

Resource Summary Report

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NCBI Sequence Read Archive (SRA)

RRID:SCR_004891

Type: Tool

Proper Citation

NCBI Sequence Read Archive (SRA) (RRID:SCR_004891)

Resource Information

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

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Description: Repository of raw sequencing data from next generation of sequencing platforms including including Roche 454 GS System, Illumina Genome Analyzer, Applied Biosystems SOLiD System, Helicos Heliscope, Complete Genomics, and Pacific Biosciences SMRT. In addition to raw sequence data, SRA now stores alignment information in form of read placements on reference sequence. Data submissions are welcome. Archive of high throughput sequencing data, part of international partnership of archives (INSDC) at NCBI, European Bioinformatics Institute and DNA Database of Japan. Data submitted to any of this three organizations are shared among them.

Abbreviations: SRA

Synonyms: Sequence Read Archive, , SRA, NCBI SRA

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

Defining Citation: [PMID:22009675](#), [PMID:21062823](#)

Keywords: sequence, blast, next-generation sequence, alignment, read placement, reference sequence, roche 454 gs system, illumina genome analyzer, applied biosystems solid system, helicos heliscope, complete genomics, pacific biosciences smrt, high-throughput sequencing, data analysis service, gold standard

Funding: NLM

Availability: Free, Available for download, Freely available

Resource Name: NCBI Sequence Read Archive (SRA)

Resource ID: SCR_004891

Alternate IDs: OMICS_01031, nlx_86174, r3d100010775

Alternate URLs: <https://doi.org/10.17616/R31S69>

Record Creation Time: 20220129T080227+0000

Record Last Update: 20260801T042551+0000

Ratings and Alerts

No rating or validation information has been found for NCBI Sequence Read Archive (SRA).

No alerts have been found for NCBI Sequence Read Archive (SRA).

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 6671 mentions in open access literature.

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

Zhu J, et al. (2026) The potential immunological mechanisms of gut microbiota dysbiosis caused by antibiotics exacerbate the lethality of influenza viruses. *Gut microbes*, 18(1), 2609451.

Yu Y, et al. (2026) *Perilla frutescens* seeds enhance lamb immunity and antioxidant capacity via the microbiota-gut-liver-muscle axis. *Journal of animal science and biotechnology*, 17(1), 1.

Baek MG, et al. (2026) Altered Phage-Related Gene Profiles in Asthmatic Airways. *Allergy*, 81(1), 252.

Walter JH, et al. (2026) Transcriptome analysis suggests the cell wall as the primary target of the antilisterial effect of carrots. *Microbiology spectrum*, 14(1), e0209125.

Obianwuna UE, et al. (2026) XOS-based prebiotic complex improves laying performance and attenuates inflammation-driven gut injury and dysbiosis under LPS challenge. *Poultry science*, 105(1), 106124.

Monteiro MP, et al. (2026) Deciphering strain differences in *codY* regulation of *Clostridioides difficile* sporulation. *Microbiology spectrum*, 14(1), e0170625.

Long Y, et al. (2026) Interactions between phytoplankton and bacterioplankton communities in Caohai plateau lake, revealed by environmental DNA metagenomics. *BMC microbiology*, 26(1), 4.

Sankar V, et al. (2026) Genetic elements promote retention of extrachromosomal DNA in cancer cells. *Nature*, 649(8095), 152.

Melino M, et al. (2025) Depleting the action of EZH2 through PI3K-mTOR inhibition to overcome metastasis and immunotherapy resistance in triple-negative breast cancer. *Molecular cancer therapeutics*.

Guerrero C, et al. (2025) Dynamics of Mutant Hematopoietic Progenitor Cells Are Not Associated with Clinical Outcomes in Multiple Myeloma. *Blood cancer discovery*, 6(3), 203.

Haltom JA, et al. (2025) Importance of De Novo Gene Evolution to Emerging Viral Threats: The ORF10 Strain-Restricted Orphan Gene of SARS-CoV-2 Promotes Pathogenesis. *Molecular biology and evolution*, 42(10).

Ma T, et al. (2025) Pan-Cancer Analyses Refine the Single-Cell Portrait of Tumor-Infiltrating Dendritic Cells. *Cancer research*, 85(19), 3596.

Smith JD, et al. (2025) Genomic Signatures of Poor Prognosis in Merkel Cell Carcinoma: A Single-Institution Prospective Study. *Molecular cancer research : MCR*.

de Groen RAL, et al. (2025) Superior survival in diffuse large B cell lymphoma of the bone with immune rich tumor microenvironment. *Blood cancer journal*, 15(1), 82.

Turner LA, et al. (2025) Differences in gene expression between high and low tolerance rainbow trout (*Oncorhynchus mykiss*) to acute thermal stress. *PloS one*, 20(1), e0312694.

Dündar T, et al. (2025) Antimicrobial resistance in coagulase negative staphylococci: Genome analysis and role of horizontal gene transfer. *Research in microbiology*, 176(5-6), 104298.

Muñoz-Mármol AM, et al. (2025) Multikinase Treatment of Glioblastoma: Evaluating the Rationale for Regorafenib. *Cancers*, 17(3).

Chen Y, et al. (2025) A Machine Learning-Based Strategy Predicts Selective and Synergistic Drug Combinations for Relapsed Acute Myeloid Leukemia. *Cancer research*, 85(14), 2753.

Ishikawa R, et al. (2025) Immunohistochemical and molecular evolutionary features of jejunoileal adenocarcinoma unveiled through comparative analysis with colorectal adenocarcinoma. *Neoplasia (New York, N.Y.)*, 66, 101180.

Han J, et al. (2025) The Glycosyltransferase XYLT1 Activates NF- κ B Signaling to Promote Metastasis of Early-Stage Lung Adenocarcinoma. *Cancer research*, 85(9), 1628.