

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

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: 20260812T044141+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 [ASWG](#) .

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.