

IDENTIFICATION

Species: *Cucumis sativus*

Locus: CsGy6G002200

Gene Model: CsGy6G002200.1

Description: CsEXPA-16

Family: Alpha Expansin

3D structure:



GENOME DATABASES

<http://cucurbitgenomics.org/>

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

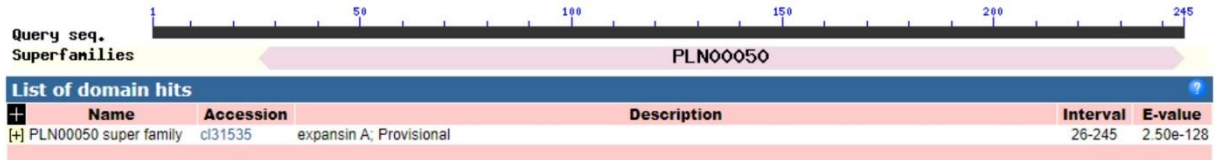
EXTERNAL RESOURCES

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GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>CsEXPA-16

MAPSSLLSSLSVFFLIFLPSISADYGHATFYGGGDASGTMGGACGYGNLYSQGYGTNT
AALSTALFNGLSCGSCYEITCNSDPKWCLPGKIIVTATNFCPPNFALSNDNGGWCNP
PLQHFDLAEP AFLQIAQYRAGIVPVSFQRVPCMKKGGIRFTINGHSYFNLVLITNVGG
AGDIHSVSIKSGKTGWQAMSRNWGQNWQSNLYLNGQSLSFQVTTSDGRTVTSYDA
VPGNWQFGQTFEGGQF

CDS (coding sequence)

>CsEXPA-16

ATGGCTCCTTCATCACTACTCTTCTCTTTCTGTTTTCTTCCTCATTTCCTTCCTT
CAATCTCTGCCGATTACGGCCACGCCACCTTCTACGGCGGTGGTGACGCTTCTGG
CACAATGGGTGGAGCTTGTGGGTATGGGAATTTGTACAGTCAAGGATATGGAAC
GAACACGGCGGCGCTTAGTACTGCTCTCTTCAACAATGGTCTCAGCTGTGGCTCTT
GCTATGAAATCACTTGCAACAGTGATCCTAAATGGTGTCTTCCCGGAAAAATCAT
CGTCACCGCCACTAATTTCTGTCCACCAAACCTTTGCTCTGTCCAACGACAATGGCG
GCTGGTGAACCCTCCTCTTCAACACTTTGATTTGGCTGAGCCTGCCTTTCTCCAA
ATCGCTCAGTACCGTGCCGGAATCGTTCCTGTTTCTTTCCAAAGAGTACCCTGTAT
GAAGAAGGGAGGAATAAGATTCACCATTAACGGACATTCATACTTCAACTTAGTT
CTAATCACCAATGTGGGCGGCGCCGGAGACATCCATTCGGTGTCAATCAAAGGTT
CGAAAACAGGGTGGCAAGCGATGTCAAGAAATTGGGGTCAGAATTGGCAGAGCA
ACAATTACTTGAATGGACAGAGCCTCTCTTCCAAGTCACCACCAGCGACGGCCG
TACCGTCACTAGCTACGACGCCGTTCCGGGGAAC TGGCAGTTCGGTCAGACGTT
GAGGGAGGCCAATTCTAA

Nucleotide

>CsEXPA-16

CTCCACCACAATTATAGCCAACTTGTACTTTTCTTCAACTGCTTTCTTTTCCCCTCT
ATTTAAATAACACCCTCTCTTCTATTCTTCCCACTCCCCACTACAAACCCTTCA
CTACAAAACCTTAAACCTTCTTCTCCCATGGCTCCTTCATCACTACTCTCTTCTC
TTTCTGTTTTCTTCCTCATTTCCTTCCCTTCAATCTCTGCCGATTACGGCCACGCCA
CCTTCTACGGCGGTGGTGACGCTTCTGGCACAATGGGTAAACTAACTAATCAAAC

TATCCATCTTCCTTTCTTCACTTTCAACCATCAACTTCAGATTTTTAACCCTTCACT
ATTTTACGATTTCAATTCTTACTTTCTCTTCCATTAACGTTTTACTCATTTGCTTTG
GGTCATTTGTATTTAAGATTACCAGAGATTGTAGATTCAAGTTGCTCCATTGTTA
CTTCTCTCTAGTTAATATCCATTTTGTTTTTCTGGTCAATGGGTGATTTATGATCG
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CTTGTGGGTATGGGAATTTGTACAGTCAAGGATATGGAACGAACACGGCGGCGCT
TAGTACTGCTCTCTTCAACAATGGTCTCAGCTGTGGCTCTTGCTATGAAATCACTT
GCAACAGTGATCCTAAATGGTGTCTTCCCGGAAAAATCATCGTCACCGCCACTAA
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CTCTTCAACACTTTGATTTGGCTGAGCCTGCCTTTCTCAAATCGCTCAGTACCGT
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TAATAACAGACTGAAACCATCCTCTTTTCTTTAACCAATTTCTTCGATTAATAACA
GACTAAAACCATCCTCTTTTCTTTTCTTTTCTTTTCTTTTCTTGTCTCATCTCTGATTTT
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CGGACATTCATACTTCAACTTAGTTCTAATCACCAATGTGGGCGGGCGCCGGAGAC
ATCCATTCGGTGTCAATCAAAGGTTGAAAACAGGGTGGCAAGCGATGTCAAGA
AATTGGGGTCAGAATTGGCAGAGCAACAATTA CTGAATGGACAGAGCCTCTCTT
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GAACTGGCAGTTCGGTCAGACGTTTCGAGGGAGGCCAATTCTAAAAAGAAGCTCA
GAGAGGGTAAAACACAGGGTAGAGTAGGAAGATCTCCGGGCGCCCTCGTTTCGG
TGGCCGGCTATGGCAGTGGTGGTTGACTCACACCCGCTAGGTCTTTGGGATTTAA
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