IDENTIFICATION

Species: *Citrus clementina*

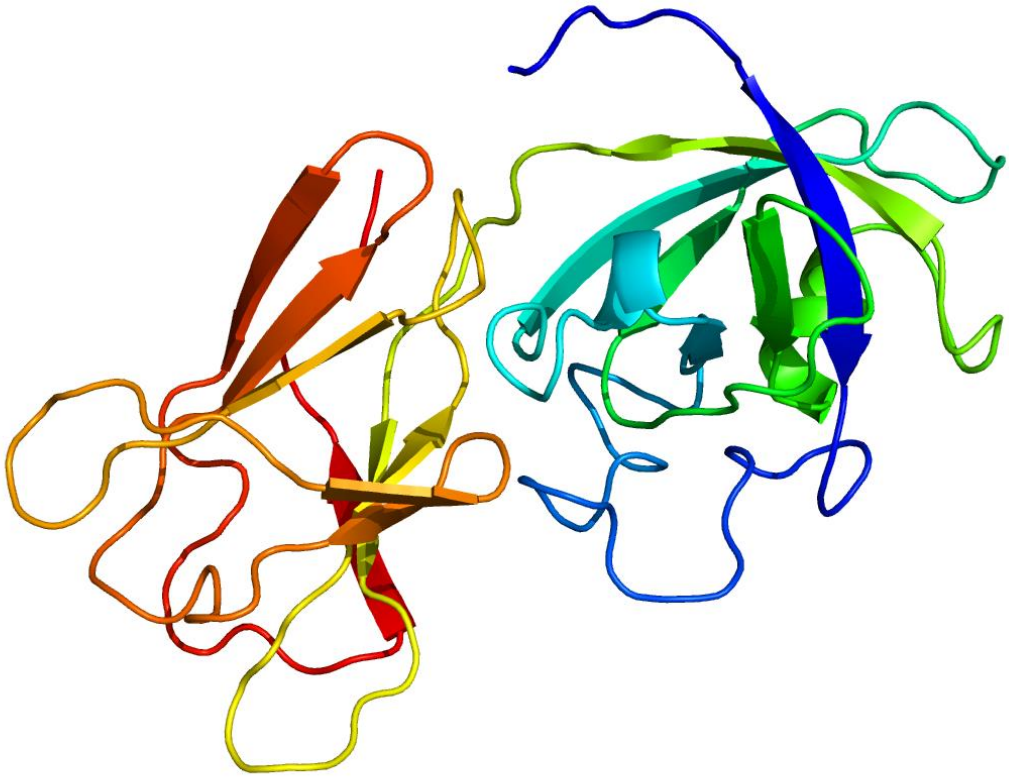
Locus: Ciclev10024605

Gene Model: Ciclev10024605m

Description: CclEXPA-03

Family: Alpha Expansin

3D structure:



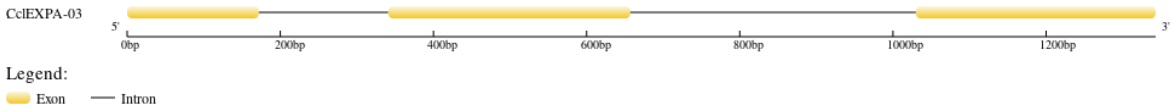
GENOME DATABASES

Phytozome: https://phytozome-next.jgi.doe.gov/info/Cclementina_v1_0
KEGG: https://www.genome.jp/entry/T02982

EXTERNAL RESOURCES

https://www.citrusgenomedb.org/organism/Citrus/clementina

GENE STRUCTURE



DOMAIN ARCHITECTURE

List of domain hits

Name	Accession	Description	Interval	E-value
[+] PLN00193 super family	cl33423	expansin-A; Provisional	35-265	7.45e-93

SEQUENCES

Peptide

>CclEXPA-03

MASFFRSFGFNFILVVLILAIAGKSNALGYTHPIFRPGPWRLAHATFYGDESASETMG
GACGYGNLFSNGYGTDTAALSSTLFNNGYACGTCYQIKCYNSPHCYKYVPFTTVTAT
NLCPPNWSQDSNNGGWCNPPRAHFDMSKPAFMKIGAWKAGIVPVLFRRVPCIKPGGI
RFAFQGNGYWLLVYVMNVAGGGDIASMWVKGTRTGWISMSHNWGASYQAFATLG
GQALSFKIQSYSTKETIIAYNVAPANWNVGLTYKSNVNFH*

CDS (coding sequence)

>CclEXPA-03

ATGGCTTCTTTTTTTCGATCATTCGGATTTAACTTCATATTAGTTGTTTTGATTTTG
GCAATCGCCGGGAAGTCAAACGCTTTGGGTTATACACATCCTATTTTCCGGCCAG
GTCCATGGAGGCTTGCTCACGCCACCTTTTATGGCGATGAGTCTGCTTCCGAAAC
CATGGGAGGAGCTTGTGGGTATGGAAACTTGTTTTCTAATGGTTACGGAACAGAC
ACAGCGGCTTTGAGCTCCACATTGTTCAACAATGGATACGCTTGTGGGACTTGTT
ACCAGATAAAGTGCTATAATTCGCCTCATTGCTATAAATATGTACCATTCACCAC
AGTTACAGCCACAAACCTCTGCCCGCCAAATTGGTCCCAGGACTCCAATAATGGA
GGCTGGTGCAATCCCCCTCGCGCCCATTTTGATATGTCCAAGCCCGCGTTCATGA
AGATCGGCGCTTGGAAGGCCGGTATTGTCCCAGTCCTGTTTCGCAGGGTGCCATG
CATAAAGCCCGGTGGGATTCGATTTGCTTTCCAGGGAAATGGATACTGGTTGTTG
GTGTATGTGATGAATGTTGCAGGCGGCGGAGATATAGCCAGCATGTGGGTTAAG
GGAACCAGAACAGGATGGATTAGCATGAGCCATAACTGGGGAGCTTCATATCAA
GCATTTGCAACTCTGGGAGGCCAAGCTCTTTCTTTCAAGATCCAGTCATATTCAAC
CAAGGAGACTATTATAGCTTACAATGTTGCTCCTGCTAACTGGAACGTAGGATTG
ACTTACAAGTCAAATGTGAACTTCCATTAA

Nucleotide

>CclEXPA-03

ATGGCTTCTTTTTTTCGATCATTCGGATTTAACTTCATATTAGTTGTTTTGATTTTG
GCAATCGCCGGGAAGTCAAACGCTTTGGGTTATACACATCCTATTTTCCGGCCAG
GTCCATGGAGGCTTGCTCACGCCACCTTTTATGGCGATGAGTCTGCTTCCGAAAC
CATGGGTACGTATATTTATACATATACTCAATTCAATATTTTTCAATTTAAAAAAA

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GACATCTGCCCACTAATACCTGCCCATCTTTTATAATTTGTGGGAAGGGGATTAA
ATTTTGAGGACAGGGAACTTGAACCGGTGTGTCGAAGGCCACAGCCCAACGCTA
AACAACAATTGAGCCTAAGTGGCGCGGGAATTAATAATATTAAGGACAAGGGGA
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TCTAATTATTTATATGTATGTATATATTCTTGTAGGGTGCCATGCATAAAGCCCGG
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AATGTTGCAGGCGGCGGAGATATAGCCAGCATGTGGGTTAAGGGAACCAGAACA
GGATGGATTAGCATGAGCCATAACTGGGGAGCTTCATATCAAGCATTTGCAACTC
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