

IDENTIFICATION

Species: *Carica papaya*

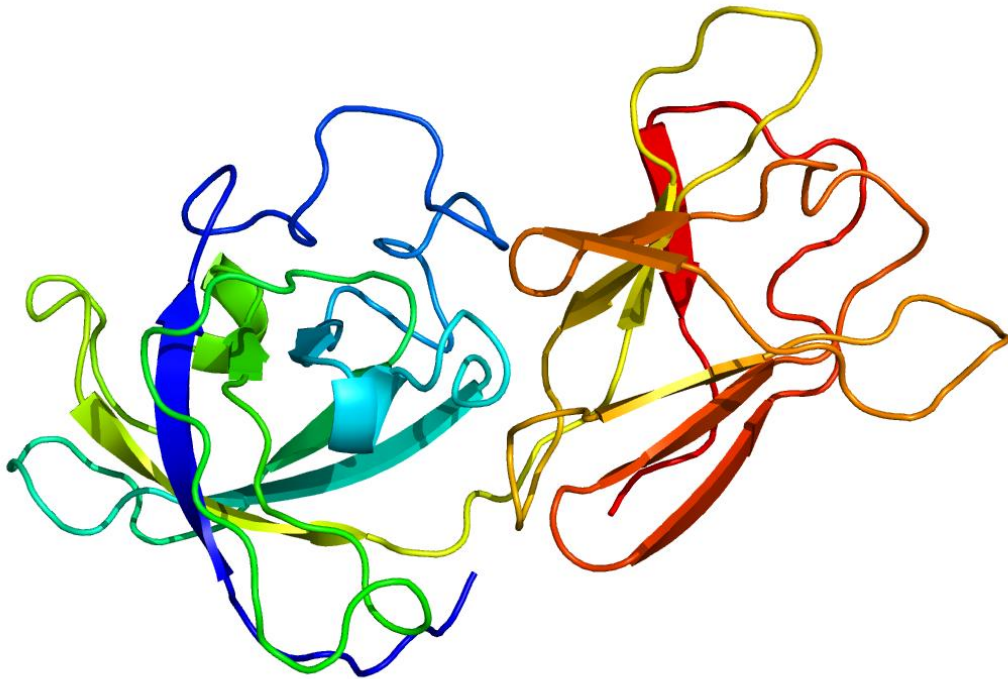
Locus: evm.model.supercontig_976.1

Gene Model: evm.model.supercontig_976.1

Description: CpEXPA-17

Family: Alpha Expansin

3D structure:



GENOME DATABASES

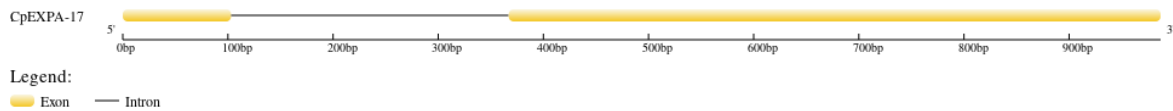
Phytozome: https://phytozome-next.jgi.doe.gov/info/Cpapaya_ASGPBv0_4

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

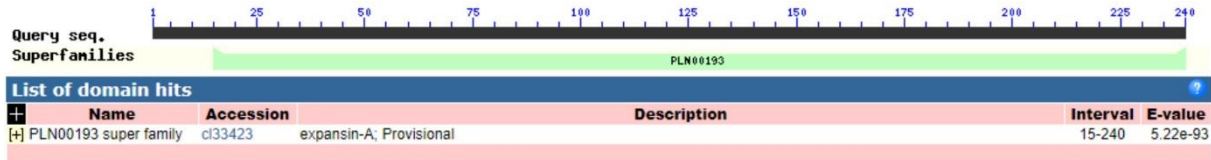
EXTERNAL RESOURCES

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

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>CpEXPA-17

MLFASLIIGESKLDSTWYDAHATFYGDIGGSETMQGACGYNDLHQQGYGLETTALST
ALFNNGKTCGACFEIKCVNNPKWCKPNAIHKVTATNFCPPNYSKPNGNWCNPPLKHF
DLSLKMFLALAEYKAGIIPVQYRRVTCTKQGGVKFEIKGNPYWILVLVYNVGGVVDI
TNVQIRGSETSSWIPMSRNWGVNWQTGKNLVGQSLSFQVTTSDGKMLEFKDIAASN
WQFGATFDGKINF*

CDS (coding sequence)

>CpEXPA-17

ATGTTGTTTGCTAGTTTGATAATTGGTGAAAGCAAAGCTAGATTCGACATGGTATG
ATGCTCATGCAACATTTTATGGCGACATTGGTGGATCCGAAACAATGCAAGGAGC
TTGTGGGTATAACGATCTCCATCAACAAGGATATGGACTAGAGACAACAGCTTTA
AGCACTGCACTATTCAACAATGGAAAACTTGTGGAGCTTGTTTTGAGATCAAGT
GCGTAAATAATCCTAAATGGTGCAAACCAATGCTATTATTAAAGTAACAGCAAC
AACTTTTGTCTCCTAATTACTCTAAACCCAACGGAAATTGGTGCAATCCTCCAC
TAAACACTTTGATTTGTCTTTAAAAATGTTCCCTCGCTCTTGCCGAGTACAAAGCT
GGCATTATTCCTGTCCAGTATCGTCGCGTCACGTGCACCAAACAAGGAGGAGTTA
AATTTGAAATCAAGGGAAACCCATATTGGATTTTAGTATTAGTTTACAATGTTGG
TGGTGTGGTGACATTACTAATGTCCAAATTAGGGGCTCTGAAACCAGTTCTTGG
ATACCAATGTCACGCAACTGGGGAGTTAATTGGCAAAGCTGGAAAAAATCTTGTA
GACAAAGTTTGTCTGTTCCAAGTTACAACAAGTGATGGGAAAATGTTGGAATTCAA
AGATATTGCGGCCTCTAATTGGCAATTTGGTGCTACTTTTGACGGAAAAATTAATT
TTTAG

Nucleotide

>CpEXPA-17

ATGTTGTTTGCTAGTTTGATAATTGGTGAAAGCAAAGCTAGATTCGACATGGTATG
ATGCTCATGCAACATTTTATGGCGACATTGGTGGATCCGAAACAATGCGTAAATT
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AGTATTTGAAGCTCTTTTTTTTTTTTTCTGTGTTTTCTCCTAAATATTTACAATATA
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ATTCACTGTAACGTTCTTAGTACTTTAAAATTATTTATAATTTTGTGACTGTATGT
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CATCAACAAGGATATGGACTAGAGACAACAGCTTTAAGCACTGCACTATTCAACA
ATGGAAAACTTGTGGAGCTTGTTTTGAGATCAAGTGCGTAAATAATCCTAAATG
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TACTCTAAACCCAACGGAAATTGGTGCAATCCTCCACTAAAACACTTTGATTTGT
CTTTAAAATGTTCCCTCGCTCTTGCCGAGTACAAAGCTGGCATTATTCCTGTCCAG
TATCGTCGCGTCACGTGCACCAAACAAGGAGGAGTTAAATTTGAAATCAAGGGA
AACCCATATTGGATTTTAGTATTAGTTTACAATGTTGGTGGTGGTGGTGGACATTAC
TAATGTCCAAATTAGGGGCTCTGAAACCAGTTCTTGGATACCAATGTCACGCAAC
TGGGGAGTTAATTGGCAAACCTGGAAAAAATCTTGTAGGACAAAGTTTGTCTGTTCC
AAGTTACAACAAGTGATGGGAAAAATGTTGGAATTCAAAGATATTGCGGCCTCTAA
TTGGCAATTTGGTGCTACTTTTGACGGAAAAATTAATTTTGTAG