

IDENTIFICATION

Species: *Medicago truncatula*

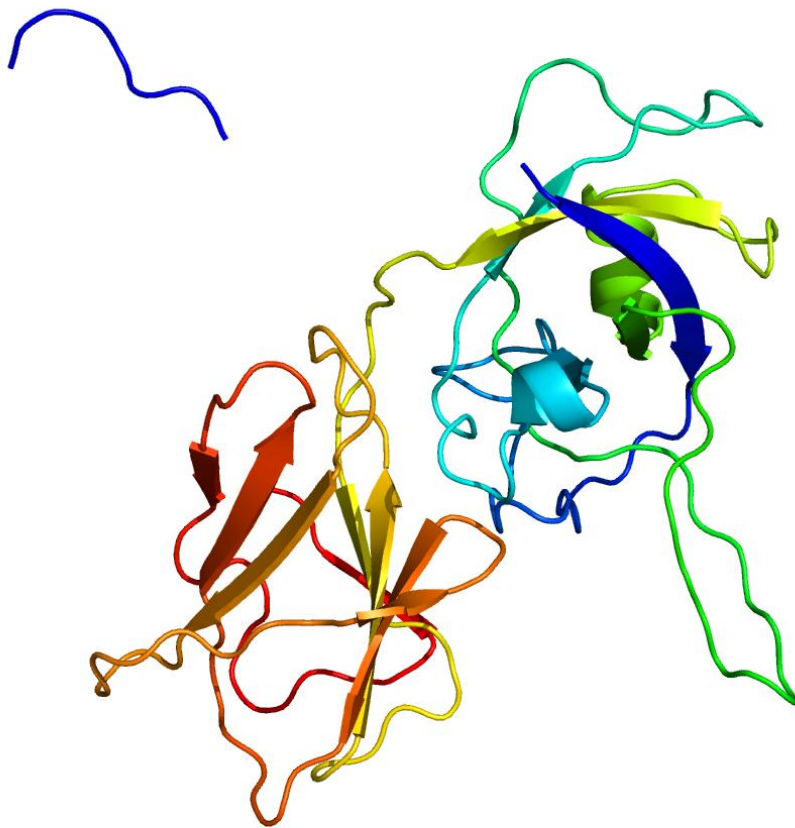
Locus: Medtr4g124340

Gene Model: Medtr4g124340.1

Description: MtrEXPA-14

Family: Alpha Expansin

3D structure:



GENOME DATABASES

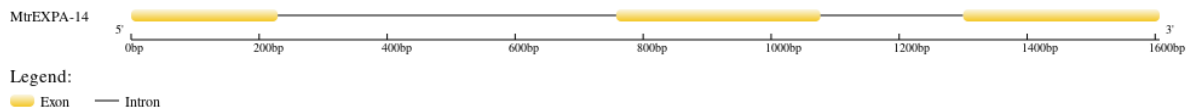
Phytozome: https://phytozome-next.jgi.doe.gov/info/Mtruncatula_Mt4_0v1

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

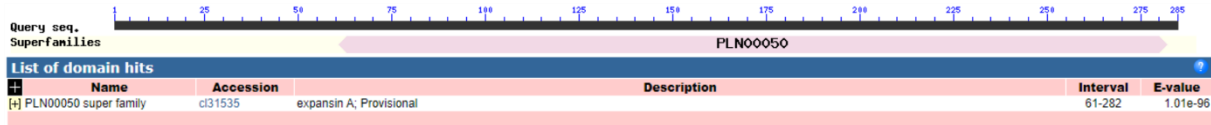
EXTERNAL RESOURCES

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GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>MtrEXPA-14

MALSSGPLVTSLLLFLVAFSLHNAHASINSSWKNAAHNNIGPKKLSTPKQNRHMLLAGSWKKAHATFYEGGSGTFGGACGYEDVVKDGYGLDTAAVSTVLFNKGLACGACYEIRCVDSPQGCKPGQASIKVTATDLCPPNFAQSSSENGGWCNPPREHFDLAKPAYLKIAEYKAGIIPVQYRRVPCRKQGGIHFTITGNPYFNLIKVANVGGAGDVVKVQVKGEDKLTWTDLKRNWGEKWETGAMLTGETLTFKVTTS DGRCSERITPKGWQFGQTFVGKNA*

CDS (coding sequence)

>MtrEXPA-14

ATGGCATTATCTTCGGGACCTCTTGTGACTTCATTATTGCTCTTTCTTGTTGCTTTT
TCACTTCATAATGCCCATGCAAGCATCAACTCCTCATGGAAAAATGCAGCTCACA
ATAATATTGGACCTAAAAAACTGATCAGTACCCCTAAACAAAACCGCCACATGCT
TTAGCTGGTTCATGGAAAAAAGCACATGCCACTTTCTATGAGGGAGGCTCAGGA
ACATTTGGTGGAGCATGCGGATATGAGGATGTGGTTAAAGATGGTTATGGCCTAG
ACACAGCAGCAGTGAGCACAGTTTTGTTCAACAAAGGTCTAGCATGTGGTGCATG
TTATGAAATCAGATGTGTGGACTCTCCTCAAGGGTGTAAAGCCAGGGCAAGCCTCT
ATTAAAGTGACGGCAACAGACCTTTGTCTCCCAATTTTGCCCAATCAAGTGAGA
ATGGAGGATGGTGCAACCCACCACGTGAGCACTTTGATTTAGCCAAACCTGCTTA
TCTTAAAATTGCTGAATACAAAGCTGGAATTATACCAGTCCAATATCGCAGGGTA
CCATGCAAGAGGCAGGGAGGTATTCATTTACGATCACAGGGAATCCTTACTTTA
ACCTAATTAAGTGGCGAATGTCGGAGGAGCAGGTGATGTGGTAAAAGTGCAAG
TGAAGGGTGAAGACAAGCTGACATGGACAGACTTGAAGAGAAATTGGGGTGAGA
AATGGGAGACTGGTGCCATGTAACTGGAGAGACATTGACCTTCAAGGTGACGA
CAAGTGATGGCAGGTGTATCCTCTGAACGTATAACCCCAAAGGTTGGCAGTT
TGGTCAGACCTTTGTAGGCCAAAAACGCATAA

Nucleotide

>MtrEXPA-14

ATGGCATTATCTTCGGGACCTCTTGTGACTTCATTATTGCTCTTTCTTGTTGCTTTT
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TACTCATTATGCAAACATGCATGGTTTACTTTATAAGTTGTCCTTTTAGGTTGGAG
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GAGGATGTGGTTAAAGATGGTTATGGCCTAGACACAGCAGCAGTGAGCACAGTT
TTGTTCAACAAAGGTCTAGCATGTGGTGCATGTTATGAAATCAGATGTGTGGACT
CTCCTCAAGGGTGTAAAGCCAGGGCAAGCCTCTATTAAGTGACGGCAACAGACCT
TTGTCCTCCCAATTTTGCCCAATCAAGTGAGAATGGAGGATGGTGCAACCCACCA
CGTGAGCACTTTGATTTAGCCAAACCTGCTTATCTTAAAATTGCTGAATACAAAG
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CCTCTGAACGTATAACCCCCAAAGGTTGGCAGTTTGGTCAGACCTTTGTAGGCAA
AAACGCATAA