

## IDENTIFICATION

**Species:** *Gossypium raimondii*

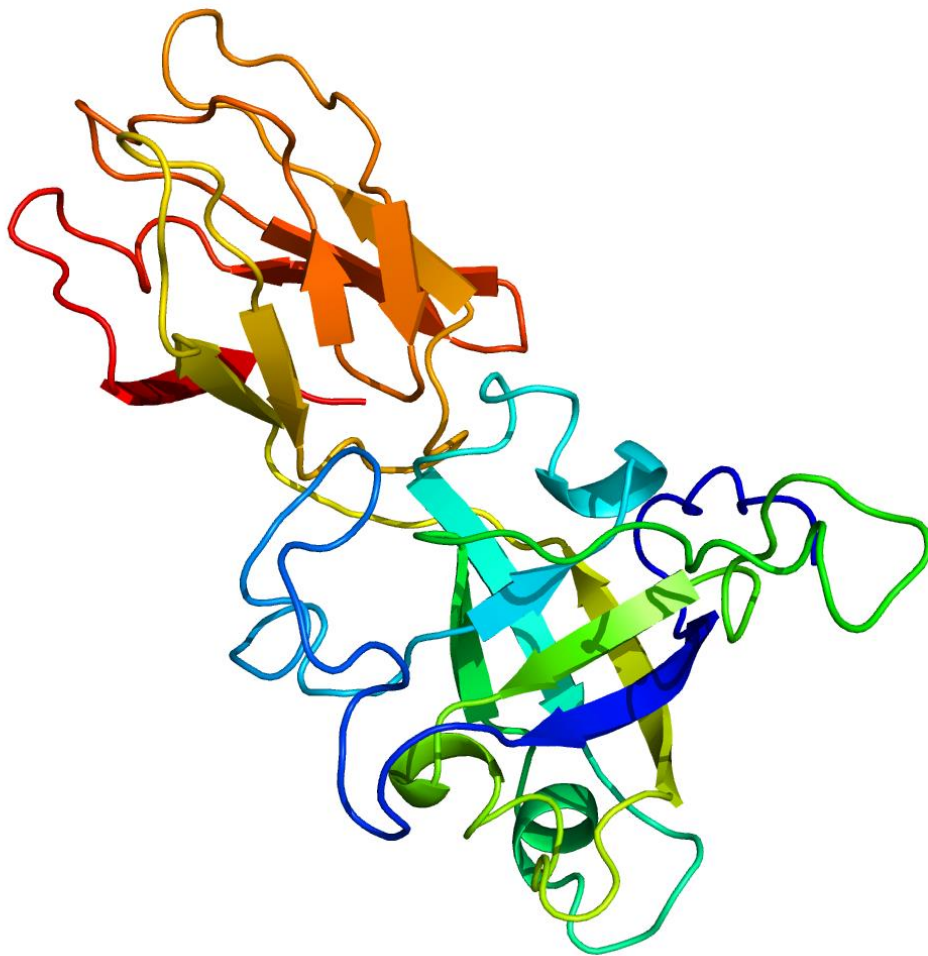
**Locus:** Gorai.006G172400

**Gene Model:** Gorai.006G172400.1

**Description:** GrEXPA-17

**Family:** Alpha Expansin

**3D structure:**



## GENOME DATABASES

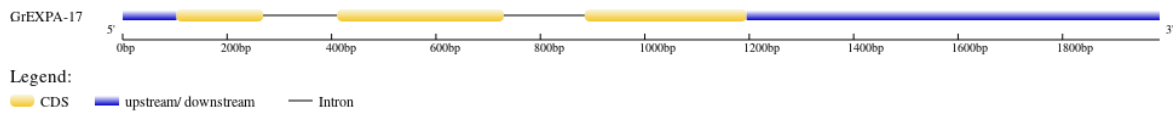
Phytozome: [https://phytozome-next.jgi.doe.gov/info/Graimondii\\_v2\\_1](https://phytozome-next.jgi.doe.gov/info/Graimondii_v2_1)

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

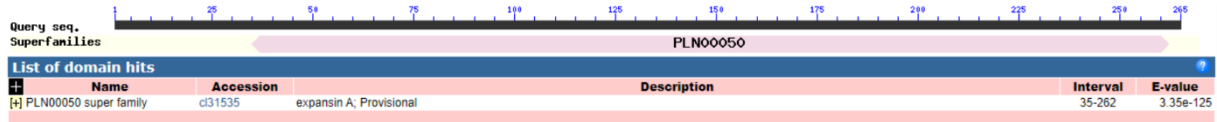
## EXTERNAL RESOURCES

[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-17

MSAVAPSFSLSVLCFASLLSFLAVVNARIPGVYTGGAWESAHAATFYGGSDASGTMGG  
ACGYGNLYSQGYGVNTAALSTALFNGLSCGGCFEIKCANDPRWCHSGSPSIITATN  
FCPPNYALPNDNGGWCNPPRPHFDLAMPFLKIAEYRAGIVPVSYRRVPCRKQGGIR  
FTINGFRYFNLVLVTNVAGAGDIVKVKVKGNTNWLSMSRNWQNWQSNVAVLVGQ  
ALSFRVTGSDRRTSTSLNVAPANWQFGQTFTGKNFRV\*

### CDS (coding sequence)

>GrEXPA-17

ATGTCGCTGTTGCTCCTTCTTTTCCTTGAGTGTGCTCTGTTTTGCTTCATTGCTC  
TCCTTTTTGGCTGTGGTGAATGCAAGAATCCCTGGAGTTTATACTGGTGGAGCTTG  
GGAAAGTGCCCATGCTACATTTTATGGTGGAAAGCGATGCTTCTGGAACAATGGGC  
GGTGCATGTGGGTACGGGAATCTCTACAGTCAAGGCTATGGCGTGAATACAGCA  
GCTTTAAGCACTGCACTTTTCAACAATGGCCTTAGCTGCGGTGGTTGCTTTGAGAT  
TAAGTGCGCAAACGACCCAGATGGTGTCACTCCGGCAGCCCTTCCATTATTATC  
ACTGCCACTAACTTTTGCCCTCCTAACTATGCTCTCCCAAATGACAATGGCGGCTG  
GTGCAACCCTCCACGCCCTCACTTTGACCTTGCCATGCCTATGTTCCCTCAAATCG  
CCGAGTACCGTGCTGGTATTGTCCCGTCTCTTACCGTAGAGTGCCATGCCGAAA  
GCAAGGGGGGATACGATTCACCATTAATGGATTCCGTTACTTCAACTTGGTTTTG  
GTCACCAACGTCGCGGGTGCAGGGGATATCGTGAAGGTGAAGGTGAAGGGAACC  
AACACCAATTGGTTGAGCATGAGCCGTAAGTGGGTCAAACCTGGCAGTCAAAC  
GCCGTTTTGGTGGGTCAGGCACTCTCGTTCAGAGTCACGGGCAGTGACAGGCGAA  
CCTCCACTTCGTTGAACGTGGCACCTGCTAATTGGCAATTCGGCCAAACCTTCAC  
GGGAAAGAATTTCCGCGTTTGA

### Nucleotide

>GrEXPA-17

CAATAAGTACCCCCACCATCTTCCCGCATTCAACACTTCAGCATTCTCTTTCTTT  
ACTCTCTTATCAATTTTCCCCCATCTTAAACTAAAGAAAATTAACAATGTCCGCT  
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CTGTGGTGAATGCAAGAATCCCTGGAGTTTATACTGGTGGAGCTTGGGAAAGTGC  
CCATGCTACATTTTATGGTGGAAAGCGATGCTTCTGGAACAATGGGTATTTATTTT  
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CGGTGGTTGCTTTGAGATTAAGTGCGCAAACGACCCAGATGGTGTCACTCCGGC  
AGCCCTTCCATTATTATCACTGCCACTAACTTTTGCCCTCCTAACTATGCTCTCCC  
AAATGACAATGGCGGCTGGTGCAACCCTCCACGCCCTCACTTTGACCTTGCCATG  
CCTATGTTCCCTCAAATCGCCGAGTACCGTGCTGGTATTGTCCCCGTCTCTTACCG  
TAGGTGAGTCCCCAAAATCTTTCCCCTTTTACTTCAATGGGTTTTCTGCCATTGTT  
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AGATTATATTTACTGCGATTAATTAAGTGTGCTTATTTTTGACAGAGTGCCATGC  
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CAAACGCCGTTTTGGTGGGTCAGGCACTCTCGTTCAGAGTCACGGGCAGTGACAG  
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GACCATGTGCTGTTAGTCTGGCACTCGCCCTTGCCGTCCATTTAACTTTCTTTTTAT  
GTTTTAGCTTCCATGGCTCCACCCCCACAACCCCTT