

## IDENTIFICATION

**Species:** *Arabidopsis halleri*

**Locus:** Araha.1146s0002

**Gene Model:** Araha.1146s0002.1

**Description:** AhEXPA-03

**Family:** Alpha Expansin

**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)

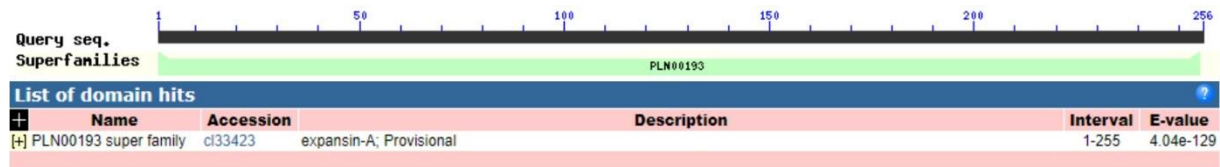
## EXTERNAL RESOURCES

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

## GENE STRUCTURE



## DOMAIN ARCHITECTURE



## SEQUENCES

### Peptide

>AhEXPA-03

MTKIFSLLVAMIFSTMFFMQISSVSAGWLQAHATFYGGSDASGTMGGACGYGNLYT  
DGYKTNTAALSTALFNDGKSCGGCYQILCDATKVPQWCLKGRSITITATNFCPPNFA  
QASDDGGWCNPPRPHFDMAQPAFLTIAKYKAGIVPILYKRVGCRRSSGMRFTINGRN  
YFELVLISNVAGAGEISKVWIKGSKSNKWETMSRNWGANYQSNTYLNGQSLSFQVQ  
LSDGRIKAALNVVPSNWQFGQSFKSNINF\*

### CDS (coding sequence)

>AhEXPA-03

ATGACGAAGATTTTCTCTCTATTGGTCGCAATGATCTTCTCCACGATGTTCTTCAT  
GCAGATCAGCTCAGTTTCTGCTGGTTGGTTGCAAGCTCATGCGACCTTTTATGGCG  
GAAGTGATGCTTCTGGTACAATGGGTGGAGCTTGTGGTTATGGAAACCTATACAC  
AGACGGTTACAAGACAAACACAGCAGCGTTAAGCACGGCACTGTTCAACGACGG  
CAAGTCATGCGGTGGATGTTACCAAATCTTGTGTGATGCAACCAAAGTACCACAA  
TGGTGTCTTAAAGGAAGATCAATCACAATCACAGCCACAACTTCTGTCCACCAA  
ACTTTGCTCAGGCAAGCGACGATGGAGGATGGTGAACCCACCAAGACCTCACTT  
TGACATGGCTCAGCCTGCGTTTCTAACCATCGCTAAGTACAAAGCTGGTATCGTT  
CCCATTCTCTACAAAAGGGTTGGATGTAGAAGAAGCGGAGGGATGAGATTTACG  
ATCAATGGTAGAACTATTTGAGCTTGTCTCATATCAAACGTAGCAGGAGCTG  
GTGAGATCTCTAAAGTTTGGATCAAAGGATCTAAGAGCAACAAATGGGAGACAA  
TGTCAGAAATTGGGGAGCTAACTATCAGAGCAACACTTACCTTAATGGTCAATC  
TCTCTTTTCAAAGTTCAACTCAGTGATGGAAGAATCAAAGCAGCTCTCAACGTT  
GTTCTTCGAATTGGCAGTTTGGTCAGAGCTTCAAGAGCAACATCAACTTCTGA

## Nucleotide

>AhEXPA-03

CAACAATCATCAACTTCTTCTCTAATCAAAAAGTTAAACACCTAAGACATTGAAAG  
AAAAACAAATGACGAAGATTTTCTCTCTATTGGTCGCAATGATCTTCTCCACGAT  
GTTCTTCATGCAGATCAGCTCAGTTTCTGCTGGTTGGTTGCAAGCTCATGCGACCT  
TTTATGGCGGAAGTGATGCTTCTGGTACAATGGGTAAGTCTCAGAACTTCACTCA  
GTTTGGTTTAAACATTTTAAATTTTACGGTTAATTCAATTAGGAGAATAAAAAGAA  
AGATTTCTTCTTCAACAAGAAACCCTCTCATAGTTTTTCTTCTTCAGGTGGAGCTT  
GTGGTTATGGAAACCTATACACAGACGGTTACAAGACAAACACAGCAGCGTTAA  
GCACGGCACTGTTCAACGACGGCAAGTCATGCGGTGGATGTTACCAAATCTTGTG  
TGATGCAACCAAAGTACCACAATGGTGTCTTAAAGGAAGATCAATCACAATCAC  
AGCCACAAACTTCTGTCCACCAAACCTTGTCTCAGGCAAGCGACGATGGAGGATGG  
TGCAACCCACCAAGACCTCACTTTGACATGGCTCAGCCTGCGTTTCTAACCATCG  
CTAAGTACAAAGCTGGTATCGTTCCATTCTCTACAAAAGGGTTGGATGTAGAAG  
AAGCGGAGGGATGAGATTTACGATCAATGGTAGAAACTATTTTCGAGCTTGTTC  
ATATCAAACGTAGCAGGAGCTGGTGAGATCTCTAAAGTTTGGATCAAAGGATCTA  
AGAGCAACAAATGGGAGACAATGTCAAGAAATTGGGGAGCTAACTATCAGAGCA  
ACACTTACCTTAATGGTCAATCTCTCTCTTTCAAAGTTCAACTCAGTGATGGAAGA  
ATCAAAGCAGCTCTCAACGTTGTTCTTCTCGAATTGGCAGTTTGGTCAGAGCTTCA  
AGAGCAACATCAACTTCTGATCTCAGTAATGATTGGGTTTATGGTTTTTATCCATC  
TTTTGTATTTACTTTCATTGGGTATTTTTGCTTCTCTGTTGCATCATCATCGTCTG  
CGAGATAAGCTGCTTGTTTTATAGCCTTATTATAGTCTTGCTTCCAGAGAGTTTAT  
AATCTGGAGAAGACTCAAGCAGTGATGATTGTATTTGTACATTTATGGAAGAATA  
TGTTTACTATATATGAAAGGATATATA