

# Resource Summary Report

Generated by T1D on Aug 2, 2026

## NCBI BioSample

RRID:SCR\_004854

Type: Tool

### Proper Citation

NCBI BioSample (RRID:SCR\_004854)

### Resource Information

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

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**Description:** Database containing descriptions of biological source materials used in experimental assays. Sources include: GenBank, Sequence Read Archive (SRA), Coriell, ATCC. Submissions are supported by a web-based Submission Portal that guides users through a series of forms for input of rich metadata describing their samples. As the capacity and complexity of biological data sets expands, databases face new challenges in ensuring that the information is adequately organized and described. The NCBI BioSample database is being developed to help address the challenges by providing the means by which data generators can organize and describe a broad range of sample types, and link to corresponding sets of experimental data in archival databases.

**Abbreviations:** BioSample

**Synonyms:** BioSample Database, NCBI BioSample Database

**Resource Type:** database, data or information resource

**Defining Citation:** [PMID:22139929](#)

**Keywords:** RIN, Resource Information Network, dna, rna, cell, cell line, stem cell, biomaterial, gold standard, RRID Community Authority

**Funding:** NLM

**Availability:** The community can contribute to this resource

**Resource Name:** NCBI BioSample

**Resource ID:** SCR\_004854

**Alternate IDs:** nlx\_143929, r3d100012828, OMICS\_01024

**Alternate URLs:** <https://doi.org/10.17616/R31NJME4>

**Record Creation Time:** 20220129T080226+0000

**Record Last Update:** 20260803T040411+0000

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## Ratings and Alerts

No rating or validation information has been found for NCBI BioSample.

No alerts have been found for NCBI BioSample.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 410 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [T1D](#).

Maeoka R, et al. (2025) Immunotherapy using allogenic NK cells downregulates mitochondrial-related genes and inhibits the OXPHOS system of malignant meningioma. *Biomedicine & pharmacotherapy = Biomedecine & pharmacotherapie*, 187, 118099.

Ji F, et al. (2025) Liver-specific gene PGRMC1 blocks c-Myc-induced hepatocarcinogenesis through ER stress-independent PERK activation. *Nature communications*, 16(1), 50.

Payne M, et al. (2025) Characterizing *Staphylococcus aureus* genomic epidemiology with multilevel genome typing. *mSystems*, 10(10), e0093525.

Ghazawi A, et al. (2025) Comparative genomic study of blaKPC-2-carrying multidrug-resistant *Klebsiella pneumoniae* in the United Arab Emirates. *Scientific reports*, 15(1), 45259.

Alves G, et al. (2025) Biological Function Assignment Across Taxonomic Levels in Mass-Spectrometry-Based Metaproteomics via a Modified Expectation Maximization Algorithm. *bioRxiv : the preprint server for biology*.

Zhang D, et al. (2025) Genetic Profiling of Synchronous Pituitary Corticotroph Adenomas. *Research square*.

Cia C-T, et al. (2025) Infections caused by clonal spread of metallo-beta-lactamase-producing *Enterobacter cloacae* complex isolates at a southern Taiwan hospital. *Microbiology spectrum*, 13(7), e0023425.

Ahmed MA, et al. (2025) Genome-resolved adaptation strategies of Rhodobacterales to changing conditions in the Chesapeake and Delaware Bays. *Applied and environmental*

microbiology, 91(2), e0235724.

Alves G, et al. (2025) Biological Function Assignment across Taxonomic Levels in Mass-Spectrometry-Based Metaproteomics via a Modified Expectation Maximization Algorithm. *Journal of proteome research*, 24(8), 3818.

Luo S, et al. (2025) Inhibition of Tumor Lipogenesis and Growth by Peptide-Based Targeting of SREBP Activation. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 12(45), e08111.

Barjau-Aguilar M, et al. (2025) Diversity and Structure of the Prokaryotic Community in Tropical Monomictic Reservoir. *Microbial ecology*, 88(1), 12.

Ullah K, et al. (2025) ARNT-dependent HIF-2 $\alpha$  signaling protects cardiac microvascular barrier integrity and heart function post-myocardial infarction. *Communications biology*, 8(1), 440.

Qin X, et al. (2025) Thioester-containing protein TEP15 promotes malaria parasite development in mosquitoes through negative regulation of melanization. *Parasites & vectors*, 18(1), 124.

Mansueto L, et al. (2024) CannSeek? Yes we Can! An open-source single nucleotide polymorphism database and analysis portal for Cannabis sativa. *GigaByte (Hong Kong, China)*, 2024, gigabyte135.

Wang H, et al. (2024) Crop DNA extraction with lab-made magnetic nanoparticles. *PloS one*, 19(1), e0296847.

Koubínová D, et al. (2024) Microsatellite Content in 397 Nuclear Exons and Their Flanking Regions in the Fern Family Ophioglossaceae. *Plants (Basel, Switzerland)*, 13(5).

Schikora-Tamarit MÀ, et al. (2024) Recent gene selection and drug resistance underscore clinical adaptation across Candida species. *Nature microbiology*, 9(1), 284.

Ortiz-Chura A, et al. (2024) Ruminant microbiome data are skewed and unFAIR, undermining their usefulness for sustainable production improvement. *Animal microbiome*, 6(1), 61.

Alfonso P, et al. (2024) Unveiling the hidden viromes across the animal tree of life: insights from a taxonomic classification pipeline applied to invertebrates of 31 metazoan phyla. *mSystems*, 9(5), e0012424.

Meshram DD, et al. (2024) Membrane Association of the Short Transglutaminase Type 2 Splice Variant (TG2-S) Modulates Cisplatin Resistance in a Human Hepatocellular Carcinoma (HepG2) Cell Line. *Current issues in molecular biology*, 46(5), 4251.