

Resource Summary Report

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dbEST

RRID:SCR_008132

Type: Tool

Proper Citation

dbEST (RRID:SCR_008132)

Resource Information

URL: <https://www.ncbi.nlm.nih.gov/genbank/dbest/>

Proper Citation: dbEST (RRID:SCR_008132)

Description: Database as a division of GenBank that contains sequence data and other information on single-pass cDNA sequences, or Expressed Sequence Tags, from a number of organisms.

Synonyms: database Expressed Sequence Tag (EST), database Expressed Sequence Tag

Resource Type: storage service resource, data repository, service resource, database, data or information resource

Defining Citation: [PMID:8401577](#)

Keywords: data, sequence, single, pass, cDNA, express, tag, bio.tools, gold standard

Resource Name: dbEST

Resource ID: SCR_008132

Alternate IDs: biotools:dbest, nif-0000-20937, r3d100010648

Alternate URLs: <http://www.ncbi.nlm.nih.gov/dbEST/>, <https://bio.tools/dbest>, <https://doi.org/10.17616/R3FG8P>

Record Creation Time: 20220129T080245+0000

Record Last Update: 20260805T044202+0000

Ratings and Alerts

No rating or validation information has been found for dbEST.

No alerts have been found for dbEST.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 179 mentions in open access literature.

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

Tan S, et al. (2025) Movi Color: fast and accurate long-read classification with the move structure. bioRxiv : the preprint server for biology.

Joshi A, et al. (2023) Genetic Databases and Gene Editing Tools for Enhancing Crop Resistance against Abiotic Stress. Biology, 12(11).

Macharia TN, et al. (2023) In silico secretome analyses of the polyphagous root-knot nematode *Meloidogyne javanica*: a resource for studying *M. javanica* secreted proteins. BMC genomics, 24(1), 296.

Xing X, et al. (2023) The First High-quality Reference Genome of Sika Deer Provides Insights into High-tannin Adaptation. Genomics, proteomics & bioinformatics, 21(1), 203.

Shanmugasundram A, et al. (2023) TriTrypDB: An integrated functional genomics resource for kinetoplastida. PLoS neglected tropical diseases, 17(1), e0011058.

Das P, et al. (2023) A comprehensive review on genomic resources in medicinally and industrially important major spices for future breeding programs: Status, utility and challenges. Current research in food science, 7, 100579.

Lin YH, et al. (2023) A salivary GMC oxidoreductase of *Manduca sexta* re-arranges the green leaf volatile profile of its host plant. Nature communications, 14(1), 3666.

Zhou Y, et al. (2022) Assembly of a pangenome for global cattle reveals missing sequences and novel structural variations, providing new insights into their diversity and evolutionary history. Genome research, 32(8), 1585.

Raeispour Shirazi M, et al. (2021) Identification and in-silico characterization of taxadien-5??-ol-O-acetyltransferase (TDAT) gene in *Corylus avellana* L. PloS one, 16(8), e0256704.

Yasin JK, et al. (2020) Genome wide in-silico miRNA and target network prediction from stress responsive Horsegram (*Macrotyloma uniflorum*) accessions. Scientific reports, 10(1), 17203.

Gahoi S, et al. (2019) Genome-wide identification and comprehensive analysis of Excretory/Secretory proteins in nematodes provide potential drug targets for parasite control. *Genomics*, 111(3), 297.

Rocha AJ, et al. (2018) Cloning of cDNA sequences encoding cowpea (*Vigna unguiculata*) vicilins: Computational simulations suggest a binding mode of cowpea vicilins to chitin oligomers. *International journal of biological macromolecules*, 117, 565.

Woldesemayat AA, et al. (2017) An integrated and comparative approach towards identification, characterization and functional annotation of candidate genes for drought tolerance in sorghum (*Sorghum bicolor* (L.) Moench). *BMC genetics*, 18(1), 119.

Mutti JS, et al. (2017) Evolution of Gene Expression Balance Among Homeologs of Natural Polyploids. *G3* (Bethesda, Md.), 7(4), 1225.

Oppelt SA, et al. (2017) Specific regions of the brain are capable of fructose metabolism. *Brain research*, 1657, 312.

Yuan SL, et al. (2017) RNA-Seq analysis of nodule development at five different developmental stages of soybean (*Glycine max*) inoculated with *Bradyrhizobium japonicum* strain 113-2. *Scientific reports*, 7, 42248.

Guerriero G, et al. (2017) Identification of fasciclin-like arabinogalactan proteins in textile hemp (*Cannabis sativa* L.): in silico analyses and gene expression patterns in different tissues. *BMC genomics*, 18(1), 741.

Dhakal R, et al. (2017) Expression Profiling Coupled with In-silico Mapping Identifies Candidate Genes for Reducing Aflatoxin Accumulation in Maize. *Frontiers in plant science*, 8, 503.

Eschbaumer M, et al. (2016) Transcriptomic Analysis of Persistent Infection with Foot-and-Mouth Disease Virus in Cattle Suggests Impairment of Apoptosis and Cell-Mediated Immunity in the Nasopharynx. *PloS one*, 11(9), e0162750.

Padmashree D, et al. (2016) Identification and characterization of conserved miRNAs with its targets mRNA in *Trichinella Spiralis*. *Bioinformation*, 12(5), 279.