

IDENTIFICATION

Species: *Gossypium raimondii*

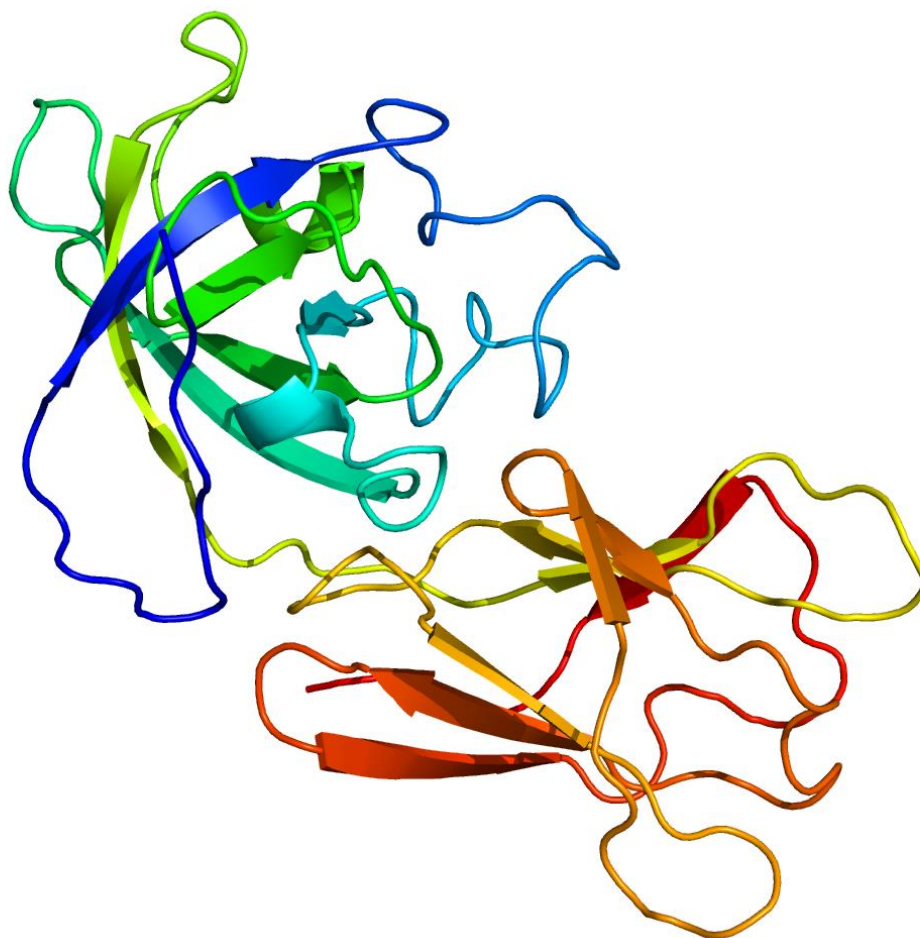
Locus: Gorai.007G022000

Gene Model: Gorai.007G022000.1

Description: GrEXPA-19

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>

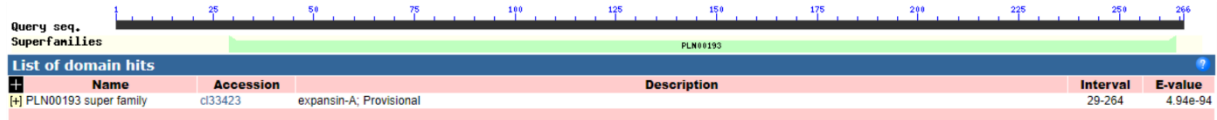
EXTERNAL RESOURCES

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

GENE STRUCTURE



DOMAIN ARCHITECTURE



SEQUENCES

Peptide

>GrEXPA-19

MNVSEKHAFRFSESEFFGRVALAIIGKPSVAAVVYRPSWALAHATFYGDETASETMG
GACGYGNLFSNGYGIDTAALSTTLFNNGFACGTCYQIKCVKSPWCYSGVQFTT²⁵VTAT
NLCPPN⁵⁰WAKDTN⁷⁵NGGWCN¹⁰⁰PPRVHFDMSKPAFMKIAQWKAGIVPIMYRRVPCIRRGG
IRFYFQNGY¹²⁵WLLVYAMNVGGGGDIAKMWVKGSKTGWIGMSHNW¹⁵⁰GASYQAFATL
TGQSL¹⁷⁵SKITSYTSKETIICWNVAPANWNVGLTYKSNVNFH*²⁰⁰

CDS (coding sequence)

>GrEXPA-19

ATGAACGTGTCAGAAAAGCATGCATTTTCGGTTTTCTGAATCCTTCTTCGGTTCGGGT
TGCATTGGCAATCATCGGCAAACCTTCTGTAGCTGCCGTAGTGTACCGGCCAAGC
CCTTGGGCACTCGCCATGCAACCTTTACGGCGATGAAACCGCCTCCGAGACTA
TGGGAGGTGCTTGTGGGTATGGGAATTTGTTAGCAATGGTTATGGTATTGACAC
AGCTGCACTGAGCACAACATTGTTCAACAATGGGTTTGCTTGTGGGACTTGTTAT
CAAATAAAGTGTGTTAAGTCGCCTTGGTGCTACAGTGGGGTTCAATTCACCACCG
TGACGGCTACAAACCTTTGCCCTCCGAATTGGGCCAAAGACACCAACAATGGTGG
GTGGTGCACCCTCCACGAGTCCATTTTGATATGTCGAAGCCCGCTTTTATGAAA
ATTGCTCAGTGGAAGCCGGCATTGTTCCATCATGTACCGAAGGGTACCGTGTA
TAAGACGAGGGGGATTTCGATTTTATTTCAAGGGAATGGGTATTGGTTGTTAGT
GTATGCGATGAATGTAGGAGGAGGCGGTGACATTGCCAAAATGTGGGTCAAAGG
AAGCAAACAGGGTGGATTGGTATGAGTCATAATTGGGGAGCTTCGTATCAAGC
ATTTGCAACTCTTACGGGCCAATCTTTATCTTTCAAGATCACTTCATACTTCCA
AGGAGACTATCATATGTTGGAATGTTGCACCTGCAAATTGGAATGTAGGTTTGAC
TTACAAGTCAAATGTCAACTTCCATTAA

Nucleotide

>GrEXPA-19

GATAACAATATCCATTTCAAAAATTTTCGAGTTTGACTTTCAGAGAATTTTAGCTT
CATGAACGTGTCAGAAAAGCATGCATTTTCGGTTTTCTGAATCCTTCTTCGGTTCGGG
TTGGT²⁵GAGTTTGCAAACACTATATAATGTGAACATGTAGAGTCAATAACAGGA
ATTAATTGCTCGTAACTTGT⁵⁰TGATCAAAGGTCTCATCGAAAAAAAAAACCATGT
CTTTTTCATTGAATTCATGGAGCTTTGTGTTTCTTTTATGACACTAACAGCATTGG
CAATCATCGGCAAACCTTCTGTAGCTGCCGTAGTGTACCGGCCAAGCCCTTGGGC
ACTCGCCCATGCAACCTTTTACGGCGATGAAACCGCCTCCGAGACTATGGGTATG

TTATGTCGCAAATTATACGTGTTTACAGGTGAATATTCAGACATGAAATCCAGAA
TAATCGGTTATAATTAATGTTTTTTCTTTACAGGAGGTGCTTGTGGGTATGGGAA
TTTGTAGCAATGGTTATGGTATTGACACAGCTGCACTGAGCACAACATTGTTCA
ACAATGGGTTTGTCTTGTGGGACTTGTTATCAAATAAAGTGTGTTAAGTCGCCTTG
GTGCTACAGTGGGGTTCAATTCACCACCGTGACGGCTACAAACCTTTGCCCTCCG
AATTGGGCCAAAGACACCAACAATGGTGGGTGGTGCAACCCTCCACGAGTCCATT
TTGATATGTCGAAGCCCGCTTTTATGAAAATTGCTCAGTGGAAAGCCGGCATTGT
TCCTATCATGTACCGAAGGTACGACTTTTTTTAATGATTTTGAATAGGGATATACC
CACGCTACATATAACCATGTTCAAAGGAGTTGTCTAAATAAATATCTATCACTTG
CTCCTCGAAAGTACGATCTCCGATAAATTATAAGGGTGAATAGTTCTTAACCATC
AAACTAAACAAGAAAGTTCCATAAAAAAATGTTATGATCGTTATTTTATAATTCG
AATTTTCGATTCCTTACAGGGTACCGTGTATAAGACGAGGGGGGATTCGATTTA
TTTTCAAGGGAATGGGTATTGGTTGTTAGTGTATGCGATGAATGTAGGAGGAGGC
GGTGACATTGCCAAAATGTGGGTCAAAGGAAGCAAACAGGGTGGATTGGTATG
AGTCATAATTGGGGAGCTTCGTATCAAGCATTTGCAACTCTTACGGGCCAATCTTT
ATCTTTCAAGATCACTTCATACACTTCCAAGGAGACTATCATATGTTGGAATGTTG
CACCTGCAAATTGGAATGTAGGTTTGACTTACAAGTCAAATGTCAACTTCCATTA
ATCTGGTCTGGCCTGATTTATGAACACATTTATTTTATTTAGTTGATTCCGTTAGTT
TTTCCTTTTTATTGGAGAATTGTATTTGTACTTTCTATAACATAGGCAATGATGAA
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TTTTCTTTTAGTTCTGTGGCGGATCTTAACATGTAATTTTTTGAGAGAACCGTCAAT
TAATACAATGTATATTTGAACTTG