

## IDENTIFICATION

**Species:** *Arabidopsis halleri*

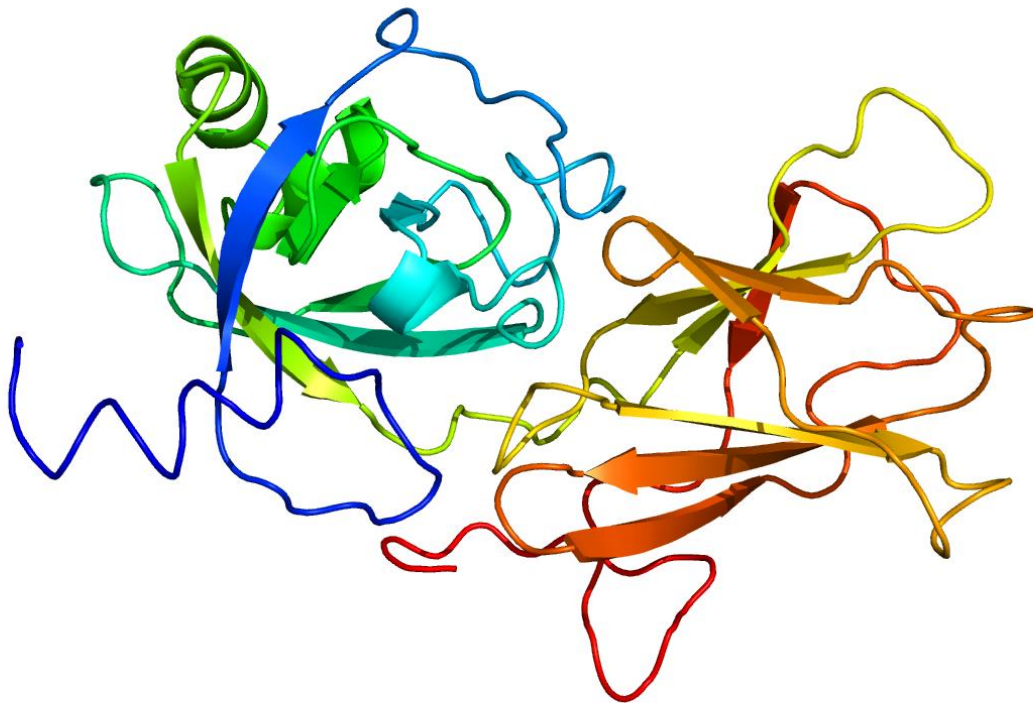
**Locus:** Araha.5281s0002

**Gene Model:** Araha.5281s0002.1

**Description:** AhEXLA-01

**Family:** Expansin Like Alpha

**3D structure:**



## GENOME DATABASES

Phytozome: [https://phytozome-next.jgi.doe.gov/info/Ahalleri\\_v1\\_1](https://phytozome-next.jgi.doe.gov/info/Ahalleri_v1_1)

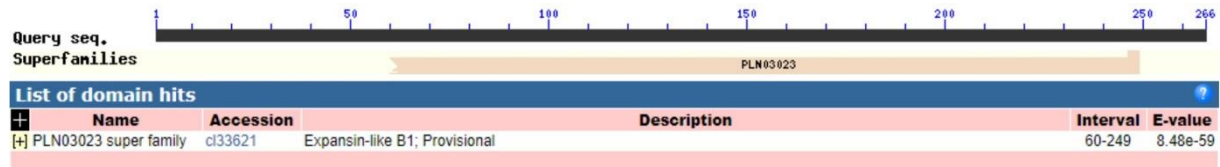
## EXTERNAL RESOURCES

[https://plants.ensembl.org/Arabidopsis\\_halleri/Info/Index](https://plants.ensembl.org/Arabidopsis_halleri/Info/Index)

## GENE STRUCTURE



## DOMAIN ARCHITECTURE



## SEQUENCES

### Peptide

>AhEXLA-01

MGNFLYLIVVIFHFSSSVNACDRCLHRSKGAYFSSASALSSGACAYDSMATSFFAGHI  
AAAIPSIYKDGAGCGACFQVRCKNPKLCSTKGTIVMITDLNKSNTDLVSSRAFR  
MAKPVVGADRDLKQGIVDIEYQVRPCDYGNKNLNVVVEEASKKPYYLEIKLLYQG  
GQTEVVSIDIAQVSSSPNWGYMTRSHGAVWATDKVPTGALQFRFIVTGGYDGMKIW  
SQSVLPSNWEAGKTYDAGVQITDIAQEGCDPCDAHIWN\*

### CDS (coding sequence)

>AhEXLA-01

ATGGGAAACTTTCTCTACCTCATCGTAGTCATCTTCCACTTCTCATCATCTGTTAA  
CGCTTGTGATCGATGCTTCCACCGTTCTAAAGGAGCTTATTTCTCCTCTGCTTCTG  
CTCTCTTTCTGGAGCTTGTGCTTATGACTCTATGGCTACGAGTTTCTTCGCCGGA  
CACATAGCCGCAGCTATACCTTCGATCTACAAAGACGGCGCTGGTTGTGGAGCTT  
GCTTTCAAGTCAGATGCAAGAACCCTAAGTTGTGTAGCACTAAAGGAACCATTGT  
GATGATCACAGACTTAAACAAGAGTAACCAAACCGATCTTGTTCTTAGTAGCAGA  
GCATTCAGAGCCATGGCTAAGCCTGTTGTTGGTGCTGATAGAGATCTTCTCAAAC  
AAGGCATTGTCGATATCGAATACCAAAGAGTTCCTTGCGATTACGGGAACAAGA  
ACCTAAACGTGAGAGTCGAAGAAGCAAGCAAAAAGCCATACTACTTAGAGATAA  
AGCTTTTATACCAAGGAGGACAAACCGAAGTAGTATCAATCGACATTGCTCAGGT  
CAGTTCATCGCCAAATTGGGGTTACATGACCAGAAGCCACGGAGCTGTATGGGCG  
ACTGACAAAGTACCAACCGGCGCTTTCAGTTCAGATTCATAGTAACCGGTGGAT  
ACGACGGTAAAATGATATGGTCACAGAGTGTCTTCCATCCAATTGGGAAGCTGG  
AAAGACTTACGACGCCGCGTTCAAATCACAGACATTGCTCAAGAAGGTTGTGAT  
CCATGCGATGCTCACATCTGGAATAA

## Nucleotide

>AhEXLA-01

CTAATTTGATCATATAGATATTTATTGTTTTCTCTTGAAAGAAACAAAAATGGGA  
AACTTTCTCTACCTCATCGTAGTCATCTTCCACTTCTCATCATCTGTAAACGCTTGT  
GATCGATGTCTTCACCGTTCTAAAGGAGCTTATTTCTCCTCTGCTTCTGCTCTCTCT  
TGTAAGCATTACATCTTCTCTGATCATTACTTCTTTTGAACACTTTTGTGTTTTC  
TTTTCTCATGTTTTGTAAATGGGTTTTTGCAGCTGGAGCTTGTGCTTATGACTCTAT  
GGCTACGAGTTTCTTCGCCGGACACATAGCCGCAGCTATACCTTCGATCTACAAA  
GACGGCGCTGGTTGTGGAGCTTGCTTTCAAGTCAGATGCAAGAACCCTAAGTTGT  
GTAGCACTAAAGGAACCATTGTGATGATCACAGACTTAAACAAGAGTAACCAAA  
CCGATCTTGTTCCTTAGTAGCAGAGCATTACAGAGCCATGGCTAAGCCTGTTGTTGGT  
GCTGATAGAGATCTTCTCAAACAAGGCATTGTCGATATCGAATACCAAAGGTTTCG  
ATTCTCAAACACCTAAACTCTTTGGTTTTCTTATAATCACATGATTTTAAATATG  
GTAATGAAAAACAGAGTTCCTTGCGATTACGGGAACAAGAACCTAACCGTGAG  
AGTCGAAGAAGCAAGCAAAAAGCCATACTACTTAGAGATAAAGCTTTTATACCA  
AGGAGGACAAACCGAAGTAGTATCAATCGACATTGCTCAGGTCAGTTCATCGCCA  
AATTGGGGTTACATGACCAGAAGCCACGGAGCTGTATGGGCGACTGACAAAGTA  
CCAACCGGCGCTCTTCAGTTCAGATTCATAGTAACCGGTGGATACGACGGTAAAA  
TGATATGGTCACAGAGTGTTCTTCCATCCAATTGGGAAGCTGGAAAGACTTACGA  
CGCCGGCGTTCAAATCACAGACATTGCTCAAGAAGGTTGTGATCCATGCGATGCT  
CACATCTGGAACCTAATTATTTATGCACACAACAAACATCCTTCATAGGTTTATGT  
ATGTATTGTGTAACAGAGTTAAAGAACATAATGTGAATGCTTAGTCTAAAGATTA  
AACAAGAGAACCAAT