

IDENTIFICATION

Species: *Capsella rubella*

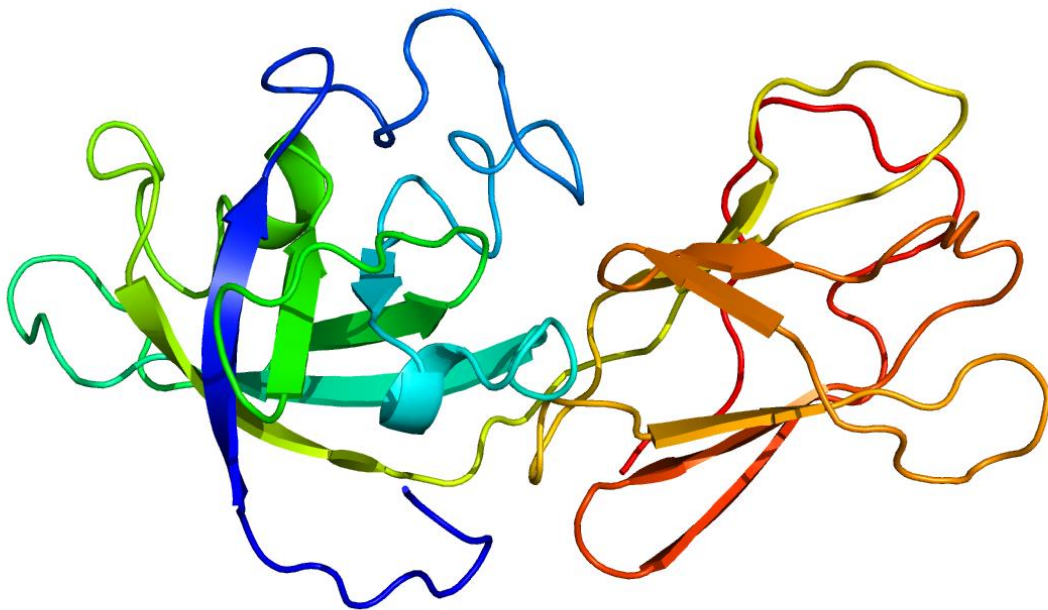
Locus: Carub.0004s2174

Gene Model: Carub.0004s2174.1.p

Description: CrEXPA-11

Family: Alpha Expansin

3D structure:



GENOME DATABASES

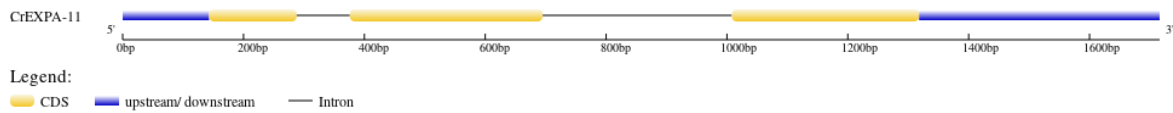
Phytozome: https://phytozome-next.jgi.doe.gov/info/Crubella_v1_1

KEGG: <https://www.genome.jp/entry/gn:T02984>

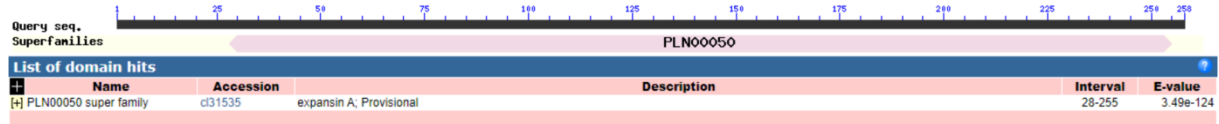
EXTERNAL RESOURCES

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GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>CrEXPA-11

MAIKLAILFTTFVLFSLADARIPGVYSGGAWQNAHATFYGGSDASGTMGGACGYGN
LYSQGYGTNTAALSTALFNNGMSCGACFELKCANDPQWCHSGSPSILITATNFCPPNL
AQPSDNGGWCNPPREHFDLAMPVFLKIAQYRAGIVPVS YRRVPCRKRGGIRFTINGH
RYFNLILITNVAGAGDIVRANVKGSRGTGWSLSRNWQNWQSNVAVLVGQALSFRVT
GSDRRSTSWNMVPSNWQFGQTFVGKNFRV*

CDS (coding sequence)

>CrEXPA-11

ATGGCTATTA AACTTGCAATTCTATTTACCACATTTGTCCTTTTTAGCCTTGCCGA
CGCTAGAATCCCCGGCGTTTACTCCGGCGGTGCGTGGCAAACGCACACGCCACT
TTCTACGGTGGCAGTGACGCCTCTGGCACTATGGGAGGAGCGTGTGGTTACGGTA
ACCTATACAGCCAAGGGTACGGGACCAACACGGCAGCTTTGAGCACGGCGCTGT
TTAACAACGGTATGAGTTGTGGAGCCTGCTTTGAGCTAAAATGCGCCAACGACCC
TCAATGGTGCCACTCTGGTAGTCCTTCGATCCTCATCACCGCAACCAATTTCTGCC
CACCAA AACTTGGCTCAGCCCAGCGACAACGGAGGATGGTGCAACCCGCCACGTG
AACACTTCGACCTAGCCATGCCTGTCTTCTCAAGATTGCTCAATATCGCGCCGGC
ATTGTCCCTGTCTCATAACCGCAGGGTGCCATGTAGAAAGAGAGGAGGAATAAGG
TTCACAATCAACGGTCACCGTTACTTCAACTTGATTCTGATTACAAACGTGGCTGG
GGCAGGAGACATAGTGAGGGCAAACGTGAAAGGTTCAAGGACTGGTTGGATGAG
TTTGAGCAGGA AACTGGGGTCAA AACTGGCAATCCAACGCTGTTCTGGTTGGTCAG
GCACTCTCGTTCCGCGTCACGGGCAGTGACCGTAGGACATCTACTTCGTGGAACA
TGGTTCCTTCTAACTGGCAGTTTGGTCAAACCTTTGTCGGGAAGAATTCAGGGTT
TAA

Nucleotide

>CrEXPA-11

TCCAATTAACAAACCTAACTCTTTCTCTTGACAAGAGCGCAAGCTCGAAGGCGC
TCTTGTTCTTTCTTTCTTTCTTCATTTTCTCCTTTTGTCACCAAACCCATAGTAC
AATTTATAACTCTCTAATTCACACACCAA AATGGCTATTA AACTTGCAATTCTATT
TACCACATTTGTCCTTTTTAGCCTTGCCGACGCTAGAATCCCCGGCGTTTACTCCG
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CACTATGGGTAAGTCCACAAAAACAGAGCATTAAAACCTTTAAAAGAGTCTTTATT
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TACGGTAACCTATACAGCCAAGGGTACGGGACCAACACGGCAGCTTTGAGCACG
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TTTCTGCCACCAAACCTTGGCTCAGCCAGCGACAACGGAGGATGGTGCAACCCG
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ACATAATAACCGGCTAAAAACAATTAGTGGATGCTATTTTTAACATTTTTTTGTT
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ATTTGAACTAATACTAGTTGAAGTCAAACCCCTCATACAAATCACACTTAATTAG
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TCACCGTACTTCAACTTGATTCTGATTACAAACGTGGCTGGGGCAGGAGACATA
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CTGTGAGAAAATTTGTAAACAGCCCGCAGCTATTAACGTGTTTTACATCTTTGGGT
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