

IDENTIFICATION

Species: *Citrus sinensis*

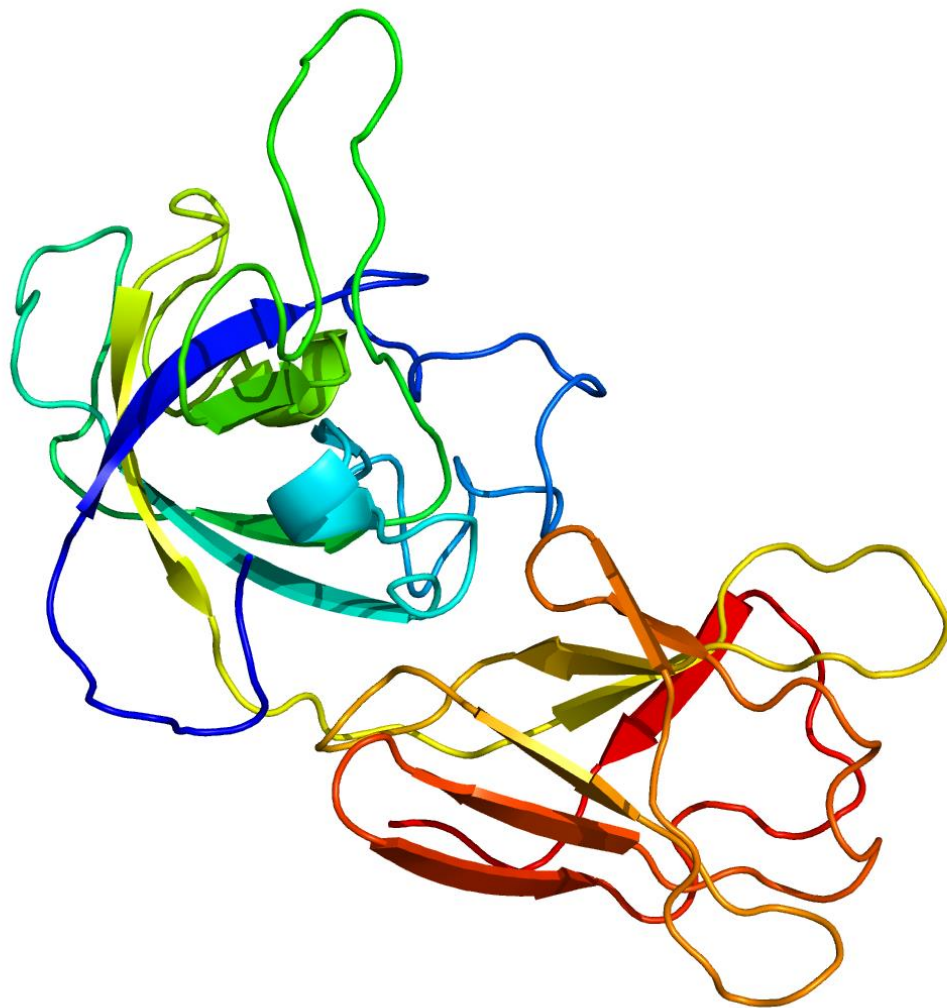
Locus: orange1.1g025298m

Gene Model: orange1.1g025298m

Description: CisEXPA-02

Family: Alpha Expansin

3D structure:



GENOME DATABASES

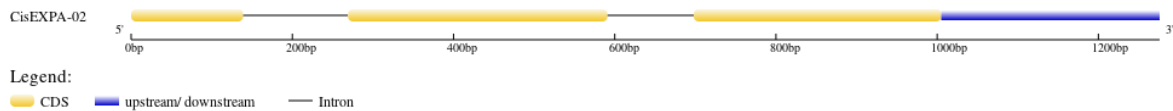
Phytozome: https://phytozome-next.jgi.doe.gov/info/Csinensis_v1_1

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

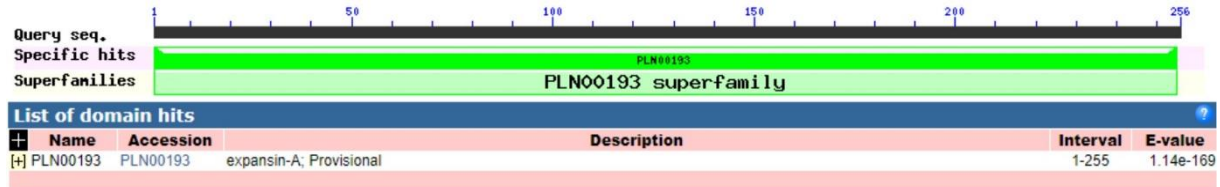
EXTERNAL RESOURCES

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

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>CisEXPA-02

MAKTLTSAILIQLCCLSVSIKAFSPSGWTQAHATFYGGSDASGTMGGACGYGNLYS
TGYGISTAALSTALFNDGASCGQCYRIMCDYKSDTRWCIKGTSVTITATNFCPPNFAL
PSDNGGWCNPPRQHFDMAYPAWQKIGIYRGGIVPVLVYQRPCKKPGGVRFTINGRD
YFELVLISNVAGAGSIKSAYIKGSSTNWMAMSRNWGANWQSNAYLNGQSLSFKVTT
TDGETRIFPNVPSNWHFGQSFASSIQF*

CDS (coding sequence)

>CisEXPA-02

ATGGCGAAAACCTTGCTTACATCTGCAATCTTGATTCAACTCTGCTGTTTAAGTGT
CAGTATCAAAGCTTTTTTCGCCTTCAGGCTGGACCCAAGCTCATGCCACATTCTACG
GAGGCAGCGATGCCTCAGGGACAATGGGGGGAGCCTGCGGGTATGGCAACTTGT
ATTCAACTGGGTATGGAATAAGCACAGCAGCATTGAGCACCGCATTGTTCAACGA
TGGAGCTTCATGTGGGCAATGCTACCGGATCATGTGTGACTATAAATCTGATACT
AGATGGTGCATAAAAGGTACATCTGTAACCATTACCGCTACAACTTTTGCCCTC
CTAACTTCGCTCTTCCAAGCGACAATGGTGGCTGGTGCAATCCTCCTCGCCAGCA
TTTTGACATGGCTTATCCCGCTTGCCAAAAGATTGGCATTACAGAGGCGGGATC
GTGCCCGTTCTGTACCAAAGGGTACCGTGCAAGAAGCCTGGTGGAGTGAGATTCA
CTATTAATGGGAGGGATTATTTGAGCTCGTATTGATTTCAAACGTGGCTGGGGC
TGGATCGATTAATCTGCATACATCAAAGTTCAAGTACAAATTGGATGGCAATG
TCAAGAACTGGGGAGCTAATTGGCAATCAAATGCTTATCTCAATGGCCAATCGC
TATCATTCAAAGTCACTACTACAGATGGTGAAACAAGAATATTTCCAATGTTGT
GCCATCTAACTGGCATTTTGGCCAATCTTTCGCTAGCAGTATCCAGTTCTAG

Nucleotide

>CisEXPA-02

ATGGCGAAAACCTTGCTTACATCTGCAATCTTGATTCAACTCTGCTGTTTAAGTGT
CAGTATCAAAGCTTTTTTCGCCTTCAGGCTGGACCCAAGCTCATGCCACATTCTACG
GAGGCAGCGATGCCTCAGGGACAATGGGTACGTAAATTTTCCTTTCATATCCCT
AGAGTTTGTTTGTAACCGTTGTGCTTCAACTTGAACCTAATTTTGAGACTACAATA

GCTAATAGAGCATATATATGTAAAAATCATCTGCATTTGGCTATAGGGGGAGCCT
GCGGGTATGGCAACTTGTATTCAACTGGGTATGGAATAAGCACAGCAGCATTGAG
CACCGCATTGTTCAACGATGGAGCTTCATGTGGGCAATGCTACCGGATCATGTGT
GACTATAAATCTGATACTAGATGGTGCATAAAAGGTACATCTGTAACCATTACCG
CTACAAACTTTTGCCCTCCTAACTTCGCTCTTCCAAGCGACAATGGTGGCTGGTGC
AATCCTCCTCGCCAGCATTTTGACATGGCTTATCCCGCTTGGCAAAAGATTGGCAT
TTACAGAGGGCGGGATCGTGCCCGTTCTGTACCAAAGGTATCATCTTGATTGCGGG
GAGTGATAGATTCTTTCAGTTGAAATAACATAGCTAGTACCACCGGCATTATGTT
TATGATGTTAATTTTGGTGTTTTTACGGAGCAGGGTACCGTGCAAGAAGCCTGGT
GGAGTGAGATTCACTATTAATGGGAGGGATTATTTTGAGCTCGTATTGATTTCAA
ACGTGGCTGGGGCTGGATCGATTAAATCTGCATACATCAAAGGTTCAAGTACAAA
TTGGATGGCAATGTCAAGAACTGGGGAGCTAATTGGCAATCAAATGCTTATCTC
AATGGCCAATCGCTATCATTCAAAGTCACTACTACAGATGGTGAAACAAGAATAT
TTCCAAATGTTGTGCCATCTAACTGGCATTTTGGCCAATCTTTCGCTAGCAGTATC
CAGTTCTAGTCAAGTTGAAAACGGCTTCAGGGTACAGGATTTGTGGTTTCAATTG
GCAGAGGCGTCCTTGTTATTTTATTGAAGCAGCCCGCCAGATTTTAATGACTTTTC
TGACTATAAGAACGGTTAATGTCAAATCTCAGGTGAACGAAATTGGAAGCAATCC
ATGAACTCGAAGCCACTGATGATTTGTTGATGCTGAAATTATTCAAAGATCATGT
TAAATAGTCATGCACAACAATAAGAAGCTCAGCCACTTAAGCTGCAGCTTCGACA
TATA