

IDENTIFICATION

Species: *Marchantia polymorpha*

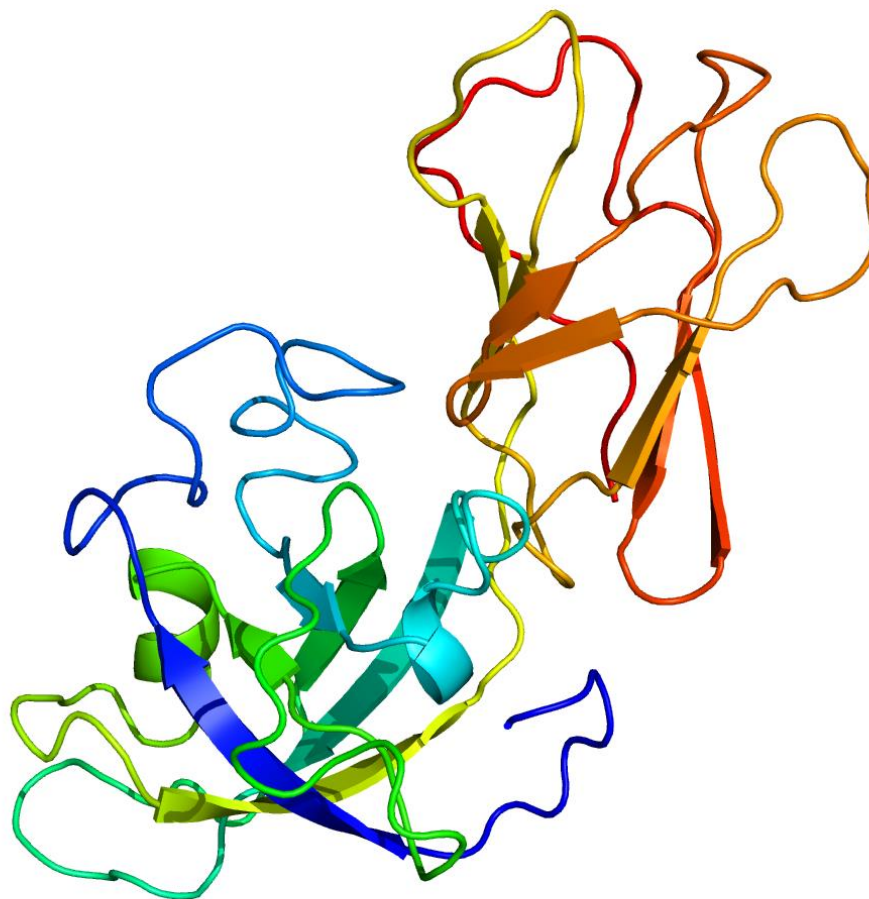
Locus: Mapoly0090s0012

Gene Model: Mapoly0090s0012.1.p

Description: MpoEXPA-25

Family: Alpha Expansin

3D structure:



GENOME DATABASES

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

KEGG:-

EXTERNAL RESOURCES

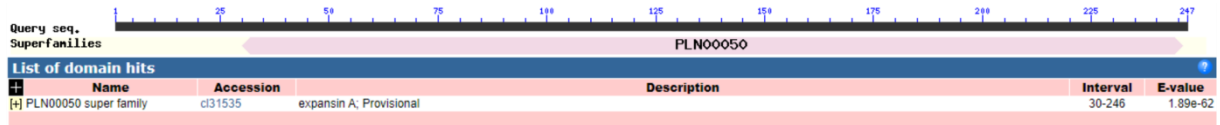
<https://marchantia.info/>

GENE STRUCTURE



Legend:
Exon

DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>MpoEXPA-25

MAQLFVAGLCVLSIFWFGESLGGVEGLKAHATFLGGSDAVGTNNGACGYSNVLA
MGYGTRTAALSAPIFREGKSCGACYKLRCRGSSEVGCRSNDGVVVVTVDVCPERSV
GGWCDGQPHFRLSEPAFAQIAEPKSGGLVEVDYEKVSCDRRGGMHFLLVGHTHFLQI
LVHNVGGCGDVAAVSVKGGTGPWIRMSRSWGQLWHTGEVLDGQALSISVTMADG
KVCVSNFAGADWKYQGQTFEGAQL*

CDS (coding sequence)

>MpoEXPA-25

ATGGCACAACTGTTTCGTGGCTGGGCTCTGCGTGCTCGTCTCCATCTTCTGGTTTGG
AGAATCGCTGGGCGGAGTCGAGGGGCTGAAAGCGCACGCGACGTTCTCGGGGG
GAGTGATGCCGTGGGCACCAACAATGGCGCCTGTGGCTATAGCAATGTTCTGGCG
ATGGGGTACGGGACGAGGACGGCGGCCCTGAGCGCCCCGATCTTCAGAGAAGGC
AAATCGTGCGGAGCTTGCTACAAGCTTCGCTGCCGGGGATCGGAGAGCGTCCGGT
GCAGGAGCAACGATGGCGTCGTCTGACGGTGACAGATGTGTGCCCTGAGCGCA
GCGTGGGCGGATGGTGCACGGCCAACCGCATTTCGACTGTCAGAACCGGCATT
CGCTCAGATCGCCGAGCCCAAGAGTGGAGGCCTGGTGGAAAGTGGATTACGAGAA
GGTTTCCTGTGACAGGAGAGGAGGCATGCACTTCCTTCTGGTGGGACACACTCAC
TTCCTGCAGATTCTCGTGCACAATGTTGGAGGCTGCGGCGATGTGGCTGCCGTGT
CGGTGAAGGGCGGAAGTGGCCCGTGGATTCGCATGAGCAGGAGCTGGGGTCAAT
TGTGGCACACGGGCGAGGTTCTCGACGGGCAGGCCCTTCAATCTCGGTGACAAT
GGCAGATGGCAAGGTCTGTGTCAGCAACAATTTTGCAGGTGCGGATTGGAAGTAT
GGTCAAACCTTCGAGGGGGCACAATTGTAA

Nucleotide

>MpoEXPA-25

ATGGCACAACTGTTTCGTGGCTGGGCTCTGCGTGCTCGTCTCCATCTTCTGGTTTGG
AGAATCGCTGGGCGGAGTCGAGGGGCTGAAAGCGCACGCGACGTTCTCGGGGG
GAGTGATGCCGTGGGCACCAACAATGGCGCCTGTGGCTATAGCAATGTTCTGGCG
ATGGGGTACGGGACGAGGACGGCGGCCCTGAGCGCCCCGATCTTCAGAGAAGGC
AAATCGTGCGGAGCTTGCTACAAGCTTCGCTGCCGGGGATCGGAGAGCGTCCGGT
GCAGGAGCAACGATGGCGTCGTCTGACGGTGACAGATGTGTGCCCTGAGCGCA
GCGTGGGCGGATGGTGCACGGCCAACCGCATTTCGACTGTCAGAACCGGCATT
CGCTCAGATCGCCGAGCCCAAGAGTGGAGGCCTGGTGGAAAGTGGATTACGAGAA

GGTTTCCTGTGACAGGAGAGGAGGCATGCACTTCCTTCTGGTGGGACACACTCAC
TTCCTGCAGATTCTCGTGCACAATGTTGGAGGCTGCGGCGATGTGGCTGCCGTGT
CGGTGAAGGGCGGAACTGGCCCGTGGATTCGCATGAGCAGGAGCTGGGGTCAGT
TGTGGCACACGGGCGAGGTTCTCGACGGGCAGGCCCTTCAATCTCGGTGACAAT
GGCAGATGGCAAGGTCTGTGTCAGCAACAATTTGCAGGTGCGGATTGGAAGTAT
GGTCAAACCTTCGAGGGGGCACAATTGTAA