

IDENTIFICATION

Species: *Cucumis sativus*

Locus: CsGy1G002410

Gene Model: CsGy1G002410.1

Description: CsEXPA-01

Family: Alpha Expansin

3D structure:



GENOME DATABASES

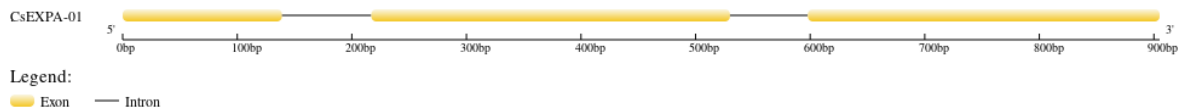
<http://cucurbitgenomics.org/>

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

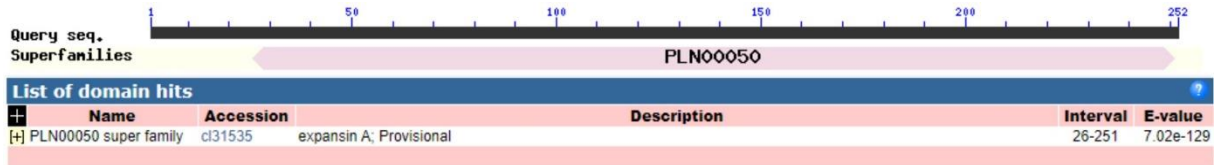
EXTERNAL RESOURCES

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GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>CsEXPA-01

MAFLGLLL VGLLLSLGCD SALANNNGGGWISAHATFYGGGDAAGTMGGACGYGNL
YSQGYGTNTAALSTALFNGLSCGACFEIKCVNDPKWCLQKSIVVTATNFCPPNNAL
PNNAGGWCNPPQHFDLSQPVFEQIAGYKAGIVPVAYRRVSCEKKGIRFTINGHSY
FNLVLVTNVGGGGDVHGVWIKGSKTGWEAMSRNWGQNWQSNSYLNQSLSFKVT
TGDGRTVISNDVAPAQWSFGQTFSGLQFR

CDS (coding sequence)

>CsEXPA-01

ATGGCGTTTCTTGGACTTCTCTTGGTGGGTCTTCTTCTATCTTTGGGATGTGATTCT
GCTCTTGCCAACAACAATGGAGGTGGTTGGATTAGTGCCCACGCCACATTCTACG
GTGGGGGTGACGCCGCTGGTACAATGGGAGGGGCTTGTGGCTATGGAAATCTGT
ACAGCCAGGGATATGGGACGAACACAGCAGCTCTGAGCACAGCTTTATTCAACA
ATGGACTGAGTTGCGGCGCTTGCTTTGAAATCAAATGTGTAAATGACCCAAAATG
GTGTCTTCAAAGTCCATTGTGGTTACTGCCACAACTTTTGTCCACCAAACAATG
CGCTCCCAAACAACGCCGGCGGCTGGTGTAAACCCTCCCAACACCATTTTCGATCT
CTCCCAACCCGTCTTCGAACAAATCGCTGGTTACAAAGCCGGCATTGTCCAGTG
GCATACAGAAGGGTATCTTGTGAGAAGAAAGGAGGCATTAGATTCACAATCAAT
GGTCATTCGTA CTTCAATTTAGTCCTTGTAAACCAACGTTGGTGGAGGTGGGGATG
TTCATGGAGTGTGGATTAAAGGGTCGAAAACAGGGTGGGAAGCAATGTTCGAGGA
ATTGGGGACAGAATTGGCAGAGCAATTCATATCTGAATGGACAAAGCTTATCGTT
CAAAGTGACCACCGCGATGGCAGAACAGTGATATCCAACGACGTAGCGCCAGC
TCAGTGGAGCTTTGGTCAAACCTTTAGTGGGTTGCAGTTCCGATGA

Nucleotide

>CsEXPA-01

ATGGCGTTTCTTGGACTTCTCTTGGTGGGTCTTCTTCTATCTTTGGGATGTGATTCT
GCTCTTGCCAACAACAATGGAGGTGGTTGGATTAGTGCCCACGCCACATTCTACG
GTGGGGGTGACGCCGCTGGTACAATGGGTATGTGAAAAGATTTATACTTGTGCAT
TTATTGAACGTCACAACCGTAGCCTTTAACGACGGACTTTCTTTTTGCAGGAGGG
GCTTGTGGCTATGGAAATCTGTACAGCCAGGGATATGGGACGAACACAGCAGCT

CTGAGCACAGCTTTATTCAACAATGGACTGAGTTGCGGCGCTTGCTTTGAAATCA
AATGTGTAAATGACCCAAAATGGTGTCTTCAAAAGTCCATTGTGGTTACTGCCAC
AACTTTTGTCCACCAAACAATGCGCTCCCAAACAACGCCGGCGGCTGGTGTAAAC
CCTCCCCAACACCATTTTCGATCTCTCCAACCCGTCTTCGAACAAATCGCTGGTTA
CAAAGCCGGCATTGTCCCAGTGGCATAACAGAAGGTACTGACTGATTTTGTAAAGT
TAAACACTATAACTGAAACAGAGACTGAGCAAATAACCAATGCAGGGTATCTT
GTGAGAAGAAAGGAGGCATTAGATTCACAATCAATGGTCATTCGTACTTCAATTT
AGTCCTTGTAACCAACGTTGGTGGAGGTGGGGATGTTTCATGGAGTGTGGATTA
GGGTCGAAAACAGGGTGGGAAGCAATGTCGAGGAATTGGGGACAGAATTGGCAG
AGCAATTCATATCTGAATGGACAAAGCTTATCGTTCAAAGTGACCACCGGCGATG
GCAGAACAGTGATATCCAACGACGTAGCGCCAGCTCAGTGGAGCTTTGGTCAA
CTTTTAGTGGGTTGCAGTTCCGATGA