

IDENTIFICATION

Species: *Citrus sinensis*

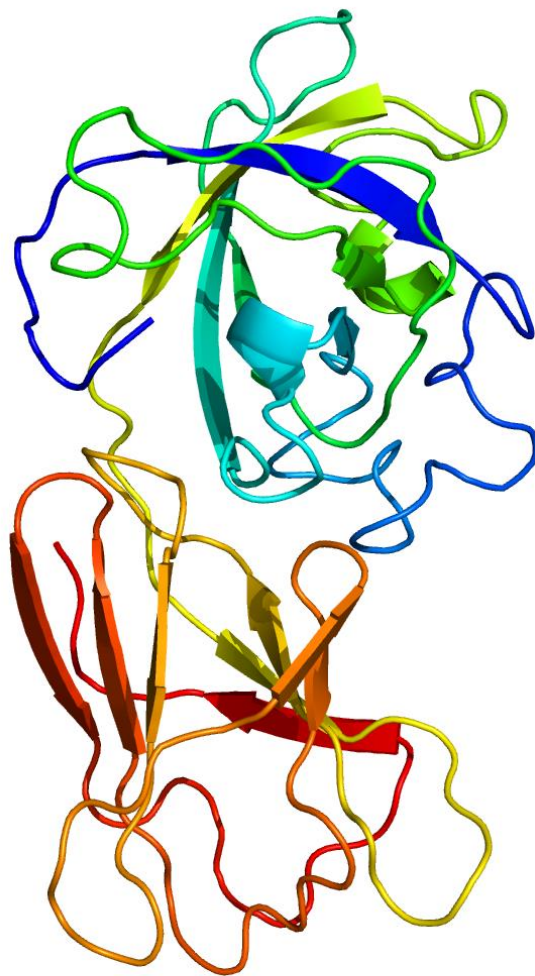
Locus: orange1.1g044678m

Gene Model: orange1.1g044678m

Description: CisEXPA-03

Family: Alpha Expansin

3D structure:



GENOME DATABASES

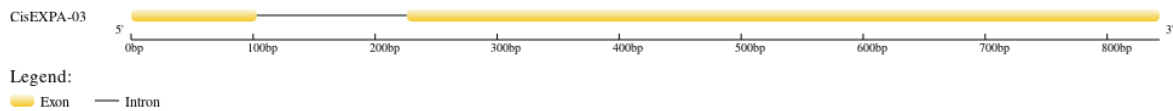
Phytozome: https://phytozome-next.jgi.doe.gov/info/Csinensis_v1_1

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

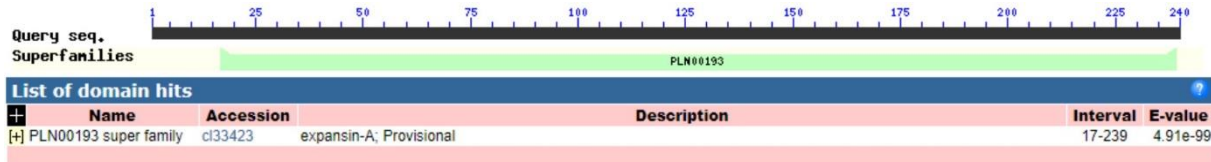
EXTERNAL RESOURCES

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

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>CisEXPA-03

MAIALSLFSSASTLNEWSPAHAATFYGDMAGNETMYGACGYGDLFKQGYGLETTALS
TALFNNGQTCGACYQIVCYNKSWCLKGAGAIGVTATNFCPPNYSKPHENWCNPPLK
HFDLSQPMFRKIAEYKGGIVPVL YRRVSCVKSGGVMFEMLGNPYWILVLVYNVGGGA
GEVINVKIKGSSTGWIQMSRNWQNWQTS AQLLGQSLSFQVTTSDGKMOVQFDDVAP
PHWQFGDVFEKGKQNF*

CDS (coding sequence)

>CisEXPA-03

ATGGCAATAGCGCTGAGTCTCTTTAGCTCAGCTTCAACGTAAATGAGTGGAGTC
CCGCACATGCAACGTTTTACGGTGACATGGCTGGCAATGAAACAATGTACGGAGC
TTGTGGCTATGGAGACCTATTTAAACAAGGGTATGGCCTCGAGACAACAGCTTTA
AGCACAGCTCTTTTCAACAATGGCCAAACTTGC GGCGCCTGTTATCAAATCGTGT
GCTATAACTCCAAATGGTGCCTGAAGGGGGCGGGTGCTATTGGCGTAACTGCGAC
AAATTTTGGCCCTCCGAATTACAGCAAACCCCATGAAAATTGGTGCAATCCTCCC
CTGAAACACTTTGATTTGTCACAACCCATGTTCCGAAAATTGCAGAGTACAAAG
GTGGCATTGTCCCTGTCTTATACCGAAGAGTGTCTTGC GTTAAATCTGGAGGGGTT
ATGTTTCAAATGCTTGGGAATCCTTATTGGATACTTGT TTTTAGTGTACAATGTTGG
GGTGCTGGTGAGGTGATTAATGTGAAGATTAAAGGATCAAGCACGGGTTGGAT
ACAAATGTGCGGAAACTGGGGCCAGAACTGGCAA ACTTCTGCACAATTA TAGG
GCAAAGCTTGTCATTTCAAGTCACTACCAGTGATGGCAA AATGGTTCAATTTGAT
GATGTTGCACCGCCGCATTGGCAATTTGGTGATGTGTTTGAGGGCAAACAGAATT
TTTAA

Nucleotide

>CisEXPA-03

ATGGCAATAGCGCTGAGTCTCTTTAGCTCAGCTTCAACGTAAATGAGTGGAGTC
CCGCACATGCAACGTTTTACGGTGACATGGCTGGCAATGAAACAATGTGTA AATT
ACTTCAACCTCAATGTCGAGATTTTCTTTTCTTTTCTTTTTCAGAAACATAGATTG
CAATCCTGAAAATTGAACCATTAATTCGTTTTTCATTTTGCACGTAACATACATG
CAGACGGAGCTTGTGGCTATGGAGACCTATTTAAACAAGGGTATGGCCTCGAGAC

AACAGCTTTAAGCACAGCTCTTTTCAACAATGGCCAAACTTGCGGCGCCTGTTAT
CAAATCGTGTGCTATAACTCCAAATGGTGCCTGAAGGGGGCGGGTGCTATTGGCG
TAACTGCGACAAATTTTTGCCCTCCGAATTACAGCAAACCCCATGAAAATTGGTG
CAATCCTCCCCTGAAACACTTTGATTTGTCACAACCCATGTTCCGAAAAATTGCA
GAGTACAAAGGTGGCATTGTCCCTGTCTTATACCGAAGAGTGTCTTGCGTTAAAT
CTGGAGGGGTATGTTTGAAATGCTTGGGAATCCTTATTGGATACTTGTTTTAGTG
TACAATGTTGGGGGTGCTGGTGAGGTGATTAATGTGAAGATTAAAGGATCAAGC
ACGGGTTGGATACAAATGTCGCGAAACTGGGGCCAGAACTGGCAAACCTTCTGCA
CAATTACTAGGGCAAAGCTTGTCATTTCAAGTCACTACCAGTGATGGCAAATGG
TTCAATTTGATGATGTTGCACCGCCGCATTGGCAATTTGGTGATGTGTTTGAGGGC
AACAGAATTTTTAA