

IDENTIFICATION

Species: *Carica papaya*

Locus: evm.model.supercontig_19.63

Gene Model: evm.model.supercontig_19.63

Description: CpEXPA-06

Family: Alpha Expansin

3D structure:



GENOME DATABASES

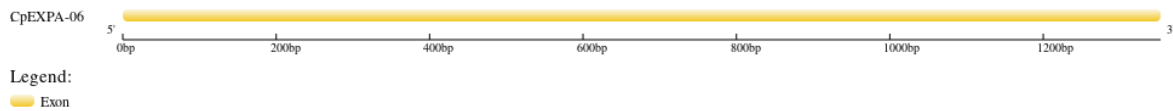
Phytozome: https://phytozome-next.jgi.doe.gov/info/Cpapaya_ASGPBv0_4

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

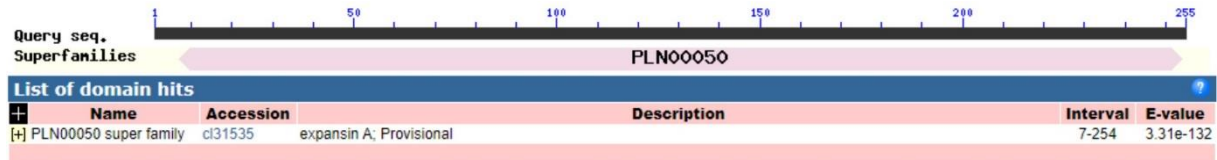
EXTERNAL RESOURCES

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

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>CpEXPA-06

MENISAFSMVSLLFVLLINSGLPVAYADYGGWTSGHATFYGGGDASGTMGGACGYG
NLYSQGYGTNTAALSTALFNGLSCGACYEMRCDNDPKWCLPGTITVTATNFCPPNF
ALSNDNGGWCNPLQHFDLAEPFLQIAQYRAGIVPVSFRRVSCGKKGIRFTINGHS
YFNLVLVTNVGGAGDVHVSIVKGSKTNWQSMSRNWGQNWQSN SYLNGQSLSFQVT
TSDGRTMTSYNLVPANWQFGQTFEGGQF*

CDS (coding sequence)

>CpEXPA-06

ATGGAAAACATTTTCAGCATTCTCCATGGTGTCTCTTCTCTTTGTCCTGCTAATCAA
CTCAGGTCTCCCCGTGGCTTATGCTGACTATGGAGGCTGGACAAGTGGCCATGCC
ACATTCTATGGTGGTGGTATGCATCCGGCACCATGGGTATGTTTTATATTTTCATA
AATATCATTACCGTCTTTCTATCAGAAACCTCTTATCATCTATATTTTCACAATTCT
ACAAAAAAGAAAGTGTTTTTTTTTTTTTTTTTTTTTTTCTTTTAGAACATTTGGTATGA
AGAATAAATTGCAAAGTGATGTATTCGTTTAACTCTGCCCAAGGAATAGCTAGG
TTTTTAATGTTAATTTAGGTGGGTTTGTATGGTGTGTTGCAGGAGGAGCATGTG
GGTATGGCAACTTATACAGCCAAGGGTATGGGACTAACACTGCAGCACTCAGCA
CAGCTCTGTTCAACAATGGTCTAAGCTGTGGAGCTTGTATGAGATGAGATGTGA
TAATGATCCTAAATGGTGTCTTCTGGAACCATAACTGTTACCGCTACCAATTTCT
GCCCTCCTAACTTTGCCCTTGCCAATGATAATGGTGGTTGGTGCAATCCTCCTCTC
CAGCATTTTGACTTGGCTGAGCCTGCCTTCTTGCAAATTGCTCAGTACAGAGCTGG
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AGACTCATTTCAGATTTTCAAATTAGAAAGTTTGTTCATTAATTGATGAAAG
TCACATCCTTTAAAGCTTTTATCCATTTTATAGATAAACTTGCAGGACCCACGGGGT
TAAACAAAAAGGGTCACTTTTTTGTGTCAATCCATTGATAAAAACCACAGCTTT
TTTTATACTATACACCTTTAAAGCCCTAATCCATTACAATAAACAACCAAA
GTCCTGAAAATAGAACTAGTATCCATAAATGTATAAAGTTAGAAGCTTTTGATAA
AGACACAGTCTTTAACATCGTTATTTCTTTCTTGGGTGAAAAACAGGGTATCCTG
TGGGAAGAAAGGAGGAATAAGGTTCCACCATCAATGGCCACTCTTACTTCAACTTG
GTATTGGTGACAAACGTTGGAGGAGCAGGAGATGTTCACTCAGTTTCAATCAAAG
GGTCCAAGACTAACTGGCAATCCATGTCAAGAACTGGGGCCAAAACCTGGCAGA

GCAACTCATACTCAATGGCCAAAGCCTCTCTTTTCAGGTCACCACCAGCGATGG
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Nucleotide

>CpEXPA-06

ATGGAAAACATTTTCAGCATTCTCCATGGTGTCTCTTCTCTTTGTCTGCTAATCAA
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AATATCATTACCGTCTTTCTATCAGAAACCTCTTATCATCTATATTTTCACAATTCT
ACAAAAAAGAAAGTGTTTTTTTTTTTTTTTTTTTTTTTTTTTTCTTTTAGAACATTTGGTATGA
AGAATAAATTGCAAAGTGTATTCGTTTAACTCTGCCCAAGGAATAGCTAGG
TTTTTAATGTTAATTTAGGTGGGTTTGTATGGTGTGTTGCAGGAGGAGCATGTG
GGTATGGCAACTTATACAGCCAAGGGTATGGGACTAACACTGCAGCACTCAGCA
CAGCTCTGTTCAACAATGGTCTAAGCTGTGGAGCTTGTTATGAGATGAGATGTGA
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AGACTCATTTCAGATTTTCAAATAGAAAGTTTTGTTCAATTAATTGATGAAAG
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TTTGAGGGTGGTCAGTTTTAG