

IDENTIFICATION

Species: *Physcomitrium patens*

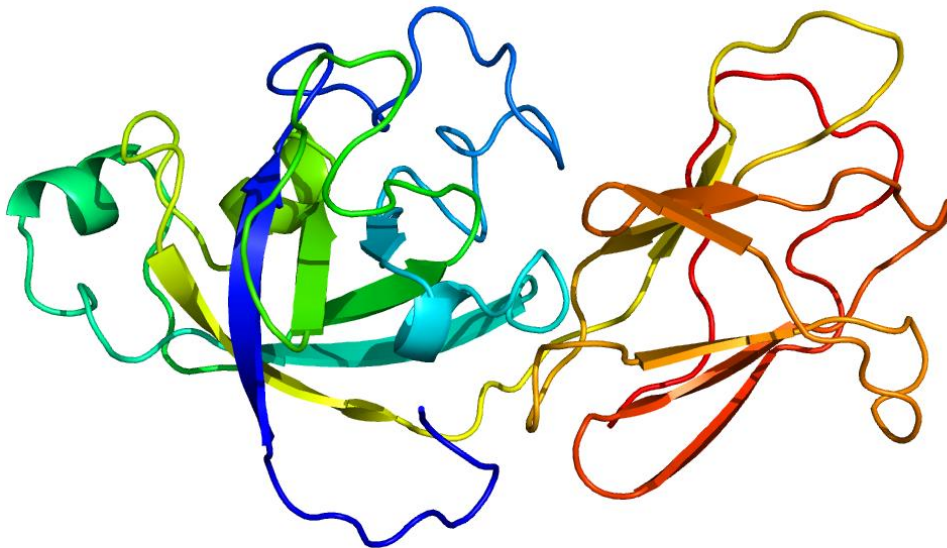
Locus: Pp3c7_12810V3

Gene Model: Pp3c7_12810V3.2.p

Description: PpEXPA-04

Family: Alpha Expansin

3D structure:



GENOME DATABASES

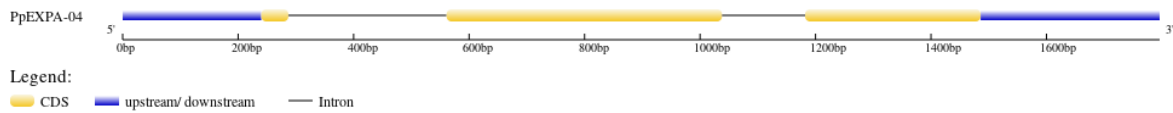
Phytozome: https://phytozome-next.jgi.doe.gov/info/Ppatens_v3_3

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

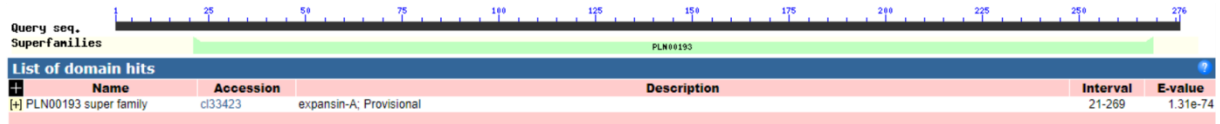
EXTERNAL RESOURCES

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GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>PpEXPA-04

MQSPGIALGRKRVLRSCTPKMSGLTRVEVTFVMFVATLVIPSVLGMPLVGVWRDAHITY
YGSPNGGGTQGGACAYQNTFSLGYGAMTAALSSPLFEGGAACGACYQLQCKRVQE
TRTVKNWCWSYSRTITITATNLCPPGSAGAWCDPPRHFDLTMFAFLTLARREGGVA
PVLYRRVKCVKRGIRFTIGGNPWFLMILIHNVAGAGDVRAVRIKTPSTDWIPMYRN
WGALWTVQRKLSGPLSFQITAGDRRQITINSAVGNAWKFGQWEGHNFR*

CDS (coding sequence)

>PpEXPA-04

ATGCAATCGCCCGGCATTGCTCTTGGCAGAAAGAGAGTGCTTTTCGAGGTGCACCC
CAAAGATGAGCGGCCTAACTCGTGTGGAGGTCACCTTTGTGCATGTTTGTGCTAC
GCTGGTTATAACCGTCGGTGCTTGAATGCCGGTTGGATGGCGCGATGCGCACATC
ACCTATTACGGGTCACCTAACGGTGGAGGAACACAGGGTGGCGCTTGC GCGTATC
AGAACACATTCTCGCTGGGCTACGGTGCCATGACTGCGGCGTTGAGCTCGCCTTT
GTTTGAGGGTGGAGCGGCTTGTGGGGCTTGCTACCAGCTTCAGTGCAAACGAGTG
CAAGAAACCCGTA CTGTGAAGAACTGGTGCTGGAGTTATTCTCGAACCATCACCA
TACTGCCACTAACCTCTGTCCACCAGGCTCTGCCGGGGCGTGGTGCGACCCTCC
AAGGCACCATTTTCGACTTGACAATGCCTGCCTTCCTAACCTGGCGAGACGTGAA
GGTGGTGTGGCTCCAGTGCTATA CAGAAGGGTTAAATGTGTCAAACGCGGTGGA
ATTCGGTTCACCATAGGAGGCAATCCTTGGTTTCTGATGATCCTCATCCACAACGT
CGCTGGCGCAGGCGATGTAAGGGCCGTTAGAATCAAGACCCCGTCCACTGACTG
GATTCCCATGTACCGCAACTGGGGTGC GTTGTGGACAGTACAAAGGAAACTCAGC
GGGCCCTCTCATTTTCAGATCACTGCCGGCGACCGCCGTCAAATCACCATCAACA
GTGCAGTAGGCAATGCATGGAAGTTTGGACAAACCTGGGAGGGCCACA ACTTCC
GCTGA

Nucleotide

>PpEXPA-04

GGCACAGATTTTCGATACTGTGGCTCCTTCGTCTGCGCAGTCAAGCGTAGCGTTCA
TAACTTCCCTTAGGAGAGAGGTTATCTATCATATATTGAGTTCGGCCAAAACCAC
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TCTTGTA ACTGTTGCTTGTCTCGT GACTGTTACAGCAGTGTGAGGATTCAATCCG

CAACTTCCACCCAGCCCCATGCAATCGCCCGGCATTGCTCTTGGCAGAAAGAGAG
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CGGGAGCAGGAATGCCGTCTTTGGTAGAACTATTTAGAGGATTGGGTCTAAGGAA
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GTGCAAACGAGTGCAAGAAACCCGTAAGTGTGAAGAACTGGTGGTGGAGTTATTCT
CGAACCATCACCATCACTGCCACTAACCTCTGTCCACCAGGCTCTGCCGGGGCGT
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GGCGAGACGTGAAGGTGGTGTGGCTCCAGTGTCTATACAGAAGGTACATTACCGC
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CAGGCGATGTAAGGGCCGTTAGAATCAAGACCCCGTCCACTGACTGGATTCCCAT
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