

IDENTIFICATION

Species: *Citrus sinensis*

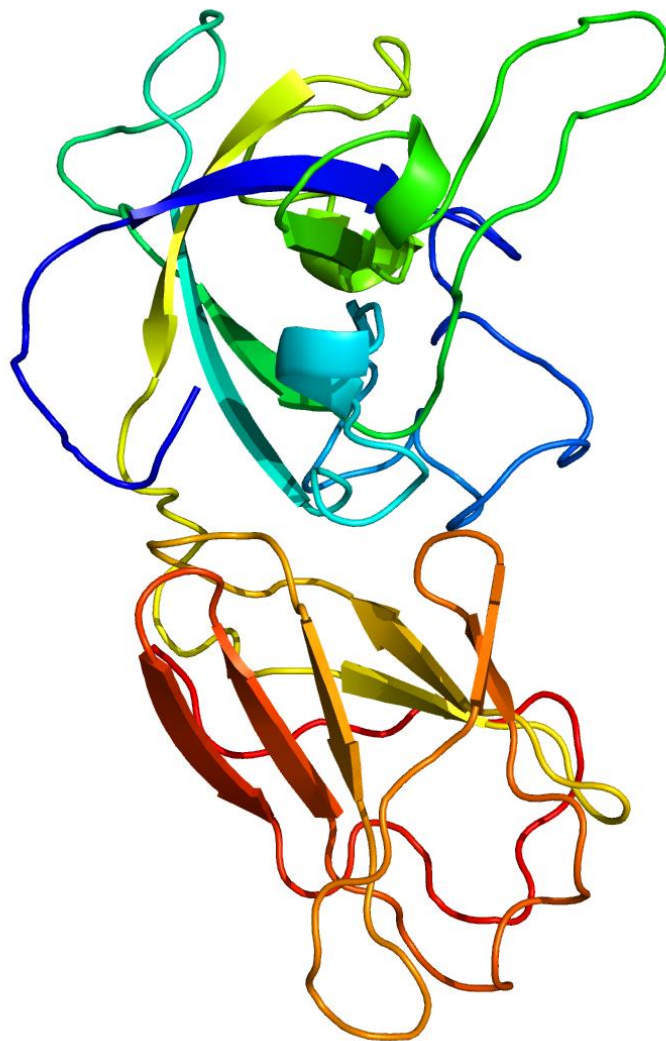
Locus: orange1.1g025617m

Gene Model: orange1.1g025617m

Description: CisEXPA-10

Family: Alpha Expansin

3D structure:



GENOME DATABASES

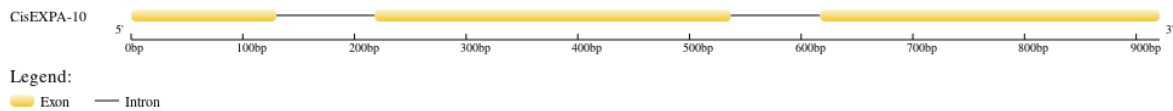
Phytozome: https://phytozome-next.jgi.doe.gov/info/Csinensis_v1_1

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

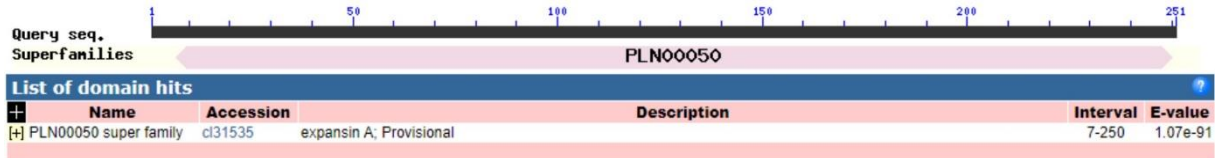
EXTERNAL RESOURCES

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

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>CisEXPA-10

MGAPQAIVFFLILLQTCKTAAQHEEWNSATATYTKETNGSIIIIEGACGYGDLHRATYG
KYSAGLSTMLFNRGSTCGACFELRCVDHILWCRPGSPSVILTATDFCPPNYGLSSDYG
GWCNFPKEHFEMSEAAFVEIAERRADIVPVQYRRVKCERRGGLRFTVSGSSHFYQVL
VTNVGLDGEVIAVKVKGSKTGWIPMARNWQNWQSNVNLTGQPLSFEVTTSNRKT
LTSYNVAPANWQFGQTYEGKQF*

CDS (coding sequence)

>CisEXPA-10

ATGGGAGCTCCTCAAGCCATTGTTTTCTTCTTGATTTTACTTCAAACATGCAAGAC
TGCAGCACAGCATGAAGAATGGAACCTCTGCTACGGCTACATACACCAAAGAAAC
AAATGGGTCTATCATCATTGAAGGTGCTTGTGGTTATGGGGACCTTCACAGGGCC
ACCTACGGAAAATACAGTGCTGGGCTTAGTACAATGTTATTCAACAGAGGGGAGTA
CTTGTGGAGCTTGCTTTGAGCTCAGATGTGTCGACCACATCTTGTGGTGCCGGCCT
GGTAGCCCATCTGTCATACTCACCGCCACAGATTTCTGCCCTCCCAATTACGGGCT
TTCGTCGGATTATGGTGGCTGGTGTAACTTTCCCAAAGAACACTTTGAGATGTCA
GAGGCCGCATTTCGTTGAAATTGCAGAGAGAAGAGCTGATATTGTACCAGTTCAAT
ACAGAAGGGTGAAGTGTGAACGCAGGGGTGGGTTGAGATTCACAGTGAGTGGAA
GCTCTCACTTCTATCAAGTTCTTGTAACCAATGTGGGTTTGGATGGTGAAGTCATT
GCTGTGAAAGTGAAGGGATCAAAAACAGGATGGATACCTATGGCAAGAACTGG
GGCCAAAACCTGGCAGTCCAACGTCAATCTTACAGGGCAGCCTCTGTCTTTTGAGG
TGACCACCAGTAACCGGAAAACACTCACATCATACAATGTTGCTCCAGCAAACCTG
GCAGTTTGGTCAGACATATGAGGGGAAACAGTTCTAG

Nucleotide

>CisEXPA-10

ATGGGAGCTCCTCAAGCCATTGTTTTCTTCTTGATTTTACTTCAAACATGCAAGAC
TGCAGCACAGCATGAAGAATGGAACCTCTGCTACGGCTACATACACCAAAGAAAC
AAATGGGTCTATCATCATTGGTACTTTCTCGCAAATTACTTTATTTAACATTGTGT
TTCATGTCTACTGAAGAGTGAAGACTGATAGGCCATCTGTTTAAATGTTGCAGAAG
GTGCTTGTGGTTATGGGGACCTTCACAGGGCCACCTACGGAAAATACAGTGCTGG

GCTTAGTACAATGTTATTCAACAGAGGGAGTACTTGTGGAGCTTGCTTTGAGCTC
AGATGTGTTCGACCACATCTTGTGGTGCCGGCCTGGTAGCCCATCTGTCATACTCA
CCGCCACAGATTTCTGCCCTCCCAATTACGGGCTTTCGTTCGGATTATGGTGGCTGG
TGTAACCTTTCCCAAAGAACAACACTTTGAGATGTCAGAGGGCCGCATTCGTTGAAATTG
CAGAGAGAAGAGCTGATATTGTACCAGTTCAATACAGAAGGTACAGCAATGCTTT
TTCCTTTTTCTGCTAGCTTGTGGATTTTAGTTAGGCACATGCTGTGATTCCGAAA
TTTGTGCAGGGTGAAGTGTGAACGCAGGGGTGGGTTGAGATTCACAGTGAGTGG
AAGCTCTCACTTCTATCAAGTTCTTGTAAACCAATGTGGGTTTGGATGGTGAAGTCA
TTGCTGTGAAAGTGAAGGGATCAAAAACAGGATGGATACTATGGCAAGAAACT
GGGGCCAAAACCTGGCAGTCCAACGTCAATCTTACAGGGCAGCCTCTGTCTTTTGA
GGTGACCACCAGTAACCGGAAAACACTCACATCATAACAATGTTGCTCCAGCAAAC
TGGCAGTTTGGTCAGACATATGAGGGGAAACAGTTCTAG