

IDENTIFICATION

Species: *Citrus sinensis*

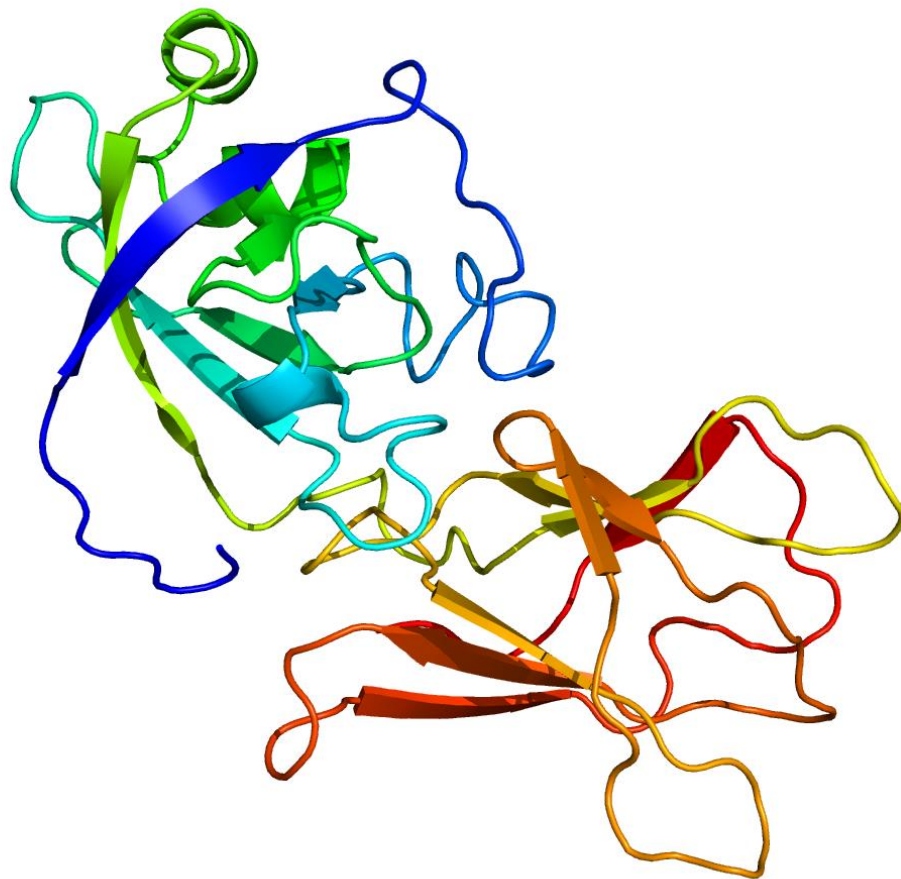
Locus: orange1.1g025007m

Gene Model: orange1.1g025007m

Description: CisEXLA-01

Family: Expansin Like Alpha

3D structure:



GENOME DATABASES

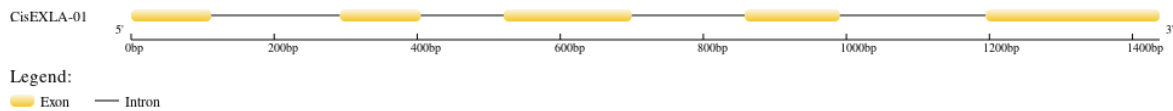
Phytozome: https://phytozome-next.jgi.doe.gov/info/Csinensis_v1_1

Kegg: <https://www.genome.jp/entry/T02983>

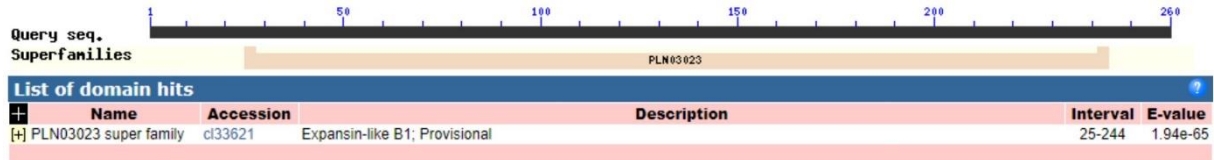
EXTERNAL RESOURCES

<https://www.citrusgenomedb.org/organism/Citrus/sinensis>

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>CisEXLA-01

MAILLCFLFFLLSSATACDHCVHQSKVSYFSKTSALSKGACGYGSLALGLGSGHIAAA
VPSIYKNGAACGGTCFQVRCKNRALCSRKGTRVIVVDLNNHNNKTDMLVLSRRAFRAL
ANKGMDNEILKQRAVDVEYIRVPCEYKHHNLA VRVEESSKNPNYLAIKVLYQGGKT
EILGVVLSEYGSPVRIDMRRKFGAVWETDRAPKGPLQFGFPIVQGFVDKWIWAKNPV
PADWKIGVTYDAGVQITDVFDTGCAECGPWN*

CDS (coding sequence)

>CisEXLA-01

ATGGCTATCTTGCTTTGCTTTCTCTTCTTTCTCTTATCATCTGCCACTGCTTGTGAT
CACTGTGTGCACCAATCCAAGGTTTCTACTTCTCCAAAACCTCCGCACTTTCAAA
GGGGGCATGTGGGTATGGCTCGTTGGCATTAGGGTTAGGTAGTGGACACATTGCT
GCTGCTGTTCCATTACAAAACGGAGCTGCCTGTGGTGGTACATGCTTTCA
GGTAAGGTGCAAGAACAGAGCTCTATGTAGCAGAAAAGGAACCAGAGTGATTGT
GACCGATCTCAATCACAACAACAAAACAGACATGGTCCTCAGCAGGAGAGCTTT
CAGGGCACTGGCCAACAAGGGCATGGACAATGAAATCTTGAAACAGAGAGCTGT
GGATGTGGAATACATAAGGGTTCCATGTGAATACAAACACCATAATTTAGCTGTG
CGCGTAGAAGAATCAAGCAAAAACCCAAATTAAGTGGCGATTAAAGTGCTATAC
CAAGGCGGTAAAACAGAAATATTAGGAGTTGTTTTATCTGAGTATGGATCTCCCG
TTCGGATCGACATGCGCAGAAAATTTGGTGCTGTTTGGGAAACGGACAGAGCACC
GAAAGGGCCATTGCAGTTTGGATTTCCAATAGTACAAGGGTTTGATGTGAAGTGG
ATTTGGGCGAAGAACCCTGTTCCAGCTGACTGGAAGATTGGGGTACATATGACG
CTGGAGTTCAGATTACTGACGTTGATTTTACGGATGGTTGTGCTGAATGTGGTCTT
TGGAAGTGA

Nucleotide

>CisEXLA-01

ATGGCTATCTTGCTTTGCTTTCTCTTCTTTCTCTTATCATCTGCCACTGCTTGTGAT
CACTGTGTGCACCAATCCAAGGTTTCTACTTCTCCAAAACCTCCGCACTTTCAAG
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GACACATTGCTGCTGCTGTTCCATTTACAAAACGGAGCTGCCTGTGGTGGT
ACATGCTTTCAGGTGTGTATAAATTATAATATACCCTCATTCTTTTTCCCCCTTT
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ACTTCAACTTAATTGATTATTATTACTATAATTTTAATGTGCAGACTAAGAGA
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TGCGTTGAATTAATTGTTCAAGGGTCCATGTGAATACAAACACCATAATTTAGCT
GTGCGCGTAGAAGAATCAAGCAAAAACCCAAATTACTTGGCGATTAAGTGCTA
TACCAAGGCGGTAAAACAGAAATATTAGGAGTTGTTTTATCTGAGGTTAGTGACA
AAATTGAGAGAAGTCTGATTGGGTGTTTCTGGTGTATACACTCGCCGCAAAGTAA
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CAGTTTGGATTTCCAATAGTACAAGGGTTTGATGTGAAGTGGATTTGGGCGAAGA
ACCCTGTTCCAGCTGACTGGAAGATTGGGGTCACATATGACGCTGGAGTTCAGAT
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