

## IDENTIFICATION

**Species:** *Arabidopsis lyrata*

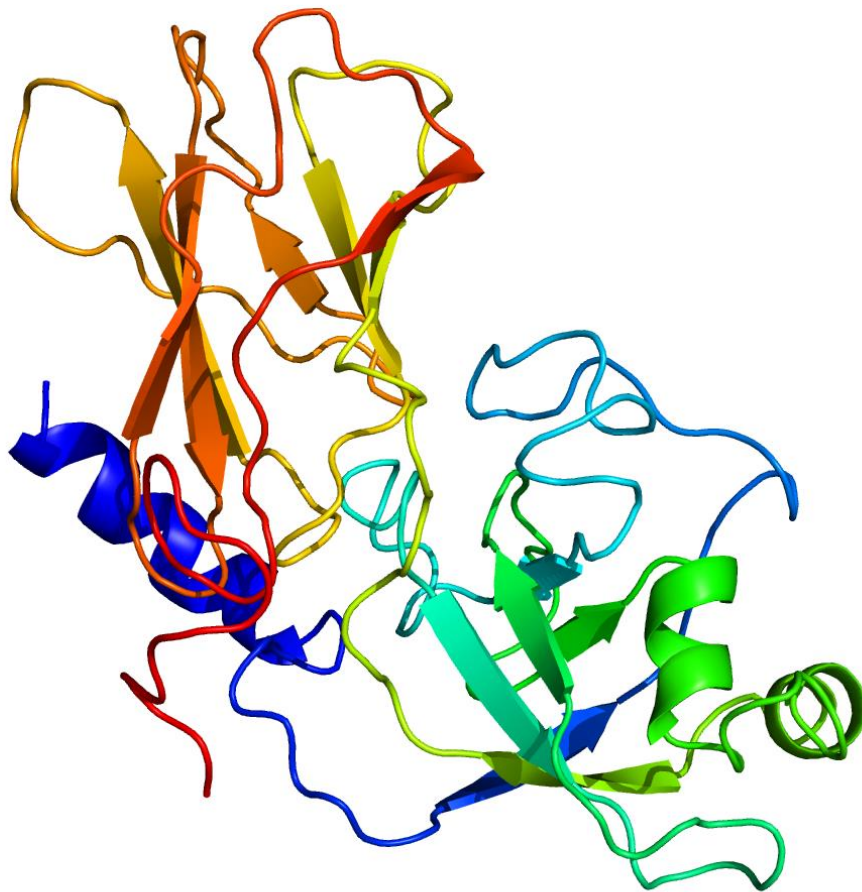
**Locus:** AL5G24660

**Gene Model:** AL5G24660.t1

**Description:** ALEXLA-01

**Family:** Expansin Like Alpha

**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>

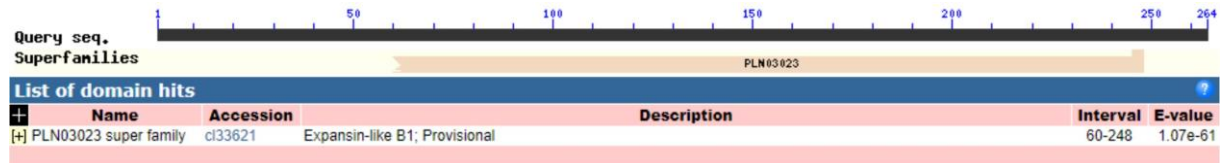
## EXTERNAL RESOURCES

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

## GENE STRUCTURE



## DOMAIN ARCHITECTURE



## SEQUENCES

### Peptide

>AIEXLA-01

MRSFLYRIVVIFLFSSSVNACDRCLHRSKAAYFSSASALSSGACAYGPMATRFFAGHI  
AAAIPSIYKDGAGCGACFQVRCKNPKLCTSKGTIVMVTDLNLSNQTDLVSSRAFRA  
MAKPVVGADKYLLRQGIVDVEYQVRPCNYGKRNLNVRVEEASKNPNYLAIKLLYQ  
GGQTEVVGIDIARVGSSQWSYMRSHGAVWATDKVPTGALQFRFTVTGGYDGTKV  
WSKRVL PANWKAGMIYDTGVQITDIAQEGCDTCGHIWD\*

### CDS (coding sequence)

>AIEXLA-01

ATGAGAAGCTTTCTCTACCGCATCGTAGTCATCTTCCTCTTCTCATCATCTGTAA  
CGCATGTGATCGATGTCTTCACCGTTCTAAAGCAGCTTATTTCTCCTCTGCTTCTG  
CTCTCTTTCCGGAGCTTGTGCTTATGGCCCTATGGCTACGAGATTCTTTGCCGGT  
CACATTGCGGCGGCTATACCTTCCATTTACAAAGATGGTGCTGGCTGTGGAGCTT  
GCTTCCAAGTCAGATGCAAGAACCCCAAGTTGTGTACCAGTAAAGGAACCATTGT  
AATGGTCACAGACTTGAACACGAGCAACCAAAGTATCTTGTCCCTTAGTAGTAGA  
GCTTTTAGGGCAATGGCTAAGCCTGTTGTTCGGTGCTGACAAATACCTTCTCAGAC  
AAGGCATTGTCGACGTTGAATACCAAAGAGTTCCTTGCAATTATGGTAAAAGGAA  
TTTGAACGTGAGAGTTGAAGAAGCAAGCAAAAATCCAAATTAATGGCGATAAA  
GCTTTTGTACCAAGGAGGCCAAACCGAAGTGGTAGGTATTGACATTGCTCGAGTG  
GGTTCGTCACAATGGAGTTACATGACTAGAAGCCACGGAGCCGTGTGGGCGACT  
GACAAAGTACCAACTGGAGCTCTACAGTTCAGGTTACGGTGACAGGCGGCTAC  
GATGGCAAACGGTTTGGTCCAAGAGGGTTCCTCCGGCCAATTGGAAAGCTGGG  
ATGATCTATGATACCGGTGTTTACAGATCACCGACATTGCTCAAGAAGGTTGTGACA  
CATGCGGTACATATGGGACTGA

### Nucleotide

>AIEXLA-01

TTTTCATCTAAATTCACATATCTCTCTACTTTGCTCATATAGATATTATTTTTTCT  
CTAGAAAAAAAAAACAATAATGAGAAGCTTTCTCTACCGCATCGTAGTCATCTTC  
CTCTTCTCATCATCTGTAAACGCATGTGATCGATGTCTTCACCGTTCTAAAGCAGC

TTATTTCTCCTCTGCTTCTGCTCTCTCTTGTGAACATTCCCATCTTCTTCTCATTACT  
TCCTTTTAACTACTTGTGTTGGTTTCTTTTTCTCATATCTTGTATCTGTTTTTGCAGC  
CGGAGCTTGTGCTTATGGCCCTATGGCTACGAGATTCTTTGCCGGTCACATTGCGG  
CGGCTATACCTTCCATTTACAAAGATGGTGCTGGCTGTGGAGCTTGCTTCCAAGTC  
AGATGCAAGAACCCCAAGTTGTGTACCAGTAAAGGAACCATTGTAATGGTCACA  
GACTTGAACACGAGCAACCAAAGTATCTTGTCCCTTAGTAGTAGAGCTTTTAGGG  
CAATGGCTAAGCCTGTTGTCGGTGCTGACAAATACCTTCTCAGACAAGGCATTGT  
CGACGTTGAATACCAAAGGTTTCGATTCTTAAAACACCTAACTTCTTGTTCCTTTT  
ATAGTCACCTGATTTACTTTTGTAAATAAAAACAGAGTTCCTTGCAATTATGGTAA  
AAGGAATTTGAACGTGAGAGTTGAAGAAGCAAGCAAAAATCCAAATTACTTGGC  
GATAAAGCTTTTGTACCAAGGAGGCCAAACCGAAGTGGTAGGTATTGACATTGCT  
CGAGTGGGTTTCGTCACAATGGAGTTACATGACTAGAAGCCACGGAGCCGTGTGG  
GCGACTGACAAAGTACCAACTGGAGCTCTACAGTTCAGGTTACGGTGACAGGC  
GGCTACGATGGCAAAACGGTTTGGTCCAAGAGGGTTCTTCCGGCCAATTGGAAAG  
CTGGGATGATCTATGATACCGGTGTTTCAGATCACCGACATTGCTCAAGAAGGTTG  
TGACACATGCGGTCACATATGGGACTGACTCATTACAATTCTCCTTATTTATAGGC  
AAACAACAACACCCTTTATAGGATTATACATGTATGTGTAACACAACAAGGA  
ACTAAAATAAAATCTATATATGTACACGGTACACCATTCACAAAAATAAAGATCT  
TGCTAAAAA