVWQTGEDLTCESLTFRVMTSDHRKATSWHVL PADWQFGV TYQ  
ASKNF\*

### CDS (coding sequence)

>McsEXPA-37

ATGTCTGGTTCGTGGATGGCGCCACCGCCTCTCCTGGTGTCGCTGCTGGTCGCCTT  
GGTCGCGGTGGCCGCCGATGTGCGCAATGCCGGCGGCGCCAATCCCCTGACGCCT  
GGCGGGCGCGTGGTGCACCACAACCACGGCAAGTTCACGGCCGGCCCGTGGAAA  
CCCGCCCACGCGACCTTCTACGGCGGCCGGGACGGGTCCGGCACCACGGCGGGC  
GCGTGCGGGTACAAGGACACGCGGTTCGGAGGGGTACGGCGTGCAGACGGTGGCC  
GTGAGCTCGGTGCTGTTTCGGCGGCGGCGCGGCCTGCGGCGGGTGCTACGAGGTGC  
GGTGC GTGACAGCCCCGACGGGTGCAAGCCCCGGCGCGGCGGCGCTGGTGGTGA  
CGGCGACTAACCTGTGCCCGCCAACGACCAGCAGTCCGGGGACAGCGGCGGGT  
GGTGCAACCCGCCGCGGGAGCACTTCGACCTACCATGCCGGCGTTCCTCCAGAT  
CGCGCAGGAGAAGGCCGGCATCGTGCCCATCTCCTACCGCAGGGTGGCGTGCGC  
GAGGCAGGGCGGCATCCGGTACACCATACCGGGAACAAGTACTTCAACATGGT  
GACGGTCACCAACGTGGGCGGCGCCGGCGACGTGGCGGTGGTGTGCGGTGAAGGG  
GAGCAAGCGCGTCAAGTGGACGGAGCTGAAGCGCAACTGGGGGATAGTGTGGCA  
GACCGGGGAGGACCTCACCTGCGAGTCGCTGACGTTCCGGGTGATGACCAGCGA  
CCACCGCAAGGCCACCTCGTGGCACGTCCCTCCCCGCCGACTGGCAGTTCGGCGTC  
ACGTACCAGGCGTCCAAGAACTTCTAA

### Nucleotide

>McsEXPA-37

ATGTCTGGTTCGTGGATGGCGCCACCGCCTCTCCTGGTGTCGCTGCTGGTCGCCTT  
GGTCGCGGTGGCCGCCGATGTGCGCAATGCCGGCGGCGCCAATCCCCTGACGCCT  
GGCGGGCGCGTGGTGCACCACAACCACGGCAAGTTCACGGCCGGCCCGTGGAAA

CCCGCCACGCGACCTTCTACGGCGGCCGGGACGGGTCCGGCACACGGCGGGC  
GCGTGCGGGTACAAGGACACGCGGTTCGGAGGGGTACGGCGTGCAGACGGTGGCC  
GTGAGCTCGGTGCTGTTTCGGCGGCCGGCGCGGCCTGCGGCGGGTGCTACGAGGTGC  
GGTGCCTGGACAGCCCCGACGGGTGCAAGCCCCGGCGCGGGCGGCGCTGGTGGTGA  
CGGCGACTAACCTGTGCCCGCCCAACGACCAGCAGTCCGGGGACAGCGGCGGGT  
GGTGCAACCCGCCGCGGGAGCACTTCGACCTCACCATGCCGGCGTTCCTCCAGAT  
CGCGCAGGAGAAGGCCGGCATCGTGCCCATCTCCTACCGCAGGGTGGCGTGCGC  
GAGGCAGGGCGGCATCCGGTACACCATCACCGGGAACAAGTACTTCAACATGGT  
GACGGTCACCAACGTGGGCGGCCGGCGACGTGGCGGTGGTGTTCGGTGAAGGG  
GAGCAAGCGCGTCAAGTGGACGGAGCTGAAGCGCAACTGGGGGATAGTGTGGCA  
GACCGGGGAGGACCTCACCTGCGAGTCGCTGACGTTCCGGGTGATGACCAGCGA  
CCACCGCAAGGCCACCTCGTGGCACGTCCTCCCCGCCGACTGGCAGTTCGGCGTC  
ACGTACCAGGCGTCCAAGAACTTCTAA