Resource Summary Report

Generated by NIF on May 8, 2025

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

Defining Citation: PMID:8401577

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

Funding:

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: 20250507T060248+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 NIF.

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.

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

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

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.

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

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.

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).

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 littoralis. Biological procedures online, 21, 14.

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.

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.

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 BC?F? Generation. International journal of molecular sciences, 19(6).

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

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