

IDENTIFICATION

Species: *Arabidopsis halleri*

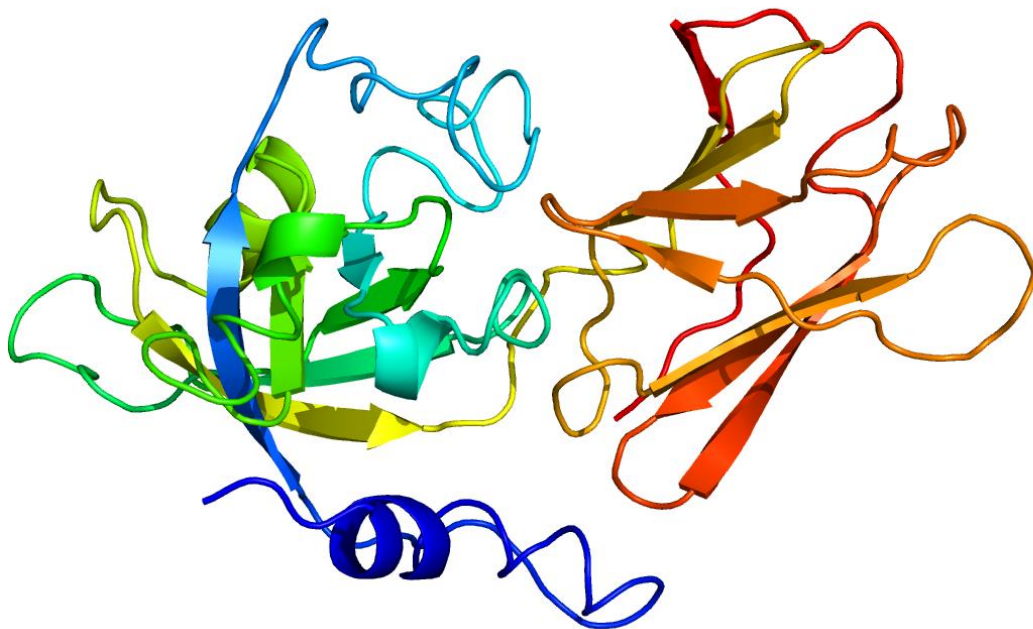
Locus: Araha.1906s0014

Gene Model: Araha.1906s0014.1

Description: AhEXPA-04

Family: Alpha Expansin

3D structure:



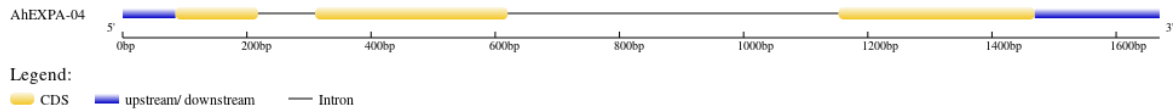
GENOME DATABASES

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

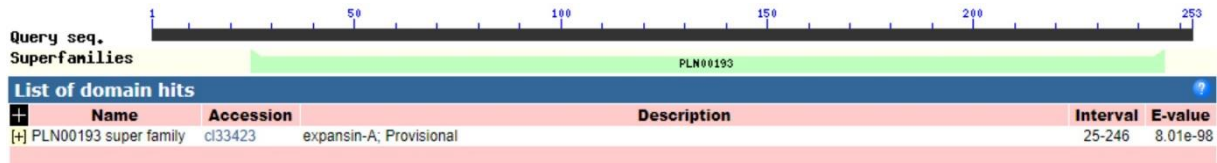
EXTERNAL RESOURCES

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

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>AhEXPA-04

MDMKGKYLVTAILLVGTLVGMCSNGWIRAHATYYGVNDSPASLGGACGYDNPYH
AGFGAHTAALSGALFRSGESCGGCYQVRCDYPADPKWCLRGAAVTVTATNFCPSNN
NNGWCNLPRHHFDMSSPAFFRIARRGNEGIVPVFYRRVGCKRRGGVRFLLRGGQNF
NMVMISNVGGGGSVRAVAVRGSKGTWLQMTRNWWGANWQSSGDLRGQRLSFKVT
LTDKKTQTFNLNVPSSWWFGQTFSSRGRQFV*

CDS (coding sequence)

>AhEXPA-04

ATGGATATGAAGGGAAAGTATCTGGTAACAGCTATTCTCTTGGTTGGTACGTTAA
GTGTGGGGATGTGTTCTAACGGTTGGATAAGAGCTCATGCAACGTATTATGGTGT
TAATGATAGCCCTGCTTCACTTGGAGGAGCTTGTGGGTATGACAATCCGTACCAC
GCCGATTTCGGAGCCACACGGCGGCTCTAAGCGGTGCGCTATTTAGAAGCGGC
GAGTCATGCGGTGGGTGCTACCAGGTGAGGTGCGACTATCCGGCGGATCCTAAGT
GGTGTCTCCGTGGAGCCCGCGTGACGGTGACGGCTACAACTTTTGTCCGTCGAA
CAACAATAATGGTTGGTGCAATCTCCCTCGCCATCACTTTGACATGTCCTCCCCCG
CTTTCTTCCGCATCGCCGTCGGGGCAATGAAGGCATCGTCCCCGTCTTCTATCGC
AGGGTGGGATGCAAAAGAAGAGGAGGCGTGAGGTTTACGTTGAGAGGGCAAGGT
AACTTCAATATGGTAATGATCTCAAACGTTGGCGGTGGCGGCTCGGTGAGAGCGG
TAGCGGTAAGAGGCTCAAAGGGAAAGACTTGGCTTCAGATGACCCGTAATTGGG
GTGCCAACTGGCAGAGCTCCGGCGATCTCCGGGGACAGAGACTCTCCTTCAAAGT
TACTCTGACTGACCGCAAACGCAGACGTTTTTGAACGTTGTTCCCTTCTTCTTGGT
GTTTTGGCCAAACCTTCTTCTTCGAGGACGCCAGTTCGTTTAA

Nucleotide

>AhEXPA-04

TGAACTCAAAGCTTTCTTTTCTCGACCTCTTTTTGTTTCAGCACGAAAGATATATA
CTTATCTGAAATCAAAGAACTTATATATATGGATATGAAGGGAAAGTATCTGGT
AACAGCTATTCTCTTGGTTGGTACGTTAAGTGTGGGGATGTGTTCTAACGGTTGG
ATAAGAGCTCATGCAACGTATTATGGTGTAAATGATAGCCCTGCTTCACTTGGTA
AAGAGTCCACTAAAGTACAGTTAATGTATTTTTTTTTGTTACTTTACTTTTTGTATA
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ATCCTAAGTGGTGTCTCCGTGGAGCCGCGGTGACGGTGACGGTACAACTTTTG
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CCTATCATTATTTCAAGTTATTAACATTATTGTTTTGTCTATAATCCATGGTAAGA
GGTTTAACTTTGATCAATTTGCTTGGTAAAATTTGGGATACTGCTTGAATCAAAA
TGATCACTAGCTAGATCATTAAAGCAACATTTGTAAGGAAAAAATCAATGAAGTT
TAGCATTGCCGTTTACAATACATCAGCATCACATTATAAGTAACATGTATAATTGT
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ACGAATCTGGAAAAGGGTTTAAACACTTGAGTTACATAAAAACATAGCATAAT
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CAGAGCTCCGGCGATCTCCGGGGACAGAGACTCTCCTTCAAAGTTACTCTGACTG
ACCGCAAACGCAGACGTTTTTGAACGTTGTTCCCTTCTTCTTGGTGGTTTTGGCCAA
ACCTTCTCTTCTCGAGGACGCCAGTTCGTTTAACTACAAAATAAGTCGTGCTCTG
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GAACTCGAC