

## IDENTIFICATION

**Species:** *Citrus sinensis*

**Locus:** orange1.1g025809m

**Gene Model:** orange1.1g025809m

**Description:** CisEXPA-18

**Family:** Alpha Expansin

**3D structure:**



## GENOME DATABASES

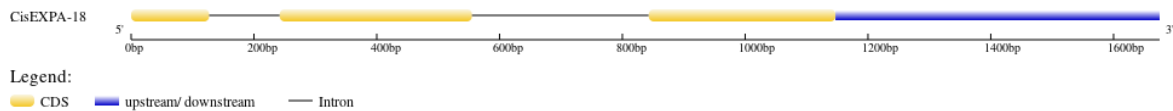
Phytozome: [https://phytozome-next.jgi.doe.gov/info/Csinensis\\_v1\\_1](https://phytozome-next.jgi.doe.gov/info/Csinensis_v1_1)

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

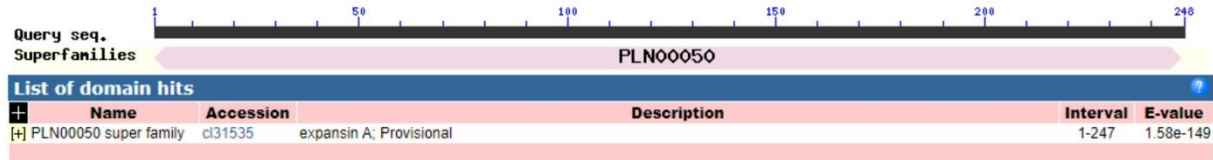
## EXTERNAL RESOURCES

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

## GENE STRUCTURE



## DOMAIN ARCHITECTURE



## SEQUENCES

### Peptide

>CisEXPA-18

MDFLGIFLVASLSMLRTIHGYAGGWSSAHATFYGGGDASGTMGGACGYGNLYSQG  
YGTSTAALSTALFNNGVTCGACFEIKCVNDNRWCLPGSIIVTATNFCPPNHALPNNAG  
GWCNPPLQHFDLSQPIFQHIAHYKAGIVPVQYRRVACRKSGGIRFTINGHSYFNLVLIT  
NVGGAGDVVSIVSIKGSRTGWQPMSRNWQNWQSN SYLNGQALS FQVTTSDGRSVIS  
INVAPPNWSFGRITYNGRQF\*

### CDS (coding sequence)

>CisEXPA-18

ATGGACTTTCTTGGGATCTTTCTAGTGGCCTCTTTGTCAATGTTGAGAACAATTCA  
TGGCTATGCCGGTGGATGGTCAAGTGCTCATGCTACGTTCTATGGCGGAGGCGAT  
GCTTCTGGCACAATGGGAGGAGCTTGTGGCTATGGAAATCTTTACAGCCAAGGTT  
ATGGCACAAGCACTGCTGCATTGAGCACTGCCCTATTCAACAACGGGGTGACTTG  
TGGAGCTTGCTTTGAGATCAAATGTGTAAATGACAATAGGTGGTGTCTTCCAGGA  
TCTATCATTGTCACAGCAACAACTTCTGCCCCCAAACCATGCCCTTCCGAATA  
ATGCAGGAGGCTGGTGTAAACCTCCTTTGCAGCACTTTGATCTTTCTCAGCCTATT  
TTCCAACACATAGCTCATTACAAAGCTGGAATCGTTCCTGTTCAATACAGAAGAG  
TTGCCCTGCAGGAAGAGTGGTGGGATCAGATTACAATAAATGGCACTCATACTT  
CAACCTTGTGCTCATAACAAACGTTGGTGGTGCCGGGGATGTTGTTTCTGTCTCCA  
TTAAAGGCTCAAGAACCGGCTGGCAACCAATGTCTCGCAACTGGGGCCAAAATT  
GGCAGAGCAATTCTTACCTTAATGGTCAAGCTCTCTCATTCCAGGTCACAACAAG  
TGATGGACGCTCTGTTATCTCCATCAATGTGGCTCCTCCCAACTGGTCTTTTGGCC  
GAACTTACAATGGGAGACAGTTTTAA

### Nucleotide

>CisEXPA-18

ATGGACTTTCTTGGGATCTTTCTAGTGGCCTCTTTGTCAATGTTGAGAACAATTCA  
TGGCTATGCCGGTGGATGGTCAAGTGCTCATGCTACGTTCTATGGCGGAGGCGAT  
GCTTCTGGCACAATGGGTAAGATGAGAATCCTAACATTCAAAGATACTCTTGAA  
AACTCTTAGCGATAGTACTTAAAAACCTTTCAACTTTTCTTTCTTGGGCGCGCGTG  
CGTACGCGTGTGTGTTACAGGAGGAGCTTGTGGCTATGGAAATCTTTACAGCCAA

GGTTATGGCACAAGCACTGCTGCATTGAGCACTGCCCTATTCAACAACGGGGTGA  
CTTGTGGAGCTTGCTTTGAGATCAAATGTGTAAATGACAATAGGTGGTGTCTTCC  
AGGATCTATCATTGTCACAGCAACAACTTCTGCCCCCAAACCATGCCCTTCCG  
AATAATGCAGGAGGCTGGTGTAAACCCTCCTTTGCAGCACTTTGATCTTTCTCAGCC  
TATTTTCCAACACATAGCTCATTACAAAGCTGGAATCGTTCCTGTTCAATACAGA  
AGGTAAAATAACATATCAATCTAGTCTCCAACTCTCACTTAGTTCTATAACCTCAA  
GAACGTGCGGTTTAATATGTTGGTTCTCCTAACGTGTACCTTTAGAATACACGTTT  
GAAGACTCTTGAGGTGCAGAACCTCAGAAAAGAGAAGCAATCCTACTGAAATGG  
CTACATCTGATGCATTTAAATGAAATAATGGCCGCATGTGATGCATTTGATTGAA  
ATTGCTATCATGGGTATATTGATTTTTCTTTTTTTTTTTGTTGTTGCTGAAAGTTTTC  
TTGTTACCGCAGAGTTGCCTGCAGGAAGAGTGGTGGGATCAGATTCACAATAAAT  
GGACTCATACTTCAACCTTGTGCTCATAACAAACGTTGGTGGTGCCGGGGATG  
TTGTTTCTGTCTCCATTAAGGCTCAAGAACCGGCTGGCAACCAATGTCTCGCAA  
CTGGGGCCAAAATTGGCAGAGCAATTCTTACCTTAATGGTCAAGCTCTCTCATTC  
CAGGTCACAACAAGTGATGGACGCTCTGTTATCTCCATCAATGTGGCTCCTCCCA  
ACTGGTCTTTTGGCCGAACCTTACAATGGGAGACAGTTTTTAACTAGTTCCAGAA  
ACCGACTAATATCCCCATCATAGGATTAGATTTTTTCAGCTCTCATTGTTAAATTGC  
CACATAACATTAGCTCTTTATCAGTATATGTAAATTTGGTATGTCGTGACATTGGC  
GTCACCAAGGGGCAAGAGCTTTTAGTGATGGCCCCGAATACCATGCCAGTTTGAT  
TTTCTTTGCTTTTTGTTTCTGATGGATTTCACTGCACGTTGTTGCCAACAAAGGGTT  
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AGAAGGAAGAAGAAATCGAGTTTCAAGCCAATCCATTTTCAATTTTAAAGTTGTAGT  
GGAGATGGTGCATTGTATTACGCTGTTTGGCTTTTTCTTTCTCACGCCATTTGCAT  
AGGACAAGAATCATAATGAATATTCTTGTAGTTTTCTACTCTGCCATGGCAACTC  
AATGAATGAACAAGCAGAACAGATCATCTTAATAGTTATGTTTGCTGTCACATGT  
GAAACTAATTAGCA