

IDENTIFICATION

Species: *Miscanthus sinensis*

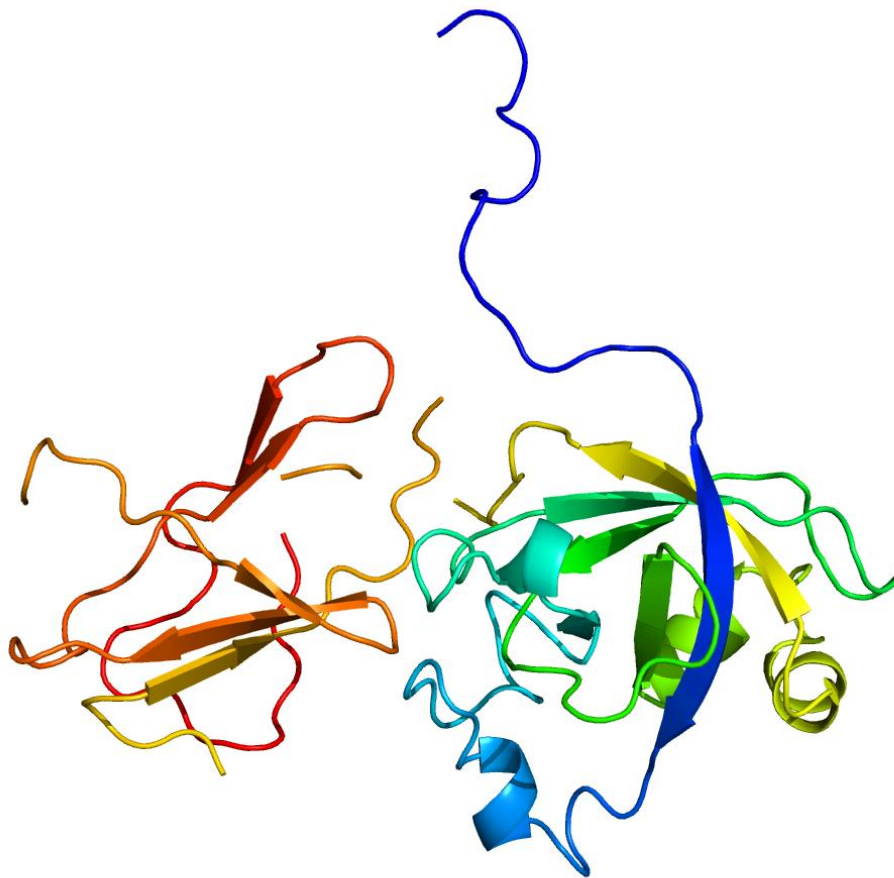
Locus: Misin02G512600

Gene Model: Misin02G512600.1.p

Description: McsEXPB-31

Family: Beta Expansin

3D structure:



GENOME DATABASES

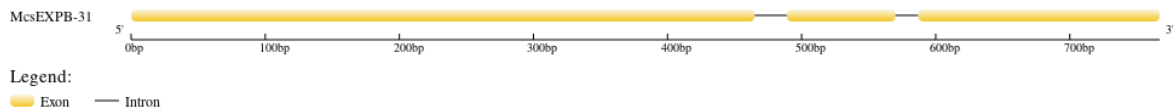
Phytozome: https://phytozome-next.jgi.doe.gov/info/Msinensis_v7_1

KEGG:-

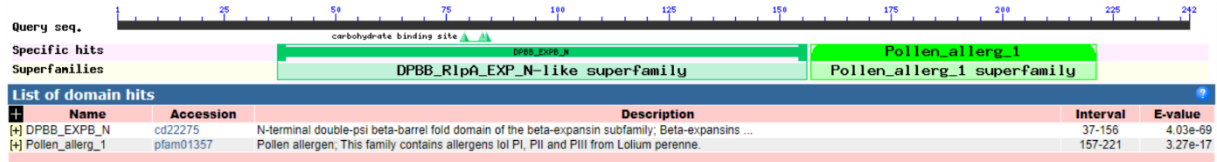
EXTERNAL RESOURCES

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

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>McsEXPB-31

MQVAAVVALAFLVGGAWCGPPKVPPGKNIMATYGSDWLEAKATWYGKPTGAGPD
DNSGGCGYKDVNKA PFNSMGACGNVPIFKDGLGCGSCFEIKCDKPAECSDEPVVYI
MDMNYEPIAAAYHFDLAGTAFGAMAKKGEEELRKGAGIIDMQFRRVTFHVEKGCNPN
YLALLVKYVDGDIVAGGDAFEPLKHSWGAIWRKDS DKPLKFPITVQITTEGGTKSIYN
DVIPEDWKPNTAYTTK*

CDS (coding sequence)

>McsEXPB-31

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GTCCTCCCAAGGTTCCCCGGGCAAGAACATCATGGCCACCTACGGCAGTGACTG
GCTAGAAGCAAAGGCAACATGGTACGGCAAGCCGACGGGCGCTGGCCCCGACGA
CAACAGCGGCGGGTGTGGGTACAAGGATGTGAACAAGGCCCCCTTCAACAGCAT
GGGCGCATGCGGCAATGTCCCATCTTCAAGGATGGCCTCGGCTGTGGCTCTTGC
TTCGAGATCAAGTGCACAAGCCGGCGGAGTGCTCTGACGAGCCCGTGGTGGTGT
ACATCATGGACATGAACTACGAGCCCATCGCCGCGTACCACTTCGACCTGGCCGG
CACGGCGTTCGGCGCCATGGCCAAGAAGGGTGAGGAGGAGAAGCTGCGCAAGGC
GGGCATCATTGACATGCAGTTCCGGCGGGTACCTTCCACGTGGAGAAGGGGTGC
AACCCCAACTACCTGGCGCTGCTGGTCAAGTATGTCGACGGCGACATTGTGGCGG
GCGGCGACGCGTTCGAGCCCCTCAAGCACTCCTGGGGCGCCATCTGGAGGAAGG
ACAGCGACAAGCCGCTCAAGTTCCCATCACCGTCCAATCACCACCGAGGGAG
GCACCAAGAGCATCTACAACGACGTCATCCCCGAAGACTGGAAGCCCAACACCG
CCTACACTACCAAATAA

Nucleotide

>McsEXPB-31

ATGCAGGTGGCGGGCGGTGGTGGCGCTGGCGTTTTTGGTGGGCGGCGCCTGGTGTG
GTCCTCCCAAGGTTCCCCGGGCAAGAACATCATGGCCACCTACGGCAGTGACTG
GCTAGAAGCAAAGGCAACATGGTACGGCAAGCCGACGGGCGCTGGCCCCGACGA
CAACAGCGGCGGGTGTGGGTACAAGGATGTGAACAAGGCCCCCTTCAACAGCAT

GGGCGCATGCGGCAATGTCCCATCTTCAAGGATGGCCTCGGCTGTGGCTCTTGC
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ACATCATGGACATGAACTACGAGCCCATCGCCGCGTACCACTTCGACCTGGCCGG
CACGGCGTTCGGCGCCATGGCCAAGAAGGGTGAGGAGGAGAAGCTGCGCAAGGC
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CACCTTCCACGTGGAGAAGGGGTGCAACCCCAACTACCTGGCGCTGCTGGTCAAG
TATGTCGACGGCGACATTGTGGCGGTGGACATCAAGGAGAGGGCGGCGACGCGT
TCGAGCCCCTCAAGCACTCCTGGGGCGCCATCTGGAGGAAGGACAGCGACAAGC
CGCTCAAGTTCCCCATCACCGTCAAATCACACCGAGGGAGGCACCAAGAGCAT
CTACAACGACGTCATCCCCGAAGACTGGAAGCCCAACACCGCCTACACTACCAA
ATAA