

IDENTIFICATION

Species: *Carica papaya*

Locus: evm.model.supercontig_1.46

Gene Model: evm.model.supercontig_1.46

Description: CpEXPA-01

Family: Alpha Expansin

3D structure:



GENOME DATABASES

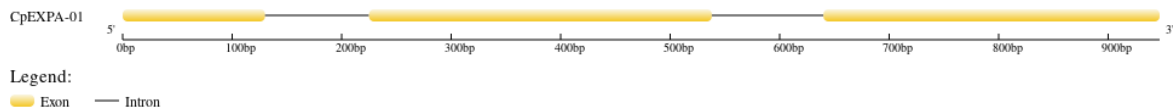
Phytozome: https://phytozome-next.jgi.doe.gov/info/Cpapaya_ASGPBv0_4

KEGG: <https://www.genome.jp/entry/T05151>

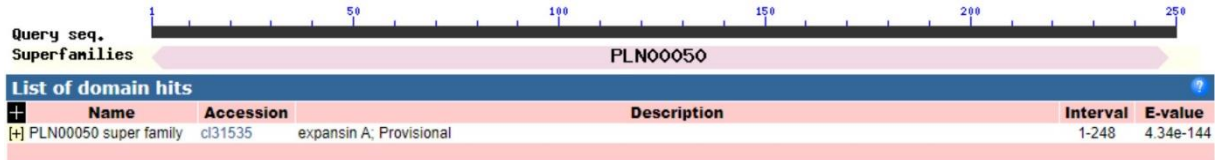
EXTERNAL RESOURCES

<http://asgpb.mhpc.hawaii.edu/papaya/>

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>CpEXPA-01

MASLIFLLTSLAVVCPVHAYGGGGWTNAHATFYGGGDASGTMGGACGYGNLYSQ
GYGTNTAALSTALFNGLSCGSCYEIRC VNDPKWCLPGSVVVTATNFCPPNNALPNN
AGGWCNPPLQHFDLSQPVFQHIAQYRAGIVPVS YRRVPCRRRGGIRFTINGHSYFNLV
LITNVGGAGDVHAVA IKGSRGTGWQAMSRNWGQNWQSN SYLNGQALSFKVTTSDGR
SVVSYNVAPSGWSFGQTFTGAQFR*

CDS (coding sequence)

>CpEXPA-01

ATGGCTTCTTTAATATTTCTGCTTTTGACTTCTCTTGCTGTGGTCTGCCCTGTTTCAT
GCATACGGCGGAGGAGGATGGACTAATGCCACGCCACCTTCTATGGTGGGGGT
GATGCCTCCGGCACAATGGGTGGGGCTTGTGGTTATGGCAACCTGTATAGCCAGG
GGTACGGTACAAACACTGCAGCTTTGAGCACTGCTCTCTTCAACAATGGTCTGAG
CTGCGGGTCTTGCTATGAGATTAGGTGCGTTAACGACCCAAAATGGTGCTTGCCA
GGCTCCGTTGTGGTCACCGCCACCAATTTCTGCCACCAAACAATGCTCTGCCAA
ATAATGCTGGTGGCTGGTGCAATCCTCCTCTCCAACATTTTGACCTCTCCCAGCCT
GTTTTCCAACACATTGCTCAGTACAGGGCAGGGATTGTTCTGTATCTTACCGAA
GGGTACCCTGCAGGAGAAGGGGAGGAATCAGATTCACCATCAACGGCCACTCAT
ACTTCAACCTGGTACTAATCACAACGTGGGTGGTGTGCTGGAGATGTGCATGCGGT
GGCCATCAAAGGGTCAAGGACAGGGTGGCAAGCTATGTCAAGGAAGTGGGGCCA
GAAGTGGCAGAGCAACAGCTACCTCAATGGCCAAGCCCTCTCCTTTAAGGTCACA
ACCAGTGATGGCCGCAGCGTGGTCTCCTACAATGTTGCCCATCTGGCTGGTCCTT
CGGCCAACTTTCACCGGCGCCAATTCCGCTGA

Nucleotide

>CpEXPA-01

ATGGCTTCTTTAATATTTCTGCTTTTGACTTCTCTTGCTGTGGTCTGCCCTGTTTCAT
GCATACGGCGGAGGAGGATGGACTAATGCCACGCCACCTTCTATGGTGGGGGT
GATGCCTCCGGCACAATGGGTATATATAATATATACATGTTTCGGCCATTTTCTTC
AACAATTTTTTAAGGAAGAACTCCTCAATGAGCTGAAATTTTGCTTCATTTCTGC
AGGTGGGGCTTGTGGTTATGGCAACCTGTATAGCCAGGGGTACGGTACAAACACT

GCAGCTTTGAGCACTGCTCTCTTCAACAATGGTCTGAGCTGCGGGTCTTGCTATGA
GATTAGGTGCGTTAACGACCCAAAATGGTGCTTGCCAGGCTCCGTTGTGGTCACC
GCCACCAATTTCTGCCACCAAACAATGCTCTGCCAAATAATGCTGGTGGCTGGT
GCAATCCTCCTCTCCAACATTTTGACCTCTCCCAGCCTGTTTTCCAACACATTGCT
CAGTACAGGGCAGGGATTGTTCCCTGTATCTTACCGAAGGTAAACTCTTAAATCCT
TAAATCCATGACTGATTTTCTTTCATTTTCTTCGAAACAAAACCCTTTTCTAACCA
GTGCTCTTATTTGATATGTTGTATTTTAGGGTACCCTGCAGGAGAAGGGGAGGAA
TCAGATTCACCATCAACGGCCACTCATACTTCAACCTGGTACTAATCACAAACGT
GGGTGGTGCTGGAGATGTGCATGCGGTGGCCATCAAAGGGTCAAGGACAGGGTG
GCAAGCTATGTCAAGGAACTGGGGCCAGA ACTGGCAGAGCAACAGCTACCTCAA
TGGCCAAGCCCTCTCCTTTAAGGTCACAACCAGTGATGGCCGCAGCGTGGTCTCC
TACAATGTTGCCCATCTGGCTGGTCCTTCGGCCAAACTTTCACCGGCGCCCAATT
CCGCTGA