

IDENTIFICATION

Species: *Aquilegia coerulea*

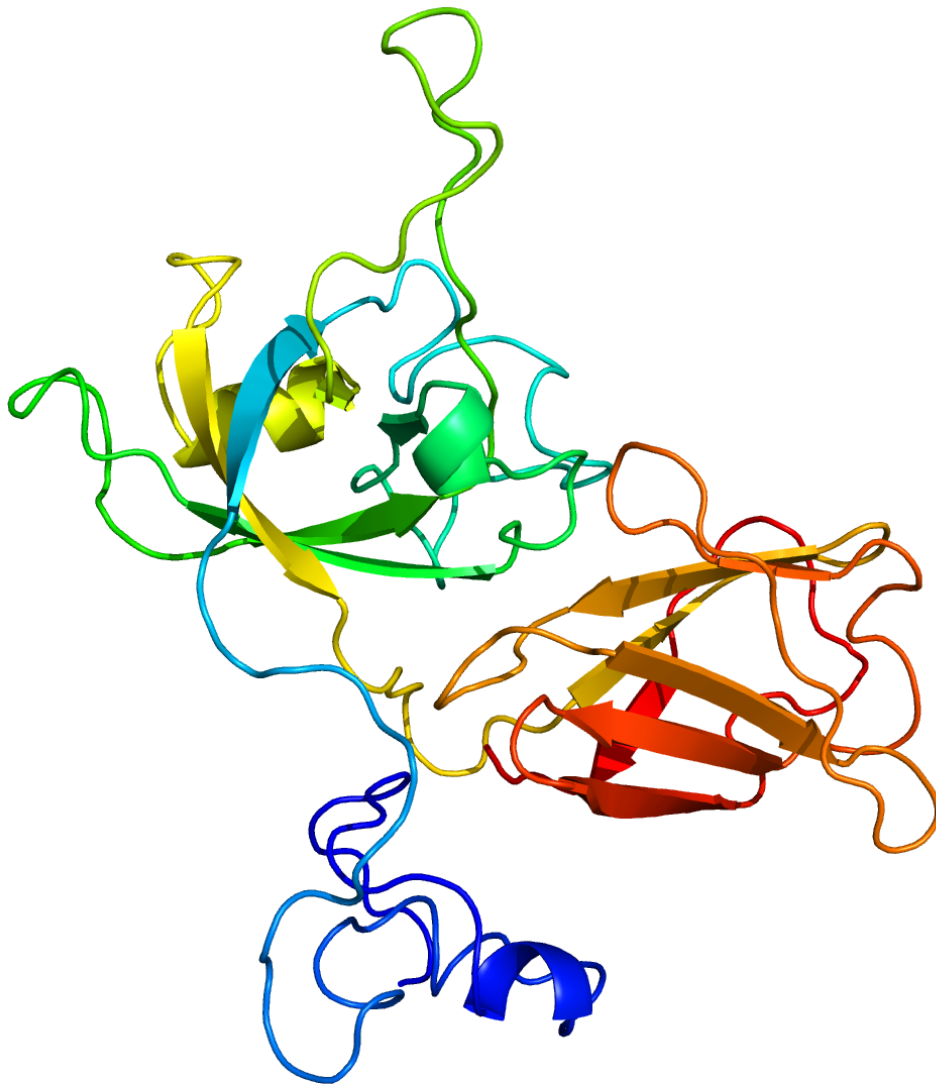
Locus: Aqcoe3G361800

Gene Model: Aqcoe3G361800.1.p

Description: AcEXPA-13

Family: Alpha Expansin

3D structure:

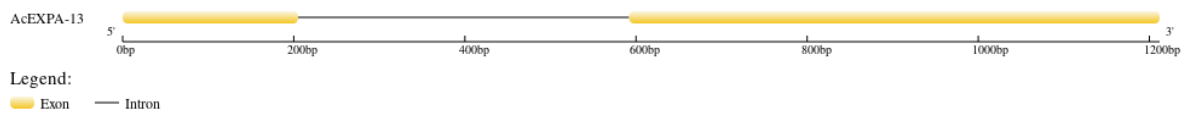


GENOME DATABASES

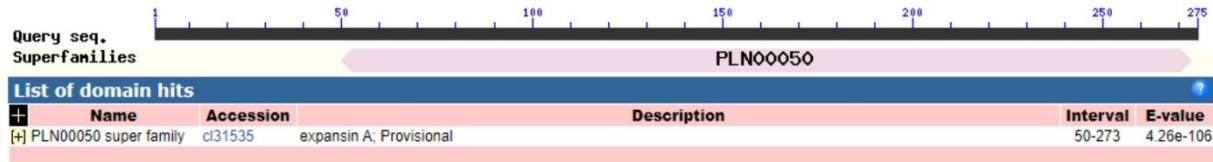
Phytozome: https://phytozome-next.jgi.doe.gov/info/Acoerulea_v3_1

EXTERNAL RESOURCES

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>AcEXPA-13

METTDLTLPPSKSDKQIAKMCCSGYLIAIIAIIAIAAFSANVVEAKHGKPYGWIKAHATF
YDISGQETMQGACGYGDLHKQGYGLETAALSTALFNDGLTCGACYEMKCYNTTQ
WCKPGIIQITATNFCPPNWSIPSDNNGWCNPPRKHFDSLMSFLKIAEYKAGIVPVLYK
RVPCVKNGGIKFEIKGNPYWTLVLVYNVAGVGNIVDVKIKSGTQWYQMSRNWGQ
NWQTGVRLQGQSLSFIVTTQGGKTVQSDNVAPANWQFGQTFEGKQFN*

CDS (coding sequence)

>AcEXPA-13

ATGGAGACCACAGACCTAACTCTGCCTCCTTCCAAGAGTGATAAACAGATTGCAA
AGATGTGTTGTTTCAGGATATTTGATTGCGATTATCGCCATCATGGCTGCTTTCTCT
GCTAATGTTGTTGAAGCCAAGCATGGCAAACCATATGGTTGGATTAAGCCCATG
CAACATTCTATGGAGACATATCTGGCCAAGAAACAATGCAAGGAGCTTGTGGGT
ACGGTGACTTACATAAACAAGGTTACGGACTAGAGACAGCTGCCTTAAGCACAG
CTCTCTTCAATGATGGACTCACCTGTGGTGCATGTTATGAGATGAAATGCTACAA
TACTACACAATGGTGCAAACCAGGAATCATTCAAATTACCGCAACCAACTTCTGC
CCTCCTAATTGGTCAATACCTAGCGACAATGGCGGGTGGTGCAATCCTCCTCGCA
AGCATTGTTGATCTCTCCATGTCAAGTTTTCTCAAGATTGCTGAGTATAAGGCTGGC
ATTGTTCCCTGTACTATAAAGAGAGTACCATGTGTGAAGAACGGTGGTATAAAAT
TTGAGATCAAGGGTAATCCATACTGGACGCTTGTTTTAGTGTACAATGTGGCAGG
AGTAGGTAATATCGTCGATGTTAAGATTAAAGGCTCAGGCACACAATGGTATCAA
ATGTCGCGTAACTGGGGTCAGAATTGGCAAACAGGGGTGAGACTGCAAGGCCAG
AGTTTGTCATTCATAGTAACTACTCAAGGGGGTAAAACCGTGCAGTCCGATAATG
TTGCACCAGCTAACTGGCAATTCGGTCAGACATTTGAAGGCAAGCAATTTAATTG
A

Nucleotide

>AcEXPA-13

ATGGAGACCACAGACCTAACTCTGCCTCCTTCCAAGAGTGATAAACAGATTGCAA
AGATGTGTTGTTTCAGGATATTTGATTGCGATTATCGCCATCATGGCTGCTTTCTCT

GCTAATGTTGTTGAAGCCAAGCATGGCAAACCATATGGTTGGATTAAAGCCCATG
CAACATTCTATGGAGACATATCTGGCCAAGAAACAATGCGTAAGTTTACATCTAC
CTACCTCCTTGTTTTCTTTTTCTATGTAGATTGCAGAAGTGCTGTTCTGCTAATATT
TTGCTTGTGAAAAGTGTCTTAAACTAGATATAAAACTATAATTCAGAATACTAGA
ACACCCTTGACTCAAAGTTCCAGCAATTGCTTACCTTGATCGGACGATTGATC
CAAGTTGTGATTTTTTTAACTGGATTTCGTCAATAAAGAAAACCAGATTGTCACA
AACTCACAATCTAGTATGGATTTTCATAATGTTGACTGGCTCAAACCTGTTTTGACT
AGTCCAGAACATCCAATTATCCCAATCCGCATCAACAATGATATCATCAATTAGT
ATATGATTTAATTTAATGTTTTATTTTTGTGATCACAGAAGGAGCTTGTGGGTACG
GTGACTTACATAAACAAGGTTACGGACTAGAGACAGCTGCCTTAAGCACAGCTCT
CTTCAATGATGGACTCACCTGTGGTGCATGTTATGAGATGAAATGCTACAATACT
ACACAATGGTGCAAACCAGGAATCATTCAAATTACCGCAACCAACTTCTGCCCTC
CTAATTGGTCAATACCTAGCGACAATGGCGGGTGGTGCAATCCTCCTCGCAAGCA
TTTTGATCTCTCCATGTCAAGTTTTCTCAAGATTGCTGAGTATAAGGCTGGCATTG
TTCCTGTACTATAACAAGAGAGTACCATGTGTGAAGAACGGTGGTATAAAATTTGA
GATCAAGGGTAATCCATACTGGACGCTTGTTTTAGTGTACAATGTGGCAGGAGTA
GGTAATATCGTCGATGTTAAGATTAAGGCTCAGGCACACAATGGTATCAAATGT
CGCGTAACTGGGGTCAGAATTGGCAAACAGGGGTGAGACTGCAAGGCCAGAGTT
TGTCATTCATAGTAACTACTCAAGGGGGTAAAACCGTGCAGTCCGATAATGTTGC
ACCAGCTAACTGGCAATTCGGTCAGACATTTGAAGGCAAGCAATTTAATTGA