

IDENTIFICATION

Species: *Carica papaya*

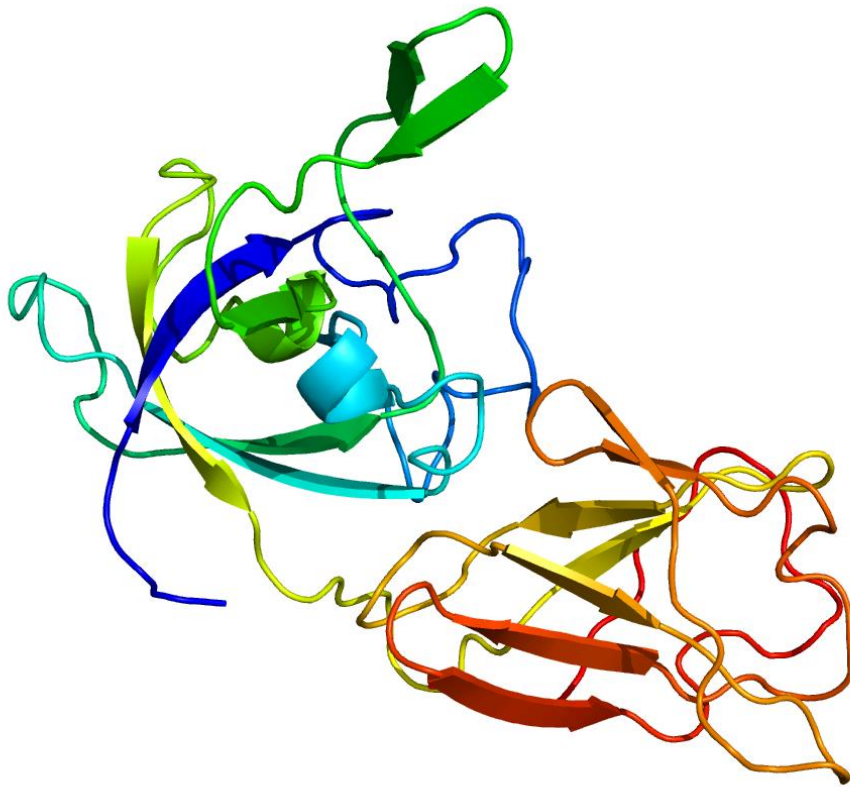
Locus: evm.model.supercontig_119.14

Gene Model: evm.model.supercontig_119.14

Description: CpEXPA-14

Family: Alpha Expansin

3D structure:



GENOME DATABASES

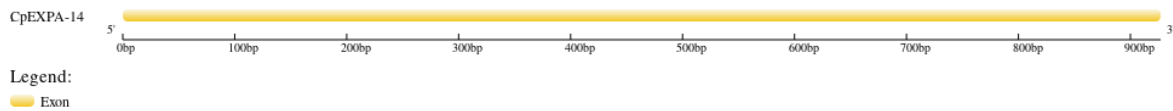
Phytozome: https://phytozome-next.jgi.doe.gov/info/Cpapaya_ASGPBv0_4

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

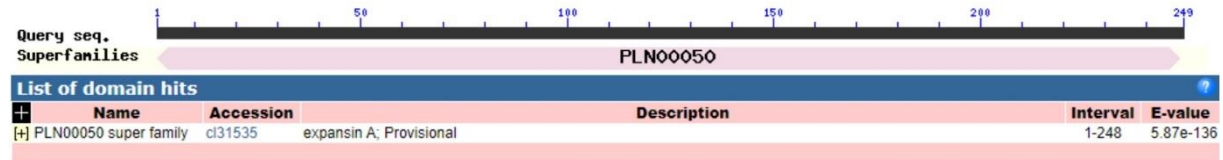
EXTERNAL RESOURCES

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

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>CpEXPA-14

MNLVWCYMLALFTTLKAVKVYIGWIDAHATFYGGGDASGTMGGACGYGNLYSQ
GYGTNTAALSTALFNGLSCGACFEIRC VNDREW CIPGSIIVTATNF CPPNLALANNA
GGWCNPPLQHF DLSQPVFLRIAKYKAGIVPVQYRRVTCRKRGGMRFTINGHSYFNLV
LITNVGGAGDVVGVSIGSKTGGWQAMSRNWGVNWQSN SYLNGQALSFKVTTSDR
RFVISNNVAPTTWTFGQTYTGKQF*

CDS (coding sequence)

>CpEXPA-14

ATGAACCTAGTCTGGTGTTATATGTTAGCACTATTCACGACATTGAAGGCTGTCA
AGGTGTATGGAATTGGGTGGATTGATGCCACGCTACTTTCTATGGAGGTGGAGA
TGCTTCTGGAACAATGGGTAAGGAAGAAAAGAACTTAAATGTCAATTTTCTTTT
CTCGCTTGAGTGCAAATAGTTTATCAATATATACATAAATATATATATGCGTGC
AGGTGGAGCTTGTGGGTATGGTAATCTTTATAGCCAAGGGTATGGGACAAACACA
GCTGCATTGAGTACAGCTTTATTCAACAATGGGTAAAGCTGTGGAGCTTGCTTCG
AGATCAGATGCGTAAATGATAGAGAATGGTGTATACCAGGCTCTATTATAGTAAC
TGCCACCAACTTTTGCCACCAAACCTTGCTCTGGCAAACAATGCTGGAGGCTGG
TGTAATCCTCCTCTGCAGCACTTTGATCTTTCACAACCTGTTTTCCTACGCATAGC
AAAATATAAAGCTGGAATTGTTCCGGTGCAGTACAGAAGGTAAGCATGCACTAA
TAGTAGGTAATAGCTCGTATTTTAATCAACTATTTTATGCCTTGAACCTAGTGCTA
GTGTTTGGTTTCAGGGTACTTGCCGGAAGAGAGGGGGAATGAGGTTCAATCA
ATGGCCACTCCTACTTCAATCTGGTGCTGATAACTAATGTTGGTGGAGCAGGTGA
TGTGGTGGGTGTGTCCATAAAGGGCTCTAAAACCTGGTGGATGGCAGGCAATGTCC
AGGAACTGGGGTGTGAACTGGCAGAGCAACTCCTACCTCAATGGTCAGGCCCTCT
CTTTCAAAGTCACAACCAGCGATAGACGCTTTGTGATCTCTAACAATGTAGCTCC
AACTACCTGGACCTTTGGCCAAACATATACTGGAAAACAGTTCTAA

Nucleotide

>CpEXPA-14

ATGAACCTAGTCTGGTGTTATATGTTAGCACTATTCACGACATTGAAGGCTGTCA
AGGTGTATGGAATTGGGTGGATTGATGCCACGCTACTTTCTATGGAGGTGGAGA

TGCTTCTGGAACAATGGGTAAGGAAGAAAAGAACTTAAATGTCAATTTTCTTT
CTCGCTTGAGTGCAAAATAGTTTATCAATATATACATAAATATATATATGCGTGC
AGGTGGAGCTTGTGGGTATGGTAATCTTTATAGCCAAGGGTATGGGACAAACACA
GCTGCATTGAGTACAGCTTTATTCAACAATGGGTTAAGCTGTGGAGCTTGCTTCG
AGATCAGATGCGTAAATGATAGAGAATGGTGTATACCAGGCTCTATTATAGTAAC
TGCCACCAACTTTTGCCACCAAACCTTGCTCTGGCAAACAATGCTGGAGGCTGG
TGTAATCCTCCTCTGCAGCACTTTGATCTTTCACAACCTGTTTTCTACGCATAGC
AAAATATAAAGCTGGAATTGTTCCGGTGCAGTACAGAAGGTAAGCATGCACTAA
TAGTAGGTAATAGCTCGTATTTAATCAACTATTTTATGCCTTGAAGTTAGTGCTA
GTGTTTGGTTTCAGGGTTACTTGCCGGAAGAGAGGGGGAATGAGGTTCAACAATCA
ATGGCCACTCCTACTTCAATCTGGTGCTGATAACTAATGTTGGTGGAGCAGGTGA
TGTGGTGGGTGTGTCCATAAAGGGCTCTAAAACCTGGTGGATGGCAGGCAATGTCC
AGGAACTGGGGTGTGAACTGGCAGAGCAACTCCTACCTCAATGGTCAGGCCCTCT
CTTTCAAAGTCACAACCAGCGATAGACGCTTTGTGATCTCTAACAATGTAGCTCC
AACTACCTGGACCTTTGGCCAAACATATACTGGAAAACAGTTCTAA