

IDENTIFICATION

Species: *Medicago truncatula*

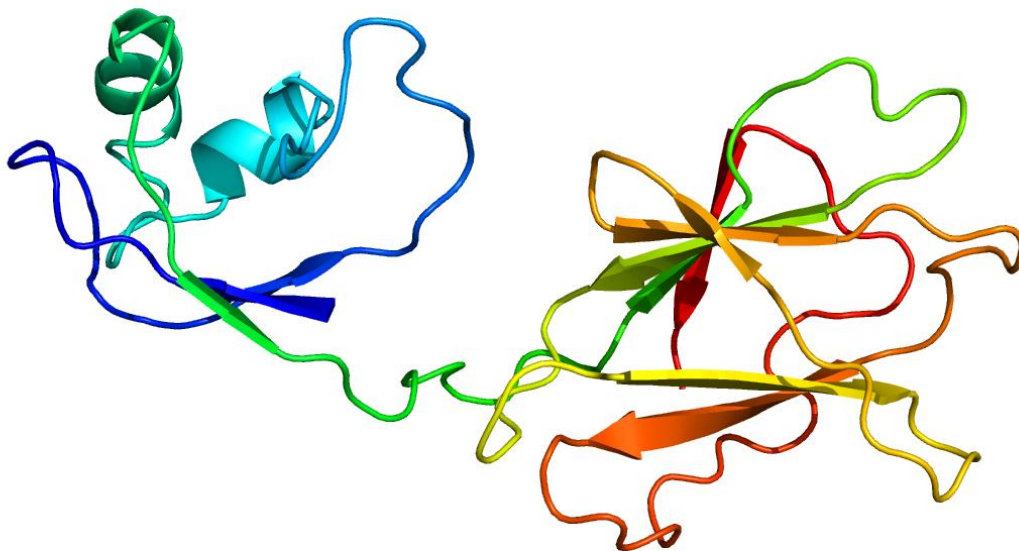
Locus: Medtr4g099400

Gene Model: Medtr4g099400.1

Description: MtrEXLB-03

Family: Expansin Like Beta

3D structure:



GENOME DATABASES

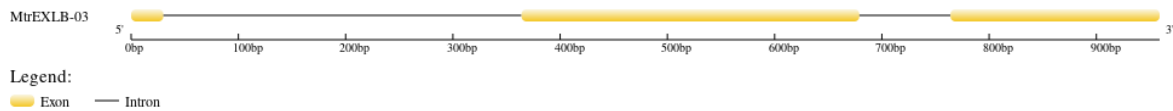
Phytozome: https://phytozome-next.jgi.doe.gov/info/Mtruncatula_Mt4_0v1

KEGG: <https://www.genome.jp/entry/T01716>

EXTERNAL RESOURCES

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GENE STRUCTURE



DOMAIN ARCHITECTURE

Query seq. MAPLTAMEIQVRCKIPQYCCDDNGALVVVTDYGEGRDTRDFIMSPRAFSGLGRNAAAS
Superfamilies PLN03023

Name	Accession	Description	Interval	E-value
PLN03023 super family	c13362.1	Expansin-like B1, Provisional	10-178	1.03e-77

SEQUENCES

Peptide

>MtrEXLB-03

MAPLTAMEIQVRCKIPQYCCDDNGALVVVTDYGEGRDTRDFIMSPRAFSGLGRNAAAS
EKLKKEYGVLDVEYKRVSCFTKGNINIVYQINEHSQNPQGYIAIVILYVGGTYDVNAVEM
WQKEQHKWEYMRRSYGAVFDYANPPKGEIRLRFQVSSNVGVNWVESRFAIPAGWK
AGATYSTKIQT*

CDS (coding sequence)

>MtrEXLB-03

ATGGCACCTCTGACGGCTATGGAAATCCAAGTGAGATGCAAATACCACAATATT
GTGATGACAATGGAGCATTGGTGGTGGTAACCGACTATGGTGAGGGAGATAGAA
CTGACTTCATAATGAGTCCACGCGCCTTCTCAGGATTGGGACGCAACGCAGCTGC
ATCTGAAAAGCTGAAGAAATATGGAGTATTGGATGTTGAATACAAAAGGGTCTC
ATGTACATTTAAAGGTAACAATATCGTGTACCAGATCAATGAGCACAGTCAAAC
CCAGGTTACATTGCTATCGTGATCCTCTACGTTGGTGGAACGTATGATGTCAATGC
TGTTGAGATGTGGCAGAAAGAACAGCACAAATGGGAGTACATGCGTCGGTCTTA
TGGGGCAGTATTTGACTATGCTAACCACCCAAAGGTGAAATCAGATTGAGGTTT
CAAGTTAGTAGCAATGTTGGGGTCAATTGGGTGGAGTCAAGGTTCCGAATACCTG
CAGGTTGGAAAGCTGGTGCTACTTATTCCACCAAGATTCAGACTTAA

Nucleotide

>MtrEXLB-03

ATGGCACCTCTGACGGCTATGGAAATCCAAGTATGTGATAATCCTCCCTTTCTAA
CTANGAGACTATGG
AAAGACAGTCAATGATGGCAGTGTAACAGCTGTGTCTGCAAAGTTGTGGAAGAA
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ATATTTCAACAACCTTAGTGAAATAAAAAAATGTTTCACATCATTATATGGAA
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AATGCATGTAAATATGATGATACATGAATTAGGTGAGATGCAAATACCACAAT
ATTGTGATGACAATGGAGCATTGGTGGTGGTAACCGACTATGGTGAGGGAGATA
GAACTGACTTCATAATGAGTCCACGCGCCTTCTCAGGATTGGGACGCAACGCAGC
TGCATCTGAAAAGCTGAAGAAATATGGAGTATTGGATGTTGAATACAAAAGGGT
CTCATGTACATTTAAAGGTAACAATATCGTGTACCAGATCAATGAGCACAGTCAA

AACCCAGGTTACATTGCTATCGTGATCCTCTACGTTGGTGGAAACGTATGATGTCA
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CATCCTCTCTTAAATATTGAATACTAGCTCTATTTTTGTTAATGATGCAGAAAGAA
CAGCACAAATGGGAGTACATGCGTCGGTCTTATGGGGCAGTATTTGACTATGCTA
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CAATTGGGTGGAGTCAAGGTTTCGCAATACCTGCAGGTTGGAAAGCTGGTGCTACT
TATCCACCAAGATTCAGACTTAA