

IDENTIFICATION

Species: *Cucumis sativus*

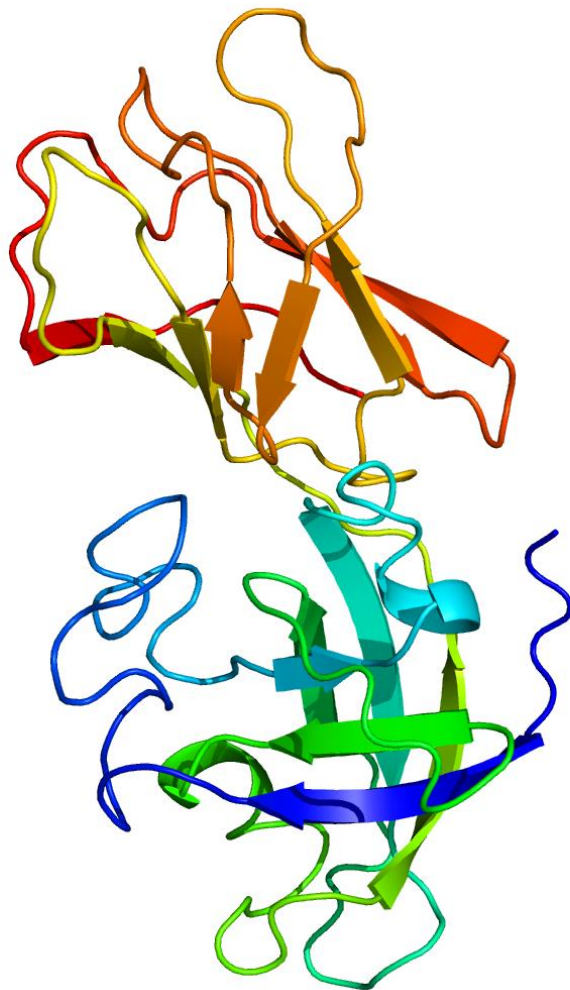
Locus: CsGy3G003370

Gene Model: CsGy3G003370.1

Description: CsEXPA-06

Family: Alpha Expansin

3D structure:



GENOME DATABASES

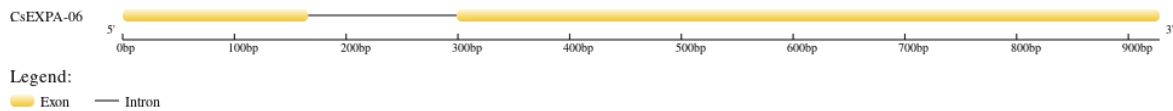
<http://cucurbitgenomics.org/>

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

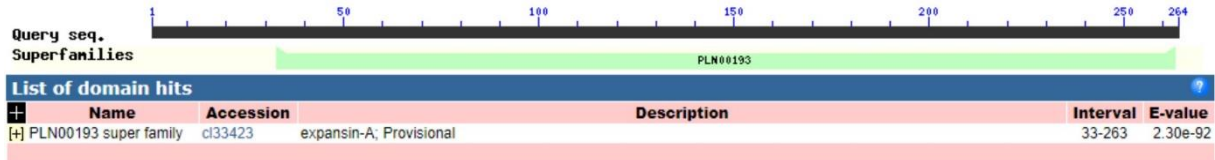
EXTERNAL RESOURCES

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GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>CsEXPA-06

MASHFPRYSLVLTIFFLSFTMPEMTTKSVLAIFRPSWKLAHATFYGDETASETMGGA
CGYGNLFTNGYGVDTAALSSTLFNNGYACGTCFQIKCAQSKACYSNVAFTT⁵⁰VTATN
LCPPNWA¹⁰⁰KPSDNGGWCNPPRVHFDMSKPAFMKIANWKAGIVPVAYRRVPCGKKGG
LRFTLQNGNGYWLLAYVMNVGGGGDVSGMWVKGSKTGWIKMSHNWGASYQAFST
LVGQSLSF¹⁵⁰RITSYTTKETIIAWNVAPSSWRFGSTYNTNVNFR²⁰⁰

CDS (coding sequence)

>CsEXPA-06

ATGGCTTCCCATTTCCTCGTTATAGTCTTGTCCTCACCATCTTTTTCTTGTCCTTT
ACAATGCCGGAGATGACA⁵⁰ACTAAATCTGTCTCGCCATCTTCCGACCAAGTCCTT
GGAAGCTCGCCCATGCCACCTTCTATGGGGATGAGACTGCATCTGAGACAATGGG
AGGAGCGTGTGGTTATGGAACTTGTTCA¹⁰⁰AAATGGGTATGGCGTTGATACGGCG
GCTCTAAGCTCTACACTCTTCAACAACGGCTACGCTTGTGGA¹⁵⁰ACTTGCTTTCAAAT
CAAATGTGCTCAATCCAAAGCTTGTTACTCTAATGTTGCTTTCACGACGGTGACTG
CCACCAACCTTTGCCCCCAAATTGGGCTAAACCTTCGGACAACGGCGGATGGTG
CAACCCTCCAAGGGTTC²⁰⁰ACTTCGACATGTCGAAGCCAGCCTTTATGAAGATCGCC
AATTGGAAGGCTGGGATCGTCCCCGTCGCGTACCGACGTGTCCCATGCGGTA²⁵⁰AAA
AAGGTGGCCTTCGGTTCACATTACAAGGAAATGGCTACTGGCTTTTGGCGTACGT
GATGAATGTCGGTGGCGGCGGACGTGTCGGGAATGTGGGTGAAAGGGAGCAA
AACAGGGTGGATCAA³⁰⁰AATGAGCCATAATTGGGGAGCTTCATATCAAGCCTTTTCA
ACTTTGGTTGGCCAATCTCTCTTTT³⁵⁰AGAATCACTTCTTACACAACCAAAGAGAC
CATCATAGCTTGGAACGTTGCTCCATCTAGTTGGAGGTTTGGTTCGACCTACAAC
ACCAACGTCAACTTCGGTTGA⁴⁰⁰

Nucleotide

>CsEXPA-06

ATGGCTTCCCATTTCCTCGTTATAGTCTTGTCCTCACCATCTTTTTCTTGTCCTTT
ACAATGCCGGAGATGACA⁵⁰ACTAAATCTGTCTCGCCATCTTCCGACCAAGTCCTT
GGAAGCTCGCCCATGCCACCTTCTATGGGGATGAGACTGCATCTGAGACAATGGG
TATCTAGACTTCTTTCATGATTTGTGTTTCTAGTGATTAAGTTTTCAA¹⁰⁰ACTCTATAT

ATACAACCTGTTTTAAAACCTTCAATAATCAATGACATATTTACTTAACATCATCG
ATCCAAACATTATTTTCAGGAGGAGCGTGTGGTTATGGAAACTTGTTACAAATG
GGTATGGCGTTGATACGGCGGCTCTAAGCTCTACACTCTTCAACAACGGCTACGC
TTGTGGAACCTTGCTTTCAAATCAAATGTGCTCAATCCAAAGCTTGTTACTCTAATG
TTGCTTTCACGACGGTGACTGCCACCAACCTTTGCCCCCAAATTGGGCTAAACCT
TCGGACAACGGCGGATGGTGCAACCCTCCAAGGGTTCACTTCGACATGTCGAAGC
CAGCCTTTATGAAGATCGCCAATTGGAAGGCTGGGATCGTCCCGTTCGCGTACCG
ACGTGTCCCATGCGGTAAAAAAGGTGGCCTTCGGTTCACATTACAAGGAAATGGC
TACTGGCTTTTGGCGTACGTGATGAATGTCGGTGGCGGGCGGCGACGTGTCGGGAA
TGTGGGTGAAAGGGAGCAAAACAGGGTGGATCAAAATGAGCCATAATTGGGGAG
CTTCATATCAAGCCTTTTCAACTTTGGTTGGCCAATCTCTCTCTTTTAGAATCACTT
CTTACACAACCAAAGAGACCATCATAGCTTGGAACGTTGCTCCATCTAGTTGGAG
GTTTGGTTCGACCTACAACACCAACGTCAACTTCCGTTGA