

IDENTIFICATION

Species: *Marchantia polymorpha*

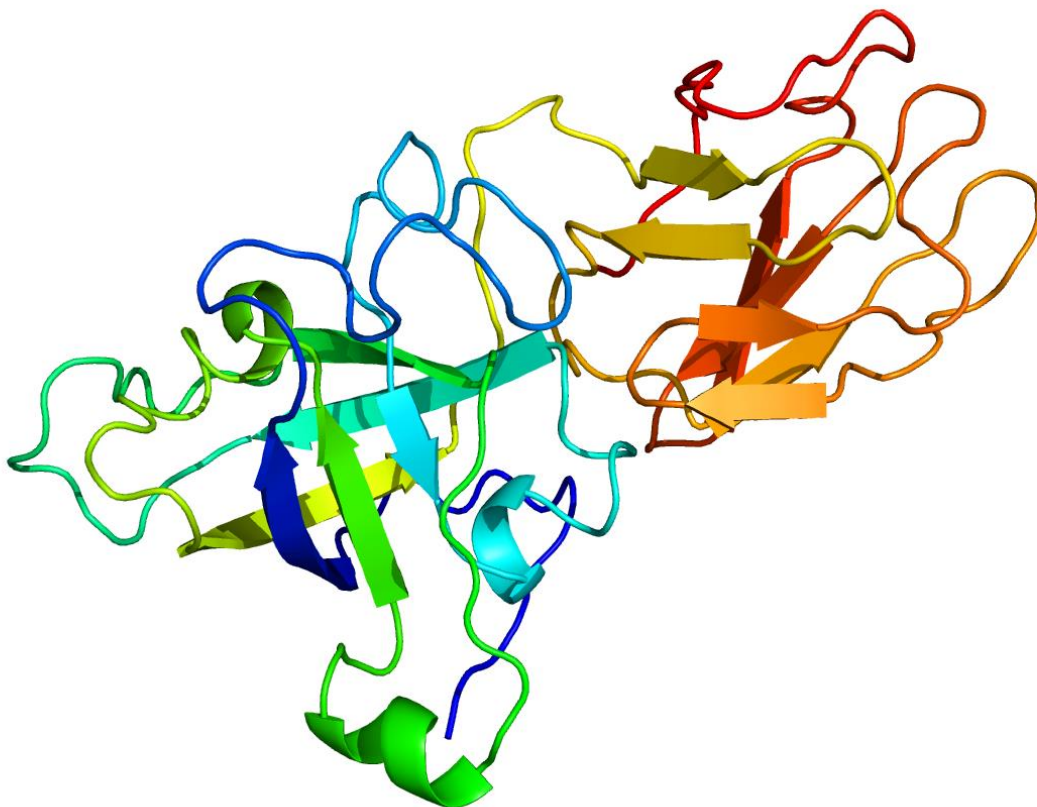
Locus: Mapoly0058s0020

Gene Model: Mapoly0058s0020.1.p

Description: MpoEXPA-13

Family: Alpha Expansin

3D structure:



GENOME DATABASES

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

KEGG:-

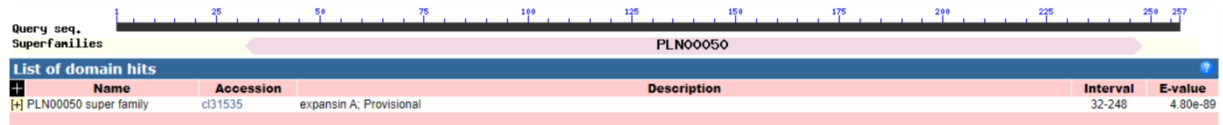
EXTERNAL RESOURCES

<https://marchantia.info/>

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>MpoEXPA-13

MEAFNRSFVVLSTLMLMLWFKLVNAVEPWAVTEWGDAAHATFYGGNDASGTMGGA
CGYGNLYSLGYGTASTALSNGLFNGLSCGACYTIECKLEGSKWCYPGKSITVTATN
ACPPGSEGGWCDPRLHFDLSYPMFQTLAQPVGGVIPVKYKRVSCNRQGGIRFTLHG
NAWFNYVLVHNVAGGDVAGVSIKGDNGGWTTMYQNWGQFWSASEHLVGQALS
FRVTLGSGRTQEFYDVASPNWYFGQTYEADNNQNF*

CDS (coding sequence)

>MpoEXPA-13

ATGGAGGCATTCAACAGATCCTTTGTGGTGCTCAGCACTTTGATGCTGATGTTGTG
GTTCAAGCTCGTAAATGCGGTTGAACCCTGGGCAGTTACAGAGTGGGGAGACGC
CCATGCAACTTTCTACGGCGGAAACGATGCCTCGGGTACAATGGGTGGTGCCCTGC
GGGTACGGCAATCTGTACTCTCTGGGTTATGGAACCGCCTCCACTGCCCTGAGCA
ACGGGCTCTTCAACAACGGGCTCAGCTGCGGGGCATGTTACACTATCGAGTGCAA
GCTCGAGGGGAGCAAATGGTGCTATCCTGGTAAAAGCATCACCGTCACCGCTACC
AATGCATGCCCGCCTGGATCAGAGGGCGGCTGGTGCGATCCTCCTCGTCTCCACT
TCGATCTGTCTTACCCCATGTTTCAGACACTCGCTCAACCAGTCGGTGGCGTCATC
CCTGTCAAGTACAAGAGGGTCTCTTGCAACAGACAAGGGGGAATCCGATTCACTT
TGCACGGAAACGCCTGGTTCAACTATGTCCTGGTCCACAATGTGGCAGGTGATGG
AGATGTGGCTGGCGTCTCCATCAAGGGAGATAACGGAGGCTGGACTACCATGTAT
CAGAATTGGGGACAATTCTGGTCCGCCAGTGAGCACCTTGTGGTCAAGCTCTCT
CTTTCCGTGTCACCTTAGGCAGCGGAAGGACTCAGGAGTTCTACGACGTTGCTTC
ACCGAATTGGTACTTTGGCCAGACTTATGAAGCCGACAACAATCAGAACTTCTAG

Nucleotide

>MpoEXPA-13

TCTGGCTTAGCTTAGAAGTCAAAGCAAAGTCAGCACTTGGAGCTGTTTAGCATT
GCATCTGGAGCTCTTCCAGCCTGTTTCCACTTACTGGTGCTTGTCTTTTACATACG
CCAGAGAAGTCATGGAGGCATTCAACAGATCCTTTGTGGTGCTCAGCACTTTGAT
GCTGATGTTGTGGTTCAAGCTCGTAAATGCGGTTGAACCCTGGGCAGTTACAGAG
TGGGGAGACGCCCATGCAACTTTCTACGGCGGAAACGATGCCTCGGGTACAATG
GGTAAGGATGCGCCTCATTGCACTCCAGATTTCAAGAGCTCTTCAATTATTGCATAT
ACTGTTTCAACAAGATCAATCTAGTTCAATCATTACTAATTGCTAAGCTATCTTAAC
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ATGCTGCATTTGAAGATTCAGAAAAGTGTGAATGTTGGCAGTAAATTTACATTGA
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GGTGGTGCCTGCGGGTACGGCAATCTGTACTCTCTGGGTTATGGAACCGCCTCCA
CTGCCCTGAGCAACGGGCTCTTCAACAACGGGCTCAGCTGCGGGGCATGTTACAC
TATCGAGTGCAAGCTCGAGGGGAGCAAATGGTGCTATCCTGGTAAAAGCATCAC
CGTCACCGCTACCAATGCATGCCCCGCTGGATCAGAGGGCGGCTGGTGCATCCT
CCTCGTCTCCACTTCGATCTGTCTTACCCCATGTTTCAGACACTCGCTCAACCAGT
CGGTGGCGTCATCCCTGTCAAGTACAAGAGGTAACCACCAGCAGAAACTTAAAA
TTTTGAAGCTGGAAGAAGATGCACTGAAATTTTCTCATCAGATTCTCTCAGAAA
TGAAAATGCCGAACTGTACTGATGTTCTATCATTCTTGTTCCTCTCAGGGTCTCTT
GCAACAGACAAGGGGGAATCCGATTCACCTTGCACGGAAACGCCTGGTTCAACT
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GGGAGATAACGGAGGCTGGACTACCATGTATCAGAATTGGGGACAATTCTGGTC
CGCCAGTGAGCACCTTGTCGGTCAAGCTCTCTCTTTCCGTGTCACCTTAGGCAGCG
GAAGGACTCAGGAGTTCTACGACGTTGCTTCACCGAATTGGTACTTTGGCCAGAC
TTATGAAGCCGACAACAATCAGAACTTCTAGTGATTGTTTCATGCAGTCTCTTTCGT
GACGGTCATTCTGAACCATGTTCAATAGAATTAGCTCTGTCTATATAGACGCAGA
CGAGGCGTGTATAAATCAACCGATTAACGCCCTCTGTTACAATATACACGGCAGG
CATAGAACAGACGAGGCGTGTAATACTTAAACCGCCCCTGTGAGGCCCACCA
TCTTCATAGTAATCCCTCAGCTGACAGAGTTGAAGTTGTAGACCAGGAATTTAG
AACGATCTGACGGAAAGACCTTCATTGTTGTCAATCAAGAGTTCGATTAATAAAT
CGAGCCATTTCA