

## IDENTIFICATION

**Species:** *Arabidopsis lyrata*

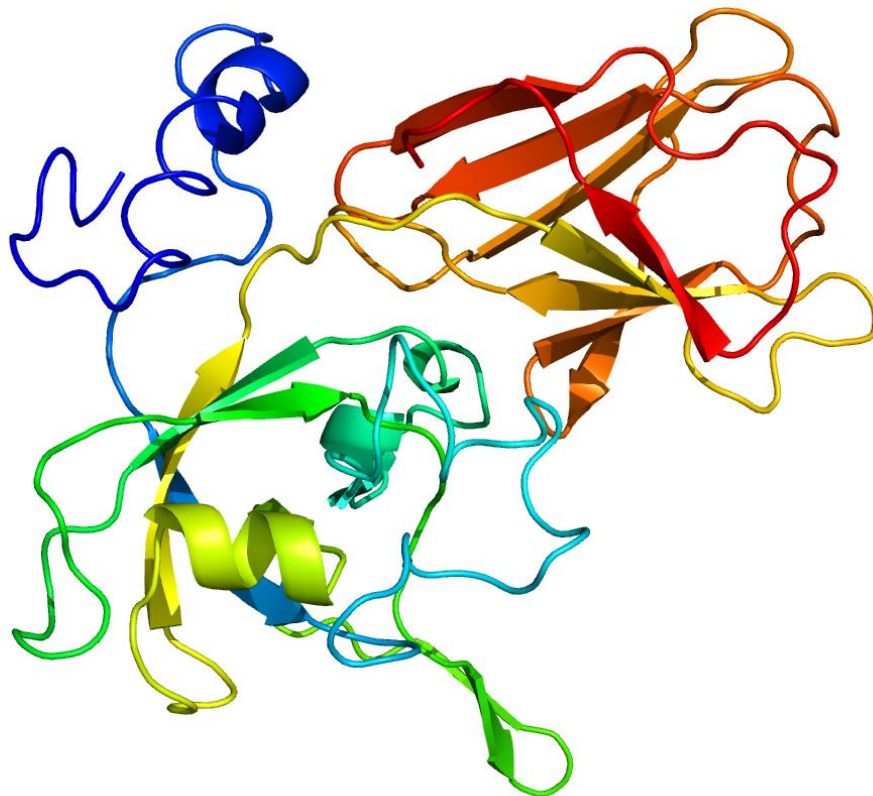
**Locus:** AL1G23910

**Gene Model:** AL1G23910.t1

**Description:** ALEXPA-01

**Family:** Alpha Expansin

**3D structure:**



## GENOME DATABASES

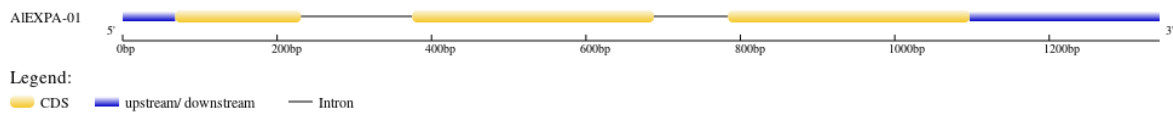
Phytozome: [https://phytozome-next.jgi.doe.gov/info/Alyrata\\_v2\\_1](https://phytozome-next.jgi.doe.gov/info/Alyrata_v2_1)

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

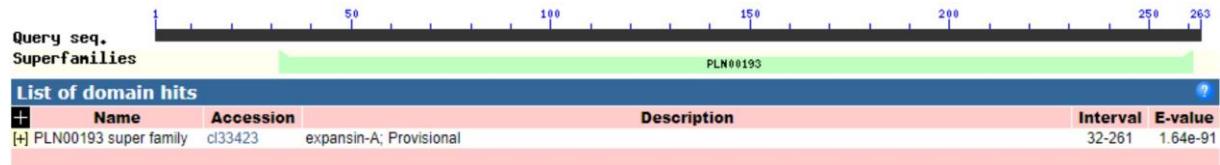
## EXTERNAL RESOURCES

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

## GENE STRUCTURE



## DOMAIN ARCHITECTURE



## SEQUENCES

### Peptide

>ALEXPA-01

MGPVSSWSFNKFFAIVCVVFAISGEFVAGYYRPGPWRYAHATFYGDETGSETMGG  
ACGYGNLFSNGYGLSTAALSTTLFKDGYGCGQCFQITCSKSPHCYYGKSTVVTATNL  
CPPNWYQDSNNGGWCNPPRTHFDMAKPAFMKLANWKAGIIPVAYRRVPCQRSGGM  
RFQFQNSYWLLVFMNVGGAGDIKSMVKGSRTNWISMSHNWGASYQAFSSLYG  
QSLFRVTSYTTGETVYAWNVPANWNAGMTYKSTANFR\*

### CDS (coding sequence)

>ALEXPA-01

ATGGGTCCAGTCTCAAGTTCTTGGAGTTTCAACAAATTCTTCGCTATAGTTTGCCT  
TGTTTTCGCCATATCCGGTGAGTTCGTCGCCGGATACTATCGACCAGGCCCATGG  
AGATATGCTCACGCCACTTTCTACGGTGATGAGACCGGTAGTGAAACCATGGGTG  
GTGCATGTGGGTACGGAAACCTTTTAAACAGCGGCTACGGACTGTCCACGGCGGC  
GCTAAGCACGACATTGTTCAAAGATGGTTACGGATGTGGCCAATGTTTTCAAATA  
ACATGTTTCGAAATCACCTCATTGTTACTACGGAAAATCAACCGTTGTCACAGCCA  
CCAATCTTTGCCCTCCTAATTGGTACCAAGACTCCAACAATGGTGGTTGGTGCAA  
TCCTCCTAGAACCCATTTGATATGGCTAAACCGGCTTTCATGAAACTCGCTAACT  
GGAAGGCCGGTATCATCCCAGTTGCCTACCGAAGAGTGCCATGCCAAAGGAGTG  
GAGGTATGAGGTTTCAATTCCAAGGTAATTCTTATTGGCTTCTCGTCTTCGTCATG  
AACGTTGGTGGCGCCGGAGACATCAAGAGCATGGCCGTGAAAGGTAGCCGCACA  
AATTGGATAAGTATGAGCCATAACTGGGGAGCCTCTTACCAAGCTTTTTCTCTCT  
TTACGGTCAATCTCTCTTTCCGGGTCACCTTCATACACCACCGGTGAAACCGTCT  
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CGCCAATTTCCGTTGA

## Nucleotide

>AEXPA-01

CAAACAAACAAACAAAACACAAACCCTAAGAAAAGTCATCGAAAATTAAGGAA  
AACGAGAAATAAACGATGGGTCCAGTCTCAAGTTCTTGGAGTTTCAACAAATTCT  
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CGACCAGGCCCATGGAGATATGCTCACGCCACTTTCTACGGTGATGAGACCGGTA  
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CGGTATCATCCCAGTTGCCTACCGAAGGTATATATATATCGTTTTGTACGACACTT  
AGTTATTCAACCTCATATATTATTCTAAA ACTATATATATAACTAATATATGTTAT  
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GTAATTCTTATTGGCTTCTCGTCTTCGTCATGAACGTTGGTGGCGCCGGAGACATC  
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TATAATGTATGTATCTAATTGTGATATAACTCTTCTTATAAAAATCATGAAGTCAA  
CACTTCTTGATCAAGAGAATTTTCGTTTTGTTATTTGTAAATTTTCTACCAATAAA  
TCGCTTGCTTTTTT