

IDENTIFICATION

Species: *Miscanthus sinensis*

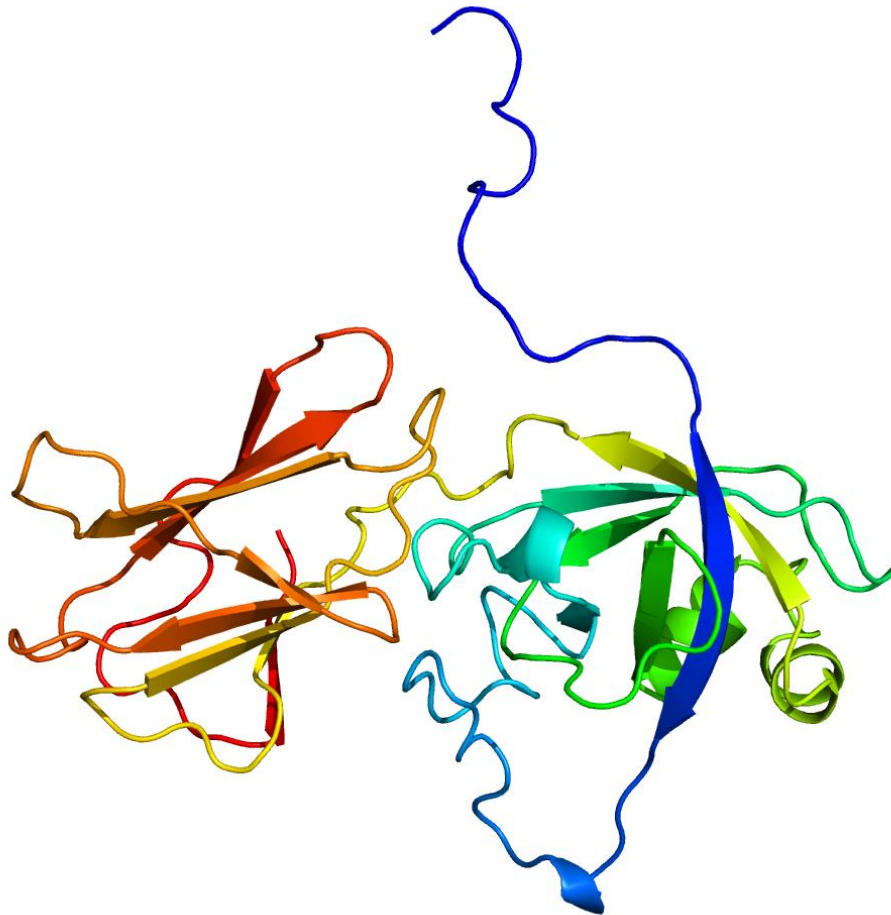
Locus: Misin02G512500

Gene Model: Misin02G512500.1.p

Description: McsEXPB-30

Family: Beta Expansin

3D structure:



GENOME DATABASES

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

KEGG:-

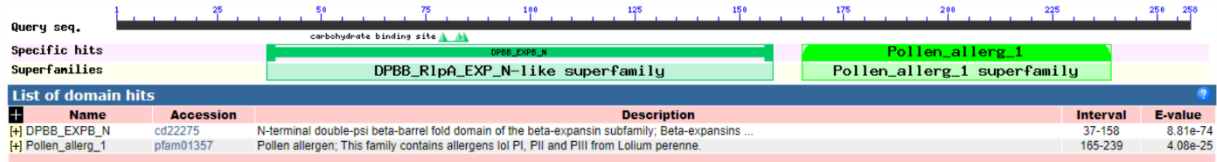
EXTERNAL RESOURCES

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

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>McsEXPB-30

MQVAVVVALAFLVGGAWCGPPKVPPGKNITATYGSDWLEAKATWYGKPTGAGPD
DNGGGCGYKDVNKA PFNSMGACGNVPIFKDGLGCGSCFEIKCDKPAECSGEPVVVYI
TDMNYEPIAAYHFDLAGTAFGAMAKKGEEKLRKAGIIDMQFRRVKCKYVEKVTFH
VEKGCNPNYLALLVKYVDGDGDIVA VDIKEKGGDAFEPLKHSWGAIWRKDS DKPLK
FPVTVQITTEGGTKSVYNDVIPEDWKPN TAYTAK*

CDS (coding sequence)

>McsEXPB-30

ATGCAGGTGGCGGTGGTGGTGGCGCTGGCGTTTCTGGTGGGCGGCGCTTGGTGCG
GTCCTCCCAAGGTTCCCCGGGCAAGA ACATCACGGCCACCTACGGCAGTGACTG
GCTAGAAGCGAAGGCGACGTGGTACGGCAAGCCGACGGGCGCCGGCCCCGACGA
CAACGGTGGTGGGTGCGGGTACAAGGATGTGAACAAGGCCCCCTTCAACAGCAT
GGGCGCGTGC GGCAATGTCCCATCTTCAAGGACGGCCTCGGCTGCGGCTCTTGC
TTTGAGATCAAGTGCGACAAGCCGGCGGAGTGCTCCGGCGAGCCCGTGGTGGTGT
ACATCACGGACATGA ACTACGAGCCCATCGCCGCGTACCACTTCGACCTGGCCGG
CACGGCGTTCGGCGCCATGGCCAAGAAGGGCGAGGAGGAGAAGTTGCGCAAGGC
GGGCATCATCGACATGCAGTTCCGGCGGGTCAAGTGCAAGTACGTTGAAAAGGT
CACCTTCCACGTGGAGAAGGGGTGCAATCCCAACTACCTGGCGCTGCTGGTCAAG
TACGTTCGACGGCGACGGTGACATTGTGGCGGTGGACATCAAGGAGAAGGGCGGC
GACGCGTTCGAGCCCCTCAAGCACTCCTGGGGCGCCATCTGGAGGAAGGACAGC
GACAAGCCGCTCAAGTTCCTGTACCCGTCCAAATCACCACCGAGGGAGGCACCA
AGAGCGTCTACAACGACGTCATCCCCGAAGACTGGAAGCCCAACACAGCCTACA
CCGCCAAATAA

Nucleotide

>McsEXPB-30

ATGCAGGTGGCGGTGGTGGTGGCGCTGGCGTTTCTGGTGGGCGGCGCTTGGTGCG
GTCCTCCCAAGGTTCCCCGGGCAAGA ACATCACGGCCACCTACGGCAGTGACTG
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CAACGGTGGTGGGTGCGGGTACAAGGATGTGAACAAGGCCCCCTTCAACAGCAT
GGGCGCGTGCGGCAATGTCCCATCTTCAAGGACGGCCTCGGCTGCGGGCTCTTGC
TTTGAGATCAAGTGCGACAAGCCGGCGGAGTGCTCCGGCGAGCCCGTGGTGGTGT
ACATCACGGACATGAACTACGAGCCCATCGCCGCGTACCACTTCGACCTGGCCGG
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GGGCATCATCGACATGCAGTTCCGGCGGGTCAAGTGCAAGTACGTTGAAAAGGT
CACCTTCCACGTGGAGAAGGGGTGCAATCCCAACTACCTGGCGCTGCTGGTCAAG
TACGTCGACGGCGACGGTGACATTGTGGCGGTGGACATCAAGGAGAAGGGCGGC
GACGCGTTCGAGCCCCTCAAGCACTCCTGGGGCGCCATCTGGAGGAAGGACAGC
GACAAGCCGCTCAAGTTCCTGTACCGTCCAAATCACCACCGAGGGAGGCACCA
AGAGCGTCTACAACGACGTCATCCCCGAAGACTGGAAGCCCAACACAGCCTACA
CCGCCAAATAA