

IDENTIFICATION

Species: *Citrus clementina*

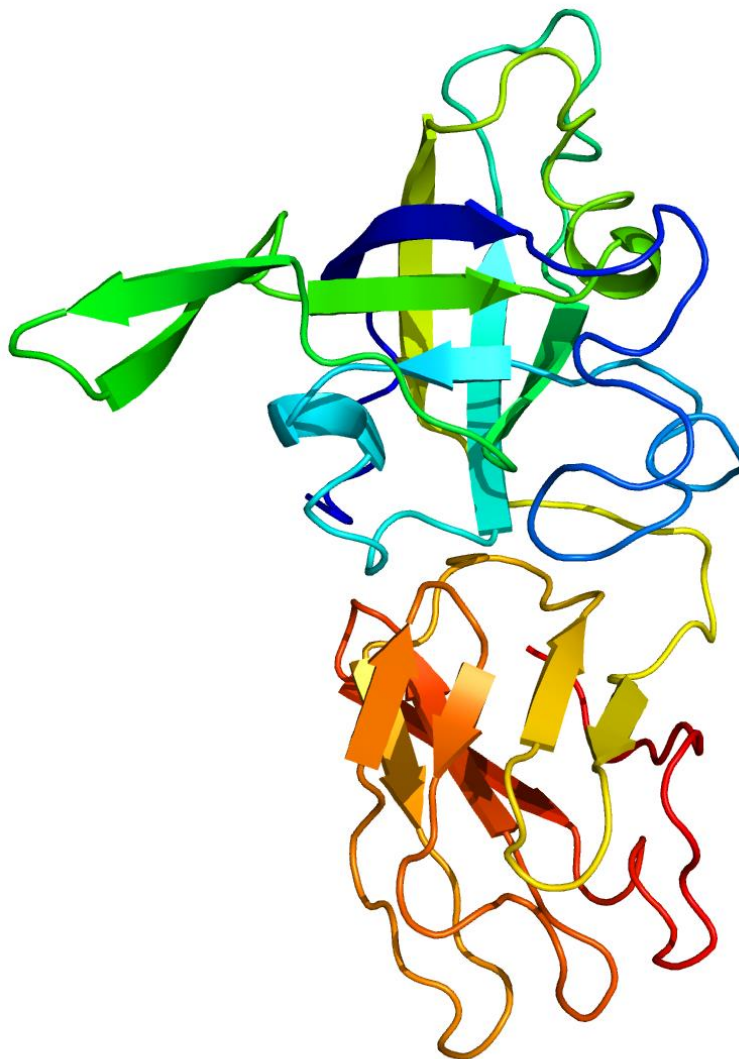
Locus: Ciclev10017738

Gene Model: Ciclev10017738m

Description: CclEXPA-02

Family: Alpha Expansin

3D structure:



GENOME DATABASES

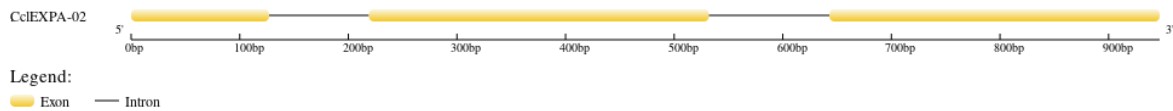
Phytozome: https://phytozome-next.jgi.doe.gov/info/Cclementina_v1_0

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

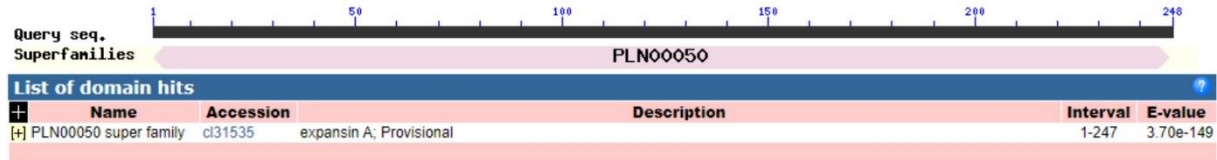
EXTERNAL RESOURCES

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

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>CclEXPA-02

MAILGYIIIALFTVFKAAVGGKAGWTNAHATFYGGGDASGTMGGACGYGNLYSQGY
GTNTAAVSTALFNNGLNCGACYAIKCVNDRWCLPGSIIVTATNFCPPNFALSNTNG
GWCNPLHFDLSQPVFLKIAQYKAGIVPVQYRRVACKKSGGIRFTINGHSYFNLVLI
TNVGGAGDVVAVSIKGSKTGWQALS RNWGQNWQSNSYLNQALSFKVTTSDGRTV
ISNNVAPANWNFGQTYTGRQF*

CDS (coding sequence)

>CclEXPA-02

ATGGCAATTCTTGGCTATATCATAATAGCCCTTTTCACAGTTTTTAAAGCAGCTGT
TGGAAAAGGAGCCGGGTGGACTAATGCTCATGCTACCTTCTATGGAGGTGGTGAT
GCTTCTGGCACAATGGGTGGGGCTTGTGGGTATGGGAATCTTTACAGCCAAGGTT
ATGGAACAAACACAGCTGCGGTGAGCACAGCTTTATTCAACAATGGGTTGAATTG
TGGAGCTTGTTATGCTATTAATGTGTAAATGACAATAGATGGTGCTTACCAGGC
TCCATTATAGTCACTGCCACTAATTTCTGTCCGCCAAATTTTGCTCTCTCTAATAC
CAATGGAGGTTGGTGTAATCCTCCCCTTCATCACTTTGATCTCTCTCAGCCTGTAT
TCCTCAAATCGCTCAGTACAAAGCCGGCATAAGTTCCGGTTCAATACAGGAGGGT
CGCCTGCAAGAAGAGTGGAGGGATCAGATTCACAATCAATGGACATTCTTACTTC
AATCTAGTGCTGATAACAAATGTTGGTGGAGCAGGTGATGTTGTTGCTGTGTCCA
TAAAAGGTTCTAAAAGTGGCTGGCAAGCATTGTCCAGGAATTGGGGGCAGAACT
GGCAGAGCAACTCTTACCTCAATGGCCAAGCCCTGTCTTTCAAGGTCACAACTAG
CGATGGCCGCACTGTCATCTCCAATAATGTAGCTCCAGCCAAGTGAATTTTGGC
CAAACCTACACCGGCCGCCAGTTCTAA

Nucleotide

>CclEXPA-02

ATGGCAATTCTTGGCTATATCATAATAGCCCTTTTCACAGTTTTTAAAGCAGCTGT
TGGAAAAGGAGCCGGGTGGACTAATGCTCATGCTACCTTCTATGGAGGTGGTGAT
GCTTCTGGCACAATGGGTAAGTTTCAGGAAGAAAAAAGATTGATGAATCAAAT
AGATGTTTGAATTGTTATATAATGAAAGTTTAATTTGTTAAATGATTGATACAGGT
GGGGCTTGTGGGTATGGGAATCTTTACAGCCAAGGTTATGGAACAAACACAGCTG

CGGTGAGCACAGCTTTATTCAACAATGGGTTGAATTGTGGAGCTTGTTATGCTATT
AAATGTGTAAATGACAATAGATGGTGCTTACCAGGCTCCATTATAGTCACTGCCA
CTAATTTCTGTCCGCCAAATTTTGCTCTCTCTAATACCAATGGAGGTTGGTGTAAT
CCTCCCCTTCATCACTTTGATCTCTCTCAGCCTGTATTCCCTCAAATCGCTCAGTA
CAAAGCCGGCATAGTTCCGGTTCAATACAGGAGGTAATAATATATGAAACGAAA
CAAACCAAGATTAGCTAATTCTCTCACTTTTACCCGTACGTGCAAATTAAGTACA
GGCGTACTGATGTTCTGAACTCTTGATAACTTCAGGGTCGCCTGCAAGAAGAGTG
GAGGGATCAGATTCACAATCAATGGACATTCTTACTTCAATCTAGTGCTGATAAC
AAATGTTGGTGGAGCAGGTGATGTTGTTGCTGTGTCCATAAAAGGTTCTAAAAC
GGCTGGCAAGCATTGTCCAGGAATTGGGGGCAGAACTGGCAGAGCAACTCTTAC
CTCAATGGCCAAGCCCTGTCTTTCAAGGTCACAACACTAGCGATGGCCGCACTGTCA
TCTCCAATAATGTAGCTCCAGCCAACCTGGAATTTGGCCAACTTACACCGGCCG
CCAGTTCTAA