

IDENTIFICATION

Species: *Marchantia polymorpha*

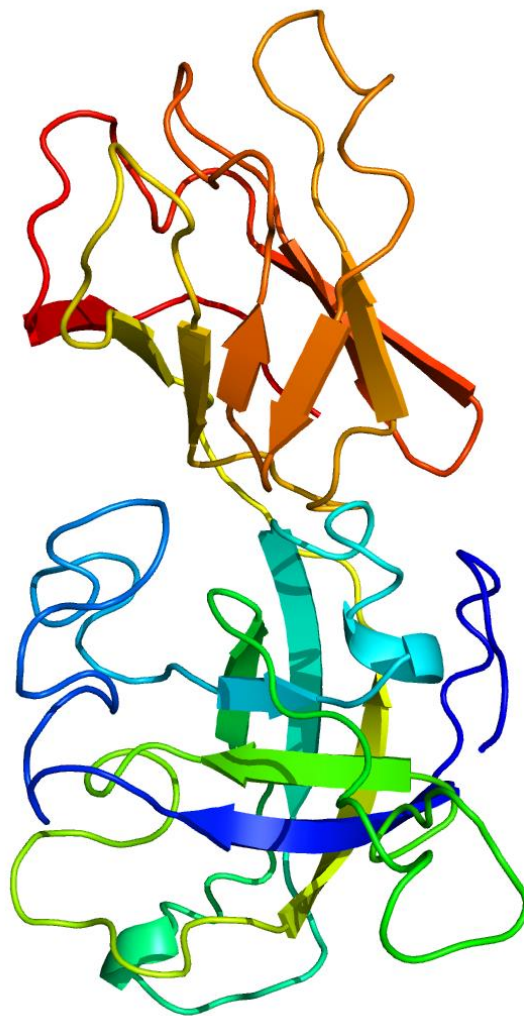
Locus: Mapoly0178s0009

Gene Model: Mapoly0178s0009.1.p

Description: MpoEXPA-38

Family: Alpha Expansin

3D structure:



GENOME DATABASES

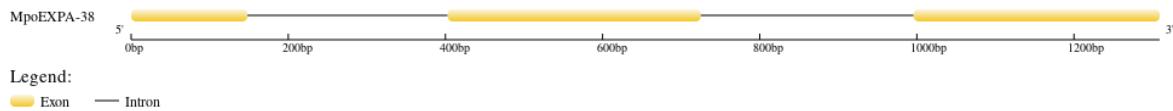
Phytozome: https://phytozome-next.jgi.doe.gov/info/Mpolymorpha_v3_1

KEGG:-

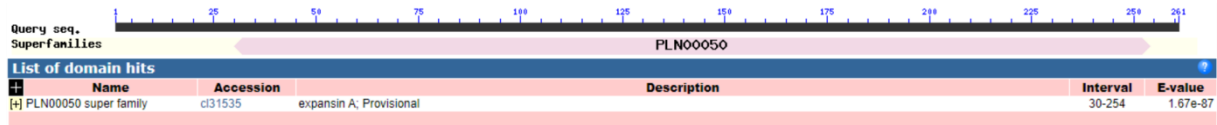
EXTERNAL RESOURCES

<https://marchantia.info/>

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>MpoEXPA-38

MVRDLLSFNVLLILIFASTSVNAGPVYANTEWTDSHATFNDGNNAQGTMGGACGYG
NISSRGYGLETTALSSTLFNSTLFCGACFEIKCKVENSTWCFPNAGSIKVTATDLCPAN
PAMPTNNGGWCNPPRTHFDLSYQMFTRLAKAEGAIIPVQFRRVPCVKVGGIRFTMNG
NPWFNLVLSNVAGAGNVVNLQMKSSSETNWFWM TARQISGQYWELNQNLMGQNI
SFRVTLGNGKVMIANNVVPANWNFQQT FESDINF*

CDS (coding sequence)

>MpoEXPA-38

ATGGTTCGTGATCTGCTTAGCTTCAACGTTCTGTTGATCCTCATATTTGCATCCAC
GTCCGTCAATGCCGGGCTGTATACGCTAACACCGAATGGACGGACTCCCATGCG
ACTTTCAACGATGGAAATAATGCTCAAGGAACGATGGGAGGCGCATGCGGATAT
GGAAATATCTCCTCCAGAGGTTATGGTCTGGAGACCACGGCCTTGAGCTCAACTC
TCTTCAACAGTGGGCTTACTTGTGGCGCCTGCTTCGAAATCAAGTGCAAAGTGGA
AAACAGCACATGGTGCTTTCCCAACGCTGGTTCATCAAGGTCCTGCGACGGAC
CTCTGCCCTGCAAATCCTGCGATGCCACCAACAATGGTGGATGGTGCAACCCGC
CCAGGACTCATTTCGATCTGTCGTATCAGATGTTCACTCGCCTGGCCAAAGCAGA
AGGAGCCATCATCCCCGTGCAGTTTCGGAGAGTACCATGTGTGAAGGTTGGAGGC
ATACGTTTTACAATGAACGGCAATCCATGGTTCAACCTCGTGCTCGTTTCCAATGT
GGCTGGAGCTGGAAATGTGGTGAACCTGCAGATGAAAAGTTCCGAAACCAACTG
GTTTTGGATGACGGCGAGGCAGATTTCCGGACAGTACTGGGAACTCAATCAGAA
CCTGATGGGACAAAATATATCGTTCCGGGTGACACTTGGTAATGGAAAGGTGATG
ATTGCCAACACGTGGTCCCAGCAAACCTGGAACCTCCAACAGACATTTGAATCCG
ATATCAACTTTTAG

Nucleotide

>MpoEXPA-38

ATGGTTCGTGATCTGCTTAGCTTCAACGTTCTGTTGATCCTCATATTTGCATCCAC
GTCCGTCAATGCCGGGCTGTATACGCTAACACCGAATGGACGGACTCCCATGCG
ACTTTCAACGATGGAAATAATGCTCAAGGAACGATGGGTGCGTTCTAGATTTCTC
ACATGAGCAGCATTAGCATTAGCATGTAACCTGAGCTCTGCAATGCTTATCTGAA
GCTATTTGAACTCCTAGAAGTGTGCATGTCATCATCATTCTGTGCAACATAGTCAA
CGTGTCCGAGATAATTCGTGGTGAATTCCTCTCGACAGATACGTGGGGACTGAT
TTTGGGTAGTCATAGTAAGCGTTCATTCTTGAAGGTTGAAATTTGAGACTTTGCAT

TTCTCCTATCTCCAGGAGGCGCATGCGGATATGGAAATATCTCCTCCAGAGGTTA
TGGTCTGGAGACCACGGCCTTGAGCTCAACTCTCTTCAACAGTGGGCTTACTTGT
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ACGCTGGTTCCATCAAGGTCACCTGCGACGGACCTCTGCCCTGCAAATCCTGCGAT
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TCGCTCCTGCTGTTTCCGATTATGTTTCTGTCTTCTTTCCACGGTGACATCGAACTT
GCTCTAACGTAGGGCTCATGAGGTGCAAACCGCTTGCATAAATGCGAAGATAGC
ACCATAAATAGATGCATGGCCATTTCTGAGATTGCAACATCTGTTATGGATCGTG
AGTAACACGCATCAATTACAAATTCGAAACGTCTGACGGGTCCTTTGGTACTGCA
GAGTACCATGTGTGAAGGTTGGAGGCATACGTTTTACAATGAACGGCAATCCATG
GTTCAACCTCGTGCTCGTTTCCAATGTGGCTGGAGCTGGAAATGTGGTGAACCTG
CAGATGAAAAGTTCCGAAACCAACTGGTTTTGGATGACGGCGAGGCAGATTTG
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GTGACACTTGGTAATGGAAAGGTGATGATTGCCAACAACGTGGTCCCAGCAA
GAACTTCCAACAGACATTTGAATCCGATATCAACTTTTAG