

## IDENTIFICATION

**Species:** *Citrus clementina*

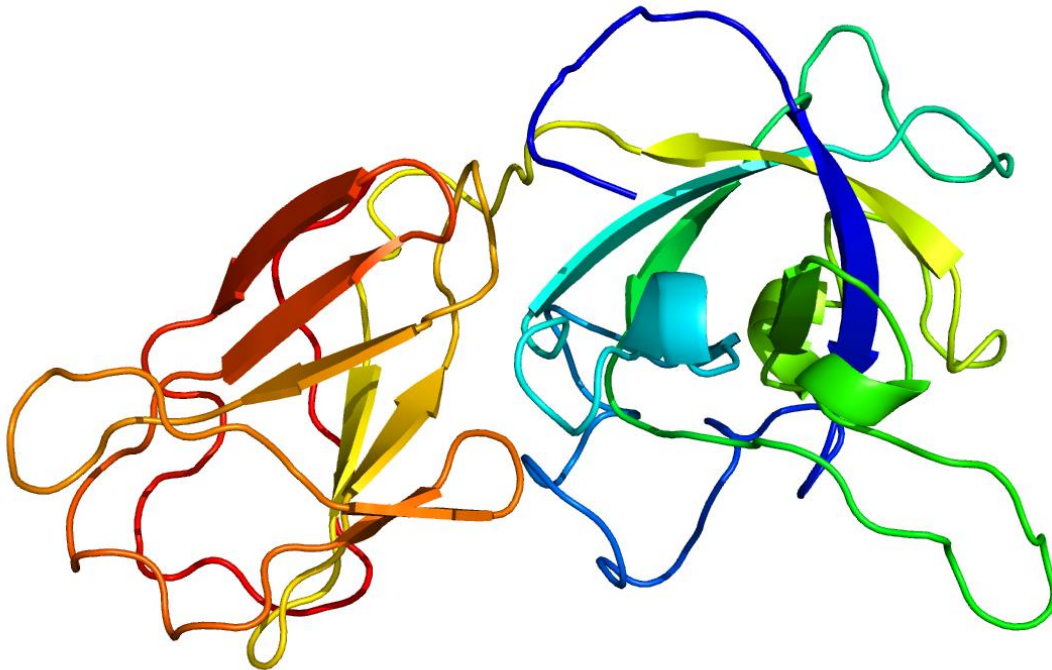
**Locus:** Ciclev10029135

**Gene Model:** Ciclev10029135m

**Description:** CclEXPA-18

**Family:** Alpha Expansin

**3D structure:**



## GENOME DATABASES

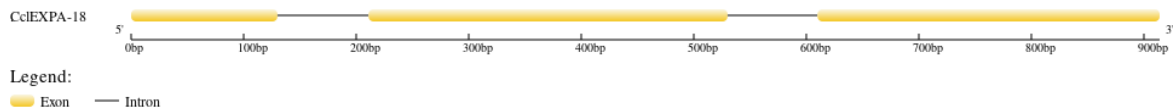
Phytozome: [https://phytozome-next.jgi.doe.gov/info/Cclementina\\_v1\\_0](https://phytozome-next.jgi.doe.gov/info/Cclementina_v1_0)

KEGG: <https://www.genome.jp/entry/T02982>

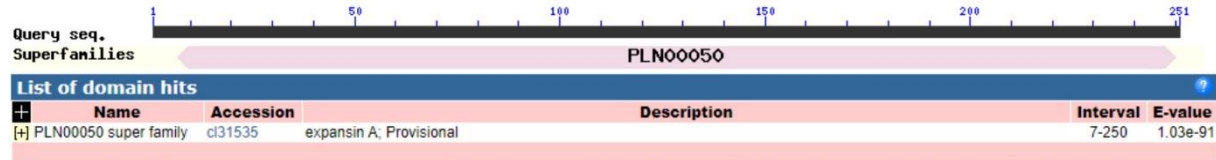
## EXTERNAL RESOURCES

<https://www.citrusgenomedb.org/organism/Citrus/clementina>

## GENE STRUCTURE



## DOMAIN ARCHITECTURE



## SEQUENCES

### Peptide

>CclEXPA-18

MGAPQAIVFFLILLQTCKTAAQHEEWNSATATYTKETNGSIIIIEGACGYGDLHRATYG  
KYSAGLSTMLFNRGSTCGACFELRCVDHILWCRPGSPSVILTATDFCPPNYGLSSDYG  
GWCNFPKEHFEMSEAAFVEIAERRADIVPVQYRRVKCERRGGLRFTVSGSSHFYQVL  
VTNVGLDGEVIAVKVKGSKTGWIPMARNWQONWQSNVNLTGQPLSFEVTTSNRKT  
LTSYNVAPANWQFGQTYEGKQF\*

### CDS (coding sequence)

>CclEXPA-18

ATGGGAGCTCCTCAAGCCATTGTTTTCTTCTTGATTTTACTTCAAACATGCAAGAC  
TGCAGCACAGCATGAAGAATGGAACCTCTGCTACGGCTACATACACCAAAGAAAC  
AAATGGGTCTATCATCATTGAAGGTGCTTGTGGTTATGGGGACCTTCACAGGGCC  
ACCTACGGAAAATACAGTGCTGGGCTTAGTACAATGTTATTCAACAGAGGGAGTA  
CTTGTGGAGCTTGCTTTGAGCTCAGATGTGTGCGACCACATCTTGTGGTGCCGGCCT  
GGTAGCCCATCTGTCATACTCACCGCCACAGATTTCTGCCCTCCCAATTACGGGCT  
TTCGTCGGATTATGGTGGCTGGTGTAACTTTCCCAAAGAACACTTTGAGATGTCA  
GAGGCCGCATTTCGTTGAAATTGCAGAGAGAAGAGCTGATATTGTACCAGTTCAAT  
ACAGAAGGGTGAAGTGTGAACGCAGGGGTGGGTTGAGATTCACAGTGAGTGGAA  
GCTCTCACTTCTATCAAGTTCTTGTAAACCAATGTGGGTTTGGATGGTGAAGTCATT  
GCTGTGAAAGTGAAGGGATCAAAAACAGGATGGATACCTATGGCAAGAAACTGG  
GGCCAAAACCTGGCAGTCCAACGTCAATCTTACAGGGCAGCCTCTGTCTTTTGAGG  
TGACCACCAGTAACCGGAAAACACTCACATCATACAATGTTGCTCCAGCAAACCTG  
GCAGTTTGGTCAGACATATGAGGGGAAACAGTTCTAG

### Nucleotide

>CclEXPA-18

ATGGGAGCTCCTCAAGCCATTGTTTTCTTCTTGATTTTACTTCAAACATGCAAGAC  
TGCAGCACAGCATGAAGAATGGAACCTCTGCTACGGCTACATACACCAAAGAAAC  
AAATGGGTCTATCATCATTGGTACTTTCTTGTCAAATTACTTTATTTAATATTGTGTT  
TCATGTCCACTGAAGACTGATAGGCCATCTGTTTAATGTTGCAGAAGGTGCTTGT  
GGTTATGGGGACCTTCACAGGGCCACCTACGGAAAATACAGTGCTGGGCTTAGTA

CAATGTTATTCAACAGAGGGAGTACTTGTGGAGCTTGCTTTGAGCTCAGATGTGT  
CGACCACATCTTGTGGTGCCGGCCTGGTAGCCCATCTGTCATACTCACC GCCACA  
GATTTCTGCCCTCCCAATTACGGGCTTTCGTCGGATTATGGTGGCTGGTGTA ACTT  
TCCCAAAGAACA CTTTGAGATGTCAGAGGCCGCATTCGTTGAAATTGCAGAGAGA  
AGAGCTGATATTGTACCAGTTCAATACAGAAGGTACAGCAATGCTTTTTCTTTTT  
CTGCTAGCTTGTGGATTTTAGTTAGGCACATGCTGTGATTCCGAAATTTGTGCAG  
GGTGAAGTGTGAACGCAGGGGTGGGTTGAGATTCACAGTGAGTGGAAGCTCTCA  
CTTCTATCAAGTTCTTGTAACCAATGTGGGTTTGGATGGTGAAGTCATTGCTGTGA  
AAGTGAAGGGATCAAAAACAGGATGGATACCTATGGCAAGAACTGGGGCCAAA  
ACTGGCAGTCCAACGTCAATCTTACAGGGCAGCCTCTGTCTTTTGAGGTGACCAC  
CAGTAACCGGAAAACACTCACATCATA CAATGTTGCTCCAGCAA ACTGGCAGTTT  
GGTCAGACATATGAGGGGAAACAGTTCTAG