

IDENTIFICATION

Species: *Citrus sinensis*

Locus: orange1.1g041395m

Gene Model: orange1.1g041395m

Description: CisEXPA-05

Family: Alpha Expansin

3D structure:



GENOME DATABASES

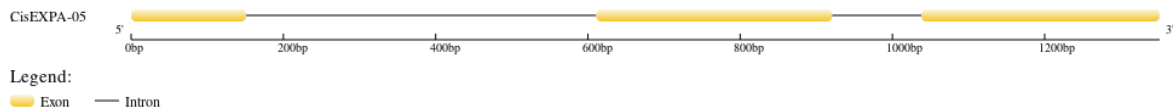
Phytozome: https://phytozome-next.jgi.doe.gov/info/Csinensis_v1_1

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

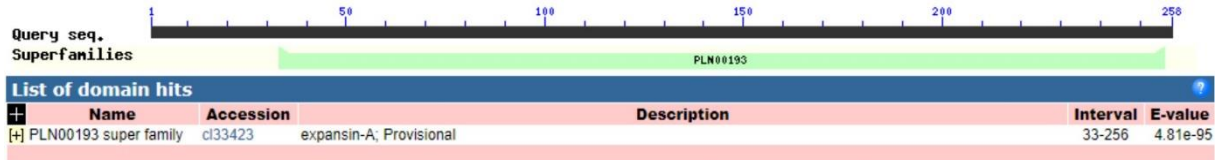
EXTERNAL RESOURCES

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

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>CisEXPA-05

MGPVVA VVPPRFWHFFLILSMGFV GINGQVNRWLNAHATYYGADQSPSTLGGACGY
DNTIHAGFGVNTAAVSGVLFRRGGQACGACYQLMCDYRADPKWCLR HATVTLTATN
FCPPNNHGGWCDPPRQHFDMSMPAFFRIARQNEGIVPILYKRVACKRRGGVHFTLK
GQSNFNMVMFSNVGGSGDLKGAWVRGSRTKTWIAMQRNWGANWSSSVDLRIQRL
SFKLTLVDGRTQLFFNVVPSSWSFGQTFSSRNQFY*

CDS (coding sequence)

>CisEXPA-05

ATGGGTCCAGTTGTTGCCGTTGTTCCCTCCTCGATTTTGGCACTTTTCTTGATTTTG
AGTATGGGTTTTGTGGGCATCAATGGCCAGGTTAACCGCTGGCTTAATGCTCATG
CTACTTACTATGGTGCTGATCAAAGCCCCTCCACTCTTGGAGGAGCTTGTGGGTAT
GATAACACAATCCACGCTGGATTCGGAGTGAACACAGCCGCCGTGAGTGGTGTTCC
TTTTCCGGGGCGGCCAAGCCTGCGGGCGCTTGCTACCAGTTGATGTGTGACTACAG
GGCCGACCCCAAGTGGTGTGTTGCGCCACGCCACGGTCACCTTGACAGCCACCAAC
TTCTGCCCTCCGAATAACCACGGGGGTTGGTGTGACCCTCCCCGCCAACATTTG
ACATGTCCATGCCCGCATTCTTCCGAATTGCACGACAAGGCAACGAAGGCATTGT
TCCATACTCTATAAAAGGGTGGCGTGCAAGAGGAGAGGGGGAGTGCATTTTAC
ATTGAAGGGGCAGTCAAATTTCAACATGGTGATGTTCTCAAACGTGGGGGGAAG
CGGGGACCTGAAGGGTGCATGGGTTAGAGGGTCAAGGACAAAGACATGGATAGC
CATGCAAAGAACTGGGGAGCTAATTGGTCCAGCAGCGTCGACCTTCGAATCCA
AAGATTGTCTTTAAGCTCACTTTGGTTGATGGAAGAACCCAATTGTTCTTCAATG
TTGTGCCTTCTTCTTGGAGTTTCGGCCAGACTTTTTCTTCCCGAAATCAGTTTTATT
AA

Nucleotide

>CisEXPA-05

ATGGGTCCAGTTGTTGCCGTTGTTCCCTCCTCGATTTTGGCACTTTTCTTGATTTTG
AGTATGGGTTTTGTGGGCATCAATGGCCAGGTTAACCGCTGGCTTAATGCTCATG
CTACTTACTATGGTGCTGATCAAAGCCCCTCCACTCTTGGTAAATATTCTAATTAA
TTATTTGCATCCACAACTAGTTATGCTTTTGTATTGTTACTTTCGTTATTATTTAA

TGGTGCAAAATTTATATATATATATAAATTATTTTCAAGTACGGCACCCCTCTATT
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TATATTATAAAATCGTGCAGTTTAAATAGTATTAGAATATGATTTTATAAAACCGC
ACGGCTTAAAAGTGTACTCGCATGAGGAAAATGAGAGACTCACACCAAAGAAGG
ATTATATATATATATATATAGTTTAAATTTATGTAAATATTTGGATTGATAATTCT
ATATCAATTAATTAAGTTTAGATTTATGAAAAATTCTATACGTACTTTGTGTGATC
ACATGGAAGGTGCACATCAATTTATTATAAACAATTTATGTAAATATTATTAGGA
GGAGCTTGTGGGTATGATAACACAATCCACGCTGGATTCGGAGTGAACACAGCC
GCCGTGAGTGGTGTCTTTTTCCGGGGCGGCCAAGCCTGCGGGCGCTTGCTACCAGT
TGATGTGTGACTACAGGGCCGACCCCAAGTGGTGTGTTGCGCCACGCCACGGTCAC
CTTGACAGCCACCAACTTCTGCCCTCCGAATAACCACGGGGGTTGGTGTGACCCT
CCCCGCCAACATTTTGACATGTCCATGCCCGCATTCTTCCGAATTGCACGACAAG
GCAACGAAGGCATTGTTCCCATACTCTATAAAAGGTAACCATAGAATATACGTTA
TATGTTATAGCTAATATCAAATTCGCATTTTAAAATGTGACGCACATCATTCATT
TTAGTAATCACGAAAGTAATAGCTTATGCATATTGCGTAGGGTGGCGTGCAAGAG
GAGAGGGGGAGTGCATTTACATTGAAGGGGCAGTCAAATTTCAACATGGTGAT
GTTCTCAAACGTGGGGGGAAGCGGGGACCTGAAGGGTGCATGGGTTAGAGGGTC
AAGGACAAAGACATGGATAGCCATGCAAAGAACTGGGGAGCTAATTGGTCCAG
CAGCGTCGACCTTCGAATCCAAAGATTGTCTTTAAGCTCACTTTGGTTGATGGAA
GAACCCAATTGTTCTTCAATGTTGTGCCTTCTTCTTGGAGTTTCGGCCAGACTTTTT
CTTCCCGAAATCAGTTTTATTAA