

IDENTIFICATION

Species: *Arabidopsis halleri*

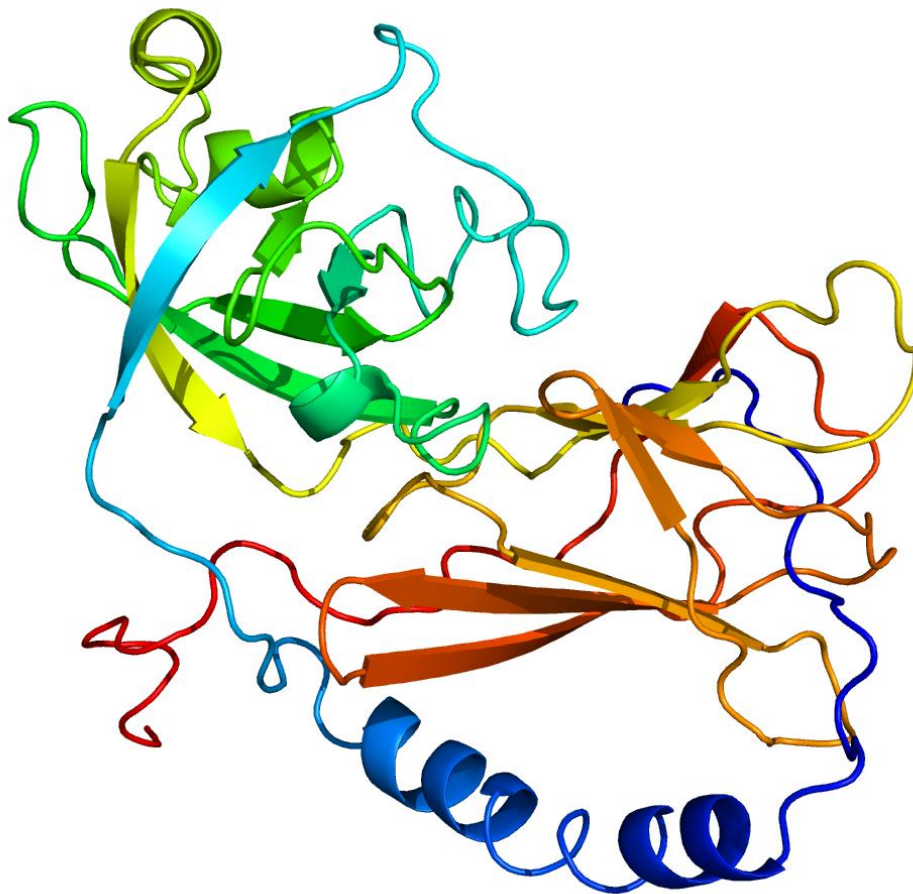
Locus: Araha.48675s0002

Gene Model: Araha.48675s0002.1

Description: AhEXLA-03

Family: Expansin Like Alpha

3D structure:



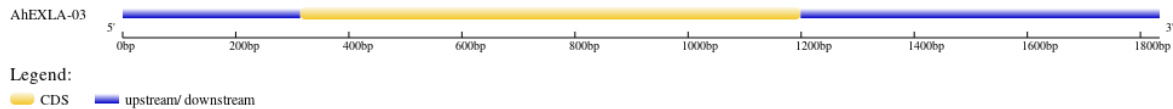
GENOME DATABASES

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

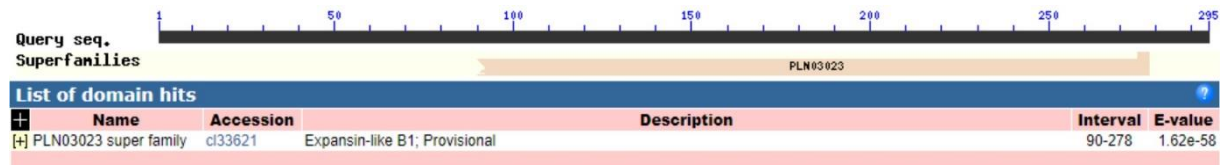
EXTERNAL RESOURCES

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

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>AhEXLA-03

MGFIHSLPLLIFRRIPHPINNIIGFFKMEGFLFLLSVVFLFSSSAAACDRCLHRSKAA
YFSSASALSSGACAYGSMATGFFAGHIAAALPSIYKDGS GCGACFQVRCTNPTLCSSK
GTTVMLTDLNKSNTDLILSSRAFRAMAKPVVGS DRDLLKQGLVDIEYRRVPCDYG
NKKMNRVEESSINPNYLAIKLLYQGGQTEVVAIDIAHVGSSHWSYMTRSHGAVVW
TDKVPTGALQFRFVVTAGYDGKMVWSQRVLPANWEAGKTYDAGVQITDIAQEGCD
PCDDHIWN*

CDS (coding sequence)

>AhEXLA-03

ATGGGGTTCATTCACTCTCTCCTTCCTCCTCCTCATTTCGTCGCATCCCCACCAC
CCCATTAATAATATTATTGGTTTCTTCAAGAAAATGGAAGGCTTCTCTTCCTCCT
CTCAGTCGTCTTCTCTTCTCCTCATCTGCAGCCGCCTGCGACCGATGTCTTACC
GTTCTAAGGCTGCTTATTTCTCCTCTGCCTCTGCTCTCTCCTCCGGAGCTTGTGCCT
ATGGCTCTATGGCTACGGGTTTCTTCGCCGGACACATTGCCGCGGCTCTGCCTTCC
ATCTACAAAGACGGCTCCGGCTGCGGAGCTTGCTTCCAGGTCAGATGTACGAACC
CGACGCTTTCAGCAGCAAAGGAACAACGGTGATGCTCACAGACCTGAACAAGA
GCAACCAAACCGATCTTATCCTTAGCAGCAGAGCCTTAGGGCCATGGCTAAGCC
TGTTGTTGGCTCCGACAGAGATCTTCTCAAACAAGGCCTTGTGACATTGAATAC
AGGAGAGTTCCTTGCATTACGGGAACAAGAAGATGAACGTGCGAGTTGAAGAA
TCAAGCATAAATCCAACTACTTGGCGATAAAGCTCTTGTACCAAGGAGGCCAAA
CCGAAGTGGTAGCCATCGACATTGCTCACGTTGGTTCGTCACATTGGAGTTACAT
GACCAGAAGCCACGGAGCCGTGTGGGTTACTGACAAAGTACCAACCGGAGCTCT
GCAGTTCAGGTTCTGTTGACCGCAGGCTACGACGGCAAAATGGTCTGGTTCGCAG
AGGGTCCTTCCCGCTAACTGGGAAGCTGGGAAGACCTATGACGCCGGCGTTCAGA
TCACCGACATTGCTCAGGAAGGTTGTGATCCATGCGACGATCACATCTGGAAC TG
A

Nucleotide

>AhEXLA-03

CCTCTTAAGTGAATAAAATGTCTCTTAGTTAAGGAACGTTTGTTAACTTTAATAGT
GATTTATCATTTAATTTTTATTAGTTATTACCTAAGATTTTTGCTAAGGAACTACC
GTTAATGATGGCCTTACACACTACACACTACTACAGTACTGCTACTCAAACCTC
AAGTCAATAAATAATGAACACGCCTACTCTTGTGCCAGCTGCTTCTATTTACGAC
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CTGCGGAGCTTGCTTCCAGGTCAGATGTACGAACCCGACGCTTTGCAGCAGCAA
GGAACAACGGTGATGCTCACAGACCTGAACAAGAGCAACCAAACCGATCTTATC
CTTAGCAGCAGAGCCTTTAGGGCCATGGCTAAGCCTGTTGTTGGCTCCGACAGAG
ATCTTCTCAAACAAGGCCTTGTCGACATTGAATACAGGAGAGTTCCTTGCGATTA
CGGGAACAAGAAGATGAACGTGCGAGTTGAAGAATCAAGCATAAATCCAAACTA
CTTGGCGATAAAGCTCTTGTACCAAGGAGGCCAAACCGAAGTGGTAGCCATCGA
CATTGCTCACGTTGGTTCGTACATTGGAGTTACATGACCAGAAGCCACGGAGCC
GTGTGGGTTACTGACAAAGTACCAACCGGAGCTCTGCAGTTCAGGTTTCGTGGTGA
CCGCAGGCTACGACGGCAAATGGTCTGGTCGCAGAGGGTCCTTCCCCTAACTG
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GTATCTCC