

## IDENTIFICATION

**Species:** *Gossypium raimondii*

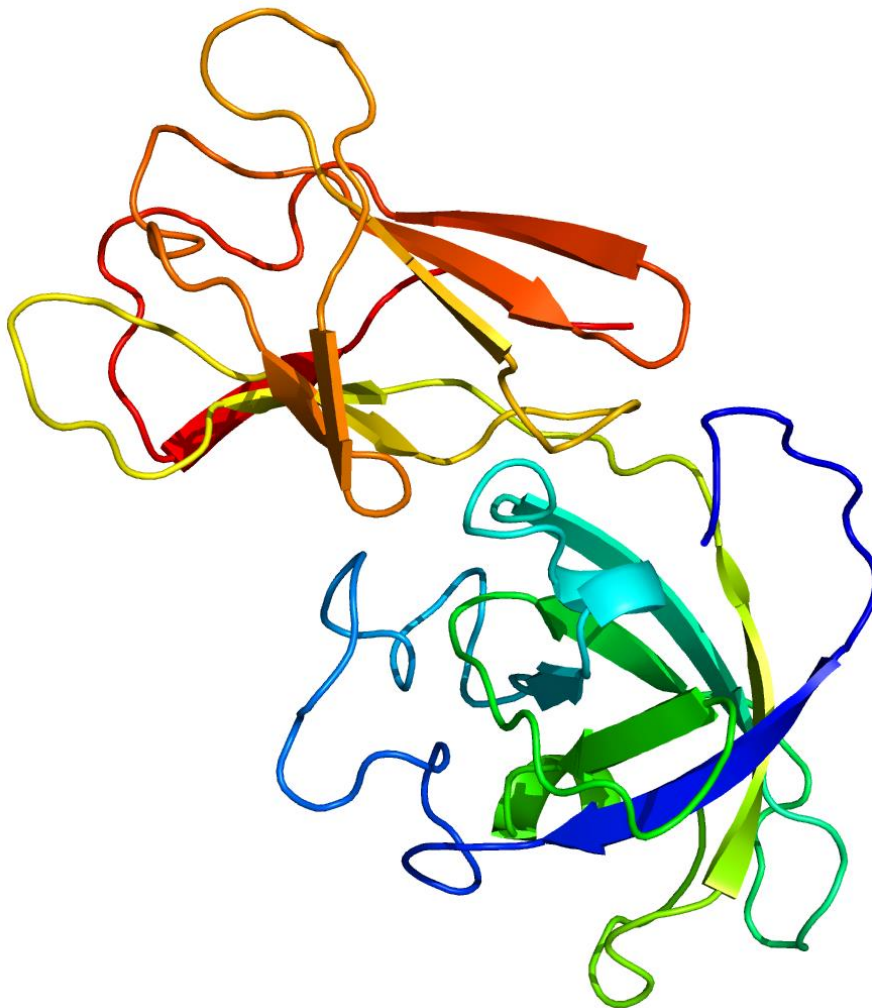
**Locus:** Gorai.004G206100

**Gene Model:** Gorai.004G206100.1

**Description:** GrEXPA-11

**Family:** Alpha Expansin

**3D structure:**



## GENOME DATABASES

Phytozome: [https://phytozome-next.jgi.doe.gov/info/Graimondii\\_v2\\_1](https://phytozome-next.jgi.doe.gov/info/Graimondii_v2_1)

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

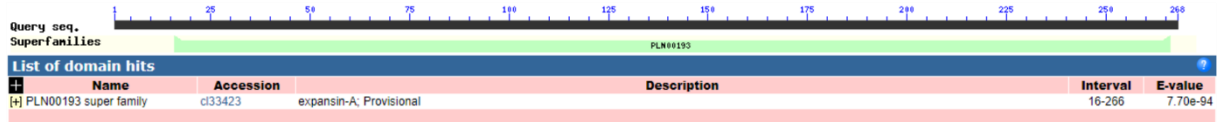
## EXTERNAL RESOURCES

[https://www.cottongen.org/species/Gossypium\\_raimondii/jgi\\_genome\\_221](https://www.cottongen.org/species/Gossypium_raimondii/jgi_genome_221)

## GENE STRUCTURE



## DOMAIN ARCHITECTURE



## SEQUENCES

### Peptide

>GrEXPA-11

MTSFDPWSFNFFSMTLATLAIIVSKSSVTVALPIEFRPSPWSLAHATFYGDETASETLG  
GACGYGNLFSNGYGTDTAALSTTLFNNGFACGTCYQIQCVESTWCYPGVPFTT<sup>1</sup>VTAT  
NLCPPNWAQDSNYGGWCNPPRVHFDMSKPAFMKIAQWKAGIVPVMYRRVPCVRPG  
GLRFYFQNGYWLLIYVMNVGGGGDIAQMWVKGSKTGWISM<sup>2</sup>SHNWGATYQAFAT  
LGGQSL<sup>3</sup>SKITSYTSKETIIAWDVAPANWN<sup>4</sup>VGSTYT<sup>5</sup>TTD<sup>6</sup>VNFH\*

### CDS (coding sequence)

>GrEXPA-11

ATGACTTCTTTTGATCCATGGAGTTTCAACTTCTTTTCGATGACGCTTGCAACGTT  
GGCCATCATCGTCAGCAAATCTTCAGTCACTGTTGCATTACCAATCGAGTTC<sup>1</sup>CCGG  
CCAAGCCCTTGGTCTCTTGCCCATGCCACCTTTTATGGCGACGAAACCGCCTCCGA  
GACGCTGGGAGGAGCTTGTGGTTATGGGAATTTGTTTAGCAATGGTTATGGTACG  
GACACAGCTGCTCTAAGTACAACGTTGTTCAACAATGGTTT<sup>2</sup>TGCTTGTGGGACAT  
GTTACCAGATACAGTGTGTTGAGTCAACTTGGTGCTACCCTGGGGTTCATT<sup>3</sup>CACC  
ACAGTGACTGCTACCAATCTTTGCCCTCCAAATTGGGCCCAAGACTCCA<sup>4</sup>ACTACG  
GTGGCTGGTGCAACCCTCCACGAGTCCACTTCGACATGTCCAAGCCC<sup>5</sup>GCTTTTAT  
GAAAATTGCACAATGGAAAGCTGGCATTGTCCCTGTCATGTATAGAAGGGT<sup>6</sup>TCCA  
TGTGTAAGGCCGGGGGGCCTTCGATTTTATTTCCAAGGAAATGGGTACTGGTTGT  
TGATATACGTGATGAATGTAGGAGGCGGGGGTGACATTGCCCAAATGTGGGTTA  
AAGGAAGCAAACAGGGTGGATTAGCATGAGCCATAACTGGGGAGCTACATATC  
AGGCATTTGCAACTCTTGGAGGCAATCTCTTTCCTTTAAGATCACTTCATACACA  
TCCAAGGAGACTATCATTGCCTGGGATGTTGCACCTGCTAATTGGAATGTAGGAT  
CCACTTACACCACAGATGTGAACTTCCATTAA

### Nucleotide

>GrEXPA-11

ATGACTTCTTTTGATCCATGGAGTTTCAACTTCTTTTCGATGACGCTTGCAACGTT  
GGCCATCATCGTCAGCAAATCTTCAGTCACTGTTGCATTACCAATCGAGTTC<sup>1</sup>CCGG  
CCAAGCCCTTGGTCTCTTGCCCATGCCACCTTTTATGGCGACGAAACCGCCTCCGA  
GACGCTGGGTATGTT<sup>2</sup>CATCATATAATCATCTTCATAATGGCTAGTTATTGATGAGT  
GCATATTTCACTTGT<sup>3</sup>TATGGTGACAGGAGGAGCTTGTGGTTATGGGAATTTGTTT  
AGCAATGGTTATGGTACGGACACAGCTGCTCTAAGTACAACGTTGTTCAACAATG  
GTTT<sup>4</sup>TGCTTGTGGGACATGTTACCAGATACAGTGTGTTGAGTCAACTTGGTGCTAC

CCTGGGGTTCCATTCACCACAGTGACTGCTACCAATCTTTGCCCTCCAAATTGGGC  
CCAAGACTCCAACACTACGGTGGCTGGTGCAACCCTCCACGAGTCCACTTCGACATG  
TCCAAGCCCGCTTTTATGAAAATTGCACAATGGAAAGCTGGCATTGTCCCTGTCA  
TGTATAGAAGGTATATTTAAATTTTCAGTTTGATTATTCAACATGAATTTACATAT  
GAAGAAGGACGTTATGAACCATGATCAACTTGGATTCCAATGGTTGCAGGGTTCC  
ATGTGTAAGGCCGGGGGGCCTTCGATTTTATTTCCAAGGAAATGGGTACTGGTTG  
TTGATATACGTGATGAATGTAGGAGGCCGGGGGTGACATTGCCCAAATGTGGGTTA  
AAGGAAGCAAAACAGGGTGGATTAGCATGAGCCATAACTGGGGAGCTACATATC  
AGGCATTTGCAACTCTTGGAGGCCAATCTCTTTCCTTTAAGATCACTTCATACACA  
TCCAAGGAGACTATCATTGCCTGGGATGTTGCACCTGCTAATTGGAATGTAGGAT  
CCACTTACACCACAGATGTGAACTTCCATTAATCCACAAATTCACAATACCTCTTT  
TTGTTTTTTAGCTTGCCCTTTTTTTCTAGCCTCTATTTTCATTTGTACTTTCTACAGC  
ATAGGCAACTGAGTAGCTCCATGGTTCAATTTTTTCTTTTACATGTAAAACTATT  
TCTGCAGATAAATTGTATTTTGATCAATATCTGCTAAGATTGAAATAAAGAAATC  
AAAAGATTTGCTATTATAATTC