

IDENTIFICATION

Species: *Arabidopsis halleri*

Locus: Araha.22287s0007

Gene Model: Araha.22287s0007.1

Description: AhEXPA-14

Family: Alpha Expansin

3D structure:



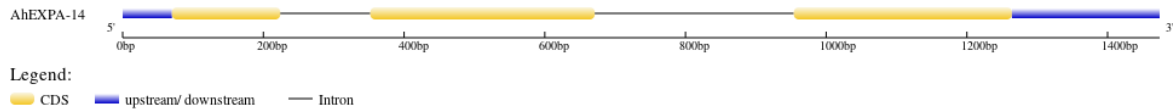
GENOME DATABASES

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

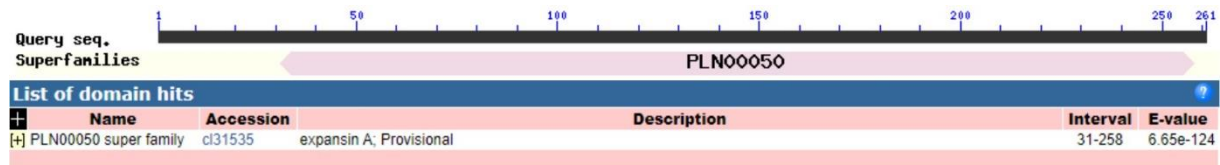
EXTERNAL RESOURCES

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

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>AhEXPA-14

MAINPMILLTIFSLFLLLSFTNAGIPGVYSGGSWQTAHATFYGGNDASGTMGGACGY
GNLYSQGYGTNTAALSTALFNSGQSCGACFEIKCVNDPKWCHPGTPSVFVTATNFCP
PNLAQPSDNGGWCNPPRSHFDLAMPVFLKIAEYRAGIVPISYRRVACRKSGGIRFTIN
GHRYFNLVLITNVAGAGDILRTSVKGSKTGWMSLTRNWGQNWQSNVAVLVGQSLSF
RVTASDRRTSTSWNIAPSNWQFGQTFVGKNFRV*

CDS (coding sequence)

>AhEXPA-14

ATGGCAATCAATCCAATGATTCTATTAACCATATTCTCACTTTTTCTCCTCTTGAG
CTTCACCAACGCCGGAATCCCTGGCGTCTACTCAGGCGGCTCTTGGCAAACCTGCT
CACGCCACTTTCTACGGTGGCAACGATGCTTCCGGAACAATGGGTGGCGCGTGTG
GATACGGGAATCTGTACAGTCAAGGATACGGAACAAACACGGCGGCCCTGAGCA
CAGCGTTGTTCAACAGTGGCCAAAGCTGCGGCGCATGCTTTGAAATCAAATGTGT
TAATGATCCTAAATGGTGTACCCGGGTACTCCTTCTGTCTTCGTAACCGCAACCA
ACTTTTGCCCTCCAAACTTAGCCCAACCTAGCGACAATGGCGGATGGTGCAACCC
GCCACGCTCTCATTTGACCTCGCCATGCCCGTTTTCTCAAGATCGCTGAGTATC
GCGCCGGCATTGTTCCCATATCTTACCGCAGGGTGGCATGTAGGAAGAGTGGAGG
GATAAGGTTACGATCAACGGTCACCGTACTTCAACTTGGTGCTGATAACGAAT
GTGGCCGGAGCAGGAGATATCCTGAGGACGAGCGTGAAAGGTTCAAAGACTGGT
TGGATGAGTTTAACTAGGAACTGGGGACAGAACTGGCAGTCTAATGCTGTTCTCG
TTGGTCAGTCACTTTCCTTCCGTGTACAGCCAGTGACCGTAGAACCTCTACTTCA
TGGAACATCGCTCCTTCGAACTGGCAGTTTGGACAAACCTTTGTCGGAAAGAATT
TCAGGGTCTAA

Nucleotide

>AhEXPA-14

TCCTCACTTAGCCTTCTAGTCTAACAATCTTCTTAACATTTCTAAATCTCAATCAC
AAATATTCACCAATATGGCAATCAATCCAATGATTCTATTAACCATATTCTCACTT
TTTCTCCTCTTGAGCTTCACCAACGCCGAATCCCTGGCGTCTACTCAGGCGGCTC
TTGGCAAACCTGCTCACGCCACTTTCTACGGTGGCAACGATGCTTCCGGAACAATG
GGTCAGTCCACTCTCCTTAAGCACAAATTACAAGAACCATACTTCGTTTATCATT
TACCAACTCTCTAAAACAGAGCACTCTGTTTTTTTTCTTTCATTTACTTTTTGTTTT
GTTGTTGTTATTTTAGGTGGCGCGTGTGGATACGGGAATCTGTACAGTCAAGGAT
ACGGAACAAACACGGCGGCCCTGAGCACAGCGTTGTTCAACAGTGGCCAAAGCT
GCGGCGCATGCTTTGAAATCAAATGTGTTAATGATCCTAAATGGTGTACCCCGG
TACTCCTTCTGTCTTCGTAACCGCAACCAACTTTTGCCCTCCAACTTAGCCCAAC
CTAGCGACAATGGCGGATGGTGCAACCCGCCACGCTCTCATTTCGACCTCGCCAT
GCCCGTTTTCTCAAGATCGCTGAGTATCGCGCCGGCATTGTTCCCATATCTTACC
GCAGGTATACTTAACATATCCAATTATAGAGTTTGGTTAGGGTCATTCAGTTTTCT
GAGTCTTAGATTTAGATGGTCAAAAACACTACTAATTTCAAAATATTTTTTTGTCA
TACTAAAGGTAAATTGTTTTATAATAAATTTTTCTTTTTTTTTCCATACGATCGT
TTGATTTATACGGATTAACATTCCTATATATAGCGTACGATGCGATAAATGATTT
GTATATAAAAGAAGTTGCAATGAATCAACTTGCTAAGGTTGAGAAATGTGGGTTT
TCTATAGGGTGGCATGTAGGAAGAGTGGAGGGATAAGGTTACAGATCAACGGTC
ACCGTTACTTCAACTTGGTGCTGATAACGAATGTGGCCGGAGCAGGAGATATCCT
GAGGACGAGCGTGAAAGGTTCAAAGACTGGTTGGATGAGTTTAACTAGGAACTG
GGGACAGAACTGGCAGTCTAATGCTGTTCTCGTTGGTCAGTCACTTTCCTTCCGTG
TCACAGCCAGTGACCGTAGAACCTCTACTTCATGGAACATCGCTCCTTCGAACTG
GCAGTTTGGACAAACCTTTGTCGGAAAGAATTTAGGGTCTAAAGTGAATTGAGG
ATATCGAAACATTTGAAGTGGTAGACACAACAAGAAGCTCCACTTTC AATTTGAA
CATCTTTGACTTTATATTTTCTATAAATCTTTTTACTGTGATTTGGAGTGTAATTGG
GAAGTGGTGTGGTAATATAGGGAAGTGTGAGAAAAGAGAAGCTGAAGTGGCTGT
TGAAAAAGTTGTAAACAGCCCGCAGCTCTTAA