

IDENTIFICATION

Species: *Cucumis sativus*

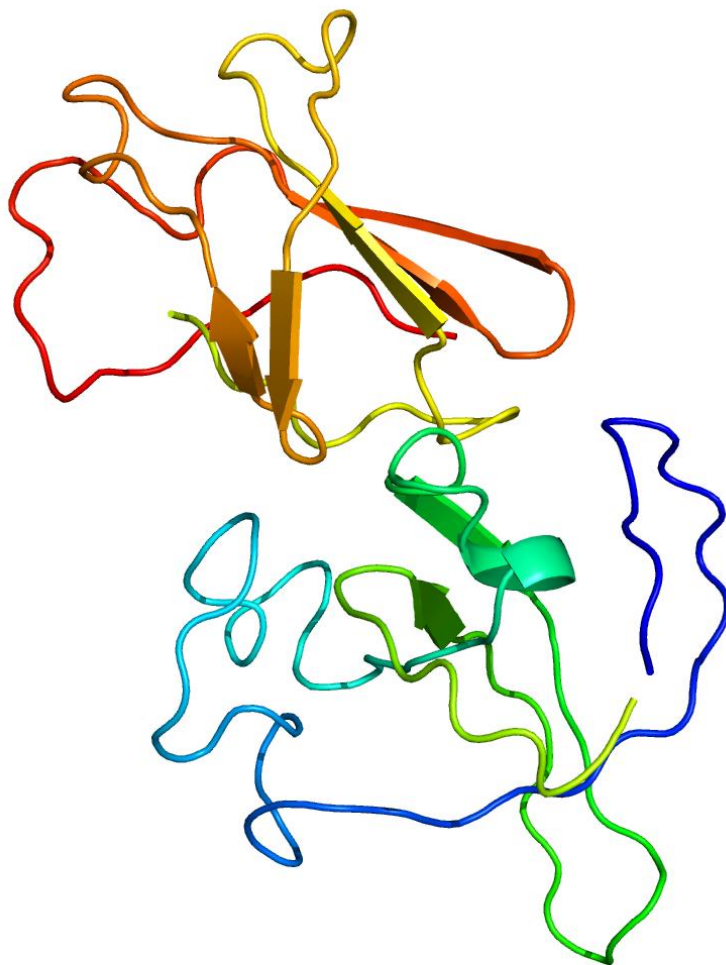
Locus: CsGy5G028430

Gene Model: CsGy5G028430.1

Description: CsEXPA-15

Family: Alpha Expansin

3D structure:



GENOME DATABASES

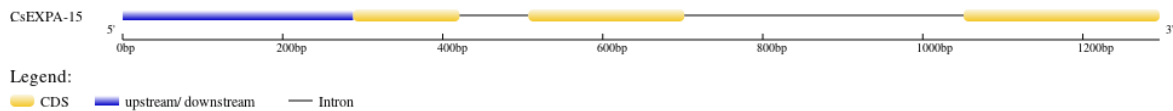
<http://cucurbitgenomics.org/>

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

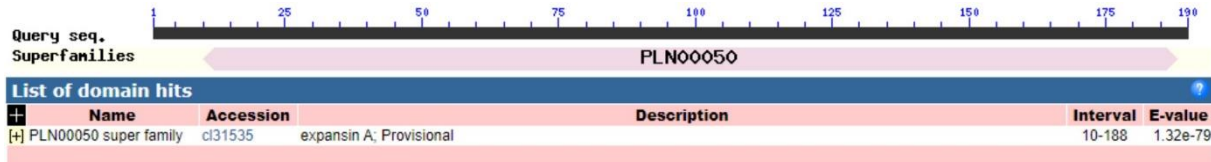
EXTERNAL RESOURCES

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GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>CsEXPA-15

MAIITTVLQLLLFFPIFSSVNGDYGGWISAHATFYGGSDASGTMGGACGYGNLYSQ
YGTNTAALSTALFDNGLSCGACFELRCVNDPQWCLPGTIVVTATNFCPPGGCLLITNV
GGAGDIHSVAIKGSKTRWQPMSRNWGQNWQNSYLNQSL SFLVTASDGRKVL SY
NVAPSGWSFGQTYVGGQFRY

CDS (coding sequence)

>CsEXPA-15

ATGGCAATCATAACAACAGTCCTCCAATTGCTTCTTTTTTTCCCAATCTTCTCCTCT
GTTAATGGAGATTATGGAGGTTGGATCAGCGCTCATGCCACTTTCTATGGTGGAA
GTGATGCTTCAGGAACAATGGGCGGCGCTTGTGGGTATGGGAATTTGTACAGCCA
AGGCTATGGGACGAACACTGCAGCGTTGAGCACGGCGCTTTTCGATAATGGACTC
AGTTGTGGCGCTTGTTTTGAGCTACGCTGTGTCAATGACCCTCAGTGGTGTCTTCC
TGGCACCATTGTTGTCACTGCCACTAATTTCTGTCCTCCTGGTGGCTGCTTACTAA
TCACAAACGTGGGGGGAGCCGGGGATATTCATTCGGTGGCGATTAAGGGTTCGA
AAACAAGATGGCAACCGATGTCTAGAAATTGGGGCCAAAACCTGGCAGTCCAATT
CTTATCTGAACGGACAAAGCCTCTCATTTTTGGTCACCGCCAGCGACGGCCGGAA
AGTCCTCTCCTACAACGTAGCTCCCTCCGGTTGGTCCTTTGGCCAAACTTATGTCG
GCGGCCAATTCGTTATTAA

Nucleotide

>CsEXPA-15

TTTTTTTTTATCAAAAATCATTTCGTAACATTTATGTGGTGGATTGATTGTAGAAA
ATAATAGAGCCGTCGTAGTCCGTAAAAAATGAGGGCAAGTCAGTAATTAACA
GAGAGATAATGATGTGATGAAACTTGGGGAAAAGTTGCCCCACACTTGAATTG
AGAATTAATTTACAAAACAAAAACACACAAATGAGTAAACGCGGTTTCAA
TTAAAATCACACACACACCACCCTCTATTTATTCCCATTTC AATCCTCACTTCTCTT
CTTCAATTTTTCAATGGCAATCATAACAACAGTCCTCCAATTGCTTCTTTTTTTCCC
AATCTTCTCCTCTGTTAATGGAGATTATGGAGGTTGGATCAGCGCTCATGCCACTT
TCTATGGTGGAAAGTATGCTTCAGGAACAATGGGTTTGTAATTTGCTCCCTTTTG

CTCTTTGTTTCCTCATTCTAATTCTAAATTGTTGTTTAATTTGTTGGTTTGTTTTAT
CACAGGCGGCGCTTGTGGGTATGGGAATTTGTACAGCCAAGGCTATGGGACGAA
CACTGCAGCGTTGAGCACGGCGCTTTTCGATAATGGACTCAGTTGTGGCGCTTGT
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GTGGAGGAATAAGATTCACAATCAACGGGCATTCATATTTCAACTTAGTACTAAT
CACAAACGTGGGGGGAGCCGGGGATATTCATTCGGTGGCGATTAAGGGTTCGAA
AACAAAGATGGCAACCGATGTCTAGAAATTGGGGCCAAAACCTGGCAGTCCAATTC
TTATCTGAACGGACAAAGCCTCTCATTTTTGGTCACCGCCAGCGACGGCCGGAAA
GTCCTCTCCTACAACGTAGCTCCCTCCGGTTGGTCCTTTGGCCAAACTTATGTCGG
CGGCCAATTCGTTATTAA