

IDENTIFICATION

Species: *Arabidopsis lyrata*

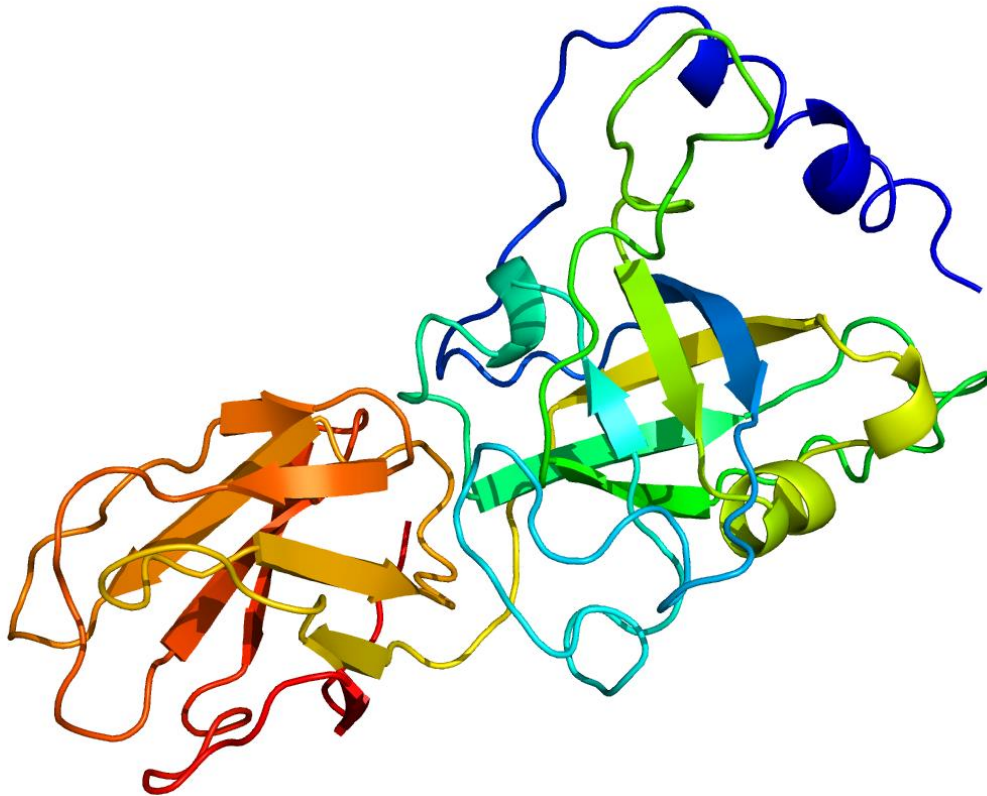
Locus: AL5G36650

Gene Model: AL5G36650.t1

Description: ALEXPA-14

Family: Alpha Expansin

3D structure:



GENOME DATABASES

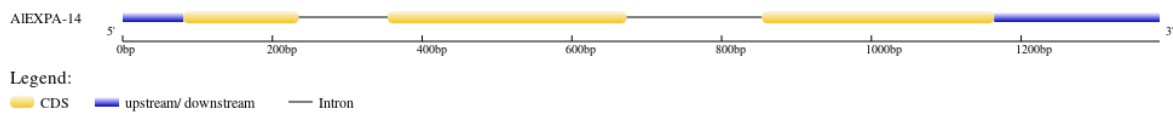
Phytozome: https://phytozome-next.jgi.doe.gov/info/Alyrata_v2_1

Kegg: <https://www.genome.jp/entry/T01578>

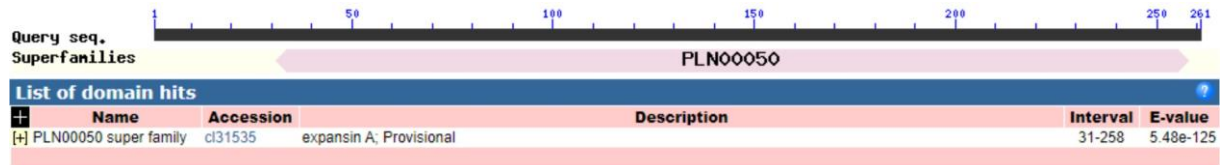
EXTERNAL RESOURCES

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

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>AIEXPA-14

MAINQMILLTIFPLFLLLSFTDAGIPGVYSGGSWQTAHATFYGGNDASGTMGGACGY
GNLYSQGYGTNTAALSTALFNSGQSCGACFEIKCVNDPKWCHPGNPSVFTATNFCP
PNLAQPSDNGGWCNPPRSHFDLAMPVFLKIAEYRAGIVPISYRRVACRKS GGIRFTIN
GHRYFNLVLITNVAGAGDILRTSVKGSKTGWMSLTRNWGQNWQSNVAVLVGQSLSF
RVTTSDRRTSTSWNIAPSNWQFGQTFVGKNFRV*

CDS (coding sequence)

>AIEXPA-14

ATGGCAATCAATCAAATGATTCTCTTAACCATATTCCCCTCTTTCTCCTCTTGAG
CTTCACCGACGCCGAATCCCTGGCGTCTACTCAGGCGGCTCTTGGCAAACCGCT
CACGCCACTTTCTATGGTGGCAACGATGCTTCCGGAACAATGGGTGGCGCGTGTG
GATACGGGAATCTGTACAGTCAAGGATACGGAACAACACGGCGGCCCTGAGCA
CAGCGTTGTTCAACAGTGGCCAAAGCTGCGGCGCATGCTTCGAAATCAAATGTGT
TAATGATCCTAAATGGTGTACCCGGGTAATCCTTCTGTCTTCGTAACCGCAACCA
ACTTTTGCCCTCCAACTTAGCCCAGCCTAGCGACAATGGCGGATGGTGCAACCC
GCCACGCTCTCATTTCGACCTCGCCATGCCCGTTTTCCTCAAGATCGCTGAGTATC
GTGCCGGCATTGTCCCATCTCTTACCGCAGGGTGGCATGTAGGAAGAGTGGAGG
GATAAGGTTACGATCAACGGTCACCGTTACTTCAACTTGGTGCTGATCACGAAT
GTGGCCGGAGCAGGAGATATCCTGAGGACGAGCGTGAAAGGTTCAAAGACTGGT
TGGATGAGTTTAACTAGGAACTGGGGACAGA ACTGGCAGTCTAATGCTGTTCTCG
TTGGTCAGTCACTTTCCTTCCGTGTCACAACAGTGACCGTAGAACCTCTACTTCA
TGGAACATCGCTCCTTCGAACTGGCAGTTTGGACAAACCTTTGTCGGAAAGAATT
TCAGGGTCTAA

Nucleotide

>AIEXPA-14

CATCCTCAAGTTCCTCACTTAGCCTTCTAGTCTAACAAATCTTCTTATCATTTCTGAA
TTTCAATCACAAATATTCACCAAAATGGCAATCAATCAAATGATTCTCTTAACCA
TATCCCCTCTTTCTCCTCTTGAGCTTACCGACGCCGAATCCCTGGCGTCTAC

TCAGGCGGCTCTTGGCAAACCGCTCACGCCACTTTCTATGGTGGCAACGATGCTT
CCGGAACAATGGGTCAGTTCACTCTCCTAAAACACATATTTCAAGAACCGTACCA
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ATACGGAACAAACACGGCGGCCCTGAGCACAGCGTTGTTCAACAGTGGCCAAAG
CTGCGGGCGCATGCTTCGAAATCAAATGTGTTAATGATCCTAAATGGTGTACCCG
GGTAATCCTTCTGTCTTCGTAACCGCAACCAACTTTTGCCCTCCAAACTTAGCCCA
GCCTAGCGACAATGGCGGATGGTGAACCCGCCACGCTCTCATTTTCGACCTCGCC
ATGCCCGTTTTCTCAAGATCGCTGAGTATCGTGCCGGCATTGTCCCCTCTCTTA
CCGCAGGTATACTTAACATATCTAATTATGGAATGATGGTAAAAAACTACTAATA
ATAATTTTTTTCTTTTTTTTCGATACGATCGTTTGATTTATAAGGATTAAACATTCCT
ATATATAGCTTCCTATTCGTAAGAAGTTGCAATGAATCAACTTGATAAGGTTGA
GAAATGTGGGTTTTCTATAGGGTGGCATGTAGGAAGAGTGGAGGGATAAGGTTT
ACGATCAACGGTCACCGTTACTTCAACTTGGTGCTGATCACGAATGTGGCCGGAG
CAGGAGATATCCTGAGGACGAGCGTGAAAGGTTCAAAGACTGGTTGGATGAGTT
TAACTAGGAACTGGGGACAGAAGTGGCAGTCTAATGCTGTTCTCGTTGGTCAGTC
ACTTTCCTTCCGTGTCACAACCAGTGACCGTAGAACCTCTACTTCATGGAACATCG
CTCCTTCGAACTGGCAGTTTGGACAAACCTTTGTCGGAAAGAATTTTCAGGGTCTA
AAGTGAAAATGAGGATATCGAAACATTCAAAGTGGTAGACACAAAAAGAAGCTC
CACTTTCAATTTGAACATCTTTGACTTTATATTTTCTATTACTTTTTTTTCTGTGAT
TTGGAGTGTAATTGGGAGGTGGTGTGGTAATATATATAGGGCAGTGTGAGAAAA
GAGAACTGAAGTGGCTGTTGAAAAAGTTGTAAACAGCCCGCAGCTCTTAAAATT
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