

IDENTIFICATION

Species: *Citrus sinensis*

Locus: orange1.1g025193m

Gene Model: orange1.1g025193m

Description: CisEXPA-17

Family: Alpha Expansin

3D structure:



GENOME DATABASES

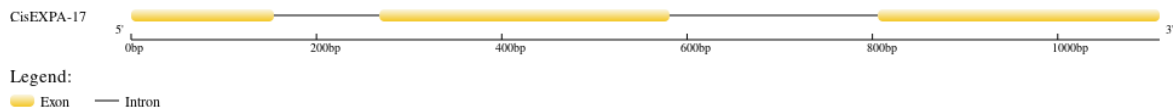
Phytozome: https://phytozome-next.jgi.doe.gov/info/Csinensis_v1_1

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

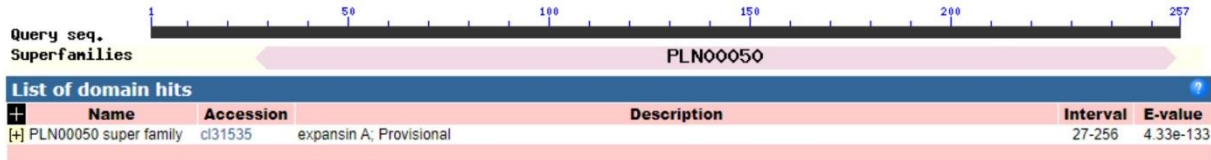
EXTERNAL RESOURCES

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

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>CisEXPA-17

MATKANAMKNFPFLVLFFFISIFVHAINGDYGGWQIAHATFYGGSDASGTMGGACG
YGNLYSQGYGTNTAALSTALFNGLSCGACYEIRCANDPQWCLPGTITVTATNFCPP
NYALSNDNGGWCNPPLQHFDLAQPSFLHIAQYRAGIVPVLFRRVPCVKKGGIRFTING
HSYFNLVLITNVGGAGDVKAVFIKGSKTGWQAMSRNWGQNWQSNLYLDGQSLSK
VTTSDGRITTSYNVVPANWKFGQTFEGSQL*

CDS (coding sequence)

>CisEXPA-17

ATGGCCACTAAAGCTAATGCCATGAAAACTTTCCATTTCTTGTTTTGTTCTTTTT
CATCAGCATTTTTGTTACGCTATAAATGGGGACTACGGTGGCTGGCAAATTGCA
CATGCCACATTTTATGGTGGCAGTGATGCCTCTGGCACAATGGGGGGAGCTTGTG
GGTATGGAACTTGTACAGCCAGGGTTATGGCACAAACACAGCAGCTCTAAGCA
CGGCTCTGTTCAACAATGGCTTGAGCTGCGGTGCATGCTATGAGATACGTTGCGC
CAATGATCCACAATGGTGCCTCCCTGGCACCATCACTGTGACTGCCACCAACTTTT
GCCCTCCTAATTATGCTTTGTCTAATGACAATGGCGGCTGGTGAATCCCCCTCTT
CAACATTTTGATTTGGCCCAGCCTTCTTTCTTGACATTGCACAATATCGAGCTGG
AATCGTACCCGTCCTCTTCAGAAGGGTACCATGTGTGAAGAAAGGGGGCATAAG
ATTCACCATCAATGGTCATTCATACTTTAACTTGGTTTTGATAACAAATGTGGGAG
GTGCTGGCGATGTGAAGGCTGTGTTCAAGGGGTCAAAAACAGGGTGGCAAG
CAATGTCCAGAAATTGGGGCCAAAATTGGCAGAGTAATTCTTACTTGGATGGCCA
AAGCCTCTCCTTTAAAGTTACCACAAGTGACGGAAGA ACTATTACCAGCTACAAT
GTTGTGCCTGCGAATTGGAAGTTTGGGCAGACTTTTGAAGGAAGTCAATTATAG

Nucleotide

>CisEXPA-17

ATGGCCACTAAAGCTAATGCCATGAAAACTTTCCATTTCTTGTTTTGTTCTTTTT
CATCAGCATTTTTGTTACGCTATAAATGGGGACTACGGTGGCTGGCAAATTGCA
CATGCCACATTTTATGGTGGCAGTGATGCCTCTGGCACAATGGGTGAGTTCTCATT
TTCATTTTCCATTTCTTTCCATAGCTAATAGGTATATATGTGTGTGCACTTAGTTA
TATGTATATATTAATGATTATTTACTTTATAATTAATTTCTAGGGGGAGCTTGTG

GGTATGGAAACTTGTACAGCCAGGGTTATGGCACAAACACAGCAGCTCTAAGCA
CGGCTCTGTTCAACAATGGCTTGAGCTGCGGTGCATGCTATGAGATACGTTGCGC
CAATGATCCACAATGGTGCCTCCCTGGCACCATCACTGTGACTGCCACCAACTTTT
GCCCTCCTAATTATGCTTTGTCTAATGACAATGGCGGGCTGGTGCAATCCCCCTCTT
CAACATTTTGATTTGGCCCAGCCTTCTTTCTTGACATTGCACAATATCGAGCTGG
AATCGTACCCGTCCTCTTCAGAAGGTATTTTTGTAGTTGCTTGCTCCAAAACTTA
AGCTGTCAGAACGAGTCCTTCAGGTAAAACCTAGACTTGATATTGTTCAAGTCTTT
CTATTATGATTTGAAACTAATGCTTGCAATCCAAGCAAGCACCCCAATTTCTTAA
ACATCGCTAAAATCAGTGTGTCGTCGTCATCATCATTATCATTATTATTATTATTGT
TCTTTAAATTTTTGGTTTTGTGATGCAGGGTACCATGTGTGAAGAAAGGGGGCATA
AGATTCACCATCAATGGTCATTCATACTTTAACTTGGTTTTGATAACAAATGTGGG
AGGTGCTGGCGATGTGAAGGCTGTGTTTCATCAAGGGGTCAAAAACAGGGTGGCA
AGCAATGTCCAGAAATTGGGGCCAAAATTGGCAGAGTAATTCTTACTTGGATGGC
CAAAGCCTCTCCTTTAAAGTTACCACAAGTGACGGAAGAAGTATTACCAGCTACA
ATGTTGTGCCTGCGAATTGGAAGTTTGGGCAGACTTTTGAAGGAAGTCAATTATA
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