

## IDENTIFICATION

**Species:** *Medicago truncatula*

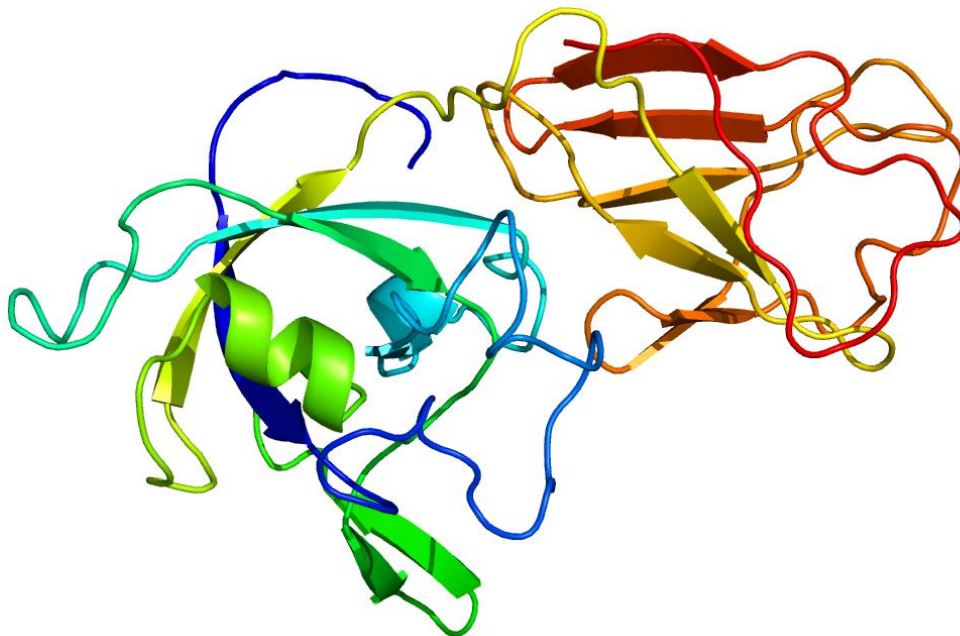
**Locus:** Medtr3g094060

**Gene Model:** Medtr3g094060.1

**Description:** MtrEXPA-10

**Family:** Alpha Expansin

**3D structure:**



## GENOME DATABASES

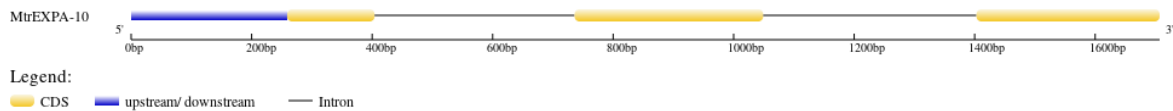
Phytozome: [https://phytozome-next.jgi.doe.gov/info/Mtruncatula\\_Mt4\\_0v1](https://phytozome-next.jgi.doe.gov/info/Mtruncatula_Mt4_0v1)

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

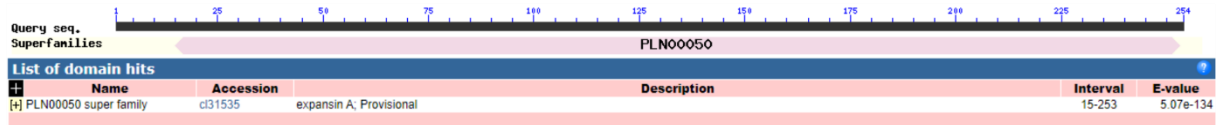
## EXTERNAL RESOURCES

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## GENE STRUCTURE



## DOMAIN ARCHITECTURE



## SEQUENCES

### Peptide

>MtrEXPA-10

MAIVATSFISTLFFVLSLCLKGTFFGDYGGGWENAHATFYGGGDASGTMGGACGYGN  
LYSQYGTNTAALSTALFNGLSCGSCYEMKCNSDPKWCLPGSILVTATNFCPPNFA  
ESNTNGGWCNPLQHFDLAEPFLQIAQYKAGIVPISFRRVPCVKKGGIRFTINGHSYF  
NLVLVTNVGGAGDVHVSIVIKGSKTGWQAMSRNWGQNWQSNNYLNGQSLSFQVTT  
DGRITTSNNVPGNWQFGQFTTGRQF\*

### CDS (coding sequence)

>MtrEXPA-10

ATGGCAATAGTAGCAACCTCATTCAATTTCTACTCTTTTCTTTGTTCTTAGCTTATGC  
CTTAAAGGCACTTTTGGTGACTACGGAGGTGGATGGGAAAATGCTCATGCCACAT  
TTTATGGTGGAGGAGATGCATCAGGCACAATGGGAGGTGCTTGTGGTTATGGAAA  
TTTGTATAGCCAAGGCTATGGAACCAACACTGCTGCACTAAGTACTGCTCTTTTCA  
ACAATGGATTGAGTTGTGGGTCTTGCTACGAGATGAAATGTAACAGTGACCCTAA  
ATGGTGCCTTCCCTGGTAGCATATTGGTTACTGCTACAACTTCTGCCCCCAA  
TTGCAGAGTCTAATAACCAATGGTGGATGGTGAACCCCTCCCTTCAGCACTTTGA  
TCTTGCTGAGCCTGCTTTCTTACAAATTGCTCAATACAAAGCTGGAATTGTTCTTA  
TTTCTTCAGAAGAGTCCCCTGTGTGAAGAAAGGAGGAATCAGATTCACAATAAA  
TGGACACTCATACTTCAACTTGGTTTTGGTCAAAATGTTGGTGGAGCTGGAGAT  
GTACATTCTGTGTCCATCAAGGGATCAAAGACTGGATGGCAAGCTATGTCTAGGA  
ACTGGGGGCAGAAGTGGCAAAGCAATAACTATCTCAATGGTCAAAGCCTCTCATT  
CCAAGTCACTACAAGTGATGGTAGAACTATCACTAGCAACAACGTTGTGCCTGGC  
AATTGGCAATTTGGACAGACATTTACAGGGAGACAGTTTTAG

### Nucleotide

>MtrEXPA-10

AAACATTTCCATGTGCACATATGAATAAGTTTTTTGTTGTTTTGGCTCTCTCTCTTT  
AGACCCTAAGAAATGCTAACATGTCTCTTTCTATATCTCAGTCTTTAGTATCCCCA  
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ACCAAGCACTAAAGCTACTTCTCTATCTTAAAATCCTTTGCAACCCTAACTTCT  
CAAGAAGTAAGTACTACTAGAAGTAGTAACACACAATGGCAATAGTAGCAACCT  
CATTCAATTTCTACTCTTTTCTTTGTTCTTAGCTTATGCCTTAAAGGCACTTTTGGTG

ACTACGGAGGTGGATGGGAAAATGCTCATGCCACATTTTATGGTGGAGGAGATG  
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CAACACTGCTGCACTAAGTACTGCTCTTTTCAACAATGGATTGAGTTGTGGGTCTT  
GCTACGAGATGAAATGTAACAGTGACCCTAAATGGTGCCTTCCTGGTAGCATATT  
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