

IDENTIFICATION

Species: *Arabidopsis halleri*

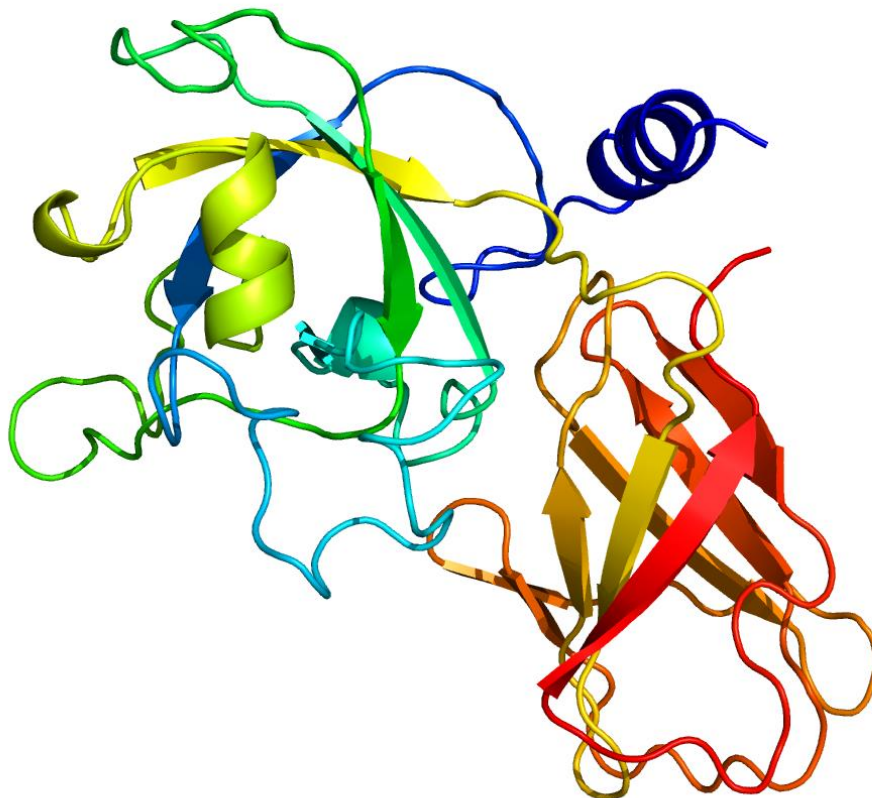
Locus: Araha.18708s0001

Gene Model: Araha.18708s0001.1

Description: AhEXPA-12

Family: Alpha Expansin

3D structure:



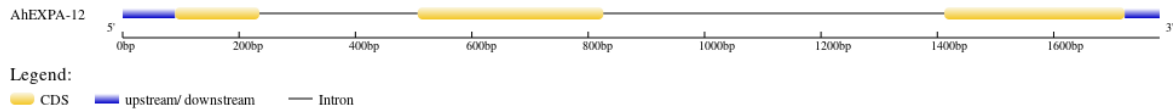
GENOME DATABASES

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

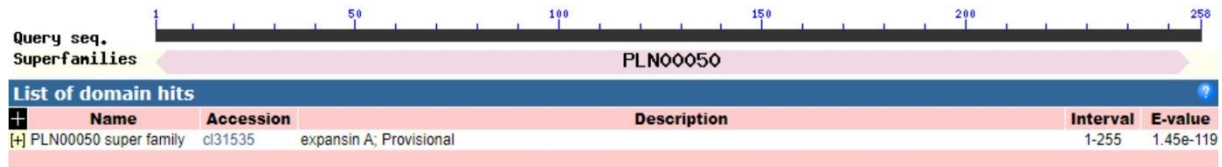
EXTERNAL RESOURCES

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

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>AhEXPA-12

MRMLGLVLSVLTILALSEARIPGVYNGGGWETAHATFYGGSDASGTMGGACGYGN
LYSQYGVNTAALSTALFNNGFSCGACFELKASDPRWCHSGSPSIFITATNFCPPNF
AQPSDNGGWCNPPRPHFDLAMPFLKIAEYRAGIVPVSFRRVPCRKRGGIRFTINGFR
YFNLVLVTNVAGVGNIVRLGVKGTHTSWMSMSRNWQNWQSNVSVGQSLFRVT
GSDRRSSTSWNIAPANWQFGQTFMGKNFRV*

CDS (coding sequence)

>AhEXPA-12

ATGAGAATGTTGGGTTTGGTTTTATCTGTTCTTACCACAATTCTTGCATTGTCTGA
AGCAAGAATCCCAGGAGTTTACAATGGAGGTGGTTGGGAAACTGCTCATGCCACT
TTCTATGGTGGCTCTGATGCTTCTGGAACCATGGGTGGTGCTTGTGGTTATGGTAA
CTTATACAGCCAAGGCTATGGTGTTAACACGGCGGCTCTAAGCACGGCTCTGTTC
ACAATGGTTTTAGCTGTGGTGCTTGTTTTGAGCTCAAGTGTGCGAGTGATCCAA
GATGGTGCCATTCTGGTAGTCCTTCAATCTTCATCACTGCGACTAATTTCTGTCTC
CCGAACCTTTGCTCAGCCTAGTGACAATGGCGGTTGGTGTAACCCTCCTAGGCCTC
ACTTTGATCTTGCTATGCCTATGTTCCCTTAAGATTGCTGAGTATCGCGCCGGAATC
GTCCCCGTCTCTTCCCGCGTGTGCCATGCCGGAAGAGAGGAGGAATAAGGTTCA
CGATCAACGGTTTCCGTTACTTTAACTTGGTTCTAGTCACAAACGTCGCCGGTGTC
GGAAACATAGTCCGACTAGGAGTGAAAGGAACATACTTCGTGGATGAGCATG
AGTCGTAACCTGGGGGCAAACTGGCAATCTAACTCAGTTTTGGTTGGTCAGTCAC
TTTCTTTTAGAGTCACAGGCAGTGACCGTAGAAGCTCGACGTCGTGGAACATTGC
TCCGGCGAATTGGCAGTTTGGTCAGACTTTCATGGGAAAGAACTTCAGAGTCTGA

Nucleotide

>AhEXPA-12

AGACACTCCAATAGACTCTTCTTCTTCTTCTTCCTCTGCCTCTTTCTCCCAAACGT
CTCTCTATTTTCTCACACTCTCTCTCTCATTATGAGAATGTTGGGTTTGGTTTTA
TCTGTTCTTACCACAATTCTTGCATTGTCTGAAGCAAGAATCCCAGGAGTTTACAA
TGGAGGTGGTTGGGAAACTGCTCATGCCACTTTCTATGGTGGCTCTGATGCTTCTG
GAACCATGGGTATGTCTCTCTCTCTCTTCTCTTCCACATTCTAATCAATCTTAAC
CTAAAGTTCCAATCTTTTTTTGTAACCACATTGTGAAAATGTTAAAATCTTGATTT
TGTACCTTAAAGATTTCAACTTTAATAAAAACCCAACCTTAAAGTTCCAATCTTTTT
GTTTCATCTTTGCTAAACCAAACCTACCACATTGTCAAATTAACGGTTTTTATTGCAT
CTTCTTGATTTTGAACCCCAAAAAGGTTTAAACTTTTTGCTCTGTTTTCTTTTTTCAGG
TGGTGCTTGTGGTTATGGTAACTTATACAGCCAAGGCTATGGTGTAAACACGGCG
GCTCTAAGCACGGCTCTGTTCAACAATGGTTTTAGCTGTGGTGCTTGTTTTGAGCT
CAAGTGTGCGAGTGATCCAAGATGGTGCCATTCTGGTAGTCCTTCAATCTTCATC
ACTGCGACTAATTTCTGTCTCCGAACCTTGTCTCAGCCTAGTGACAATGGCGGTTG
GTGTAACCCTCCTAGGCCTCACTTTGATCTTGTCTATGCCTATGTTCCCTAAGATTG
CTGAGTATCGCGCCGGAATCGTCCCCGTCTCTTCCGCCGGTAAGAAGAACAAC
TCCTAGGCTTTTAGATTGGTTTCTTGAATTAGAAAAAATTGGGGTTAACTTTAGTA
TATTATGAACCTTTGGGGTGTGAAATTTAATATCTTAGAAGTATTGGGGTTGCTGTT
GGGAAGTCCAATGATTGGGGTTATTGCCGACAGAATTAAGTTTGGGGTATTA
AACATAACATTTTTATAAATACCATGGTGCAGTTGTAAATTCTTATTTCTAGATTC
TGAATAATTTGGGTAAATGTGAAAGAATTTAAAGTTTGGGGTGTAAATATAAAA
TTTTTGAAGTATAGGGGTATGGTTGAAAAGTCTGTCTTTGATTCTTGGCGCGAGTC
GGTGCGACATTTATGTCGGGTCTCTAGTACTTGGCTAAATTACCAAATCTAAAAG
ATCTTATTTTCTGCAAAAAGACGAAACTGTCCTTCCAACAATCTCTATTTTACCTA
TCAGTACTATTTGCAAAAAGTCAAGAGTAACAATAATGAAATGGTGTCTTTTAGT
CAACAACGCGTTTTCTCCTTTTTATTGAAATGACGTAACCTTGACTTGTTTG
TTTTAATTACAACAGTGTGCCATGCCGGAAGAGAGGAGGAATAAGGTTACGATC
AACGTTTCCGTTACTTTAACTTGGTTCTAGTCACAAACGTCGCCGGTGTCCGAA
ACATAGTCCGACTAGGAGTGAAAGGAACACATACTTCGTGGATGAGCATGAGTC
GTAACCTGGGGGCAAACTGGCAATCTAACTCAGTTTTGGTTGGTCAGTCACTTTC
TTTTAGAGTCACAGGCAGTGACCGTAGAAGCTCGACGTCGTGGAACATTGCTCCG
GCGAATTGGCAGTTTGGTCAGACTTTCATGGGAAAGAATTCAGAGTCTGAGGGC
AAAATCGGAAACTCATCTATCTATTTAGTATTTTTATTATTATTAAAATTTCC