

## IDENTIFICATION

**Species:** *Citrus sinensis*

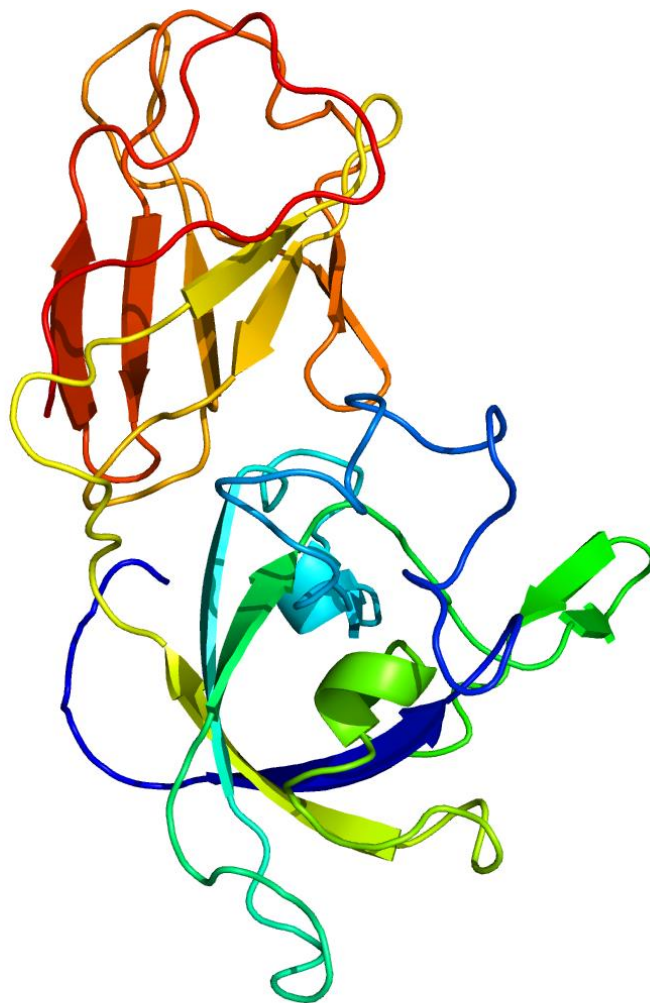
**Locus:** orange1.1g025827m

**Gene Model:** orange1.1g025827m

**Description:** CisEXPA-15

**Family:** Alpha Expansin

**3D structure:**



## GENOME DATABASES

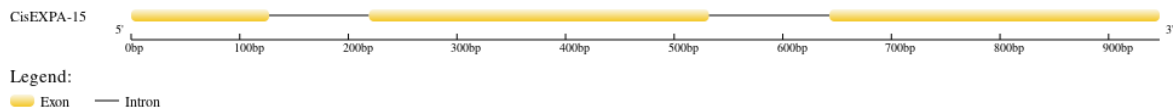
Phytozome: [https://phytozome-next.jgi.doe.gov/info/Csinensis\\_v1\\_1](https://phytozome-next.jgi.doe.gov/info/Csinensis_v1_1)

Kegg: <https://www.genome.jp/entry/T02983>

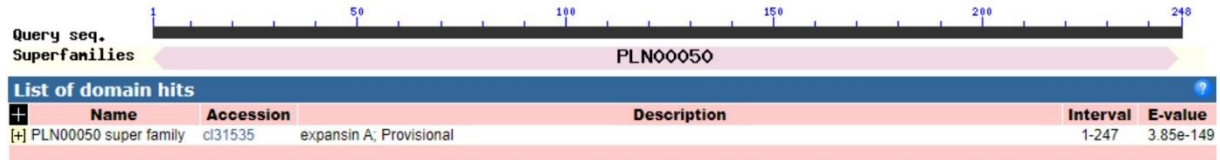
## EXTERNAL RESOURCES

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

## GENE STRUCTURE



## DOMAIN ARCHITECTURE



## SEQUENCES

### Peptide

>CisEXPA-15

MAILGYIIIALFTVFKAAVGGKAGWTNAHATFYGGGDASGTMGGACGYGNLYSQGY  
GTNTAAVSTALFNNGLNCGACYAIKCVNDRWCLPGSIIVTATNFCPPNFALSNTNG  
GWCNPLHFDLSQPVFLKIAQYKAGIVPVQYRRVACKKSGGIRFTINGHSYFNLVLI  
TNVGGAGDVVAVSIKGSKTGWQALSARNWGQNWQSN SYLNGQALSFKVTTSDGRTV  
ISNNVAPANWNFGQTYTGRQF\*

### CDS (coding sequence)

>CisEXPA-15

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

### Nucleotide

>CisEXPA-15

ATGGCAATTCTTGGCTATATCATAATAGCCCTTTTCACAGTTTTTAAAGCAGCTGT  
TGGAAAAGGAGCCGGGTGGACTAATGCTCATGCTACCTTCTATGGAGGTGGTGAT  
GCTTCTGGCACAATGGGTAAGTTTCAGGAAGAAAAAAGATTGATGAATCAAAT  
AGATGTTTGAATTGTTATATAATGAAAGTTTAATTTGTTAAATGATTGATACAGGT  
GGGGCTTGTGGGTATGGGAATCTTTACAGCCAAGGTTATGGAACAAACACAGCTG

CGGTGAGCACAGCTTTATTCAACAATGGGTTGAATTGTGGAGCTTGTTATGCTATT  
AAATGTGTAAATGACAATAGATGGTGCTTACCAGGCTCCATTATAGTCACTGCCA  
CTAATTTCTGTCCGCCAAATTTTGCTCTCTCTAATACCAATGGAGGTTGGTGTAAT  
CCTCCCCTTCATCACTTTGATCTCTCTCAGCCTGTATTCTCTCAAATCGCTCAGTA  
CAAAGCCGGCATAAGTTCCGGTTCAATACAGGAGGTAAAAATATATGAAACGAAA  
CAAACCAAGATTAGCTAATTCTCTCACTTTTACCCGTACGTGCAAATTAAGTACA  
GGCGTACTGATGTTCTGAACTCTTGATAACTTCAGGGTCGCCTGCAAGAAGAGTG  
GAGGGATCAGATTCACAATCAATGGACATTCTTACTTCAATCTAGTGCTGATAAC  
AAATGTTGGTGGAGCAGGTGATGTTGTTGCTGTGTCCATAAAAGGTTCTAAAAC  
GGCTGGCAAGCATTGTCCAGGAATTGGGGGCAGAACTGGCAGAGCAACTCTTAC  
CTCAATGGCCAAGCCCTGTCTTTCAAGGTCACAACACTAGCGATGGCCGCACTGTCA  
TCTCCAATAATGTAGCTCCAGCCAACCTGGAATTTGGCCAACTTACACCGGCCG  
CCAGTTCTAA