

## IDENTIFICATION

**Species:** *Arabidopsis lyrata*

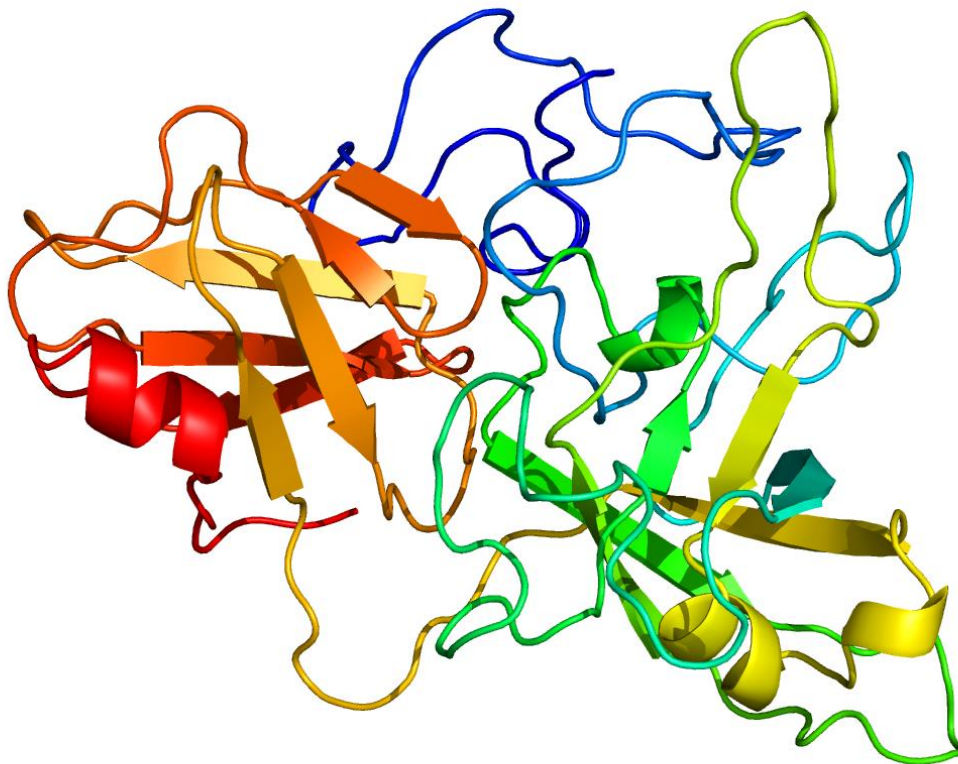
**Locus:** AL7G51170

**Gene Model:** AL7G51170.t1

**Description:** ALEXPA-19

**Family:** Alpha Expansin

**3D structure:**



## GENOME DATABASES

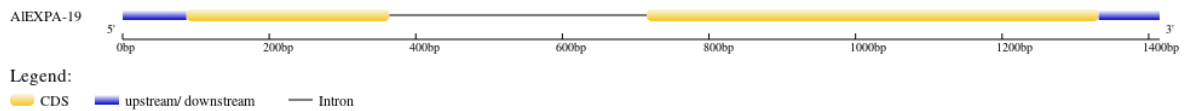
Phytozome: [https://phytozome-next.jgi.doe.gov/info/Alyrata\\_v2\\_1](https://phytozome-next.jgi.doe.gov/info/Alyrata_v2_1)

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

## EXTERNAL RESOURCES

[https://plants.ensembl.org/Arabidopsis\\_lyrata/Info/Index](https://plants.ensembl.org/Arabidopsis_lyrata/Info/Index)

## GENE STRUCTURE



## DOMAIN ARCHITECTURE



## SEQUENCES

### Peptide

>AIEXPA-19

MVMVIWIAPMTYGHGHATHVPGGRTGPPMTGAHPSHGAHPSHG VHP SHGSQPSHG  
AHP SHGAHPSHGGLGPHSGWGHGRATFYGDINGGETQQGACGYGDLHKQGYGLET  
AALSTALFNNGSRCGACFEIKCVDAPQWCLPGSIKITATNFCPPDFSKPKDCWCNPPQ  
KHF DLSQPMFLKIAKYKAGVVPVKFRRVPCAKIGGVKFEIKGNPHFLMILPYNVGG A  
GDVRAMQIKGTRTEWIAMKKNWGQIWSTGVVLTGQCLSFRVTTSDGITKEFIDVTPP  
DWKCNQGSFQDGKINF\*

### CDS (coding sequence)

>AIEXPA-19

ATGGTAATGGTGATATGGATAGCACCTATGACATACGGTCATGGTCATGCAACCC  
ACGTACCCGGTGGAAGAACCGGCCACCCATGACTGGTGCCACCCCTTCCCATGG  
TGCCACCCCTTCCCATGGCGTCCACCCATCCCATGGCTCCCAACCTTCCCATGGCG  
CCCACCCATCCCATGGCGGCCATCCATCCCATGGCGGCCTTGGGCCGCATTCTGG  
TTGGGGTTCATGGCCGTGCCACATTTTACGGTGACATCAATGGTGGAGAACTCAA  
CAGGGAGCTTGTGGATATGGTGATCTACACAAACAAGGATATGGTCTAGAGACA  
GCAGCACTAAGCACCGCACTATTTAACAACGGCTCAAGGTGTGGGGCTTGTTCG  
AGATCAAGTGCGTAGATGCTCCACAATGGTGTTTGCCAGGTTCCATCAAGATCAC  
AGCTACAAACTTCTGTCCACCAGATTTCTCCAAGCCCAAAGACTGTTGGTGCAAC  
CCGCCACAAAACACTTTGATCTCTCGCAACCAATGTTCCCTCAAAATTGCCAAAT  
ACAAAGCCGGGGTTGTCCCGGTTAAATTTAGACGTGTTCCCTTGTGCGAAAATCGG  
AGGTGTCAAGTTTGAAATCAAGGGAACCCCTCATTCTTAATGATCTTACCGTAC  
AATGTAGGAGGAGCTGGAGATGTTAGGGCCATGCAAATTAAGGGAACGAGGACC  
GAGTGGATTGCGATGAAGAAGAATTGGGGACAGATTTGGAGCACTGGTGTGTG  
TTGACCGGACAATGTTTATCGTTTAGGGTTACGACAAGTGATGGAATTACGAAAG  
AGTTTATTGACGTTACCCCGCCGGATTGGAATGTAATGGACAGAGTTTTGATGG  
AAAGATTAATTTTATAG

## Nucleotide

>A1EXPA-19

ATCGTCAATAAAATTAATAAGATTTGATAAAAAGAGAGATAAAGTCATGGAACTCT  
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CCACCCATGACTGGTGCCACCCTTCCCATGGTGCCACCCTTCCCATGGCGTCCA  
CCCATCCCATGGCTCCCAACCTTCCCATGGCGCCACCATCCCATGGCGCCCATC  
CATCCCATGGCGGCCTTGGGCCGCATTCTGGTTGGGGTCATGGCCGTGCCACATT  
TTACGGTGACATCAATGGTGGAGAACTCAACGTAAGCAGCTAAATATATACTAA  
TAATTCAAAAATCTCGAGACCTGTAAAAATGTTAAGATTGTTTAGACGTATACAA  
AAGCCAACATGAAGACGTACGTAGTAAATGATACTCATGAATCTTTGACCACTAG  
ACTAATATTGTTTGCTTATGCATTTACACAATTAACCAAAAAAGTTTAGAAATATT  
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ATGCATGCAAACGAAAAATAACGAAGCCACATAATTAATTAATTTTTCTTCAC  
ATAATTAGTTTTGTTTTTGAAAGTAATACATAGTTTTTTTTCTATTTAATAGAGG  
GAGCTTGTGGATATGGTGATCTACACAACAAGGATATGGTCTAGAGACAGCAG  
CACTAAGCACCGCACTATTTAACAACGGCTCAAGGTGTGGGGCTTGTTCGAGAT  
CAAGTGCGTAGATGCTCCACAATGGTGTTCGCCAGGTTCCATCAAGATCACAGCT  
ACAACTTCTGTCCACCAGATTTCTCCAAGCCAAAGACTGTTGGTGCAACCCGC  
CACAAAAACACTTTGATCTCTCGCAACCAATGTTCCCTCAAATGCCAAATACAA  
AGCCGGGGTTGTCCCGGTTAAATTTAGACGTGTTCCCTTGTGCGAAAATCGGAGGT  
GTCAAGTTTGAAATCAAGGGAAACCCTCATTCTTAATGATCTTACCGTACAATG  
TAGGAGGAGCTGGAGATGTTAGGGCCATGCAAATTAAGGGAACGAGGACCGAGT  
GGATTGCGATGAAGAAGAATTGGGGACAGATTTGGAGCACTGGTGTTGTGTTGAC  
CGGACAATGTTTATCGTTTAGGGTTACGACAAGTGATGGAATTACGAAAGAGTTT  
ATTGACGTTACCCCGCCGGATTGGAAATGTAATGGACAGAGTTTTGATGGAAAGA  
TTAATTTTTAGAAAAAGAATTTGAGTTTTGTTAGCTAACACTTGCAATAACTAAG  
AAATCCGTTGTTATTAGTTAACAAAACCTATGTCCATTAC