

Resource Summary Report

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Nucleotide database

RRID:SCR_004630

Type: Tool

Proper Citation

Nucleotide database (RRID:SCR_004630)

Resource Information

URL: <http://www.ncbi.nlm.nih.gov/nucest>

Proper Citation: Nucleotide database (RRID:SCR_004630)

Description: Nucleotide database as collection of sequences from several sources, including GenBank, RefSeq, TPA and PDB. Genome, gene and transcript sequence data provide the foundation for biomedical research and discovery.

Abbreviations: nucest

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

Defining Citation: [PMID:8401577](#)

Keywords: Genome, gene, transcript sequence data, GenBank, RefSeq, TPA, PDB, gold standard

Availability: Free, Freely available

Resource Name: Nucleotide database

Resource ID: SCR_004630

Alternate IDs: SCR_016578, nlx_62971

Record Creation Time: 20220129T080225+0000

Record Last Update: 20260728T043205+0000

Ratings and Alerts

No rating or validation information has been found for Nucleotide database.

No alerts have been found for Nucleotide database.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 167 mentions in open access literature.

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

Kabir N, et al. (2022) RAD gene family analysis in cotton provides some key genes for flowering and stress tolerance in upland cotton *G. hirsutum*. *BMC genomics*, 23(1), 40.

Zhao P, et al. (2021) Mining Unknown Porcine Protein Isoforms by Tissue-based Map of Proteome Enhances Pig Genome Annotation. *Genomics, proteomics & bioinformatics*, 19(5), 772.

Ching KH, et al. (2020) Expression of human lambda expands the repertoire of OmniChickens. *PloS one*, 15(1), e0228164.

Shen WW, et al. (2020) EHD2 is a Predictive Biomarker of Chemotherapy Efficacy in Triple Negative Breast Carcinoma. *Scientific reports*, 10(1), 7998.

Simonovic S, et al. (2020) Limited utility of qPCR-based detection of tumor-specific circulating mRNAs in whole blood from clear cell renal cell carcinoma patients. *BMC urology*, 20(1), 7.

Cheng RL, et al. (2020) Nudivirus Remnants in the Genomes of Arthropods. *Genome biology and evolution*, 12(5), 578.

Bay?r M, et al. (2020) Identification and Characterization of Carnitine Palmitoyltransferase 1 (cpt 1) Genes in Nile Tilapia, *Oreochromis niloticus*. *Evolutionary bioinformatics online*, 16, 1176934320913255.

Wang W, et al. (2020) Comprehensive analysis of the *Gossypium hirsutum* L. respiratory burst oxidase homolog (Ghrboh) gene family. *BMC genomics*, 21(1), 91.

Haenig C, et al. (2020) Interactome Mapping Provides a Network of Neurodegenerative Disease Proteins and Uncovers Widespread Protein Aggregation in Affected Brains. *Cell reports*, 32(7), 108050.

Mathew R, et al. (2019) The genome of the migratory nematode, *Radopholus similis*, reveals signatures of close association to the sedentary cyst nematodes. *PloS one*, 14(10), e0224391.

Zhao J, et al. (2019) A MIF-like effector suppresses plant immunity and facilitates nematode parasitism by interacting with plant annexins. *Journal of experimental botany*, 70(20), 5943.

Chen S, et al. (2019) Genome-Wide Analysis of Serine/Arginine-Rich Protein Family in Wheat and *Brachypodium distachyon*. *Plants* (Basel, Switzerland), 8(7).

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.

Luukkonen J, et al. (2019) Osteoclasts secrete osteopontin into resorption lacunae during bone resorption. *Histochemistry and cell biology*, 151(6), 475.

Yu J, et al. (2019) Insight into the evolution and functional characteristics of the pan-genome assembly from sesame landraces and modern cultivars. *Plant biotechnology journal*, 17(5), 881.

Fatemi F, et al. (2019) Exploiting Differential Gene Expression to Discover Ionic and Osmotic-Associated Transcripts in the Halophyte Grass *Aeluropus litoralis*. *Biological procedures online*, 21, 14.

Tran HTM, et al. (2018) Use of a draft genome of coffee (*Coffea arabica*) to identify SNPs associated with caffeine content. *Plant biotechnology journal*, 16(10), 1756.

Filippenkov IB, et al. (2018) Multi-step splicing of sphingomyelin synthase linear and circular RNAs. *Gene*, 654, 14.

Magwanga RO, et al. (2018) GBS Mapping and Analysis of Genes Conserved between *Gossypium tomentosum* and *Gossypium hirsutum* Cotton Cultivars that Respond to Drought Stress at the Seedling Stage of the BC₂F₂ Generation. *International journal of molecular sciences*, 19(6).

McLean F, et al. (2018) Improving the annotation of the *Heterorhabditis bacteriophora* genome. *GigaScience*, 7(4).