

IDENTIFICATION

Species: *Physcomitrium patens*

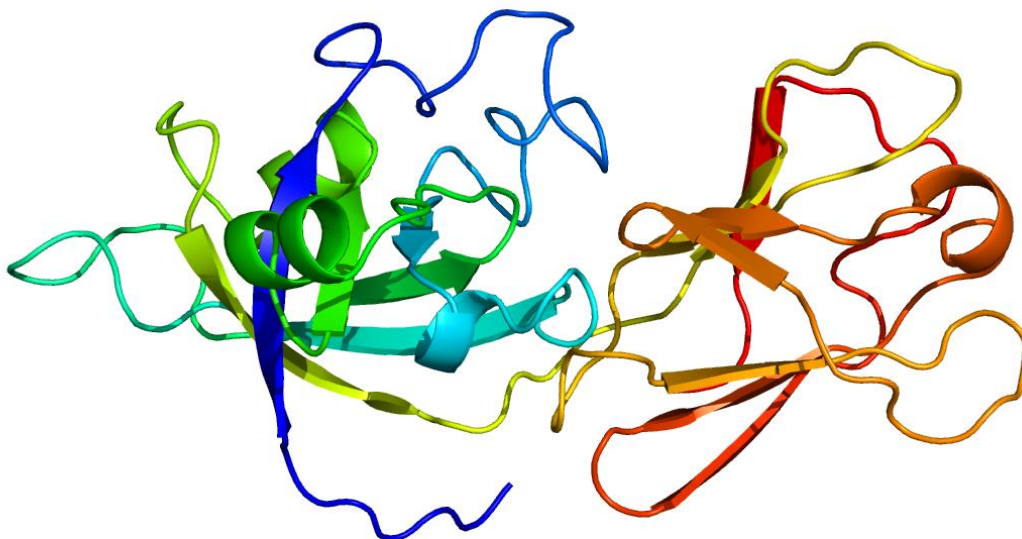
Locus: Pp3c1_37980V3

Gene Model: Pp3c1_37980V3.1.p

Description: PpEXPB-01

Family: Beta Expansin

3D structure:



GENOME DATABASES

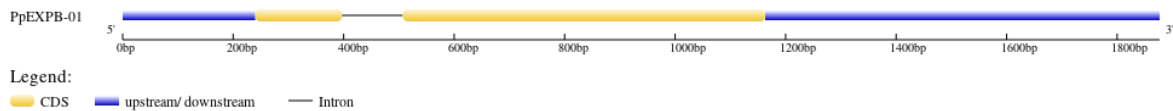
Phytozome: https://phytozome-next.jgi.doe.gov/info/Ppatens_v3_3

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

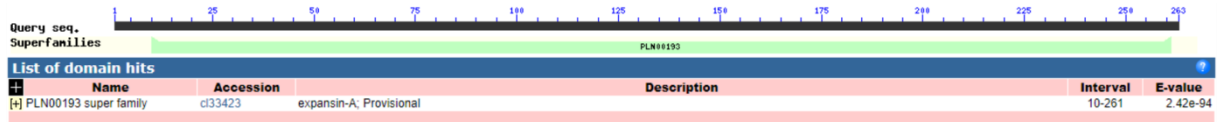
EXTERNAL RESOURCES

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GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>PpEXPB-01

MAMVVRGNAFAAVLTLVVALDLVARVMLVQASSYLGTNWVSGRAHATFYGGADAS
GTQGGACGYGNLYSTGYGTSTAALSSALFNSGLSCGACYELTCDTSGSKYCLPGNPSI
ILTATNYCPQNSNGGWCDAPKQHFDLAHPMFVSLAEERGGVIPVNYRRVPCAkkGG
MRFQMNGNPWFLLVLVTNVGGAGDVQQLSIKGSNSGWYQMKRNWGMWQLTGN
SNMPGQALSFRVLSDGTTVESLDAAPANWHFGQMFEGSQA*

CDS (coding sequence)

>PpEXPB-01

ATGTCGACGGCTTTCCAAGCGGTGTGGCTGGTGTGTGTGGGCCTTTTGAGCCTGC
AAGCAGCCGAAGCGGGCTATTTGGCCCAGAATGGATACCACGAGCGATGGGTCC
GCGCTCGCGGCACCTGGTACGGGGATCCTTATGGCGAAGGCTCTAGCGGAGGAA
ACTGCGGATACACTAAGCTTTGGGGCACACCCATCGGGCCTAAAATTGTTGCCGG
AAGCAGGTCAATCTATGCTAATGGGCAGGGTTGCGGCCAATGCTATCAAATCAGG
TGTGTTGATCCAAACGGAGGACCCAGGCTCTGCAATCCTCAAGGCACGAACGTCG
TCGTGACTGATTTCTGTCCCGGTGGAACCTTACTGCAGCACCGGGGAAAATGCCTT
CGACATGAGCGGGGCCGCGATAAATGCAATGGCGTTGCGTGGGAGAGAAGGCCA
GCTCCGCAACCGTGGTTTGTACAACCTGCTCTACAAGAGAGTCCCTTGTGCGATAC
AGGGGTACCAATATAGAATTCCTGTGTTGATAACGGCTCCAGTCCCTTCTGGCTCA
GTATTTTGATAAAGTACGTGGGAGGGCCTGGTGACATTGGTCAGGTGTACATTAG
GATGGCGAACTGGTATAAGTTCCAGCCGATGAGGCATGCGTGGGGCGCTAACTG
GATGATTTCCAACTACGACGGGAAGCCGTTTCAGGGGCCCCATGGATATTAGAATT
GTATCGAGATTGAACCGTCACACAGTGCTTGCTAGAGGAGTCATTCCCGCCTACT
TCAGACCTGGAACGTCTTACAGGTCTAGAGTGCAAATGGCTTTTTAG

Nucleotide

>PpEXPB-01

ACCGCAAACAGTTAGTATGTTATTGGTTTACTTTTCTTCTTCCTCCACCCTCGAAC
CCCCATATAAACTTCATCCTCGTTCTCAAGTGACATCGATCAAGAATCTGCAGGT
GAAGCATTCTGTCTCATTTCGGTTAATTAATTTTCAGGTTTCAGCGATGTTGTAGCA
GCACCGGAACGTCAGTCGGTTACCTTGGTTCTCAGCAAGGTCGGATTCCCCGAGA
GCTCACAGCGTTACTGCTATGTCGACGGCTTTCCAAGCGGTGTGGCTGGTGTGTG

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AGGCACGAACGTCGTCGTGACTGATTTCTGTCCCGGTGGAACCTTACTGCAGCACC
GGGGAAAATGCCTTCGACATGAGCGGGGCCGCGATAAATGCAATGGCGTTGCGT
GGGAGAGAAGGCCAGCTCCGCAACCGTGGTTTTGTACAACCTGCTCTACAAGAGA
GTCCCTTGTGATACAGGGGTACCAATATAGAATTCCGTGTTGATAACGGCTCCA
GTCCCTTCTGGCTCAGTATTTTGATAAAGTACGTGGGAGGGCCTGGTGACATTGG
TCAGGTGTACATTAGGATGGCGAACTGGTATAAGTTCAGCCGATGAGGCATGCG
TGGGGCGCTAACTGGATGATTCCCAACTACGACGGGAAGCCGTTTCAGGGGCCCC
ATGGATATTAGAATTGTATCGAGATTGAACCGTCACACAGTGCTTGCTAGAGGAG
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