

IDENTIFICATION

Species: *Citrus sinensis*

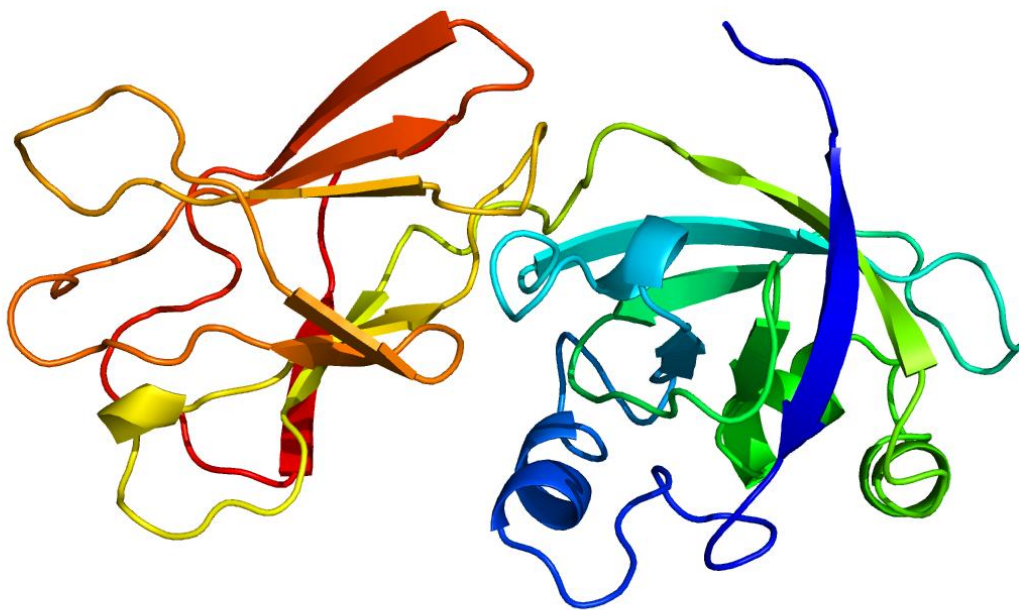
Locus: orange1.1g025808m

Gene Model: orange1.1g025808m

Description: CisEXLB-02

Family: Expansin Like Beta

3D structure:



GENOME DATABASES

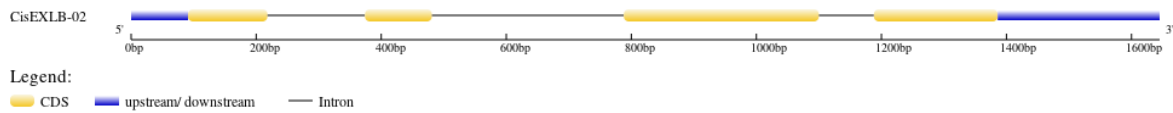
Phytozome: https://phytozome-next.jgi.doe.gov/info/Csinensis_v1_1

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

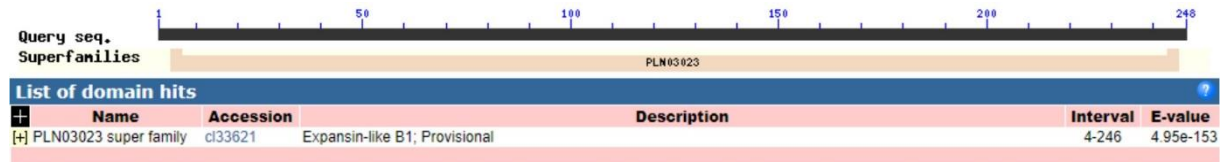
EXTERNAL RESOURCES

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

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>CisEXLB-02

MGLYQYYLLSVMLLLPALCYSHYTSTYSRATYYGSPDSLGTPTGACGFGEYGRTVN
DANVAGVSRWLKNGTGCGACYQVRCKVPQLCTDYGVYVVVTDYGECDKTDIFILSP
RAYGRMALPKSAELYSYGVVNVFRRVPCWYKGYNLQFKVHENSRYPHYLAAIL
YVAGQNDVLAVEIWQEDYQEWVAMRRAFGAVFDISSPPEGAI SLRFQVSGSAGLTW
VVANNAIPSDWKAGVAYESEIQLK*

CDS (coding sequence)

>CisEXLB-02

ATGGGGTTATATCAATACTACCTTCTTTCCGTCATGCTGCTTTTGCCTGCATTGTGT
TACTCTCATTACACATCCACATATTCTAGAGCTACATACTATGGTAGCCCTGATAG
TTTAGGGACACCAACTGGTGCTTGCGGGTTTGGTGAATATGGAAGAACTGTAAAT
GATGCTAACGTGGCCGGTGTGTCGAGGCTTTGGAAAAATGGAAGTGGTTGTGGAG
CTTGCTATCAAGTCAGGTGCAAGGTACCACAACCTTGCACAGATTATGGGGTGTA
CGTGGTGGTGACTGACTACGGTGAAGGAGACAAAACAGACTTCATCCTCAGCCC
GCGCGCATATGGAAGAATGGCACTTCCAGATAAGTCAGCAGAGCTCTATTCTTAT
GGTGTGGTCAACGTTGAATTCCGGAGAGTCCCTTGCTGGTACAAAGGCTACAACC
TTCAGTTCAAGGTCCATGAAAACAGCAGGTACCCACATTACTTGGCCATAGCCAT
TCTGTACGTAGCTGGCCAAAATGATGTCCTAGCAGTTGAAATATGGCAGGAGGAT
TATCAAGAATGGGTGGCAATGAGAAGGGCTTTCGGTGCAGTATTTGACATCTCTA
GTCCACCAGAAGGAGCAATTAGTTTGAGGTTTCAAGTGAGTGGCAGCGCGGGGC
TCACATGGGTGTGGCAAACAATGCTATTCCTAGCGATTGGAAGGCTGGCGTTGC
TTATGAGTCAGAAATTCAGCTTAAATAA

Nucleotide

>CisEXLB-02

GCCATTAACATTTGTTAGCAACCCATCTCATAACTTGTTATTATTCCTCTTCCTCCT
TCGTATTGCTAACAAAGATTTCCATATTTTGCAAATGGGGTTATATCAATACTACC
TTCTTTCCGTCATGCTGCTTTTGCCTGCATTGTGTTACTCTCATTACACATCCACAT
ATTCTAGAGCTACATACTATGGTAGCCCTGATAGTTTAGGGACACCAAGTACGTA
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ACTATTAGTTCATGTCATTATGACTTAGAGAATTTTTGTTTTTGTATATGTTTATAT
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AACTTCAGGTCAGGTGCAAGGTACCACAACCTTTGCACAGATTATGGGGTGTACGT
GGTGGTGACTGACTACGGTGAAGGAGACAAAACAGACTTCATCCTCAGCCCGCG
CGCATATGGAAGAAATGGCACTTCCAGATAAGTCAGCAGAGCTCTATTCTTATGGT
GTGGTCAACGTTGAATTCCGGAGAGTCCCTTGCTGGTACAAAGGCTACAACCTTC
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CATGTAATGCTTTTGTGGTGCAGGAGGATTATCAAGAATGGGTGGCAATGAGAA
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GAGGTTTCAAGTGAGTGGCAGCGCGGGGCTCACATGGGTTGTGGCAAACAATGC
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CTCCTTAATACTTAAGTGTGCTAAATAAATAGTGG