

IDENTIFICATION

Species: *Miscanthus sinensis*

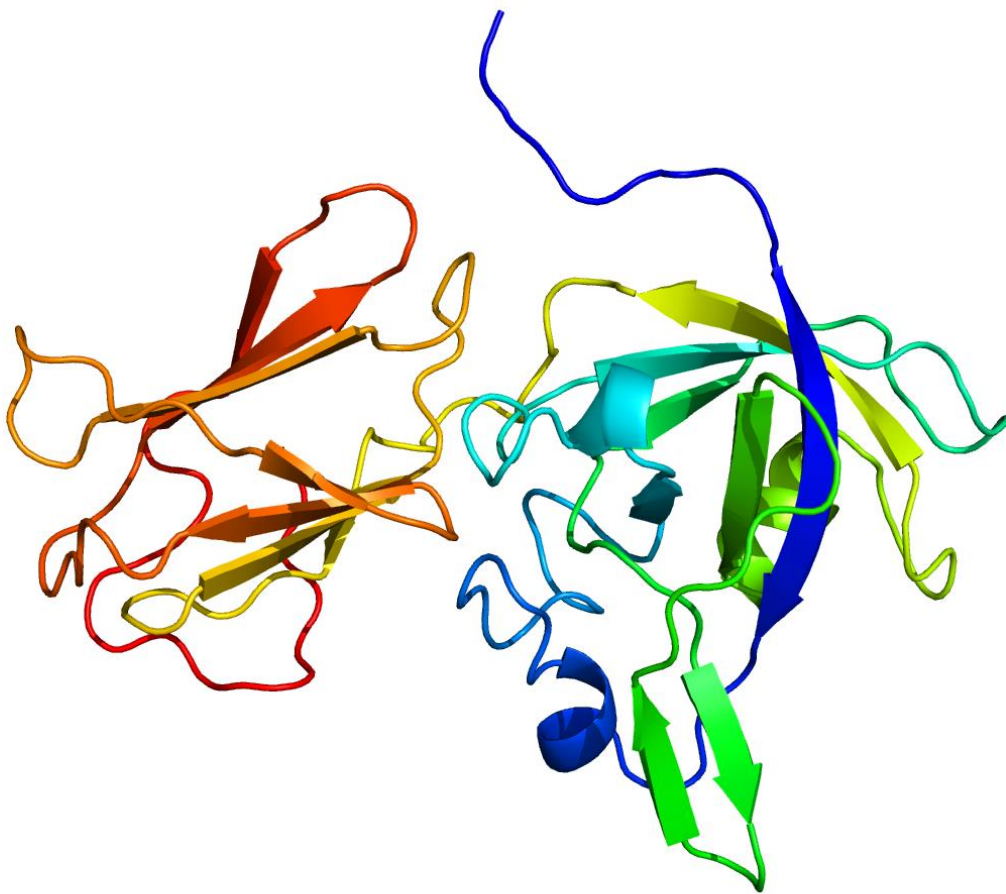
Locus: Misin05G126800

Gene Model: Misin05G126800.1.p

Description: McsEXPA-28

Family: Alpha Expansin

3D structure:



GENOME DATABASES

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

KEGG:-

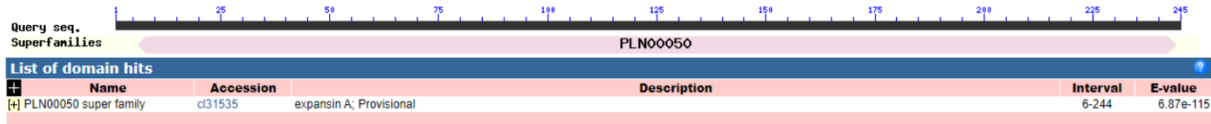
EXTERNAL RESOURCES

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

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>McsEXPA-28

MGSVGLLVLAIAAVLELTRADSWNGGRATFYGGDDASGTMGGACGYGNLYNAGY
GKNTAALSTALFNNGQSCGACFEIRCTGSGSCLSGSAIVTATNFCPPNYALPNNNGG
WCNPPQPHFDLAEPVFTQIAIAGAGVVPVQYRRVPCVKQGGIRFTINGHSYFILLITN
VGGAGDLTAVSIKGSRSGWQTMSRNWGANWNNGALLDGQALSFQVTASDGRTVTS
ENAAPDGWSYGQTYTGKQF*

CDS (coding sequence)

>McsEXPA-28

ATGGGGTCCGTAGGCTTGCTGGTTCTAGCGATCGCCGCCGTGCTGGAGCTACCA
GAGCCGACTCCTGGAACGGCGGCCGCGCCACGTTCTACGGCGGCGATGACGCCTC
TGGCACTATGGGAGGAGCGTGTGGGTATGGCAACTTGTACAATGCAGGATACGG
GAAGAACACCGCGGCGCTGAGCACCGCGCTGTTCAACAATGGGCAGAGCTGCGG
CGCGTGCTTTGAGATCCGGTGCACCGGCAGTGGCAGCTGCCTGTCTGGTTCCGCC
ATTGTGACAGCGACCAACTTCTGCCACCCAATTATGCGCTCCCCAACAACAATG
GTGGATGGTGCAACCCGCCGACCCGCACTTCGACCTCGCCGAGCCGGTCTTCAC
CCAGATCGCTATCGCCGGTGCCGGCGTTCGTGCCTGTCCAATACAGGAGGGTGCCG
TGCGTCAAGCAGGGTGGCATCCGGTTCACCATCAACGGCCACTCCTACTTCATCC
TGTTGCTGATCACAAATGTGGGCGGCGCTGGTGACTTGACGGCGGTATCGATAAA
GGGCTCGCGGTCGGGCTGGCAGACCATGAGCCGCAACTGGGGCGCCAACTGGAA
TAACGGCGCCCTGCTCGACGGCCAGGCACTGTCGTTCCAGGTCACCGCCAGTGAT
GGCCGCACCGTCCAGTCCGAGAACGCCGCACCAGACGGCTGGAGCTACGGCCAG
ACCTACACCGGCAAACAGTTCTAA

Nucleotide

>McsEXPA-28

TAGCTAGATCTAACTATCTTAGTTTGTTCCTCTACTAACACTCTTTTTTATGTTTT
TTTGTAGAAGTATATACTACACATGGGGTCCGTAGGCTTGCTGGTTCTAGCGATC
GCCGCCGTGCTGGAGCTCACCAGAGCCGACTCCTGGAACGGCGGCCGCGCCACG
TTCTACGGCGGCGATGACGCCTCTGGCACTATGGGTGAGCATCTATCTATACATT
GAGCAGTTGAAGATATCAATGGCTCGTTAGCTATTGGTTGCATCACATGACATGT
TGATCTTTGTGTCTGACATGCAGGAGGAGCGTGTGGGTATGGCAACTTGTACAAT

GCAGGATACGGGAAGAACACCGCGGCGCTGAGCACCGCGCTGTTCAACAATGGG
CAGAGCTGCGGCGCGTGCTTTGAGATCCGGTGCACCGGCAGTGGCAGCTGCCTGT
CTGGTTCGCCATTGTGACAGCGACCAACTTCTGCCACCCAATTATGCGCTCCCC
AACAAACAATGGTGGATGGTGCAACCCGCCGCAGCCGCACTTCGACCTCGCCGAG
CCGGTCTTCACCCAGATCGCTATCGCCGGTGCCGGCGTCGTGCCTGTCCAATACA
GGAGGTACGTACGTGACACTGTCACACTCACACTAACACCAGCCAGGTGCTCAAA
GTGGGCGGCCCGTGCGTATGATCACACGCGTGATGCCTATGTGATGTTAATTTGT
GCTTGTGCAGGGTGCCGTGCGTCAAGCAGGGTGGCATCCGGTTCACCATCAACGG
CCTACTCCTACTTCATCCTGTTGCTGATCACAAATGTGGGCGGCGCTGGTGACTTGA
CGGCGGTATCGATAAAGGGCTCGCGGTCGGGCTGGCAGACCATGAGCCGCAACT
GGGGCGCCAACTGGAATAACGGCGCCCTGCTCGACGGCCAGGCACTGTCGTTCCA
GGTCACCGCCAGTGATGGCCGCACCGTCACGTCCGAGAACGCCGCACCAGACGG
CTGGAGCTACGGCCAGACCTACACCGGCAAACAGTTCTAA