IDENTIFICATION

Species: *Physcomitrium patens*

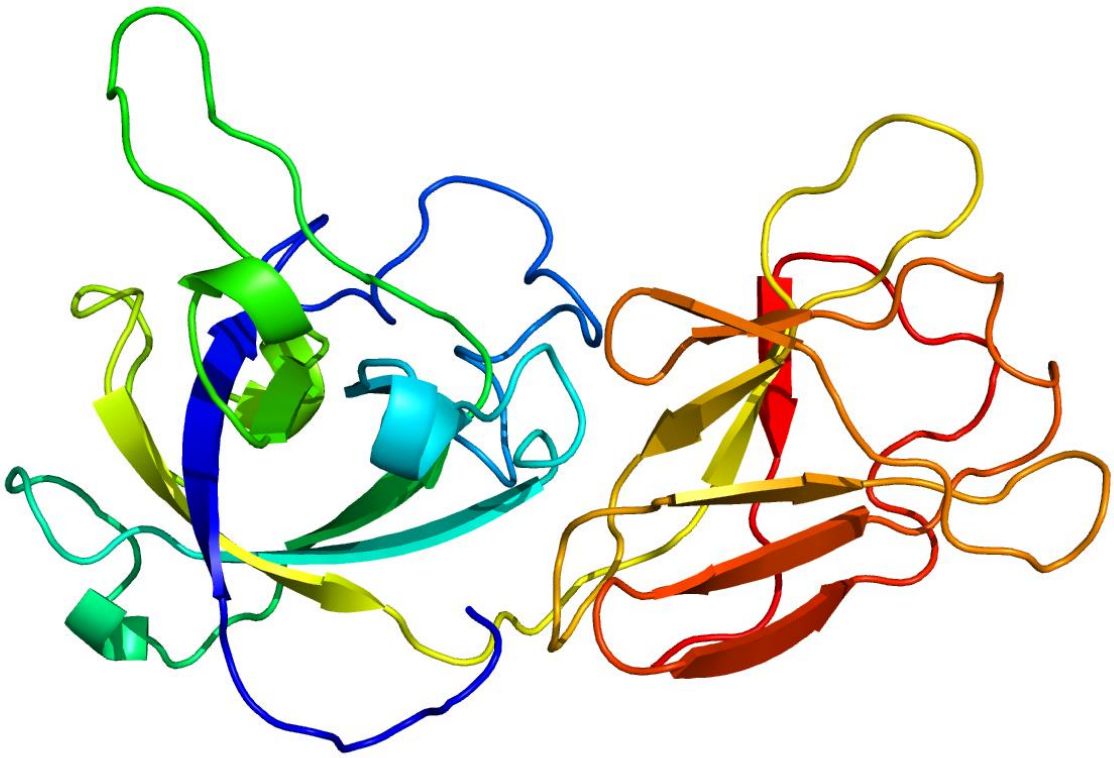
Locus: Pp3c20_5780V3

Gene Model: Pp3c20_5780V3.1.p

Description: PpEXPA-32

Family: Alpha Expansin

3D structure:



GENOME DATABASES

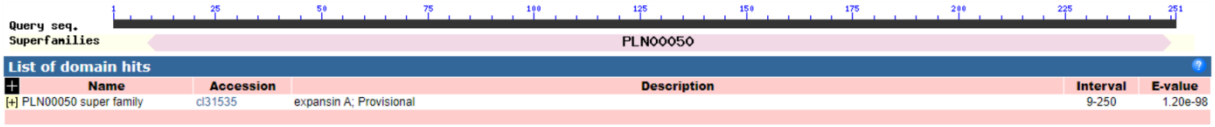
Phytozome: https://phytozome-next.jgi.doe.gov/info/Ppatens_v3_3
KEGG: https://www.genome.jp/entry/gn:T01041

EXTERNAL RESOURCES

-

GENE STRUCTURE

DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>PpEXPA-32

MAKFSAQIVVAFMVLLAQQVRAESGWNEAHATFYGGSDAGGTTGGACGYGDLYST
GYGTSTVAISSALFDRGLACGACYQVKCAGSSSECRSDSPAIQVTVTNFCPPNPSLPED
NGGWCNLPLHHFDMSMPAFEQIATYKAGIVPVMYRRTSCVRTGGIHFTMSGHNFMN
LVLVTNVGGMGDVQSVSIRGSKTSWVTMTRNFGQIWQSTVNMSGQSLSFMVTTSDG
KTVVSNNVAPPDWAFGQTYEGSQF*

CDS (coding sequence)

>PpEXPA-32

ATGGCAAAGTTCTCAGCCCAGATTGTGGTGGCGTTCATGGTGTTGTTGGCGCAAC
AAGTTCGTGCTGAAAGTGGATGGAACGAAGCTCATGCTACATTTTACGGTGGTAG
CGATGCCGGTGGCACAACAGGTGGTGCTTGCGGGTACGGAGATCTCTACAGCACT
GGCTATGGCACCAGCACAGTCGCCATAAGCTCAGCTCTTTTCGACCGTGGCCTCG
CATGCGGTGCGTGCTACCAGGTGAAGTGTGCGGGGAGTTCCTCCGAGTGCCGCTC
TGACAGCCCAGCTATTCAAGTTACTGTCACCAACTTCTGCCCTCCTAATCCCTCCT
TGCCTGAAGACAACGGCGGATGGTGCAACCTCCCTCTGCATCATTTCGACATGTC
CATGCCTGCCTTCGAGCAAATCGCAACTTACAAGGCCGGCATTGTGCCTGTGATG
TACCGAAGGACTTCTTGTGTAAGGACTGGTGGCATTCACTTCACCATGAGCGGTC
ACAACTTCATGAACTTGGTGCTTGTCACCAACGTCGGAGGCATGGGGGACGTGCA
ATCCGTGTCCATTCGAGGTTCCAAAACTAGTTGGGTGACAATGACCAGGAACTTT
GGGCAGATATGGCAGAGTACCGTCAACATGAGCGGCCAGAGCCTCTCCTTTATGG
TGACGACTAGCGACGGCAAGACTGTGGTCTCCAACAACGTAGCGCCTCCCGATTG
GGCGTTCGGCCAAACATACGAAGGATCGCAATTCTGA

Nucleotide

>PpEXPA-32

TGATAACGGGGGTACTTAGTCCGGCCGACGCTGTAGGGGGCAGCCATGCACATG
ACTGACTGACCGACCGACCGCCGCTGTTGCTGCTTCTGCTGCTCGCTCTCCGCCTG
CGCGCTTCGCATCCGCCCTCGCTGCGGCACCAGCACCAGCACCACCAAGGCACGC
GAGGCTACATCACGTCAGTGCGCTGTGAACGGGGGATTTTGAGCCGGGGCAGGG
GCTGTTGTTGGTCCCTGCAGCTTCATTCATTCATTCACTCACATACACACACTTAC
ATAGATACACATACCCTCCCACCCACTCATCCACCCACTCATGCACCCACTCTTCC

CGGCGCTGCATGTTATGATCCTCATCACCTGCTGTGACCAAACGCTCTCCCTGCTT
CTGCTACTCCACAGATTGCATGTGTGCTTCTCGTGCGTGTCTCTCCTGCACCAAGA
GCTAACCCCGTGAAACCGACGCCCTTGTCTGCTGGGTTATTTCCCCGCCCGTGAA
GGTTGCGAGATTGGGTTGTGATCGCGTGGTGGTGTTCGTTGTGTGAAGTGTGACA
ACTTTCTTGTCCAGCGTATAGACTTTCGAAGTATGGCCATGGGTTTGGTGCATTTG
TGCTTATTCTTAGCAATCTTGTCGTGTGTTGGTTATTGCATTTGCTTGTGTGGTGCT
CTTAGGTTACCGAGTGATGTCCCCAAGCGAAGTTGGGGTAAACATTTTAAGTGAA
AAAATGCAGGGTAAATGAAGCTCTTGTGATGAGCGTCGTGAATAGGACTTCTGGG
TGCAGATCGAGACAGAAGAGGTGTAGCTCAGGATCAGGGTATTGAGATTGAGTA
TGTGCGAGCTATTAGTTTCGGGGTTCTGAAGCTGCCGCAGTCAGTGCAAGGGCGT
TTAAGAATCAACGACGGCGTTCTTTTATCGCCATGTCAATTTGCACATGCTCTGCA
ATAATGATTTAGTAGTGGGGTTGAGCGTGGCCTAATCAGAGGACGGAATGGGCTT
ATTCCTTGTGCAGAACTATGGCAAAGTTCTCAGCCCAGATTGTGGTGGCGTTCAT
GGTGTTGTTGGCGCAACAAGTTCGTGCTGAAAGTGGATGGAACGAAGCTCATGCT
ACATTTTACGGTGGTAGCGATGCCGGTGGCACAACAGGTACTCGAGGCTCCACCA
TAGCCGAGTCCAAACTTGCAACTCGTTCACTTAACTCACTGCCCTAAGGTTGTGTA
GTTAAGACATAAAGTGAATCTCTCCGGTTGTTCATTCAGGTGGTGCTTGCGGGTA
CGGAGATCTCTACAGCACTGGCTATGGCACCAGCACAGTCGCCATAAGCTCAGCT
CTTTTCGACCGTGGCCTCGCATGCGGTGCGTGCTACCAGGTGAAGTGTGCGGGGA
GTTCCTCCGAGTGCCGCTCTGACAGCCCAGCTATTCAAGTTACTGTCACCAACTTC
TGCCCTCCTAATCCCTCCTTGCCTGAAGACAACGGCGGATGGTGCAACCTCCCTCT
GCATCATTTCGACATGTCCATGCCTGCCTTCGAGCAAATCGCAACTTACAAGGCC
GGCATTGTGCCTGTGATGTACCGAAGGTGTGCAGTTGTGATTTGCACGCTCATTGT
CAGTTTTGGAATCCTCGAGAATTTTCCGACAGGTCGTGATTGTTAACTTGTGTGAT
GTTTTTGAAAATTTCAGGACTTCTTGTGTAAGGACTGGTGGCATTCACTTCACCAT
GAGCGGTCACAACTTCATGAACTTGGTGCTTGTCACCAACGTCGGAGGCATGGGG
GACGTGCAATCCGTGTCCATTCGAGGTTCCAAAACTAGTTGGGTGACAATGACCA
GGAACTTTGGGCAGATATGGCAGAGTACCGTCAACATGAGCGGCCAGAGCCTCT
CCTTTATGGTGACGACTAGCGACGGCAAGACTGTGGTCTCCAACAACGTAGCGCC
TCCCGATTGGGCGTTCGGCCAAACATACGAAGGATCGCAATTCTGACTCCAAATC
AAAGACGTAGAATGTCTACTAAACCATTCCTGACTTGCATCAGCTCCATGTTCAC
TTGAACATTCAGGAGGATCAGTGCATTGGGTGAATTCATTTTTGAAGTTATTGAA
GCAATGGGTGCCACATTGGCTAATGCGGTGTTAGAGCTATAGCCATCCATGGCCC
ACGGTGAGGATGCTAAGTACGGCAACCCAATGTGGTGGAGAATTATTAATATGTG
TATATGCAGTAGACAGTCCAGATCTGAAGAAGAGTAGGAGCTTAGGTTATCTAGT
CTGAGTGGCCGGTACAACACCCCTAAAATCGTTCAAGCTTGTACATTGTCGGTGT
CTCTTTCCACTGTGGTCTTCACCTTTCCTTTCAATGCAACAGTTGAAACTAAGTCC
CTTGTACTTAACGCGGTGCATTTGTATCCGTTGTGTTTCAGTGAATAATATCACGT
TGTGAAGTGTGGATAGTAGAGATTTAACTCGTGCTCACATGTCAAATCTGTGATG
CAGTTGAGGAAGTGCAGCTTGTGACACTGTTGAAATCAATGTTTTGTAATTAATG
CCAAGCAGAGTCTAGTGGTGACTCGTGAACCTTGTG