

## IDENTIFICATION

**Species:** *Gossypium raimondii*

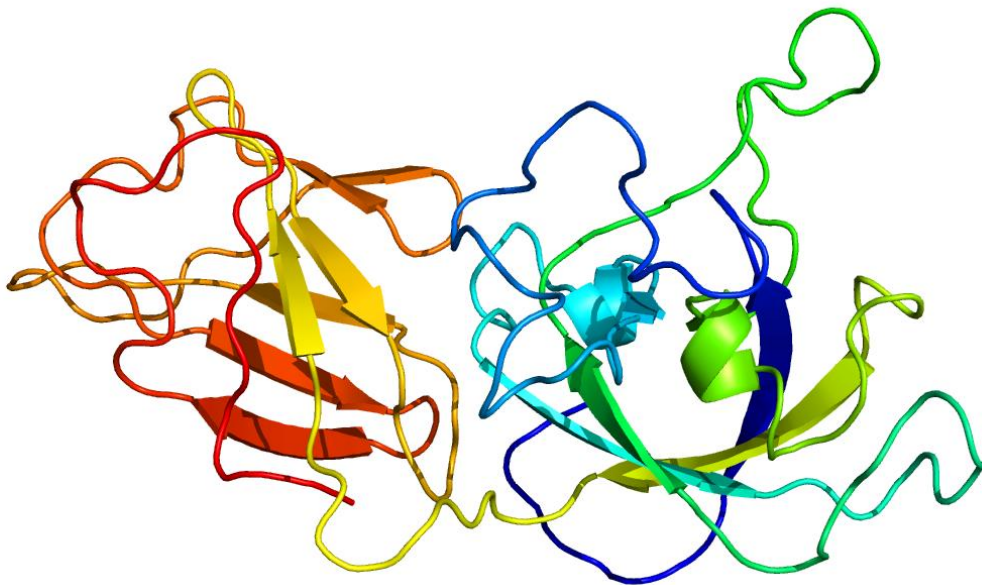
**Locus:** Gorai.004G148200

**Gene Model:** Gorai.004G148200.1

**Description:** GrEXPA-10

**Family:** Alpha Expansin

**3D structure:**



## GENOME DATABASES

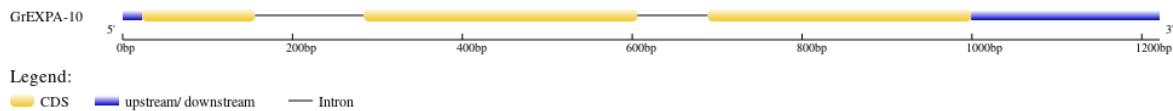
Phytozome: [https://phytozome-next.jgi.doe.gov/info/Graimondii\\_v2\\_1](https://phytozome-next.jgi.doe.gov/info/Graimondii_v2_1)

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

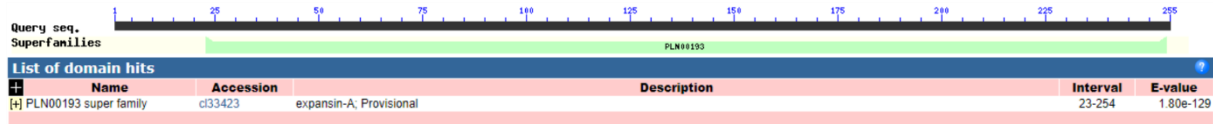
## EXTERNAL RESOURCES

[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-10

MESAYLFITALFLVGLFSTQTDAAATWFSAHATFYGGSDASGTMGGACGYGNLYTD  
GYGTKTAALSTALFNDGKSCGGCYQIVCDAKKAPQWCLKSR YITITATNFCPPNYAL  
PSDNGGW CNPPRPHFDM SQPAFETIAKYKAGIVPILYRKVKCERSGGLRFTINGRNYF  
ELVLISNVGGAGEISMVWIKGSKTNKWETMSRNWGANWQSLSYLNQSLFRVQVS  
NGRIRTALNVVPSNWQFGQSFKSNIQF\*

### CDS (coding sequence)

>GrEXPA-10

ATGGAGAGTGCCTATCTATTCATTACAGCCTTATTCCTAGTGGGTTTATTTCCAC  
TCAAACAGATGCTGCTGCAACTTGGTTCTCAGCCCATGCAACATTCTACGGTGGG  
AGTGATGCTTCTGGTACAATGGGTGGAGCTTGTGGCTATGGTAATCTTTATACAG  
ATGGTTATGGAACAAAACAGCTGCACTCAGTACAGCTTTGTTTAACGATGGCAA  
GTCATGCGGAGGGTGCTATCAGATAGTTTGTGATGCTAAAAAAGCACCTCAATGG  
TGTCTCAAGAGTAGATACATTACCATCACTGCTACCAACTTCTGTCTCCCAATTA  
TGCACTCCCAAGTGACAATGGTGGTTGGTGAATCCTCCCCGTCGCGCATTTTCGAC  
ATGTCTCAACCTGCATTTCGAGACCATTGCCAAATACAAGGCTGGAATTGTACCAA  
TCCTCTACAGGAAGGTTAAATGCGAGAGAAGTGGAGGCCTTAGATTACCCATCAA  
CGGAAGAACTATTTTGAGCTAGTGTGATATCAAATGTAGGGGGTGCTGGGGAG  
ATATCCATGGTGTGGATAAAGGGTTCTAAAACAAATAAATGGGAAACCATGTCC  
AGAAACTGGGGAGCCA ACTGGCAGAGCTTAAGCTATCTCAATGGTCAGAGCTTAT  
CCTTCAGGGTTCAAGTCAGTAATGGAAGGATTCGAACAGCTCTGAATGTGGTGCC  
TTCCAATTGGCAATTTGGACAGTCTTTCAAAGCAACATCCAGTTTTAG

### Nucleotide

>GrEXPA-10

GAAAAAAAAACCATTGTATTTAGATGGAGAGTGCCTATCTATTCATTACAGCCTT  
ATTCCTAGTGGGTTTATTTCCACTCAAACAGATGCTGCTGCAACTTGGTTCTCAG  
CCCATGCAACATTCTACGGTGGGAGTGATGCTTCTGGTACAATGGGTAAGTTTTT  
AACCTTTTCTATTTTCTTTTAAA ACTATACTGGTCTCAAGGTATATATACTTCC  
AATATAAAGAGCTCTTGGTCTTGA ACTAAGGATGATTATTAATGCTATGTGGGTT  
TTTTTAGGTGGAGCTTGTGGCTATGGTAATCTTTATACAGATGGTTATGGAACAA  
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CTATCAGATAGTTTGTGATGCTAAAAAAGCACCTCAATGGTGTCTCAAGAGTAGA

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TCGAGACCATTGCCAAATACAAGGCTGGAATTGTACCAATCCTCTACAGGAAGTA  
TGTTCAAAAGTTTATTCTTCAATTAAAAAAACTTGGAATTTTAAGCATTATCTCTC  
AATAATTTGTTTTGTGCTTGGCAGGGTTAAATGCGAGAGAAGTGGAGGCCTTAGA  
TTCACCATCAACGGAAGAACTATTTTGAGCTAGTGTTGATATCAAATGTAGGGG  
GTGCTGGGGAGATATCCATGGTGTGGATAAAGGGTTCTAAAACAAATAAATGGG  
AAACCATGTCCAGAAACTGGGGAGCCAACTGGCAGAGCTTAAGCTATCTCAATG  
GTCAGAGCTTATCCTTCAGGGTTCAAGTCAGTAATGGAAGGATTCGAACAGCTCT  
GAATGTGGTGCCTTCCAATTGGCAATTTGGACAGTCTTTCAAAAGCAACATCCAG  
TTTTAGACTTTCCTTAATTAGTACCTACCTCTCTTATGTATTTTTCTTTGATATACA  
ACTATTTGTTTTCTTCTTTTCTTTGGGTAGATAAAAGTCGCCGCTTAGATTGTGGCT  
TAGCCTAGTGGTTTACAAAACATTATATATATATGCCATCTATTGAAAACCTCTATG  
TATTACAATGTTACTATAGGCCTTGTATTGTTACAAGTAACAGTTTTATACAGTCA  
AA