

IDENTIFICATION

Species: *Medicago truncatula*

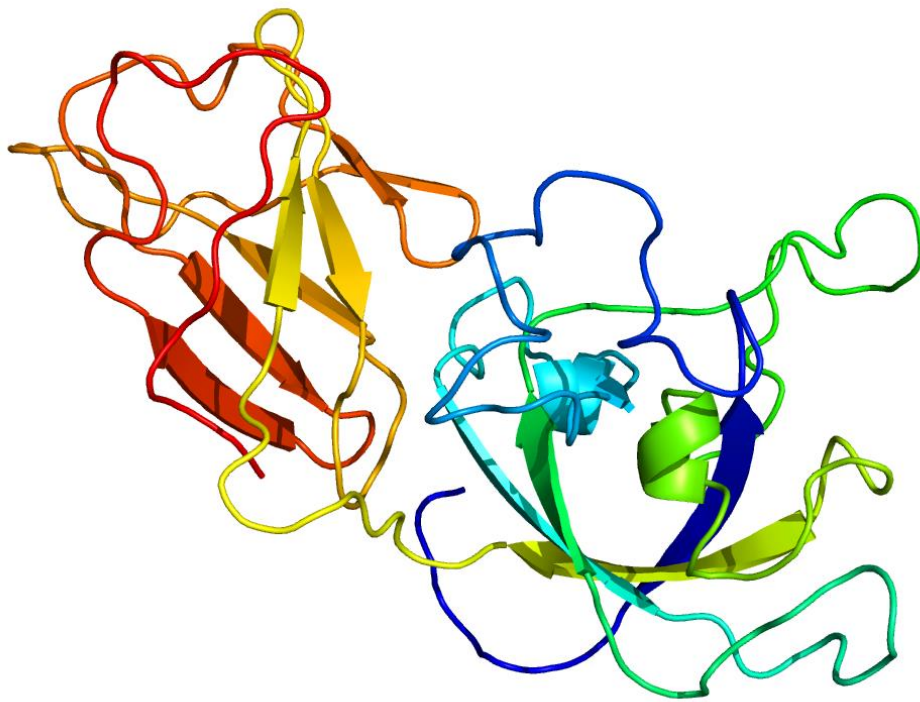
Locus: Medtr1g085460

Gene Model: Medtr1g085460.1

Description: MtrEXPA-02

Family: Alpha Expansin

3D structure:



GENOME DATABASES

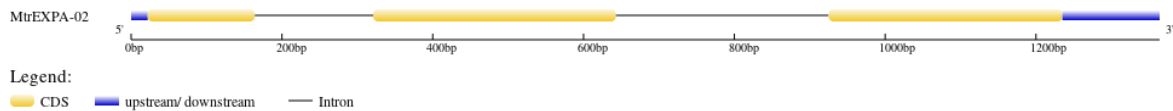
Phytozome: https://phytozome-next.jgi.doe.gov/info/Mtruncatula_Mt4_0v1

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

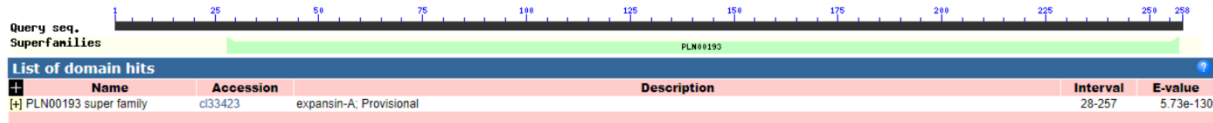
EXTERNAL RESOURCES

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GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>MtrEXPA-02

MERASFIGAVVLVVLVGLFTSEVRVESAAWQKAHATFYGGSDASGTMGGACGYGD
LYKDGYGIKTAALSTALFNDGKSCGGCYQIVCDASQVPQWCLRGTSTITATNFCPPN
FALPSDNGGWCNPPRPHFDMSQPAFQMIAKYKAGIVPILYRKVECKKSGGIRFKINGR
DYFELVLISNVGGAGDISKVWIKGSKMRNWESMSRNWGANWQSLSYLNQSLFRV
QLSNGKTLTAVNVVPSSWRFQSFISKVQF*

CDS (coding sequence)

>MtrEXPA-02

ATGGAAAGGGCAAGTTTCATTGGTGCAGTAGTACTAGTAGTGCTTGTGGGGTTGT
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CTATGGTGGAAGTGATGCCTCAGGAAGTATGGGGGGTGCATGTGGGTATGGAGA
CTTGTACAAAGATGGTTATGGAATAAAAACAGCTGCATTGAGTACTGCTTTGTTT
AATGATGGAAAGTCATGTGGTGGTTGCTATCAGATTGTTTGTGATGCAAGTCAAG
TTCCCAATGGTGCCTCAGGGGAAGTCCATAACAATTACTGCCACTAATTTTTGT
CCCCAACTTTGCTCTTCTAGTGACAATGGTGGTTGGTGTAACTCCTAGACC
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TGA

Nucleotide

>MtrEXPA-02

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GATGCAAGTCAAGTTC C C C C A A T G G T G C C T C A G G G G A A C T T C C A T A A C A A T T A C T G
C C A C T A A T T T T T G T C C C C C A A A C T T T G C T C T T C C T A G T G A C A A T G G T G G T T G G T G T
A A T C C T C C T A G A C C A C A T T T T G A C A T G T C C C A A C C T G C T T T T C A A A T G A T C G C C A A
A T A T A A G G C T G G G A T T G T T C C A A T C C T T T A C A G A A A G T A T G T T A T A C T T G T G T T T A
C T G T C T T A T T T T T C A A T T T A T T T T T T C T T A T T A G G A A T C G A G T T C G G T A C T C T G G A
G T T T A C A A C A C T C G C A C A C T T T G T G C A T T A T T A A C C A T T T G T T C T A A A A A A A T C T G
T C T A T T C T A A G A A A A A T C T T T T T T T A C T T A C A T G T A G T A C A G T T T T C C A T C A A A T T
T T C T C C G G A A A A A C C A T T T A G A A A G T T A A A A C T T G T T A A A G T G A T T A A G C T A G C T
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C T C T C A C G G C T G T T A A T G T G G T A C C C T C T A G T T G G A G A T T T G G T C A G T C T T T C A T C
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A G T C T T C A C T T C A T C C T T T T A C A A A T A T A C A T C C A T G T C A A T T T A C T G A C T T G T C T T
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