

IDENTIFICATION

Species: *Citrus sinensis*

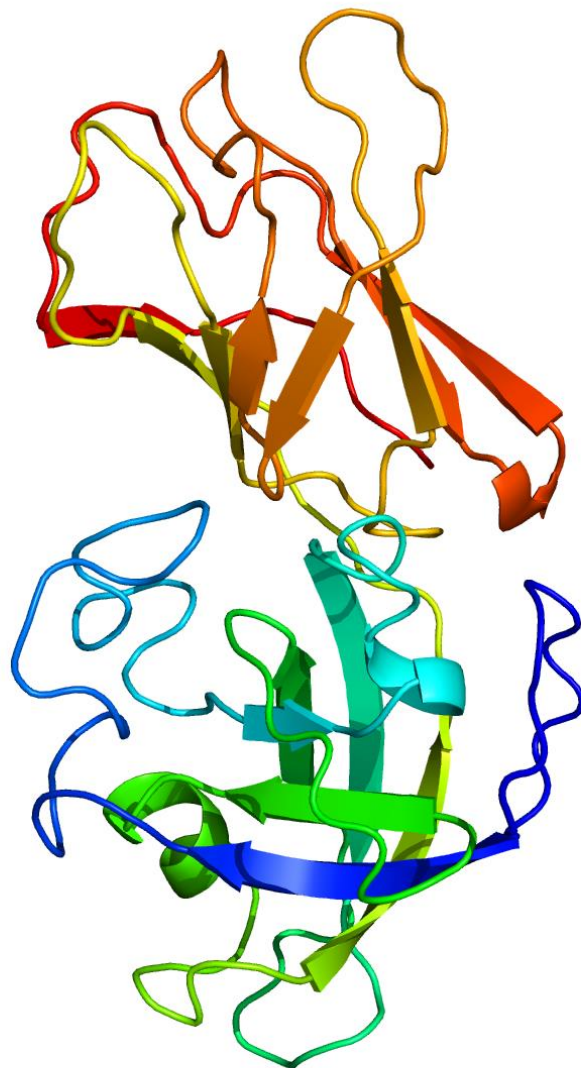
Locus: orange1.1g024520m

Gene Model: orange1.1g024520m

Description: CisEXPA-12

Family: Alpha Expansin

3D structure:



GENOME DATABASES

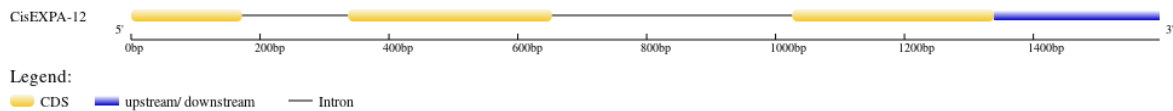
Phytozome: https://phytozome-next.jgi.doe.gov/info/Csinensis_v1_1

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

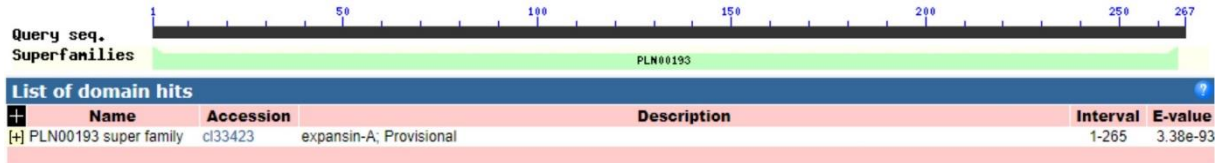
EXTERNAL RESOURCES

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

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>CisEXPA-12

MASFLRSFGFNFILVVLILAIAGKSNALGYTHPIFRPGPWRLAHATFYGDESASETMG
GACGYGNLFSNGYGTDTAALSSTLFNNGYACGTCYQIKCYNSPHCYKYVPFTT¹VTAT
NLCPPNWSQDSNNGGWCNPPRAHFDMSKPAFMKIGAWKAGIVPVLFRRVPCIKPGGI
RFAFQNGYWLLVYVMNVAGGGDIASMWVKGTRTGWISM²SHNWGASYQAFATLG
GQALSFKIQSYSTKETIIAYNVAPANWNVGLTYKSNVNFH*

CDS (coding sequence)

>CisEXPA-12

ATGGCTTCTTTTCTTCGATCATTTCGGATTTAACTTCATATTAGTTGTTTTGATTTG
GCAATCGCCGGGAAGTCAAACGCTTTGGGTTATACACATCCTATTTCCGGCCAG
GTCCATGGAGGCTTGCTCACGCCACCTTTTATGGCGATGAGTCTGCTTCCGAAAC
CATGGGAGGAGCTTGTGGGTATGGAACTTGT¹TTTCTAATGGTTACGGAACAGAC
ACAGCGGCTTTGAGCTCCACATTGTTCAACAATGGATACGCTTGTGGGACTTGTT
ACCAGATAAAGTGCTATAATTCGCCTCATTGCTATAAATATGTACCATTCACCAC
AGTTACAGCCACAAACCTCTGCCCGCCAAATTGGTCCCAGGACTCCAATAATGGA
GGCTGGTGCAATCCCCCTCGCGCCATTTTGATATGTCCAAGCCC²CGGTT³CATGA
AGATCGGCGCTTGGAAGGCCGGTATTGTCCCAGTCCTGTTTCGCAGGGTGCCATG
CATAAAGCCCGGTGGGATTCGATTTGCTTTCCAGGGAAATGGATACTGGTTGTTG
GTGTATGTGATGAATGTTGCAGGCGGCGGAGATATAGCCAGCATGTGGGTTAAG
GGAACCAGAACAGGATGGATTAGCATGAGCCATAACTGGGGAGCTTCATATCAA
GCATTTGCAACTCTGGGAGGCCAAGCTCTTTCTTTCAAGATCCAGTCATATTCAAC
CAAGGAGACTATTATAGCTTACAATGTTGCTCCTGCTAACTGGAACGTAGGATTG
ACTTACAAGTCAAATGTGAACTTCCATTAA

Nucleotide

>CisEXPA-12

ATGGCTTCTTTTCTTCGATCATTTCGGATTTAACTTCATATTAGTTGTTTTGATTTG
GCAATCGCCGGGAAGTCAAACGCTTTGGGTTATACACATCCTATTTCCGGCCAG
GTCCATGGAGGCTTGCTCACGCCACCTTTTATGGCGATGAGTCTGCTTCCGAAAC
CATGGGTACGTATATTTATACATATGCTCAATTCAATATTTTCAATTTAAAAATT

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ACTAGAATGATGTTACTGGATGTTAAATGTTCTTTTTCTCTGGACCATCTAATTAC
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GCGGCTTTGAGCTCCACATTGTTCAACAATGGATACGCTTGTGGGACTTGTTACC
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TCTTTCGAAGTTGTTAAGAGATATTACGACATGGAGTTTGAATTCATGACAATCTT
AGAGCTCTACTGAGGATGACTTGGAATATGTGCCAATTAGAGAGGAGAGACAT
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AGGACAGGGAACCTGAACCGGTGTGTCGAAGGCCACAGCCCAACGCTAAACAAC
AATTGAGCCTAAGTGGCGCGGAATTAATAATATTAAGGACAAGGGGAAAATGA
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ATAAACGGGAAGCATTTATGTATGTTTCGACCAGCTAATAAA