

IDENTIFICATION

Species: *Arabidopsis halleri*

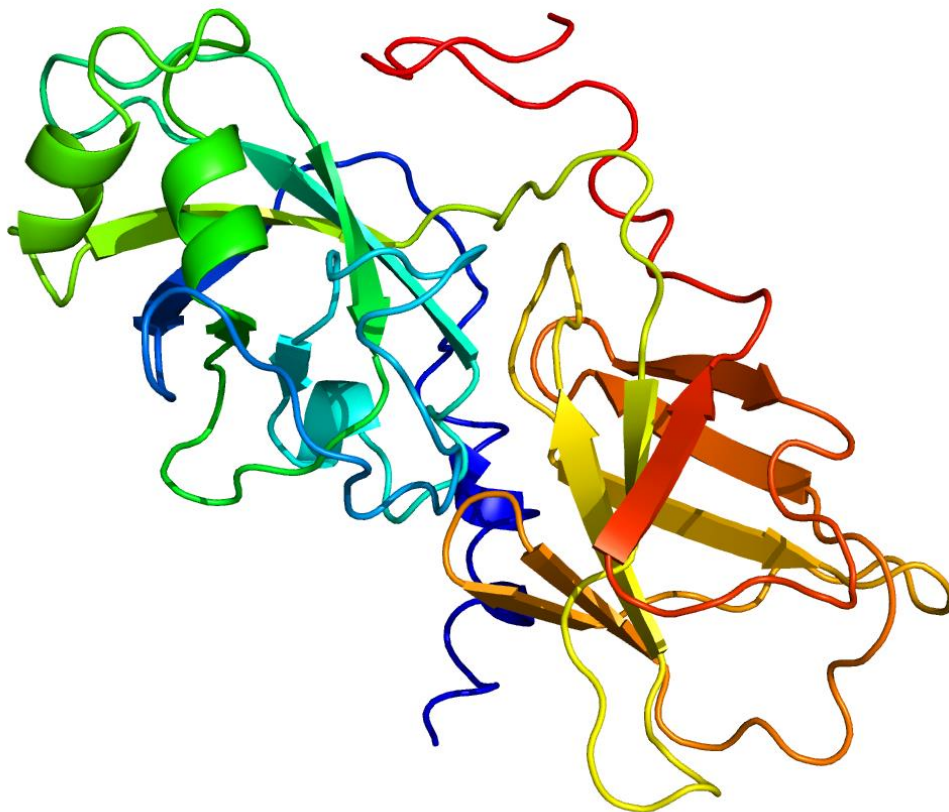
Locus: Araha.35044s0003

Gene Model: Araha.35044s0003.1

Description: AhEXLA-02

Family: Expansin Like Alpha

3D structure:



GENOME DATABASES

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

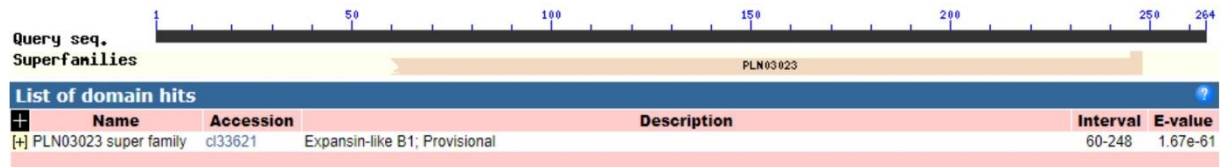
EXTERNAL RESOURCES

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

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>AhEXLA-02

MKSFLYLIVVIFLFSNVNACDRCLHRSKAAYFSSASALSSGACAYGPMATRFFAGHIS
AAIPSIYKDGAGCGACFQVRCKNPKLCSSKGTIVMVTDLNTSNQTDLVLSSRAFRAM
AKPVVGADKYLKQGIQVDEYQRVPCNYGTRNLNVRVEEASKGPNYLAIKLLYQGG
QTEVVGIDIARVDSSQWSYMTRSHRAVWATDKVPTGALQFRFTVTGGYDGMVWS
KRVLPANWKAGMIYDTGVQITDIAQEGCDTCGHIWN*

CDS (coding sequence)

>AhEXLA-02

ATGAAAAGCTTTCTCTACCTCATCGTTGTCATCTTTCTCTTCTCATCATCTGTTAAC
GCATGTGATCGATGTCTTCATCGTTCTAAAGCAGCTTATTTCTCCTCTGCTTCTGCT
CTCTCTTCTGGAGCTTGTGCTTATGGCCCTATGGCTACGAGATTCTTTGCGGGCCA
CATTTCAGCGGCTATACCTTCCATTTACAAAGATGGTGCTGGCTGTGGAGCTTGT
TCCAAGTCAGATGCAAGAACCCCAAGTTGTGTAGCAGTAAAGGAACCATTGTGAT
GGTCACTGACTTGAACACGAGCAACCAAAGTATCTTGTCTTAGTAGTAGAGCT
TTTAGGGCAATGGCTAAGCCTGTTGTTGGTGCTGACAAATACCTTCTCAAACAAG
GCATTGTGACGTTGAATACCAAAGAGTTCCTTGCAATTATGGTACAAGGAATTT
GAACGTGAGAGTGGAAGAAGCAAGTAAAGGGCCAAATTACTTGGCGATAAAGCT
TTTGTACCAAGGAGGCCAAACCGAAGTGGTAGGTATCGACATTGCTCGAGTGGAT
TCGTCACAATGGAGTTACATGACTAGAAGCCACAGAGCCGTGTGGGCGACGGAT
AAAGTACCAACTGGAGCTCTACAGTTCAGGTTACGGTGACAGGCGGCTACGATG
GCAAAATGGTTTGGTCCAAGAGAGTTCTTCCGGCCAATTGGAAAGCTGGGATGAT
CTATGATAACGGTGTTCAGATAACCGACATTGCTCAAGAAGGTTGTGATACATGC
GGTCACATATGGAAGTGA

Nucleotide

>AhEXLA-02

CTCTACTTTGCTCATATAGATATTATTTTTTTCCTCTAGAAAAAAAAACAAAATG
AAAAGCTTTTCTCTACCTCATCGTTGTCATCTTTCTCTTCTCATCATCTGTAAACGCA
TGTGATCGATGTCTTCATCGTTCTAAAGCAGCTTATTTCTCCTCTGCTTCTGCTCTC
TCTTGAAACTACCCCATCTTCTTCTCATTACTTCCTTTTAACTATATAGAATTTAA
GAGAAAGAAATCAAGAACTCAAAGAATAACTCTCTTTTATTACTTTAGAAAATA
TCTCAAAACTAAAGTCTCCTCTCAATCTCTCTCAAACCTCTTAAGGTTAGCCACAC
CATTGGCAACTCTTATATAGAGACTTGACTTGATAACTCCAAATCAAACCTAGGAC
TAAACTTAGATAACTCCTAAACATTATTTAGATAACTCCTAAATAATTCTAGTAA
TATCTCTTCCTTTATTTTAGTAACTTCAAGCTCAAGTACTCTTCAAGCTTATCAAC
AAACTACTTGTTTGTTCCTTTTCTCATATCTTGTTCCTTGTATCTGTTTTTGCAGCTG
GAGCTTGTGCTTATGGCCCTATGGCTACGAGATTCTTTCGCGGCCACATTTTCAGCG
GCTATACCTTCCATTTACAAAGATGGTGCTGGCTGTGGAGCTTGCTTCCAAGTCA
GATGCAAGAACCCCAAGTTGTGTAGCAGTAAAGGAACCATTTGTGATGGTCACTG
ACTTGAACACGAGCAACCAAACCTGATCTTGTCTTAGTAGTAGAGCTTTTAGGGC
AATGGCTAAGCCTGTTGTTGGTGCTGACAAATACCTTCTCAAACAAGGCATTGTC
GACGTTGAATACCAAAGGTTTCGATTCTTGAACACTTAACTTCTTGGTTTTTTAAT
AGTCACTTGATTTACTTTAGTACTAATAATAAGAAGGTTTTGGAAATGAAACAGA
GTTCTTGAATTATGGTACAAGGAATTTGAACGTGAGAGTGAAGAAGCAAGT
AAAGGGCCAAATTACTTGGCGATAAAGCTTTTGTACCAAGGAGGCCAAACCGAA
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GAAGCCACAGAGCCGTGTGGGCGACGGATAAAGTACCAACTGGAGCTCTACAGT
TCAGGTTACGGTGACAGGCGGCTACGATGGCAAATGGTTTGGTCCAAGAGAG
TTCTTCCGGCCAATTGGAAAGCTGGGATGATCTATGATACCGGTGTTTCAGATAAC
CGACATTGCTCAAGAAGGTTGTGATACATGCGGTCACATATGGAACCTGACTTATT
ACAATTTTCCTTATTTATAGGCAAACAACAACATATGGAACCGACATGTTTTTTTT
TCCCTTTATAGGATTATACATGTATGTGTAACACAACAAGGAACTAAAATAAAA
TCTATATATGTACACGGTACACC