

## IDENTIFICATION

**Species:** *Citrus clementina*

**Locus:** Ciclev10012518

**Gene Model:** Ciclev10012518m

**Description:** CclEXPA-13

**Family:** Alpha Expansin

**3D structure:**



## GENOME DATABASES

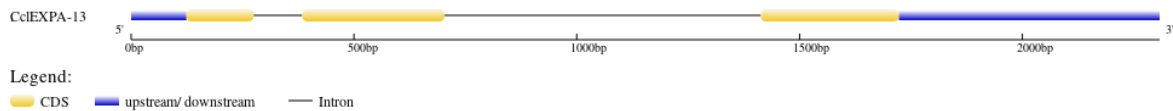
Phytozome: [https://phytozome-next.jgi.doe.gov/info/Cclementina\\_v1\\_0](https://phytozome-next.jgi.doe.gov/info/Cclementina_v1_0)

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

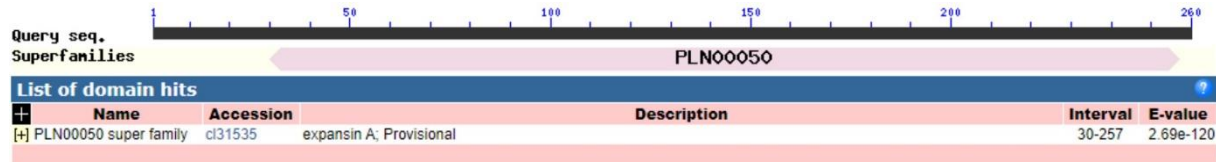
## EXTERNAL RESOURCES

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

## GENE STRUCTURE



## DOMAIN ARCHITECTURE



## SEQUENCES

### Peptide

>CclEXPA-13

MALFRMLCFFSLALSFLFATANAKIPGVFAGGPWQSAHATFYGGSDASGTMGGACGY  
GNLYSQGYGVNTAALSTALFNGLSCGACFELKCGGDPQWCNPGNPAILITATNFCP  
PNFAQPSDNGGWCNPPRPHFDLAMPMLKLAQYRAGIVPVSYRRVPCRKRGGIRFTI  
NGFRYFNLVLVTNVAGAGDIVRVSVK GANTQWLSMSRNWGQNWQSNAQLVGQAL  
SFRVTGSDRRTSTSWNVAPANWQFGQTFSGKNFRV\*

### CDS (coding sequence)

>CclEXPA-13

ATGGCTCTTTTCAGAATGCTCTGCTTTTTTCTCACTGGCACTCTCCTTATTTGCGACG  
GCCAACGCCAAGATTCCCGGTGTCTTCGCCGGTGGCCCCTGGCAATCGGCCACG  
CCACTTTTTACGGTGGCAGCGACGCTTCCGGCACTATGGGTGGTGCTTGTGGGTA  
CGGGAATCTGTACAGCCAGGGCTATGGAGTGAACACGGCGGCTCTCAGTACGGC  
GCTGTTCAACAACGGCTTGAGCTGCGGCGCGTGCTTCGAGTTAAAGTGCGGCGGC  
GACCCGCAATGGTGTAACCCGGGTAACCCGGCCATTCTGATCACGGCGACAACT  
TTTGCCCCCGAACTTCGCTCAGCCCTCCGATAATGGCGGGTGGTGCAACCCTCCT  
CGCCCTCATTTTCGATCTGGCCATGCCTATGTTCTCAAGCTCGCCAGTACCGCGC  
TGGTATCGTCCCCGTTTCTTACCGCAGGGTGCCCTGCAGAAAGCGAGGCGGAATC  
AGATTACAATTAACGGTTTCCGTTACTTCAACTTGGTCTTGGTCACCAACGTCGC  
GGGCGCAGGGGATATCGTGCGCGTGAGCGTGAAGGGGCCAACACCCAATGGCT  
GAGCATGAGCCGCAACTGGGGACAAA ACTGGCAATCCAACGCTCAGCTCGTGGG  
CCAGGCACTTTTCGTTTAGAGTCACGGGCAGTGACAGAAGGACCTCAACCTCTTGG  
AACGTGGCGCCAGCGAATTGGCAGTTCGGTCAAACCTTTTCGGGAAAGAATTTCC  
GCGTCTAG

### Nucleotide

>CclEXPA-13

CTCTTTACCCTAACGTACCCCTTTAAGTACCCCCACTTCCTTCCCGCTTTCTCCATT  
CGCCACCTCCTGCGCGCTCACTCACTCACTCACTCAACTCTGTCTCCCTCTCTTC  
AACTCCAACAATGGCTCTTTTCAGAATGCTCTGCTTTTTTCTCACTGGCACTCTCCT

TATTTGCGACGGCCAACGCCAAGATTCCCGGTGTCTTCGCCGGTGGCCCCTGGCA  
ATCGGCCACGCCACTTTTTACGGTGGCAGCGACGCTTCCGGCACTATGGGTATA  
CTTTAGTTCTATCTCCTTACATCTCTCCATTTCTCATTCTTTTTTTTTCTTTTTTTCA  
AAGAACTTTTCTAACGGTGATATGTGTATATATTTTTTTGTGCAGGTGGTGCTTGT  
GGGTACGGGAATCTGTACAGCCAGGGCTATGGAGTGAACACGGCGGCTCTCAGT  
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AACTTTTTGCCCCCGAACTTCGCTCAGCCCTCCGATAATGGCGGGTGGTGCAAC  
CCTCCTCGCCCTCATTTTCGATCTGGCCATGCCTATGTTCCCTCAAGCTCGCCAGTA  
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CTTTGTCTCCAAGTTTTGTTTGAATGTCTTCTTTGGAAGAAATACCGGAAACCCGG  
GAAAAGTCGGGCTGTTTAAATGTGTGTTTTTATTTTAAATATTTTCCCTTTTCTTTTC  
TTCGCAAACAAACAGAACCCGGAAATAAGTTTACTGATCAGTAGTTTATGTCGTT  
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ATTAATTATAATAATTTACCAAATTTTCTACATGAAAACCTTGTAATACTTCAAGC  
TCAGGACAAGTCAAATAATTACCAA