

IDENTIFICATION

Species: *Marchantia polymorpha*

Locus: Mapoly0050s0035

Gene Model: Mapoly0050s0035.1.p

Description: MpoEXPA-11

Family: Alpha Expansin

3D structure:



GENOME DATABASES

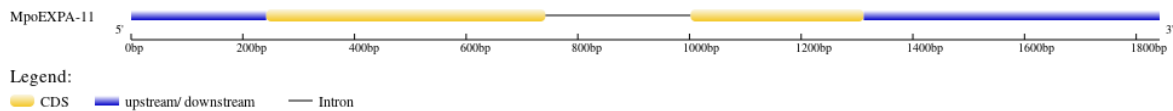
Phytozome: https://phytozome-next.jgi.doe.gov/info/Mpolymorpha_v3_1

KEGG:-

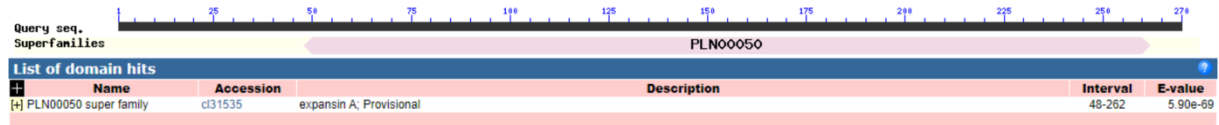
EXTERNAL RESOURCES

<https://marchantia.info/>

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>MpoEXPA-11

MFCRKMTEMRRISRLAWSCLAVAATALLVLLAADVAEANESFAVGRTSFGDATAT
FYGGSDAAGTAGGFCGYENPFTRGYGVTTVALSDSLLSNGLNCGACYEVKCKWEAS
DYTKKYCYQGM TIVSATNLSPPGLNGEHHFDLTYPMFVKISNPESGRIPIQYRRVPC
QKQGGIRFSMVGNPFWNLVLVYNVGGWGNVHSLYVRGSRTDWYYMNRNWGQNW
QCSVNLTGQKLSFRVVLGNGQTSVFNNVADSNWKHGQTYEASSNFW*

CDS (coding sequence)

>MpoEXPA-11

ATGTTCTGCAGGAAGATGACTGAAATGAGGAGGATCAGTAGACTGGCATGGAGC
TGCAGCTTGGCAGTGGCAGCCACGGCATTGCTCGTGCTTCTGGCGGCAGATGTGG
CGGAGGCCGAACGAATCATTCCGCGTGGGCGGCACATCATTCCGAGACGCCACTG
CGACGTTTTATGGCAGGAAGCGACGCTGCAGGAACGGCTGGGGGGTTCTGTGGGT
ACGAGAACCCCTTCACTCGAGGGTATGGAGTCACAACGGTGGCGCTCAGTGACA
GCCTGCTCAGCAATGGGCTCAATTGTGGCGCTTGTATGAGGTCAAGTGCAAGTG
GGAGGCCTCGGACTACACCAAGAAGTACTGCTACCAGGGCATGACCACGATTGT
CTCCGCCACCAACCTCAGCCCCCGGGCTCAATGGCGAGCACCATTTCGACTTG
ACGTACCCCATGTTTCGTCAAGATTTCCAACCCGGAATCTGGCCGCATCCCCATCC
AGTACCGAAGGGTGCCTTGTGAGAAGCAAGGAGGAATAAGGTTCTCCATGGTGG
GAAATCCCTTCTGGAATCTGGTCTCGTCTACAATGTGGGCGGCTGGGGGAACGT
CCACTCTCTGTACGTCAGAGGCTCTCGAACCGATTGGTATTACATGAACAGAAAC
TGGGGTCAA AATTGGCAGTGTCTGTCAACTTGACGGGCCAGAAGTTGTCGTTCC
GTGTAGTTCTTGGGAATGGGCAAACGAGTGTGTTCAACAACGTAGCTGACTCGAA
TTGGAAGCACGGCCAGACCTACGAGGCGAGCAGCAATTTCTGGTGA

Nucleotide

>MpoEXPA-11

GACTCATAACCGTACCCCCCTCCTCGCCTTGATAATCGACATCGACCCCAAGCTT
CAAGACTCGCATGTTTATCGTCGTGCTTAATAGAAGCGAACATTGTTTTCGGACTC
GTATCGAATCTCTCTCTGGGAGTTCACAAAGGAGGCCAGAGGCAA ACTCTCATGA
CTGACTCTGTTTCGTTCCCTCGCACCTCGTTCCTCCAGTCGAGTGGAGCTGGTCCTA
ACGCGTTGAGCTCGCTCCAATGTTCTGCAGGAAGATGACTGAAATGAGGAGGATC
AGTAGACTGGCATGGAGCTGCAGCTTGGCAGTGGCAGCCACGGCATTGCTCGTGC
TTCTGGCGGCAGATGTGGCGGAGGCCGAACGAATCATTCCCGTGGGCGGCACATC

ATTCGGAGACGCCACTGCGACGTTTTATGGCGGAAGCGACGCTGCAGGAACGGC
TGGGGGGTTCTGTGGGTACGAGAACCCCTTCACTCGAGGGTATGGAGTCACAACG
GTGGCGCTCAGTGACAGCCTGCTCAGCAATGGGCTCAATTGTGGCGCTTGTTATG
AGGTCAAGTGCAAGTGGGAGGCCTCGGACTACACCAAGAAGTACTGCTACCAGG
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GCACCATTTGACTTGACGTACCCCATGTTCGTCAAGATTTCCAACCCGGAATCTG
GCCGCATCCCATCCAGTACCGAAGGTAAGACCGTGCCCCACTGCCTGCCCATGC
AGTCTCCCGTCAGACCTCAGCTCAGCTGTCGATAGAACATCTCGTCTTGTAGCAC
ATTTGTGAGCATTTCGTACGAGGTTTTAGGTCTTACGAAGGTCGTTGATTGAGTG
CATGCTGTCTTCGATCGTGACTTTGGTTGCATTACGGTGTGGGCTGGTGAGCATT
GCGATGCCATGGCCGGGAAGGAGCTGTGCTTATATTCTGTGGACTCGCTTGTGAT
GTTATCAGGGTGCCCTGTCAGAAGCAAGGAGGAATAAGGTTCTCCATGGTGGGA
AATCCCTTCTGGAATCTGGTCCCTCGTCTACAATGTGGGGCGGCTGGGGGAACGTCC
ACTCTCTGTACGTCAGAGGCTCTCGAACCGATTGGTATTACATGAACAGAACTG
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GTAGTTCTTGGGAATGGGCAAACGAGTGTGTTCAACAACGTAGCTGACTCGAATT
GGAAGCACGGCCAGACCTACGAGGCGAGCAGCAATTTCTGGTGAAGTGGGTCGT
GGGGATGTCTGTATGAAGAATGCGCCGATCAATGGAACGGAGCGTTTTGAAATA
AGTTCAGTTGCAGCGAAGCAGAGGTGGCGTGTTAATATCACCGTATGGTTGCGCC
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TTGTCAATGTGAACCTGGGTCCCGATGCTGCTGTACGTGTCTGACGATCTCGTAGG
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AATAAAGAGTCAAATCTTGACCGA