## IDENTIFICATION

**Species:** *Citrus sinensis*

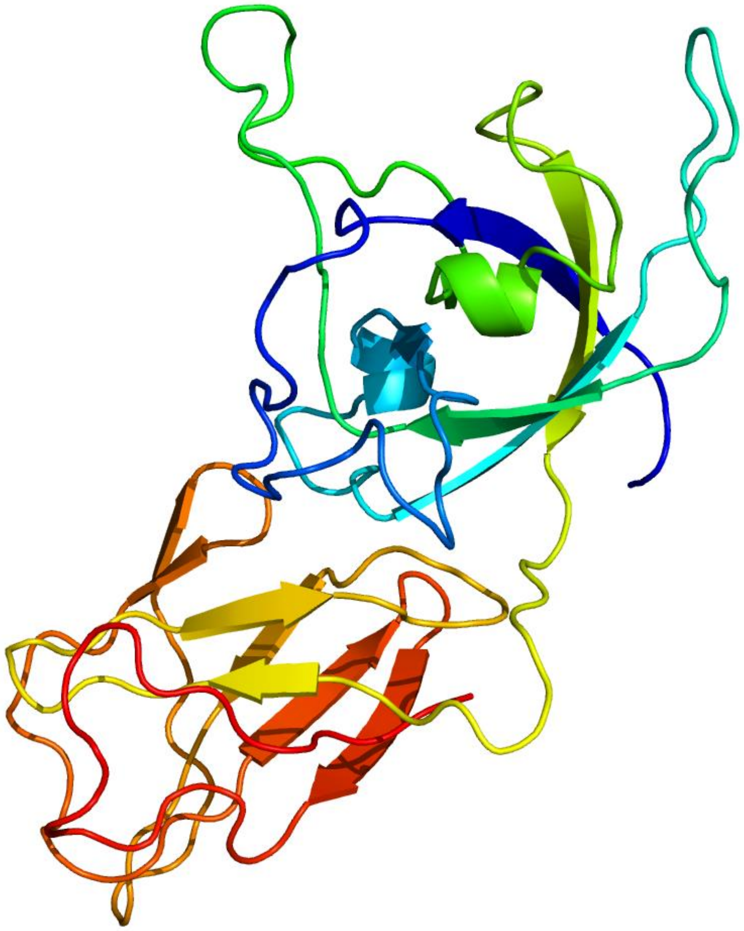
**Locus:** orange1.1g048775m

**Gene Model:** orange1.1g048775m

**Description:** CisEXPA-20

**Family:** Alpha Expansin

**3D structure:**



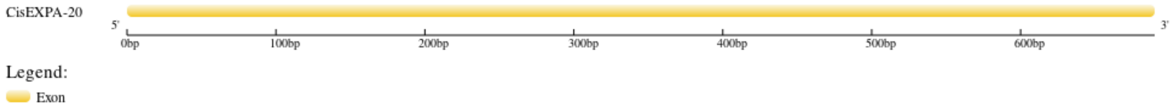
## GENOME DATABASES

Phytozome: https://phytozome-next.jgi.doe.gov/info/Csinensis_v1_1
Kegg: https://www.genome.jp/entry/T02983

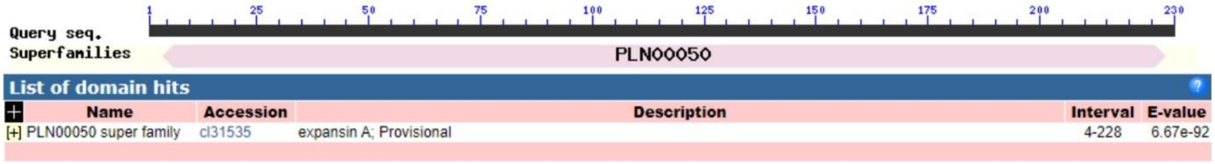
## EXTERNAL RESOURCES

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

## GENE STRUCTURE



## DOMAIN ARCHITECTURE



List of domain hits

| Name | Accession | Description | Interval | E-value |
|---|---|---|---|---|
| [+] PLN00050 super family | cl31535 | expansin A; Provisional | 4-228 | 6.67e-92 |

## SEQUENCES

### Peptide

>CisEXPA-20

PGPWKHAHATFYTGDTGSFGGACGYSDVTREGYGEGTTALSTTLFHNGAACGACFE
IKCIDDPKSCIPGQPSLFVTATNFCPPNFHQDANDGGWCNPPREHFDIAYPAFKHIAEY
KAGIVPVAYRRVSCKKQGGIKFTITGTQHWTLVTIWNVGGAGDISHVEVKGDNKLN
WTPLHKNWGSKWQTSCSLEEESLTFKVTTSDGRFVISPNVTPNKYWKYGQTFEGLNF
R*

### CDS (coding sequence)

>CisEXPA-20

CCTGGCCCGTGGAAACATGCTCATGCCACCTTTTACACCGGAGACACCGGATCAT
TTGGTGGAGCTTGTGGTTACTCGGATGTTACAAGAGAAGGATACGGTGAGGGAA
CAACAGCTTTGAGCACAACTTTGTTTCACAATGGGGCAGCTTGTGGTGCTTGTTTT
GAGATCAAATGTATTGACGACCCTAAATCTTGCATTCCCGGGCAACCATCTCTCTT
TGTCACAGCCACAAACTTTTGCCCACCAAATTTCCATCAAGACGCTAACGATGGC
GGTTGGTGCAATCCACCGCGTGAACATTTTGATATTGCTTATCCGGCATTCAAAC
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AAGAAGCAAGGAGGTATCAAGTTTACCATTACTGGCACTCAACACTGGACTCTAG
TCACAATATGGAACGTAGGTGGTGCTGGAGATATATCACACGTCGAAGTGAAGG
GTGATAACAAGTTGAATTGGACACCATTGCATAAAAATTGGGGTTCAAAATGGCA
AACAAGTTGCAGCCTTGAAGAAGAGAGCCTCACTTTTAAAGTTACCACAAGTGAT
GGCAGATTCGTTATCTCACCGAATGTTACCCCAAACAAGTATTGGAAATATGGCC
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### Nucleotide

>CisEXPA-20

CCTGGCCCGTGGAAACATGCTCATGCCACCTTTTACACCGGAGACACCGGATCAT
TTGGTGGAGCTTGTGGTTACTCGGATGTTACAAGAGAAGGATACGGTGAGGGAA
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GAGATCAAATGTATTGACGACCCTAAATCTTGCATTCCCGGGCAACCATCTCTCTT
TGTCACAGCCACAAACTTTTGCCCACCAAATTTCCATCAAGACGCTAACGATGGC
GGTTGGTGCAATCCACCGCGTGAACATTTTGATATTGCTTATCCGGCATTCAAAC

ACATTGCTGAGTACAAGGCTGGCATTGTTCCTGTTGCATATCGTAGGGTTTCATGC
AAGAAGCAAGGAGGTATCAAGTTTACCATTACTGGCACTCAACACTGGACTCTAG
TCACAATATGGAACGTAGGTGGTGCTGGAGATATATCACACGTCGAAGTGAAGG
GTGATAACAAGTTGAATTGGACACCATTGCATAAAAATTGGGGTTCAAAATGGCA
AACAAGTTGCAGCCTTGAAGAAGAGAGCCTCACTTTTAAAGTTACCACAAGTGAT
GGCAGATTCGTTATCTCACCGAATGTTACCCCAAACAAGTATTGGAAATATGGCC
AGACTTTTGAGGGCCTCAACTTCCGCTAA