

## IDENTIFICATION

**Species:** *Cucumis sativus*

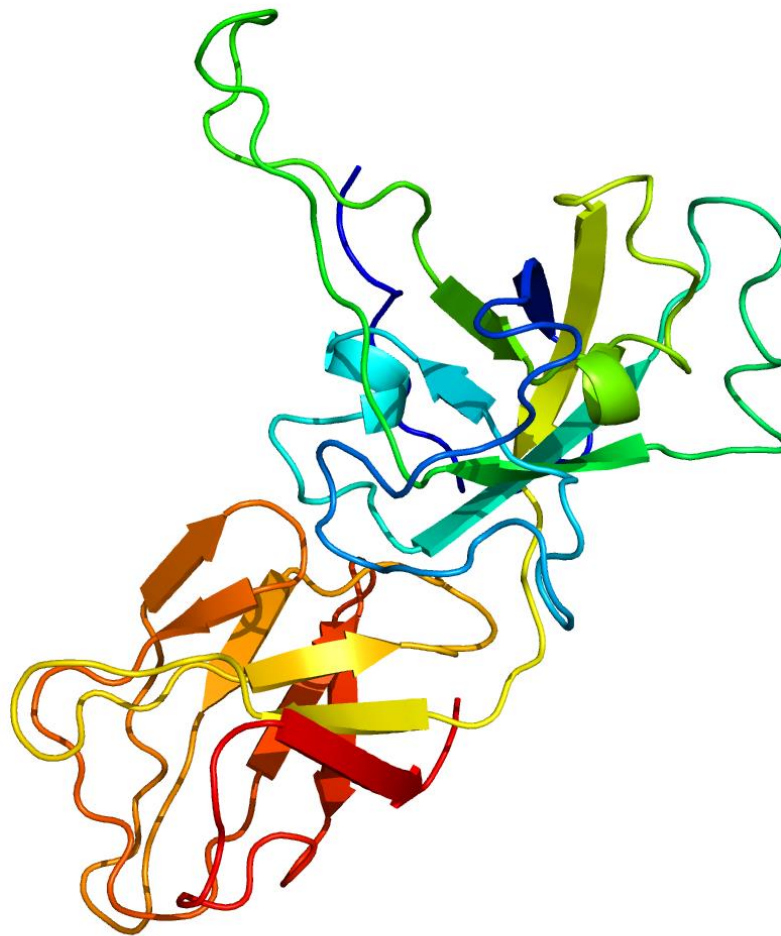
**Locus:** CsGy6G024340

**Gene Model:** CsGy6G024340.1

**Description:** CsEXPA-19

**Family:** Alpha Expansin

**3D structure:**



## GENOME DATABASES

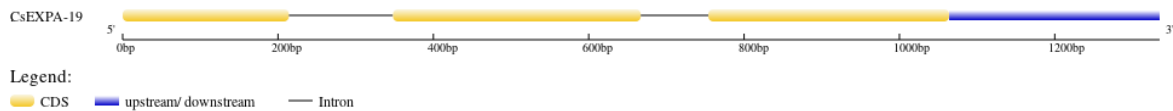
<http://cucurbitgenomics.org/>

KEGG: <https://www.genome.jp/entry/T02486>

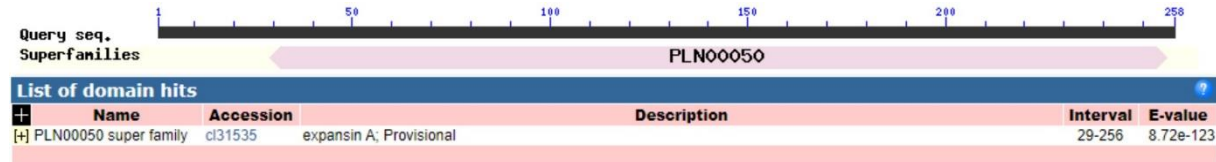
## EXTERNAL RESOURCES

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## GENE STRUCTURE



## DOMAIN ARCHITECTURE



## SEQUENCES

### Peptide

>CsEXPA-19

MQRVWGFLVIMLWLSIIGDATNLGATLKRAKRHRQLGEGATIHKQHRRPPFKPGPWN  
HAHATFYEGSGTFGAACGYEDVEKEGYGMQTAALSTALFNNGQSCGACYEIKCVD  
DPQWCKPGQPSLVVTGTNHCPPNHNLPNDNGGWCNPPLEHFDIAKPVFLNIAEFKAG  
IVPITYRRVPCCKGGGIRFTITGNPYYNQVLVWNVGGAGDLKSVQVKGHRKCLKWTS  
MSRSWGQKWITNAMLVGESLTFKVRASDGRFSTSWHVAPPTWQFGQTFEGKNFK

### CDS (coding sequence)

>CsEXPA-19

ATGCAAAGGGTATGGGGATTTTTGGTGATTATGTTGTGGCTAAGTATAATTGGGG  
ATGCAACAAATTTAGGAGCCACATTGAAACGTGCAAACGGCATAGGCAATTAG  
GAGAAGGGGCGACGATTATTAACAGCATCGTAGGCCGCCGTTTAAGCCCGGCC  
CTTGAACACGCTCATGCTACCTTCTATGAAGGTGGCTCCGGAACTTTTGGTGCT  
GCGTGTGGGTACGAAGACGTGGAAGGAAGGGTATGGGATGCAGACGGCGGC  
GCTGAGCACGGCGCTGTTCAACAACGGGCAGAGCTGCGGCGCTTGCTATGAAAT  
AAAATGCGTGGACGATCCCCAATGGTGAAGCCCGGGCAGCCTTCCCTAGTGGTG  
ACGGGTACCAACCACTGCCCGCCAATCACAACCTTCCTAATGACAACGGTGGAT  
GGTGAATCCCCACTCGAGCATTTCGACATTGCCAAGCCTGTTTTCTCAACATT  
GCTGAGTTCAAGGCTGGCATTGTCCCTATCACTACCGCAGGGTTCCATGCAAGA  
AAGGAGGAGGAATTCGATTTACAATAACTGGAAATCCATATTACAACCAAGTTTT  
AGTATGGAACGTGGGAGGAGCTGGAGATTTGAAGAGTGTCCAAGTGAAGGGTCA  
CCGTAAGCTCAAATGGACGTCCATGTCTCGTTCGTGGGGTCAAAAATGGATCACC  
AACGCCATGCTGGTTGGCGAGTCCCTCACCTTTAAGGTTTCGAGCCAGTGATGGCA  
GATTCTCCACTTCATGGCACGTTGCTCCCCCAACTTGGCAGTTTGGTCAGACCTTT  
GAAGGCAAAAACCTTTAAGTAA

### Nucleotide

>CsEXPA-19

ATGCAAAGGGTATGGGGATTTTTGGTGATTATGTTGTGGCTAAGTATAATTGGGG  
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CTTGGAACCACGCTCATGCTACCTTCTATGAAGGTGGCTCCGGAACTTTTGGTATG  
GATAAAAAGGATATATTCAATCTTAAATCTACCGTAACTCATCAGTCAATTAATA  
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TACCGCAGGTATGTTATACTGTGTTTTTCTTTTATCATACTTAGTTCAAGGTATGG  
TGTGAAAATAATTTTAGTGATTGTTGTTGTTATTATTAGGGTTCCATGCAAGAAAG  
GAGGAGGAATTCGATTTACAATAACTGGAAATCCATATTACAACCAAGTTTTAGT  
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TAAGCTCAAATGGACGTCCATGTCTCGTTCGTGGGGTCAAAAATGGATCACCAAC  
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GGCAAAAACTTTAAGTAAATCTAAATCACTTTGTTTCGCGTAATTCGTTCCATTTG  
ATAATCATTTTCATCTTTTGTCTTGATTTTTAAAACATTTTTTTGGGTTTTTTAAAAAC  
TTATTTCAAACAGTAAAACCTGCATAAGATATGTACAAAGCCTTAGTAAAATGTTA  
GAAAATCTATAAATGATAGATATGTATAGAGTAGATTTTTAAATTTGGGTATATT  
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AGTGGTTACCT