

IDENTIFICATION

Species: *Citrus sinensis*

Locus: orange1.1g024916m

Gene Model: orange1.1g024916m

Description: CisEXPA-09

Family: Alpha Expansin

3D structure:



GENOME DATABASES

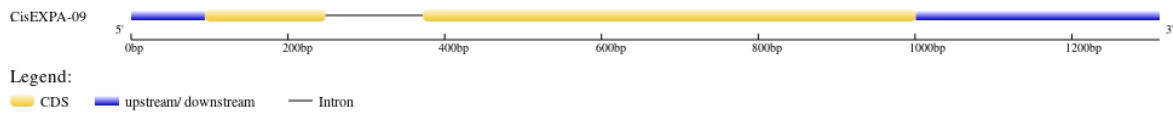
Phytozome: https://phytozome-next.jgi.doe.gov/info/Csinensis_v1_1

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

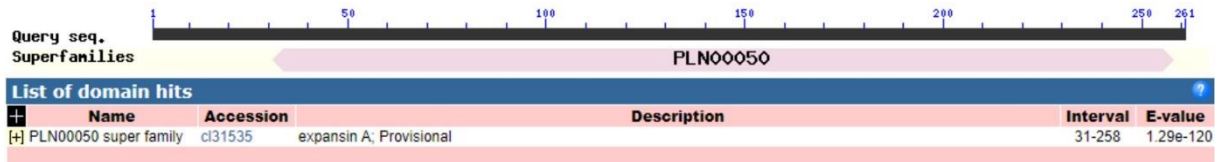
EXTERNAL RESOURCES

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

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>CisEXPA-09

MGVAVGIICIVTFVTFSSLSVDARIPGVYGGGEAWQSAHATFYGGNDASGTMGGACG
YGNLYSQGYGVNTAALSTALFNGLSCGACFEIKCANDPQWCHAGSPSIFVTATNFC
PPNFAQPSDNGGWCNPPRPHFDLAMPMLKMAEYRAGIVPVSYRRVPCRKRGGIRFT
INGFRYFNLVLITNVAGAGDIVKASVKGSRTGWMSLSRNWQNWQSNVSVLVGQSLS
FRVTGSDRRTSTSWNIVPANWQFGQTFTGKNFRV*

CDS (coding sequence)

>CisEXPA-09

ATGGGTGTCGCTGTGGGCATCATTGTATTGTGACTTTTGTACATTTCCCTCCCTT
AGTGTTGATGCGAGAATCCCCGGCGTTTACGGTGGCGAGGCATGGCAAAGCGCTC
ATGCTACATTCTATGGAGGCAATGATGCCTCAGGAACAATGGGAGGTGCTTGTGG
GTACGGCAATCTCTACAGTCAAGGATACGGCGTTAACACGGCAGCGCTAAGCAC
AGCACTGTTCAACAACGGGTTGAGCTGCGGTGCGTGTTTTGAGATTAAGTGTGCG
AATGACCCTCAATGGTGCCACGCTGGGAGCCCTTCAATCTTCGTCACTGCCACCA
ACTTTTGCCCTCCGAATTTGCTCAACCCAGCGACAATGGGGGGTGGTGCAACCC
TCCTCGCCCTCACTTCGATCTCGCCATGCCATGTTCCCTCAAGATGGCCGAATACC
GCGCCGGAATTGTCCCTGTCTCTTACCGCAGGGTCCCTTGCAGGAAGAGAGGCGG
CATCAGGTTCAACATCAACGGTTTCCGTTACTTCAACTTGGTCTTGATCACCAACG
TCGCTGGTGTGGGGATAATTGTCAAGGCTAGCGTCAAAGGTTCCAGGACTGGGTG
GATGAGCTTGAGCAGGAAGTGGGACAGAAGTGGCAGTCTAATTCTGTTTTGGTT
GGTCAGTCTCTCAGCTTCAGGGTCACTGGCAGTGACCGCCGTAATCCACTTCTTG
GAACATTGTCCCTGCTAATTGGCAATTTGGTCAAACCTTCACCGGAAAGAATTC
AGGGTTTAG

Nucleotide

>CisEXPA-09

ACACTCGCACTGTCACCCACAACACCAAGTCTTAATTTGTTTTTCTTGGGGGAGC
ATCTTATTCTTAATTAGTTGGGTTGAAATTAACCAAATGGGTGTCGCTGTGGG
CATCATTGTATTGTGACTTTTGTACATTTCCCTCCCTTAGTGTTGATGCGAGAAT
CCCCGGCGTTTACGGTGGCGAGGCATGGCAAAGCGCTCATGCTACATTCTATGGA

GGCAATGATGCCTCAGGAACAATGGGTACGCGTGCACTTAAATTTACAGTGATT
TATTTGCGTTTTGCATCAACATACATGATTATTTACCACCAGTCAACTGTTTCTGA
TTTGTTCGGTTGTGTGTAATTGTATATTTAACAAACAGGAGGTGCTTGTGGGTACG
GCAATCTCTACAGTCAAGGATACGGCGTTAACACGGCAGCGCTAAGCACAGCAC
TGTTCAACAACGGGTTGAGCTGCGGTGCGTGTTTTGAGATTAAGTGTGCGAATGA
CCCTCAATGGTGCCACGCTGGGAGCCCTTCAATCTTCGTCACTGCCACCAACTTTT
GCCCTCCGAATTTTCGCTCAACCCAGCGACAATGGGGGGTGGTGCAACCCTCCTCG
CCCTCACTTCGATCTCGCCATGCCCATGTTCCCTCAAGATGGCCGAATACCGCGCC
GGAATTGTCCCTGTCTCTTACCGCAGGGTCCCTTGCAGGAAGAGAGGGCGGCATCA
GGTTCACCATCAACGGTTTTCCGTTACTTCAACTTGGTCTTGATCACCAACGTCGCT
GGTGCTGGGGATATTGTCAAGGCTAGCGTCAAAGGTTCCAGGACTGGGTGGATG
AGCTTGAGCAGGAAGTGGGGACAGAACTGGCAGTCTAATTCTGTTTTGGTTGGTC
AGTCTCTCAGCTTCAGGGTCACTGGCAGTGACCGCCGTACTTCCACTTCTTGGAAC
ATTGTCCCTGCTAATTGGCAATTTGGTCAAACCTTTCACCGGAAAGAATTTCAGGG
TTAGTTTTCAAGCACTTTCTCCCCTCCATGTTTTTGTGTTTTTTTCGCTTTTTTTGTT
TTATCCCGGAAAGTGAGAAAGAAAATGAGGGAAAGTATACTGTGTAAGTCTGTC
CCTGTGAGTGTGAACTTTTTGACTTTGACGGATTTGGTTGGGGACTGGGTTTGGTT
TCTGTTTTGGTTGAAGTGAAATGTAAAAGCTGAAGTGGCTTCAAAGTAATAGAGA
GCCCGCAGCTTCCAAAGTTAAATAGATTCGGTTTTATATTATATGTTTACAGTTA
CTTCACATGATAGTGATAATCATCTACGTACAAGTGT