

## IDENTIFICATION

**Species:** *Citrus sinensis*

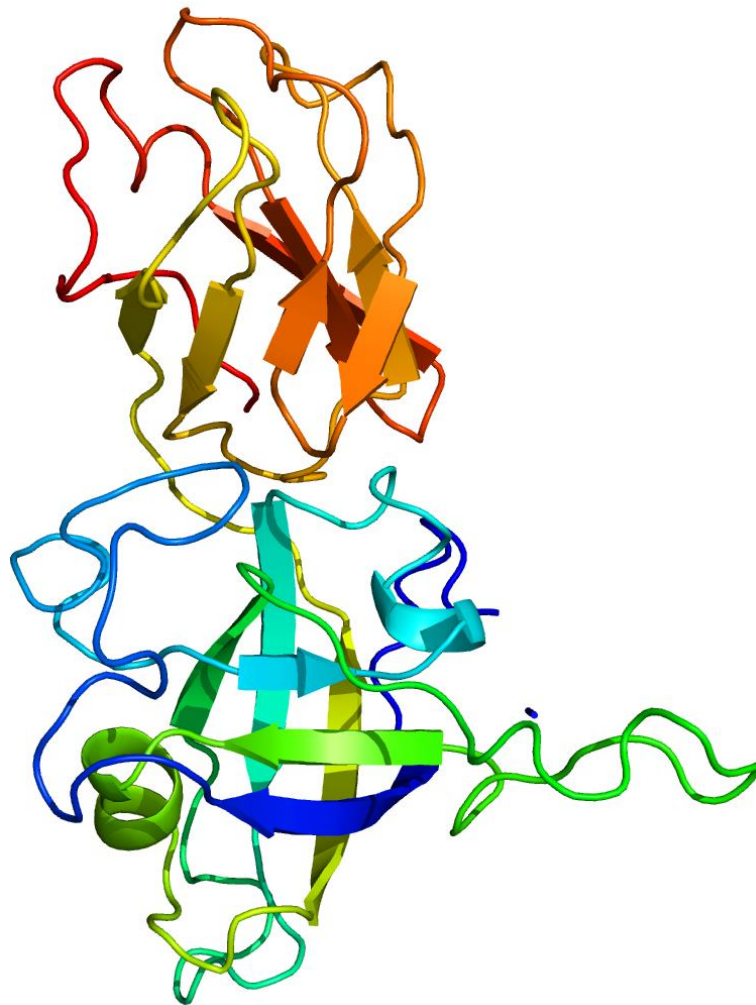
**Locus:** orange1.1g024457m

**Gene Model:** orange1.1g024457m

**Description:** CisEXPA-13

**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>

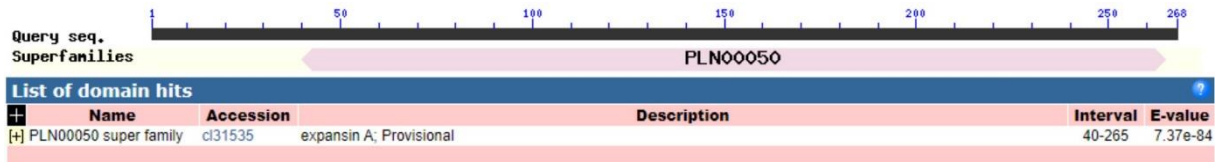
## EXTERNAL RESOURCES

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

## GENE STRUCTURE



## DOMAIN ARCHITECTURE



## SEQUENCES

### Peptide

>CisEXPA-13

MSPQLLTLVIQLLLLFTPAPTTVTSHYNYNFTSTSPPSQSEWRPARATFYAASDPRDK  
VGGACGYGDLEKAGYQGATAGLSEILFERGQICGACFELRCFEDIRWCIPGTSIIIVTVT  
NFCAPNYGFNPDGGGHCNPPNKHVFLPIEAFEKIAIWKAGNMPVQYRRYNFILLSIRF  
TIDGSDIFISALISNVAGAGDVVAVKIKGSRTGWLPMGRNWGQNWHINANLKNQPLS  
FEVTTSDGLTVTSYNVAPKNWNFGQTFEGKQFES\*

### CDS (coding sequence)

>CisEXPA-13

ATGTCGCCACAACCTGTTAACTCTTGTAATAACAACCTGCTGCTTCTGTTACACACCAGC  
ACCGACAACAGTCACCTCACACTACAACCTACAACCTTCACTTCCACGTCTCCCCCA  
TCGCAATCCGAGTGGCGGCGCCGACGCGCCACTTTCTACGCGGCCTCCGATCCCC  
GTGACAAGGTGGGCGGCGCGTGC GGGTACGGCGACCTCGAAAAGGCAGGCTACG  
GTCAGGCCACCGCTGGACTGTCTGAGATTCTCTTCGAGCGCGGCCAGATCTGCGG  
CGCCTGCTTTGAGCTCCGCTGTTTCGAGGATATCCGATGGTGCATTCTGGAACCT  
CTATAATTGTCACTGTCACTAACTTTTGTGCTCCTAATTACGGTTTTAACCCCGAT  
GGCGGTGGCCACTGTAATCCTCCTAATAAGCATTTTGTTCTTCCCATCGAGGCTTT  
CGAGAAAATCGCCATTTGGAAAGCTGGCAACATGCCCGTCCAGTACCGCAGGTAT  
AATTTTATTTTAATTTTAAGCATTTCGATTTACGATTGATGGTTTCGGATATCTTCATT  
TCAGCGTTGATCAGCAATGTTGCAGGTGCTGGAGATGTGGTTGCAGTGAAGATCA  
AGGGTTCAAGAACCGGTTGGCTTCCAATGGGTCGGAATTGGGGCCAAAACCTGGC  
ACATAAATGCCAATCTGAAAAATCAACCTCTCTCATTTGAGGTCACCACTAGTGA  
TGGCCTCACGGTTACATCTTATAATGTTGCTCCTAAGAATTGGAACCTTGGGCAG  
ACCTTTGAAGGCAAACAATTTGAGTCTTAG

### Nucleotide

>CisEXPA-13

ATGTCGCCACAACCTGTTAACTCTTGTAATAACAACCTGCTGCTTCTGTTACACACCAGC  
ACCGACAACAGTCACCTCACACTACAACCTACAACCTTCACTTCCACGTCTCCCCCA  
TCGCAATCCGAGTGGCGGCGCCGACGCGCCACTTTCTACGCGGCCTCCGATCCCC

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GTCAGGCCACCGCTGGACTGTCTGAGATTCTCTTCGAGCGCGGCCAGATCTGCGG  
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CTGCTTTTTTTTTTTTTTTTTTTTTGGGTGTCGCAAGGCAGTGAGTATATAACCCAGAG  
GTTGATCGTATGAAGTAGATGTCTTGAATTTGACTATCTGGTGTGTGAGTTGAG  
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CCAAAATGGCACATAAATGCCAATCTGAAAATCAACCTCTCTCATTTGAGGTC  
ACCACTAGTGATGGCCTCACGGTTACATCTTATAATGTTGCTCCTAAGAATTGGA  
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TAAAATTTTTTATCCTCACTAATACGAAACCAGGAAATTGCTACCTTACAACG  
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