

IDENTIFICATION

Species: *Physcomitrium patens*

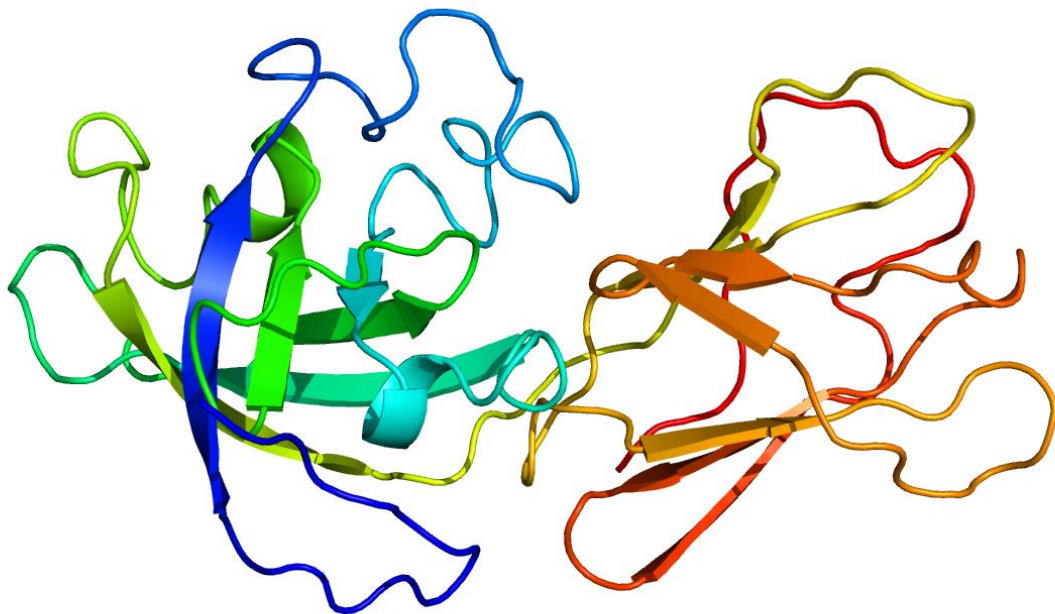
Locus: Pp3c8_15200V3

Gene Model: Pp3c8_15200V3.1.p

Description: PpEXPA-16

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>

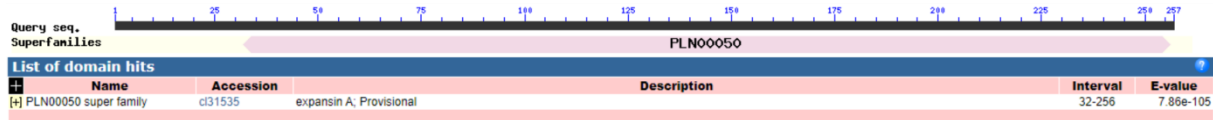
EXTERNAL RESOURCES

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GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>PpEXPA-16

MAKINLLFLPAQFVFSMAFLVQDIAGSDSHCGWSNAHATFYGGHDAHGTLGGSCGY
GNVIARGYGTNTVALSSALYGSGLSCGSCFEIKCAGGEGCIPGSGAVTVTATNFCPPN
PHRLPNNGGWCNMPRQHFDMAQPAFLRIAQYRVGIVPVL YRRAACRRSGGMHFTM
NGHKFHNLVLISNVGGDGNIRAVKIRGSKTGWQPMWRNWGQNWQFSSNLFQSLSF
MVTGTDGRTVTSMNVPVPPFWKYGQTFQGLQF*

CDS (coding sequence)

>PpEXPA-16

ATGGCGAAGATCAACCTCCTGTTCCCTACCCGCGCAATTCGTGTTTTTCGATGGCCTT
TCTCGTGCAAGATATAGCTGGTTCGGACAGCCACTGCGGGTGGAGTAATGCTCAT
GCAACCTTCTATGGCGGCCATGACGCCCATGGAACCTTGGGTGGTTCCTGCGGCT
ATGGAACGTCATCGCTCGCGGTTATGGAACCAACACCGTAGCGCTGAGCTCTGC
ACTTTACGGCAGCGGACTCTCATGCGGGTCGTGCTTCGAAATCAAGTGCGCAGGG
GGAGAAGGTTGCATTCCAGGCAGTGGTGTGTAAGTGTACTGCTACCAATTTTT
GCCACCAAACCCGCACAGACTTCCAACAATGGAGGCTGGTGCACATGCCCA
GACAACACTTCGATATGGCTCAGCCTGCATTTCTGCGCATTGCCAGTACCGCGT
GGGTATTGTGCTGTACTGTACAGAAGAGCTGCGTGCAGGAGGAGTGGGGGAAT
GCACTTCACCATGAATGGGCACAAGTTCCACAACCTTGTCTCATTTCAAACGTA
GGTGGCGATGGAATATCCGAGCAGTGAAAATCAGAGGATCAAAGACTGGGTGG
CAGCCGATGTGGCGCAACTGGGGTCAGAACTGGCAATTCAGCAGTAACTTGTTTCG
GGCAGAGTCTCTCATTTATGGTCACTACAGGAGATGGCCGCACGGTGACTAGCAT
GAATGTTGTCCCACCGTTTTTGGAGATATGGGCAGACTTTTCAAGGGTTGCAGTTCT
GA

Nucleotide

>PpEXPA-16

CCGCCCCCGCCATCTCCACAGAAATTCCTCTCCCTTCAGCCGCCTTCATGATCA
TGCACTAGCTTTGCGCTTCGACCACTACCGTCTTTTTTCTTTTTTCTTTTTTCTTTTCC
AATTTACACCCCTATGATTTTAATTTTCGGAACATTTTTCTCCTTCGTCTGAGTTGT
CTCAAGCCTGAAAGTTTATCTAGCCTCCATTTAGTTTGTGAGTGATCATCGCGGTC
ATACTTTCAGATGTGCCGAACGTCTCCCCGTGTAATCTGGAGGTTTTCAAGGCTG

CGTGTGATTGCATTAGCAACTCGTACTGCCAGCTGAGGTTGATAGATTTCATCTTC
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TTTCTCTATTTGTGATCGCAACATGCTCATCTTTAGCTCATCTGTATGAGACCTGC
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CCAAACCCGCACAGACTTCCCAACAATGGAGGCTGGTGCAACATGCCCAGACAA
CACTTCGATATGGCTCAGCCTGCATTTCTGCGCATTGCCCAGTACCGCGTGGGTAT
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CAAGGATCAGATAGAGAAGCAATTCGCACAAAAAAAAGCATGGTATTAATAAC
GTGAACCCTTTACGGCGAGAAAATCAACAAGCAGCTGAATACCGACAGAAGCAG
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CATTTCGTGAAAAGAGAATGCAGCAACAACCTCAGGTTCCCTCAATGACACAGATGA
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