

## IDENTIFICATION

**Species:** *Marchantia polymorpha*

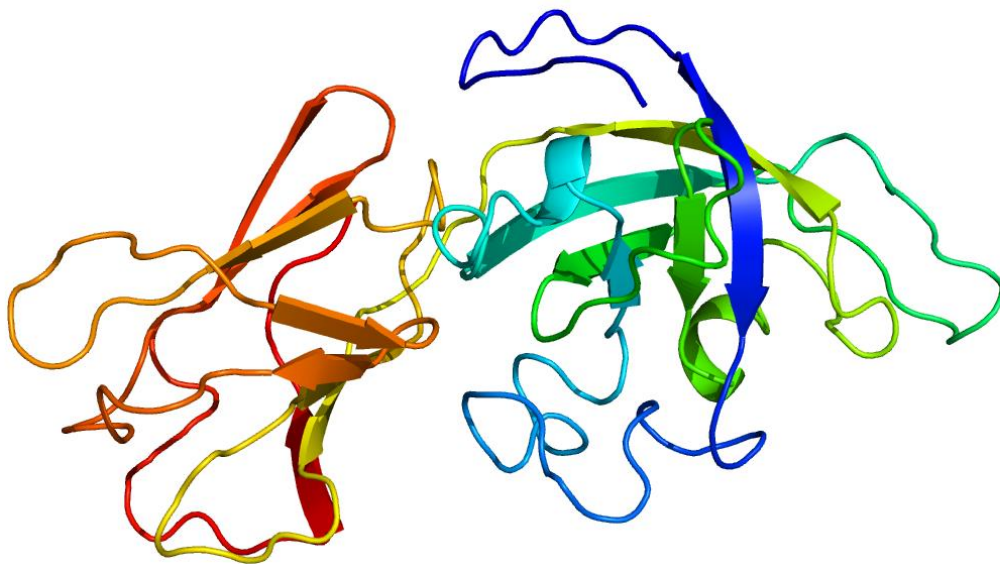
**Locus:** Mapoly0050s0034

**Gene Model:** Mapoly0050s0034.1.p

**Description:** MpoEXPA-10

**Family:** Alpha Expansin

**3D structure:**



## GENOME DATABASES

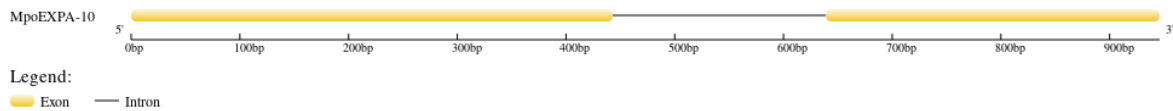
Phytozome: [https://phytozome-next.jgi.doe.gov/info/Mpolymorpha\\_v3\\_1](https://phytozome-next.jgi.doe.gov/info/Mpolymorpha_v3_1)

KEGG:-

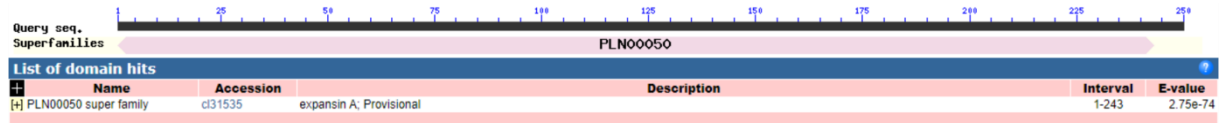
## EXTERNAL RESOURCES

<https://marchantia.info/>

## GENE STRUCTURE



## DOMAIN ARCHITECTURE



## SEQUENCES

### Peptide

>MpoEXPA-10

MNLILSTLFLILSLDGLSEAGESGAVSRTTFGDATATFYGGTDAAGTAGGSCGYENPFRG  
YGVTTAALSNSLLSDGLNCGACFEVKCNFGASDYTRKYCYNGKSVVITSTNLSPPGLH  
GEHHFDLTYPMFTQISNMIAGRIPVQYRRVPCKKQGGIKFNINGNPYFNLVLVY  
NVAGGGNVYAMAMKGGNSAWCTMGRNWWGQNWQSSVKLTGQGLSFRVTLGSGKMLV  
FNNVAPSSWQFGQTYQASSNF\*

### CDS (coding sequence)

>MpoEXPA-10

ATGAACCTCATTTTATCCACTTTGTTCCCTCATTCTCTCGCTTGACGGCCTGTCAGA  
AGCTGGAGAATCAGGAGCTGTCAGCCGCACAACCTTTCGGAGATGCTACAGCAAC  
GTTTACGGAGGCACTGATGCTGCTGGTACAGCGGGAGGTTTCATGTGGTTATGAA  
AATCCGTTACGAGAGGTTACGGTGTGACCACAGCTGCGCTGAGCAACAGCTTAC  
TCAGTGACGGTCTGAATTGCGGAGCCTGCTTTGAAGTCAAGTGCAATTTTCGGTGC  
ATCAGATTATACGAGAAAATACTGCTATAACGGCAAATCAGTCGTTATCACGTCCG  
ACAAACCTCAGCCCTCCTGGTCTCCATGGAGAACACCACTTCGACCTGACCTACC  
CAATGTTCACTCAGATTTTGAATATGATCGCTGGACGCATCCCGGTTCAATACCG  
AAGAGTGCCATGTAAAAAGCAGGGAGGAATTAATTCAATATCAATGGCAATCC  
TACTTCAATCTCGTGCTCGTGTATAACGTAGCTGGTGGTGGAAACGTTTATGCCA  
TGGCGATGAAAGGTGGCAACAGTGCCTGGTGTACAATGGGACGAAACTGGGGAC  
AAAATTGGCAATCCTCCGTGAAGCTTACTGGGCAGGGACTGTCTTCCGTGTCAC  
GTTGGGCAGTGGCAAGATGCTAGTGTTCAACAACGTAGCTCCATCGTCGTGGCAG  
TTCGGTCAGACGTACCAGGCGAGCAGTAACTTCTGA

### Nucleotide

>MpoEXPA-10

ATGAACCTCATTTTATCCACTTTGTTCCCTCATTCTCTCGCTTGACGGCCTGTCAGA  
AGCTGGAGAATCAGGAGCTGTCAGCCGCACAACCTTTCGGAGATGCTACAGCAAC  
GTTTACGGAGGCACTGATGCTGCTGGTACAGCGGGAGGTTTCATGTGGTTATGAA  
AATCCGTTACGAGAGGTTACGGTGTGACCACAGCTGCGCTGAGCAACAGCTTAC  
TCAGTGACGGTCTGAATTGCGGAGCCTGCTTTGAAGTCAAGTGCAATTTTCGGTGC  
ATCAGATTATACGAGAAAATACTGCTATAACGGCAAATCAGTCGTTATCACGTCCG  
ACAAACCTCAGCCCTCCTGGTCTCCATGGAGAACACCACTTCGACCTGACCTACC  
CAATGTTCACTCAGATTTTGAATATGATCGCTGGACGCATCCCGGTTCAATACCG

AAGGTGAATGAATGCACACAGAGCTCAGGAATGTCCATTAGAGTTAAACGAAAC  
TAATGCGCACCTCGCAGAGTACATGCAGAAGAAGTTGACATGATTTGGATGTGAG  
GTGTATACTGACAGCGAGGATGGATTGAATCATGCCATGCTACACGTGCATGATC  
AGCAATTAACATTCTCCTGACAATGTTCCATGCAGAGTGCCATGTAAAAAGCAGG  
GAGGAATTAATTCAATATCAATGGCAATCCTTACTTCAATCTCGTGCTCGTGTAT  
AACGTAGCTGGTGGTGGAAACGTTTATGCCATGGCGATGAAAGGTGGCAACAGT  
GCCTGGTGTACAATGGGACGAAACTGGGGACAAAATTGGCAATCCTCCGTGAAG  
CTTACTGGGCAGGGACTGTCTTTCCGTGTCACGTTGGGCAGTGGCAAGATGCTAG  
TGTTCAACAACGTAGCTCCATCGTCGTGGCAGTTCGGTCAGACGTACCAGGCGAG  
CAGTAACTTCTGA