

IDENTIFICATION

Species: *Marchantia polymorpha*

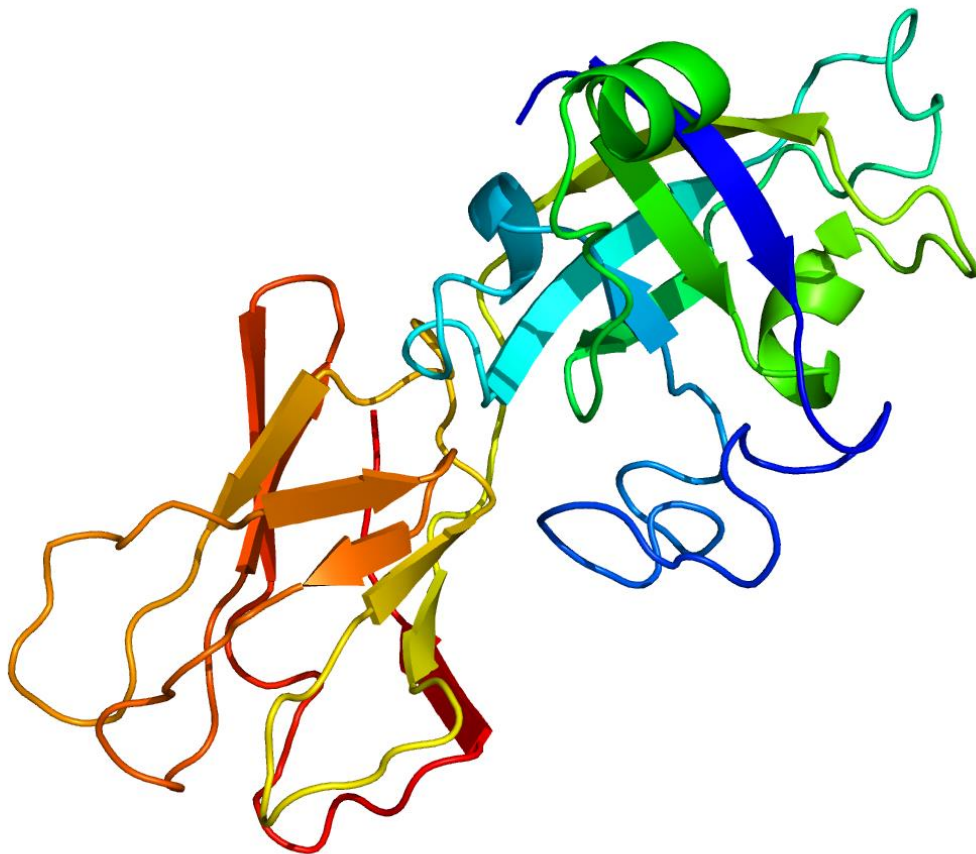
Locus: Mapoly0105s0025

Gene Model: Mapoly0105s0025.1.p

Description: MpoEXPA-26

Family: Alpha Expansin

3D structure:



GENOME DATABASES

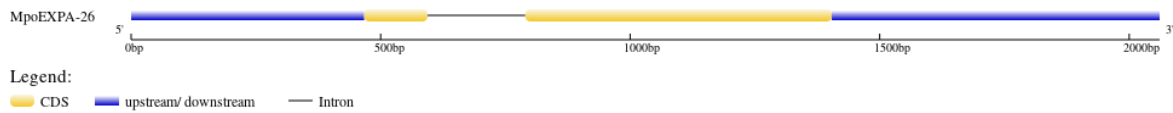
Phytozome: https://phytozome-next.jgi.doe.gov/info/Mpolymorpha_v3_1

KEGG:-

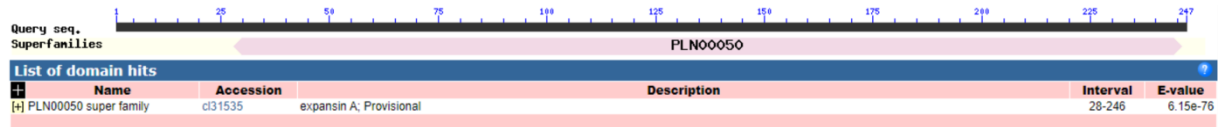
EXTERNAL RESOURCES

<https://marchantia.info/>

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>MpoEXPA-26

MRTMILNSTTFLISFMLLCRQSVDCIPATATFYGGNDASGTNTGACAYPNVLAMGYG
TMNAALSSAIFDHGKTCGACFQLVCTYVPYGNLRLCLRGRITVTATNYCPQGSKGGW
CDAPRSHFDLAEPAFVQIAPYNAGVVHVDYQRVNCQRSGEIRYRLYGFTYFLQVLVY
NVAGTGDVTAMSIKGSSEGRWISMTRSWGQLWTTGVVLEHQALSFMVTISDGRITIT
VNDVANEYWRYGQTYEGGQF*

CDS (coding sequence)

>MpoEXPA-26

ATGAGGACAATGATATTGAACAGCACGACGTTTCTCATCAGCTTCATGCTCTTGT
GTAGACAATCAGTCGATTGTATACCAGCGACTGCCACATTCTACGGTGGGAACGA
TGCTTCAGGCACAAATACTGGTGCCTGCGCATATCCAAACGTGCTGGCGATGGGC
TACGGGACGATGAACGCTGCTCTGAGTTCTGCAATCTTCGACCACGGCAAACAT
GTGGAGCTTGCTTCCAGCTCGTGTGCACCTACGTGCCCTACGGCAACCTTCGCTGC
CTGCGCGGAAGAATCACGGTGAAGTCAACGAACTATTGTCCGCAGGGAAGCAAG
GGAGGATGGTTCGACGCGCCAGATCCCACTTCGACCTTGGCGAGCCGGCCTTCG
TGCAGATCGCCCTTACAATGCCGGCGTTGTGCACGTCGACTATCAGCGCGTGAA
CTGCCAGAGGAGCGGCGAAATTCGGTATCGCCTCTACGGCTTCACTTATTTCTG
CAGGTCTTGGTTTACAACGTGGCGGGCACGGGCGACGTCACGGCGATGTCCATCA
AAGGCTCGTCTGAGGGTTCGGTGGATCTCCATGACTCGGAGCTGGGGTTCAGTTGTG
GACCACGGGAGTCGTGCTCGAGCACCAGGCTCTCTCGTTCATGGTCACCATCAGC
GATGGGAGA ACTATTACCGTCAACGACGTGGCCAACGAGTACTGGAGGTATGGA
CAGACTTACGAAGGAGGACAGTTTTGA

Nucleotide

>MpoEXPA-26

TCCTGGGAGTCGTGAGGGCAAACGAGCCTTGAGTGAGGATTGGGAGGTCTGAGC
AGTGCTCCTGACCTCGACTTCGACTGATGGGATCGTCTGATACGTGGCATGGGGT
CACCTCCAATTTCTACAGTCTGGCTGAAAGCAGGTCCAAGCCTCCGTGTTAGAAT
TGCTTTCTGAGAGAATGGCAAGTGATGCGATAAAGTGAGGGAGTGAGTAAATCA
GTCAGTCAGACTGTAAAGGCAGCCGCATATATTAGGCTGACAGAGGAGTACAAT
GCAGAAAGCATCAGTCTGAGACGGAGGTCGCGTTTGTCTGATCCTACAACAGC
AGCACGTACAAGCTCGAGTTTTTCGCGTCCC GCACTTGAAGTGCTTGTACTCGAAG
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ATACACGCATGTAATACAACATCGGCCGCCATGAGGACAATGATATTGAACAGC
ACGACGTTTCTCATCAGCTTCATGCTCTTGTGTAGACAATCAGTCGATTGTATACC
AGCGACTGCCACATTCTACGGTGGGAACGATGCTTCAGGCACAAATAGTATGTCC
CTTCAAACCTCTGAATCCTGTGAATTATCGGGCATAACGATGAAAACGTATGACGCT
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TGGGCTACGGGACGATGAACGCTGCTCTGAGTTCTGCAATCTTCGACCACGGCAA
AACATGTGGAGCTTGCTTCCAGCTCGTGTGCACCTACGTGCCCTACGGCAACCTT
CGCTGCCTGCGCGGAAGAATCACGGTGACTGCAACGAACTATTGTCCGCAGGGA
AGCAAGGGAGGATGGTGCACGCGCCAGATCCCCTTCGACCTTGCGGAGCCG
GCCTTCGTGCAGATCGCCCCTTACAATGCCGGCGTTGTGCACGTCGACTATCAGC
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TTTCTGCAGGTCCTGGTTTACAACGTGGCGGGCACGGGCGACGTCACGGCGATG
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AGTTGTGGACCACGGGAGTCGTGCTCGAGCACCAGGCTCTCTCGTTCATGGTCAC
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ATCGTCCAAAGATCTGTATAAAGTGGT