

## IDENTIFICATION

**Species:** *Citrus sinensis*

**Locus:** orange1.1g045913m

**Gene Model:** orange1.1g045913m

**Description:** CisEXPA-11

**Family:** Alpha Expansin

**3D structure:**



## GENOME DATABASES

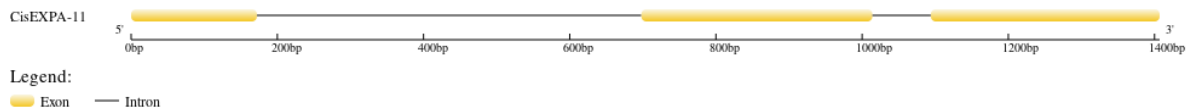
Phytozome: [https://phytozome-next.jgi.doe.gov/info/Csinensis\\_v1\\_1](https://phytozome-next.jgi.doe.gov/info/Csinensis_v1_1)

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

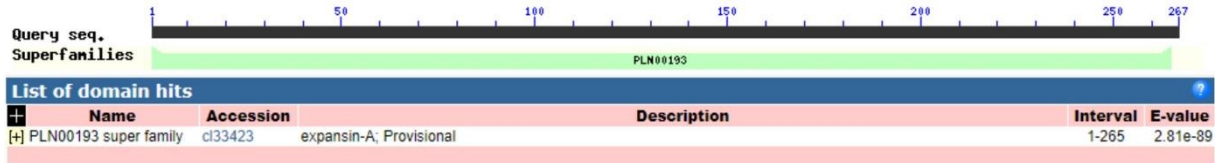
## EXTERNAL RESOURCES

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

## GENE STRUCTURE



## DOMAIN ARCHITECTURE



## SEQUENCES

### Peptide

>CisEXPA-11

MASFLRSFGFSYLLVVLILIAIEKSNASGYTRPIFRSGAWQLAHATFYGDQSASETMG  
GACGYGNLRINGYGTDTAALSSMLFNNGGYACGTCYQIKCHDSPHCYTYVSFTTVTA  
TNLCPPNWSQDSNNGGWCNPPRAHFDMSKPAFMKIADWKAGIIPVIYRRVPCVKAG  
GLRFAFQNGYWLLVYVLNVAGGGDIANMWVKGTRTGWISMShNWGASYQAFAT  
LGGQALSFKLTSYSSKETIFAYNVAPPNWNVGLTYSSDVNFH\*

### CDS (coding sequence)

>CisEXPA-11

ATGGCTTCTTTCCTTCGATCATTGGATTTAGCTACCTATTGGTTGTTTTGATTTG  
GCAATCGCTGAAAAGTCAAATGCTTCGGGCTATACACGTCCTATTTCCGTTTCAG  
GTGCATGGCAGCTTGCTCACGCCACCTTTTACGGTGATCAGTCTGCCTCTGAGACC  
ATGGGTGGAGCTTGCGGGTATGGAACTTGC GGATTAATGGATACGGGACAGAC  
ACAGCGGCATTGAGCTCTATGTTGTTCAACGGTGGATACGCTTGTGGGACTTGTT  
ATCAGATAAAGTGCCACGATTCGCCTCATTGCTATACATATGTATCGTTCACAAC  
AGTTACAGCCACAAACCTTTGCCC GCCAAATTGGTCCCAGGACTCCAATAATGGT  
GGCTGGTGCAATCCTCCTCGGGCCATTTTGACATGTCCAAGCCCGCATTCATGA  
AGATTGCTGACTGGAAGGCCGGCATTATCCCCGTCATCTACCGAAGAGTGCCATG  
CGTGAAGGCTGGAGGGTTGCGATTTCGCTTCCAGGGAAATGGTACTGGTTGTTG  
GTGTATGTACTGAATGTTGCGGGCGGAGGAGACATTGCCAACATGTGGGTTAAAG  
GAACAAGAACGGGATGGATTAGCATGAGCCATAACTGGGGAGCTTCATATCAAG  
CATTTGCAACTCTAGGTGGCCAAGCTCTTTCTTTCAAGCTCACTTCCTATTCCTCC  
AAGGAGACAATTTTGCATACAATGTTGCTCCTCCTAACTGGAACGTAGGATTGA  
CTTACAGTTCAGATGTAACTTCCATTGA

### Nucleotide

>CisEXPA-11

ATGGCTTCTTTCCTTCGATCATTGGATTTAGCTACCTATTGGTTGTTTTGATTTG  
GCAATCGCTGAAAAGTCAAATGCTTCGGGCTATACACGTCCTATTTCCGTTTCAG  
GTGCATGGCAGCTTGCTCACGCCACCTTTTACGGTGATCAGTCTGCCTCTGAGACC  
ATGGGTATGCTATTTACATTTTTTGTCTAAATTATATATAGTTTTAATAATTATTTTC

AGATAAAATATGACTGAAAATTAATTTTTCTACCCACTCATATCAGCGTAATCGT  
TTATCTTGTGTAGCTAAAATATTACACGAATGTACGTACAAAAGAATGTCATTC  
ATTTGGTTAGATTAATAAAAAAATAAATACTTTTTTCAAATAGAAATGTGATTA  
CAGTAAAAAGATTATCACACGGGGCAGAAGGAAAACCTATGTAGAGGCCTGGTCC  
CTGAAACCGAAAAATTCAAATAAAGAAAAGGGTCTTCATTGGAATTTTACTCATT  
TTATATTGTAGTTATCAGGTTTATTGTATACACGTTATAGCCTTACATATAAAATA  
ATATGTTTAACCCACATTTTTTGC GGTTTCTAACATTATGTGCACCTCTAACCAAAA  
TCATAGTTGCATTCGCCGCTGCTTAGAAATGTTTCACCATAAAATGTTTTACTGTAT  
GTTAAAATGTTGTTAACTCTGGATTACAGGTGGAGCTTGCGGGTATGGAACTT  
GCGGATTAATGGATACGGGACAGACACAGCGGCATTGAGCTCTATGTTGTTCAAC  
GGTGGATACGCTTGTGGGACTTGTTATCAGATAAAGTGCCACGATTTCGCCTCATT  
GCTATACATATGTATCGTTCACAACAGTTACAGCCACAAACCTTTGCCCGCCAAA  
TTGGTCCCAGGACTCCAATAATGGTGGCTGGTGAATCCTCCTCGGGCCCATTTTTG  
ACATGTCCAAGCCCGCATTTCATGAAGATTGCTGACTGGAAGGCCGGCATTATCCC  
CGTCATCTACCGAAGGTACTAATGTGGACATGAATGTGAAAGTCCTCATAATTGG  
TGTTATATTTAATTCAAATGACTAAAGTTTGGTTTTGTAGAGTGCCATGCGTGAAG  
GCTGGAGGGTTGCGATTTCGCTTTCCAGGGAAATGGTACTGGTTGTTGGTGTATG  
TACTGAATGTTGCGGGCGGAGGAGACATTGCCAACATGTGGGTAAAGGAACAA  
GAACGGGATGGATTAGCATGAGCCATAACTGGGGAGCTTCATATCAAGCATTTCG  
AACTCTAGGTGGCCAAGCTCTTTCTTTCAAGCTCACTTCCTATTCTCCAAGGAGA  
CAATTTTTGCATACAATGTTGCTCCTCCTAACTGGAACGTAGGATTGACTTACAGT  
TCAGATGTAACTTCCATTGA