

## IDENTIFICATION

**Species:** *Aquilegia coerulea*

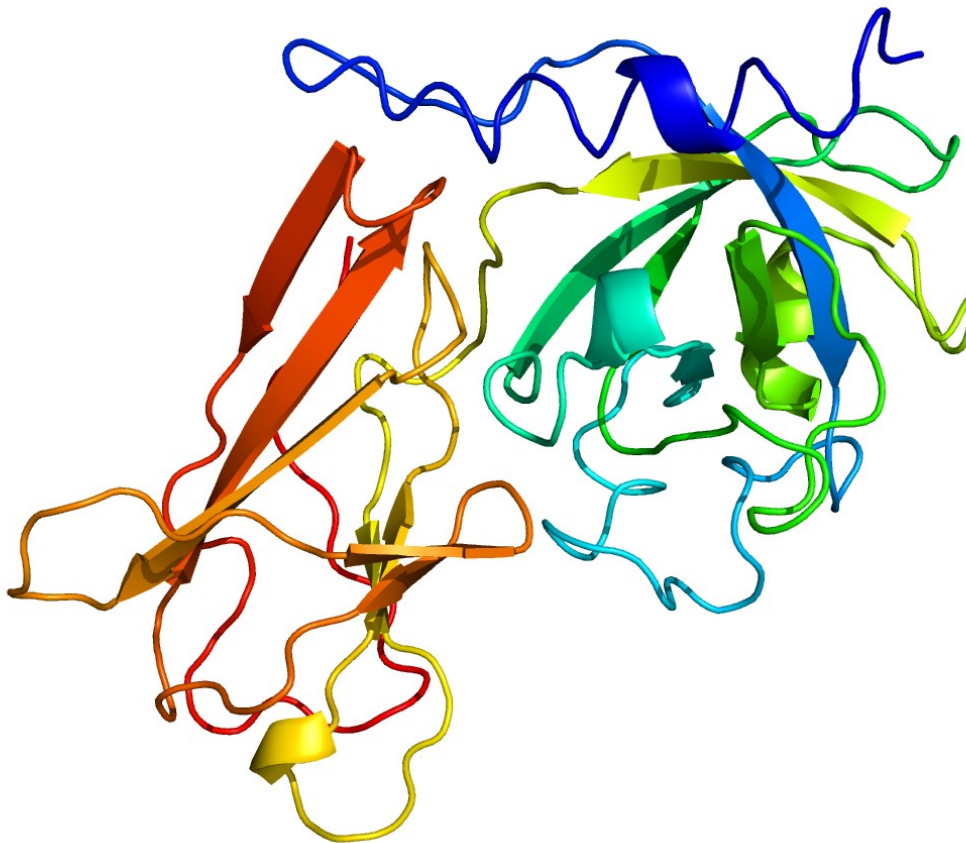
**Locus:** Aqcoe3G253300

**Gene Model:** Aqcoe3G253300.1.p

**Description:** AcEXLB-01

**Family:** Expansin Like B

**3D structure:**

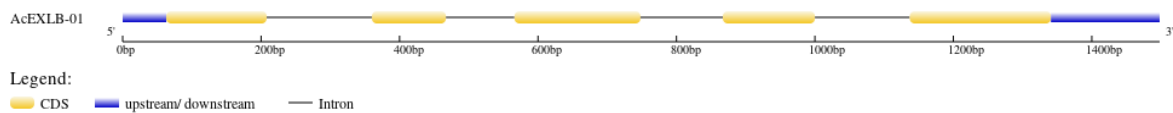


## GENOME DATABASES

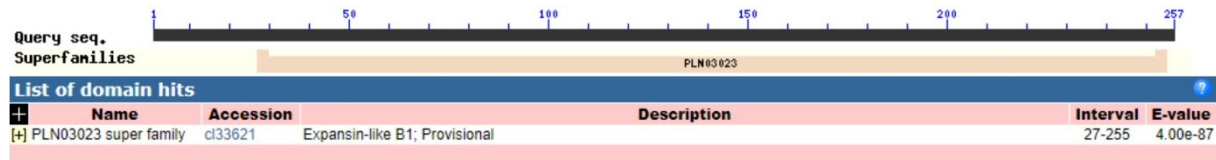
Phytozome: [https://phytozome-next.jgi.doe.gov/info/Acoerulea\\_v3\\_1](https://phytozome-next.jgi.doe.gov/info/Acoerulea_v3_1)

## EXTERNAL RESOURCES

## GENE STRUCTURE



## DOMAIN ARCHITECTURE



## SEQUENCES

### Peptide

>AcEXLB-01

MTLYLQPLTLLLVCVLLRQTLVDGATCKDCFIHSRAAHYPNSDEMGTETGACGFGSF  
GAIINGGDVSAASNLYRDGVGCGACYQVRCTNSMYCSDKGVTVVITDSGSGDNTDFI  
LSRRAYAKMSQTTYAAASLLALGVVDIEYRRVPCSYPYKNITFKIDENSYPHYLAF  
VIWYQQGKKDVTAVQLCETTNLCKLLDRSHGAVWTVVTPPSGPLSIRMLLSVDVDD  
GEETWVPLNNIPQNWKAGDIYDSGIQVE\*

### CDS (coding sequence)

>AcEXLB-01

ATGACTCTTTATCTTCAACCCCTTACCTTACTCCTTGTTTGTGTGCTTCTTAGGCAA  
ACTCTTGTAGATGGGGCAACATGCAAAGATTGTTTTATCCATTCCAGAGCTGCTC  
ACTATCCGAACTCAGATGAAATGGGAACAGAACTGGAGCTTGTGGATTCGGTTC  
ATTTGGAGCTATAATCAATGGTGGAGATGTTTCTGCTGCATCCAACCTTTACAGG  
GATGGTGTAGGATGTGGGGCATGCTACCAAGTGAGGTGCACAAACAGCATGTAC  
TGTTACAGACAAAGGTGTGACCGTGGTGATTACTGATAGTGGTTCGGGTGATAACA  
CTGATTTCATACTAAGTAGACGAGCTTATGCGAAAATGTCTCAAACAACATATGC  
AGCAGCATCATTACTAGCTCTTGGTGTGTTGACATTGAATATAGACGTGTTCCAT  
GCAGTTATCCATATAAGAATATCACCTTCAAGATTGATGAAAACAGCAATTACCC  
TCACTACTTGGCCTTTGTCATATGGTATCAACAAGGCAAGAAGGATGTTACTGCT  
GTACAACATATGTGAGACTACAAATTTATCATGCAAGCTATTGGACCGAAGTCATG  
GAGCCGTTTGGACAGTTGTTACACCACCAAGTGGACCTTTGTCCATTAGGATGTT  
ATTGAGTGATGTTGATGATGGAGAGGAAACATGGGTGGTGGCCCTCAACAACAT  
ACCCAGAACTGGAAAGCTGGAGACATATATGATTCAGGGATACAAGTGGAATA  
A

### Nucleotide

>AcEXLB-01

TCCTCTTCTTCTACTACTGCTTCAATATTTCTTCCAATATCCTCTGCTTAGAGTTT  
ATCACAATGACTCTTTATCTTCAACCCCTTACCTTACTCCTTGTTTGTGTGCTTCTT  
AGGCAAACCTTGTAGATGGGGCAACATGCAAAGATTGTTTTATCCATTCCAGAG

CTGCTCACTATCCGAACTCAGATGAAATGGGAACAGAAAGTGAGTGGGAAGCCC  
CAACCAACATGATCAAATAAAGAAAAATGCAGATCGATTATAATTACTAGTACTA  
GCTAGGATAAGTTTTGATGTTCTATATATAATATGTTCGATCGAAGTACCTATTTGC  
TAAATTGTTTTCTTAATGTCATGCAGCTGGAGCTTGTGGATTCGGTTCATTTGGAG  
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CGAGCTTATGCGAAAATGTCTCAAACAACATATGCAGCAGCATCATTACTAGCTC  
TTGGTGTGTTGACATTGAATATAGACGGTATGATCATCAGGCATCAGCACAGTG  
GGATTCATGTATTCAAATAATTTAAGCATAACTATTTATATTAACAAATGATATAT  
ATTAACATAACATGCATGGTGGTTCCTTTGATTTACAGTGTTCATGCAGTTATCCAT  
ATAAGAATATCACCTTCAAGATTGATGAAAACAGCAATTACCCTCACTACTTGGC  
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ATTTTATTTCCCTCAATAATATTTTGCCGTGCTTCTTATGATCGATCGTGTTCCTTAA  
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AAAA