

IDENTIFICATION

Species: *Capsella rubella*

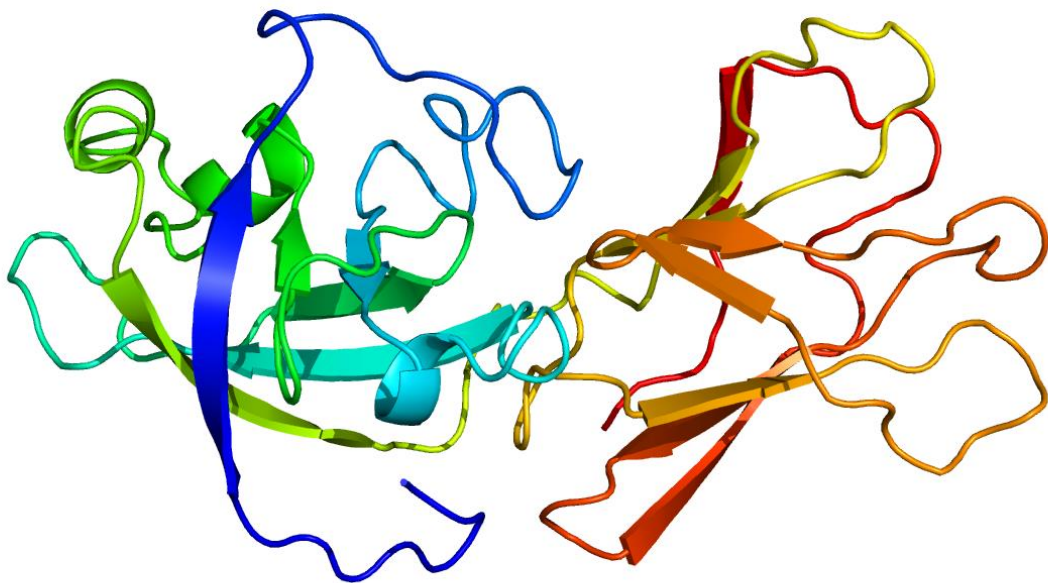
Locus: Carub.0005s1181

Gene Model: Carub.0005s1181.1.p

Description: CrEXLA-03

Family: Expansin Like Alpha

3D structure:



GENOME DATABASES

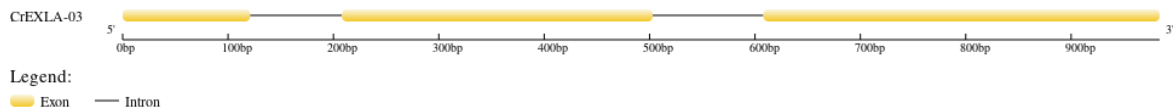
Phytozome: https://phytozome-next.jgi.doe.gov/info/Crubella_v1_1

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

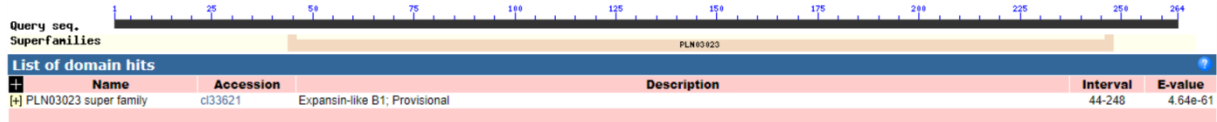
EXTERNAL RESOURCES

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GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>CrEXLA-03

MRSFLYILVIVFLFSSSVNACDRCVHSSKAA YFSSASALSSGACGYGSMATRFVAGHI
AAATPSIYKNGAGCGACFQVRCKNPKLCTSKGTIVMVTDLNTNSHTDLVLSNRAFRA
MAKPVGSADKYLLKQGIVDIEYQRVPCNYGKRNLQVRVEEASKKPYLAIKLLYQG
GQTEVVGDIAQVGSSQWSYMTRS YGGVWATDKVPTGALQFRVTVTGGYDGKT VV
AKRVL PANWEAGRIYDSGVQITDIAQESCNTCSNIWK*

CDS (coding sequence)

>CrEXLA-03

ATGAGAAGCTTTCTCTACATACTTGTGATAGTGTTCCCTCTTCTCATCATCTGTTAA
CGCATGTGACCGATGTGTTTCATAGTTCTAAAGCAGCTTATTTCTCATCTGCCTCTG
CTCTCTCTTCCGGAGCTTGTGGTTATGGCTCTATGGCTACAAGATTCGTTGCTGGA
CACATTGCGGCGGCTACACCTTCCATATACAAAATGGTGCTGGCTGTGGAGCTT
GCTTCCAAGTCAGATGCAAGAACCCAAAGTTGTGTACAAGTAAAGGAACCATTGT
GATGGTCACGGACTTGAACACGAACAGCCACACTGATCTAGTCCCTTAGTAATAGA
GCTTTTAGGGCTATGGCTAAACCTGTTGGTAGTGCTGACAAGTACCTTCTTAAAC
AAGGCATTGTCGACATCGAATACCAAAGAGTTCCTTGCAACTATGGGAAAAGGA
ATTTGCAAGTGAGAGTGGAAGAAGCAAGCAAAAAGCCATATTACTTGGCGATAA
AGCTTTTGTACCAAGGAGGCCAAACCGAAGTGGTAGGTATCGACATTGCTCAAGT
TGGTTCGTCACAATGGAGTTACATGACAAGAAGCTACGGAGGCGTGTGGGCAAC
TGACAAAGTACCAACGGGAGCTCTACAGTTTAGGGTCACGGTGACAGGCGGCTA
TGATGGCAAACGGTTTGGGCGAAGAGAGTTCTTCCAGCCA ACTGGGAAGCTGG
GAGGATCTATGATTCCGGGGTTCAGATCACTGACATTGCTCAAGAAAGTTGTAAT
ACATGCAGTAACATATGGAAGTGA

Nucleotide

>CrEXLA-03

ATGAGAAGCTTTCTCTACATACTTGTGATAGTGTTCCCTCTTCTCATCATCTGTTAA
CGCATGTGACCGATGTGTTTCATAGTTCTAAAGCAGCTTATTTCTCATCTGCCTCTG
CTCTCTCTTGTAAATTAACATTCTTCTATTGTCTCATTACTTCTTATAACTACTTGT
TATTTCTTTACTCATGTCTTGTAAATGGGGTTTTTGCAGCCGGAGCTTGTGGTTAT
GGCTCTATGGCTACAAGATTCGTTGCTGGACACATTGCGGCGGCTACACCTTCCA

TATACAAAATGGTGCTGGCTGTGGAGCTTGCTTCCAAGTCAGATGCAAGAACCC
AAAGTTGTGTACAAGTAAAGGAACCATTTGTGATGGTCACGGACTTGAACACGAA
CAGCCACACTGATCTAGTCCTTAGTAATAGAGCTTTTAGGGCTATGGCTAACCT
GTTGGTAGTGCTGACAAGTACCTTCTTAAACAAGGCATTGTCGACATCGAATACC
AAAGGTTTGATTCTTAAAACACATAACTTCTTTTTTTTTTTTTTTTTTTGTTATGGTCACT
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GTAGGTATCGACATTGCTCAAGTTGGTTCGTCACAATGGAGTTACATGACAAGAA
GCTACGGAGGCGTGTGGGCAACTGACAAAGTACCAACGGGAGCTCTACAGTTTA
GGGTCACGGTGACAGGCGGCTATGATGGCAAACGGTTTGGGCGAAGAGAGTTC
TTCCAGCCAACTGGGAAGCTGGGAGGATCTATGATTCCGGGGTTCAGATCACTGA
CATTGCTCAAGAAAGTTGTAATACATGCAGTAACATATGGAAGTGA