

IDENTIFICATION

Species: *Aquilegia coerulea*

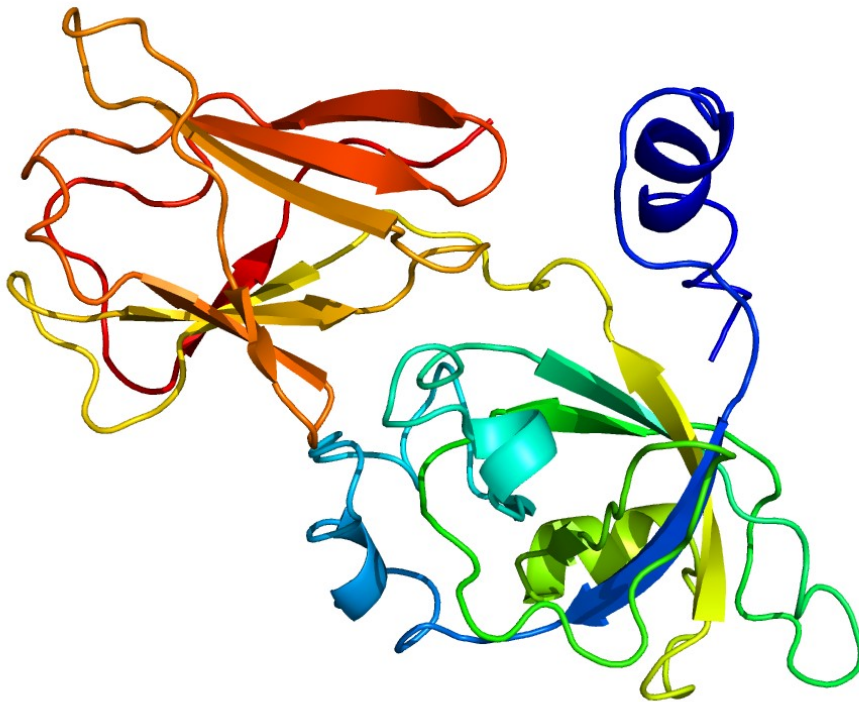
Locus: Aqcoe1G269900

Gene Model: Aqcoe1G269900.1.p

Description: AcEXPA-03

Family: Alpha Expansin

3D structure:



GENOME DATABASES

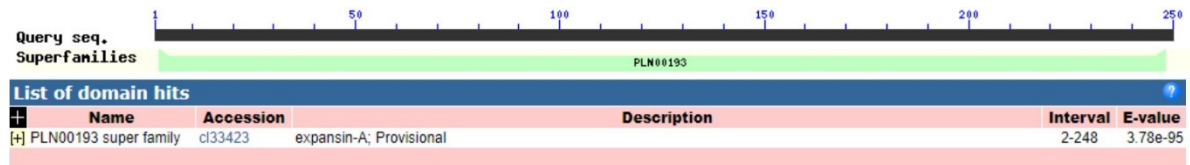
Phytozome: https://phytozome-next.jgi.doe.gov/info/Acoerulea_v3_1

EXTERNAL RESOURCES

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>AcEXPA-03

MVALQVVWLFVLFCCVFLVIKGTNAWFNGHATYYGASENPATLGGACGYENTFRAG
FGINTAALSGALFRSGEACGACYQLRCDARQDPKWCLRSGTVTITATNFCPSNNNGG
WCNAPRQHFDMSAPAFFRIARQGNELIIPVIYRRVPCRRGGVRFITLKGQSNFNMVM
ITNIGGSGDVKAAWIKGSKTRQWVQMRNWGANWQSSIDVSSQRLSFRITLVDGKT
LLFSNVVPPTWKFGQTFASQLQFA*

CDS (coding sequence)

>AcEXPA-03

ATGGTGGCCCTTCAAGTTGTTTGGTTGTTTCTCTTTTGTGTTGTTTTCTTGTTATT
AAAGGA ACTAATGCTTGGTTTAATGGCCATGCAACATATTATGGTGCTTCTGAGA
ACCCTGCCACCCTTGGAGGTGCATGTGGTTATGAAAACACTTTTCGTGCTGGATT
GGCATAAACACTGCAGCATTAAAGTGGTGCCTCTTCAGAAGTGGTGAAGCCTGTG
GTGCATGCTATCAGCTCAGGTGTGACGCACGGCAAGACCCAAAATGGTGCCTTCG
AAGTGGGACTGTAACCATCACTGCCACCAACTTCTGTCCATCAAACAATAATGGA
GGATGGTGTAATGCTCCTCGTCAGCATTGACATGTCTGCACCTGCTTTCTTTTCG
CATTGCTCGCCAGGGTAATGAAGGCATAATCCTGTTATCTACAGAAGGGTGCCA
TGCAAAGAAGAGGTGGAGTTCGATTCACACTGAAGGGACAGTCAAATTTCAAT
ATGGTGATGATCACTAACATAGGCGGGAGCGGAGATGTTAAGGCTGCATGGATT
AAAGGATCAAAGACAAGACAATGGGTACAAATGCATAGGAACTGGGGAGCAAA
CTGGCAAAGCAGCATTGATGTTAGTAGCCAAAGACTGTCTTTTCAGAATCACTTTA
GTCGACGGGAAAACACTACTTTTCTCCAATGTTGTCCCTCCAACATGGAAGTTTG
GACAAACTTTTGCTTCCCAATTGCAGTTTGCTTAA

Nucleotide

>AcEXPA-03

TCTTCTTCGATCATTTTATTATTAAGGAAACAAGAGCTAGAAGAAGGAAAAAGAA
AATGGTGGCCCTTCAAGTTGTTTGGTTGTTTCTCTTTTGTGTTGTTTTCTTGTTAT
TAAAGGAACTAATGCTTGGTTAATGGCCATGCAACATATTATGGTGCTTCTGAG
AACCTGCCACCCTTGGTACGATTACAGATTTGCATGTAAAATCGAAGTGCAGCA
ATTTAATTTGCATGTAGTGGTGTATAAACTTATATGCATTAGAGTCTTGTGCTCT
TTGAAATCATATACTTTTCTATTGTTTGATCAAAGAGCATGCTGACTTGTGTTCTT
GTTCTATTTTAGGAGGTGCATGTGGTTATGAAAACACTTTTCGTGCTGGATTTGGC
ATAAACACTGCAGCATTAAAGTGGTGCCTTTCAGAAGTGGTGAAGCCTGTGGTG
CATGCTATCAGCTCAGGTGTGACGCACGGCAAGACCCAAAATGGTGCCTTCGAAG
TGGGACTGTAACCATCACTGCCACCAACTTCTGTCCATCAAACAATAATGGAGGA
TGGTGTAATGCTCCTCGTCAGCATTTTGACATGTCTGCACCTGCTTTCTTTCGCATT
GCTCGCCAGGGTAATGAAGGCATAATTCCTGTTATCTACAGAAGGTATTAATTGA
AAATATCACATATCAAATCCTCAGTTTAATTTTCCTAGTTATACTGTATATAGCAT
TTAAGAATTTTCGTTTTAATTTTCTCTGAAGGGTGCCATGCAAAAAGAAGAGGTGGA
GTTTCGATTCACACTGAAGGGACAGTCAAATTTCAATATGGTGATGATCACTAACA
TAGGCGGGAGCGGAGATGTAAAGGCTGCATGGATTAAGGATCAAAGACAAGAC
AATGGGTACAAATGCATAGGAACTGGGGAGCAAACCTGGCAAAGCAGCATTGATG
TTAGTAGCCAAAGACTGTCTTTCAGAATCACTTTAGTCGACGGGAAAACACTACT
TTTCTCCAATGTTGTCCCTCCAACATGGAAGTTTGGACAAACTTTTGCTTCCAAT
TGCAGTTTGCTTAATAACAAGAACTACATATACAAGCACCACAGAAATAACTATG
AAAAGTTCATCCAATTACTTACAGTTCATATAGTTTCC