

## IDENTIFICATION

**Species:** *Marchantia polymorpha*

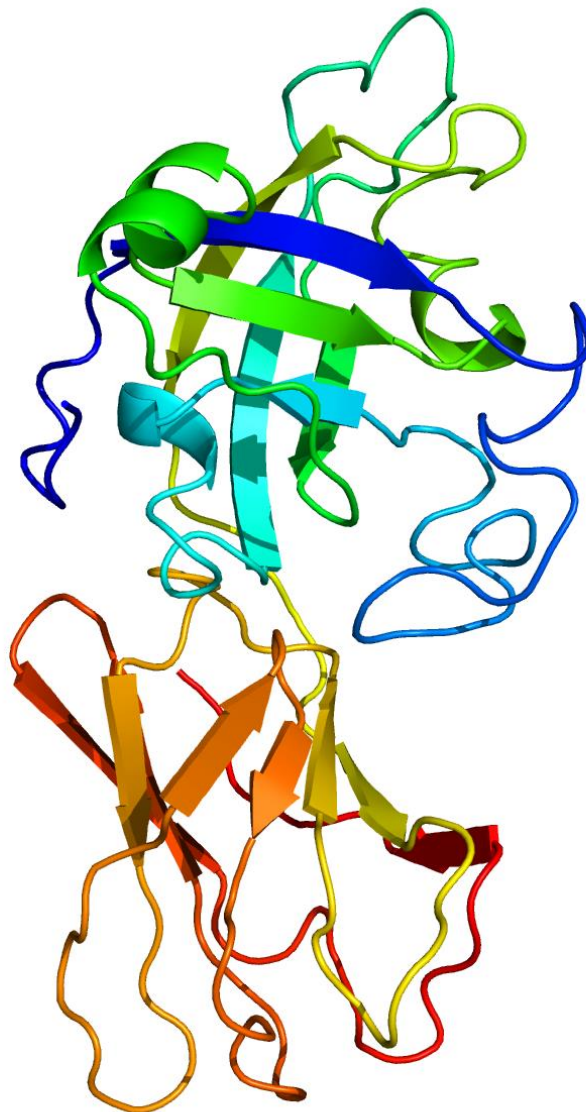
**Locus:** Mapoly0022s0139

**Gene Model:** Mapoly0022s0139.1.p

**Description:** MpoEXPA-05

**Family:** Alpha Expansin

**3D structure:**



## GENOME DATABASES

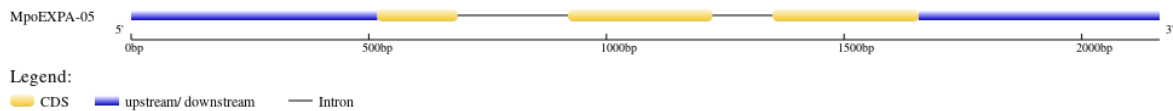
Phytozome: [https://phytozome-next.jgi.doe.gov/info/Mpolymorpha\\_v3\\_1](https://phytozome-next.jgi.doe.gov/info/Mpolymorpha_v3_1)

KEGG:-

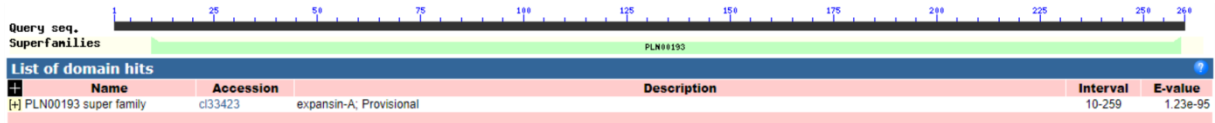
## EXTERNAL RESOURCES

<https://marchantia.info/>

## GENE STRUCTURE



## DOMAIN ARCHITECTURE



## SEQUENCES

### Peptide

>MpoEXPA-05

MAASMHAGRSVQLLVGSLVLLCLKVATVNAAQAWAVTDWADAHATFYGGSDASG  
TMGGACGYGNLYSLGYGTSSTALSINALFNGLSCGACFLIQCKLEGSKYCYPGQSIT  
VTATNACPPGSEGGWCDPPRSHFDLSFPMFQKLAQPVGGVIPVRYKRVSCTKQGGVR  
FTLHGPNPYFNYVLVHNVAGWGDVSSLAIKGDQTGWYYMSQNWGQYWSASAKLTG  
QALSFKVTLGNGKSLEFYNVADKNWGFQGTYESDYNF\*

### CDS (coding sequence)

>MpoEXPA-05

ATGGCTGCGTCGATGCATGCGGGTTCGGTCTGTGCAGCTCCTCGTGGGGAGCGTGC  
TGCTTCTCTGCCTCAAAGTGGCAACGGTGAATGCCGCCCAAGCTTGGGCAGTAAC  
AGACTGGGCGGATGCCACGCGACGTTTTATGGAGGATCAGACGCGTCTGGAAC  
GATGGGTGGCGCTTGTGGATATGGAAACCTGTACTCGCTCGGGTACGGGACTTCA  
TCGACCGCCCTGAGCAACGCGCTCTTCAACAACGGGCTCAGCTGCGGAGCTTGCT  
TCTTGATCCAGTGCAAGTTGGAGGGCAGCAAATACTGCTACCCCGGCCAGAGCAT  
CACTGTCACCGCCACCAACGCCTGCCCCCAAGGCTCTGAGGGAGGCTGGTGCAC  
CCTCCAAGGTCCCCTTCGACCTGTCCTTCCCCATGTTCCAGAAGCTCGCCAGCC  
CGTCGGCGGTGTCATCCCGTCAGATAACAAGAGAGTGTCTGCACCAAGCAAGG  
AGGTGTGCGCTTACCCCTCCACGGCAACCCCTACTTCAACTACGTCTTGGTCCACA  
ATGTTGCCGGCTGGGGAGATGTTTTCGTCTTTGGCGATCAAGGGAGACCAGACTGG  
ATGGTACTACATGAGCCAGAAGTGGGGCCAGTACTGGTCTGCGAGCGCCAAGCT  
AACGGGACAGGCACTCTCCTTCAAAGTCACTCTGGGAAATGGCAAGAGTCTGGA  
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TACAACTTCTAG

### Nucleotide

>MpoEXPA-05

GACCCTGCCTCTACTCCTATCCCCTCCACTCCATCGATATCCGCACACTCTTATAA  
ATTGTCCCTGCACTGCCATTCAATTCAGCACGCAGTCGGTCTGTCTGTCAATCCG  
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CTGTGCCTTCTCTCCGGAGTCGGTTGCCCCCCTCGCCCTCCAAGGTATACTTCT  
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TTCTCAAGGGGCATATAGATGGGACGATGAGGCGGCAAGGGCATTGCCCTGAAG  
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GCTGAGACTGTCTCCTCAACATTTGTGCAGGTGGCGCTTGTGGATATGGAAACCT  
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AGGCTCTGAGGGAGGCTGGTGCAGCCCTCCAAGGTCCCCTCGACCTGTCCTTC  
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CATGCCCCACCAACGTCACCAAATTGGTTCGAGACCTCACATGGATTCTATTCAT  
GTATTTTCTACGATGGAACAATCGATGGTATTAGTAATAAAAAGTTTTTTTTGGTGT  
ACATCAGACA