

IDENTIFICATION

Species: *Marchantia polymorpha*

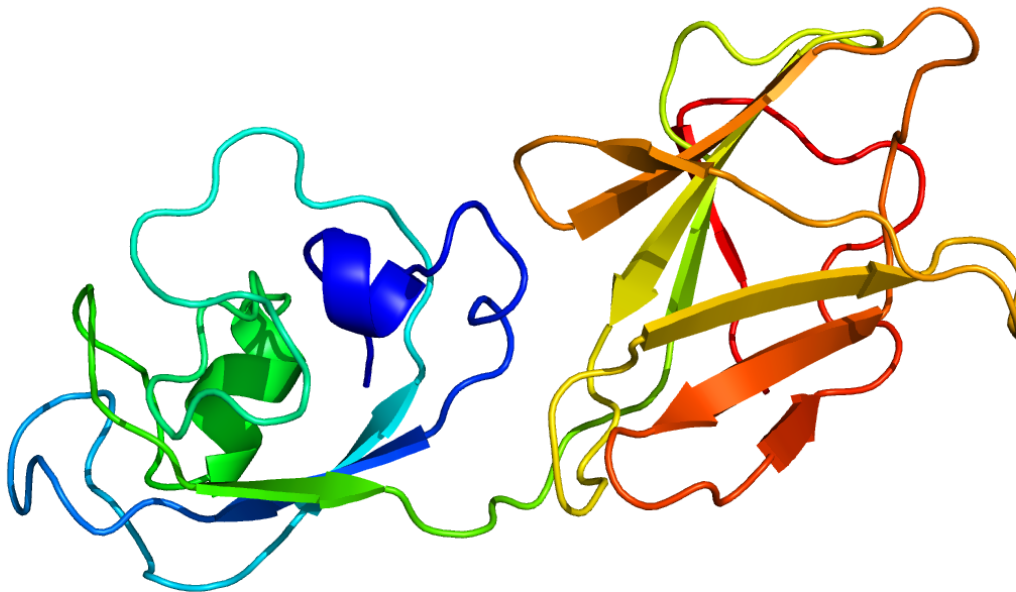
Locus: Mapoly0085s0014

Gene Model: Mapoly0085s0014.1.p

Description: MpoEXPA-18

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

Query seq. MNTALSGALYNGGEACGACFKIQCVSIPFGNLQCLPGSIVVTATNLCPQGSTGGWCD
EPRSHFDLAEP AFQHLAPPVAGVVNVEYERVSCLRSGGIRFLIQGHPYFMQVLVYNV
GGMGDVTAVSVKGSSSDWIQMDRNWGQLWTTGTVLDGQALSFSVTTSDGRTVASN
GVADSDWQYGQTFEGNQF#

Superfamilies PLN00050

Name	Accession	Description	Interval	E-value
PLN00050 super family	d31535	expansin A; Provisional	4-187	8.70e-73

SEQUENCES

Peptide

>MpoEXPA-18

MNTALSGALYNGGEACGACFKIQCVSIPFGNLQCLPGSIVVTATNLCPQGSTGGWCD
EPRSHFDLAEP AFQHLAPPVAGVVNVEYERVSCLRSGGIRFLIQGHPYFMQVLVYNV
GGMGDVTAVSVKGSSSDWIQMDRNWGQLWTTGTVLDGQALSFSVTTSDGRTVASN
GVADSDWQYGQTFEGNQF*

CDS (coding sequence)

>MpoEXPA-18

ATGAACACTGCGTTGAGTGGTGCATTATACAATGGTGGAGAAGCCTGTGGAGCTT
GCTTCAAGATAACAATGCGTCTCCATTCCGTTTGGAAATCTTCAATGCCTGCCAGG
GAGCATAGTGGTCACAGCCACCAACTTGTGCCCGCAAGGTAGCACTGGCGGCTG
GTGCGACGAGCCCAGGAGTCACTTCGATCTTGCCGAGCCTGCTTCCAGCATTG
GCTCCGCCTGTAGCAGGAGTGGTGAACGTAGAATACGAGAGGGTAAGCTGTCTG
AGAAGTGGCGGTATCCGTTTCCTCATT CAGGGCCATCCGATTTTATGCAGGTCTC
CGTTTACAATGTGGGTGGGATGGGTGATGTGACAGCAGTATCTGTGAAGGGTCC
AGCTCCGATTGGATACAAATGGATCGAACTGGGGTCAGCTCTGGACTACAGGA
ACCGTGCTTGATGGGCAAGCTCTCTTTCTCGGTGACAACAAGCGATGGCAGAA
CTGTGGCAAGTAATGGTGTAGCTGACTCTGACTGGCAGTATGGCCAGACCTTTGA
GGGCAACCAATTCTAG

Nucleotide

>MpoEXPA-18

TGGATCGTGTGGGTACCCAAATGTGCTAACAATCGACGGACCGATGAACACTGCG
TTGAGTGGTGCATTATACAATGGTGGAGAAGCCTGTGGAGCTT GCTTCAAGATAC
AATGCGTCTCCATTCCGTTTGGAAATCTTCAATGCCTGCCAGGGAGCATAGTGGT
CACAGCCACCAACTTGTGCCCGCAAGGTAGCACTGGCGGCTGGTGTGCGACGAGCC
CAGGAGTCACTTCGATCTTGCCGAGCCTGCTTCCAGCATTGGCTCCGCCTGTAG
CAGGAGTGGTGAACGTAGAATACGAGAGGGTAAGCTGTCTGAGAAGTGGCGGTA
TCCGTTTCCTCATT CAGGGCCATCCGATTTTATGCAGGTCTCCTCGTTTACAATGTG
GGTGGGATGGGTGATGTGACAGCAGTATCTGTGAAGGGTTCCAGCTCCGATTGGA
TACAAATGGATCGAACTGGGGTCAGCTCTGGACTACAGGAACCGTGCTTGATGG
GCAAGCTCTCTTTCTCGGTGACAACAAGCGATGGCAGAACTGTGGCAAGTAAT
GGTGTAGCTGACTCTGACTGGCAGTATGGCCAGACCTTTGAGGGCAACCAATTCT
AGTATCTAGCATAATCTATACGCTCTACGTTCTGCACATTGCATTAACCTTCGGATA

TCTGAAAAGTTTCAGAATCGTCCATCCACAAACTGATTCGTTTGAGATTCGGTCGT
CCTGCATAGCATTTCAGTTAGTGCCAATGCTACGGAGGTGTTCTCCGCGGCATGTC
TACGATGCACCTCTATTTTACATATTGATAAGGAGCATTACTTATCAGCGTACATC
CTTATACAGTGCTGTAGAAGCTTGTTGAGGCTACACAACAGCGACAATTATATAT
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GCTTTGCATTTATGGATACGCGACTCAAATAATTTACATGCATTGGTTTTTAGTC
ATGATTCATGACTGAAAACATGAGTCATGACTCATGAACAAGTACTGTGCGCG
GGCAGAGACACAATGGGTATTTATATAAATCCTAGTGGAACAATGC