

IDENTIFICATION

Species: *Arabidopsis halleri*

Locus: Araha.13516s0016

Gene Model: Araha.13516s0016.1

Description: AhEXPA-08

Family: Alpha Expansin

3D structure:



GENOME DATABASES

Phytozome: https://phytozome-next.jgi.doe.gov/info/Ahalleri_v1_1

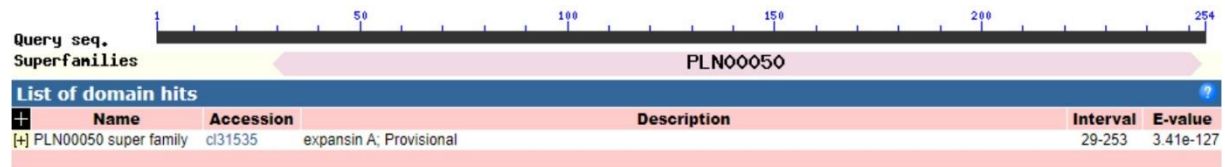
EXTERNAL RESOURCES

https://plants.ensembl.org/Arabidopsis_halleri/Info/Index

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>AhEXPA-08

MKLTEYSHILFLSLFTINFYIINSDDNGGWERGHATFYGGDDASGTMGGACGYGNLH
SQGYGLQTAALSTALFNSGQKCGACFELQCEDDPEWCIPGSIIVSATNFCPPNFALAN
DNGGWCNPLKHFDLAEP AFLQIAQYRAGIVPVAFRRVPCKEGGIRFTINGNPYFDL
VLITNVGGAGDIRAVSLKGSKSDQWQSMSRNWQNWQSNTYLRGQSLSFQVTTSDG
RTVVSYDVVPQDWQFGQTFEGRQF*

CDS (coding sequence)

>AhEXPA-08

ATGAAGCTTACAGAATATTCCCATATTTTATTTCTTTCACTATTCACCATCAACTT
CTACATTATAAACTCGGACGACAACGGAGGCTGGGAGAGAGGCCATGCTACCTT
CTACGGTGGAGATGATGCATCCGGCACAATGGGTGGTGTGCTTGTGGGTACGGTAAC
TTACACAGCCAAGGCTATGGGCTACAAACCGCGGCTTTGAGCACGGCTTTGTTCA
ATAGTGGGCAGAAATGTGGGGCCTGCTTTGAGCTACAGTGTGAGGATGATCCTGA
GTGGTGCATCCCTGGTTCCATCATCGTCTCAGCTACAAACTTCTGTCTCCAAACT
TTGCCTTAGCCAATGATAATGGTGGTTGGTGCAATCCTCCTCTCAAGCACTTTGAC
TTGGCCGAGCCTGCCTTCCCTCCAGATCGCTCAGTACCGGGCTGGAATCGTTCCTGT
CGCATT CAGAAGGGTTCCATGTGAGAAAGGTGGAGGGATAAGGTT CACGATAAA
CGGGAATCCGTATTTT GACCTCGTGTGATCACAAATGTGGGTGGTGTGCTGGAGAT
ATAAGGGCCGTCTCTTTGAAAGGCTCAAAGTCTGATCAGTGGCAATCCATGTCAA
GAAACTGGGGACAGAATTGGCAAAGTAACACTTACCTCAGAGGTCAAAGCCTCT
CCTTCCAGGTC ACTACTAGTGATGGTCCGACTGTTGTGAGCTACGATGTTGTGCCT
CAGGATTGGCAGTTCGGTCAAACCTTTTGAAGGCAGGCAATTCTAG

Nucleotide

>AhEXPA-08

ATGAAGCTTACAGAATATCCCATATTTTATTTCTTTCACTATTCACCATCAACTT
CTACATTATAAACTCGGACGACAACGGAGGCTGGGAGAGAGGCCATGCTACCTT
CTACGGTGGAGATGATGCATCCGGCACAATGGGTACTTAAAACATTTTCTTTTAC
TCGCACACACATATATCATTAAAACATCACAATTGGATACTTTTAACATATTTGAC
CGTTCAAGTGTTGATGTTTTTTAGGTGGTGCTTGTGGGTACGGTAACTTACACAGC
CAAGGCTATGGGCTACAAACCGCGGCTTTGAGCACGGCTTTGTTCAATAGTGGGC
AGAAATGTGGGGCCTGCTTTGAGCTACAGTGTGAGGATGATCCTGAGTGGTGCAT
CCCTGGTTCCATCATCGTCTCAGCTACAAACTTCTGTCCTCCAAACTTTGCCTTAG
CCAATGATAATGGTGGTTGGTGCAATCCTCCTCTCAAGCACTTTGACTTGGCCGA
GCCTGCCTTCCTCCAGATCGCTCAGTACCGGGCTGGAATCGTTCCTGTTCGATTCA
GAAGGTAAAAACAAATTGTAGCCAAAAAAAATTCCTTTGTAAACAAATTTTTTTT
TAAAAAACTCTACGTACCATTTATGTCCTCTTATAATGATAGGGTTCCATGTGAGA
AAGGTGGAGGGATAAGGTTACGATAAACGGGAATCCGTATTTTGACCTCGTGTT
GATCACAAATGTGGGTGGTGCTGGAGATATAAGGGCCGTCTCTTTGAAAGGCTCA
AAGTCTGATCAGTGGCAATCCATGTCAAGAACTGGGGACAGAATTGGCAAAGT
AACACTTACCTCAGAGGTCAAAGCCTCTCCTTCCAGGTCACTACTAGTGATGGTC
GGACTGTTGTGAGCTACGATGTTGTGCCTCAGGATTGGCAGTTCGGTCAAACCTTT
GAAGGCAGGCAATTCTAG