

IDENTIFICATION

Species: *Miscanthus sinensis*

Locus: Misin02G208500

Gene Model: Misin02G208500.1.p

Description: McsEXPA-10

Family: Alpha Expansin

3D structure:



GENOME DATABASES

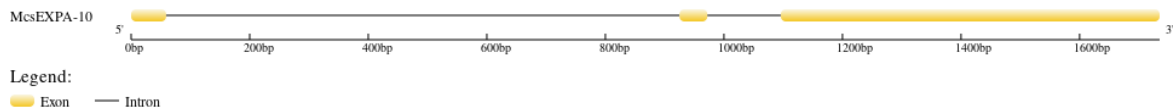
Phytozome: https://phytozome-next.jgi.doe.gov/info/Msinensis_v7_1

KEGG:-

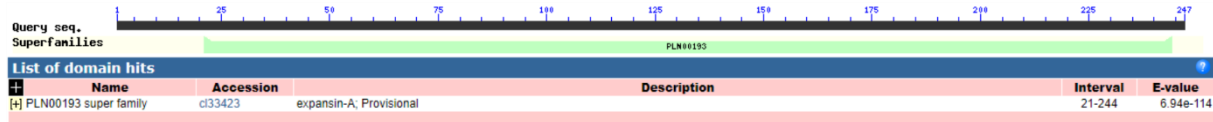
EXTERNAL RESOURCES

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

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>McsEXPA-10

MAPSPSTTPRRQGGRLAVGGTATFYGGSDASGTMGGACGYGNLYATGYGQYTAA
LSQVLYNDGASCGQCYQISCDPQTDARWCRQGAGAVTVAATNLCPPNYAYS GSDG
GWCNPPRAHFDMSQPAWLQIGIYQGGIIPVLYQRVSCAKAGVRFITGFNY YELVLIS
NVGGSGSVASAWVQGSNTNLVPMSRNWGANWQSLAGIAGQALTFGVTSTGGQTIV
FLNVVPQNWVFGMSFTSNLQFSY*

CDS (coding sequence)

>McsEXPA-10

ATGGCCCCTTCCCCTTCCACGACGCCTCGACGCCAGGGCGGGCGGGGGTTGGCCG
TTGGGGGCACCGCCACGTTCTACGGCGGCAGCGACGCCTCGGGCACAATGGGCG
GGGCGTGCGGGTACGGCAACCTGTACGCGACGGGCTACGGTCAGTACACGGCGG
CGCTGAGCCAGGTCCTGTACAACGACGGCGCGTCTGTCGGGGCAGTGCTACCAGAT
CTCCTGCGACCCGACAGACGGACGCGCGGTGGTGCCGGCAGGGCGCCGGCGCCGT
CACCGTCGCCGCCACCAACCTCTGCCCGCCCAACTACGCCTACTCCGGCAGCGAC
GGCGGCTGGTGCAACCCGCCGCGGGCGCACTTCGACATGTTCGACGCCGGCGTGG
CTCCAGATCGGCATCTACCAGGGCGGCATCATCCCGGTGCTGTACCAGCGCGTGT
CCTGCGCGAAGGCTGGCGTTCGCTTACCATCACC GGCTTCAACTACTACGAGCT
GGTGCTCATCTCCAACGTCGGTGGCAGCGGCTCCGTGGCCAGCGCCTGGGTCCAG
GGCTCCAACACCAACCTGGTGCCCATGAGCAGGAACTGGGGCGCCAACTGGCAG
TCGCTTGCCGGGATCGCCGGCCAGGCGCTCACCTTCGGCGTTACGTCCACCGGCG
GACAGACCATCGTCTTCTGAACGTCGTGCCGCAGAACTGGGTGTTCCGGCATGTC
ATCACCAGCAACTTGCAGTTCTCCTACTGA

Nucleotide

>McsEXPA-10

ATGGCCCCTTCCCCTTCCACGACGCCTCGACGCCAGGGCGGGCGGGGGTTGGCCG
TTGGGTACGTCGACCGCCGCCGGCCTCACGTGACCGGCATGTGCCCATGTTCGAA
TCGAATAACAGATGGGTTTACTTGTCGGAGCGATGGCGATGCTAGGATACTATCT
GTCGAGTTGTTGCTTATCAGCGCTAGCTTCTTCTTATTACTTATCAACGCGTCCAA
TAGACGACCGCCAGTTCATCTCTAATCATTCTGTCCACGGAATCAACCCTTTGTT
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AGAATGGGAGTATAACTGCACTTAGATCAGAATCTTGTATACTGGTTGCTTGATG
GCCGGCCATGCGCGCATGTTACGTTCTTGAATTAACAAGAGTCCGCCGGGCGCGG
GCGGAGAGCAAGAGCACTCGACCAGAAACGCACCCACGCCATGCAGGCATGCAC
TTGCACTTGCAGCGCCGATCTGAATCTGATCGGCTATCGGCATGCATGCGCAGCG
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CACCTATCGTCGGACGTACAGTTCCTTGATCCCTACATCGTGAGCTTCGTCCTTCG
TGTGATCCATCTTCACTTGCCTGATCCTGCTGTACTGTTTGAGACGCAAAGCTA
AGGGTGGTAGTAATTGGAGACACCCAAACCTCTGGCCTTGCTGTTCTCGCGGTT
GTCGCGCTGGCTGCCACGTCGGCAGTCGACGCCTGGTTCAGGGGCACCGCCACGT
TCTACGGCGGCAGCGACGCCTCGGGCACAATGGGTACGTACCCTACCCATGCTTA
CTACGTATAGGAGTAGTAGATTTTCAAGATTTCACTGCATGCATGTTATGTCGCGCTC
CGATCCAGTTCTCATCCAGTATGTAAACTGCCACATGATCGATCAGGCGGGGCGT
GCGGGTACGGCAACCTGTACGCGACGGGCTACGGTCAGTACACGGCGGCGCTGA
GCCAGGTCTGTACAACGACGGCGCGTCGTGCGGGCAGTGCTACCAGATCTCCTG
CGACCCGCAGACGGACGCGCGGTGGTGCCGGCAGGGCGCCGGCGCCGTCACCGT
CGCCGCCACCAACCTCTGCCCCGCCAACTACGCCTACTCCGGCAGCGACGGCGGC
TGGTGCAACCCGCCGCGGGCGCACTTCGACATGTTCGAGCCGGCGTGGCTCCAGA
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GCTCATCTCCAACGTCGGTGGCAGCGGCTCCGTGGCCAGCGCCTGGGTCCAGGGC
TCCAACACCAACCTGGTGCCCATGAGCAGGAACCTGGGGCGCCAACTGGCAGTCG
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AGACCATCGTCTTCTGAACGTCGTGCCGAGAACTGGGTGTTCCGGCATGTCATT
CACCAGCAACTTGCAGTTCTCCTACTGA