

IDENTIFICATION

Species: *Aquilegia coerulea*

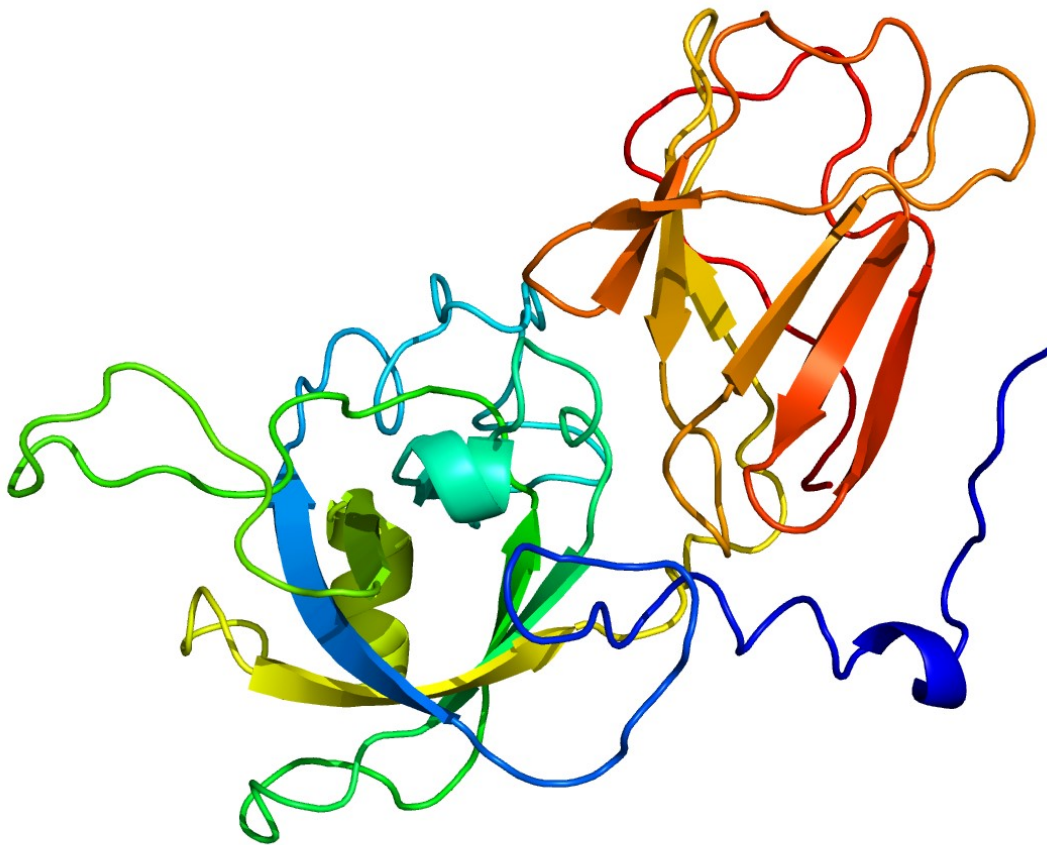
Locus: Aqcoe7G366800

Gene Model: Aqcoe7G366800.1.p

Description: AcEXPA-20

Family: Alpha Expansin

3D structure:

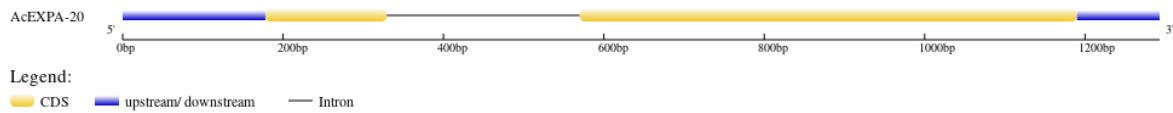


GENOME DATABASES

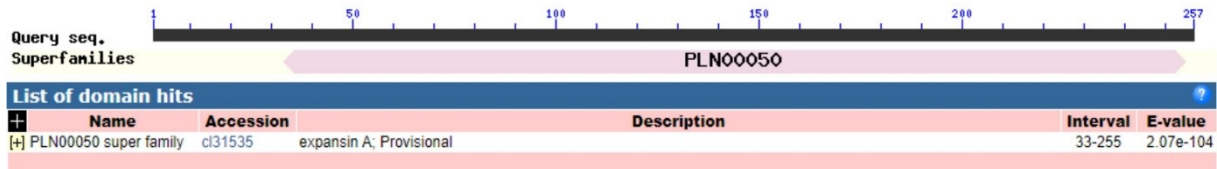
Phytozome: https://phytozome-next.jgi.doe.gov/info/Acoerulea_v3_1

EXTERNAL RESOURCES

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>AcEXPA-20

MGFSCYIVGFITMMAFFFSVLIEAKILAKTHPWMPAQATFYGDMSGQETMQGACGY
GNLSRQGYGLETTALSTTLFNNGLTCGACYELKCFNSSQWCIPGTIRVTATNFCPPNW
DIPSDNGGWCNPPRKHFDSLMPMFVQIAPYEAGIVPVL YRRVPCFKQGGIKFEIKGNP
YWILVLVYNVAGVGNIIDVKIKGSNTGWIKMSRNWGQNWQTFTRLQGQSLSFQVTS
QTGTMVQSDSVAPSNWQFGQTFEGRQFG*

CDS (coding sequence)

>AcEXPA-20

ATGGGGTTTTTCATGCTATATAGTTGGATTTCATAACGATGATGGCCTTCTTCTTTTC
TGTTCTAATTGAAGCAAAAATTCTTGCCAAAACACATCCATGGATGCCTGCACAG
GCAACATTCTACGGAGATATGTCTGGCCAAGAAACCATGCAAGGAGCTTGTGGAT
ATGGTAATCTATCTCGACAAGGATATGGACTAGAGACCACTGCCTTGAGCACAAC
TCTCTTCAACAATGGCCTCACATGTGGTGCCTGCTACGAGTTAAAATGCTTTAATT
CTTCACAATGGTGCATACCAGGAACCATCCGTGTGACTGCAACCAATTTCTGCCC
TCCTAACTGGGATATACCTAGTGACAATGGAGGTTGGTGCAACCCTCCTCGTAAG
CATTTTCGATTTGTCCATGCCAATGTTTGTCCAGATTGCTCCCTATGAGGCCGGTAT
TGTTCTGTACTATATCGTCGTGTACCATGTTTCAAGCAAGGTGGTATAAAGTTTG
AGATCAAGGGTAATCCATATTGGATTCTTGTACTAGTTTACAATGTGGCAGGCGT
AGGCAACATTATCGATGTAAAGATCAAAGGATCAAATACAGGTTGGATAAAAAT
GTCACGCAATTGGGGTCAGAATTGGCAAACATTTACGCGATTGCAAGGACAGAG
TTTGTCAATTTCAAGTAACGTCCCAAACACTGGTACGATGGTGCAGTCTGATAGTGTG
CACCATCTAATTGGCAATTTGGTCAGACATTTGAAGGTAGACAATTTGGATAA

Nucleotide

>AcEXPA-20

TATCTAGATTCAGTTTTATATTTATCTTTCCAAAAGAAATCTTTCTGTTCTAGCCAT
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TATTTATTTTAGTAGTTTGTGGCTTTGTTCAATAGATAGAGAGAGAGAAGTTAGA
GTTTCTTGGGATGGGGTTTTTCATGCTATATAGTTGGATTTCATAACGATGATGGCCT

TCTTCTTTTCTGTTCTAATTGAAGCAAAAATTCTTGCCAAAACACATCCATGGATG
CCTGCACAGGCAACATTCTACGGAGATATGTCTGGCCAAGAAACCATGCGTAAGT
TTCCATTTTGTGCCGCATACAGTCTTTTAGGATCAATTGCTCCAATATCATGTGTG
CTGAAATATTGAATAGTGTTTCCTTTCATATATTATATTGCTACACTTCATGTGGC
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TAGTCCGAAAAAAAATCCTGCCAAGATAATATGGCTAACAAAATGAGTTGCACG
TTTTTCAATTGCAGAAGGAGCTTGTGGATATGGTAATCTATCTCGACAAGGATAT
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GTGCGTGCTACGAGTTAAAATGCTTTAATTCTTCACAATGGTGCATACCAGGAAC
CATCCGTGTGACTGCAACCAATTTCTGCCCTCCTAACTGGGATATACCTAGTGAC
AATGGAGGTTGGTGC AACCCCTCCTCGTAAGCATTTCGATTTGTCCATGCCAATGTT
TGCCAGATTGCTCCCTATGAGGCCGGTATTGTTCCCTGTACTATATCGTCGTGTAC
CATGTTTCAAGCAAGGTGGTATAAAGTTTGAGATCAAGGGTAATCCATATTGGAT
TCTTGTAAGTTTACAATGTGGCAGGCGTAGGCAACATTATCGATGTTAAGATC
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CAAACATTTACGCGATTGCAAGGACAGAGTTTGTCAATTTCAAGTAACGTCCCAA
CTGGTACGATGGTGCAGTCTGATAGTGTTGCACCATCTAATTGGCAATTTGGTCA
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AAAGGGTGATAAAAAGAAGTGTAAGTATAAAAATTTTCTTCCTTTCATTCAATTT
GCAACAAATGGTCTAATGGTA