

## IDENTIFICATION

**Species:** *Physcomitrium patens*

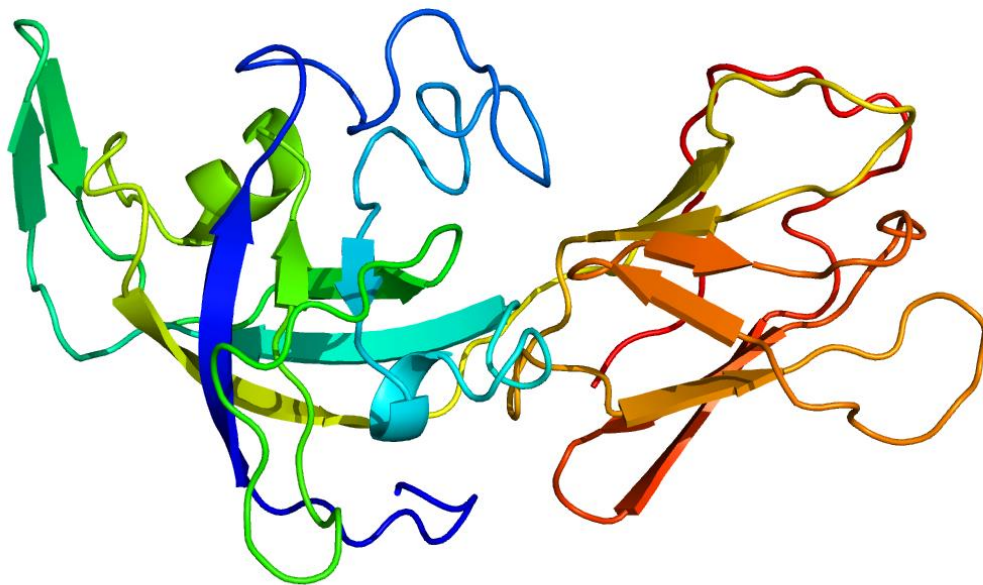
**Locus:** Pp3c14\_18590V3

**Gene Model:** Pp3c14\_18590V3.1.p

**Description:** PpEXPA-28

**Family:** Alpha Expansin

**3D structure:**



## GENOME DATABASES

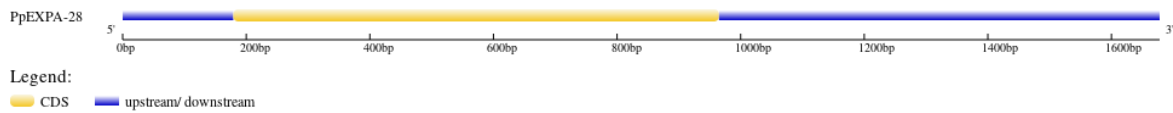
Phytozome: [https://phytozome-next.jgi.doe.gov/info/Ppatens\\_v3\\_3](https://phytozome-next.jgi.doe.gov/info/Ppatens_v3_3)

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

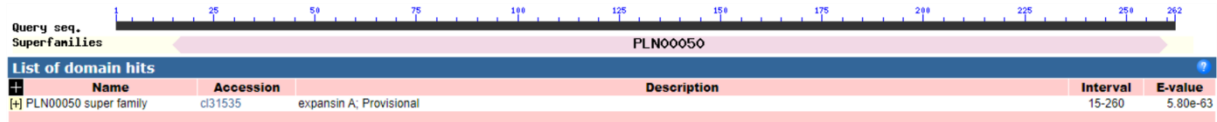
## EXTERNAL RESOURCES

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## GENE STRUCTURE



## DOMAIN ARCHITECTURE



## SEQUENCES

### Peptide

>PpEXPA-28

MRTPGAASTMKVAACIGMAALMALSVLPCVVGAPYGWNEAHITYYGTANGGGTQ  
GGACGYPNTFAMGYGAMTAALSYPFLFQGGKACGGCYQLRCKWVTPTRTVHNWCW  
SYSRTITVTATNSCPPGSHGGWCNWRPHFDLPMPAFLTLARREGGVAPVYYRKVRC  
AKRGGIRFTIGGNPYFLMILIHNVGGAGDLKAVKVRGGNGYWVPMWRNWGALWTC  
KTRMSGALSQITTDGRTLTYYKAVGGYWRFGQTWEGSQFR\*

### CDS (coding sequence)

>PpEXPA-28

ATGAGGACCCCGGGCGCTGCATCCACCATGAAGGTCGCAGCTTGCATTGGCATGG  
CCGCCTTGATGGCGCTGAGCGTCCTGCCTTGCCTGCGTGGTGGGAGCGCCGTACGGGTG  
GAACGAGGCGCACATCACGTAATGGAACAGCTAATGGCGGGGGCACGCAGGG  
AGGCGCCTGCGGGTATCCGAACACCTTTGCGATGGGATACGGGGCGATGACCGC  
AGCGTTGAGTTATCCTCTGTTCCAGGGGGAAAGGCATGCGGCGGGTGCTATCAG  
TTGCGGTGCAAGTGGGTGACGCCAACCCGAACCGTGCACAACCTGGTGCTGGAGCT  
ACTCTCGCACCATCACCGTGACCGCAACAACTCGTGCCCTCCAGGGTCGCACGG  
AGGTTGGTGCAACTGGAGACCTCACTTCGACTTGCCAATGCCTGCTTTCCTGACG  
CTGGCACGGCGTGAGGGAGGAGTGGCTCCGGTGTATTACAGGAAGGTCGGGTGT  
GCGAAGCGCGGCGGAATTCGGTTCACCATCGGAGGCAACCCGTACTTCTTGATGA  
TCCTGATTCACAACGTGGGAGGGGCGGGCGATTTGAAGGCAGTGAAGGTCAGGG  
GAGGAAACGGATATTGGGTGCCATGTGGCGCAACTGGGGCGCGCTGTGGACAT  
GCAAAACGAGGATGAGCGGAGCACTGTCTTTCCAGATTACGACGGGCGACGGGC  
GCACTTTGACGACTTACAAAGCCGTGGGCGGGTACTGGAGGTTTCGGACAGACCTG  
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### Nucleotide

>PpEXPA-28

ACATTCCCGCTGCATCTGATGTATTAGGCCGTGAGCTCCCTTCGATCCCTCCACTT  
GCAGGACCAAGTTCATGTACCATCTCATCCTGATGAGCGCACACAGAAACCGAG  
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CTAACACGTCGTCATGAGGACCCCGGGCGCTGCATCCACCATGAAGGTCGCAGCT  
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CGTACTTCTTGATGATCCTGATTCACAACGTGGGAGGGGGCGGGCGATTTGAAGGC  
AGTGAAGGTCAGGGGAGGAAACGGATATTGGGTGCCCATGTGGCGCAACTGGGG  
CGCGCTGTGGACATGCAAACGAGGATGAGCGGAGCACTGTCTTTCAGATTACG  
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GAAGCGGATCTTGCAAGTCCCATCGACGAGACGACAACGTGTGGAGATGTAGAA  
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ATGTGATCGCATTGGAATCGTGCGCTTGTCAAGTCCCATTTGCCGGTCATGCCAC  
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