

## IDENTIFICATION

**Species:** *Arabidopsis halleri*

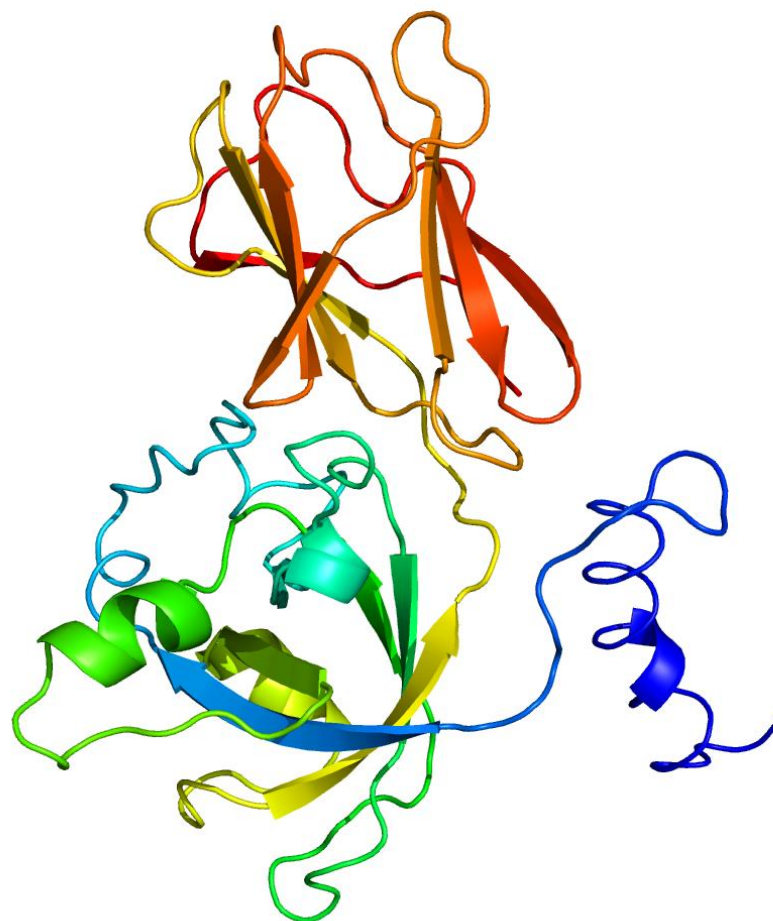
**Locus:** Araha.17420s0006

**Gene Model:** Araha.17420s0006.1

**Description:** AhEXPA-10

**Family:** Alpha Expansin

**3D structure:**



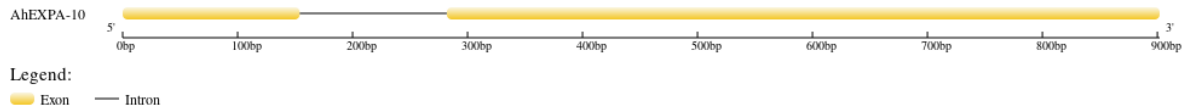
## GENOME DATABASES

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

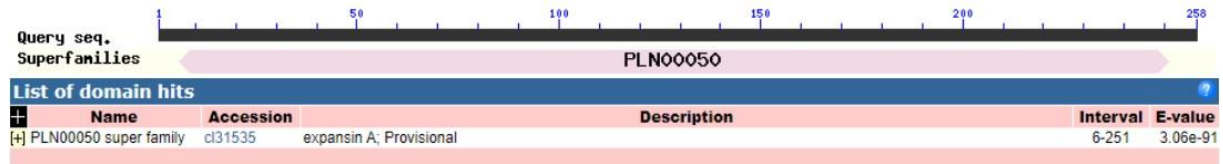
## EXTERNAL RESOURCES

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

## GENE STRUCTURE



## DOMAIN ARCHITECTURE



## SEQUENCES

### Peptide

>AhEXPA-10

MNRSMTFVVLLAILVSVANLGLAHVGLTNIDPSWYDAHATFYGDMSGGETMQGAC  
GYGDLFKEGYGLETAALSTALFNNGQTCGACFELMCMNSKWCKPNAGSIKITATNF  
CPPNYDEPVQYHWCNPPNKHFDLSMKMFTSMAEYKGGIVPVKFRVMCHKRGGVR  
FEIKGNPYFIMVLVYNVGGAGDVNNVEIRGHKSNWIVMKRNWQIWNVTGVDLVGQ  
KLSFVVRTSDGRSMTFFNVAPASWGFQTFEAKLNF\*

### CDS (coding sequence)

>AhEXPA-10

ATGAACCGATCAATGACTTTTGTGTTGTTACTGGCGATTCTTGTCTCGGTGGCTAA  
CCTTGGCTTAGCTCATGTCGGTCTTACTAATATCGACCCTTCGTGGTACGACGCAC  
ATGCGACGTTTTATGGCGATATGAGCGGCGGAGAAACCATGCAAGGAGCATGTG  
GTTACGGGGATCTATTCAAAGAAGGTTACGGCTTAGAGACGGCGGGCGCTAAGCA  
CGGCTCTTTCAACAACGGGCAGACTTGTGGTGCTTGTTCGAGCTCATGTGTATG  
AACTCAAAGTGGTGCAAACCAAACGCTGGTTCAATCAAATCACAGCCACTAATT  
TCTGCCCACCAAATTATGATGAACCGGTTCAATACCATTGGTGCAACCCTCCTAA  
CAAACACTTTGATCTATCCATGAAAATGTTCACTTCGATGGCCGAGTACAAAGGA  
GGGATAGTTCCGGTGAAGTTCAGGCGAGTGATGTGTCATAAGAGAGGTGGTGTG  
AGGTTTGAGATTAAGGGTAATCCTTATTTTATCATGGTTTTGGTGTATAACGTTGG  
AGGTGCAGGAGATGTGAATAACGTTGAAATTAGAGGGCATAAGAGTAATTGGAT  
CGTTATGAAGAGGAATTGGGGGCAAATTTGGAATACTGGTGTGGATTTGGTTGGA  
CAAAGCTCTCGTTTGTGGTTCGGACCAGTGATGGTAGGAGCATGACGTTCTTCA  
ATGTTGCGCCTGCGAGTTGGGGGTTCCGGTCAAACTTTTGAAGCAAACCTGAACTT  
TTAG

## Nucleotide

>AhEXPA-10

ATGAACCGATCAATGACTTTTGTGTGTTACTGGCGATTCTTGTCTCGGTGGCTAA  
CCTTGGCTTAGCTCATGTCGGTCTTACTAATATCGACCCTTCGTGGTACGACGCAC  
ATGCGACGTTTTATGGCGATATGAGCGGCGGAGAAACCATGCGTTAGTATTTTTT  
ATTATTTTATTATAATGTCTTTTTCTCATTTTGTTAATGATTTCTTTATGATTTTTT  
TAAGTATTAATCGTATGTAGTTTTTAAATTTTATTTTAATACTGTTTGGTGTGACA  
GAAGGAGCATGTGGTTACGGGGATCTATTCAAAGAAGGTTACGGCTTAGAGACG  
GCGGCGCTAAGCACGGCTCTTTCAACAACGGGCAGACTTGTGGTGCTTGTTCG  
AGCTCATGTGTATGAACTCAAAGTGGTGCAAACCAAACGCTGGTTCAATCAAAT  
CACAGCCACTAATTTCTGCCACCAAATTATGATGAACCGGTTCAATACCATTGG  
TGCAACCCTCCTAACAACACTTTGATCTATCCATGAAAATGTTCACTTCGATGGC  
CGAGTACAAAGGAGGGATAGTTCCGGTGAAGTTCAGGCGAGTGATGTGTCATAA  
GAGAGGTGGTGTGAGGTTTGAGATTAAGGGTAATCCTTATTTTATCATGGTTTTG  
GTGTATAACGTTGGAGGTGCAGGAGATGTGAATAACGTTGAAATTAGAGGGCAT  
AAGAGTAATTGGATCGTTATGAAGAGGAATTGGGGGCAAATTTGGAATACTGGT  
GTGGATTTGGTTGGACAAAAGCTCTCGTTTGTGGTTCGGACCAGTGATGGTAGGA  
GCATGACGTTCTTCAATGTTGCGCCTGCGAGTTGGGGGTTTCGGTCAAACCTTTGA  
AGCAAAACTGAACTTTTAG