

IDENTIFICATION

Species: *Citrus sinensis*

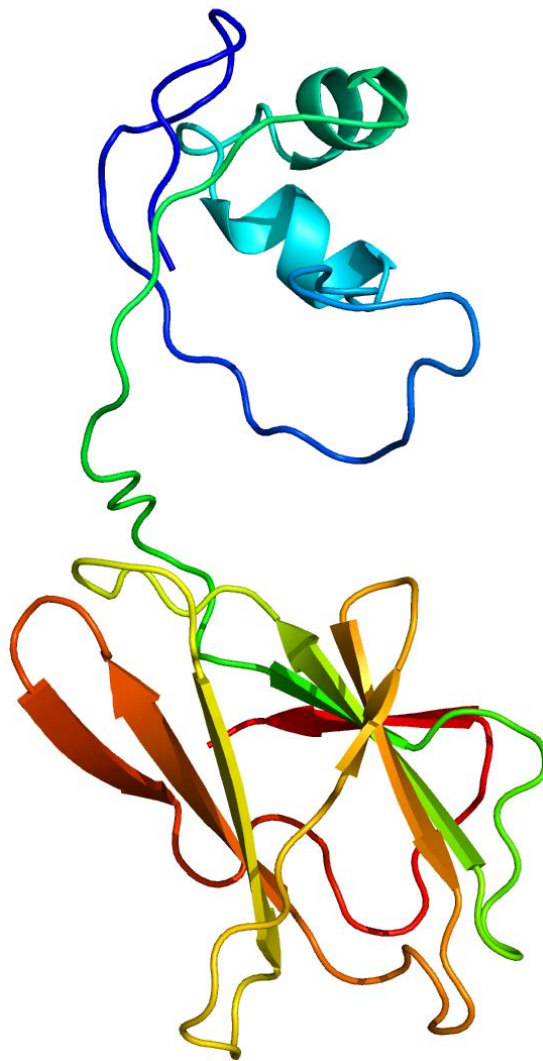
Locus: orange1.1g029804m

Gene Model: orange1.1g029804m

Description: CisEXLA-03

Family: Expansin Like Alpha

3D structure:



GENOME DATABASES

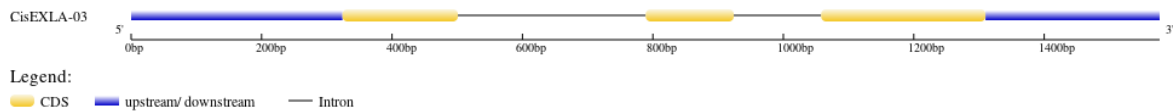
Phytozome: https://phytozome-next.jgi.doe.gov/info/Csinensis_v1_1

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

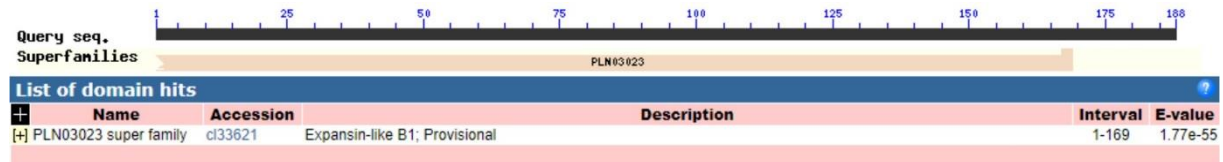
EXTERNAL RESOURCES

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

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>CisEXLA-03

MRCKNPTLCSGRGTRVILTDLNHSNQDFVISSRAFMALSNQGKGQDILKLGVV DVE
YKRVPC EYKNQNLAVRVEESSQKPNYLAVKVL YQGGQTEMVAMDVAQV GSSNWG
YMSRNYGAVW DTSRVPNGALQFRFVVTSGYD GKWIWAKNVLPADWKP GMIYNSG
VQITDIAKEGCSESECGDGSWK*

CDS (coding sequence)

>CisEXLA-03

ATGAGATGCAAGAACCCA AACTCTGTGTAGCGGCAGAGGAACCAGAGTGATTCTG
ACTGATCTCAATCACAGCAACCAAACAGATTTTGT TATCAGCAGCAGAGCTTTCA
TGGCCTTATCCAACCAGGGCAAGGGCCAAGACATTTTAAA AACTTGGAGTTGTCGA
TG TAGAATAACAAAAGGGTTCCATGTGAATATAAAA ACCAGA AACTTGGCTGTGCGT
GTGGAAGAATCAAGTCAAAAACCAAATTATTTAGCAGTTAAAGTGT TGTATCAGG
GTGGTCAAACAGAAATGGTAGCAATGGATGTAGCTCAGGTTGGTTCTTCAA AACTG
GGGTTACATGAGCAGAAATTATGGGGCAGTTTGGGATA CAAGTAGAGTGCCAAA
TGGGGCATTGCAGTTCAGATTTGTGGTAACATCAGGCTATGATGGCAAGTGGATT
TGGGCAAAAAATGTTCTTCCAGCTGATTGGAAACCTGGAATGATTTACA AACTCTG
GAGTTCAGATCACTGATATTGCCAAAGAGGGATGCTCCGAATCTGAATGTGGTGA
TGGAAGCTGGAAATGA

Nucleotide

>CisEXLA-03

ATGATCACTCTTTCGTA CTTTATTA AAAATCAAATTTGGCATTGACCCAGATGGTAT
TTTTGTAAGAATTTAAATGGGTAATATCTTTTTTTTGGTAAATTGATGCAGCCGGGG
CATGTGGATATGGTTCATTAGCATTAAAGCTTCAATGGTGGACACCTTGCTGCTGGT
GTTCCCTCCCTTTACAAAGATGGAGCTGGTTGTGGTGCATGCTTTCAAGTATGTAT
TATTAGCTTTCAATTTCA TTTTTCATTCTTTTGT TATTGATTGTGTTATCAA AATTG
GTTTTTCGAACTTAATTTGGGTACCAACATTTGTTTTGATCAGATGAGATGCAAGA
ACCAACTCTGTGTAGCGGCAGAGGAACCAGAGTGATTCTGACTGATCTCAATCA
CAGCAACCAAACAGATTTTGT TATCAGCAGCAGAGCTTTCATGGCCTTATCCAAC
CAGGGCAAGGGCCAAGACATTTTAAA AACTTGGAGTTGTTCGATGTAGAATAACAAA

AGGCAAGCAAATATTCTCAACTTCTCTATATTAATTGTTAATGCAGCATAGCTTAT
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CTATCCCTACCCCGGGACAAAATATCAGGCACACATTAATTGCTTATAACGGTCC
CAATTTGTATCTTATCGTAGACTAATCATACTAATAAATGCATTTGCTCTTCTGGG
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AAAATGAACACACATGATAAGTGCACATCATTTAGTTTACACGGCCCCAAAAGCC
TGGCGCAAATGTAGTTCAAAAACCGATGATGATTATGATTGCTGTTGCAAATTTT
GCAGGTTGGTTCTTCAAACCTGGGGTTACATGAGCAGAAATTATGGGGCAGTTTGG
GATACAAGTAGAGTGCCAAATGGGGCATTGCAGTTCAGATTTGTGGTAACATCAG
GCTATGATGGCAAGTGGATTTGGGCAAAAAATGTTCTTCCAGCTGATTGGAAACC
TGGAATGATTTACAACCTCTGGAGTTCAGATCACTGATATTGCCAAAGAGGGATGC
TCCGAATCTGAATGTGGTGATGGAAGCTGGAAATGAAAGAGATAAAGAGTTTGAT
TGCCACCACTACTTATTTATGTGAATACACATAAATTTTGATTTGATTTCTTTCAC
ATACAATCAGTATAATCAAATAACTTAGAGGATTAGAAAGTGAAGACGTATAGA
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TGTAACATTGTTCTTTTGCTGCTAAAGTAATAAATGCCCTATTGTTTCAGAATTC
TGTGTCTCTTTTCTCACTCTCGTTT