

IDENTIFICATION

Species: *Arabidopsis halleri*

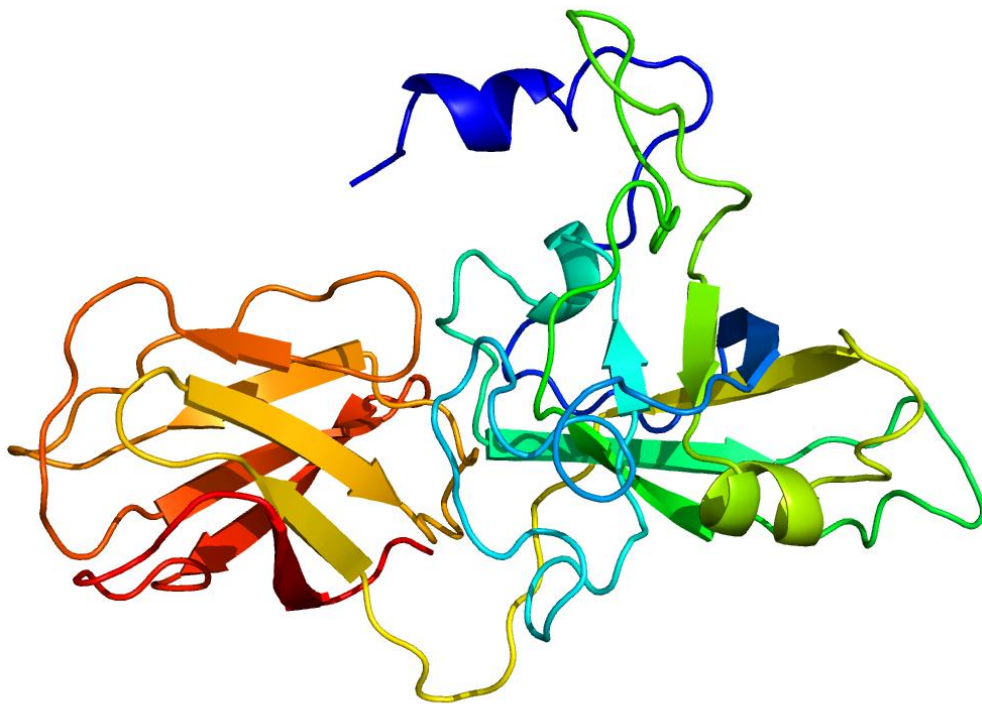
Locus: Araha.0898s0002

Gene Model: Araha.0898s0002.1

Description: AhEXPA-02

Family: Alpha Expansin

3D structure:



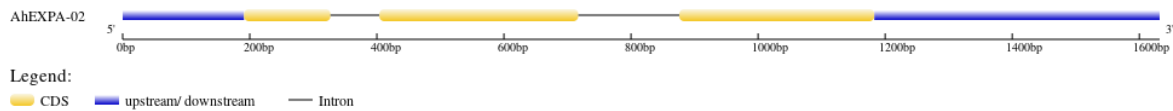
GENOME DATABASES

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

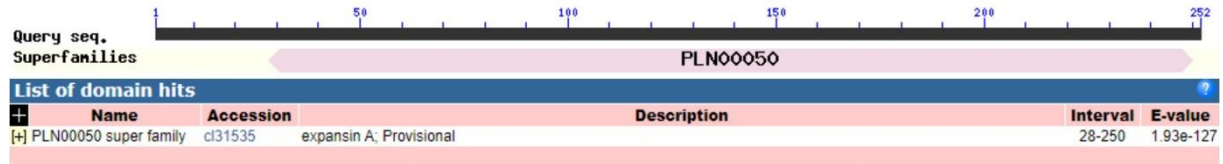
EXTERNAL RESOURCES

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

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>AhEXPA-02

MCHLGFLVMVMVGVMASSVSGYGGGGGWINAHATFYGGGDASGTMGGACGYGN
LYSQYGTSTAALSTALFNGLSCGSCFEIRCENDGKWCLPGSIVVTATNFCPPNNAL
ANNNGGWCNPPLEHFDLAQPVFQRIAQYRAGIVPVSYRRVPCRRRGGIRFTINGHSYF
NLVLITNVGGAGDVHSAAIKGSRTGWQAMSRNWQNWQSN SYLNGQALSFKVTT
DGRTVVSYNAAPAGWSYGQTFAGGQFR*

CDS (coding sequence)

>AhEXPA-02

ATGTGTCATCTTGGATTCTTAGTTATGGTTATGGTAGGAGTTATGGCTTCTTCAGT
GAGCGGCTACGGTGGCGGTGGCGGTTGGATCAACGCTCACGCCACTTTCTACGGT
GGAGGCGATGCTTCCGGCACAATGGGTGGTGCTTGTGGATATGGTAATCTATATA
GCCAAGGCTACGGGACAAGCACGGCTGCTTTGAGCACGGCTTTGTTCAACAATGG
ACTTAGTTGTGGTTCTTGCTTTGAGATAAGATGTGAAAACGATGGTAAATGGTGT
TTACCTGGCTCAATCGTTGTAACCGCTACAACTTCTGCCCGCCAATAACGCGTT
AGCGAACAATAATGGTGGTTGGTGAATCCTCCTCTTGAACACTTTGACCTTGCTC
AGCCTGTTTTTCAACGCATTGCTCAGTACAGAGCTGGAATCGTCCCTGTTTCATAT
AGAAGGGTACCATGCAGGAGAAGGGGAGGAATAAGATTCACGATAAACGGCCA
CTCATACTTCAACCTTGTGCTGATCACAAACGTCGGTGGTGCCGGAGATGTTAC
TCGGCGGCGATCAAGGGTTCAAGAACAGGTTGGCAAGCTATGTCAAGGAAGTGG
GGACAAAATTGGCAAAGCAACTCTTACCTCAACGGTCAAGCACTTTCCTTTAAGG
TCACCACCAGCGACGGCCGACCGTTGTATCCTACAACGCCGCTCCTGCCGGCTG
GTCTTACGGCCAGACTTTTGCCGGTGGACAGTTCCGCTGA

Nucleotide

>AhEXPA-02

CAGATTTTACATATCTCTCTTTCTTTCTTTTTCTTGAAGGAAAGAAGAAGATCT
CCAAATCCAAGTAACTACTTTCTCCACTTACATTCAATTGTTTCTCGTTTATTTCTC
GAATACACATTTACTTGAGCTAAAAGTCATGGACTTTATATCACCCATTTGCAGG
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GTTTTTTTCTTAAAACAGAGTATATGCTAAGTTTAGTAACAGAGTTCTTGAATAAA
TGGTCCAAAATTTTAACTTTTCGATACTTTGGTGTTTTATAGGGTACCATGCAGGA
GAAGGGGAGGAATAAGATTCACGATAAACGGCCACTCATACTTCAACCTTGTGCT
GATCACAAACGTCGGTGGTGCCGGAGATGTTCACTCGGCGGCGATCAAGGGTTCA
AGAACAGGTTGGCAAGCTATGTCAAGGAACTGGGGACAAAATTGGCAAAGCAAC
TCTTACCTCAACGGTCAAGCACTTTCCTTTAAGGTCACCACCAGCGACGGCCGCA
CCGTTGTATCCTACAACGCCGCTCCTGCCGGCTGGTCTTACGGCCAGACTTTTGCC
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