

IDENTIFICATION

Species: *Citrus sinensis*

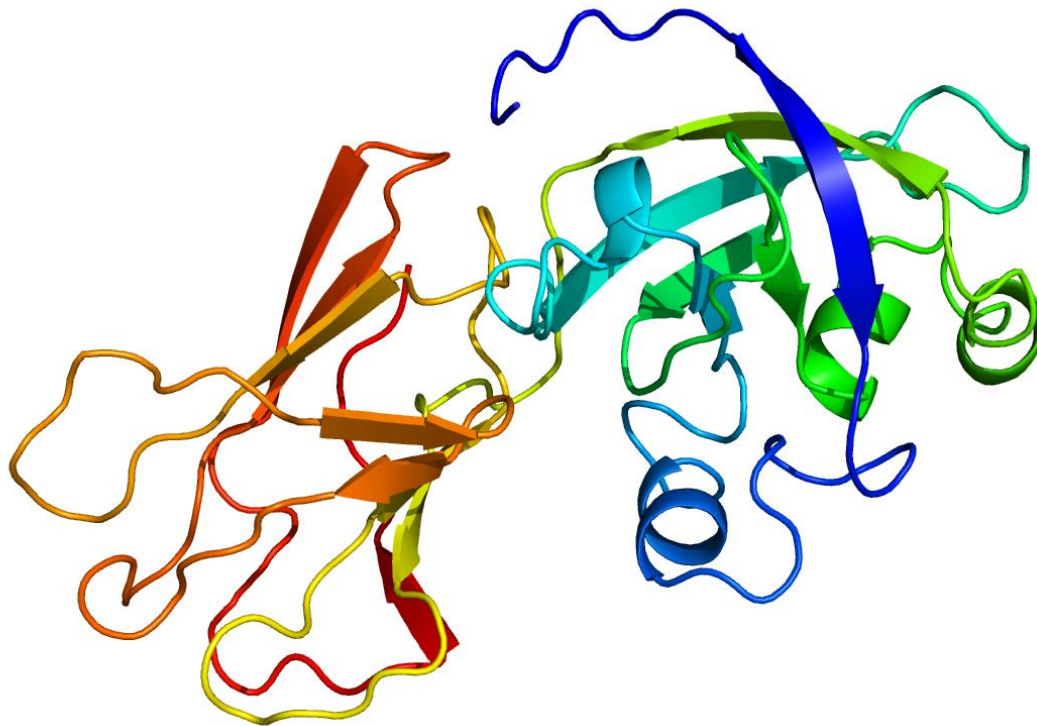
Locus: orange1.1g025837m

Gene Model: orange1.1g025837m

Description: CisEXLB-01

Family: Expansin Like Beta

3D structure:



GENOME DATABASES

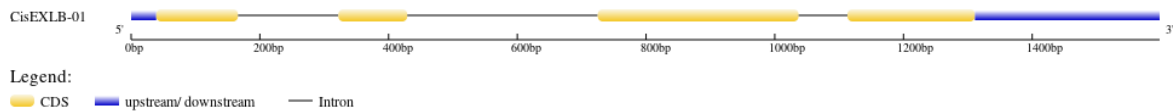
Phytozome: https://phytozome-next.jgi.doe.gov/info/Csinensis_v1_1

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

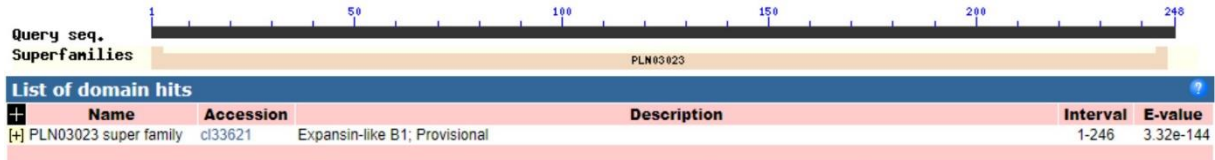
EXTERNAL RESOURCES

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

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>CisEXLB-01

MGLCQYYLLSVVM LLPALCYSQYSFTNSRATYYGSPDGLGTP TGACGFGGYGRNVN
DANVAGVSR LWNNGAGCGTCYQVRCTVPEICTDEGVSVVVTDY GEGDDTDFILSPR
AYGRMAVADKSEEL YSHGVVDVEFERVPCRFRGYNV MFKVHENSRY PQYLAVSML
YVSGQNDVLA VEIWQKDCRDWVPMRRAFGAVFDISNP SPGEINLRFQVSGSAGFTW
VVANNAIPRAWKAGVAYGSAIQLE*

CDS (coding sequence)

>CisEXLB-01

ATGGGGTTATGTCAACTACCTTCTTTCCGTCGTGATGCTTTTGCCTGCATTGTG
TTACTCTCAGTACTCATTCAAAATTCTAGAGCTACATACTATGGTAGCCCTGACG
GTTTGGGGACACCAACTGGTGCTTGC GGGTTTGGTGGATATGGAAGAAATGTA
TGATGCTAACGTGGCCGGTGTGTCGAGGCTTTGGAATAATGGAGCTGGTTGTGGA
ACTTGTTATCAGGTCAGATGCACTGTACCAGAAATTTGCACAGATGAGGGGGTGT
CCGTGGTGGT GACTGACTATGGTGAAGGAGACGACACAGACTTCATCCTCAGCCC
ACGCGCATATGGAAGAATGGCAGTTGCAGATAAGTCAGAAGAGCTTTATTCTCAT
GGTGTGTCGTCGACGTTGAATTCGAGAGAGTCCCTTGCCGGTTCAGAGGCTACAACG
TCATGTTCAAGGTCCATGAAAACAGCAGGTACCCACAGTACTTGGCCGTATCCAT
GCTGTACGTATCTGGCCAAAATGACGTCCTAGCAGTTGAAATATGGCAGAAGGAT
TGTCGAGACTGGGTGCCGATGAGAAGGGCTTTCCGGTGCAGTATTTGACATCTCTA
ATCCATCACCAGGAGAAATTAATTTGAGGTTTCAAGTGAGTGGCAGCGCGGGGTT
CACATGGGTTGTGGCAAACAATGCTATTCCCAGAGCATGGAAGGCTGGAGTTGCT
TATGGGTCAGCAATTCAGCTTGAATAA

Nucleotide

>CisEXLB-01

CTCCTTCG TACTGCTAACAAAGATTTTGATATTTTGCAAATGGGGTTATGTCAATA
CTACCTTCTTTCCGTCGTGATGCTTTTGCCTGCATTGTGTTACTCTCAGTACTCATT
CACAAATTCTAGAGCTACATACTATGGTAGCCCTGACGGTTTGGGGACACCAAGT
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AATCTTTTAGATTA ACTAATGTT CATGTTGATGATTCATCAGCTGGTGCTTGCGGG
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TTTGGAATAATGGAGCTGGTTGTGGA ACTTGTATCAGGTAATGGTTATTA ACTTT
CAACCCACTCAATCATTGCAGTTTATTGTAAAGCTATATAATAAATGTGTAAAGT
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CTGACTATGGTGAAGGAGACGACACAGACTTCATCCTCAGCCCACGCGCATATGG
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GTTGAATTCGAGAGAGTCCCTTGCCGGTTCAGAGGCTACAACGTCATGTTCAAGG
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ACTTCTAAACAATTGATTTTTTGGCCCGTCCATCGCATGTAATGCTTTTGTGGTGC
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GAGTTGCTTATGGGTCAGCAATTCAGCTTGAATAAATTTGAGATATCCCAAGCTT
TATTATTACTGGTTCCTGGTTATCAGCTTCTTAATGTCATTAAGGTATTCTAGTAT
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