Resource Summary Report

Generated by RRID on May 23, 2025

NCBI BioSample

RRID:SCR_004854

Type: Tool

Proper Citation

NCBI BioSample (RRID:SCR_004854)

Resource Information

URL: http://www.ncbi.nlm.nih.gov/biosample

Proper Citation: NCBI BioSample (RRID:SCR_004854)

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: data or information resource, database

Defining Citation: PMID:22139929

Keywords: RIN, Resource Information Network, dna, rna, cell, cell line, stem cell,

biomaterial, gold standard

Funding: NLM

Availability: The community can contribute to this resource

Resource Name: NCBI BioSample

Resource ID: SCR_004854

Alternate IDs: nlx_143929, OMICS_01024

Record Creation Time: 20220129T080226+0000

Record Last Update: 20250523T054437+0000

Ratings and Alerts

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

No alerts have been found for NCBI BioSample.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 398 mentions in open access literature.

Listed below are recent publications. The full list is available at RRID.

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.

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.

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.

Bergström A, et al. (2024) Improving data archiving practices in ancient genomics. Scientific data, 11(1), 754.

Choi S, et al. (2024) Dissemination of pathogenic bacteria is reinforced by a MARTX toxin effector duet. Nature communications, 15(1), 6218.

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.

Wang Z, et al. (2024) Distinct prophage gene profiles of Staphylococcus aureus strains from atopic dermatitis patients and healthy individuals. Microbiology spectrum, 12(8), e0091524.

Knjaz M, et al. (2024) First regional reference database of northern Adriatic diatom transcriptomes. Scientific reports, 14(1), 16209.

Chu YH, et al. (2024) Molecular mechanisms underlying gene regulatory variation of maize metabolic traits. The Plant cell, 36(9), 3709.

Dong W, et al. (2024) An expanded database and analytical toolkit for identifying bacterial virulence factors and their associations with chronic diseases. Nature communications, 15(1), 8084.

Aguilar-Rangel EJ, et al. (2024) Increases in the soil ammonia oxidizing phylotypes and their rechange due to long-term irrigation with wastewater. PloS one, 19(4), e0299518.

Chen Y, et al. (2024) LncRNA LINK-A Remodels Tissue Inflammatory Microenvironments to Promote Obesity. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 11(10), e2303341.

Wang Z, et al. (2024) Genomic and functional divergence of Staphylococcus aureus strains from atopic dermatitis patients and healthy individuals: insights from global and local scales. Microbiology spectrum, 12(10), e0057124.

Acuña-Castillo C, et al. (2024) A retrospective study suggests 55 days of persistence of SARS-CoV-2 during the first wave of the pandemic in Santiago de Chile. Heliyon, 10(7), e24419.

Tapia AC, et al. (2024) RNA-clique: a method for computing genetic distances from RNA-seq data. BMC bioinformatics, 25(1), 205.

Kambara K, et al. (2024) Data from collection and analysis of RNA sequencing data from pearl millet. Data in brief, 55, 110592.