

IDENTIFICATION

Species: *Citrus sinensis*

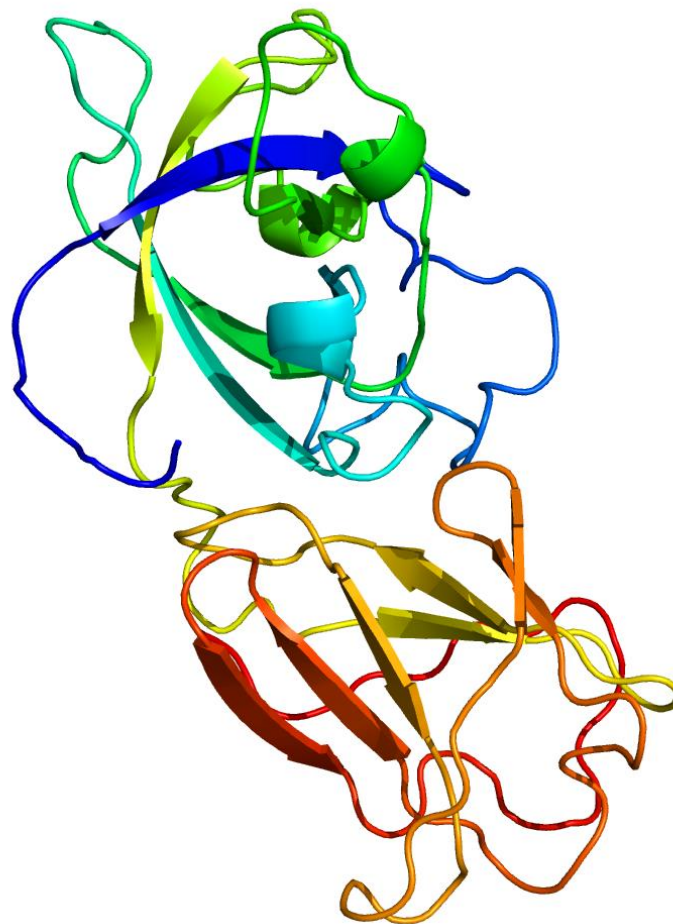
Locus: orange1.1g026331m

Gene Model: orange1.1g026331m

Description: CisEXPA-07

Family: Alpha Expansin

3D structure:



GENOME DATABASES

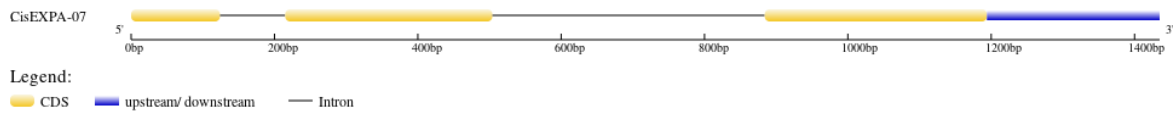
Phytozome: https://phytozome-next.jgi.doe.gov/info/Csinensis_v1_1

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

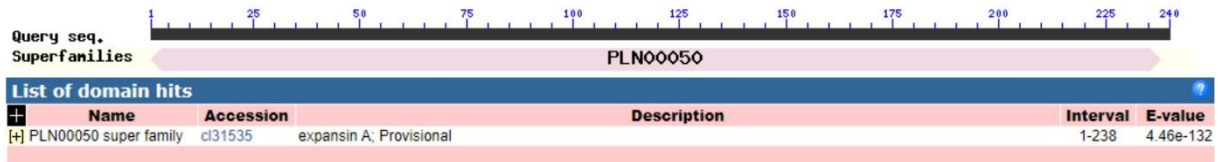
EXTERNAL RESOURCES

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

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>CisEXPA-07

MALWVILCVGFLSLVSSVQGYGGWINAHATFYGGGDASGTMGGACGYGNLYSQGY
GTNTAALSTALFNGLSCGACFQIMCANDPQWCLRGSIIVTATNFCPPGGWCDPPNH
HFDLSQPVFQHIAQYRAGIVPVIYRRVRCKRNGGIRFTINGHSYFNLVLITNVGGAGD
VRAVSIKGSRTRWQPMSRNWQNWQSN SYLNGQSLSFVVTTSNHGSVVSYNVAPPN
WSFGQTYTGRQFRY*

CDS (coding sequence)

>CisEXPA-07

ATGGCTCTTTGGGTGATTCTTTGTGTTGGGTTTCTCTCATTGGTCTCATCCGTTCAA
GGTTATGGAGGTTGGATTAATGCTCATGCAACTTTCTATGGAGGTGGTGATGCTT
CTGGCACAATGGGGGGCGCTTGTGGGTACGGCAATTTGTACAGCCAAGGTTATGG
TACTAATACCGCAGCACTTAGCACTGCTTTGTTCAACAATGGCCTAAGTTGTGGA
GCTTGCTTTCAAATTATGTGCGCTAATGACCCGCAATGGTGCCTGCGTGGCTCCAT
CATTGTCACTGCCACTAACTTTTGCCCTCCTGGAGGCTGGTGTGATCCTCCTAACC
ACCACTTIGATCTCTCAGCCTGTCTTCCAACACATTGCCCAGTATAGAGCTGGT
ATTGTTCTGTAATCTACAGAAGGGTGAGATGCAAGAGAAATGGGGGCATAAGG
TTCACAATCAATGGCCATTCTTACTTCAATTTAGTTCTAATAACAAACGTGGGTGG
AGCTGGTGACGTGCGTGCTGTATCCATCAAAGGTTCAAGGACTAGATGGCAACCG
ATGTTCGAGAACTGGGGCCAAAACCTGGCAAAGCAACTCGTATCTTAATGGACAA
AGCCTCTCTTTTGTGTTGTGACCACAAGTAATGGCCACAGTGTTGTTTCTTACAATGT
TGCCCCTCCTAATTGGTCATTTGGGCAGACTTATACCGGCAGACAATTCGATATT
AG

Nucleotide

>CisEXPA-07

ATGGCTCTTTGGGTGATTCTTTGTGTTGGGTTTCTCTCATTGGTCTCATCCGTTCAA
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AGTAAAATTTCAATGTGGTGATTGTATTTTGGTAAACTTTTCTTTTAGGGGGCGCT
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GCACTGCTTTGTTCAACAATGGCCTAAGTTGTGGAGCTTGCTTTCAAATTATGTGC
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TTGCCCTCCTGGAGGCTGGTGTGATCCTCCTAACCACCACTTTGATCTCTCTCAGC
CTGTCTTCCAACACATTGCCCAGTATAGAGCTGGTATTGTTCCCTGTAATCTACAGA
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AATATGTTTGCATAGGTCTCTACTTTTCGCCTTTTGTGTGAGAAGCATGTTTGATGT
CAATCTTGTACGCTAAAGAGGCTTGGTAAATACTGTTTAATTTTTGTGAGCCATAT
TCAGGCTTAATCATTTGGTATCAGTCTTGCATTATTTACTAATTTTCAGATCTTCA
ACGACCGGCTTAAGCTGTTAAACCTGACTTTATGCAAACCTTTTTCAGGGTGAGAT
GCAAGAGAAATGGGGGCATAAGGTTCAACAATCAATGGCCATTCTTACTTCAATTT
AGTTCTAATAACAAACGTGGGTGGAGCTGGTGACGTGCGTGCTGTATCCATCAAA
GGTTCAAGGACTAGATGGCAACCGATGTCGAGAACTGGGGCCAAAACCTGGCAA
AGCAAACCGTATCTTAATGGACAAAGCCTCTCTTTTGTGTGACCACAAGTAATG
GCCACAGTGTTGTTTCTTACAATGTTGCCCTCCTAATTGGTCATTTGGGCAGACT
TATACCGGCAGACAATTTTCGATATTAGGCTTAATTTAAGTTAAAATCAAGCAACC
CTTTAAGTATTTTTAATTAGCTCTAGCGATATGGGTACGTACAAAATTATTTCTGA
ATTGGCCCTTGTGTGCTTCAGTACCATTTATGAGAGTGTTTGCATGCAGTTTTTTC
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