

IDENTIFICATION

Species: *Citrus sinensis*

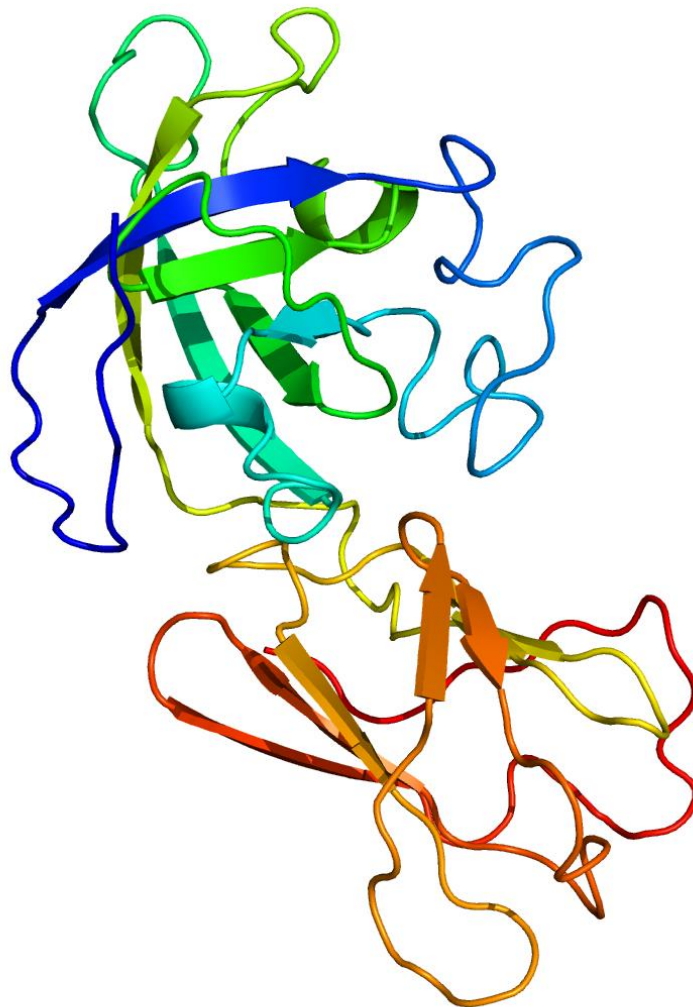
Locus: orange1.1g025025m

Gene Model: orange1.1g025025m

Description: CisEXPA-16

Family: Alpha Expansin

3D structure:



GENOME DATABASES

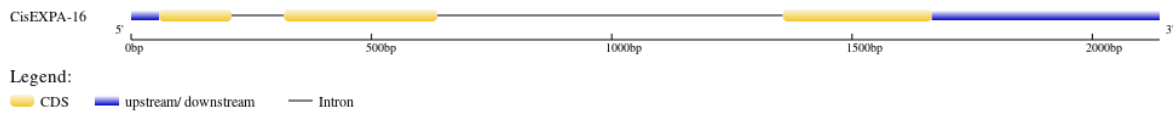
Phytozome: https://phytozome-next.jgi.doe.gov/info/Csinensis_v1_1

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

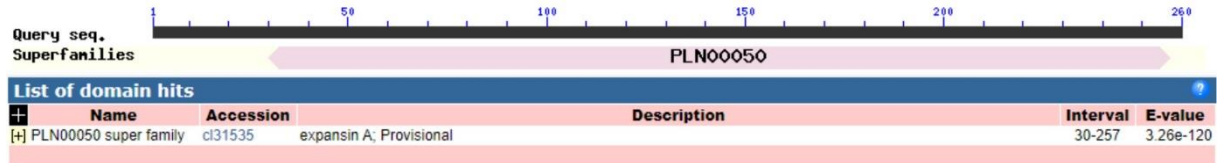
EXTERNAL RESOURCES

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

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>CisEXPA-16

MALFRMLCFFSVALSFLFATANAKIPGVFAGGPWQSAHATFYGGSDASGTMGGACGY
GNLYSQGYGVNTAALSTALFNGLSCGACFELKCGGDPQWCNPGNPAILITATNFCP
PNFAQPSDNGGWCNPPRPHFDLAMPFLKLAQYRAGIVPVSYRRVPCRKRGGIRFTI
NGFRYFNLVLVTNVAGAGDIVRVSVKGANTQWLSMSRNWGQNWQSNAQLVGQAL
SFRVTGSDRRTSTSWNVAPANWQFGQTFSGKNFRV*

CDS (coding sequence)

>CisEXPA-16

ATGGCTCTTTTCAGAATGCTCTGCTTTTTCTCAGTGGCACTCTCCTTATTTGCGACG
GCCAACGCCAAGATTCCCGGTGTCTTCGCCGGTGGCCCCTGGCAATCGGCCACG
CCACTTTTTACGGTGGCAGCGACGCTTCCGGCACTATGGGTGGTGCTTGTGGGTA
CGGGAATCTGTACAGCCAGGGCTATGGAGTGAACACGGCGGCTCTCAGTACGGC
GCTGTTCAACAACGGCTTGAGCTGCGGCGCGTGCTTCGAGTTAAAGTGCGGCGGC
GACCCGCAATGGTGTAAACCCGGGTAACCCGGCCATTCTGATCACGGCGACCAACT
TTTGCCCCCGAACTTCGCTCAGCCCTCCGATAATGGCGGGTGGTGCAACCCTCCT
CGCCCTCATTTTCGATCTGGCCATGCCTATGTTCTCAAGCTCGCCAGTACCGCGC
TGGTATCGTCCCCGTTTCTTACCGCAGGGTGCCCTGCAGAAAGCGAGGCGGAATC
AGATTCACAATTAACGGTTTCCGTTACTTCAACTTGGTCTTGGTCACCAACGTCGC
GGGCGCAGGGGATATCGTGCGCGTGAGCGTAAAGGGGCCAACACCCAATGGCT
GAGCATGAGCCGCAACTGGGGACAAAACCTGGCAATCCAACGCTCAGCTCGTGGG
CCAGGCACTTTTCGTTTAGAGTCACGGGCAGTGACAGAAGGACCTCAACCTCTTGG
AACGTGGCGCCAGCGAATTGGCAGTTCGGTCAAACCTTTTCGGGAAAGAATTTCC
GCGTCTAG

Nucleotide

>CisEXPA-16

CTGCGCGCTCACTCACTCACTCACTCAACTCTCTGTCTCCCTCTCTTCAACTCCAA
CAATGGCTCTTTTCAGAATGCTCTGCTTTTTCTCAGTGGCACTCTCCTTATTTGCGA
CGGCCAACGCCAAGATTCCCGGTGTCTTCGCCGGTGGCCCCTGGCAATCGGCCCA

CGCCACTTTTTACGGTGGCAGCGACGCTCCGGCACTATGGGTATACTTTAGTTCT
ATCTCCTTACATCTCTCCATTTCTCATTTCTTTTTTTTTCTTTTTTTCAAAGAACTTT
TCTAACGGTGATATGTGTATATATTTTTTTGTGCAGGTGGTGCTTGTGGGTACGGG
AATCTGTACAGCCAGGGCTATGGAGTGAACACGGCGGCTCTCAGTACGGCGCTGT
TCAACAACGGCTTGAGCTGCGGGCGCTGCTTCGAGTTAAAGTGCGGGCGGCGACCC
GCAATGGTGTAACCCGGGTAACCCGGCCATTCTGATCACGGCGACCAACTTTTGC
CCCCGAACTTCGCTCAGCCCTCCGATAATGGCGGGTGGTGCAACCCTCCTCGCC
CTCATTTTCGATCTGGCCATGCCTATGTTCCCTCAAGCTCGCCCAGTACCGCGCTGGT
ATCGTCCCCGTTTCTTACCGCAGGTGAGTGTTAGAGTTGCTGTGATTTTACTCAA
ATGCCCTGCTAAAGTTTACATTTTTATTTAATATGTGGTTTCTTTTCTTTGTCTCC
AAGTTTTGTTTGAATGTCTTCTTTGGAAGAAATACCGGAAACCCGGGAAAAAGTC
GGGCTGTTAATGTGTGTTTTTATTTAATATTTCCCTTTTCTTTTCTTCGCAAAC
AAACAGAACCCGGAAATAAGTTTACTGATCAGTAGTTTATGTCGTTTATCCCAAC
ACAGCCAACGGCAAACCGTTCAGCCCTTGTGCCCTTTTCACCCTTGTACTTTTCGG
TGTTGTTTAAATTATAATTATTTTTATAACTAAAATATGCTCGCATGTATGTAATT
GTTAATTTCTACGAGGACATTGTCGTCAAATAAAATAAGGGTGCTTTAGTAATTT
TACGTTTCTCAAATATTACCGGAAAATCAGGATTGGGTGGTGGTTCTAAGTCAGA
AAATCTGGGGCACAGTTCACGTTCTCCCACGCGTGTGTCTGTTACCATTTTTTGG
GACCTTGTACCTAATTACTGAAGTATTTATTTTTTAATTTTTTTAATTTATTTAAC
CAGTCAAGGTTTTAGTCTTCAAACGGGGCCTAAAAGTTGCCCTCAAACCGTAGGG
CACTGTTATGGCAGGTCTTAACTGCGACGTTACCCATTTTTTTAAATAATAATTATT
ATTTTGTCTTTGCAGGGTGCCCTGCAGAAAGCGAGGCGGAATCAGATTCACAATT
AACGGTTTCCGTTACTTCAACTTGGTCTTGGTCACCAACGTCGCGGGCGCAGGGG
ATATCGTGCGCGTGAGCGTGAAAGGGGCCAACACCCAATGGCTGAGCATGAGCC
GCAACTGGGGACAAAACCTGGCAATCCAACGCTCAGCTCGTGGGCCAGGCACTTTC
GTTTAGAGTCACGGGCAGTGACAGAAGGACCTCAACCTCTTGGAACGTGGCGCC
AGCGAATTGGCAGTTCGGTCAAACCTTTTCGGGAAAGAATTTCCGCGTCTAGTGA
TATTTAATCTTTTTTCAACATTTTCATGTTTCCCGCCTTCCAAGATTTTTTTCTCCTT
TATTTCCCGGAAAAAAAATTGAAGCGAAGGAAAAGGGGGTTATGGGGGGTTCGT
GTTAGGTTTTTAAAGTAAAAGTGGGTCAAATCAAATGATGGTGATAGGTAGTA
GAAAAAAGTGACAAAAGGATGTAGTGTGTGGTGGGGTAACTTCTGTTTATTT
TCAGTTTTTACTGTTTTTGTGTTTACTTGTGTTACCGGGGCTGGTGGTAATAGT
AAAAACCAGTCTCGTGGGTGAAAGTGTAGTGGCTGAAGTGGCTGCAGGAACAAA
CTAAAAAACATGTAGCCCGCAGCTGATATGATTTACTATATATGGTATAATTA
TCTTCAATGTTTCAAATGTCTATTGTTAAGTAATAATGCTAATGTTGTTATAAGTA
ATAATGCTAAAGTTGTTATACTTTGAG