

IDENTIFICATION

Species: *Citrus sinensis*

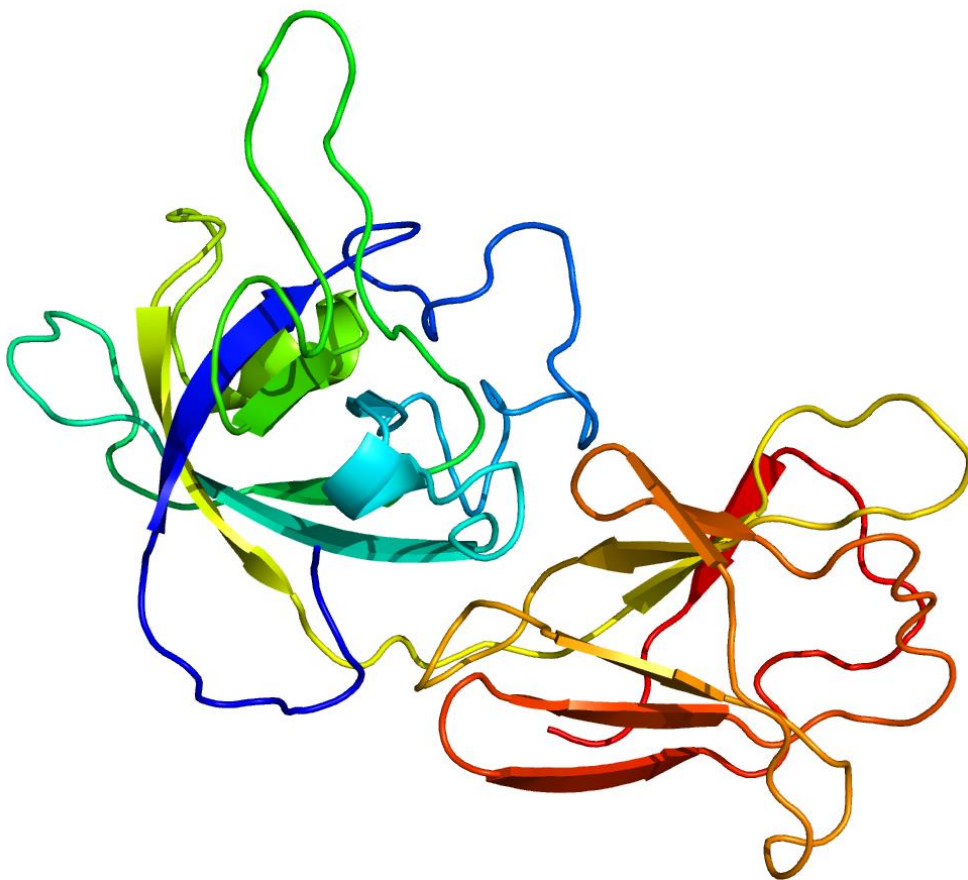
Locus: orange1.1g025919m

Gene Model: orange1.1g025919m

Description: CisEXPA-14

Family: Alpha Expansin

3D structure:



GENOME DATABASES

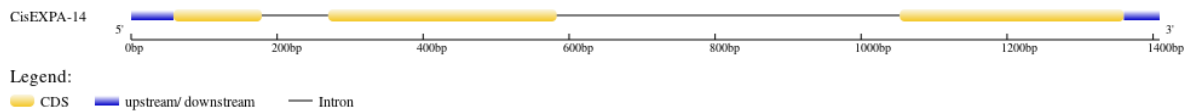
Phytozome: https://phytozome-next.jgi.doe.gov/info/Csinensis_v1_1

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

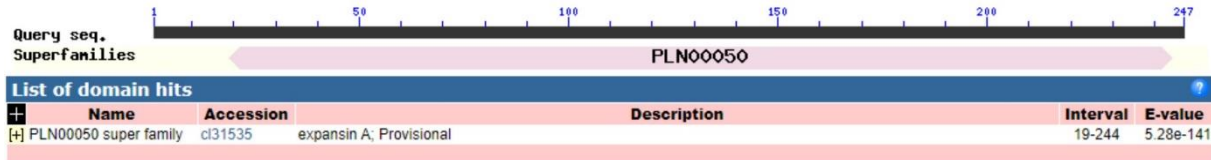
EXTERNAL RESOURCES

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

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>CisEXPA-14

MAFLGLLLLGILSLVSSVYGQGWTDAAHATFYGGGDASGTMGGACGYGNLYSEGYG
TNTAALSTALFNNGMSCGACFEIKCVNDPRWCRPGSIFVTATNFCPPNNALPNNAGG
WCNPPQQHFDLSQPVFEQIAQYKAGIVPVSYRRVPCSRKGGIRFTINGHSYFNLVLITN
VGGAGDVRAVSIKGSRTDWQPMsrNWGQNWQSNsYLNQsLSFKVTTSDGHTVVS
NNVAPAGWSFGQTFsGLQVP*

CDS (coding sequence)

>CisEXPA-14

ATGGCATTCTTGGGCTGCTGTTGTTGGGGATTCTTTCTTTAGTCTCATCTGTTTAT
GGCCAGGGATGGACTGATGCTCATGCCACTTTTTATGGTGGGGGTGATGCCTCTG
GTACAATGGGTGGCGCTTGTGGGTATGGAACTTATACAGCGAGGGATATGGGA
CAAACACAGCAGCTCTGAGCACTGCACCTTTTCAACAATGGCATGAGCTGTGGGGC
TTGTTTTGAGATCAAGTGTGTTAATGACCCAAGATGGTGCCGTCCGGGCTCCATTT
TTGTTACTGCCACAAATTTTTGCCCTCAAATAATGCTCTCCCAAACAATGCCGGT
GGCTGGTGCAATCCTCCCCAGCAACATTTTGACCTCTCTCAGCCTGTGTTTGAACA
AATTGCTCAGTACAAAGCTGGGATAGTACCTGTGTCTTACAGAAGGGTTCCATGC
AGTAGGAAGGGAGGCATCAGATTCACGATCAACGGCCATTCTTACTTCAACTTAG
TCCTAATCACAAACGTCGGAGGCGCTGGTGATGTGCGTGCTGTTTCAATCAAAGG
GTCAAGAAGTGAATGGCAACCCATGTCAAGGAACTGGGGTCAAACTGGCAAAG
TAACAGTTACCTCAATGGCCAAAGCCTCTCATTTAAGGTCACCACAAGTGATGGC
CACACTGTTGTCTTAACAATGTTGCCCCAGCTGGCTGGTCCTTTGGCCAAACCTT
CAGTGGCCTGCAAGTTCCTGA

Nucleotide

>CisEXPA-14

GCAAGAACCTCTCTTTCTCTCTTACAAAAAGATACGCAAGCAAAAGGGTTTCAGG
AACATGGCATTCTTGGGCTGCTGTTGTTGGGGATTCTTTCTTTAGTCTCATCTGTT
TATGGCCAGGGATGGACTGATGCTCATGCCACTTTTTATGGTGGGGGTGATGCCT
CTGGTACAATGGGTACGTCGATGCCTGTCATAAACCTTTTTCGTTTCATGTTATT
TTGATCAACATTAAAACCAAATTGCTGATGATTAATTAATTATTCAGGTGGCGCTT

GTGGGTATGGAACTTATACAGCGAGGGATATGGGACAAACACAGCAGCTCTGA
GCACTGCACTTTTCAACAATGGCATGAGCTGTGGGGCTTGTTTTGAGATCAAGTG
TGTTAATGACCCAAGATGGTGCCGTCCGGGCTCCATTTTTGTTACTGCCACAAATT
TTTGCCCTCCAAATAATGCTCTCCCAAACAATGCCGGTGGCTGGTGCAATCCTCCC
CAGCAACATTTTGACCTCTCTCAGCCTGTGTTTGAACAAATTGCTCAGTACAAAG
CTGGGATAGTACCTGTGTCTTACAGAAGGTGACCCGTTTGAATCCTACAAATATT
CATATTGTTTTTTACTCGGGCACTATTTGGTCCTGTGTTTAACTAGCAAGCAGTTA
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AGAGCACATAACAAAAAAGTGTTTGGTAAACAAAAAATCAAATAAAAGAC
AGGAAAACACATATATTCTATTACATGTTTTTTGGACTTTAGCTATTTAGTCGAAAC
ATTCAATAGAAATTAGAAGACAGCTGATTTTATCCTACGGCTGTTTCGATGCATGC
ATCGGTATACTTTCACTCGATAGCTAGTGGTTCCAATTTACGACAACGGAGCCTT
AAATAGTTTATTTGGTTAGCTTCTGATCCTGTGTTATGTGTTGGCAATGCCAGGG
TTCCATGCAGTAGGAAGGGAGGCATCAGATTCACGATCAACGGCCATTCTTACTT
CAACTTAGTCCTAATCACAAACGTCGGAGGCGCTGGTGATGTGCGTGCTGTTTCA
ATCAAAGGGTCAAGAACTGATTGGCAACCCATGTCAAGGAACTGGGGTCAAAC
TGGCAAAGTAACAGTTACCTCAATGGCCAAAGCCTCTCATTTAAGGTCACCACAA
GTGATGGCCACACTGTTGTCTCTAACAATGTTGCCCCAGCTGGCTGGTCCTTTGGC
CAAACCTTCAGTGGCCTGCAAGTTCCTGAAGTTGAAACTCAGCCTCCAAAATCC
AGCAGTTTTTTTTTTTTCACATTTT