

IDENTIFICATION

Species: *Marchantia polymorpha*

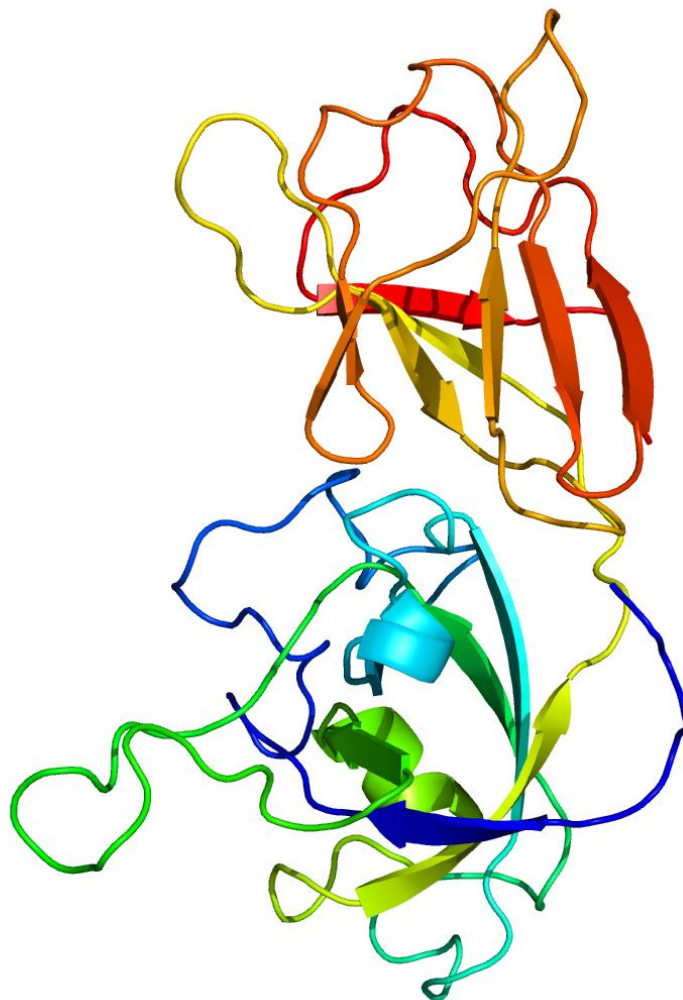
Locus: Mapoly0131s0018

Gene Model: Mapoly0131s0018.1.p

Description: MpoEXPA-33

Family: Alpha Expansin

3D structure:



GENOME DATABASES

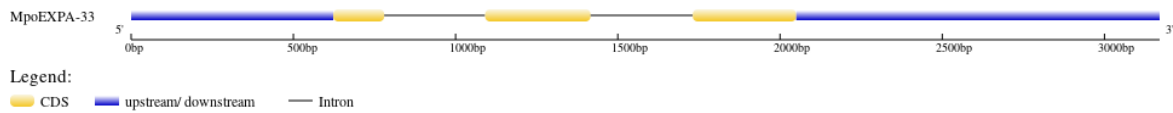
Phytozome: https://phytozome-next.jgi.doe.gov/info/Mpolymorpha_v3_1

KEGG:-

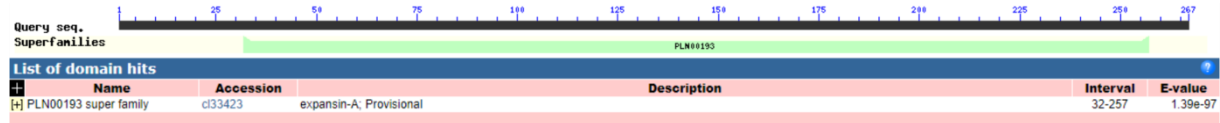
EXTERNAL RESOURCES

<https://marchantia.info/>

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>MpoEXPA-33

MARMCTSKEWAILLCTLSMCMVVGSLAGVPGVPSGWKAAHATFYGGSSNAQGTMGGA
CGYGNLYNTGYGLETAAALSSTLFNNGKTCGACYEMFCNYRQQSRWCYKAQPHIKV
TATNLCPANWNRPTNRGGWCNPPRVHFDLPQPMFIKMARYVGGIVPVA YRRVPCVK
KGGVKFTMNGNPWFNLILISNVAGPGDIKAVAVKGSKQKSWTSARQNWGQKWEVK
QKLQGQALSFRLTSGSGKVLVLYNAVPRTWRFGSTYMARSNWKGL*

CDS (coding sequence)

>MpoEXPA-33

ATGGCCAGGATGTGCACCTCGAAAGAATGGGCCATTATACTATGCACGTTATCTA
TGTGCGTCGTTGGCTCCCTGGCTGGTGTTCGGGAGTTCCAAGTGGATGGAAAGC
GGCCCATGCTACATTCTACGGAGGATCTAATGCCCAAGGGACTATGGGTGGAGCT
TGTGGATACGGAAACCTTTACAACACCGGGTATGGGTGGAAACTGCTGCTCTCA
GTTCAACATTATTCAACAACGGCAAGACCTGCGGAGCTTGCTACGAAATGTTCTG
CAATTATCGTCAGCAATCTCGATGGTGTATAAAGCACAAACCCACATCAAAGTC
ACTGCCACCAACTTGTGTCCAGCTAACTGGAACCGACCCACGAACAGAGGAGGA
TGGTGCAACCCTCCGAGGGTCCACTTCGATTTACCTCAGCCTATGTTTCATCAAGAT
GGCTAGATATGTCGGAGGAATCGTCCCGGTTGCATACAGAAGAGTTCCTGCGTA
AAGAAGGGTGGAGTCAAGTTCACAATGAACGGTAATCCATGGTTCAACCTGATTC
TCATCAGCAATGTTGCGGGGCCCGGAGACATCAAGGCAGTCGCGGTGAAGGGCT
CGAAGCAAAAGTCCTGGACATCAGCCAGACAGAACTGGGGTCAGAAGTGGGAAG
TGAAGCAAAAGCTTCAAGGTCAAGCGCTTTCCTTCCGACTCACTTCAGGAAGCGG
CAAAGTACTGGTCCTCTACAACGCTGTACCGAGAACCCTGGAGATTTGGCAGCACT
TACATGGCCAGATCTAACTGGAAGGGCTTGTAG

Nucleotide

>MpoEXPA-33

AGCACAGCCCTCTACAGCGTCGATCGATCGTGCAAAGCGGGGAGAGAGATTTCCG
TGGGTGGGTGGGACGTGAGCTCCGGCGGGCGCTTCTGACAGTTCAAGTTCCCCCG
GCAAAGCCCAAGGTGGGGACGTGCGAGTGCATGCGAATTTCCGGTAGTCAACTGT
GTTCTAGGCGCGCTCTGGATTTTCTTCTCAGAGGGAGCGAGACATATATCTGAG
CAATTCCTCTTCCACCCTCCACAAGGTTACACTCGACGATCTCTGAAACACTGGCT
TACAACCTCGCACCAGTTTTTCTTGGAAATCCTCTTCCCGTAGCTGGACTTCGATTGA
AGTTGCTCGGGTATGCATGTGATTCCATCCCTCTGCATCCATCCTCTCCTGCTGT

GGGATCGTTCTAGATCTCATAATGGCTTGGCAGTTAGACCTGCATTGTACTCTCAG
CTACATCAGTTGTTGCCTGCATAGCTTGTAGTTCAGGTCAACGTGCAAAATGGCA
CTCACTGAATGGTTACAGCAGTATCTGGTTCAGAGTTCAAACAGTTTGTGATTTCC
AGTTTCAAAACTCGATTCTTTAGCTGATTACACGTTCTGAACCAAGTTTCGGCTTT
CGTTCTGCAGAAGGATGGCCAGGATGTGCACCTCGAAAGAATGGGCCATTATACT
ATGCACGTTATCTATGTGCGTCGTTGGCTCCCTGGCTGGTGTCCGGGAGTTCCAA
GTGGATGGAAAGCGGCCCATGCTACATTCTACGGAGGATCTAATGCCCAAGGGA
CTATGGGTAAAGTGGACAGGCAAACATTGACCAAATGTGTGTAATTCGATCTTTT
TTCTTGGAACACGCAATTTAGACAGTTAAGCACCCATTTATTTACAAATTAATTGA
AGAATTGTATCTTCTTTTACAATGTCGTCCATATCTTCAGTACACATGTTGAGTC
CTATACACATAACTTCCACTTTTGTACCTTGTATATGCATATACGAGAGAACGCC
AACTGCTGCTTGTGCGCAAATCAAGAGTTTTTGTGCTTTGATTTGGTTTCGATC
TACGATATATTCAACATCACTCGGATGTTTGTCTATAGGTGGAGCTTGTGGATAC
GGAAACCTTTACAACACCGGGTATGGGTGGAAACTGCTGCTCTCAGTTCAACAT
TATTCAACAACGGCAAGACCTGCGGAGCTTGTACGAAATGTTCTGCAATTATCG
TCAGCAATCTCGATGGTGTATAAAGCACAACCCACATCAAAGTCACTGCCACC
AACTTGTGTCCAGCTAACTGGAACCGACCCACGAACAGAGGAGGATGGTGC AAC
CCTCCGAGGGTCCACTTCGATTTACCTCAGCCTATGTTTCATCAAGATGGCTAGATA
TGTCGGAGGAATCGTCCCGGTTGCATACAGAAGGTGCTCTTCACATTACACGTTT
CAAACGATCGCCACCTATCAAGCGCTTGTAGCTTCTTGTACTCCAATTGCTTTGA
CAATGTAGACCTTTCTCCGTGTCGATTTTTCATGAGTCGGCTTCGAAGCTGCTCATG
CCAGCCGTATTACTCGTATAATTACAGTATTTGAACCAGTCATCGCTCGACTGAA
GCATAAAAGATGTACATGTGGAGTGTGTAACCAGTTCATCCAAATGTAATAACA
TTGTTTGTATGGTTCACAGATCCGTGAGATTTTGTCAAAGGTACTAACAACTA
ATCGGGTAATTGCAGAGTTCCTGCGTAAAGAAGGGTGGAGTCAAGTTCACAATG
AACGGTAATCCATGGTTC AACCTGATTCTCATCAGCAATGTTGCGGGGCCCCGGAG
ACATCAAGGCAGTCGCGGTGAAGGGCTCGAAGCAAAAGTCCTGGACATCAGCCA
GACAGAACTGGGGTCAGAAGTGGGAAGTGAAGCAAAAGCTTCAAGGTCAAGCGC
TTTCTTCCGACTCACTTCAGGAAGCGGCAAAGTACTGGTCCTCTACAACGCTGT
ACCGAGAACCTGGAGATTTGGCAGCACTTACATGGCCAGATCTAACTGGAAGGG
CTTGTAGATCTGGTCCAAACATTTTATTTGTTTTAATTTACGTTACACATGCAGG
AACATCAGCTAGATCTGAGGGATATCTATCGTAGAATCTAGCTAGCCCGTAAACC
CAGCTTCTCGGAAAGCTTCATTAAGCTTCGTTCTGATCTGAGGATTTAGCGCTCGT
TGTCTAATCTTTTATGTCTGACGGCCAAGGCCCTTGTAGATAGACAGCCGGCGTT
GAAAGGGGGTTCATCGTTTGAATGATTGATTGAGGGAGAGAAAGGGAGGT
AGAGTGAGTGAGGAGTAAGGGAGGGAAAGGAGAGAGAGAAAGAGGAGCATTCA
TCAGCAACGATTTGGGAGGATCTTGGGCAAGATTCTTACATTCTACAAGCTGATC
TACCTGCCGACAGTACAGTACTGCCGACATACTTGAGTGACGACATTTAGTTGCT
TCATGCATGTAGAAGTCGAAGTCTATCACA ACTGTCACGCTTAACCTCAGATCTG
TAATATGTACGTGATATGAAGTACTCTGATTCAAGGCTCTAGCTGCAGTTACAGC
TAACCTTAATCAAGAGCCTCAAGCACTATCTTTAGCCAGAAGGAAGGTGCTTAGC
TTCTAGTTGTACGATCTTCAGTATACGAGTTGGAGTGTAATATTTCACTCGGTCTA
CATTTAGTGCTCTACTGTCCTGGCGTCGAGGTGAGCCAGCGGAGCCGCCACTCC
AGATGCGAGCTTCAATAGGTCCTCTATGGGATGAGCGAGCGATCTTCTACA ACTG
TGTCACGCCTCTACGTGTTTGAAGTTGAGTACTGCTTCTGCATCTGATTCATGCACC
AAAAGCCTCTTTTTGGCTCAATCGTTTCGCAGCTCCAGGAACCTGGTCTTCTAATG
AATCTTCAGTCGGGATATAGAGGATGCGGCGAGGAGAATCGATCTTCTTGCGAAA
TTTCTATACTCTAATCGCGGAGGTGCAGGAGAAGAAAGGGTTGCTGAAGCGACA
AATTGTTCTTGAAGCTTCAGACGAAGGGATGTGTACTTTTGTTC AATGATATATTT

GTATAAATTCGAGGATCACCACCACTTAAACACAGCATTATTTAGCTGGTGGAAA
TAAATTCAGAACTTCTCAATTGTA