

## IDENTIFICATION

**Species:** *Miscanthus sinensis*

**Locus:** Misin05G113100

**Gene Model:** Misin05G113100.1.p

**Description:** McsEXPA-27

**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:-

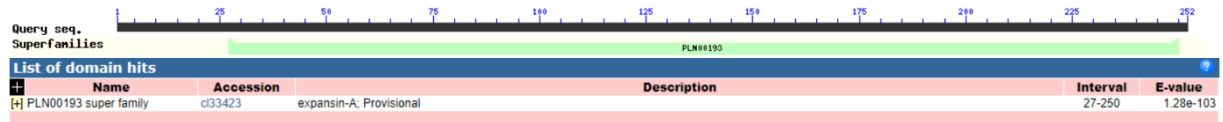
## EXTERNAL RESOURCES

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

## GENE STRUCTURE



## DOMAIN ARCHITECTURE



## SEQUENCES

### Peptide

>McsEXPA-27

MDQMAMLLLLLSLCAFRLGGAVAQQYWTPATATFYGGSDASGTMGGSCGYGDLYS  
AGYGTQTTALSTALYGDGASCGACYLITCDASRTQYCKPGSSSVTVTATNFCPPNYG  
DPNGWCNSPRQHFDMSQPAWETIGVYQAGVVPVNYRRVSCQRSGGIRFSISGHDYFE  
LVTITNVGGAGAVAAA WIMGTGTDWLTMSRNWGENWQSGAYLTGKALSFKVQTD  
DGKVVVAYNVAPANWQFGSTYEASANFY\*

### CDS (coding sequence)

>McsEXPA-27

ATGGACCAGATGGCGATGCTGCTCTTGCTGCTGAGCTTGTGCGCCTTTCGGCTCG  
GCGGTGCAGTGGCGCAGCAGTACTGGACGCCGGCCACCGCGACGTTCTACGGCG  
GGAGCGACGCGTCCGGCACCATGGGCGGGTCGTGCGGGTACGGCGACCTGTACA  
GCGCCGGGTACGGTACGCAGACGACGGCGCTGAGCACGGCGCTCTACGGCGACG  
GCGCCTCCTGCGGCGCGTGCTACCTCATCACCTGCGACGCGTCGCGGACGCAGTA  
CTGCAAGCCGGGGTTCGTCCGTCACCGTCACGGCCACCAACTTCTGCCCGCCC  
AACTACGGCGACCCCAACGGGTGGTGCAACTCGCCGCGGCAGCACTTCGACATGT  
CGCAGCCGGCCTGGGAGACCATCGGCGTGTACCAGGCCGGCGTCGTCCCGTCAA  
CTACCGGAGGGTCTCGTGCCAGCGGTCCGGCGGGATCAGGTTTCAGCATCAGCGGC  
CACGACTACTTCGAGCTCGTCACCATACCAACGTCGGCGGGCGCCGGCGCGGTGG  
CCGCGGCGTGGATCATGGGGACCGGCACGGACTGGCTGACCATGAGCCGCAACT  
GGGGGAGA ACTGGCAGAGCGGGGCTATCTCACCGGAAAGGCCCTGTCTGTTA  
AGGTGCAGACGGACGATGGCAAGGTCGTCTGTGGCGTATAACGTGGCGCCGGCGA  
ACTGGCAGTTTGGCAGCACCTACGAGGCCTCGGCCAACTTCTACTAG

### Nucleotide

>McsEXPA-27

CTCGCCGGCAGTTGCAAGCTTATAAGTACCACACAAGCAGAGAAAACAGTGTGC  
ATCAGTCACAACAGACCGCAAGTGATCTGGCTTGGCAGGCAACATCCTAGTGAG  
AGACGATGGACCAGATGGCGATGCTGCTCTTGCTGCTGAGCTTGTGCGCCTTTCG  
GCTCGGCGGTGCAGTGGCGCAGCAGTACTGGACGCCGGCCACCGCGACGTTCTAC  
GGCGGGAGCGACGCGTCCGGCACCATGGGTAACACTGTCACTGACTGACCATTTT  
CTTGGCAATCCA ACTCTGATCCACGCGTTCGTTTCGTCTGCACTGATGCGCGTGTACT

TGTCGTGCTGCGCGTGCGCATGCAGGCGGGTCGTGCGGGTACGGCGACCTGTACA  
GCGCCGGGTACGGTACGCAGACGACGGCGCTGAGCACGGCGCTCTACGGCGACG  
GCGCCTCCTGCGGCGCGTGCTACCTCATCACCTGCGACGCGTCGCGGACGCAGTA  
CTGCAAGCCGGGGTCGTCCGTACCGTCACGGCCACCAACTTCTGCCCCGCC  
AACTACGGCGACCCCAACGGGTGGTGCAACTCGCCGCGGCAGCACTTCGACATGT  
CGCAGCCGGCCTGGGAGACCATCGGCGTGTACCAGGCCGGCGTCGTCCCCGTCAA  
CTACCGGAGGGTCTCGTGCCAGCGGTCCGGCGGGATCAGGTTTCAGCATCAGCGGC  
CACGACTACTTCGAGCTCGTCACCATCACCAACGTCGGCGGGCGCCGGCGCGGTGG  
CCGCGGCGTGATCATGGGGACCGGCACGGACTGGCTGACCATGAGCCGCAACT  
GGGGGGGAGAAGTGGCAGAGCGGGGCCTATCTCACCGGAAAGGCCCTGTCGTTTA  
AGGTGCAGACGGACGATGGCAAGGTTCGTTCGTGGCGTATAACGTGGCGCCGGCGA  
ACTGGCAGTTTGGCAGCACCTACGAGGCCTCGGCCAACTTCTACTAGGCCAGTT  
GGCCGCGCCACTTCAGATTCAACTGAGTGGGCCATGTAACTAACAGCCCATGAG  
TCGGAGAAAATCCTTACAGTGAACACGTGTATAATTTTTTTTTTTATTTTGATAATA  
CAAAAACCTGATAAGCGCACTTAAGTTCCTATATAATTGTTAGAAAGTAGAGAAT  
GAGAGAGATCGATTGATGCAAATGATTATCTGTTGTATTCCCAATGAACAATGTG  
TACATATATATACAGGCCACGTGGACGGTTACAAGTG