

IDENTIFICATION

Species: *Miscanthus sinensis*

Locus: MisinT004900

Gene Model: MisinT004900.1.p

Description: McsEXPA-60

Family: Alpha Expansin

3D structure:



GENOME DATABASES

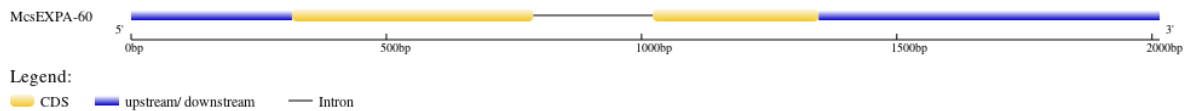
Phytozome: https://phytozome-next.jgi.doe.gov/info/Msinensis_v7_1

KEGG:-

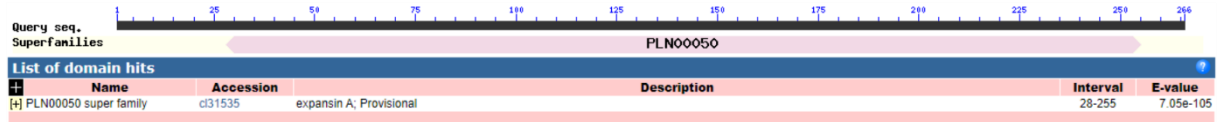
EXTERNAL RESOURCES

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

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>McsEXPA-60

MICCLPLSSSSRPGHQLGRRPAQGTWGGGPWQSAHATLYGGSDASGTMGGACGYG
NLYSEGYGVETGALSTPLFNGLTCGACFQIKSSGSSSGGGCHPGSPSVVITATNFCP
PNYALPSDAGGWCNPPRHHLDLSPAFRLIADYRAGIVPVTYRRVACRKS GGIRFSV
NGFRYFNLVLISNVGGAGDVVRAAVKASHTEWLPLARNWGQNWQCSSILVGGALSF
RVTTSDRRTLTSWNVAGPAWRFGQTF TG GKNFRIAAAP*

CDS (coding sequence)

>McsEXPA-60

ATGATCTGCTGCTTGCCATTGTCATCCTCCTCCAGGCCCGGGCATCAGCTGGGCCG
GCGGCCGGCGCAGGGCACATGGGGCGGGCGGGCCGTGGCAGAGCGCGCACGCCAC
CTTGTACGGTGGCAGCGACGCGTCGGGCACCATGGGCGGCGCCTGCGGGTACGG
CAACCTCTACAGCGAGGGATACGGCGTGGAGACGGGGGGCGCTCAGCACGCCGCT
CTTCAACAACGGACTCACCTGCGGCGCCTGCTTCCAGATCAAGTGCAGCTCCGGT
TCCAGCAGCGGGCGGGCTGCCACCCCGGGAGCCCCTCCGTGGTGATCACGGCCA
CCAACTTCTGCCCGCCAACTACGCGCTGCCCTCGGACGCCGGCGGGTGGTGCAA
CCCGCCGCGCCACCACTTGGACCTCTCCATGCCGGCATTCTCCGCATCGCAGAC
TACCGCGCCGGCATCGTCCCCGTCACATACCGGAGGGTGGCGTGCCGCAAGTCCG
GCGGCATCCGGTTCAGCGTCAACGGCTTCCGCTACTTCAACCTGGTGCTGATCAG
CAACGTGGGCGGCGCCGGCGACGTGGTCCGCGCCGCGTCAAGGCCTCGCACAC
GGAGTGGCTGCCCTGGCGCGCAACTGGGGACAGA ACTGGCAGTGCAGCTCCAT
CCTCGTGGGCGGGGCGCTCTCCTTCCGCGTCACCACCAGCGACCGCCGCACCCTC
ACCTCCTGGAACGTCGCCGGACCAGCCTGGCGCTTTGGACAGACATTCACCGGCG
GCAAAA ACTTCAGGATCGCCGCCGCCCTAG

Nucleotide

>McsEXPA-60

AATTATAAGTCAGAAGTACTGCTAGCTGGTTTGGTGTGATTGAAAAATATTGTTTT
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CGCCCGGTAGTGTGGCTGCTGCTGCCTGCGCATGAACAAGTGCCCACTTCCCCTC
CACCGACCGGCGATCCCTTTCAGTCTTTCACCAGGCCACCGCGCGGCAGCCACCA

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CATTGTCATCCTCCTCCAGGCCCGGGCATCAGCTGGGCGGGCGGGCCGGCGCAGGG
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CCAACCTACGCGCTGCCCTCGGACGCCGGCGGGTGGTGCAACCCGCCGCGCCACCA
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CAATCTCTCTGCAGGACGGACAGATCATGCATTGCGAATTAACGTACTACTGA
TGTACGTATGTGATCGATGCAGCTAAGTAGTACTGTGTACTGGGCGCAGGATGCT
CGTGAGCTTTAATTTTCTTCTGTCCCGATACCGATCCCAAGAATGCCAGTCCCCGG
CCTCTACAAGCTTTCCTTACCTTGTGTGTTGCAGGGTGGCGTGCCGCAAGTCCGGC
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