

IDENTIFICATION

Species: *Arabidopsis halleri*

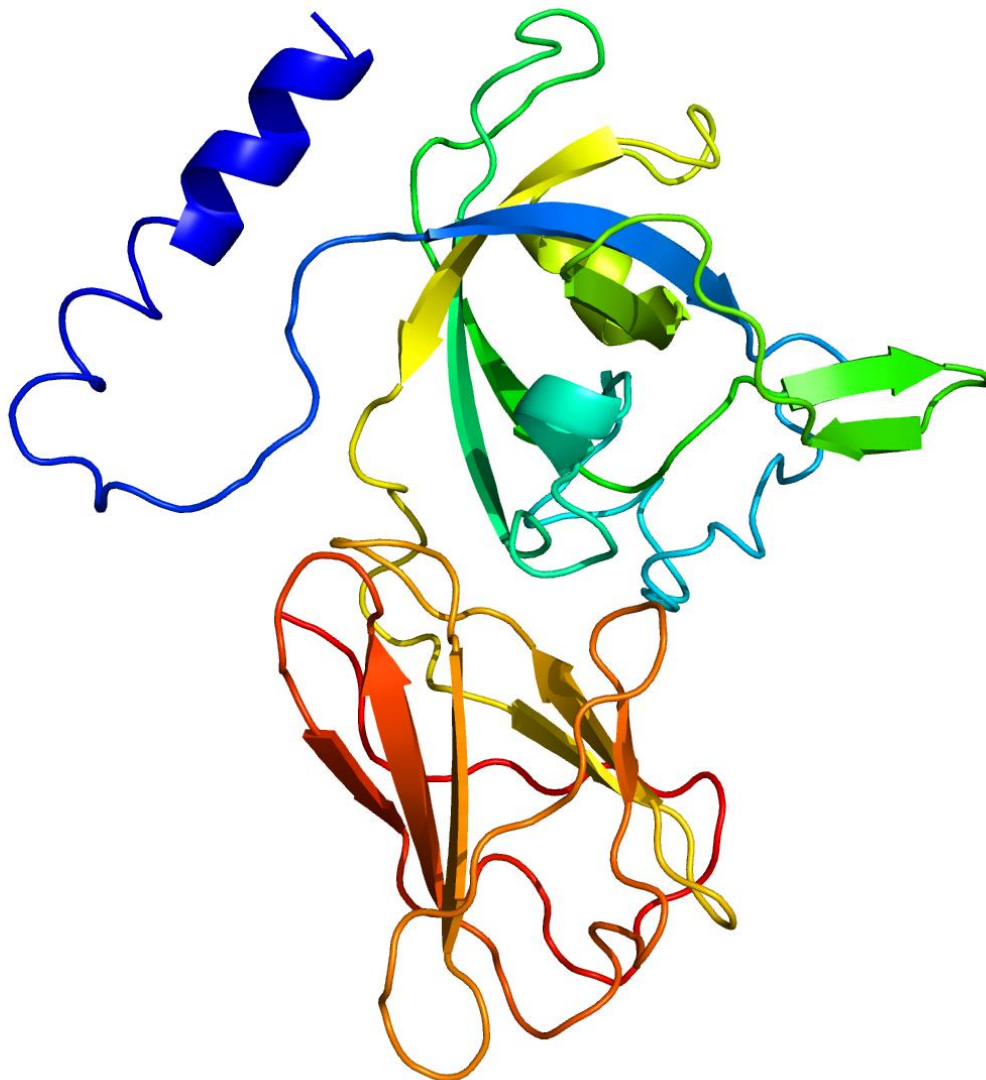
Locus: Araha.20073s0002

Gene Model: Araha.20073s0002.1

Description: AhEXPA-13

Family: Alpha Expansin

3D structure:



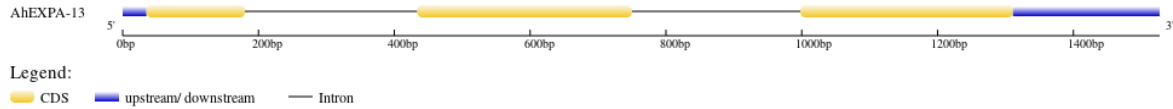
GENOME DATABASES

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

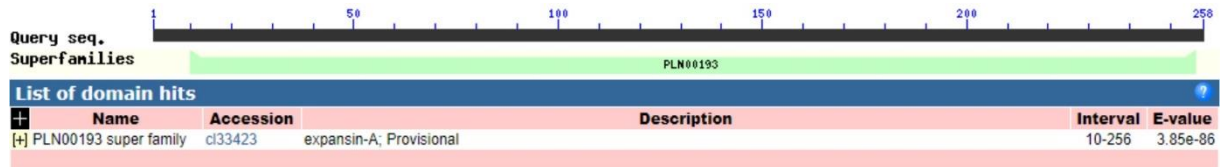
EXTERNAL RESOURCES

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

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>AhEXPA-13

MDQONLYHKCLVILSMMAMIGTSM AAYAGTPWRTASATFYGDETGSATMGGACGY
GNMWDSGYGVATTALSTALFNDGYACGQCFQIRCVSSPNCYYGSPATVVTATNICPP
NYGQASNNGGWCNPPQVHFDLAKPAFMKIANWKAGIVPLSYRRVACKRTGGIRFKF
EGNGYWLLVYVMNVGGAGDIKTMAVKGSRTGWINMSHNWGASYQAFSSLYGQSL
SFRLTSYTTRQTIYA YNGAPASWSAGKTYQSKANFN*

CDS (coding sequence)

>AhEXPA-13

ATGGATCAA AATTTGTATCAC AAGTGCTTGGTTATTTTATCGATGATGGCAATGAT
CGGCACATCAATGGCGGCATATGCCGGGACCCCATGGCGTACGGCCTCAGCCACT
TTTTACGGTGACGAGACCGGTAGCGCAACTATGGGTGGGGCGTGTGGCTATGGTA
ACATGTGGGACAGCGGCTACGGCGTAGCCACGACTGCGCTGAGCACAGCTCTGTT
CAACGACGGTTATGCATGCGGTCAATGTTTCCAGATAAGGTGTGTGTCGTCGCCT
AACTGCTACTACGGTTCACCAGCCACCGTGGTGACTGCGACCAACATATGTCCAC
CGAATTATGGCCAAGCCTCCAACAATGGTGGATGGTGTAAATCCGCCACAAGTCCA
TTTTGATTTGGCTAAACCAGCTTTCATGAAGATCGCTAATTGGAAGGCTGGTATTG
TTCCCCTCTCATACCGCAGAGTGGCATGTAAGAGAACCGGAGGAATAAGGTTTAA
ATTTGAAGGAAATGGGTATTGGCTACTTGTGTACGTGATGAACGTAGGTGGTGCA
GGTGACATCAAGACCATGGCCGTGAAAGGTAGCCGCACAGGGTGGATTAATATG
AGCCATAATTGGGGAGCTTCGTACCAAGCCTTTTCTTCTCTCTACGGTCAGTCTCT
CTCGTTCGGGCTCACCTCTTACACCACTCGTCAGACCATTTACGCTTATAATGGTG
CTCCGGCTAGCTGGAGCGCCGGCAAGACCTACCAGAGCAAGGCTAATTTTAACTG
A

Nucleotide

>AhEXPA-13

ATAAGAGTAGGAGCCCTCGAGAAAACAGAGTAAAAATGGATCAAAATTTGTATC
ACAAGTGCTTGGTTATTTTATCGATGATGGCAATGATCGGCACATCAATGGCGGC
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AAGTAGAACACAACTATATATGACTCAATTGCATATTATTTGAAAAAATTGTTT
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CACGATGAAACAATTATGGCTTATATATAAATACATGAATCTTTAATTTCGAAGA
TCATTA AAAATGTATTGACAATTTTTAACATGACCATGTATATCGATCAGGTGGGG
CGTGTGGCTATGGTAACATGTGGGACAGCGGCTACGGCGTAGCCACGACTGCGCT
GAGCACAGCTCTGTTCAACGACGGTTATGCATGCGGTCAATGTTTCCAGATAAAG
TGTGTGTCGTCGCCTAACTGCTACTACGGTTCACCAGCCACCGTGGTGACTGCCA
CCAACATATGTCCACCGAATTATGGCCAAGCCTCCAACAATGGTGGATGGTGTAA
TCCGCCACAAGTCCATTTTGATTTGGCTAAACCAGCTTTCATGAAGATCGCTAATT
GGAAGGCTGGTATTGTTCCCCTCTCATACCGCAGGTAATATCCACTACATAAGTA
CATACTAAATATAACAATTTTCACTTTTTTGGGAAGAGATGTGTATATAACAAGGACT
AACGTTTTATAATTACAGAGGTA TAGATTGAAAACGTAAAGAAATTGTTTATAT
AACCATTGTGAATTCAGTATATTTATATTCAAATATTTTTAAATGAGGTCTTGTTT
GAAAGCACATTTTGCACATGCCTAAAATACGATAATTTTGTTCATATATATATATA
TGCAGAGTGGCATGTAAGAGAACCGGAGGAATAAGGTTTAAATTTGAAGGAAAT
GGGTATTGGCTACTTGTGTACGTGATGAACGTAGGTGGTGCAGGTGACATCAAGA
CCATGGCCGTGAAAGGTAGCCGCACAGGGTGGATTAATATGAGCCATAATTGGG
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GAGCGCCGGCAAGACCTACCAGAGCAAGGCTAATTTTAACTGAGTTAGGTCATAT
TCATTTCTGAAAAACCGGTTATTCGAATTTACGGTTTTGCTACTTGTATTGAGGC
TGATCGATCCAGAGGTTGATCTTTTTCTAATTAATAACTCCCTTTGATTATATGGT
AGTCACTAATTCTTGTATATCCATTCCATCGTTGGTTGAGGAAAAATTGTTGATTT
TTTGTGTATTTAAGTTTTTGAATTTTATTTTCATTT