

IDENTIFICATION

Species: *Mimulus guttatus*

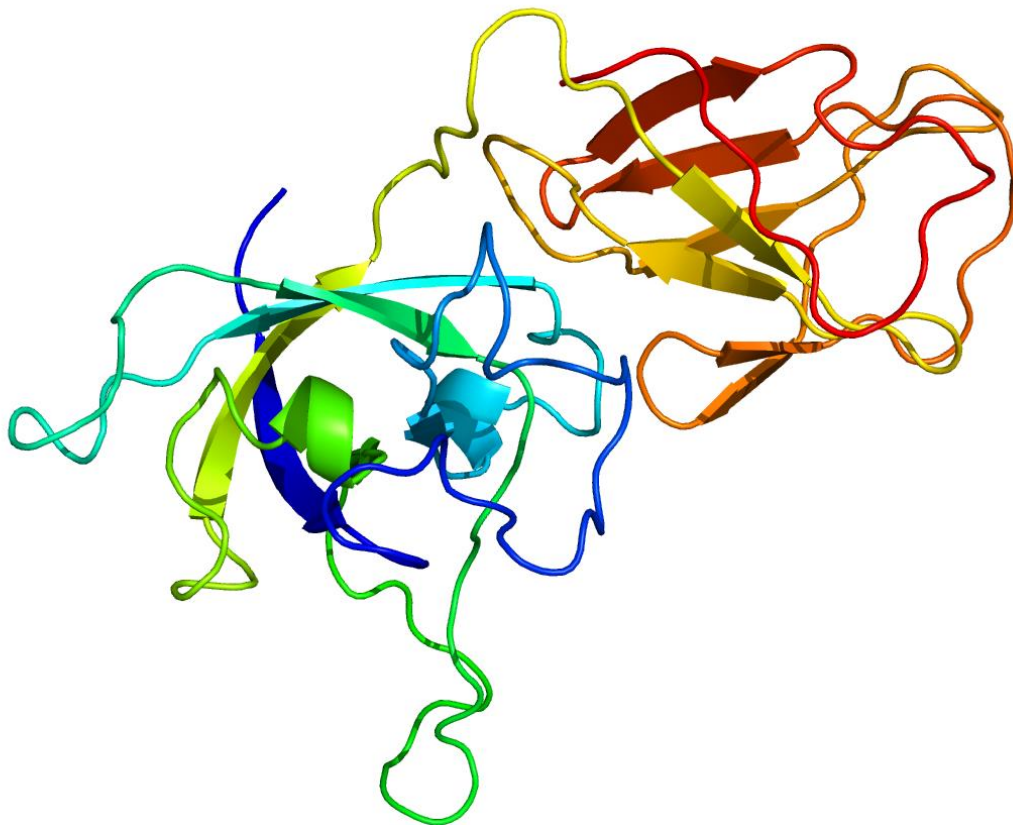
Locus: Migut.D00821

Gene Model: Migut.D00821.1.p

Description: MgEXPA-03

Family: Alpha Expansin

3D structure:



GENOME DATABASES

Phytozome: https://phytozome-next.jgi.doe.gov/info/Mguttatus_v2_0

KEGG:-

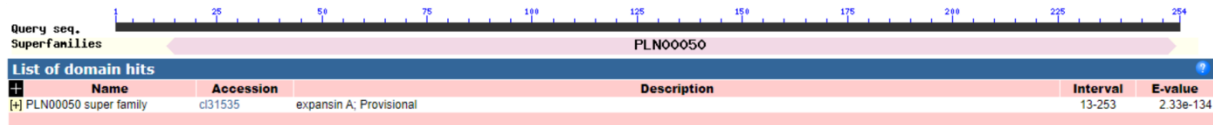
EXTERNAL RESOURCES

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GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>MgEXPA-03

MVAKSLSLATFSFFILNLLRFHSVEADYGGWENGHATFYGGGDASGTMGGACGYGN
LYSQYATNTAALSTALFNGLTCGACYEMRCENDPKWCLSGTITITATNFCPPNFA
LPNDNGGWCNPLQHFDMAEPAFLQIAQYRAGIVPVAFRRVPCMKKGGIRFTINGHS
YFNLVLITNVGGAGDIHALSIKGSKTGWQPMsrNWGQNWQSNsYLNQsLSFQVTA
SDGRtITSYDVAPSNWQFGQTYEGGQF*

CDS (coding sequence)

>MgEXPA-03

ATGGTTGCTAAATCACTTTCTCTTGCCACTTTTTCTTTCTTCATTCTGAATTTACTC
CGGTTTCATAGTGTTGAGGCTGATTACGGAGGATGGGAAAACGGTCACGCCACGT
TTTACGGCGGTGGCGATGCTTCGGGGACGATGGGAGGAGCATGTGGGTACGGGA
ATTTGTACAGCCAAGGGTACGCGACCAACACGGCAGCGCTCAGCACGGCCCTATT
CAACAACGGGCTAACGTGCGGAGCGTGCTACGAAATGCGGTGCGAAAACGACCC
CAAGTGGTGCCTTTCCGGAACCATCACCATCACCGCCACCAATTTCTGCCACCA
AACTTTGCTCTGCCTAACGACAACGGTGGGTGGTGCAATCCTCCCCTCCAGCATT
CGACATGGCCGAGCCCGCTTTCCTTCAAATCGCTCAATACCGGGCCGGCATCGTG
CCCGTTGCTTTTCGAAGGGTGCCATGTATGAAGAAAGGTGGGATTAGGTTACGA
TCAACGGCCACTCGTACTTCAACTTGGTTTTGATCACCAACGTCGGAGGCGCAGG
AGATATCCATGCACTCTCGATCAAAGGGTCCAAAACCGGCTGGCAACCGATGTGC
AGGAATTGGGGCCAAAATTGGCAGAGCAATTTCGTACCTCAACGGTCAAAGCCTCT
CCTTTCAGGTCACCGCCAGTGACGGTAGAACCATCACTAGCTATGACGTGGCGCC
CTCTAATTGGCAGTTCGGTCAAACCTACGAGGGGGGTCAATTCTAA

Nucleotide

>MgEXPA-03

ATGTTATATTTTATATGTAATTGATAAAAAAAAAAATTAAATATTCCAATGTATATAG
GAGGAGCATGTGGGTACGGGAATTTGTACAGCCAAGGGTACGCGACCAACACGG
CAGCGCTCAGCACGGCCCTATTCAACAACGGGCTAACGTGCGGAGCGTGCTACG
AAATGCGGTGCGAAAACGACCCCAAGTGGTGCCTTTCCGGAACCATCACCATCAC
CGCCACCAATTTCTGCCACCAAATTTGCTCTGCCTAACGACAACGGTGGGTGG
TGCAATCCTCCCCTCCAGCATTTTCGACATGGCCGAGCCCGCTTTCCTTCAAATCGC
TCAATACCGGGCCGGCATCGTGCCCGTTGCTTTTCGAAGGTTTCGGAAATTTTGTAT
TCCATATATTGACTTTAATTTAAATATTAATTAAGAGATAAAACCTCTCAAAGA

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CCTTTCAGGTCACCGCCAGTGACGGTAGAACCATCACTAGCTATGACGTGGCGCC
CTCTAATTGGCAGTTCGGTCAAACCTACGAGGGGGGTCAATTCTAAAAGATCATA
TTTATACATACTTTGAATTA AAAAGATTGAGACGAATGAAATTGTTAATTA
CAAAAATACATAACCATTTCTCTTAAAATGTACGAATGTACGTATGTACGTATATG
TATGTATGTATTTATGTATGTATGTATGCATGCATGCTAAGTTTTTTGGGCATGGT
AAGTAATTTGTTAGGGTTATAGAAAGTGTTGAAGTGGTGGCTAATGGCTGCTTAC
ACCGGCCGCTTGGCCTTATATATTTACCGGATTAATAATATTGAAGAGATTAATT
AACATCTT