

IDENTIFICATION

Species: *Marchantia polymorpha*

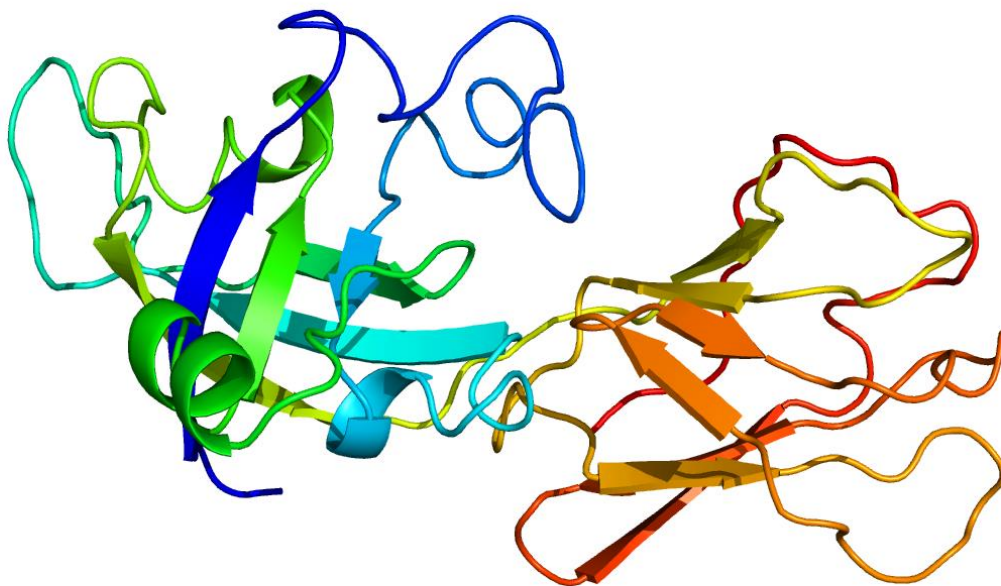
Locus: Mapoly0085s0015

Gene Model: Mapoly0085s0015.1.p

Description: MpoEXPA-19

Family: Alpha Expansin

3D structure:



GENOME DATABASES

Phytozome: https://phytozome-next.jgi.doe.gov/info/Mpolymorpha_v3_1

KEGG:-

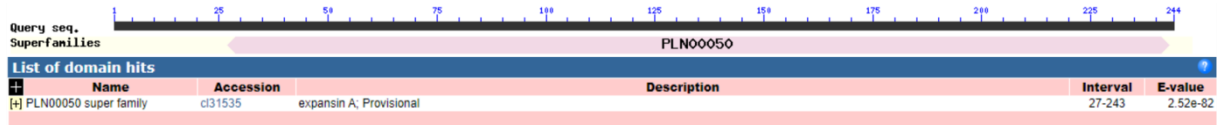
EXTERNAL RESOURCES

<https://marchantia.info/>

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>MpoEXPA-19

MTTCTTYLWIMLLLHMLISEANAIPATATFYGGNDASGTNTGSCGYPNVLTIDGPM
NTALSGALYNGGEACGACFKIQCVSIPFGNLQCLPGSIVVTATNLCPQGSTGGWCDEP
RSHFDLAEPAFQHLAPPVAGVVNVEYERVSCLRSGGIRFLIQGHPYFMQVLVYNVGG
MGDVTAVSVKGSSSDWIQMDRNWQQLWTTGTVLDGQALSFSVTTSDGRTVASNGV
ADSDWQYQGQTFEGNQF*

CDS (coding sequence)

>MpoEXPA-19

ATGACCACTTGCACGACCTACCTCTGGATCATGTTGCTGTTGATGCATATGTTGAT
ATCAGAGGCCAACGCAATACCAGCAACAGCCACGTTTTATGGTGGAAACGATGC
GTCTGGCACAACACTGGATCGTGTGGGTACCCAAATGTGCTAACAAATCGACGGA
CCGATGAACACTGCGTTGAGTGGTGCATTATACAATGGTGGAGAAGCCTGTGGAG
CTTGCTTCAAGATACAATGCGTCTCCATTCCGTTTGGAAATCTTCAATGCCTGCCA
GGGAGCATAGTGGTCACAGCCACCAACTTGTGCCCGCAAGGTAGCACTGGCGGC
TGGTGCGACGAGCCCAGGAGTCACTTCGATCTTGCCGAGCCTGCTTTCCAGCATT
TGGCTCCGCCTGTAGCAGGAGTGGTGAACGTAGAATACGAGAGGGTAAGCTGTC
TGAGAAGTGGCGGTATCCGTTTCTCATTACAGGGCCATCCGTATTTTATGCAGGTC
CTCGTTTACAATGTGGGTGGGATGGGTGATGTGACAGCAGTATCTGTGAAGGGTT
CCAGCTCCGATTGGATACAAATGGATCGAAACTGGGGTCAGCTCTGGACTACAGG
AACCGTGCTTGATGGGCAAGCTCTCTCTTTCTCGGTGACAACAAGCGATGGCAGA
ACTGTGGCAAGTAATGGTGTAGCTGACTCTGACTGGCAGTATGGCCAGACCTTTG
AGGGCAACCAATTCTAG

Nucleotide

>MpoEXPA-19

GTGAGTACAATTAATTGAGCAAGCATTCTGGCAGCTACTGTAAGAGCTGCCAGCA
TCAAATTCATTTCTTCTTTCAGTTTGAGAGCTACAGACATTCCTGACGTGGCCCT
GTGACCATTCATATGCACTCCTTACCCATTCTTTATTGTTTTAATAAGCATTGACT
GTATTTGGTACTAGAGATTTTCGTGTTTCATGTCGATAGATCGAGAGGTTCTGCATGT
ATACTGTCGTTTTTAAATTTAAAACACGTTCTGAAGTATAGAGTGACAAAAGTGA
AGACTAATCACAATCATAACGTACCTGCTACCGTCGGTTCTCCTCGAGTAGACTC
AAATTCGCACAAGTCCATCTTTTGTGAGCCCATCATAGTTTTCTCACATTCTTTG
CATAACGTCTCGAGATTCTTCTTTTTCAGAAGTTTCTGTTTCTATTTGAGGTTGGT

TAACCATGACCACTTGCACGACCTACCTCTGGATCATGTTGCTGTTGATGCATATG
TTGATATCAGAGGCCAACGCAATACCAGCAACAGCCACGTTTTATGGTGGAAACG
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GTGCATTATACAATGGTGGAGAAGCCTGTGGAGCTTGCTTCAAGATACAATGCGT
CTCCATTCCGTTTGGAAATCTTCAATGCCTGCCAGGGAGCATAGTGGTCCACAGCC
ACCAACTTGTGCCCCGCAAGGTAGCACTGGCGGCTGGTGGCAGCAGCCAGGAGT
CACTTCGATCTTGCCGAGCCTGCTTTCCAGCATTTGGCTCCGCCTGTAGCAGGAGT
GGTGAACGTAGAATACGAGAGGGTAAGCTGTCTGAGAAGTGGCGGTATCCGTTT
CCTCATT CAGGGCCATCCGATTTTTATGCAGGTCCTCGTTTACAATGTGGGTGGGA
TGGGTGATGTGACAGCAGTATCTGTGAAGGGTTCAGCTCCGATTGGATACAAAT
GGATCGAAACTGGGGTCAGCTCTGGACTACAGGAACCGTGCTTGATGGGCAAGC
TCTCTCTTCTCGGTGACAACAAGCGATGGCAGAACTGTGGCAAGTAATGGTGTA
GCTGACTCTGACTGGCAGTATGGCCAGACCTTTGAGGGCAACCAATTCTAGTATC
TAGCATAATCTATACGCTCTACGTTCTGCACATTGCATTA ACTTCGGATATCTGAA
AAGTTTCAGAATCGTCCATCCACAACTGATTCGTTTGAGATTCGGTCGTCCTGCA
TAGCATT CAGTTAGTGCCAATGCTACGGAGGTGTTCTCCGCGGCATGTCTACGAT
GCACCTCTATTTTACATATTGATAAGGAGCATTACTTATCAGCGTACATCCTTATA
CAGTGCTGTAGAAGCTTGTTGAGGCTACACAACAGCGACAA