

IDENTIFICATION

Species: *Marchantia polymorpha*

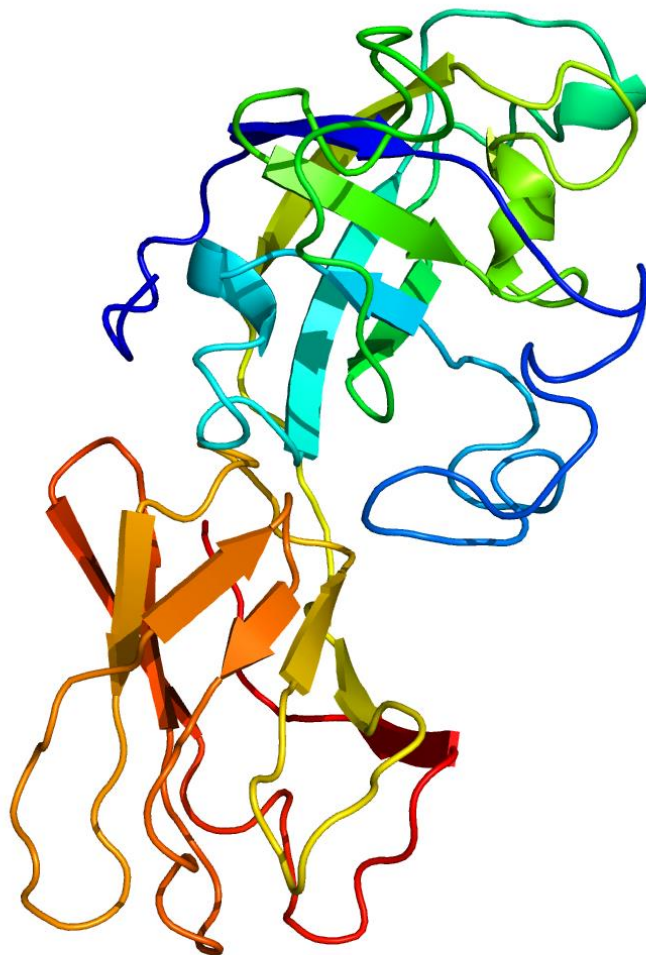
Locus: Mapoly0085s0051

Gene Model: Mapoly0085s0051.1.p

Description: MpoEXPA-20

Family: Alpha Expansin

3D structure:



GENOME DATABASES

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

KEGG:-

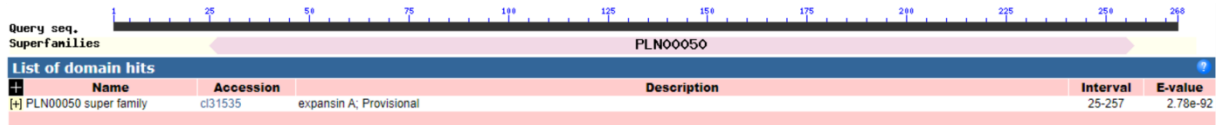
EXTERNAL RESOURCES

<https://marchantia.info/>

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>MpoEXPA-20

MAIFSRAALAAGLFASALVIFSEHLSFVSAYEPYAVTSWTASDATFYGGNSGAGTMG
GACGYGNMYNTGYGLNTAALSPVLFNNGLSGACFELKCNLTGKWCYPSAGSITV
TATNLCPANPARTTDGWCNPPRTHFDLSYTMFAILAQPVAGIPIQYRRVSCVKTGGV
RFVINGNPWFNLVLIYNVGGDGNVVTAMMKGENTEWYSMTRNWGQNWQLSQKLH
GQALSFQLTTGYGTTLVCSADVAPANWQFGQTFEAYTNMYDLY*

CDS (coding sequence)

>MpoEXPA-20

ATGGCGATTTTTTCCAGAGCTGCGCTAGCTGCTGGCTTATTTGCCAGCGCTCTGGT
CATCTTCTCGGAGCATCTGTCGTTTGTGAGTGCCTACGAGCCATATGCTGTACAT
CTTGGACGGCATCTGATGCAACCTTCTACGGAGGAAACAGTGGAGCTGGAACAA
TGGGTGGAGCTTGTGGATATGGAAACATGTACAACACGGGTTATGGACTCAACAC
CGCTGCTCTGAGCCCGGTCTTCAATAATGGACTGAGCTGTGGAGCTTGTTTTG
AGCTTAAGTGCAATCTCACTGGTACCAAGTGGTGCTACCCGAGCGCAGGTTCCAT
CACCGTCACAGCTACCAATCTGTGCCCTGCAACCCGGCCAGAACCACCGACGGA
TGGTGCAACCCTCCCAGGACACACTTCGATTTGTCATACACGATGTTTCGCTATACT
CGCCCAACCAGTTGCAGGAATCATTCCAATTCAGTACCGCAGAGTGTCTTGCCTG
AAGACTGGAGGCGTCCGCTTCGTCATCAACGGCAACCCCTGGTTCAATCTGGTGC
TCATATAACAACGTGGGCGGTGACGGAAACGTCGTGACAGCCATGATGAAAGGAG
AGAACACAGAGTGGTATTCCATGACTAGAACTGGGGGCAAACTGGCAGCTGA
GCCAGAAGCTTCACGGTCAGGCCCTCTTTCCAGCTCACGACGGGTTATGGCAC
GACCTTGGTGTGCAGCGACGTAGCGCCAGCCAACCTGGCAATTCGGCCAGACGTT
GAAGCCTACACGAACATGTATGACCTCTACTGA

Nucleotide

>MpoEXPA-20

GGAATTTTGGATAAAAAGATGAACGAGCTGCATTGTGAAGGAAGAAATGAGTGAA
TGGCACGATAACGAAGACCAATATCGATAGTGATGATCCCCTGGAGGTCGGTAG
ACTTAGCCCATGCATCAGCACAGCATTGCAAAGCAGGTCGACCCAGACAGG
ATCCAAGGTCCAGTGAGCCGTAGCTTTTGACGCAAAGACGCGAGTCCGACTGCTG
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GACCAGCCGACTAATCTTCGAATGTGGGGTTCGAGACTTGCCTGCTGGCCTTTGAT
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ACCAGATTACCTTTCCTGCCCTTCAATTTTCTGTCTGAACTCGATCAGCACAGAAG
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CTGGTCATCTTCTCGGAGCATCTGTCGTTTGTGAGTGCCTACGAGCCATATGCTGT
CACATCTTGGACGGCATCTGATGCAACCTTCTACGGAGGAAACAGTGGAGCTGGA
ACAATGGGTAAGCGACAGGTCACATCACTTCTGCCTCTAGCTTCTTCGAGTTCAA
ATTCACATCAGACGACGAATATTGTCAAAGAACATGATTTTGTGGTGCAATTCG
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CCCGTCGATGACTTCAACTCCGTGGCGATAAATTGCAGGTGGAGCTTGTGGATAT
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TCTTCAATAATGGACTGAGCTGTGGAGCTTGTTTTGTGAGCTTAAGTGCAATCTCACT
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