

IDENTIFICATION

Species: *Arabidopsis halleri*

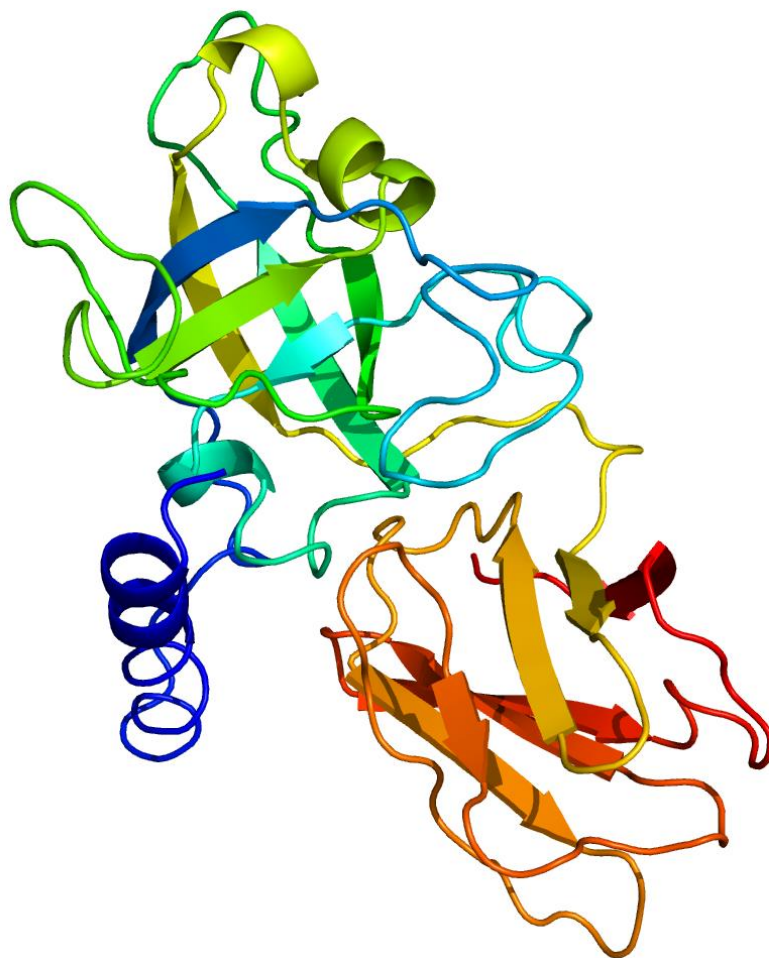
Locus: Araha.0846s0004

Gene Model: Araha.0846s0004.1

Description: AhEXPA-01

Family: Alpha Expansin

3D structure:



GENOME DATABASES

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

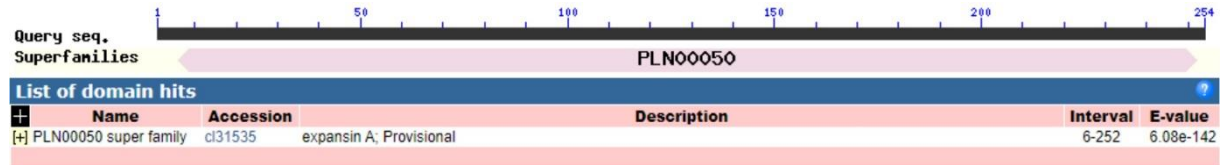
EXTERNAL RESOURCES

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

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>AhEXPA-01

MFMGKMSLLGFALLCYAAMVCSVHAYDAGWVNAHATFYGGSDASGTMGGACGY
GNLYSQGYGTNTAALSTALFNGLSCGACFEIKCQSDGAWCLPGAIIVTATNFCPPNN
ALPNNAGGWCNPLHHFDLSQPIFQRIAQYKAGVVPVSYRRVPCMRGGIRFTINGH
SYFNLVLTNVGGAGDVHSAVKGSRTRWQQMSRNWQNWQSNLLNGQALSFK
VTASDGRTVVSNNIAPASWSFGQTFGRQFR*

CDS (coding sequence)

>AhEXPA-01

ATGTTTCATGGGAAAGATGAGTCTTTTGGGATTTGCTCTGTTGTGTTATGCTGCAAT
GGTGTGCTCTGTTTCATGCTTATGACGCTGGATGGGTCAATGCTCATGCTACCTTCT
ATGGTGGAAGTGATGCTTCAGGAACAATGGGTGGAGCATGTGGCTATGGGAATC
TCTATAGTCAAGGATACGGTACCAACACGGCGGCGTTGAGCACTGCTCTGTTCAA
TAACGGTCTTAGCTGCGGCGCGTGTTCGAGATCAAGTGTCAGAGCGACGGCGCG
TGGTGTTTACCTGGTGCTATCATAGTCACAGCCACCAATTTCTGTCCTCCTAACAA
CGCTCTTCCCAATAACGCTGGTGGTTGGTGTAACCTCCGCTTCATCATTTCGATC
TCTCTCAGCCGATTTTCCAACGCATTGCCCAGTACAAAGCTGGTGTGTCCTGTT
TCTTACAGAAGGGTTCCTGCATGAGAAGGGGAGGCATAAGGTTACAATCAAT
GGCCACTCTTACTTCAACCTGGTTTTGGTGACCAATGTTGGTGGTGCTGGAGATGT
TCACTCTGTAGCGGTTAAAGGTTCAAGAACAAGGTGGCAACAAATGTCAAGAAA
CTGGGGTCAAACTGGCAAAGCAACAATCTTTAAATGGTCAAGCATTGTCCTTT
AAGGTTACTGCTAGTGATGGTCGTACCGTCGTCTCTAACAAACATTGCTCCGGCTA
GTTGGTCTTTTGGACAAACCTTCACCGGCCGTCAATTCCGTTGA

Nucleotide

>AhEXPA-01

CATTCTATAAATTCCACTTCAACCATCAACCTTCTTCTTCACTCCCATCAACTATCT
TTCTCCTTCACATTCCATTTTCTTACTCTCCTCCATTAAGCTCTGCACTTTCTC
AAAGAGAATGTTTCATGTAATAACCATCTTCTTTCAAATCCATCTTTAACTTTT
TTTCTCTTGCTTATAATGTATAAAGTTCTAATTTTTGTTTGAAATTTTGTTCAATTG

CAGGGGAAAGATGAGTCTTTTGGGATTTGCTCTGTTGTGTTATGCTGCAATGGTGT
GCTCTGTTTCATGCTTATGACGCTGGATGGGTCAATGCTCATGCTACCTTCTATGGT
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GTGTCAGAGCGACGGCGCGTGGTGTTTACCTGGTGCTATCATAGTCACAGCCACC
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TCCGCTTCATCATTTTCGATCTCTCTCAGCCGATTTTCCAACGCATTGCCAGTACA
AAGCTGGTGTGTCCCTGTTTCTTACAGAAGGTAAAACATAGATCTTTACTGTTAC
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GGTCTTCATAATTGCTCTGTTTCTTAAAGAAGTTGAAGACTTTAATGGCGAAAGTT
TCAATCTTTATTCAATTTTCTCGTTGTCACTGTTGGTGAAAGCTCCAATCTTTATTC
AATTTTGGATCTGAGTATCGATAATCTTACAATGCGTCTTCATAAATTTTGTATAT
TCTCGGTTTCTCTCTGTTATTA ACTGATGTTTTTTTTGTTTGCTTTATGTGTAGGGT
CCGTGCATGAGAAGGGGAGGCATAAGGTTCAATCAATGGCCACTCTTACTTCA
ACCTGGTTTTGGTGACCAATGTTGGTGGTGCTGGAGATGTTCACTCTGTAGCGGTT
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CAAAGCAACAATCTTTTAAATGGTCAAGCATTGTCCTTTAAGGTTACTGCTAGTG
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ACCTTCACCGGCCGTCAATTCCGTTGAAATTGTGTCAAGTTCGGTTTTATATAGTT
TAGGGTTTTGTGTAGTAGTGGTTGAGGAAAGAGGAGAGAAAGAGACAGGGTTTAA
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GTAAAATGGAGAAAAGAGCTTATTT