

IDENTIFICATION

Species: *Citrus sinensis*

Locus: orange1.1g040256m

Gene Model: orange1.1g040256m

Description: CisEXPA-08

Family: Alpha Expansin

3D structure:



GENOME DATABASES

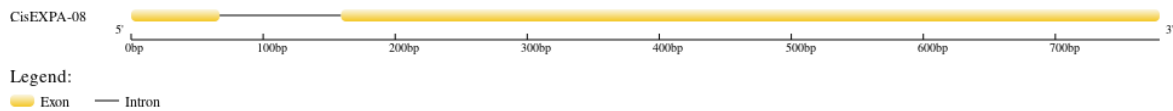
Phytozome: https://phytozome-next.jgi.doe.gov/info/Csinensis_v1_1

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

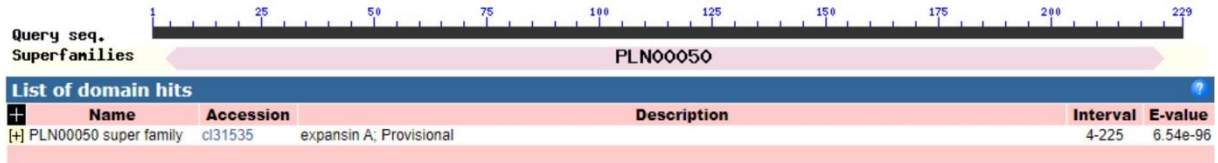
EXTERNAL RESOURCES

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

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>CisEXPA-08

MNGAWEDAHATFYGDMSGGETMQGACGYGDLKRQGYGLETAALSTALFNNGSTC
GACFEIICVNDPQWCLKGAGSIKITATNFCPPNYTKTKDIWCNPPQKHFDLSMPMFVK
LAPSKAGIIPVRYRRILCSKQGGVKFEVKGPNPNWTLVLVYNVGGAGDVTAVQVKGS
STGWLPMsrnwGQNWQTGTVLLGQGLSFQVTTSDGKTLQFDNVAPRNWQFGQTFQ
GRGNF*

CDS (coding sequence)

>CisEXPA-08

ATGAATGGTGCCTGGGAAGATGCTCATGCTACATTTTATGGTGACATGTCTGGAG
GAGAAACCATGCAGGGAGCTTGTGGTTATGGTGATCTCAAGAGACAAGGATATG
GCCTTGAGACAGCAGCTCTAAGCACAGCACTCTTCAACAATGGCTCAACTTGCAG
TGCTTGTTTCGAAATCATTGTGTGAATGATCCTCAATGGTGCTTAAAAGGTGCCG
GCTCAATCAAAATCACAGCAACCAATTTCTGCCACCAAACTACACAAAGACAA
AGGACATCTGGTGCAATCCTCCCCAGAAACACTTTGATCTTTCGATGCCTATGTTT
GTCAAATTAGCTCCTTCAAAGCGGGGATCATTCTGTGAGATACCGCAGAATCT
TGTGTAGCAAGCAAGGTGGTGTCAAGTTTGAAGTTAAAGGGAATCCGAAGTGA
CACTGGTTTTGGTGTACAATGTTGGGGGTGCTGGTGATGTTACCGCTGTGCAGGT
CAAGGGATCAAGCACAGGCTGGCTGCCATGTCTCGGAACTGGGGCCAGAATTG
GCAAACAGGAACAGTGCTTCTGGGGCAGGGTTTGTCATTTTCAGGTGACTACAAGT
GATGGGAAGACGCTGCAGTTTGATAATGTTGCCCTAGAAATTGGCAATTTGGCC
AAACCTTTCAGGGAGAGGAAATTTCTAG

Nucleotide

>CisEXPA-08

ATGAATGGTGCCTGGGAAGATGCTCATGCTACATTTTATGGTGACATGTCTGGAG
GAGAAACCATGCAGTAAGCGCGTCAATATCATATTTTGTAGATAAGTCTGA
CATATATTACATATTCAAGTTTTTATGACAATTAATAATGACAGAGGGAG
CTTGTGGTTATGGTGATCTCAAGAGACAAGGATATGGCCTTGAGACAGCAGCTCT
AAGCACAGCACTCTTCAACAATGGCTCAACTTGCAGGTGCTTGTTCGAAATCATT
GTGTGAATGATCCTCAATGGTGCTTAAAAGGTGCCGGCTCAATCAAAATCACAGC

AACCAATTTCTGCCACCAAACACTACACAAAGACAAAGGACATCTGGTGCAATCCT
CCCCAGAAACACTTTGATCTTTCGATGCCTATGTTTGTCAAATTAGCTCCTTCAA
AGCGGGGATCATTCTGTGAGATACCGCAGAATCTTGTGTAGCAAGCAAGGTGGT
GTCAAGTTTGAAGTTAAAGGGAATCCGAACCTGGACACTGGTTTTGGTGTACAATG
TTGGGGGTGCTGGTGATGTTACCGCTGTGCAGGTCAAGGGATCAAGCACAGGCTG
GCTGCCCATGTCTCGGAACTGGGGCCAGAATTGGCAAACAGGAACAGTGCTTCTG
GGCAGGGTTTTGTCATTTACAGGTGACTACAAGTGATGGGAAGACGCTGCAGTTTG
ATAATGTTGCCCTAGAAATTGGCAATTTGGCCAAACCTTTCAAGGGAGAGGAAA
TTTCTAG