

Resource Summary Report

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[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: 20260819T044125+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 432 mentions in open access literature.

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

Sáenz JS, et al. (2026) The chicken gut virome: spatial structuring and extensive diversity of 19,778 viral populations. *mSystems*, 11(4), e0019126.

Hu B, et al. (2026) Metagenomics reveals potential interactions between Patescibacteriota and their phages in groundwater ecosystems. *mSystems*, 11(2), e0120425.

de Sousa LLF, et al. (2026) Integrated molecular and metatranscriptomic evidence of Tacaribe virus and the brain virome profile of *Molossus molossus* bat sampled in Brazil. *Microbiology spectrum*, 14(3), e0196025.

Tascini C, et al. (2026) In vitro activity of cefepime/zidebactam against *Klebsiella pneumoniae* carrying bla KPC variants conferring resistance to ceftazidime/avibactam. *JAC-antimicrobial resistance*, 8(1), dlag026.

Kim N-H, et al. (2026) Comparative genomic analyses of *Escherichia coli* ST405 strains from Pakistan. *mSystems*, 11(4), e0168525.

Romanenko MN, et al. (2026) *Psychrobacillus syltrankelensis* sp. nov., a new species isolated from soil in the North Caucasus, Russia. *Microbiology spectrum*, 14(6), e0291925.

Greco JPG, et al. (2026) A pangenome-based strategy for designing a multi-epitope vaccine against non-toxin antigens of necrotic enteritis-associated *Clostridium perfringens*. *Brazilian journal of microbiology* : [publication of the Brazilian Society for Microbiology], 57(1).

Chongdar N, et al. (2026) Genomic Survey of Carbon Monoxide Dehydrogenases Reveals Their Widespread Distribution in Marine Habitats. *Environmental microbiology reports*, 18(3), e70375.

Mullet JI, et al. (2026) Phage-plasmid-like elements are found throughout diverse environments and encode niche-specific functional traits. PloS one, 21(5), e0350027.

Uzun H?, et al. (2026) Valorisation of cheese whey into single-cell protein by *Lactococcus garvieae*: dual waste nitrogen supplementation and uncertainty-informed process evaluation. World journal of microbiology & biotechnology, 42(5).

Hirsch RM, et al. (2026) CD73 restrains mutant β -catenin oncogenic activity in endometrial carcinomas. JCI insight, 11(2).

Özdemir K, et al. (2026) Characterization of a Boron-Tolerant *Nocardia niigatensis* Isolated from Boron-Rich Soils: Physiological, Enzymatic, and Genomic Insights. Microorganisms, 14(2).

Ji X, et al. (2026) ResMicroDb: a comprehensive database and analysis platform for the human respiratory microbiome. Nucleic acids research, 54(D1), D858.

Guan J, et al. (2026) Emergence of a high-risk multidrug-resistant *Acinetobacter baumannii* clone ST697 in nosocomial settings. Microbiology spectrum, 14(6), e0229325.

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.

Zeng X, et al. (2025) Identification and characterization of an invasive, hyper-aerotolerant *Campylobacter jejuni* strain causing bacteremia in a pediatric leukemia patient. ASM case reports, 1(3).

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.

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.