

IDENTIFICATION

Species: *Aquilegia coerulea*

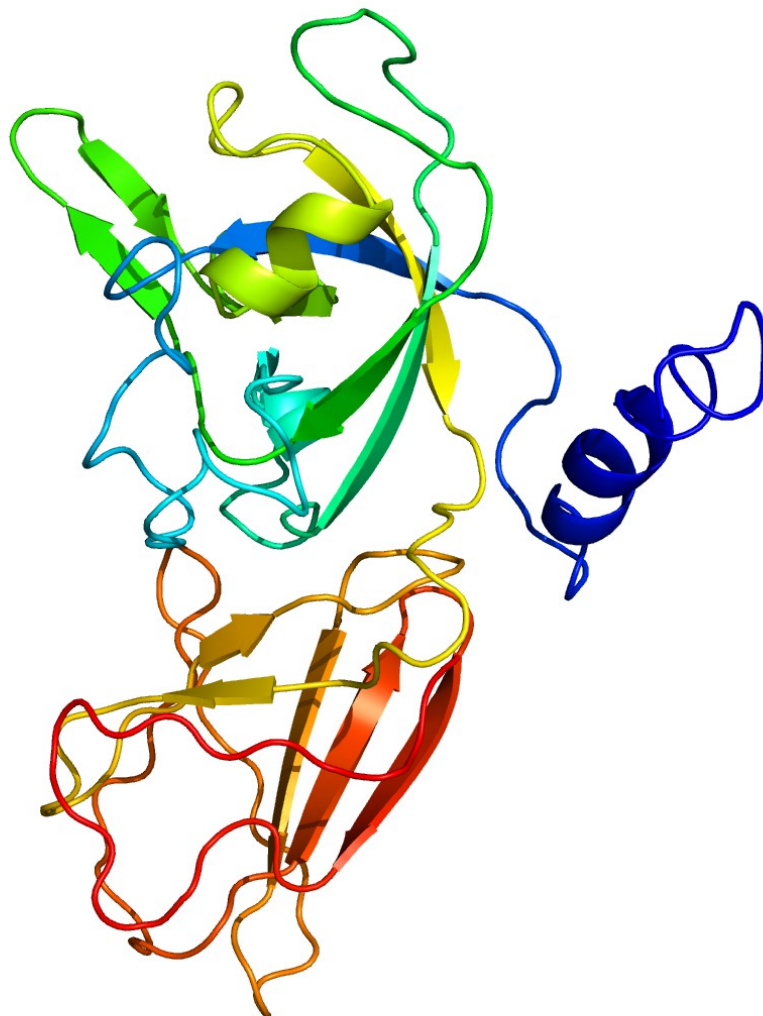
Locus: Aqcoe2G236500

Gene Model: Aqcoe2G236500.1.p

Description: AcEPXA-08

Family: Alpha Expansin

3D structure:



GENOME DATABASES

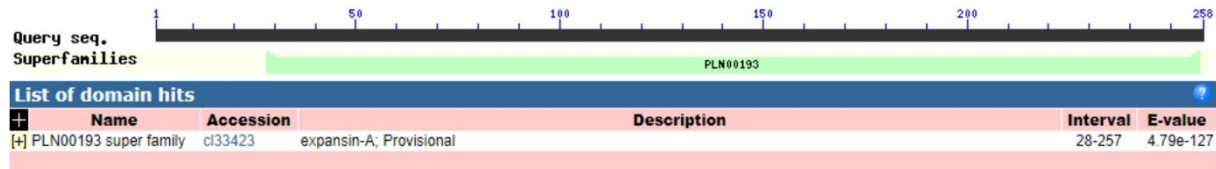
Phytozome: https://phytozome-next.jgi.doe.gov/info/Acoerulea_v3_1

EXTERNAL RESOURCES

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>AcEXPA-08

MENSSFSRFSFIIIVAVLAC SINSSFAAWQLAHATFYGGDASGTMGGACGYGNLYT
DYG IKTAA LSTALFNSGQSCGACYQIVCDGSQAPRWCLKGGYITITATNFCPPNYNL
PSNNGGWCNPPRQHFDMSQPAFQKIAVYKAGIVPVLRYKVSCKRTGGVRF TINGRD
YFELVLISNVGGAGDIAKVWIKGSKTNRWEPMSRNWGSNWQSSTYLN RQSLSFRIQT
SNGRKTAYNVAPSNWVFGRSYSSNVQF*

CDS (coding sequence)

>AcEXPA-08

ATGGAGAATTCCAGTAGTTTTCTAGGTTTCAGTTTTATTATAATTGTTGCAGTGTT
GGCTTGTAGCATTAAACAGCAGCTTTGCTGCTTGGCAGCTTGCCCATGCAACTTTCT
ATGGAGGTGGCGATGCTTCGGGGACAATGGGGGGCGCTTGTGGTTATGGGAACC
TCTACACAGATGGCTATGGTATCAAACAGCGGCATTGAGCACAGCCCTCTTCAA
CAGTGGCCAGTCATGTGGAGCATGTTATCAGATTGTTTGTGATGGGAGTCAAGCG
CCACGATGGTGCTTAAAGGGGGGCTATATAACCATTACTGCAACAAATTTCTGTC
CACCAAATTACAATCTCCCTAGCAACAATGGTGGATGGTGCAACCCGCCACGACA
ACACTTTGACATGTGCAACCTGCATTTCAAGAAGATTGCAGTTTACAAGGCCGGC
ATTGTGCCTGTGCTCTATAGAAAGGTTAGTTGCAAGAGAACTGGAGGAGTTCGAT
TTACCATCAACGGACGAGATTACTTCGAACTGGTCCTCATAAGTAATGTAGGAGG
AGCTGGGGATATAGCAAAGGTCTGGATTAAAGGGTCCAAAACAAATAGATGGGA
ACCAATGTCCAGAACTGGGGATCAAACCTGGCAAAGCTCGACCTATCTGAATCGC
CAGAGTTTATCATTTAGAATCCAGACAAGCAATGGACGTACGAAAACAGCATAT
AATGTGGCGCCTTCTAATTGGGTATTTGGCAGATCTTACTCCAGCAATGTTTCAGTT
CTAA

Nucleotide

>AcEXPA-08

AATATAAGCAAAACAGATATTGAAAACCTAGCTAGCTGGGTTATCCTTAAGTTGTT
TAAAATCGAGACAAGGAAAGAGAATGGAGAATTCCAGTAGTTTTTCTAGGTTCA
GTTTTATTATAATTGTTGCAGTGTTGGCTTGTAGCATTAAACAGCAGCTTTGCTGCT
TGGCAGCTTGCCCATGCAACTTTCTATGGAGGTGGCGATGCTTCGGGGACAATGG
GTGAGTACTTAGCTGTCTGTGTGACTCACACTGTCATAGTAGATATGATAGATAA
TAAGTAATATGCCATTAAGTGTATTGATTGAATTTATTTAACGATGCAAGTATAAT
TTGCAGGGGGCGCTTGTGGTTATGGGAACCTCTACACAGATGGCTATGGTATCAA
AACAGCGGCATTGAGCACAGCCCTCTTCAACAGTGGCCAGTCATGTGGAGCATGT
TATCAGATTGTTTGTGATGGGAGTCAAGCGCCACGATGGTGCTTAAAGGGGGGCT
ATATAACCATTACTGCAACAAATTTCTGTCCACCAAATTACAATCTCCCTAGCAA
CAATGGTGGATGGTGCAACCCGCCACGACAACACTTTGACATGTCGCAACCTGCA
TTTCAGAAGATTGCAGTTTACAAGGCCGGCATTGTGCCTGTGCTCTATAGAAAGT
ATGTTTCCATATCATATATCAACCACCACCAAATTTACATTTACATGAATTA AAAA
CTGATATGTTATCTACCTCTGTCTGTATATCTCAGGGTTAGTTGCAAGAGA ACTGG
AGGAGTTCGATTTACCATCAACGGACGAGATTACTTCGAACTGGTCCTCATAAGT
AATGTAGGAGGAGCTGGGGATATAGCAAAGGTCTGGATTAAGGGTCCAAAACA
AATAGATGGGAACCAATGTCCAGAACTGGGGATCAA ACTGGCAAAGCTCGACC
TATCTGAATCGCCAGAGTTTATCATTTAGAATCCAGACAAGCAATGGACGTACGA
AAACAGCATATAATGTGGCGCCTTCTAATTGGGTATTTGGCAGATCTTACTCCAG
CAATGTT CAGTTCTAAGACATC