

IDENTIFICATION

Species: *Physcomitrium patens*

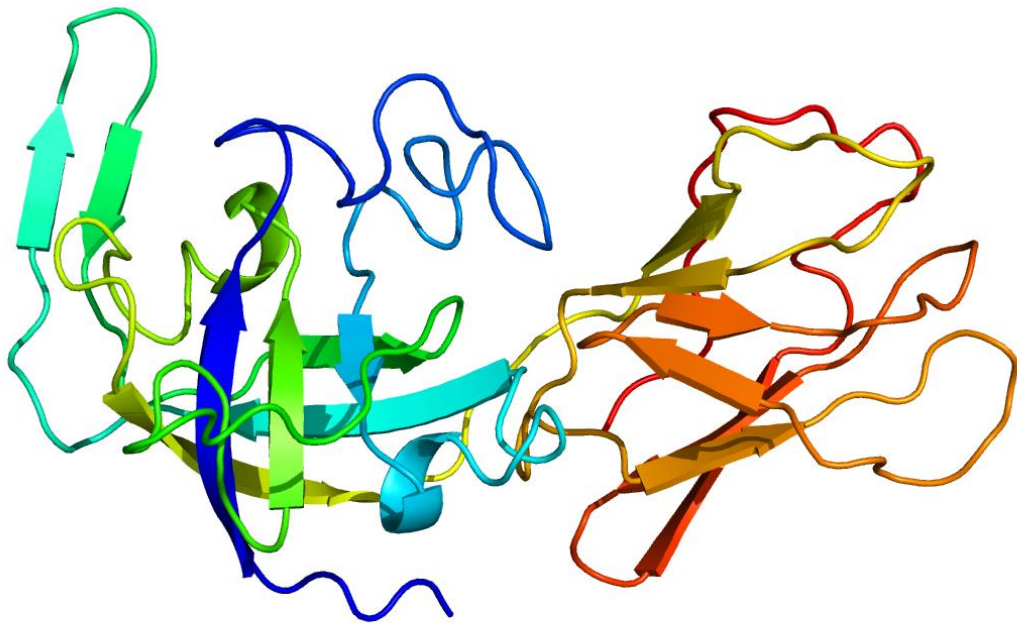
Locus: Pp3c7_12940V3

Gene Model: Pp3c7_12940V3.1.p

Description: PpEXPA-06

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>

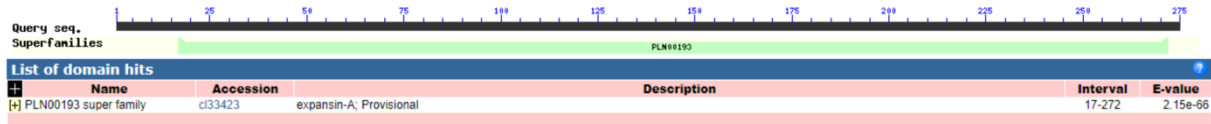
EXTERNAL RESOURCES

-

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>PpEXPA-06

MMLAMFNCSSSNRKMSAASCMKLAVFLLVQLVLFAPAVLGAPPRGWSSGRITYYYGS
 PNGGGTQGGACGYQNTVSLGYGFMTAALSTPLFNGGAACGACYQLQCAPVHETPK
 NLLQRNWCWKVGRRITITATNLCPPGSEGGWCDPPQHHFDLPMPAFTALAKREGGV
 VPIYYRRVRCAKQGGIRFTMGGNPWFLMILIHNVAGAGDVVAVKIKCPTSDWCDMY
 RNWGAFWTVQKKMEGPLSFQITTGDRRKVTTHNAVGHGWQFGQTWEGAQYR*

CDS (coding sequence)

>PpEXPA-06

ATGATGTTGGCAATGTTCAATTGCAGTTCGAGCAACAGGAAGATGAGTGCTGCAT
 CCTGTATGAAGCTCGCGGTGTTCTGCTCGTTCAGTTGGTTCTGTTTGCGCCTGCT
 GTGCTTGGTGCGCCACCGAGAGGGTGGTCGAGTGGCCGAATCACCTACTACGGCT
 CGCCTAACGGTGGAGGAACCCAGGGAGGCGCTTGCGGATACCAGAACACAGTGT
 CACTGGGGTACGGGTTCATGACTGCGGCTCTGAGCACTCCTTTGTTTAACGGCGG
 AGCAGCATGTGGGGCGTGTTATCAGCTCCAATGCGCTCCAGTGCACGAACTCCA
 AAGAATTTACTCCAGAGAAATTGGTGCTGGAAGGTGGGTCGAAGGATCACCATC
 ACCGCTACTAACTTGTGCCCTCCAGGCTCTGAGGGAGGATGGTGCGATCCTCCTC
 AGCATCACTTTGACTTGCCAATGCCCCGCTTTCACGGCCCTTGCAAAACGCGAGGG
 AGGTGTTGTTCCAATCTACTACAGGAGGGTCAGGTGTGCGAAGCAAGGTGGAATT
 CGATTCACGATGGGAGGGAACCCTTGGTTTCTGATGATCCTCATCCACAACGTAG
 CTGGCGCAGGTGATGTGGTAGCTGTGAAGATCAAGTGCCCTACTTCTGATTGGTG
 TGACATGTACCGGAACTGGGGTGCATTTTGGACTGTGCAAAAAAAGATGGAGGG
 GCCGCTTTCCTTCCAGATCACGACGGGTGATCGGCGCAAGGTGACTACCCACAAT
 GCAGTTGGTCACGGTTGGCAATTCGGGCAGACCTGGGAGGGCGCCCAATATAGG
 TGA

Nucleotide

>PpEXPA-06

GTGCCTTGTAAGGTGGTATCATTGCTGTAGCCTCCTTTGAAAGGTCTGGAAGAGT
 ATGTACTTGTTCAGCCTTCTTCATGATGTTGGCAATGTTCAATTGCAGTTCGAGC
 AACAGGAAGATGAGTGCTGCATCCTGTATGAAGCTCGCGGTGTTCTGCTCGTTC
 AGTTGGTTCTGTTTGCGCCTGCTGTGCTTGGTGCGCCACCGAGAGGGTGGTCGAG

TGGCCGAATCACCTACTACGGCTCGCCTAACGGTGGAGGAACCCAGGGAGGCGC
TTGCGGATACCAGAACACAGTGTCACTGGGGTACGGGTTCATGACTGCGGCTCTG
AGCACTCCTTTGTTTAACGGCGGAGCAGCATGTGGGGCGTGTTATCAGCTCCAAT
GCGCTCCAGTGCACGAACTCCAAAGAATTTACTCCAGAGAAATTGGTGCTGGAA
GGTGGGTCGAAGGATCACCATCACCCTACTAACTTGTGCCCTCCAGGCTCTGAG
GGAGGATGGTGCGATCCTCCTCAGCATCACTTTGACTTGCCAATGCCCGCTTTCAC
GGCCCTTGCAAAACGCGAGGGAGGTGTTGTTCCAATCTACTACAGGAGGGTCAG
GTGTGCGAAGCAAGGTGGAATTCGATTACGATGGGAGGGAACCTTGGTTTCTG
ATGATCCTCATCCACAACGTAGCTGGCGCAGGTGATGTGGTAGCTGTGAAGATCA
AGTGCCCTACTTCTGATTGGTGTGACATGTACCGGAACTGGGGTGCATTTTGGAC
TGTGCAAAAAAAGATGGAGGGGCCGCTTTCCTTCCAGATCACGACGGGTGATCG
GCGCAAGGTGACTACCCACAATGCAGTTGGTCACGGTTGGCAATTCGGGCAGACC
TGGGAGGGCGCCCAATATAGGTGACGAATCAGTCTTGCCAGTCTGCACGGAGAA
GGGATTTGATTGAAAATGATGGCTCCTACGATCCGCGCTGTGCCTGTGGCAGATC
GGCAGGCCCGCGTAGGACCACAGGGAGGGTCGCAATGTCAAATGCTAGCTTCTTG
GCGCGTAGTCGATGGGCTTCGTTTGTGAGTCTTTTAGAACTAGGTAGAAATTGAG
CTTGTTACACGCAGTTGGAAGGAATCCGTGCTGTGCTTATACTGATGTCACTCACA
AGCTGGGTGTTTTTCGATGTTTGTGTATGGGTTTTTAGGCTGCATCCGGCCGAGCAG
TGCTGATAAAAATCTGCCGCCTGGATTGATTAGTTGGCGTGGTTTAGCTGACTGC
GCAGTCGCCAATAATATGTACCCTAGGACGAAATTGTAGACATTATGCAAAATAA
GAGCACATTGACATTCTACGATTATTATTAGCTCCTCTTAAGATGTTTCTTGTTAA
AATTTAGAGATGGCTGCAGAGTTGCAGAGCTTACCAGCCATATTAGGTGACATGT
TTCGCGCAATGTTTTACACATAAATTGGCTCTAATCAGCAGTCGGACTACATAAG
ACCTTGGGCAGCATGCAGCGCCTGCCTATTCTCCCCGTAATGGAGGTTGTGGTCG
AACTAATCTTAGCCGCGACTCCCGACCTAGAACGGAAGCTACCCACCACAATCTT
ACGATTTTGCAAGTATTTGTTCCCTGGTTATTGCCGACAAAAGAATATATGAGTT
TACTTGTGAGGACGTGATGGTCACATCTTTTAATCTCAAGTTGCAATTCATTTGC
GAACAATGACGATCTATTTGAGTCATTGAAGTCAAATCGTAAGGAGCTCTTCTAT
TAATTATTTGTTTCATGAACCAGCTACGACTAGATTGTACTCCAAGAATTGAATAG
CTTGTAATTGGTTTTTTTTGTCAACATGTCAATAGTGTGAGGCTTGACTGTGGAAG
TGGCAGCACGAAGCATGATACGGATAAGTGTGTGACATGATATTGAGTAACGCA
TGTGGCATGATTTTGGGTAACCATTAGTTCTTCATGTTGGAACGATTGGAAGTGTG
CTTCATCAGGAAGTACTCGTTTGTTGACATCATCAGTCACTATTTGAAGGCATTTG
GATGACGGTAGAGAACTGGAAAATCCAGAAGACCGTGGCCGACAACAACATTAT
CAACAATTGCACCAGAACTTGAGGCTCAGTTTTACTCCAAAATTTTATACTCTCTT
TGCAGCATGAACTGGCTACAACCTTGTATTTTCCGTCGAGCATCGTGGTGTTATG
AAAAGGTTTAGACTCGCCAACCGCTCAGTGAACCTTCAGAAATGCATAGTACCCACT
GTAAAGCAGCCTTGAGAAAATTGCTTCATTATTAGTACGTGGTGAACATACTTT
CCACCCTTGCTGAACTCATGTAAACGAGTGGGGAAACGATAAATAAATAACA
AATAATGGAGGCACCAAGTGGTGACACAAGCTTGAAATATGTATGCACGCGGAT
CAGCTACGATTGTGTCTCCCTGTTTAATTATCTACTTCTCAAATGTACAGAATTA
TTGGCTTTATATTTACATCCGGCGCATCGACCGTTGTGCATCTGATGCATTCTTC
CGTCGGTCGGGCTCCGCAACCTGCGTCACTGCAGGGCTGAAGATCGGCCGCCGAA
TGTGCACCCGTGCGAGTTCCAGCCGCCCGATGAAGAAGGGCACGAATAGCGGCA
CTCGTGGTTCGCAACGCGAGGGATTCCGACGAACATCCATTCACCGGATTCCTTG
TCTATGGTTACTACGGATAATTTAGGGCTGTTGGGAATGAGAGCAACAAAAAGTA

GCAGGAACATCCCTACTTTCTGAAGCAACCATGTGGCTGGGAGGATCCATTACGA
GAAAGTCACGCCGTGCAAG