

IDENTIFICATION

Species: *Physcomitrium patens*

Locus: Pp3c13_8440V3

Gene Model: Pp3c13_8440V3.1.p

Description: PpEXPA-21

Family: Alpha Expansin

3D structure:



GENOME DATABASES

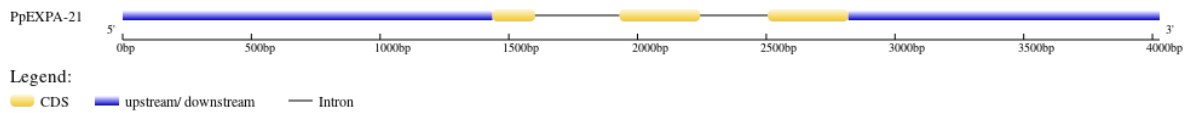
Phytozome: https://phytozome-next.jgi.doe.gov/info/Ppatens_v3_3

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

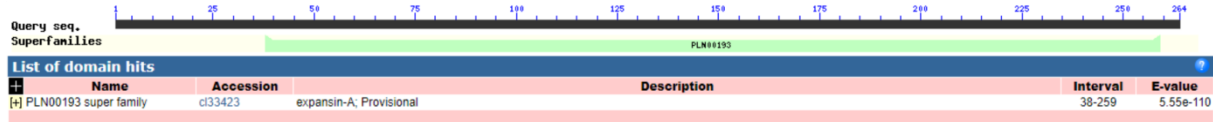
EXTERNAL RESOURCES

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GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>PpEXPA-21

MARHNATKPVTLLAALMVLSATDNVEGRHHVRDVGKNWRKAHATFYGGADASGT
MGGACGYGNLYSTGYGVDSTALSTALFNNGAKCGACFAIQCYRSQYCVPGSPVITV
TATNFCPPNHKGDGTPGWCNPPMRHFDLAQPSFTKIAKYRAGIVPVLFRVPCEKKG
GVRFTINGNKYFNLVLVHNVGGKGDVHAVDIKGSNTEWIPMKRNWGMNWQTDAV
MTGQALSFRVTTSDGKTIVSMNATPSHWSFGQTFEGGQFAMN*

CDS (coding sequence)

>PpEXPA-21

ATGGCGAGGCATAATGCAACAAAGCCTGTGACACTCATTCTTGCTGCACTGATGG
TTCTTTCAGCCACCGACAACGTCGAAGGTCGTCATCACGTCAGAGATGGAAAAAA
CTGGCGCAAAGCTCATGCAACTTTCTACGGGGGTGCTGATGCTTCAGGAACTATG
GGCGGTGCATGCGGTTACGGAAACCTCTACAGCACTGGCTATGGAGTCGATTCGA
CAGCTTTGAGTACAGCTCTTTTCAACAATGGGGCAAATGCGGAGCTTGTTTTGC
GATCCAATGCTATCGTTCACAGTATTGCGTTCAGGTTCCACCTGTAATCACTGTCA
CAGCTACAACTTCTGCCCTCCTAACCACAAAGGTGATGGCACGCCAGGATGGTG
TAATCCGCCAATGCGTCACTTCGACCTTGCGCAGCCTAGCTTCACCAAATCGCT
AAGTATAGAGCCGGCATCGTCCCCGTTCTCTTCAGAAGGGTACCATGCGAGAAAA
AAGGTGGCGTCAGGTTCACTATCAATGGAAATAAGTATTTCAATCTCGTCCTAGT
TCACAATGTTGGTGAAAAGGCGATGTGCACGCAGTAGACATCAAGGGATCCAA
TACAGAATGGATTCCCATGAAGCGAACTGGGGAATGAACTGGCAGACAGATGC
TGTTATGACTGGCCAGGCACTCTCCTTCCGAGTGACAACCAGTGATGGTAAGACC
ATAGTCTCTATGAACGCAACGCCATCTCACTGGAGCTTCGGCCAGACCTTCGAGG
GAGGTCAGTTCGCTATGAATTGA

Nucleotide

>PpEXPA-21

AATCGTGTAGCGACTGTTCCCTAGTTTTCGCACCATCACGTATGTCATAGATCCTGTC
GGGTTTTTCTTCGGTGCTTGATACCTATCTGTAAGCTCATGGCGCCTTGAACGATG
ATCTAATTAAGTTGTAGCTACTGTTTCAGCGTTAGTGACAGGAAGGTGGGAGAAAT
TTTCAGTCCACAATTCAAGCCACTCGCGCCTGTGATTTTTGCCGGCTGTAGTACGA
AGCTGAACTGATTTTGGTAAATTCTTATCTCATTGGAAGGTTGCTATCTTCTTGT

TCAATCTAAAATGGCACGCTAATTA AAAACGGGAGTCTCATCATAGTTTTGAGAGT
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AAAGTAGTCTGCATCTGTCTACATGACGCTTCGTACACTTTCCGAAATATTATATC
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ATGAGTGTAAAGAACATGAGACTAGATACTGAAAAAGATAAGAATTGTTTAGAC
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CCTCCTCTTACGCGTGTGTACATACACCCTAGCATTAAAGATAGCTTCTGTCTTT
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TCACCACTTCTTTCTCCAGTGCCAATCTGAAAGAACAGGCCAAATACGGCGCTAT
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TCCATTA AAAACAAGCCTCCCAAGGTACCATAGCAACCTTTCATCTGATCTTTG
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CCTGTTAATCATCTGAGCAGCACGAATAAAAACAATTTGACAGGCTACTTACAGA
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CCTTGAGACATCCAAGTGGTCGTCCTTCCATGTAGCTTTCATCCGGCACGAGCTGC
TCAATGAACGTCGTCTCCTGCACATGAAGAAAGCCGAAGGAAACTGAGAAATAG
TCAGAATGTGTGAAAAACAATGTGTATTACTCCAGAAAACCTATACAAGTGCAC