

IDENTIFICATION

Species: *Marchantia polymorpha*

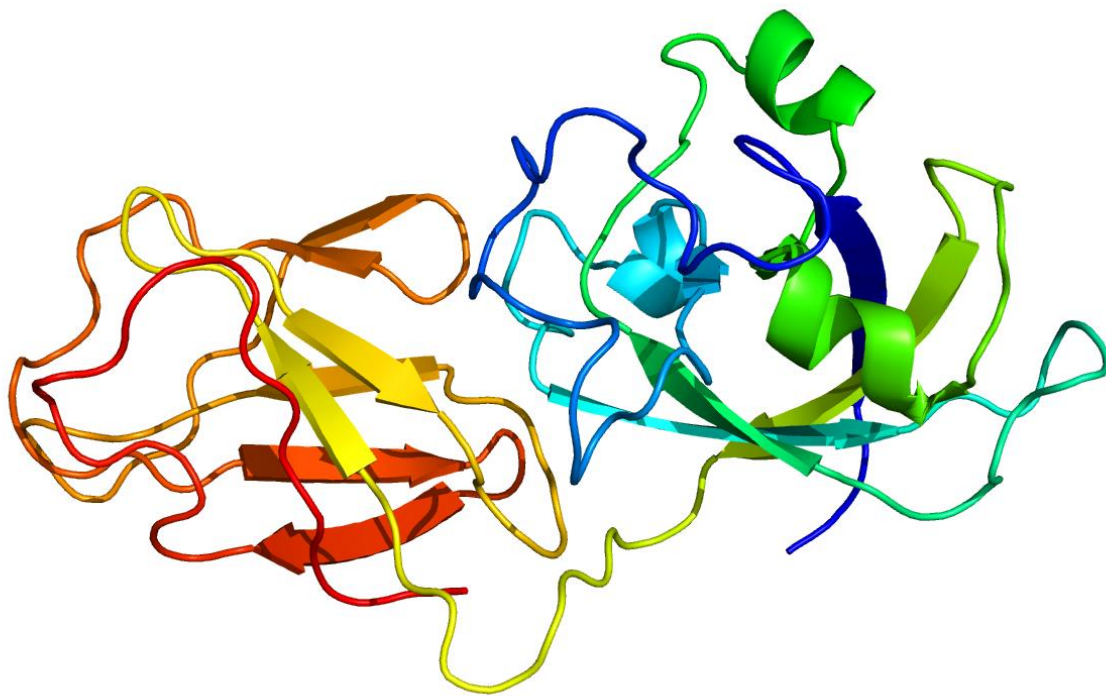
Locus: Mapoly0061s0098

Gene Model: Mapoly0061s0098.1.p

Description: MpoEXPA-16

Family: Alpha Expansin

3D structure:



GENOME DATABASES

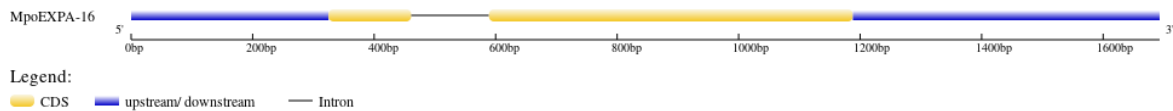
Phytozome: https://phytozome-next.jgi.doe.gov/info/Mpolymorpha_v3_1

KEGG:-

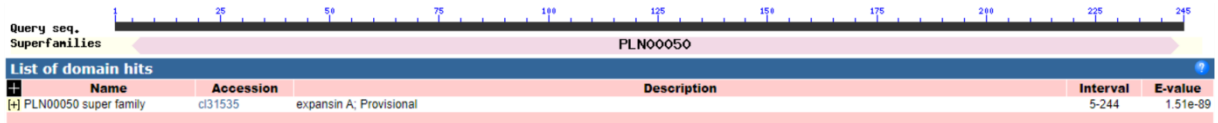
EXTERNAL RESOURCES

<https://marchantia.info/>

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>MpoEXPA-16

MVTGMRSFLMTVAVLLFTEKAFRVADGWSTAHATFYGGSDASGTNNGACGYSNVF
ALGYGTMTAALSAPLNDGLSCGACFQIQCSGDAACYSNSITVTATNLCPQGSYGGW
CDYPNAHFDSLQPAFSQLAQTAVAGHVTVNYQRVNCNRQGGVRFQIDGHTYFMQTLI
YNVGGSGDVVAVQVKGSKTGWISMTRGWGQNWQTGTVLDGQALSFSVKTSDBGKT
LYHNNVADSNWKYGQTFEGAQF*

CDS (coding sequence)

>MpoEXPA-16

ATGGTGACAGGAATGAGGAGCTTTTTGATGACTGTGGCAGTCCTTCTCTTCACAG
AGAAGGCGTTTTCGTGTAGCGGATGGGTGGTCGACTGCCACGCGACATTCTACGG
CGGGAGTGACGCATCTGGCACCAACAATGGTGCATGTGGCTACAGCAATGTCTTC
GCCCTCGGATACGGGACGATGACAGCGGCATTGAGCGCGCCGCTCTTCAACGAC
GGGCTGTCGTGCGGAGCTTGCTTCCAAATTCAGTGCTCGGGCGACGCGGCGTGCT
ACTCCAACCTCCATCACCGTCACCGCGACCAACCTCTGCCCTCAGGGCAGCTACGG
AGGCTGGTGGCGACTACCCGAACGCGCACTTCGATCTATCGCAGCCCGCGTTCTCT
CAGCTCGCCCAGACCGTCGCAGGTCACGTCACTGTCAACTACCAGAGGGTGA
GCAACAGGCAGGGAGGAGTGCCTTCCAGATCGATGGCCACACTTACTTCATGCA
GACTCTGATCTACAACGTCGGCGGCTCAGGCGACGTGGTGGCCGTCCAGGTCAAG
GGCTCCAAGACCGGCTGGATTAGCATGACAAGAGGGTGGGGCCAGAATTGGCAA
ACTGGCACGGTGCTTGACGGACAGGCGCTCTCCTTCTCCGTGAAGACCAGCGATG
GCAAGACATTGTACCACAATAATGTCGCTGACTCTAACTGGAAGTACGGGCAAAC
ATTCGAAGGGGCCAGTTCTAG

Nucleotide

>MpoEXPA-16

ACTCAATCCTTCTCTCAGCTCTCATACTACTTCCCTCTTCCCGATCCGTCCCGAG
CTTCTCTCGCGGCATCCCATCGGTCCAAGAGAAGTCTCATCCGGCATCAGGATAG
GCGTCGAGCGAGCTGCGAGCTCCAGTCACTTGGATTTCAGAGTCTGGTTGGTGGGA
CGGCAGGAGCTCTCCACCCCTGCATATTGTGAGCTTCATCTGAGGATCGCCTTGC
AAGCAGCGCATTCTGCACCGGGGCAACAGCTCCTCCAGCAGAAGGGTCTGAGCA
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GCAATGTCTTCGCCCTCGGATACGGGACGATGACAGCGGCATTGAGCGCGCCGCT
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CGCGTTCTCTCAGCTCGCCCAGACCGTCGCAGGTCACGTCACTGTCAACTACCAG
AGGGTGAAC TGCAACAGGCAGGGAGGAGTGCGCTTCCAGATCGATGGCCACACT
TACTTCATGCAGACTCTGATCTACAACGTCGGCGGCTCAGGCGACGTGGTGGCCG
TCCAGGTCAAGGGCTCCAAGACCGGCTGGATTAGCATGACAAGAGGGTGGGGCC
AGAATTGGCAAAC TGGCACGGTGCTTGACGGACAGGCGCTCTCCTTCTCCGTGAA
GACCAGCGATGGCAAGACATTGTACCACAATAATGTCGCTGACTCTAACTGGAAG
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TCGCATCCTGTAAACAGTATAAAAATCGAATCATCCATTTCCATGAAAATCGAAACC
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CTGTCACTACGACTGTGGATAATCCGGTGGCTTTGTATTTCAGAATGGTGTCTCTCC
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TGCCATCCGCCTCTCTCCATATTAGGATATCTTTGCTCGGAACACCCAAGTTATTG
TATGGTTTACCGATGATAGTGAAAATTTTACATTACGACTTATA