IDENTIFICATION

Species: *Arabidopsis lyrata*

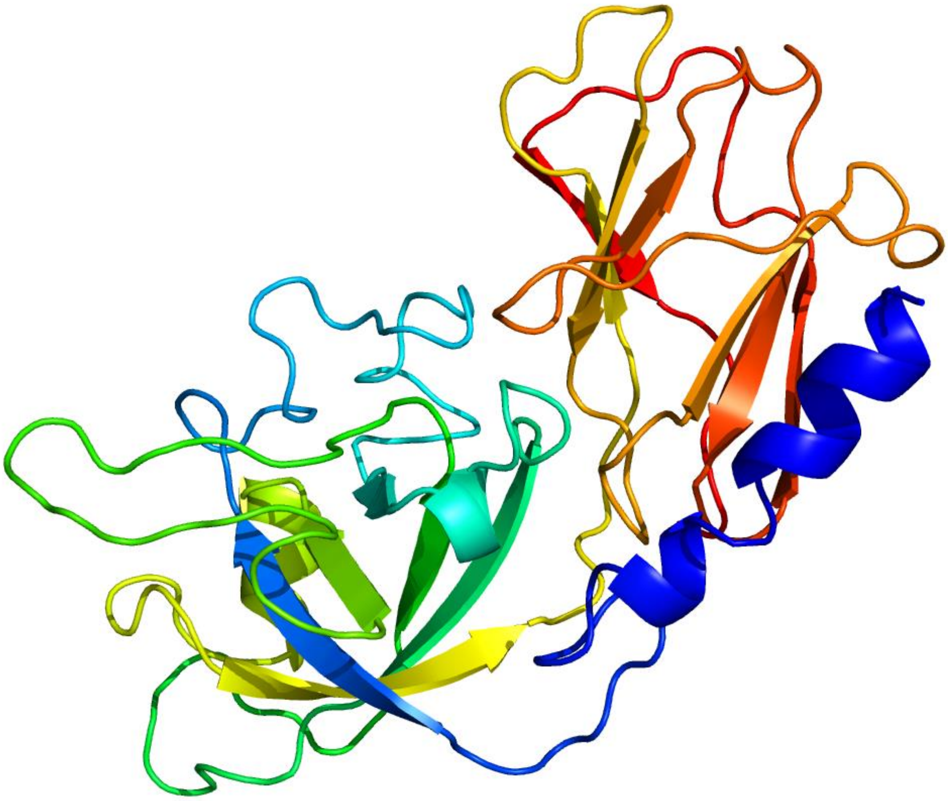
Locus: AL7G10110

Gene Model: AL7G10110.t1

Description: AlEXPA-18

Family: Alpha Expansin

3D structure:



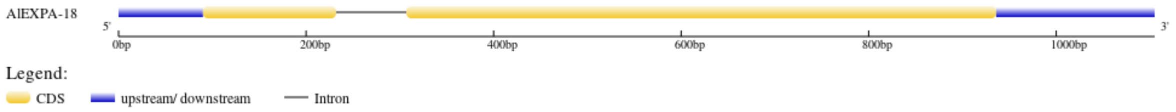
GENOME DATABASES

Phytozome: https://phytozome-next.jgi.doe.gov/info/Alyrata_v2_1
Kegg: https://www.genome.jp/entry/T01578

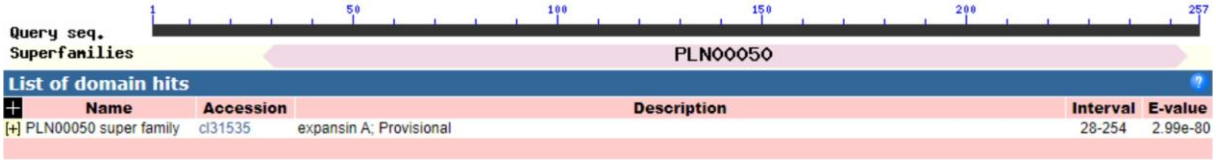
EXTERNAL RESOURCES

https://plants.ensembl.org/Arabidopsis_lyrata/Info/Index

GENE STRUCTURE



DOMAIN ARCHITECTURE



List of domain hits

Name	Accession	Description	Interval	E-value
[+] PLN00050 super family	cl31535	expansin A; Provisional	28-254	2.99e-80

SEQUENCES

Peptide

>AlEXPA-18

MDSGLQQLALCLFFILCRLFQATAEDDWKIATATLSRDRDGSSSVATGGACGYGDLR
QSSFGGYSAGLSGKLFNRGSSCGACLEVRCVNHIRWCLQGSPSVVVTATDFCPPNSG
LSSDYGGWCNFPKEHLELSHAAFTGIAETRAEMIPVQYRRVKCGRRGGLRFSLSGSS
HFFQVLISNVGLDGEVIGVKVKGHTTAWIPMARNWGQNWHSSLDLIGQSLSFEVTLK
GGKTIASYDVAPPYWRFGMTYQGKQFHS*

CDS (coding sequence)

>AlEXPA-18

ATGGATTCTGGGCTTCAGCAACTCGCATTGTGCCTCTTCTTCATTCTCTGCCGCCT
CTTTCAAGCCACTGCAGAGGATGACTGGAAGATAGCCACAGCCACGCTTTCTAGA
GACAGGGACGGCTCCTCCTCCGTCGCTACTGGAGGCGCTTGTGGGTATGGAGATC
TGAGGCAGAGCAGCTTTGGCGGGTACAGCGCAGGCCTGAGCGGGAAGCTGTTCA
ACAGGGGAAGCAGCTGCGGAGCTTGTCTAGAAGTGCGGTGCGTGAACCACATCC
GGTGGTGCCTTCAAGGCAGCCCCTCCGTGGTGGTCACCGCCACCGATTTCTGTCCT
CCCAATTCGGGACTCTCCTCCGATTACGGAGGTTGGTGCAACTTCCCAAAGGAGC
ACTTGGAACTATCTCATGCCGCTTTCACAGGGATCGCAGAAACTAGAGCCGAGAT
GATACCTGTACAGTACAGGAGGGTCAAGTGTGGGCGGAGAGGCGGGTTGAGATT
CAGCTTGAGCGGGAGCTCCCACTTCTTCCAGGTGTTGATAAGCAATGTGGGCCTC
GACGGGGAAGTGATTGGAGTGAAAGTGAAGGGCCATACAACGGCTTGGATCCCA
ATGGCCAGAAACTGGGGACAGAATTGGCACTCCTCTCTTGACCTCATTGGACAGT
CTCTCTCTTTCGAGGTTACTCTCAAAGGCGGCAAAACCATTGCCTCTTATGATGTG
GCTCCTCCATATTGGCGCTTCGGAATGACATACCAAGGAAAGCAGTTCCACTCCT
GA

Nucleotide

>AlEXPA-18

ATGATCAAAAGGAACCCCCAAAACCCTCTCAAACGCGTCACTTTTGTCTGCCACC
TGTGACTGTGAGGATCCCAACAACACTTCTTGTTCATGGATTCTGGGCTTCAGCA
ACTCGCATTGTGCCTCTTCTTCATTCTCTGCCGCCTCTTTCAAGCCACTGCAGAGG

ATGACTGGAAGATAGCCACAGCCACGCTTTCTAGAGACAGGGACGGCTCCTCCTC
CGTCGCTACTGGTTTTTTCCTCTCTCTCTCTCTCTATTTTTCTTTCTTTTTTCATCAG
GACTGACTAGACTAATTGGTCCTAATAGGAGGCGCTTGTGGGTATGGAGATCTGA
GGCAGAGCAGCTTTGGCGGGTACAGCGCAGGCCTGAGCGGGAAGCTGTTCAACA
GGGGAAGCAGCTGCGGAGCTTGTCTAGAAGTGCGGTGCGTGAACCACATCCGGT
GGTGCCTTCAAGGCAGCCCCTCCGTGGTGGTCACCGCCACCGATTTCTGTCCTCCC
AATTCGGGACTCTCCTCCGATTACGGAGGTTGGTGCAACTTCCCAAAGGAGCACT
TGGAACTATCTCATGCCGCTTTCACAGGGATCGCAGAAACTAGAGCCGAGATGAT
ACCTGTACAGTACAGGAGGGTCAAGTGTGGGCGGAGAGGCGGGTTGAGATTCAG
CTTGAGCGGGAGCTCCCACTTCTTCCAGGTGTTGATAAGCAATGTGGGCCTCGAC
GGGGAAGTGATTGGAGTGAAAGTGAAGGGCCATACAACGGCTTGGATCCCAATG
GCCAGAAACTGGGGACAGAATTGGCACTCCTCTCTTGACCTCATTGGACAGTCTC
TCTCTTTCGAGGTTACTCTCAAAGGCGGCAAAACCATTGCCTCTTATGATGTGGCT
CCTCCATATTGGCGCTTCGGAATGACATACCAAGGAAAGCAGTTCCACTCCTGAC
TCCTCCTTTATCGTCTTCAAGTCATGATTCACTTTCGGTGGCTTTATTATGACTTTG
GAGACATTAAATATCATCACTTCGTTTCAAGGTATAAATGACTTTCCACGAGTGG
CTCATCTTGTCTTCTCTTTTAGTTTTCTTTTTATATAATCAATCCTTCACAATCCT