

## IDENTIFICATION

**Species:** *Cicer arietinum*

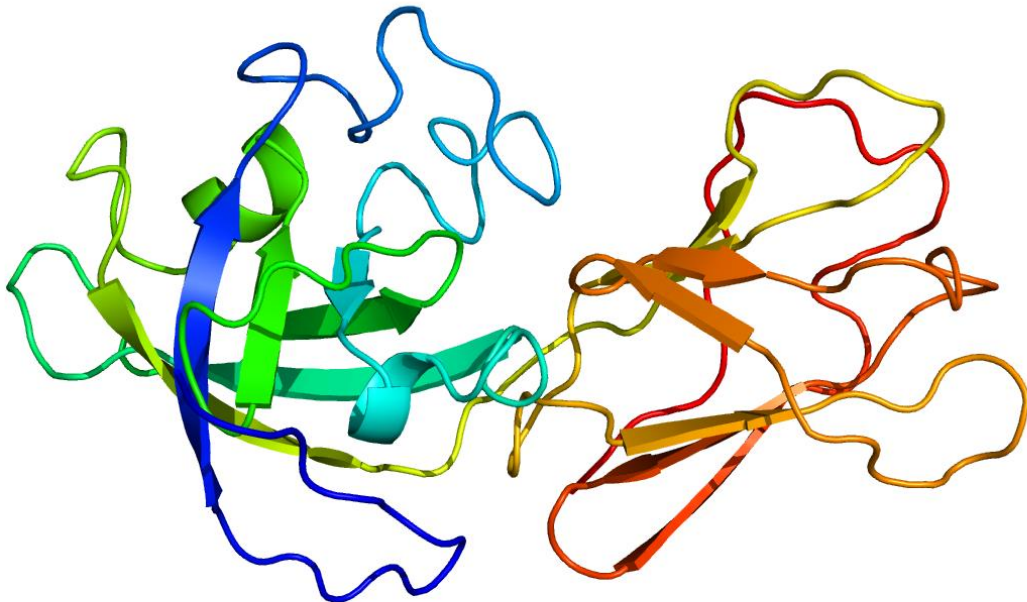
**Locus:** Ca\_14386

**Gene Model:** Ca\_14386

**Description:** CarEXPA-05

**Family:** Alpha Expansin

**3D structure:**



## GENOME DATABASES

Phytozome: [https://phytozome-next.jgi.doe.gov/info/Carietinum\\_v1\\_0](https://phytozome-next.jgi.doe.gov/info/Carietinum_v1_0)

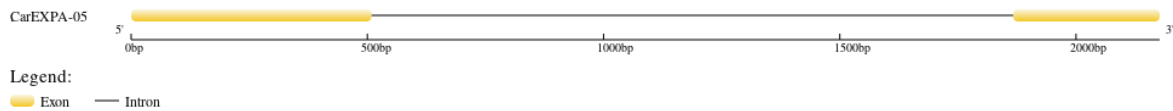
KEGG: <https://www.genome.jp/entry/T02819>

## EXTERNAL RESOURCES

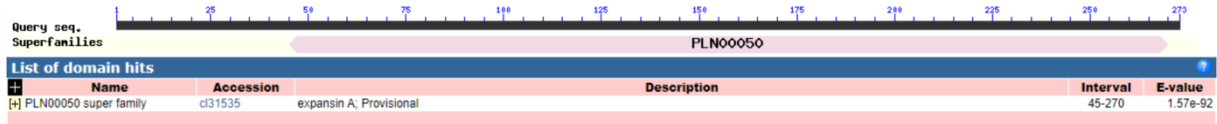
[https://www.pulsedb.org/bio\\_data/80](https://www.pulsedb.org/bio_data/80)

<http://www.cicer.info/databases.php>

## GENE STRUCTURE



## DOMAIN ARCHITECTURE



## SEQUENCES

### Peptide

>CarEXPA-05

MSLPSFFTTLTIFLITLTSTKKVTSHYSSSSSQPPYLQSSPSFTEWRSARATYYAADP  
RDTVGGACGYGDLTKAGYGMATVGLSESLFERGQICGACFELRCVEDMRWCLPGTS  
IIVTATNFCAPNYGFTSEGGGHCNPPNKHVFLPIDAFEKIAIWKAGNMPLQYRRIKCR  
REGGIRFTVTGSGIFVSVLISNVAGHGDIIAVKVKGSRTGWLPMGRNWGQNWHISAL  
LQNQPLSFEVTSSDGKTVTSYNVAPKDWSFGQTFEGKQFDT\*

### CDS (coding sequence)

>CarEXPA-05

ATGTCACTTCCTTCATTCTTCACAACATTAACAATCTTCCTCATTACACTAACATC  
AACAAAAAAGTAACCTCTCATTATTCCTCTTCATCTTCTCAACAACCACCTTATC  
TCCAATCCTCACCTTCCTTCACCGAATGGCGATCTGCACGCGCGACCTACTACGCT  
GCCGCGGATCCACGCGACACAGTAGGCGGCGCGTGTGGCTACGGCGACCTAACG  
AAAGCCGTTACGGCATGGCGACGGTAGGACTTAGTGAATCTTTGTTTCGAAAGAG  
GTCAGATCTGTGGCGCGTGCTTTGAATTACGGTGTGTGGAGGATATGCGGTGGTG  
TTTACCTGGAACCTTCGATTATTGTTACTGCGACTAATTTCTGTGCGCCGAACTATG  
GGTTTACGTCCGAGGGTGGTGGACATTGTAATCCTCCTAATAAGCATTTTGTTCTT  
CCTATTGATGCTTTTGAGAAGATTGCTATATGGAAAGCTGGTAACATGCCTCTTCA  
GTATCGTAGGATAAAGTGCAGAAGGGAAGGTGGAATTCGATTTACAGTCACTGG  
TTCTGGTATCTTCGTTTCAGTGCTGATCAGCAATGTTGCTGGCCACGGAGACATCA  
TTGCGGTGAAGGTTAAAGGCTCAAGAACAGGTTGGCTTCCAATGGGTCCGAATTG  
GGGTCAAACTGGCATATAAGCGCATTACTGCAGAATCAACCTCTTTCATTTGAG  
GTTACTAGTAGCGATGGGAAAACAGTTACGTCTTACAACGTTGCTCCCAAGGATT  
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### Nucleotide

>CarEXPA-05

ATGTCACTTCCTTCATTCTTCACAACATTAACAATCTTCCTCATTACACTAACATC  
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GATTTGTAAGATTATGAATATTTTAAAACATTACTCATATCGGTCCTTTAGATAGT  
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ATGTTCCACATCAAATGGATAGTAAATTATTAAGGGATATTGAAAGAGTTTTAAG  
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CAGCAATGTTGCTGGCCACGGAGACATCATTGCGGTGAAGGTTAAAGGCTCAAG  
AACAGGTTGGCTTCCAATGGGTCGGAATTGGGGTCAAACTGGCATATAAGCGC  
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