

IDENTIFICATION

Species: *Gossypium raimondii*

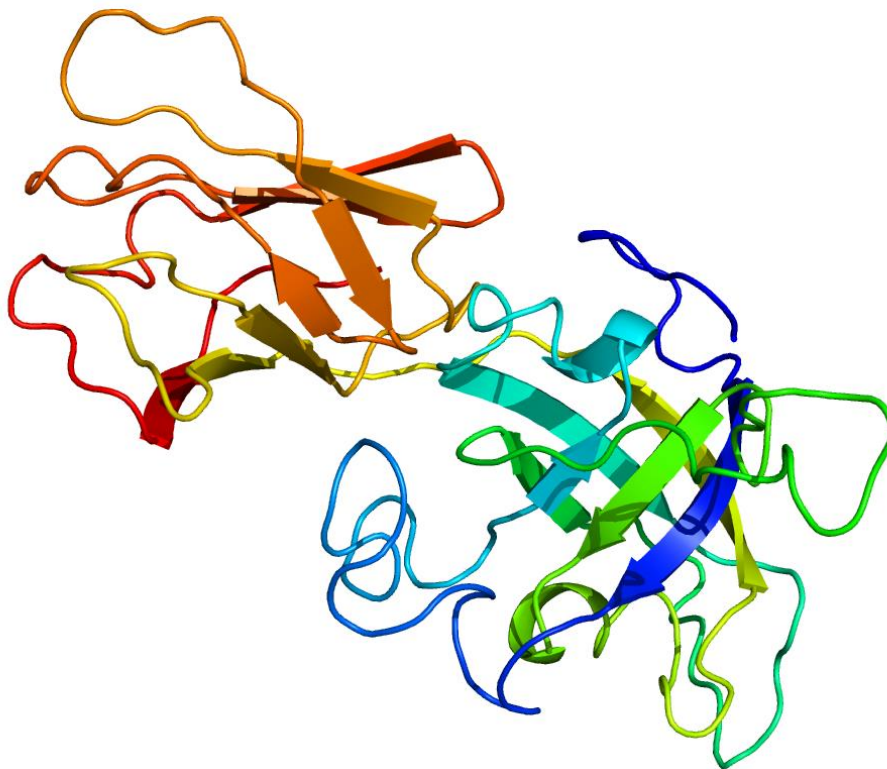
Locus: Gorai.001G148900

Gene Model: Gorai.001G148900.1

Description: GrEXPA-04

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>

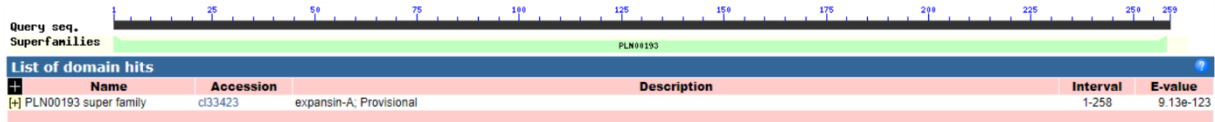
EXTERNAL RESOURCES

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

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>GrEXPA-04

MESSYQFTTAILLVGLYFSTRFNIAETAPVWFPAHATFYGGVDASGTMGGACGYGNL
FTDGYGTSSAAVSTVLFNGGKSCGGCYRIVCDAKNAPQWCVKKSITITATNFCPPN
YALPSDTGGWCNPPRPHFDMSQPAFETIAKYKAGIVPILYRKVTCRRSGGIRFTINGR
NYFQLVLISNVGGAGEINKVWVKGSRSNKWEAMSRNWGAKWQSLSYLSGQSLSFKI
QAGNGRTKAALNVVPSGWQFGQSFKSNVQF*

CDS (coding sequence)

>GrEXPA-04

ATGGAGAGTTCCTATCAATTCACTACTGCGATACTCCTTGTGGGTTTATATTTTTC
CACTAGATTTAACATAGCAGAACTGCACCAGTTTGGTTCAGCCCATGCAACA
TTCTATGGTGGGGTTGATGCTTCTGGTACAATGGGAGGAGCTTGTGGTTATGGCA
ATCTCTTACAGATGGTTATGGAACAAGCTCAGCTGCAGTTAGCACAGTTTGTGTT
AATGGTGGAAAGTCATGTGGAGGCTGCTATCGAATAGTTTGTGATGCCAAAATG
CACCCCAATGGTGTGTCAAGGGTAAATCTATTACCATCACCGCCACCAACTTCTG
TCCTCCCAACTATGCACTCCCAAGTGACACTGGTGGTTGGTGAATCCTCCCCGAC
CACACTTCGACATGTCTCAACCTGCGTTTGGAGCCATAGCCAAATACAAAGCTGG
AATTGTACCAATCCTCTACAGGAAGGTTACATGCAGGAGAAGTGGGGGCATTAG
ATTCACCATCAACGGAAGGAAGTATTTTCAGCTAGTTCTGATATCAAACGTTGGG
GGTGCTGGAGAGATTAACAAGGTATGGGTAAAGGGATCCAGAAGCAATAAATGG
GAAGCAATGTCGAGAAATTGGGGTGCCAAATGGCAGAGCTTAAGCTATCTAAGC
GGCCAGAGCTTATCCTTCAAGATCCAAGCCGGCAACGGAAGGACTAAAGCCGCT
CTTAATGTGGTACCTTCCGGTTGGCAATTTGGTCAGTCCTTCAAAGCAACGTGC
AGTTTTAG

Nucleotide

>GrEXPA-04

AAACTCATTCTTAGCTCTACGCGCATTACCATTGAAAAGAAACAATCCTTTTGTGTT
TTAGAGGAAAGGGAGAAAAGAAATAGAATAATGGAGAGTTCCTATCAATTCACT
ACTGCGATACTCCTTGTGGGTTTATATTTTCCACTAGATTTAACATAGCAGAAAC
TGCACCAGTTTGGTTCAGCCCATGCAACATTCTATGGTGGGGTTGATGCTTCTG
GTACAATGGGTAAGTTTAAACAACCTTTTCTTCCCTCTCATTGTGCTGATCTCAAT
TCATATAATTTATTTTCTATAAAAGAGCTGTTGATCTTGAACAGATGATTATTGAT
TACCATGTTGGTTTTCCAGGAGGAGCTTGTGGTTATGGCAATCTCTTTACAGATG

GTTATGGAACAAGCTCAGCTGCAGTTAGCACAGTTTTGTTTAATGGTGGAAAGTC
ATGTGGAGGCTGCTATCGAATAGTTTGTGATGCCAAAAATGCACCCCAATGGTGT
GTCAAGGGTAAATCTATTACCATCACCGCCACCAACTTCTGTCCTCCCAACTATGC
ACTCCAAGTGACACTGGTGGTTGGTGTAAATCCTCCCCGACCACACTTCGACATG
TCTCAACCTGCGTTTGAGACCATAGCCAAATACAAAGCTGGAATTGTACCAATCC
TCTACAGGAAGTATGAAATTTGATTCTTCCCTTATAACCGCAGTTAAGTACCGTA
ACATTTTTATCACGATATTAGTAACTGACATCACCGGTTTAAATCCTTGTGGTTAC
CAGGGTTACATGCAGGAGAAGTGGGGGCATTAGATTCACCATCAACGGAAGGAA
CTATTTTCAGCTAGTTCTGATATCAAACGTTGGGGGTGCTGGAGAGATTAACAAG
GTATGGGTAAAGGGATCCAGAAGCAATAAATGGGAAGCAATGTCGAGAAATTGG
GGTGCCAAATGGCAGAGCTTAAGCTATCTAAGCGGCCAGAGCTTATCCTTCAAGA
TCCAAGCCGGCAACGGAAGGACTAAAGCCGCTCTTAATGTGGTACCTTCCGGTTG
GCAATTTGGTCAGTCCTTCAAAGCAACGTGCAGTTTTAGATCTTTGTTTTAT