

IDENTIFICATION

Species: *Gossypium raimondii*

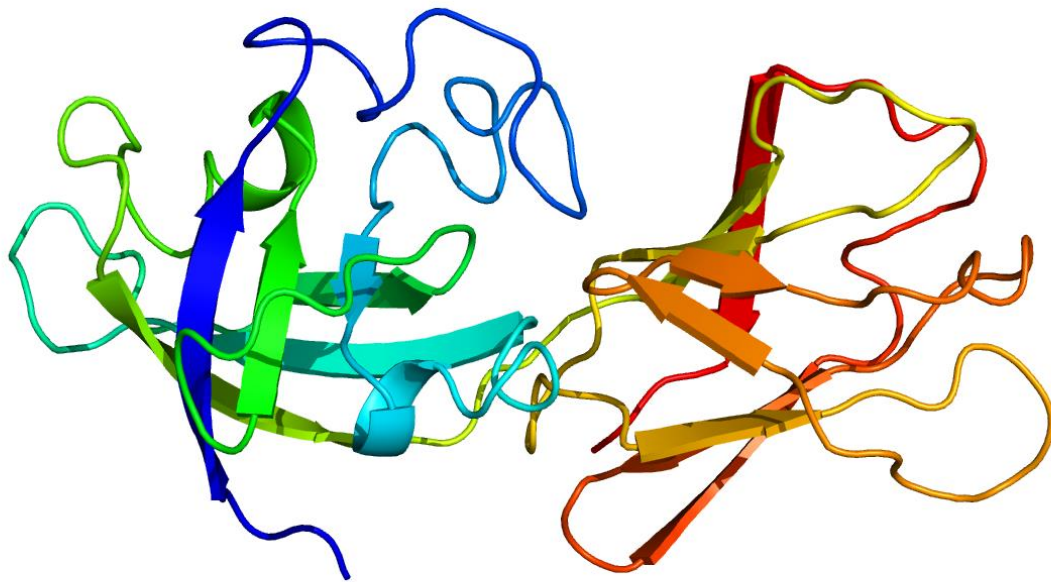
Locus: Gorai.001G083300

Gene Model: Gorai.001G083300.1

Description: GrEXPA-01

Family: Alpha Expansin

3D structure:



GENOME DATABASES

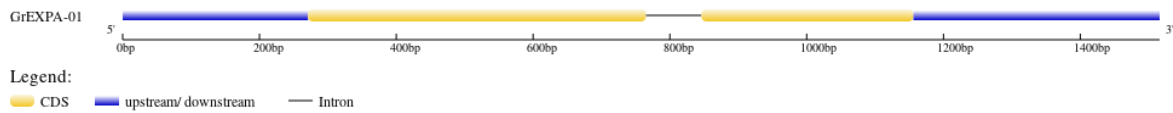
Phytozome: https://phytozome-next.jgi.doe.gov/info/Graimondii_v2_1

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

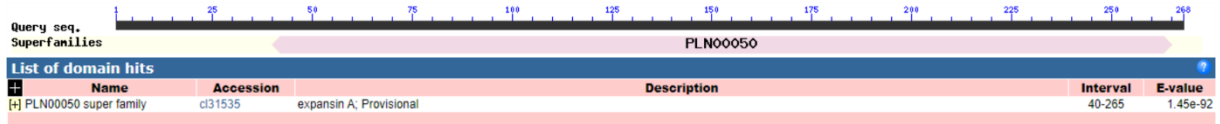
EXTERNAL RESOURCES

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

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>GrEXPA-01

MSNPSSITATAALLSLISTVTSHYSSSTFFSSPPAPQSTVWHSARATYYAASDPRDAV
GGACGYGDLVKAGYGMATVGLSEALFQRGQICGACFELRCVDDLRCIPGTSIIVTA
TNFCAPNYGFTAEGGGRCNPPNKHVFLPIEAFEKIAIWKAGNMPVQYRRIKCRKEGG
VRFTIDGSGIFVSVLISNVGGAGDIVAVKIKGSRGTGWLPMGRNWGQNWHINSDLRNQ
PLSFEVTNSDGLTLTSYNVAPKNWNFGQTFEGKQFEA*

CDS (coding sequence)

>GrEXPA-01

ATGTCCAACCCATCTTCTATAACTGCAACTGCAGCTCTTCTTCTCTCACTCATCTCT
ACTGTCACTTCCCATTACTCTTCCCTCCACCTTCTCTTCTTCCCCACCGGCGCCACAG
TCCACCGTCTGGCACTCCGCACGCGCCACTTACTACGCCGCTTCGGATCCTCGCG
ACGCCGTCGGCGGTGCTTGTGGGTATGGAGACCTAGTCAAGGCTGGGTACGGTAT
GGCGACTGTGGGTTTAAGTGAAGCTTTGTTTCAGCGTGGACAGATCTGCGGTGCT
TGTTTCGAGTTAAGGTGTGTGGACGACCTGCGGTGGTGTATACCTGGGACATCTA
TCATTGTCACCGCCACAAATTTCTGTGCTCCAAATTATGGGTTCACGGCGGAAGG
CGGTGGGCGTTGTAATCCTCCTAACAACACTTTGTACTTCCCATTGAAGCTTTTG
AAAAGATTGCTATTTGGAAAGCTGGCAACATGCCTGTCCAGTATCGAAGGATAAA
GTGCAGAAAAGAAGGAGGTGTACGATTCACCATTGATGGCTCAGGGATCTTCGTG
TCAGTTCTCATCAGCAATGTTGGAGGCGCTGGTGACATAGTTGCAGTTAAGATTA
AAGGTTCAAGAACGGGGTGGTTACCGATGGGTTCGGAATTGGGGACAAAATTGGC
ATATAAATTCTGATCTAAGGAATCAACCACTTTCAATTTGAGGTCACTAATAGTGA
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CTTTTGAAGGAAAGCAATTCGAGGCCTAA

Nucleotide

>GrEXPA-01

GAATCATAATGCACAACCCTAACGCTTTTTGAGTAAAGAAAAAAGAGGGCCCAA
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GCGTTGTAATCCTCCTAACAAACACTTTGTACTIONCCATTGAAGCTTTTGAAAAGA
TTGCTATTTGGAAAGCTGGCAACATGCCTGTCCAGTATCGAAGGTATACAAATCT
GGGTTTCTTACATTGTTGGATTTGTTGGGATAAAACATCTTAAATTCTGTCTCATT
TGTCTTAAAACAGGATAAAGTGCAGAAAAGAAGGAGGTGTACGATTCACCATTG
ATGGCTCAGGGATCTTCGTGTCAGTTCTCATCAGCAATGTTGGAGGCGCTGGTGA
CATAGTTGCAGTTAAGATTAAGGTTCAAGAACGGGGTGGTTACCGATGGGTCCG
AATTGGGGACAAAATTGGCATATAAATTCTGATCTAAGGAATCAACCACTTTCAT
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GAGAGACAAGACTGTCCTATTCTTTTCTTTCTTTTGTATCTGTTGTTTTGTACT
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CCATGTCAACCATGGTGATAT