

## IDENTIFICATION

**Species:** *Marchantia polymorpha*

**Locus:** Mapoly0118s0015

**Gene Model:** Mapoly0118s0015.1.p

**Description:** MpoEXPA-29

**Family:** Alpha Expansin

**3D structure:**



## GENOME DATABASES

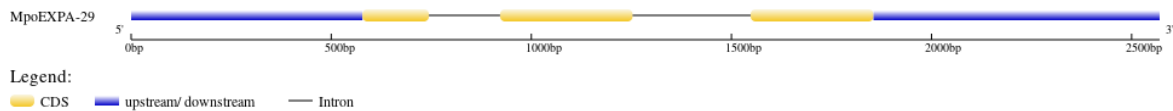
Phytozome: [https://phytozome-next.jgi.doe.gov/info/Mpolymorpha\\_v3\\_1](https://phytozome-next.jgi.doe.gov/info/Mpolymorpha_v3_1)

KEGG:-

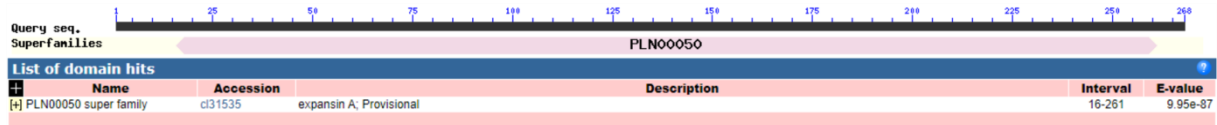
## EXTERNAL RESOURCES

<https://marchantia.info/>

## GENE STRUCTURE



## DOMAIN ARCHITECTURE



## SEQUENCES

### Peptide

>MpoEXPA-29

MVKVNQMAVLQVATITLVVLGSLVQVAKAVNAWDVTTWTPSHATFYGDSDGAAT  
MGGACGYGNLWWRGYGLATAALSDDLNNGLTCGACFEIKCNITGGESGKWCIQSN  
PSIKITATNQCPPNFDRPTDNGGWCNPPRTHFDLSLNMFRRLAQTQAGIIPISYRTRCI  
KTGGIRFYLGNAHFNLVLVYNVGGWGDVMKMQMRGKTKGWITMKRNWQONWE  
SSINYTGQSLSFIVTLGNGQVRVIRNLTPTVWYFKQTYEADTNF\*

### CDS (coding sequence)

>MpoEXPA-29

ATGGTGAAAGTCAACCAAATGGCGGTGCTCCAGGTGGCCACTATAACATTAGTGG  
TCCTCGGAAGCCTTGTGCAAGTGGCAAAGCTGTGAATGCGTGGGACGTCACAAC  
CTGGACTCCCTCGCACGCAACATTCTATGGGGACGATTCGGGTGCGGCCACCATG  
GGTGGCGCATGCGGGTATGGAAACCTGTGGTGGCGCGGATATGGACTGGCGACG  
GCTGCTTTGAGCGATACTCTCTTGAATAATGGCCTGACTTGCGGGGCTTGCTTCGA  
GATAAAGTGTAATATAACCGGGGGTGAATCAGGAAAATGGTGCATTCAGAGCAA  
CCCTTCCATCAAATTACGGCTACCAATCAATGTCCTCCGAATTCGACCGACCG  
ACCGACAACGGAGGATGGTGAACCCACCGAGAACTCACTTCGACTTATCCCTCA  
ACATGTTTCAGACGTCTCGCTCAGACTCAAGCAGGCATCATTCCCATTTCATACAG  
GAGAACGAGGTGCATCAAGACAGGCGGAATCAGATTTTATCTAGGCGGGAATGC  
GCATTTCAACCTCGTGCTGGTGTACAACGTAGGCGGATGGGGTGTATGTGATGAAG  
ATGCAGATGAGAGGAACGAAGACCGGATGGATCACGATGAAGAGAACTGGGG  
CCAAAACCTGGGAAAGCTCGATCAACTACACGGGCCAGAGTCTTTCATTCATCGTG  
ACCCTGGGAAATGGTCAGGTCCGCGTTATCAGAAATCTCACTCCAACAGTATGGT  
ACTTCAAGCAAACCTACGAAGCGGACACGAACCTTCTGA

### Nucleotide

>MpoEXPA-29

TTCAGTGTGTTATCCAAACCCGAGATGTCAACCTGAATCCCCCATATTGCTCATCT  
GTGTGCTTAGCTCCGGGACGACCTTGGAGCACCTGGCCATTGTTCTTTTACCGAGC  
TTTTTCGAGCATCTCAAAGTTGCCAGGCTGTGGAAGTTTGCTCTCGAGAGTACGA  
ACTCCATCACTAGTACTTGAGGTTCCATTGTTTCGAGCAGAGAAAATTGGAAAGAT  
ACTTGTGGACTTTGAGCGAAATCAGTGAGCTGGCTACTGTCTGTATAGTGCTATC  
GATGTCCATGATCAGTCTTCTTTCGTAGTTCACCATGGTTCAGTTCGACTTCAGT  
TTCAGACGTCTCTGCATCAGAGTCTCCCTCCTCACACATGTGTTCAAGTCCA

ATTCATGAATATCTGAAATTTATGCTCTTGAAAGAACGATGATGGCGAGGATACA  
CAGTCAAAGAGTGTACGGAATGAATCCAGCGATCCTGAGCAGCATCGACAGCA  
TAGACCCTAGTAATGTGCATCTTGTGGCGAGCTTTTCTTCATTTGTAGCAAATTA  
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CTGTGAATGCGTGGGACGTCACAACCTGGACTCCCTCGCACGCAACATTCTATGG  
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ATCACCTTCTGCTCATTTAGCTGGAATGGGGTGAATAAGCATGATCATCTGTAA  
CGCAATGAATGCCAGCCAGGTGCGACTGACTCCTACGTGCCGAAGGGTGACGTG  
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TCTCTTGAATAATGGCCTGACTTGCGGGGCTTGCTTCGAGATAAAGTGTAATATA  
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GGTGAACCCACCGAGAACTCACTTCGACTTATCCCTCAACATGTTTCAGACGTCT  
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GCAGATCCGGCCGATGAGACCAAATACCGAAAACCTAGTCTTTGTTGAGACAAGCT  
CCATGAGGACATGGCAGGCAGGCTGCCGGAAGTTAGCTCGAATCCACTAGCACG  
ACATAGAACGATAGGATCTTGAAGTGAACCTTCTCTGTCGTA CTGCTGTGAGCTGG  
TCCGGTTTCAGAGGCGTTAGATTAGCTCGTAGACTCCGAGTTCCAAGTAGCAGGA  
CCCAGAAGCTAGATTGCGCTCGACCTCTTCCATCTTCGTTACGAGTATCGAGTTCCG  
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AATAAACGTGATCTGTGATCCTCTTGTATAAAAAATTAGAGACTGTATATAGACT  
TGTAAGTCAATAAACTTGAGCCTTCACTTGATTTCGCC