

IDENTIFICATION

Species: *Arabidopsis lyrata*

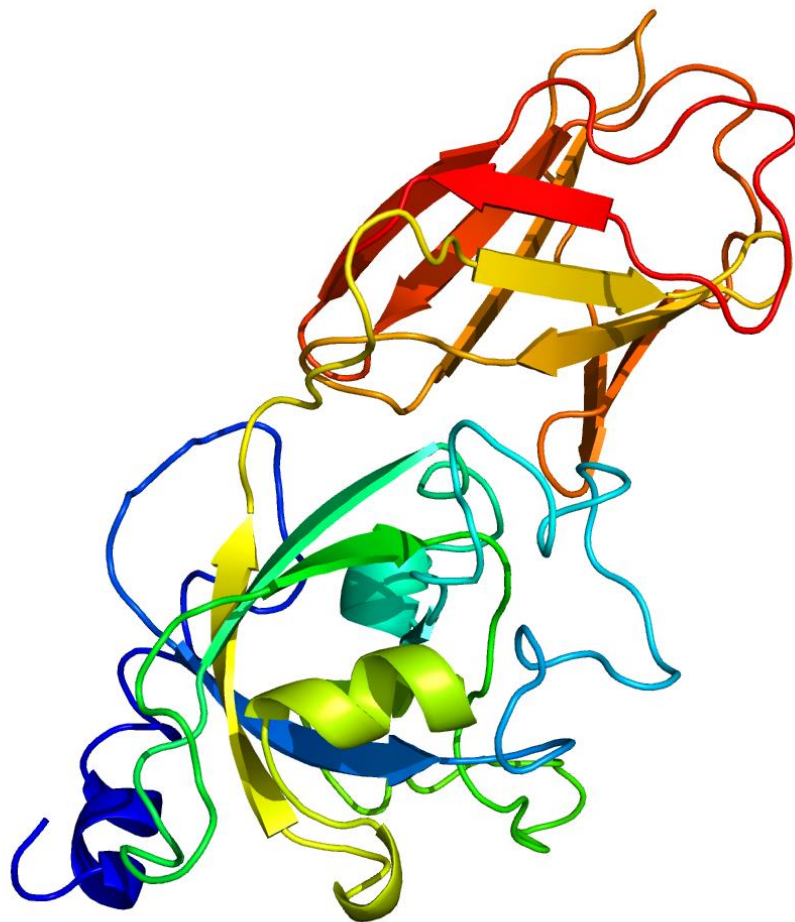
Locus: AL6G15130

Gene Model: AL6G15130.t1

Description: ALEXPA-16

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>

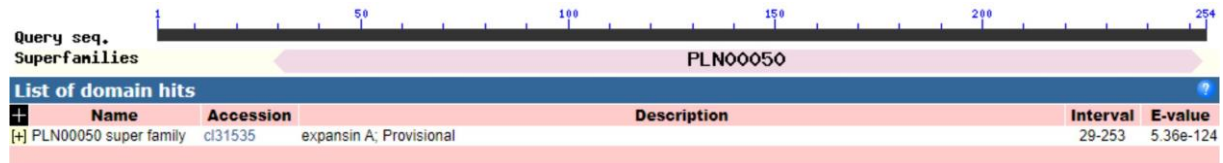
EXTERNAL RESOURCES

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

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>ALEXPA-16

MKLTEYSHILFSLFTINFYIINSDDNGGWERGHATFYGGADASGTMGGACGYGNLH
SQGYGLQTAALSTALFNSGQKCGACFELQCEDDPEWCIPGSIIVSATNFCPPNFALAN
DNGGWCNPPLKHFDLAEP AFLQIAQYRAGIVPVAFRRVPCCKGGGIRFTINGNPYFDL
VLITNVGGAGDVRAVSLKGSKTDQWQMSRNWQNWQSN TYLRGQSLSFQVTASD
GQTVVSYDVVPQDWQFGQTFEGGQF*

CDS (coding sequence)

>ALEXPA-16

ATGAAGCTTACAGAATATTCCCATATTTTATTTCTTTCACTATTCACCATCAACTT
CTACATTATAAACTCCGACGACAACGGAGGCTGGGAGAGAGGCCATGCTACCTTC
TACGGTGGAGCTGATGCATCCGGCACAATGGGTGGTGCTTGTGGGTACGGTAACT
TACACAGCCAAGGCTATGGGCTACAAACCGCGGCTTTGAGCACGGCTTTGTTCAA
TAGTGGGCAGAAATGTGGGGCCTGCTTTGAGCTACAGTGTGAGGATGATCCTGAG
TGGTGCATCCCTGGTTCCATCATCGTTTCAGCTACAAACTTCTGTCTCCAAACTT
TGCCTTAGCCAATGATAATGGTGGTTGGTGCAATCCTCCTCTCAAGCATTTTGACT
TGGCCGAGCCTGCCTTCCTCCAGATCGCTCAGTACCGGGCTGGAATCGTTCCTGT
GCATTCAGAAGGGTTCCATGTGAGAAAGGTGGAGGGATAAGGTTACGATCAAC
GGGAATCCGTATTTTCGACCTCGTGTTGATCACAAACGTGGGTGGTGCTGGAGATG
TTAGGGCCGTCTCTTTGAAAGGCTCAAAGACTGATCAGTGGCAATCTATGTCAAG
AACTGGGGACAGAATTGGCAAAGCAACTTACCTCAGAGGGCAAAGCCTATC
TTTTCAAGTCACTGCTAGTGATGGTCAGACTGTTGTGAGCTACGATGTTGTCCCTC
AGGATTGGCAGTTCGGTCAAACCTTTTGAAGGTGGACAATTCTAG

Nucleotide

>ALEXPA-16

TCTCCTTTTTCCACTTCTTACTTCTCCTCCGATCCTCTTTAGCCCCTCAGCAAATCAT
GAAGCTTACAGAATATTCCCATATTTTATTTCTTTCACTATTCACCATCAACTTCT
ACATTATAAACTCCGACGACAACGGAGGCTGGGAGAGAGGCCATGCTACCTTCT
ACGGTGGAGCTGATGCATCCGGCACAATGGGTACTTCAAACATTTTCTTTCACTC

GCACCCACACATATCATTAATTAAGTCAGCACAATTGGATACTTTTAACATATTTG
ACCGTTCAAGTGTTGATGTTTTTTAGGTGGTGCTTGTGGGTACGGTAACTTACACA
GCCAAGGCTATGGGCTACAAACCGCGGCTTTGAGCACGGCTTTGTTCAATAGTGG
GCAGAAATGTGGGGCCTGCTTTGAGCTACAGTGTGAGGATGATCCTGAGTGGTGC
ATCCCTGGTTCCATCATCGTTTCAGCTACAACTTCTGTCCTCCAACTTTGCCTT
AGCCAATGATAATGGTGGTTGGTGCAATCCTCCTCTCAAGCATTTTGACTTGGCC
GAGCCTGCCTTCCTCCAGATCGCTCAGTACCGGGCTGGAATCGTTCCTGTCGCATT
CAGAAGGTAAAAACAAAATTTTAGCCAAAAAAGGACAATTCAGTATACGTTTTCT
TATATAAAACGCTCTAGGTATCAATGTATATCATTTGTCCTTTTATAATGATAGGG
TTCCATGTGAGAAAGGTGGAGGGATAAGGTTACGATCAACGGGAATCCGTATTT
CGACCTCGTGTTGATCACAAACGTGGGTGGTGCTGGAGATGTTAGGGCCGTCTCT
TTGAAAGGCTCAAAGACTGATCAGTGGCAATCTATGTCAAGAACTGGGGACAG
AATTGGCAAAGCAACACTTACCTCAGAGGGCAAAGCCTATCTTTTCAAGTCACTG
CTAGTGATGGTCAGACTGTTGTGAGCTACGATGTTGTCCCTCAGGATTGGCAGTT
CGGTCAAACCTTTTGAAGGTGGACAATTCTAGATTATGTACCAAGATAAAGTAATA
GACATTATACGAGAAGAGGCAATGATTGTGTTTAATTAAGACAAAACCTCTGTTTT
TCATTGATCATATCCACTCTTTTATAGTAATAACTCATAAGAAAGACAATGAAAC
AGTTAATTTTGT