

IDENTIFICATION

Species: *Citrus sinensis*

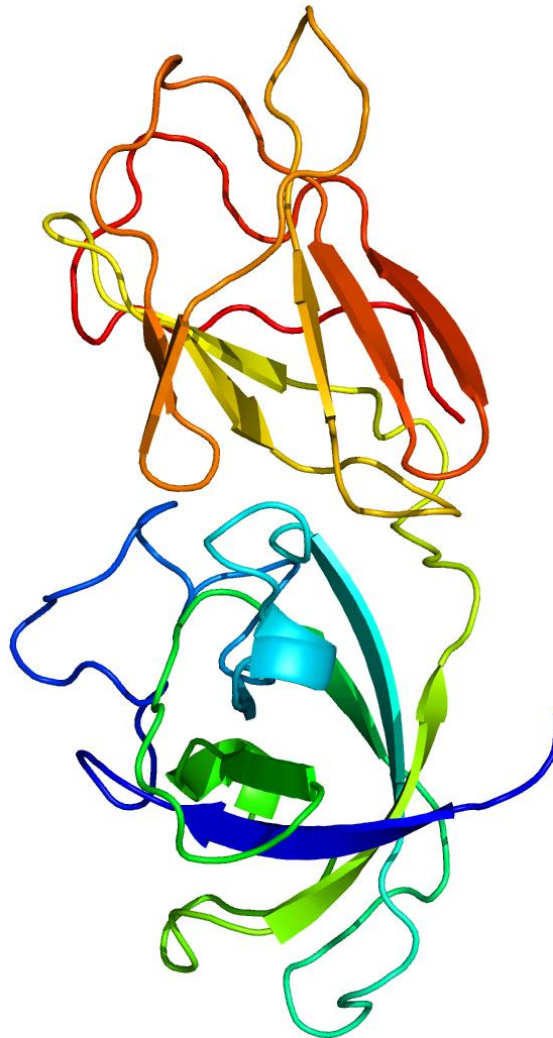
Locus: orange1.1g042474m

Gene Model: orange1.1g042474m

Description: CisEXPA-01

Family: Alpha Expansin

3D structure:



GENOME DATABASES

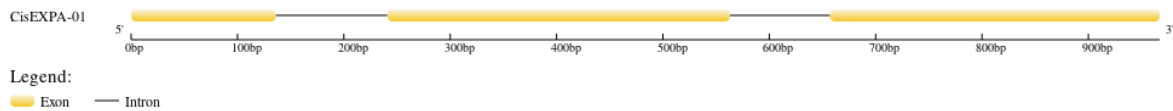
Phytozome: https://phytozome-next.jgi.doe.gov/info/Csinensis_v1_1

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

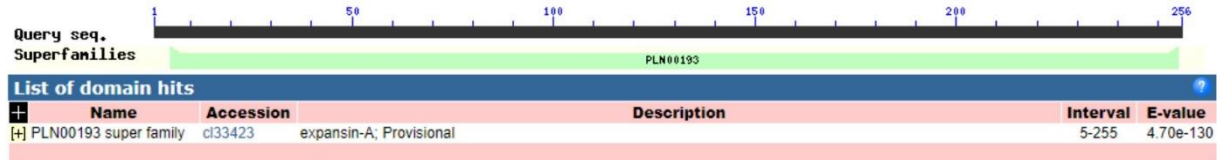
EXTERNAL RESOURCES

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

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>CisEXPA-01

MEGFFAFSVALILTLLSIKINAASAAWMQAHATFYGGSDASETMGGACGYGNLYTD
GYGTKTAALSTVLFNNGKSCGGCYHIVCDGRKVPQWCRRGTSIIITATNFCPPNYDLP
NDNGGWCNPPRAHFDMSQPAFESIAIYRAGIVPVL YRKV GCMRSGGLRFTINGRDYF
ELVLVSNVGGAGEVSNVWIKGSKMSKWQVMSRNWGANWQSLTYLNAQSLSFRVQ
TSNGRTRTAYNVAPSNWRFGQSFKSNVQF*

CDS (coding sequence)

>CisEXPA-01

ATGGAAGGTTTCTTTGCTTTCAGTTTTGTGGCGCTGATCTTAACGTTACTTTCCATT
AAAATTAATGCAGCTTCTGCTGCTTGGATGCAAGCCCATGCAACTTTCTACGGTG
GAAGTGATGCTTCAGAAACAATGGGTGGTGCTTGTGGATATGGAAACTTATACAC
AGATGGTTATGGCACAAAACACTGCAGCATTGAGCACAGTTTTGTTCAATAATGGA
AAGTCTTGTGGTGGGTGCTATCACATCGTTTGCAGCGGGAGGAAGGTGCCGCAAT
GGTGCCGCCGGGGACATCCATCATCATTACGGCTACAACTTCTGCCCGCCAAA
CTATGATCTGCCTAACGACAACGGCGGTTGGTGCAACCCTCCACGGGCGCACTTT
GACATGTCTCAGCCTGCATTTGAGTCCATTGCCATTTACAGAGCCGGAATTGTAC
CCGTA CTCTACAGAAAGGTTGGATGCATGAGAAGTGGAGGCCTTAGATT CACAAT
AAATGGAAGGGACTACTTTGAGCTTGTGCTTGTTC AAATGTTGGAGGAGCTGGA
GAGGTTTCTAATGTGTGGATCAAGGGATCCAAAATGAGCAAATGGCAAGTGATG
TCAAGGAACTGGGGAGCTAATTGGCAGAGTTTGACTTATCTCAATGCTCAGAGCT
TGTCCTTTAGAGTCCAAACTAGCAATGGAAGGACCCGCACAGCCTATAACGTTGC
ACCTTCCA ACTGGAGATTTGGCCAATCTTTCAA AAGCAATGTTCAATTCTAA

Nucleotide

>CisEXPA-01

ATGGAAGGTTTCTTTGCTTTCAGTTTTGTGGCGCTGATCTTAACGTTACTTTCCATT
AAAATTAATGCAGCTTCTGCTGCTTGGATGCAAGCCCATGCAACTTTCTACGGTG
GAAGTGATGCTTCAGAAACAATGGGTATGTTTTCTATTTATATAATGGCAAGAAT
AAACAATATGTCGCTTAATTCATTATTCATTTACATTCAATTTTATGCTAATGATT
TTGAACTTCGGCTTTCAGGTGGTGCTTGTGGATATGGAAACTTATACACAGATGG

TTATGGCACAAAACTGCAGCATTGAGCACAGTTTTGTTCAATAATGGAAAGTCT
TGTGGTGGGTGCTATCACATCGTTTGGGACGGGAGGAAGGTGCCGCAATGGTGCC
GCCGGGGGACATCCATCATCATTACGGCTACAACTTCTGCCCGCCAAACTATGA
TCTGCCTAACGACAACGGCGGTTGGTGCAACCCTCCACGGGCGCACTTTGACATG
TCTCAGCCTGCATTTGAGTCCATTGCCATTTACAGAGCCGGAATTGTACCCGTACT
CTACAGAAAGTATGTTCAATTCTTCATTAAAAAAATTTGCATTTTTGTTTCTTCTTG
GTGGGCGTCTTCTGTATATATACTGAGGTTTCTTGTCGTTCCACCAGGGTTGGATGC
ATGAGAAGTGGAGGCCTTAGATTCACAATAAATGGAAGGGACTACTTTGAGCTTG
TGCTTGTTTCAAATGTTGGAGGAGCTGGAGAGGTTTCTAATGTGTGGATCAAGGG
ATCCAAAATGAGCAAATGGCAAGTGATGTCAAGGAACTGGGGAGCTAATTGGCA
GAGTTTGACTTATCTCAATGCTCAGAGCTTGTCTTTAGAGTCCAAACTAGCAATG
GAAGGACCCGCACAGCCTATAACGTTGCACCTTCCAACCTGGAGATTTGGCCAATC
TTTCAAAGCAATGTTCAATTCTAA