

IDENTIFICATION

Species: *Arabidopsis halleri*

Locus: Araha.8490s0006

Gene Model: Araha.8490s0006.1

Description: AhEXPA-07

Family: Alpha Expansin

3D structure:



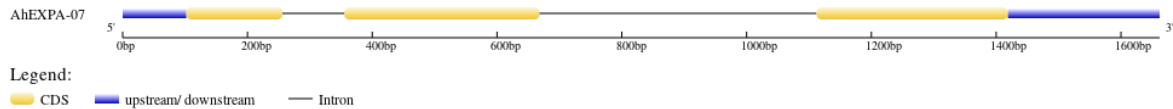
GENOME DATABASES

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

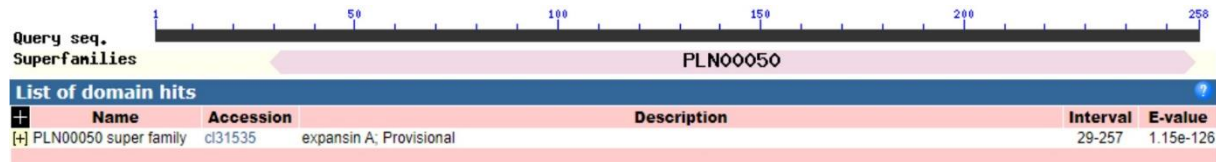
EXTERNAL RESOURCES

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

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>AhEXPA-07

MSITSASKYSIISIISLLSLSFFLQGTHGDDGGWQGGHATFYGGEDASGTMGGACGYG
NLYGQGYGTNTAALSTALFNGLTCGACYEMKCNDPRWCLGSTITVTATNFCPPN
PGLSNDNGGWCNPPLQHFDLAEP AFLQIAQYRAGIVPVSFRRVPCMKKGGIRFTINGH
SYFNLVLISNVGGAGDVHAVSIKGSKTQSWQAMSRNWGQNWQSN SYMNDQSLSFQ
VTTSDGRTLVSNDVAPSNWQFGQTYQGGQF*

CDS (coding sequence)

>AhEXPA-07

ATGTCTATCACATCAGCCTCCAAATATTCAATAATCTCAATTATATCTTTACTCAG
CTTATCATTCTTCCCTCCAAGGAATCATGGAGACGACGGAGGTTGGCAAGGTGGT
CACGCTACGTTCTACGGCGGTGAAGATGCTTCTGGCACCATGGGCGGAGCTTGTG
GCTATGGAAATTTGTATGGCCAAGGTTACGGGACGAACACGGCGGCTTTAAGTAC
GGCTTTATTCAACAACGGACTCACGTGTGGCGCGTGCTATGAGATGAAGTGTAAC
GATGACCCGAGGTGGTGTCTCGGGTCTACCATCACCGTCACAGCCACTAACTTTT
GCCACCAAACCCTGGCCTCTCCAACGATAATGGAGGTTGGTGAATCCTCCTCT
TCAACATTTGACCTAGCCGAGCCAGCTTTTCTCCAGATCGCTCAGTATCGTGCCG
GCATTGTTCTGTCTCTTTCCGAAGAGTACCATGTATGAAGAAAGGAGGAATAAG
GTTACGATCAACGGACATTCATACTTCAACCTCGTCCTGATCTCGAACGTAGGA
GGAGCAGGAGATGTCCACGCTGTCTCGATCAAAGGCTCAAAAACACAGTCGTGG
CAAGCAATGTCTAGAAATTGGGGACAAAACCTGGCAGAGCAATTCTTACATGAAC
GACCAAAGCCTTTCTTCCAGGTCACCACCAGCGATGGTTCGCACACTCGTTAGCA
ATGACGTGGCTCCTTCTAATTGGCAATTCGGACAAAACCTACCAAGGCGGTCAATT
CTGA

Nucleotide

>AhEXPA-07

TTCTCAATCCCTCCATTTGATTCCATACCAGTCTCACGATTCTCACCAAATCATAT
CCGATATCACAACCGAAATAACCAACCCCTTAAAAAAAAAAAAAAAAAATGTCTAT
CACATCAGCCTCCAAATATTCAATAATCTCAATTATATCTTTACTCAGCTTATCAT
TCTTCCTCCAAGGAACTCATGGAGACGACGGAGGTTGGCAAGGTGGTCACGCTAC
GTTCTACGGCGGTGAAGATGCTTCTGGCACCATGGGTACGTATGTCCAATAACAA
TATAAAAAAAAAAGCGTATGTTAGCTAAATTATATCTATACCCATGCGTATGTTAGC
TAACAAGCGGCATGCACAAATCAGGCGGAGCTTGTGGCTATGGAAATTTGTATGG
CCAAGGTTACGGGACGAACACGGCGGCTTTAAGTACGGCTTTATTCAACAACGGA
CTCACGTGTGGCGCGTGTCTATGAGATGAAGTGTAAACGATGACCCGAGGTGGTGTC
TCGGGTCTACCATCACCGTCACAGCCACTAACTTTTGCCACCAAACCCTGGCCTC
TCCAACGATAATGGAGGTTGGTGCAATCCTCCTTCAACATTTTCGACCTAGCCG
AGCCAGCTTTTCTCCAGATCGCTCAGTATCGTGCCGGCATTGTTCCCTGTCTCTTTC
CGAAGGTCGTTTACTTTTCTTTAACTTAGGACGCTAAATGATAAGACTGCGAC
AAAACCTCTTCACAGTTTTTAATACAGTTGTGTTTATGATTA AAAAATTTCAAATA
CTAAAAATTTTGGATTTATATTTGGAAAAAAAACACACTTTTAAACAAAGCCAA
CCTAAGGAAATTAACAAAACACACTATTTTACATGTAATTGATGTAAAGATTAAT
CACCAATCTATATTTACCAATATAATTGACTTAGAGACATGACTTTTGTAGCTACC
ATTGTTAAAACTTAAACCTAACAATAACATTAGGATATTTTGTGCCTAACAAAC
CATTATTAATTTTTTACTATTGATGCTTGCCGTGTAGAAAAGCCTAGGCAAGACCT
TTTATAAGTCCATGTTCTTAAACTAATGGCTTATGTCGGTGTTTTAACGTGATTAT
TGCAGAGTACCATGTATGAAGAAAGGAGGAATAAGGTTACGATCAACGGACAT
TCATACTTCAACCTCGTCCTGATCTCGAACGTAGGAGGAGCAGGAGATGTCCACG
CTGTCTCGATCAAAGGCTCAAAAACACAGTCGTGGCAAGCAATGTCTAGAAATTG
GGGACAAAACCTGGCAGAGCAATTCTTACATGAACGACCAAAGCCTTTCCTTCCAG
GTCACCACCAGCGATGGTCGCACACTCGTTAGCAATGACGTGGCTCCTTCTAATT
GGCAATTCGGACAAACCTACCAAGGCGGTCAATTCTGATCAGACCATCATCATCC
ACATCTCTCTGTTTTGGGTGCTGACGTGGCCGCATATTGCTGAGGTGGCTCGTAAG
CACCCGCTTTAGCTTAGCTTAGTTTTTTTTTTCTTATTTACGAATTATTGCTTCAAT
GGTTGTATTTTCATCGTGCCTACAAAGAGCAAGGTTTTTTTTTTTACATGTTTATGG
AATCTAGCCTTATTATTGGCCTTCTTTTCTTTGTAATCCAATATCGCCAAAAGCCC
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