

## IDENTIFICATION

**Species:** *Carica papaya*

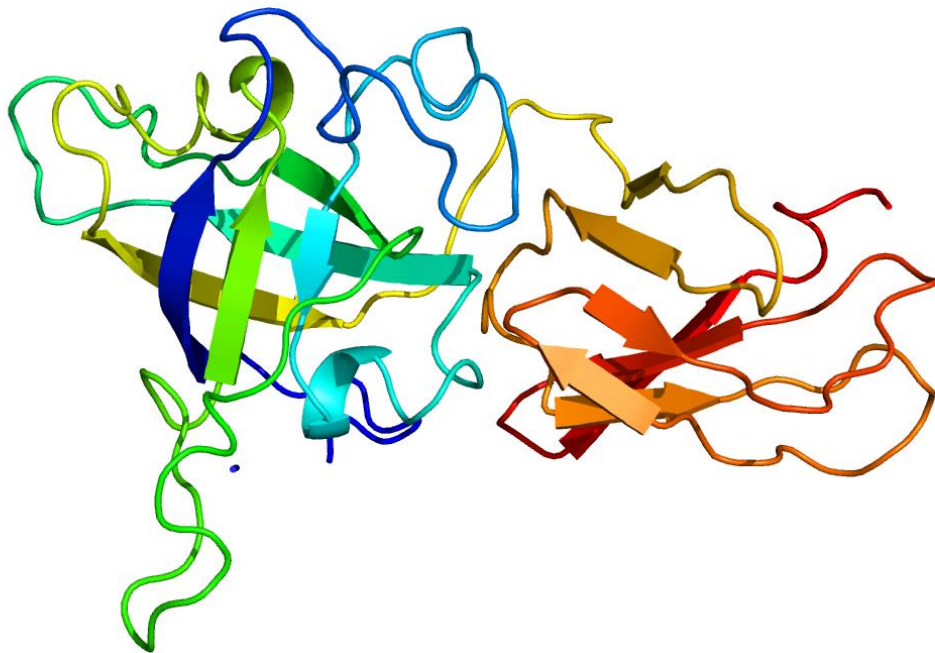
**Locus:** evm.model.supercontig\_2.303

**Gene Model:** evm.model.supercontig\_2.303

**Description:** CpEXPA-03

**Family:** Alpha Expansin

**3D structure:**



## GENOME DATABASES

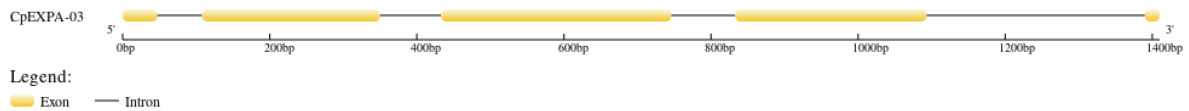
Phytozome: [https://phytozome-next.jgi.doe.gov/info/Cpapaya\\_ASGPBv0\\_4](https://phytozome-next.jgi.doe.gov/info/Cpapaya_ASGPBv0_4)

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

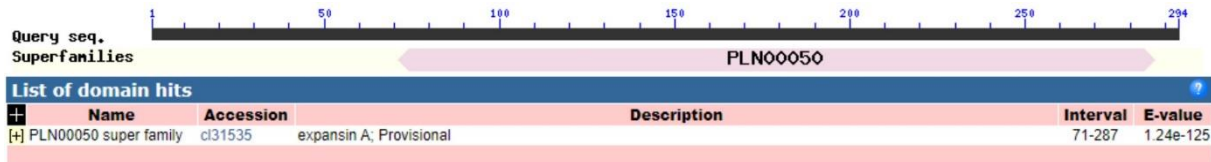
## EXTERNAL RESOURCES

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

## GENE STRUCTURE



## DOMAIN ARCHITECTURE



## SEQUENCES

### Peptide

>CpEXPA-03

MTHGHRGGAQLSSAQRPAVSDSASCNPNQSFPAKYPLTLIHS DHETNTNMAAPQKF  
FSSFLFFVFFFVHEIAADYGGWENAHATFYGGGDASGTMGGACGYGNLYSQGYGTN  
TAALSTALFNNGLSGSCYEMRCNDDPRWCLPGTITVTATNFCPPNFALSNDNGGWC  
NPPLQHFDLAEP AFLQIAQYRAGIVPVAFRRVPCMKKGGIRFTINGHSYFNLVLITNV  
GGAGDVHAVSIKGSKTGWQPMSRNWQNWQSN SYLNGQSLSFQVTASDGR T L T S Y  
D V V P E I V S S S \*

### CDS (coding sequence)

>CpEXPA-03

ATGACCCACGGCCACAGGGGTGGGGCTCAGCTCAGCTCAGCTCAGCGGCCGGCT  
GTCTCTGACTCTGCTTCCTGCAACCCTAATCAATCTTTTCCTGCTTATAAATACCC  
ACTCACTCTTATTCACTCTGACCACGAAACAAATACCAACATGGCAGCTCCTCAG  
AAATTCTTCTCCTCTTTTCTCTTCTTCGTTTTTTTTCTTCGTGCACGAAATAGCAGCA  
GATTATGGAGGCTGGGAAAATGCTCATGCTACTTTCTATGGCGGCGGTGATGCGT  
CTGGGACAATGGGAGGAGCATGTGGGTATGGGAATTTATACAGCCAAGGGTACG  
GAACCAACACCGCAGCACTGAGCACTGCCCTTTTCAACAATGGCTTGAGCTGTGG  
TTCTTGCTACGAAATGCGATGCAACGATGACCCAAGATGGTGTCTTCCC GGGACC  
ATCACTGTCACTGCTACCAACTTCTGTCCGCCAACTTTGCTCTGTCTAACGACAA  
TGGCGGGTGGTGCAATCCTCCTCTCCAGCACTTTGACTTGGCCGAGCCTGCTTTCT  
TGCAGATTGCACAGTACAGAGCTGGGATCGTCCCTGTGCGTTTTAGAAAGGGTGCC  
TTGTATGAAGAAAGGAGGGATAAGATTACACCATTAATGGACACTCTTACTTCAAC  
CTGGTGCTGATCACCAACGTCGGCGGAGCAGGAGATGTTTCATGCAGTGTCGATCA  
AAGGGTCGAAAACAGGGTGGCAACCCATGTCGAGGAACTGGGGCCAGAATTGGC  
AGAGCAACTCTTACCTTAATGGCCAGAGCTTGTCGTTTCAAGTCACAGCCAGTGA  
CGGTAGAACTCTACAAGCTACGACGTGGTGCCTGAGATTGTGAGTTCGAGTTGA

### Nucleotide

>CpEXPA-03

ATGACCCACGGCCACAGGGGTGGGGCTCAGCTCAGCTCAGCTCAGCGGTTGGTA  
AGGCAAACACTTGCATGTGCGCTCTTGATTTTCTAAATCCCCTTCTTGGCTCAGGC

CGGCTGTCTCTGACTCTGCTTCCTGCAACCCTAATCAATCTTTTCCTGCTTATAAA  
TACCCACTCACTCTTATTCCTGACCACGAAACAAATACCAACATGGCAGCTC  
CTCAGAAATCTTCTCCTCTTTTCTCTTCTTCGTTTTTTTTCTTCGTGCACGAAATAG  
CAGCAGATTATGGAGGCTGGGAAAATGCTCATGCTACTTTCTATGGCGGCGGTGA  
TGCGTCTGGGACAATGGGTAAATATCTTTACTCTCAAACCTTCATCACTTCTTCT  
TCATTCCTTCATCTCAATATATATGTAACATAATTAACCTTGCAGGAGGAGCATGTG  
GGTATGGGAATTTATACAGCCAAGGGTACGGAACCAACACCGCAGCACTGAGCA  
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GATGACCCAAGATGGTGTCTTCCCGGGACCATCACTGTCACTGCTACCAACTTCT  
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CAGCACTTTGACTTGGCCGAGCCTGCTTTCTTGCAATTGCACAGTACAGAGCTG  
GGATCGTCCCTGTCGCTTTTAGAAGGTAAAGTAACAATTCTCTCTTTTACAGAGAC  
TCTGTTTTTTGGTTTGGTGGGTGAATTGGGTGTGTGATTTTTTTTTTTTTTTTGCAGG  
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