

## IDENTIFICATION

**Species:** *Citrus clementina*

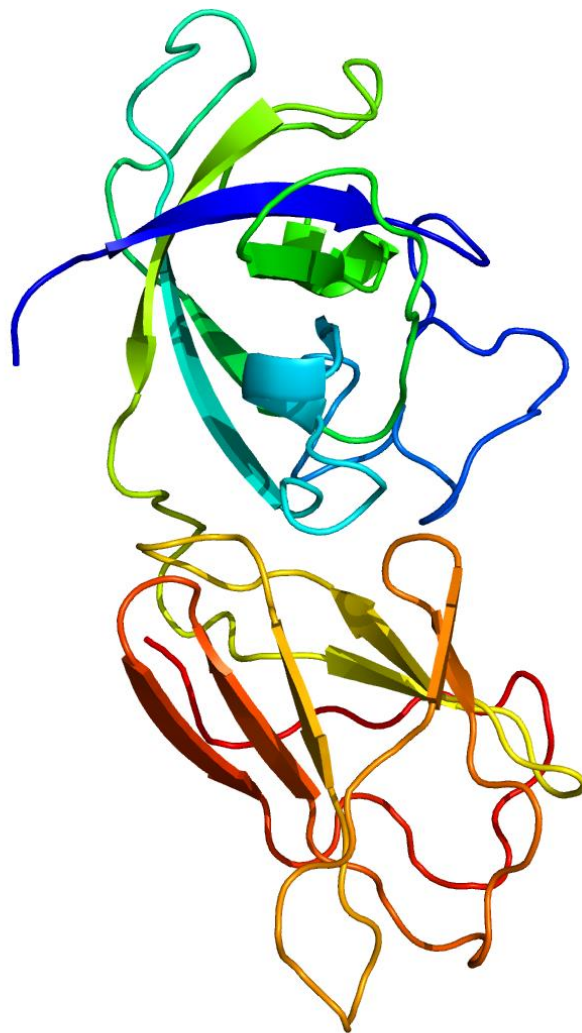
**Locus:** Ciclev10023630

**Gene Model:** Ciclev10023630m

**Description:** CclEXPA-06

**Family:** Alpha Expansin

**3D structure:**



## GENOME DATABASES

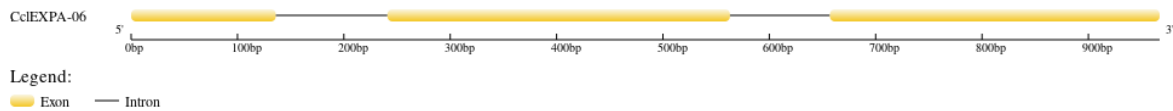
Phytozome: [https://phytozome-next.jgi.doe.gov/info/Cclementina\\_v1\\_0](https://phytozome-next.jgi.doe.gov/info/Cclementina_v1_0)

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

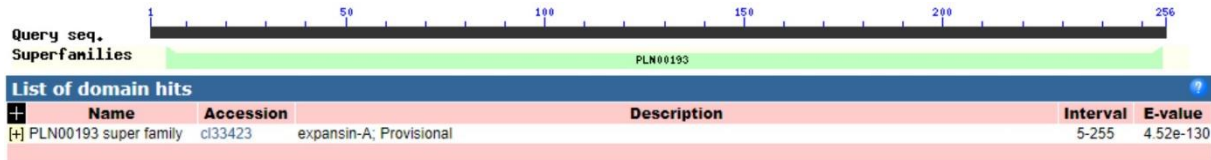
## EXTERNAL RESOURCES

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

## GENE STRUCTURE



## DOMAIN ARCHITECTURE



## SEQUENCES

### Peptide

>CclEXPA-06

MEGFFAFSFLALILTLLSIKINAASAAWMQAHATFYGGSDASETMGGACGYGNLYTD  
GYGTKTAALSTVLFNNGKSCGGCYHIVCDGRKVPQWCRRGTSIIITATNFCPPNYDLP  
NDNGGWCNPPRAHFDMSQPAFESIAIYRAGIVPVL YRKV GCMRSGGLRFTINGRDYF  
ELVLVSNVGGAGEVSNVWIKGSKMSKWQVMSRNWGANWQSLTYLNAQSL SFRVQ  
TSNGRTRTAYNVAPSNWRFGQSFKSNVQF\*

### CDS (coding sequence)

>CclEXPA-06

ATGGAAGGTTTCTTTGCTTTCAGTTTTGTGGCGCTGATCTTAACGTTACTTTCCATT  
AAAATTAATGCAGCTTCTGCTGCTTGGATGCAAGCCCATGCAACTTTCTACGGTG  
GAAGTGATGCTTCAGAAACAATGGGTGGTGCTTGTGGATATGGAAACTTATACAC  
AGATGGTTATGGCACAAAACACTGCAGCATTGAGCACAGTTTTGTTCAATAATGGA  
AAGTCTTGTGGTGGGTGCTATCACATCGTTTGCACGGGAGGAAGGTGCCGCAAT  
GGTGCCGCCGGGGACATCCATCATTACGGCTACAACTTCTGCCCGCCAAA  
CTATGATCTGCCTAACGACAACGGCGGTTGGTGCAACCCTCCACGGGCGCACTTT  
GACATGTCTCAGCCTGCATTTGAGTCCATTGCCATTTACAGAGCCGGAATTGTAC  
CCGTA CTCTACAGAAAGGTTGGATGCATGAGAAGTGAGGCCTTAGATT CACAAT  
AAATGGAAGGGACTACTTTGAGCTTGTGCTTGTTCAAATGTTGGAGGAGCTGGA  
GAGTTTCTAATGTGTGGATCAAGGGATCCAAAATGAGCAAATGGCAAGTGATG  
TCAAGGA ACTGGGGAGCTAATTGGCAGAGTTTGACTTATCTCAATGCTCAGAGCT  
TGTCCTTTAGAGTCCAAACTAGCAATGGAAGGACCCGCACAGCCTATAACGTTGC  
ACCTTCCA ACTGGAGATTTGGCCAATCTTTCAAAGCAATGTTCAATTCTAA

### Nucleotide

>CclEXPA-06

ATGGAAGGTTTCTTTGCTTTCAGTTTTGTGGCGCTGATCTTAACGTTACTTTCCATT  
AAAATTAATGCAGCTTCTGCTGCTTGGATGCAAGCCCATGCAACTTTCTACGGTG  
GAAGTGATGCTTCAGAAACAATGGGTATGTTTTCTATTTATATAATGGCAAGAAT  
AAACAATATGTCGCTTAATTCATTATTCATTTACATTC AATTTTATGCTAATGATT  
TTGAACTTCGGCTTTCAGGTGGTGCTTGTGGATATGGAAACTTATACACAGATGG

TTATGGCACAAAACTGCAGCATTGAGCACAGTTTTGTTCAATAATGGAAAGTCT  
TGTGGTGGGTGCTATCACATCGTTTGGGACGGGAGGAAGGTGCCGCAATGGTGCC  
GCCGGGGGACATCCATCATCATTACGGCTACAACTTCTGCCCGCCAAACTATGA  
TCTGCCTAACGACAACGGCGGTTGGTGCAACCCTCCACGGGGCGCACTTTGACATG  
TCTCAGCCTGCATTTGAGTCCATTGCCATTTACAGAGCCGGAATTGTACCCGTACT  
CTACAGAAAGTATGTTCAATTCTTCATTAAAAAAATTTGCATTTTTGTTTCTTCTTG  
GTGGGCGTCTTCTGTATATATACTGAGGTTTCTTGTCGTTCCACCAGGGTTGGATGC  
ATGAGAAGTGGAGGCCTTAGATTCACAATAAATGGAAGGGACTACTTTGAGCTTG  
TGCTTGTTTCAAATGTTGGAGGAGCTGGAGAGGTTTCTAATGTGTGGATCAAGGG  
ATCCAAAATGAGCAAATGGCAAGTGATGTCAAGGAACTGGGGAGCTAATTGGCA  
GAGTTTGACTTATCTCAATGCTCAGAGCTTGTCCTTTAGAGTCCAAACTAGCAATG  
GAAGGACCCGCACAGCCTATAACGTTGCACCTTCCAACCTGGAGATTTGGCCAATC  
TTTCAAAGCAATGTTCAATTCTAA