

## IDENTIFICATION

**Species:** *Arabidopsis lyrata*

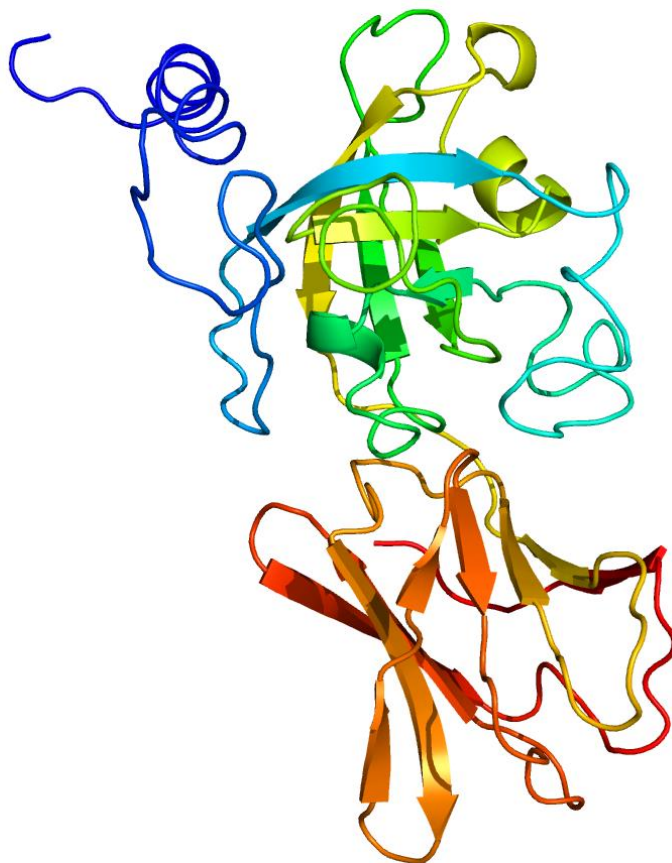
**Locus:** AL7G51200

**Gene Model:** AL7G51200.t1

**Description:** ALEXPA-22

**Family:** Alpha Expansin

**3D structure:**



## GENOME DATABASES

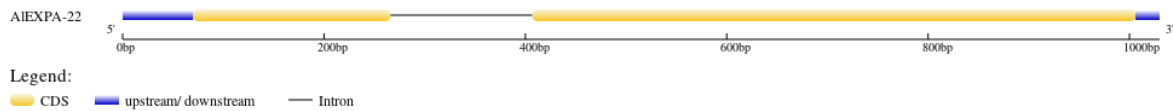
Phytozome: [https://phytozome-next.jgi.doe.gov/info/Alyrata\\_v2\\_1](https://phytozome-next.jgi.doe.gov/info/Alyrata_v2_1)

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

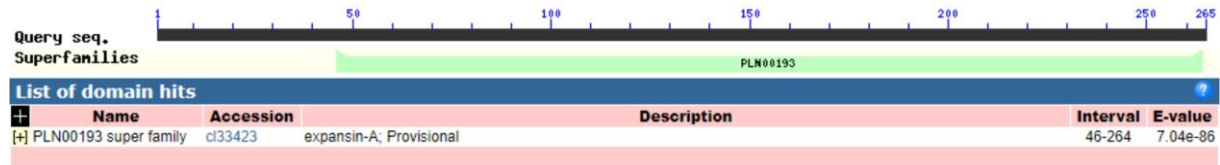
## EXTERNAL RESOURCES

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

## GENE STRUCTURE



## DOMAIN ARCHITECTURE



## SEQUENCES

### Peptide

>ALEXPA-22

MTYVECFMIIMATWFMFISYGHGADV AEPPIIDDV AASPGTNGLDTAWYDARATY  
YGDHIGIGTEQGACGYGDPNKHGYGLATAALSTALFNNGATCGACYEIMCAPNPQG  
CLSGSIKITATNLCPPDSTWCNLPNKHFDLSLPMFIKIAQVKAGIVPIRYRRVPCA  
KTG GVKFEVKGNPSFLTILPYNVGGAGDIKAVYVKGSKTGWIAMSRNWGQNWTTN  
VNL AGQSVSLRVTTSDDEVTKDFTDVM PQSWGFGQTFDGKTNF\*

### CDS (coding sequence)

>ALEXPA-22

ATGACATATGTAGAATGTTTTATGATAATAATGGCGACTTGGTTCATGTTTCATAA  
GTTATGGTCATGGAGCCGATGTAGCCGAACCACCCATGATTGATGATGTAGCCGC  
TTCACCTGGAACCAACGGACTCGATACTGCTTGGTATGATGCACGAGCCACATAT  
TATGGTGATATCCATGGTATAGGCACTGAACAGGGAGCTTGTGGATACGGTGATC  
CAAACAAACATGGATATGGTCTAGCCACAGCGGCATTGAGCACGGCGCTATTCA  
ACAACGGGGCCACATGTGGGGCTTGTTACGAGATCATGTGCGCTCCTAATCCACA  
AGGGTGTGGTCTGGATCCATCAAGATCACAGCAACAATTTATGTCCACCAGAT  
TCCACTTGGTGCAACCTACCAAATAAACACTTTGATCTCTCCTTACCAATGTTTCAT  
CAAGATCGCCCAGGTCAAAGCCGGGATCGTCCCATTAGATATAGACGTGTTCCCT  
TGTGCAAAAACCGGTGGTGTCAAGTTTGAAGTTAAAGGAAACCCTAGTTTCCTAA  
CGATCTTACCGTACAATGTAGGAGGAGCCGGAGATATTAAGCCGTGTATGTTAA  
GGGAAGCAAAAACCGGTGGATAGCAATGAGCAGAACTGGGGACAAAACCTGGA  
CCACTAATGTTAATCTAGCCGGTCAGAGTGTATCATTGAGGGTTACAACGAGTGA  
TGAGGTTACAAAAGATTTTACTGATGTGATGCCACAAAGTTGGGGATTTGGGCAG  
ACTTTTGATGGAAAGACTAACTTTTAA

### Nucleotide

>ALEXPA-22

CCATCAATTAAGCTAAAGTAAAAACAATATCATTAAAGAGGTATAATAATCATG  
AAATTGCTAGAAAAAATGACATATGTAGAATGTTTTATGATAATAATGGCGACTT  
GGTTCATGTTTCATAAGTTATGGTCATGGAGCCGATGTAGCCGAACCACCCATGAT

TGATGATGTAGCCGCTTCACCTGGAACCAACGGACTCGATACTGCTTGGTATGAT  
GCACGAGCCACATATTATGGTGATATCCATGGTATAGGCACTGAACGTAAGTTAA  
AATACTAATATTTGTCGAATCTAATTATTACATTGATGTTTTGTTTCGATATATAT  
AGGCTGGGAATGTTTTCAATATAAAGAAACAATCAAAAGTTTACATACTAACGTT  
TTATTATAATACATTCAATAGAGGGAGCTTGTGGATACGGTGATCCAAACAAACA  
TGGATATGGTCTAGCCACAGCGGCATTGAGCACGGCGCTATTCAACAACGGGGCC  
ACATGTGGGGCTTGTTACGAGATCATGTGCGCTCCTAATCCACAAGGGTGTGTTGT  
CTGGATCCATCAAGATCACAGCAACAAATTTATGTCCACCAGATTCCACTTGGTG  
CAACCTACCAAATAAACACTTTGATCTCTCCTTACCAATGTTTCATCAAGATCGCCC  
AGGTCAAAGCCGGGATCGTCCCGATTAGATATAGACGTGTTCCCTTGTGCAAAAAC  
CGGTGGTGTCAAGTTTGAAGTTAAAGGAAACCCTAGTTTCCTAACGATCTTACCG  
TACAATGTAGGAGGAGCCGGAGATATTAAGCCGTGTATGTTAAGGGAAGCAAA  
ACCGGGTGGATAGCAATGAGCAGAAACTGGGGACAAAACCTGGACCACTAATGTT  
AATCTAGCCGGTCAGAGTGTATCATTGAGGGTTACAACGAGTGATGAGGTTACAA  
AAGATTTTACTGATGTGATGCCACAAAGTTGGGGATTTGGGCAGACTTTTGATGG  
AAAGACTAACTTTTAAGAAAAATGAAATGAATTTTTTTAG