

IDENTIFICATION

Species: *Arabidopsis lyrata*

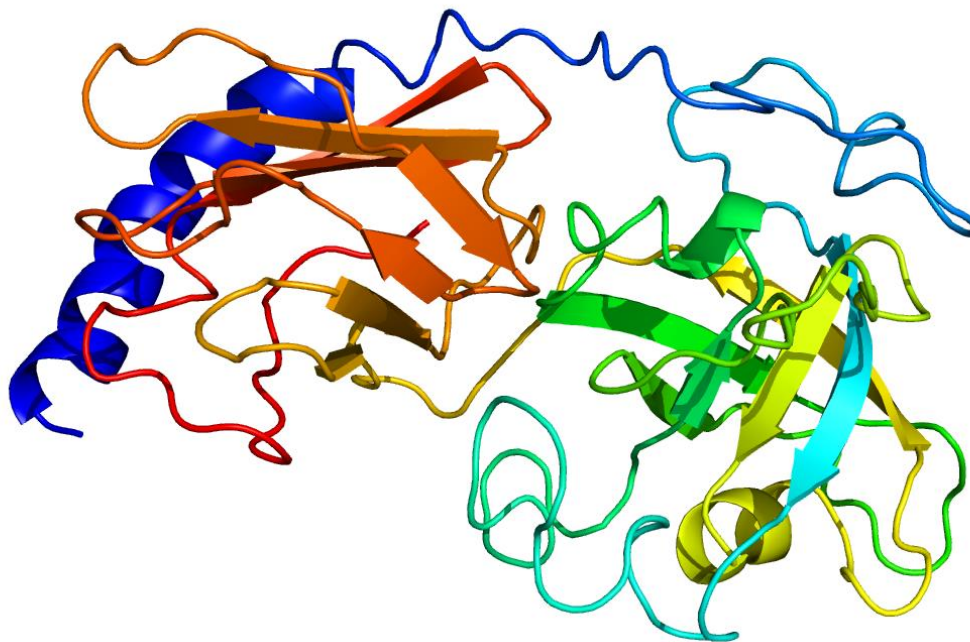
Locus: AL7G51190

Gene Model: AL7G51190.t1

Description: ALEXPA-21

Family: Alpha Expansin

3D structure:



GENOME DATABASES

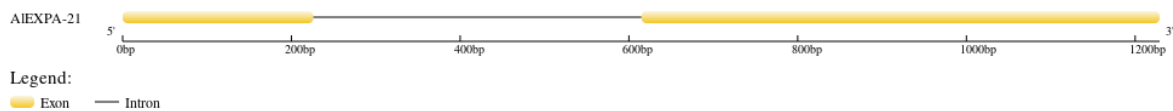
Phytozome: https://phytozome-next.jgi.doe.gov/info/Alyrata_v2_1

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

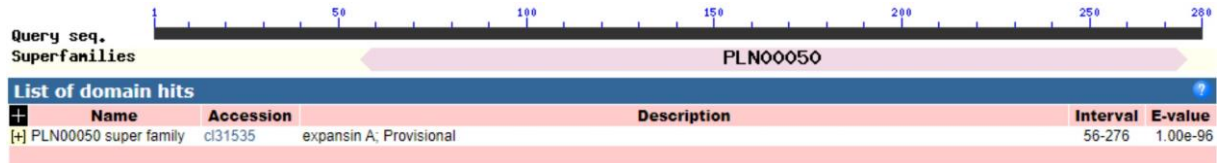
EXTERNAL RESOURCES

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

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>AIEXPA-21

MKLLLEKMIYVEFLMIIMAVWVVPMSYGHGAMIHDAEAPDVAEAPGINGPSKTLDT
NWYDARATFYGDIHGGETQQGACGYGNLFRQGYGLATAALSTALFNDGYTCGACY
EIMCARDPQWCLPGSIKITATNFCPPNYTKTVDVWCNPPQKHFDLSLPMFLKIAKFKA
GVVPVRYRRVLCAKTGGVKFETKGNPYFLMVLLYNVGGAGDVKQVQVKGKNTGWI
TMKKNWGQNWTTDTVLTGQGLSFRVTTSDGVTKDFINLMPKNWGFGQTFVVGKINF*

CDS (coding sequence)

>AIEXPA-21

ATGAAACTCTTAGAAAAAATGATATATGTAGAATTTTTGATGATAATAATGGCGG
TGTGGGTCGTACCCATGAGTTACGGTCATGGAGCGATGATTCATGATGCAGCCGA
AGCACCCGATGTAGCTGAAGCACCCGGGATTAATGGCCAAGCAAGACTCGA
CACTAATTGGTATGACGCACGGGCCACATTCTACGGTGACATCCATGGTGGAGAA
ACTCAACAGGGAGCTTGTGGATACGGTAATCTGTTTAGACAAGGCTATGGTCTAG
CCACAGCAGCGTTAAGCACGGCACTCTTCAACGACGGGTACACATGTGGCGCTTG
TTACGAAATCATGTGCGCGCGTGATCCACAATGGTGTTTACCCGGATCTATCAAG
ATTACAGCAACAAATTTCTGTCCACCAATTACACCAAAACCGTTGATGTTTGGT
GCAACCCACCACAAAAGCACTTTGATCTCTCTTACCGATGTTTCTCAAGATCGCC
AAGTTCAAGGCCGGGTTGTCCAGTCAGATACAGACGTGTTCTTTGTGCAAAAA
CTGGTGGAGTCAAGTTTGAACCAAAGGAAACCCTTATTTCTTAATGGTCTTGCT
ATACAATGTAGGAGGAGCTGGAGATGTTAAGTTCGTGCAAGTTAAAGGAAACAA
GACCGGGTGGATAACAATGAAAAAGAAGTGGGGGCAGAATTGGACCACTGATAC
AGTATTGACCGCCAAGGTTTATCGTTTAGGGTTACGACGAGTGATGGGGTTACA
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GAAAGATTAACCTTTAG

Nucleotide

>AIEXPA-21

ATGAAACTCTTAGAAAAAATGATATATGTAGAATTTTTGATGATAATAATGGCGG
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GATATAATTCATTTTTCTGATTATTACATACTCACTTTTTTTCATTATACATTCAATA
GAGGGAGCTTGTGGATACGGTAATCTGTTTAGACAAGGCTATGGTCTAGCCACAG
CAGCGTTAAGCACGGCACTCTTCAACGACGGGTACACATGTGGCGCTTGTACGA
AATCATGTGCGCGCGTGATCCACAATGGTGTTTACCCGGATCTATCAAGATTACA
GCAACAAATTTCTGTCCACCAAATTACACCAAACCGTTGATGTTTGGTGCACC
CACCACAAAAGCACTTTGATCTCTCTCTACCGATGTTTCTCAAGATCGCCAAGTTC
AAGGCCGGGGTTGTCCCAGTCAGATACAGACGTGTTCTTTGTGCAAAAACCTGGTG
GAGTCAAGTTTGAAACCAAAGGAAACCCTTATTTCTTAATGGTCTTGCTATACAA
TGTAGGAGGAGCTGGAGATGTTAAGTTCGTGCAAGTTAAAGGAAACAAGACCGG
GTGGATAACAATGAAAAAGAACTGGGGGCAGAATTGGACCACTGATACAGTATT
GACCGGCCAAGGTTTATCGTTTAGGGTTACGACGAGTGATGGGGTTACAAAAGAT
TTTATTAATCTGATGCCAAAAAATTGGGGATTTGGACAGACTTTTGTTGGAAAGA
TTAACTTTTAG