

Resource Summary Report

Generated by T1D on Sep 5, 2026

Cotton EST Database

RRID:SCR_003301

Type: Tool

Proper Citation

Cotton EST Database (RRID:SCR_003301)

Resource Information

URL: <http://150.216.56.64/index.php>

Proper Citation: Cotton EST Database (RRID:SCR_003301)

Description: Database platform for cotton expressed sequence tag (EST)-related information, covering assembled contigs, function annotation, analysis of GO and KEGG, SNP, miRNA, SSR-related marker information.

Abbreviations: Cotton EST Database

Resource Type: data or information resource, database

Defining Citation: [PMID:22087239](https://pubmed.ncbi.nlm.nih.gov/22087239/)

Keywords: expressed sequence tag, contig, indel mutant, single nucleotide polymorphism, transcription factor, protein kinase, gene, mirna, blast, est-simple sequence repeat, simple sequence repeat, pathway, function

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: Cotton EST Database

Resource ID: SCR_003301

Alternate IDs: r3d100011232

Alternate URLs: <https://doi.org/10.17616/R3X63C>

Old URLs: <http://www.leonxie.com/>

Record Creation Time: 20220129T080218+0000

Record Last Update: 20260904T000113+0000

Ratings and Alerts

No rating or validation information has been found for Cotton EST Database.

No alerts have been found for Cotton EST Database.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 10 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#).

Lyu S, et al. (2019) Identification of Appropriate Reference Genes for Normalizing miRNA Expression in Citrus Infected by *Xanthomonas citri* subsp. *citri*. *Genes*, 11(1).

Larsson C, et al. (2017) Loss of DIP2C in RKO cells stimulates changes in DNA methylation and epithelial-mesenchymal transition. *BMC cancer*, 17(1), 487.

Al-Sabah A, et al. (2016) Importance of reference gene selection for articular cartilage mechanobiology studies. *Osteoarthritis and cartilage*, 24(4), 719.

Ihara F, et al. (2016) Changes in neurotransmitter levels and expression of immediate early genes in brain of mice infected with *Neospora caninum*. *Scientific reports*, 6, 23052.

Abe C, et al. (2015) Role of the chemokine receptor CCR5-dependent host defense system in *Neospora caninum* infections. *Parasites & vectors*, 8, 5.

Li R, et al. (2015) Transcriptome Analysis of Cotton (*Gossypium hirsutum* L.) Genotypes That Are Susceptible, Resistant, and Hypersensitive to Reniform Nematode (*Rotylenchulus reniformis*). *PloS one*, 10(11), e0143261.

Wang S, et al. (2015) The potent tumor suppressor miR-497 inhibits cancer phenotypes in nasopharyngeal carcinoma by targeting ANLN and HSPA4L. *Oncotarget*, 6(34), 35893.

Artico S, et al. (2014) Transcriptome analysis of *Gossypium hirsutum* flower buds infested by cotton boll weevil (*Anthonomus grandis*) larvae. *BMC genomics*, 15(1), 854.

Ding J, et al. (2012) Finding microRNA targets in plants: current status and perspectives. *Genomics, proteomics & bioinformatics*, 10(5), 264.

McEwan IJ, et al. (2009) Nuclear hormone receptor architecture - form and dynamics: The 2009 FASEB Summer Conference on Dynamic Structure of the Nuclear Hormone Receptors. *Nuclear receptor signaling*, 7, e011.