

IDENTIFICATION

Species: *Physcomitrium patens*

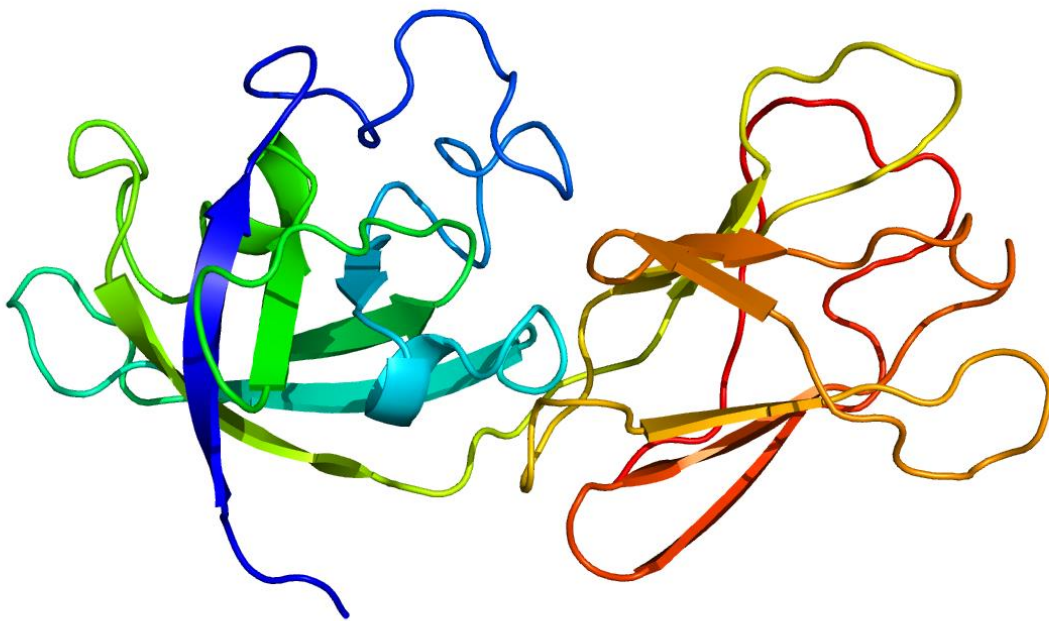
Locus: Pp3c8_15200V3

Gene Model: Pp3c8_15200V3.3.p

Description: PpEXPA-17

Family: Alpha Expansin

3D structure:



GENOME DATABASES

Phytozome: https://phytozome-next.jgi.doe.gov/info/Ppatens_v3_3

KEGG: <https://www.genome.jp/entry/gn:T01041>

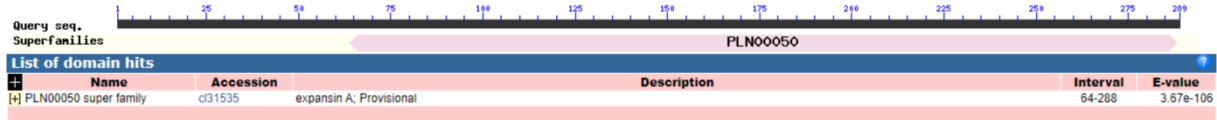
EXTERNAL RESOURCES

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GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>PpEXPA-17

MCRTSPRVLLEVFKAACDCISNSYYIEHHSVSMAKINLLFLPAQFVFSMAFLVQDIAG
SDSHCGWSNAHATFYGGHDAHGTLGGSCGYGNVIARGYGTNTVALSSALYGSGLSC
GSCFEIKCAGGEGCIPGSGAVTVTATNFCPPNPHRLPNNGGWCNMPRQHFDMAQPAF
LRIAQYRVGIVPVL YRRAACRRSGGMHFTMNGHKFHNLV LISNVGGDGNIRAVKIRG
SKTGWQPMWRNWGQNWQFSSNLFGQSLFMVTTGDGRTV TSMNVVPPFWKYGQT
FQGLQF*

CDS (coding sequence)

>PpEXPA-17

ATGTGCCGAACGTCTCCCCGTGTA CTTCTGGAGGTTTTCAAGGCTGCGTGTGATTG
CATTAGCAACTCGTACTATATTGAACACCATAGTGTATCGATGGCGAAGATCAAC
CTCCTGTTCCTACCCGCGCAATTCGTGTTTTCGATGGCCTTTCTCGTGCAAGATAT
AGCTGGTTCGGACAGCCACTGCGGGTGGAGTAATGCTCATGCAACCTTCTATGGC
GGCCATGACGCCCATGGAACCTTGGGTGGTTCTTGCGGCTATGGAAACGTCATCG
CTCGCGTTATGGAACCAACACCGTAGCGCTGAGCTCTGCACTTTACGGCAGCGG
ACTCTCATGCGGGTCGTGCTTCGAAATCAAGTGCGCAGGGGGAGAAGGTTGCATT
CCAGGCAGTGGTGCTGTA ACTGTC ACTGCTACCAATTTTTGCCACCAAACCCGC
ACAGACTTCCCAACAATGGAGGCTGGTGCAACATGCCCAGACAACACTTCGATAT
GGCTCAGCCTGCATTTCTGCGCATTGCCCAGTACCGCGTGGGTATTGTGCCTGTAC
TGACAGAAGAGCTGCGTGCAGGAGGAGTGGGGGAATGCACTTCACCATGAATG
GGCACAAGTTCACAACCTTGTCTCATTTCAAACGTAGGTGGCGATGGAAATAT
CCGAGCAGTGAAAATCAGAGGATCAAAGACTGGGTGGCAGCCGATGTGGCGCAA
CTGGGGTCAGAACTGGCAATTCAGCAGTAACTTGTTTCGGGCAGAGTCTCTCATTT
ATGGTCACTACAGGAGATGGCCGCACGGTGACTAGCATGAATGTTGTCCCACCGT
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Nucleotide

>PpEXPA-17

CCGCCCCCGCCATCTCCACAGAAATTC ACTCTCCCCTTCAGCCGCCTTCATGATCA
TGCACTAGCTTTGCGCTTCGACCACTACCGTCTTTTTTCTTTTTTCTTTTTTCTTTTCC
AATTCACACCCTATGATTTTAATTCGGAACATTTTTCTCCTTCGTCTGAGTTGT

CTCAAGCCTGAAAGTTTATCTAGCCTCCATTTAGTTTGTGAGTGATCATCGCGGTC
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ACTTTGTATCACTCGTTTCTTGAATCAAGAGCATGTTTCCCTCGGGACTGCTGAACC
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CAACCTCCTGTTCCCTACCCGCGCAATTCGTGTTTTTCGATGGCCTTTCTCGTGCAAG
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CAAGGATCAGATAGAGAAGCAATTCGCACAAAAAAAAGCATGGTATTAATAAC
GTGAACCCTTACGGCGAGAAAATCAACAAGCAGCTGAATACCGACAGAAGCAG
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CATTCGTGAAAAGAGAATGCAGCAACAACCTCAGGTCCTCAATGACACAGATGA
AGTAGACTAGTAAGCCTGTGCATATATATA