

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: data or information resource, data repository, database, service resource, storage service 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: 20260829T182326+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 186 mentions in open access literature.

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

MacDonald ZG, et al. (2026) Genome assembly for the Sierra Nevada Parnassian (*Parnassius behrii*) and a brief review of butterfly genome sizes. *The Journal of heredity*, 117(4), 888.

Tan S, et al. (2025) Movi Color: fast and accurate taxonomic classification with the move structure. *ACM-BCB ... : the ... ACM Conference on Bioinformatics, Computational Biology and Biomedicine. ACM Conference on Bioinformatics, Computational Biology and Biomedicine*, 2025.

Wang B, et al. (2025) Genome-wide comprehensive analysis the molecular phylogenetic evolution, functional divergence and tissue-specific expression of GH3 gene family in *Salvia miltiorrhiza*, *Arabidopsis thaliana*, and *Oryza sativa*. *Frontiers in plant science*, 16, 1644853.

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).

Liu QR, et al. (2023) Novel Hominid-Specific IAPP Isoforms: Potential Biomarkers of Early Alzheimer's Disease and Inhibitors of Amyloid Formation. *Biomolecules*, 13(1).

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

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.

Jiang H, et al. (2023) Development of simple sequence repeat markers for sugarcane from data mining of expressed sequence tags. *Frontiers in plant science*, 14, 1199210.

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.

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.

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.

Liu X, et al. (2022) Identification of Differentially Expressed Genes in Resistant Tetraploid Wheat (*Triticum turgidum*) under *Sitobion avenae* (F.) Infestation. *International journal of molecular sciences*, 23(11).

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.

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

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.