

## IDENTIFICATION

**Species:** *Marchantia polymorpha*

**Locus:** Mapoly0107s0006

**Gene Model:** Mapoly0107s0006.1.p

**Description:** MpoEXPA-27

**Family:** Alpha Expansin

**3D structure:**



## GENOME DATABASES

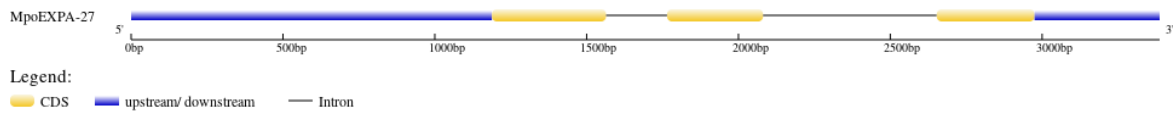
Phytozome: [https://phytozome-next.jgi.doe.gov/info/Mpolymorpha\\_v3\\_1](https://phytozome-next.jgi.doe.gov/info/Mpolymorpha_v3_1)

KEGG:-

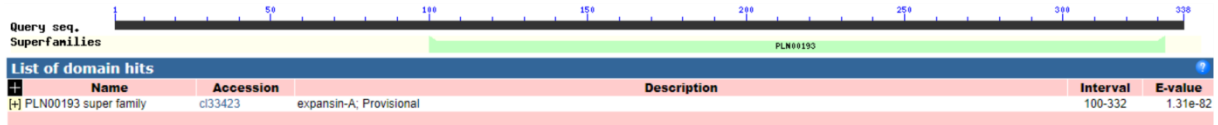
## EXTERNAL RESOURCES

<https://marchantia.info/>

## GENE STRUCTURE



## DOMAIN ARCHITECTURE



## SEQUENCES

### Peptide

>MpoEXPA-27

MVQFLASRSSTDFSLLLLRLLLVTSSLNPGACSQVPRGADSAATAENPLTRIVGVDPQ  
QQDGRVQAMHPVSPLLTSEEVERLNSFDGEPSEVAAGVTRRVAPFSVGQWNYAHAT  
FYGDETAQDTMQGACGYGNMYQQGYGTATTALSSTLFDNGFACGRCFEIRCVASW  
ACYLGNPSTIVTATNFCPANWLKPTNNGGWCNPPRQHFDMSKPAFEKIAAWRAGIVP  
VAYRRVPCSKQGSMEFRIEGNPWWHIVFITNVGGPGDIGEVYIRGSGTKRWVRMSHN  
WGVGFQVFGGYLGQGLSFMVISSNLETVMAWNVVPANWRLGQTFSGGQFQHPR\*

### CDS (coding sequence)

>MpoEXPA-27

ATGGTTCAATTTCTCGCCTCGAGATCCAGCACTGACTTTAGCCTCCTTCTCTTACG  
ATTGCTTCTGGTTACAAGTTCTTTGAATCCAGGAGCGTGCAGTCAAGTCCCTCGTG  
GAGCAGATTCTGCTACTGCTGCAGAGAATCCACTGACGAGAATCGTGGGAGTAG  
ATCCACAGCAGCAGGATGGCCGCGTGCAAGCAATGCATCCGGTGTCTCCACTTTT  
GACTTCTGAAGAAGTTGAACGATTGAACAGCTTCGATGGAGAGCCTTCTGTGGAA  
GCTGCTGGCGTTACGAGAAGAGTGGCTCCGTTCTCCGTTGGGCAATGGA ACTATG  
CACACGCGACTTTCTACGGAGACGAAACAGCTCAAGACACGATGCAAGGTGCGT  
GCGGTTATGGTAACATGTATCAGCAAGGATATGGCACGGCCACGACAGCCTTGA  
GCTCCACCCTGTTTCGACAACGGATTCGCATGTGGACGCTGCTTCGAGATTCGATG  
CGTCGCTTCATGGGCTTGCTACTTGGGGAACCCGTCTACGATCGTGACGGCCACA  
AACTTCTGCCCCGCGAACTGGCTCAAGCCAACGAACAACGGAGGATGGTGCAAC  
CCTCCTCGCCAACACTTCGACATGTCGAAGCCAGCTTTTGAAAAGATTGCTGCCT  
GGCGGGCCGGAATCGTTCCTCGTTGCATATCGCAGAGTCCCCTGCTCGAAACAGGG  
GAGCATGGAGTTCAGAATCGAGGGCAACCCGTGGTGGCATATAGTATTCATAACC  
AACGTTCGGAGGCCCGGCGACATCGGGGAGGTTTACATTCGAGGCTCCGGCACG  
AAGCGCTGGGTTTCGCATGAGCCACA ACTGGGGAGTGGGGTTCCAAGTCTTCGGA  
GGCTACCTCGGCCAAGGCCTGTCGTTTCATGGTCATCTCGAGCTCCAACCTCGAGA  
CCGTCATGGCCTGGAACGTGGTTCGCGGCAACTGGCGACTGGGTCAAACATTCAG  
CGGCGGCCAATTCCAACACCCTCGCTGA

### Nucleotide

>MpoEXPA-27

GCGAGAAAAGTGCCTTTTCGCCGAAATTGTCCGAGAACGAAAATCCAAGAGGAG  
GTGCAGGCATTGGCGTGGCTAAATTCCACGAGTGGATTTTGGCCCCGAAGACAGT

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TCTAGTGGCTCGGATGATAAGCGGGGGGTCGGTACCGTTACGCAGCCCAATTCT  
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AGCCCCCTCCGCGCTTCGACCCTTCATTCGCTGGATTCGAGTCTGAGATTGTCTGG  
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GTACTTTCTTTGTCCCATAAGATCCCCTTCGAGTAACTTGTACCGAACGCCCTGGG  
AGGCTGTTTCGATCCGAGTTGACCTGAAATATTGGAGCGAGCATCAGTGAGAAGTC  
GATTGGTCAAAGGCAGGCCTCAGCATTCTGCCTGCACTTAGTAAAAATCTCTCT  
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ACGTGCTACTGAATGATGATTTTGTCTCGAAAGCAGCGCAAACCTGGAATTCTGAA  
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TCGAGATTTCGATGCGTCGCTTCATGGGCTTGCTACTTGGGGAACCCGTTACGAT  
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AGGATGGTGC AACCCTCCTCGCCAACACTTCGACATGTCGAAGCCAGCTTTTGAA  
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TCATGGTCATCTCGAGCTCCAACCTCGAGACCGTCATGGCCTGGAACGTGGTTCC  
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GAGCTAATGTGGAGTTGTATACTGCCAGTCACCATTTGCATATCCGTGTACTCGTT  
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TTCTCATTACCGCTGCGATGTA ACTCTAGATTTGCAATCAGAATCGGTATTATGT  
CCTCCACCCAAGGATGCATGGAGAATTGTTACAAGCTCTGAATCTCACACTGCGA  
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CATGTCCTTCGATCTGTTTGTGCGAC