

IDENTIFICATION

Species: *Carica papaya*

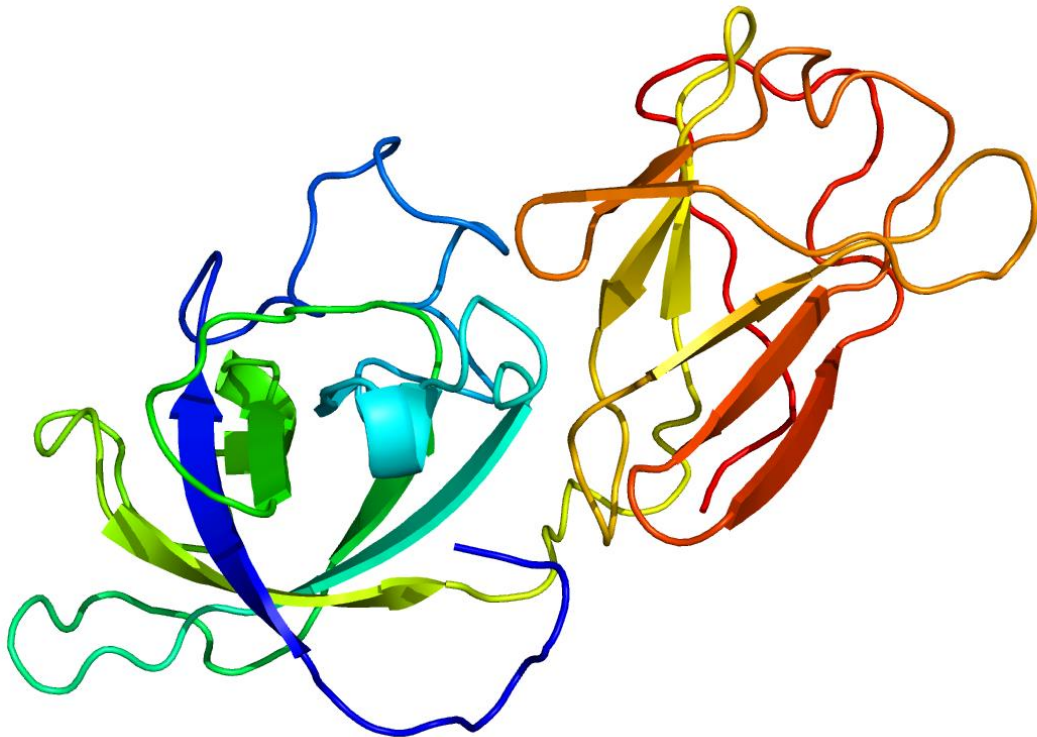
Locus: evm.model.supercontig_26.280

Gene Model: evm.model.supercontig_26.280

Description: CpEXPA-07

Family: Alpha Expansin

3D structure:



GENOME DATABASES

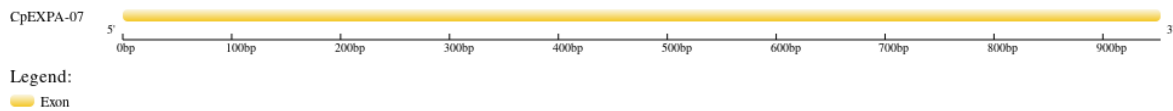
Phytozome: https://phytozome-next.jgi.doe.gov/info/Cpapaya_ASGPBv0_4

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

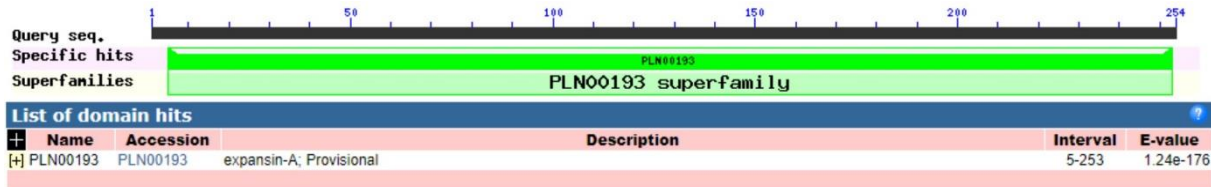
EXTERNAL RESOURCES

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

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>CpEXPA-07

MAQLAAILLGFFCYLTITVHAFLPSGWTKAHATFYGGSDASGTMGGACGYGNLYST
GYGTRTAALSTALFNDGASCGQCYKIMCDYQVDPKWCKKGVSVTITATNFCPPNYA
LPNNNGGWCNPPPLQHFDMAQPAWEKIGIYRGGIVPVIFQRVPCCKKHGGVRFTINGRD
YFELVLISNVAGAGSIKSVSIKGSKTGWTAMSRNWGANWQSN SYLNGQSLSFQVTTT
DGVTRVFPNVVPSNWAFGQSFSTKIQF*

CDS (coding sequence)

>CpEXPA-07

ATGGCCCAACTCGCAGCCATCTTGCTTGGATTCTTCTGCTATCTTACCATCACAGT
CCACGCATTTTTGCCTTCTGGGTGGACTAAAGCTCATGCCACGTTTTATGGAGGCA
GCGATGCATCAGGAACAATGGGTATTTACCATTTTCACTTGTCTTTTTCTCATCT
TTCTGATAACTAAACCAGATGAATCTTAGCTTAAATGATTAATATACTTTGGTCGT
TGTAGGGGGAGCCTGTGGTTATGGTAATCTATATTCTACTGGGTACGGAACAAGG
ACTGCTGCTCTTAGCACTGCGTTATTTAACGATGGAGCTTCATGTGGACAATGCTA
CAAGATCATGTGCGACTACCAAGTAGATCCCAAGTGGTGCAAGAAAGGAGTATC
CGTCACCATTACTGCAACAACTTCTGCCCTCCTAACTATGCTCTCCCAAACAACA
ATGGCGGCTGGTGCAACCCTCCTCTCCAGCATTTTGATATGGCTCAGCCTGCTTGG
GAAAAGATCGGTATTTACAGAGGTGGGATCGTGCCTGTTATCTTCCAGAGGTACA
GATTAATCTGAATAGCTAGTCCTATTAATGTGTTTATAATATTTAATACCATGTT
TCTGAATATCAACAACTCTTGAAATTGGTGCAGGGTGCCCTGCAAAAAGCATGG
TGGAGTTAGATTCACCATCAATGGCAGGGACTACTTCGAGCTTGTTTTGATCAGC
AACGTAGCTGGAGCTGGATCCATCAAATCAGTATCCATCAAAGGATCAAAAACA
GGTTGGACAGCAATGTCAAGGAACTGGGGAGCTAATTGGCAATCCAACCTCTACC
TCAATGGCCAATCTTTGTCTTCCAGGTCACCACTACAGATGGGGTAACCAGAGT
CTTCCAAACGTTGTGCCATCAAACCTGGGCATTTGGTCAATCCTTCTCCACCAAAA
TACAGTTCTAA

Nucleotide

>CpEXPA-07

ATGGCCCAACTCGCAGCCATCTTGCTTGGATTCTTCTGCTATCTTACCATCACAGT
CCACGCATTTTTGCCTTCTGGGTGGACTAAAGCTCATGCCACGTTTTATGGAGGCA
GCGATGCATCAGGAACAATGGGTATTTACCATTTCACCTTGTCTTTTTCTCATCT
TTCTGATAACTAAACCAGATGAATCTTAGCTTAAATGATTAATATACTTTGGTCGT
TGTAGGGGGGAGCCTGTGGTTATGGTAATCTATATTCTACTGGGTACGGAACAAGG
ACTGCTGCTCTTAGCACTGCGTTATTTAACGATGGAGCTTCATGTGGACAATGCTA
CAAGATCATGTGCGACTACCAAGTAGATCCCAAGTGGTGCAAGAAAGGAGTATC
CGTCACCATTACTGCAACAACTTCTGCCCTCCTAACTATGCTCTCCCAAACAACA
ATGGCGGCTGGTGCAACCCTCCTCTCCAGCATTTTGATATGGCTCAGCCTGCTTGG
GAAAAGATCGGTATTTACAGAGGTGGGATCGTGCCTGTTATCTTCCAGAGGTACA
GATTAATCTGAATAGCTAGTCCTATTAATGTGTTTATAATATTTAATACCATGTT
TCTGAATATCAACAACTCTTGAAATTGGTGCAGGGTGCCCTGCAAAAAGCATGG
TGGAGTTAGATTCACCATCAATGGCAGGGACTACTTCGAGCTTGTTTTGATCAGC
AACGTAGCTGGAGCTGGATCCATCAAATCAGTATCCATCAAAGGATCAAAAACA
GGTTGGACAGCAATGTCAAGGAACTGGGGAGCTAATTGGCAATCCAATCCTACC
TCAATGGCCAATCTTTGTCCTTCCAGGTCACCACTACAGATGGGGTAACCAGAGT
CTTTCCAAACGTTGTGCCATCAAACCTGGGCATTTGGTCAATCCTTCTCCACCAAAA
TACAGTTCTAA