

## IDENTIFICATION

**Species:** *Gossypium raimondii*

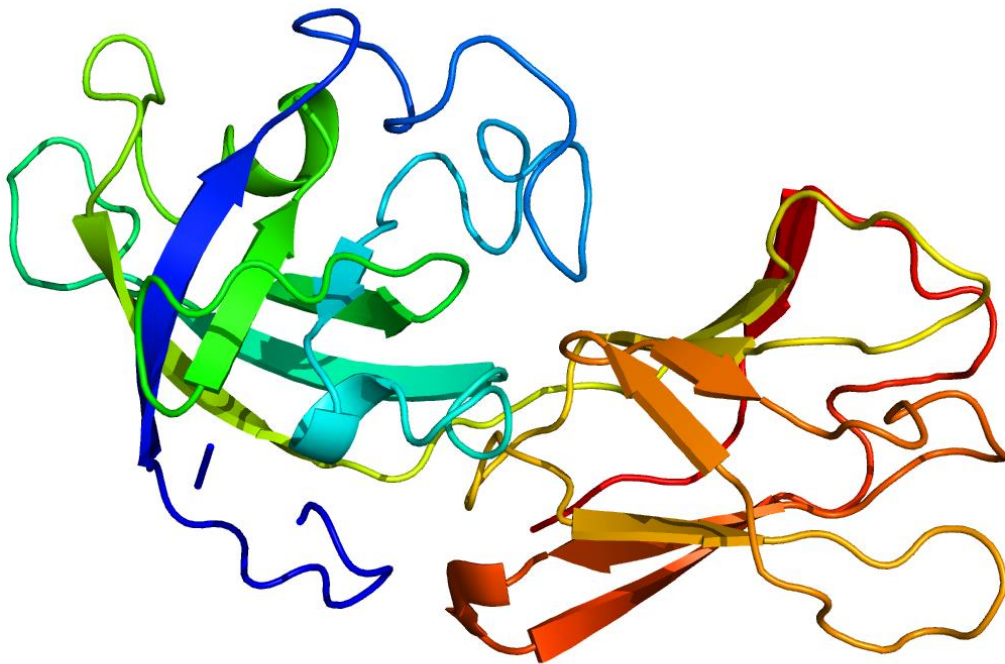
**Locus:** Gorai.006G210800

**Gene Model:** Gorai.006G210800.1

**Description:** GrEXPA-18

**Family:** Alpha Expansin

**3D structure:**



## GENOME DATABASES

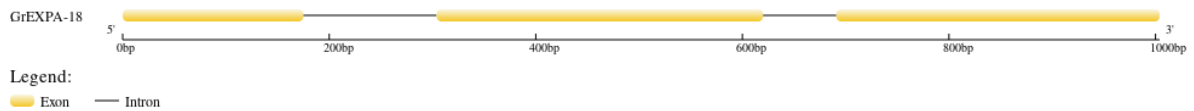
Phytozome: [https://phytozome-next.jgi.doe.gov/info/Graimondii\\_v2\\_1](https://phytozome-next.jgi.doe.gov/info/Graimondii_v2_1)

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

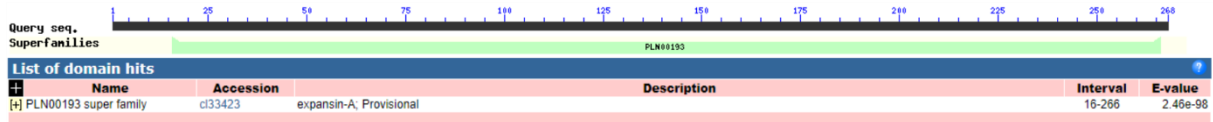
## EXTERNAL RESOURCES

[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-18

MASFTSWSFKFLMFLATFAIISKPSLAVAVAVPVFQSSPWAAAHATFYGDESASQT  
MGGACGYGDLFSNGYGTDTAALSTTLFNDGFACGTCYQIKCVDSPWCYSGVPSTTV  
TATNICPPNWAQESNNGGWCNPPRAHFDMSKPAFMKIATWKAGIVPVMYRRVPCER  
PGGVRFQNGYWLLVYVMNVGGGGDIANMWVKGSKTGWINMSHNWGFQAF  
ATLGGQSLFKLTSYSTKETIIAWNVAPENWNVVGSTYKTDVNFH\*

### CDS (coding sequence)

>GrEXPA-18

ATGGCTTCTTTACTTCATGGAGCTTTAAGTTCTTGTTTATGACACTTGCAACCTTT  
GCCATCATCAGCAAACCTTCCCTTGCGGTTGCGGTTGCGGTTCCGGTTTTCCAATC  
AAGCCCTTGGGCTGCTGCCCATGCCACCTTTTATGGCGATGAATCTGCCTCTCAA  
CAATGGGAGGAGCTTGTGGGTACGGGGATTTGTTTCAGCAATGGTTATGGTACAGA  
CACTGCTGCACTGAGCACAACATTGTTCAACGATGGCTTTGCTTGTGGGACTTGT  
ACCAAATAAAGTGTGTTGACTCACCTTGGTGCTACTCTGGGGTTCCATCCACCAC  
AGTGACAGCAACCAACATTTGCCCTCCAAATTGGGCCCAAGAATCCAACAATGGC  
GGCTGGTGCAACCCTCCTCGAGCCCATTTTCGACATGTCCAAGCCTGCTTTCATGA  
AAATCGCAACATGGAAAGCTGGCATTGTCCCCGTCATGTACCGAAGGGTACCTTG  
TGAGAGGCCAGGAGGGGTTAGATTTTCATTCCAAGGCAATGGGTATTGGTTATTG  
GTGTATGTGATGAACGTAGGAGGAGGTGGTGACATTGCAAACATGTGGGTCAA  
GGAAGCAAACAGGGTGGATTAACATGAGCCATAACTGGGGAGCTTCGTTTCAG  
GCATTTGCCACACTTGGTGGCCAATCACTTTCTTTCAAGCTTACTTCATATTCAAC  
CAAGGAAACCATCATAGCTTGAATGTTGCACCTGAAAATTGGAATGTAGGGTCA  
ACTTACAAGACAGATGTGAACTTCATTAA

### Nucleotide

>GrEXPA-18

ATGGCTTCTTTACTTCATGGAGCTTTAAGTTCTTGTTTATGACACTTGCAACCTTT  
GCCATCATCAGCAAACCTTCCCTTGCGGTTGCGGTTGCGGTTCCGGTTTTCCAATC  
AAGCCCTTGGGCTGCTGCCCATGCCACCTTTTATGGCGATGAATCTGCCTCTCAA  
CAATGGGTACTTTTCGATTTTTTTATATTATATATCCGTTTCATCTTTAAATGATA  
TATTGCAGATTTAAAATTCGAATATCAATATCTGCAATTATCTTCAATCATCTTTT  
TCTATTACTGAGCTTATAGGAGGAGCTTGTGGGTACGGGGATTTGTTCAGCA  
ATGGTTATGGTACAGACACTGCTGCACTGAGCACAACATTGTTCAACGATGGCTT

TGCTTGTGGGACTTGTTACCAAATAAAGTGTGTTGACTCACCTTGGTGCTACTCTG  
GGGTTCCATCCACCACAGTGACAGCAACCAACATTTGCCCTCCAAATTGGGCCCA  
AGAATCCAACAATGGCGGCTGGTGCAACCCTCCTCGAGCCCATTTCGACATGTCC  
AAGCCTGCTTTCATGAAAATCGCAACATGGAAAGCTGGCATTGTCCCCGTCATGT  
ACCGAAGGTACACAACATCTTCGATCTCTTAAAAGTGATTACATGAACCGGTTGA  
AATATGTGTTTAAATCCTTGTAGGGTACCTTGTGAGAGGCCAGGAGGGGTTAGAT  
TTCATTCCAAGGCAATGGGTATTGGTTATTGGTGTATGTGATGAACGTAGGAGG  
AGGTGGTGACATTGCAAACATGTGGGTCAAAGGAAGCAAAACAGGGTGGATTAA  
CATGAGCCATAACTGGGGAGCTTCGTTTCAGGCATTTGCCCACACTTGGTGGCCAA  
TCACTTCTTTCAAGCTTACTTCATATTCAACCAAGGAAACCATCATAGCTTGGAA  
TGTTGCACCTGAAAATTGGAATGTAGGGTCAACTTACAAGACAGATGTGAACTTC  
CATTAA