

IDENTIFICATION

Species: *Gossypium raimondii*

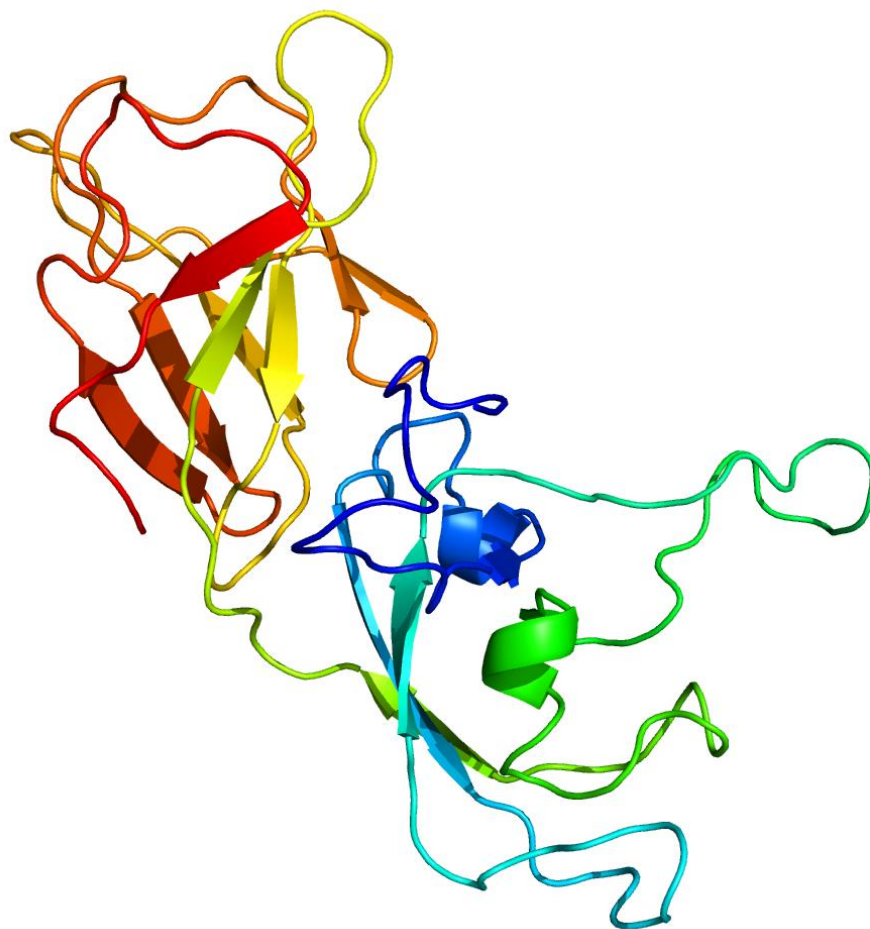
Locus: Gorai.001G148900

Gene Model: Gorai.001G148900.2

Description: GrEXPA-05

Family: Alpha Expansin

3D structure:



GENOME DATABASES

Phytozome: https://phytozome-next.jgi.doe.gov/info/Graimondii_v2_1

Kegg: <https://www.genome.jp/entry/T04129>

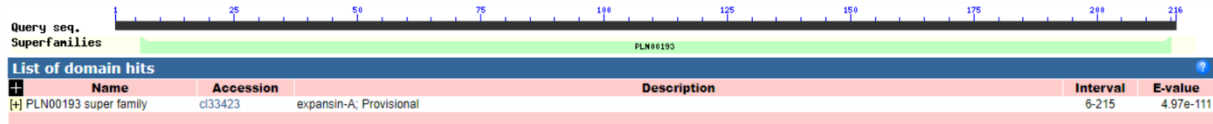
EXTERNAL RESOURCES

https://www.cottongen.org/species/Gossypium_raimondii/jgi_genome_221

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>GrEXPA-05

MLVFPGGACGYGNLFTDGYGTSSAAVSTVLFNNGKSCGGCYRIVCDAKNAPQWCV
KGKSITITATNFCPPNYALPSDTGGWCNPPRPHFDMSQPAFETIAKYKAGIVPILYRKV
TCRRSGGIRFTINGRNYFQLVLISNVGGAGEINKVWVKGSRSNKWEAMSRNWGAKW
QSLSYLSGQSLSFKIQAGNGRKAALNVVPSGWQFGQSFKSNVQF*

CDS (coding sequence)

>GrEXPA-05

ATGTTGGTTTTCCAGGAGGAGCTTGTGGTTATGGCAATCTCTTTACAGATGGTTA
TGGAACAAGCTCAGCTGCAGTTAGCACAGTTTTGTTTAATGGTGGAAAGTCATGT
GGAGGCTGCTATCGAATAGTTTGTGATGCCAAAAATGCACCCCAATGGTGTGCA
AGGGTAAATCTATTACCATCACCGCCACCAACTTCTGTCCTCCCAACTATGCACTC
CCAAGTGACACTGGTGGTTGGTGTAAATCCTCCCCGACCACACTTCGACATGTCTC
AACCTGCGTTTGGAGACCATAGCCAAATACAAAGCTGGAATTGTACCAATCCTCTA
CAGGAAGGTTACATGCAGGAGAAGTGGGGGCATTAGATTCACCATCAACGGAAG
GAACTATTTTCAGCTAGTTCTGATATCAAACGTTGGGGGTGCTGGAGAGATTAAC
AAGGTATGGGTAAAGGGATCCAGAAGCAATAAATGGGAAGCAATGTCGAGAAAT
TGGGGTGCCAAATGGCAGAGCTTAAGCTATCTAAGCGGCCAGAGCTTATCCTTCA
AGATCCAAGCCGGCAACGGAAGGACTAAAGCCGCTCTTAATGTGGTACCTTCCGG
TTGGCAATTTGGTCAGTCCTTCAAAGCAACGTGCAGTTTTAG

Nucleotide

>GrEXPA-05

AAACTCATTCTTAGCTCTACGCGCATTACCATTGAAAAGAAACAATCCTTTTTGTTT
TTAGAGGAAAGGGAGAAAAGAAATAGAATAATGGAGAGTTCCTATCAATTCACCT
ACTGCGATACTCCTTGTGGGTTTATATTTTTCCACTAGATTTAACATAGCAGAAAC
TGCACCAGTTTGGTTCCAGCCCATGCAACATTCTATGGTGGGGTTGATGCTTCTG
GTACAATGGGTAAAGTTTAAACAACCTTTTTCTTCTCCTCCTCATTGTGCTGATCTCAAT
TCATATAATTTATTTTCTATAAAAGAGCTGTTGATCTTGAACAGATGATTATTGAT
TACCATGTTGGTTTTCCAGGAGGAGCTTGTGGTTATGGCAATCTCTTTACAGATG
GTTATGGAACAAGCTCAGCTGCAGTTAGCACAGTTTTGTTTAATGGTGGAAAGTC
ATGTGGAGGCTGCTATCGAATAGTTTGTGATGCCAAAAATGCACCCCAATGGTGT
GTCAAGGGTAAATCTATTACCATCACCGCCACCAACTTCTGTCCTCCCAACTATGC
ACTCCCAAGTGACACTGGTGGTTGGTGTAAATCCTCCCCGACCACACTTCGACATG

TCTCAACCTGCGTTTGAGACCATAGCCAAATACAAAGCTGGAATTGTACCAATCC
TCTACAGGAAGTATGAAATTTGATTCTTCCCTTATAACCGCAGTTAAGTACCGTA
ACATTTTTATCACGATATTAGTAACTGACATCACCGGTTTAAATCCTTGTGGTTAC
CAGGGTTACATGCAGGAGAAGTGGGGGCATTAGATTCACCATCAACGGAAGGAA
CTATTTTCAGCTAGTTCTGATATCAAACGTTGGGGGTGCTGGAGAGATTAACAAG
GTATGGGTAAAGGGATCCAGAAGCAATAAATGGGAAGCAATGTCGAGAAATTGG
GGTGCCAAATGGCAGAGCTTAAGCTATCTAAGCGGCCAGAGCTTATCCTTCAAGA
TCCAAGCCGGCAACGGAAGGACTAAAGCCGCTCTTAATGTGGTACCTTCCGGTTG
GCAATTTGGTCAGTCCTTCAAAAGCAACGTGCAGTTTTAGATCTTTGTTTTAT