

IDENTIFICATION

Species: *Gossypium raimondii*

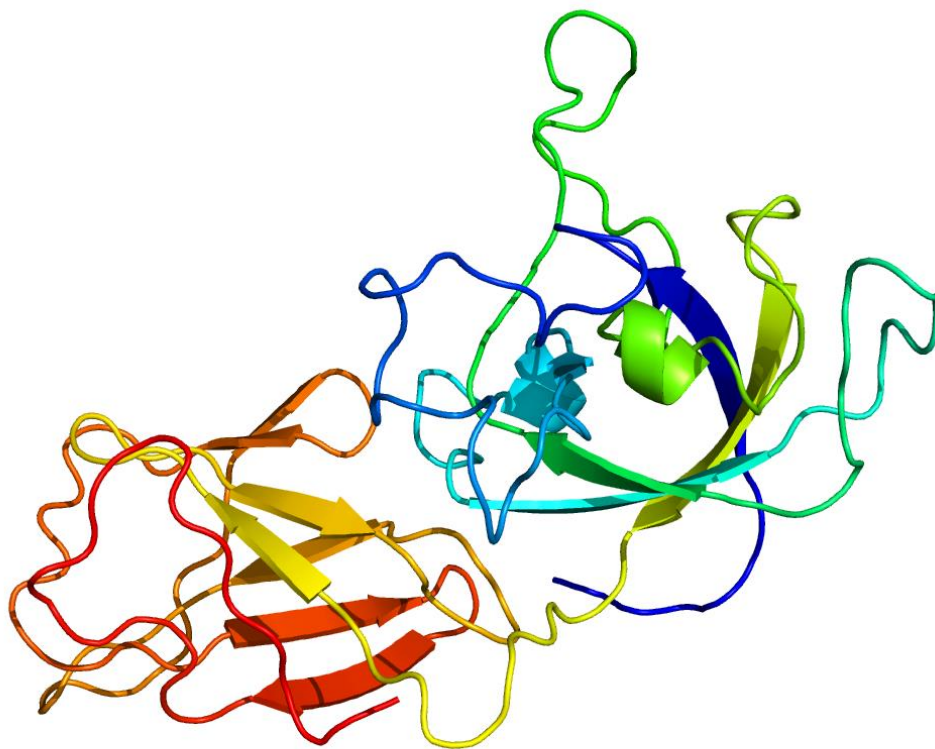
Locus: Gorai.007G118900

Gene Model: Gorai.007G118900.1

Description: GrEXPA-20

Family: Alpha Expansin

3D structure:



GENOME DATABASES

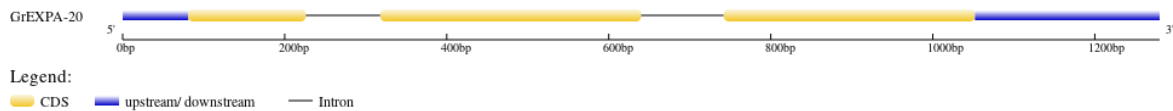
Phytozome: https://phytozome-next.jgi.doe.gov/info/Graimondii_v2_1

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

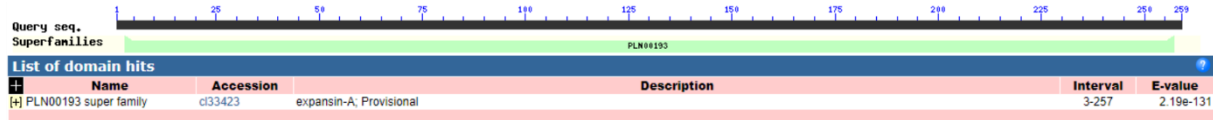
EXTERNAL RESOURCES

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

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>GrEXPA-20

MDSA YLFTTAVLIVGLYFSPKFHVADAAHTWLSAHATFYGGSDASGTMGGACGYG
NLYTDGYGTNTAALSTALFNDGKACGGCYQITCDARQVPQWCLKGKYITITATNFCP
PNYALPSDNGGWCNPPRPHFDMSQPAFETIAKYRAGIVPPLYRRVTCRRKGGMRFTI
NGRNYFELVLISNVGGSGEISRVIKWSKTNKWESMSRNWGANWQSLSYLNQSL
FRIQASNGRIRYALNVVPSNWQFGQSFKTNVQI*

CDS (coding sequence)

>GrEXPA-20

ATGGACAGTGCCTATCTGTTCACTACTGCCGTAATGTTGGGCTTATACTTTTC
CCCTAAATTTTCATGTAGCAGATGCAGCTCATACTGGCTTTCGGCACATGCAACG
TTCTATGGTGGAAAGTGATGCTTCTGGAAGTATGGGTGGAGCTTGTGGTTATGGCA
ATCTCTATACAGATGGTTATGGAACAAACACAGCTGCACTCAGCACTGCTTTGTT
TAATGATGGCAAAGCATGCGGAGGGTGCTATCAGATAACTTGTGATGCAAGACA
GGTGCCTCAATGGTGTCTCAAGGGTAAATACATTACCATCACTGCCACCAACTTC
TGCCCTCCCAACTATGCACTCCCAAGTGATAATGGGGGCTGGTGTAATCCACCCC
GACCACACTTCGACATGTCTCAACCTGCATTCGAGACCATAGCTAAATACAGGGC
TGGAATTGTACCAGTCCTCTACAGGAGGGTTACATGCAGGAGAAAGGGAGGCAT
GAGATTCACCATCAATGGAAGGAATTATTTTGAGCTAGTGCTCATATCGAACGTT
GGAGTTCTGGAGAGATTTCCAGGGTATGGATAAAGGGATCCAAAACCAATAAA
TGGGAAAGCATGTCCAGGAACTGGGGTGCCAATTGGCAGAGCTTAAGCTATCTA
AATGGTCAGAGCTTATCTTTTCAGGATTCAAGCTAGTAATGGCAGGATTCGATATG
CTCTTAATGTGGTGCCTTCCAATTGGCAATTTGGTCAGTCTTTTAAAACCAATGTT
CAGATTTAG

Nucleotide

>GrEXPA-20

ATCTGCGGTATCAAACATCACATTCTCTAGCATAAAAAGAAAAGAAAATTTCC
ATTGTTTTTAGAGGAAGAGAACTCGATGGACAGTGCCTATCTGTTCACTACTGC
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ATACTTGGCTTTCGGCACATGCAACGTTCTATGGTGGAAAGTGATGCTTCTGGAAC
TATGGGTAAGTTTTCTTTCTTTTTCTTTTTAATTCTCTTTCTTATTTTTGTTCTT
CTCATTGAATGACTTAGACAAACATGTTGGTTTTGCAGGTGGAGCTTGTGGTTAT
GGCAATCTCTATACAGATGGTTATGGAACAAACACAGCTGCACTCAGCACTGCTT

TGTTTAATGATGGCAAAGCATGCGGAGGGTGCTATCAGATAACTTGTGATGCAAG
ACAGGTGCCTCAATGGTGTCTCAAGGGTAAATACATTACCATCACTGCCACCAAC
TTCTGCCCTCCCAACTATGCACTCCCAAGTGATAATGGGGGCTGGTGTAAATCCAC
CCCGACCACACTTCGACATGTCTCAACCTGCATTCGAGACCATAGCTAAATACAG
GGCTGGAATTGTACCAGTCCTCTACAGGAGGTATGTCCATTGTTTCTTCCATAAAA
AACTTGAAGGCGTAAGCAATGGTGGTGAAAAATGGCTTAAGAGTATCTCCGAGT
AATTTGTTTTGTGTTTTGCCAGGGTTACATGCAGGAGAAAGGGAGGCATGAGATT
CACCATCAATGGAAGGAATTATTTTGAGCTAGTGCTCATATCGAACGTTGGAGGT
TCTGGAGAGATTTCCAGGGTATGGATAAAGGGATCCAAAACCAATAAATGGGAA
AGCATGTCCAGGAAGTGGGGTGCCAATTGGCAGAGCTTAAGCTATCTAAATGGTC
AGAGCTTATCTTTCAGGATTCAAGCTAGTAATGGCAGGATTCGATATGCTCTTAA
TGTGGTGCCTTCCAATTGGCAATTTGGTCAGTCTTTTAAAACCAATGTTTCAGATTT
AGAACTCTGCATATCATCTCACATGTATTTATGTATTTTGTTTTTACTTTGGTTTCA
TTTACTTCAAATTGTATCATAAAGTGTCACTAAGGCTGTGGCTCAGCGTTTT
GCAATGAAGCCCGGCAAGTGATTTATTTATAAAATATATTAGCCGACTAGTGGC
TGCTTTATTGTAATGGTATTCATAAATGCAAGTATGCAATGAATCTTCCAAATTC
CAATTA