

IDENTIFICATION

Species: *Marchantia polymorpha*

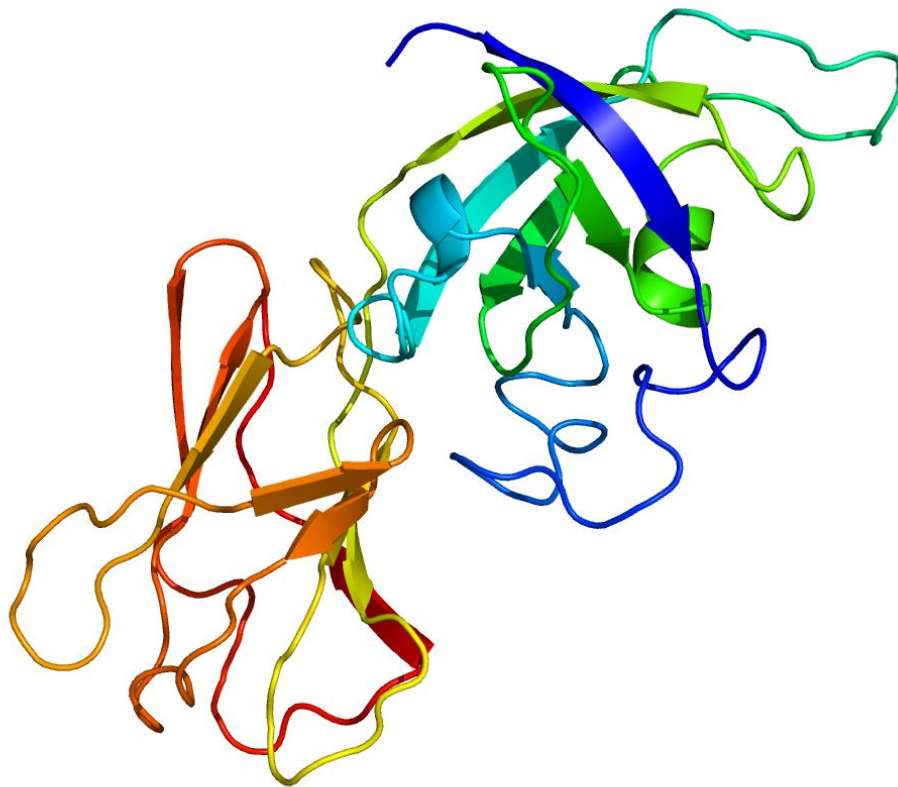
Locus: Mapoly0050s0035

Gene Model: Mapoly0050s0035.2.p

Description: MpoEXPA-12

Family: Alpha Expansin

3D structure:



GENOME DATABASES

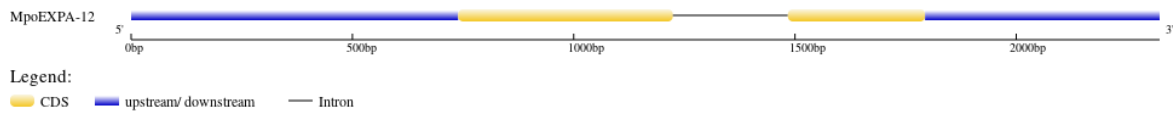
Phytozome: https://phytozome-next.jgi.doe.gov/info/Mpolymorpha_v3_1

KEGG:-

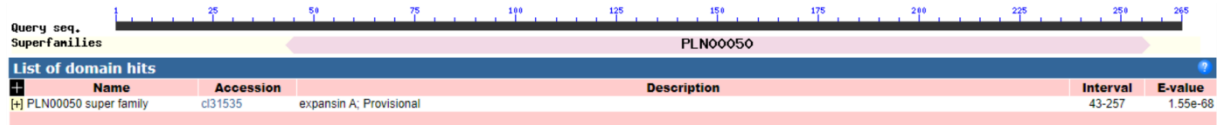
EXTERNAL RESOURCES

<https://marchantia.info/>

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>MpoEXPA-12

MTEMRRISRLAWSCSLAVAATALLVLLAADVAEANESFAVGRTSFGDATATFYGGS
DAAGTAGGFCGYENPFTRGYGVTTVALSDSLLSNGLNCGACYEVKCKWEASDYTK
KYCYQGMTTIVSATNLSPPGLNGEHHFDLTYPMFVKISNPESGRIPIQYRRVPCQKQG
GIRFSMVGNPFWNLVLVYNVGGWGNVHSLYVRGSRDWWYMNRNWQNWQCSV
NLTGQKLSFRVVLGNGQTSVFNNVADSNWKHGGQTYEASSNFW*

CDS (coding sequence)

>MpoEXPA-12

ATGACTGAAATGAGGAGGATCAGTAGACTGGCATGGAGCTGCAGCTTGGCAGTG
GCAGCCACGGCATTGCTCGTGCTTCTGGCGGCAGATGTGGCGGAGGGCGAACGAA
TCATTCGCCGTGGGCCGCACATCATTCCGAGACGCCACTGCGACGTTTTATGGCG
GAAGCGACGCTGCAGGAACGGCTGGGGGGTTCTGTGGGTACGAGAACCCCTTCA
CTCGAGGGTATGGAGTCACAACGGTGGCGCTCAGTGACAGCCTGCTCAGCAATG
GGCTCAATTGTGGCGCTTGTTATGAGGTCAAGTGCAAGTGGGAGGCCTCGGACTA
CACCAAGAAGTACTGCTACCAGGGCATGACCACGATTGTCTCCGCCACCAACCTC
AGCCCCCGGGCTCAATGGCGAGCACCATTTCGACTTGACGTACCCATGTTCG
TCAAGATTTCCAACCCGGAATCTGGCCGCATCCCCATCCAGTACCGAAGGGTGCC
CTGTCAGAAGCAAGGAGGAATAAGGTTCTCCATGGTGGGAAATCCCTTCTGGAAT
CTGGTCTCTGCTACAATGTGGGCGGCTGGGGGAACGTCCACTCTGTACGTCA
GAGGCTCTCGAACCGATTGGTATTACATGAACAGAACTGGGGTCAA AATTGGC
AGTGTCTGTCAACTTGACGGGCCAGAAGTTGTTCGTTCCGTGTAGTTCTTGGGAAT
GGGCAAACGAGTGTGTTCAACAACGTAGCTGACTCGAATTGGAAGCACGGCCAG
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Nucleotide

>MpoEXPA-12

TCAAGCCCTATTCTTCGTCGCGTGCGAGGCTCGTGAAAAAATTCTCACCCCGCTT
CGGCGGTCGACGTGTTCCCGGGGACTCGAGGCGAAGGCAGGAGCAGCTCCACG
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CGCCGGCCAATTTAACCGGGTCCACTCTGCCTGCTCTGCTCCGCCCTGCCCTGCTC
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TCGTCTGTGCTTAATAGAAGCGAACATTGTTTTCGGACTCGTATCGAATCTCTCTCT
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TGCGACGTTTTATGGCGGAAGCGACGCTGCAGGAACGGCTGGGGGGTTCTGTGG
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AGCCTGCTCAGCAATGGGCTCAATTGTGGCGCTTGTTATGAGGTCAAGTGCAAGT
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ATATCAGCTGCAGGATTCTGCGAGATGGATGCATTGATTGTA CTATACTGTTCTCT
GTA CTCTCGGCCGACTGAGGAACTTCGCGGACGTGGACATGGTCCATAGAGGTCTCC
CGCTGCGGAACAGCTGCCGATTGGCTTTTAAATCATATTTTAAATAAAGAGTCAA
TCTTGACCGA