

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, database, service resource, storage 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: 20260821T193729+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 7247 mentions in open access literature.

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

Hayashida H, et al. (2026) Genome-wide screening identifies ZFP91 as a key regulator of EVI1 in myeloid leukemia. *Oncogene*, 45(23), 2237.

Gumpert N, et al. (2026) Recurrent Immunogenic Neoantigens and Their Cognate T-cell Receptors in Treatment-Resistant Metastatic Prostate Cancer. *Cancer discovery*, 16(2), 250.

Fan K, et al. (2026) Monitored food intake in early pregnancy modulates the maternal microbiome in the obese BPH/5 mouse model of superimposed preeclampsia. *Physiological genomics*, 58(3), 144.

Ianevski A, et al. (2026) Multiomics Profiling of T-cell Leukemia and Lymphoma Enables Targeted Therapeutic Discovery. *Cancer research*, 86(2), 295.

Li J, et al. (2026) FNDC4 Drives Metastasis and Immune Evasion in Pancreatic Cancer. *Cancer research*, 86(2), 349.

Yue L, et al. (2026) The mechanism of m6A methylation analysis of the transcriptome to regulate the diameter of Alpine Merino wool fiber. *Animal bioscience*, 39(2), 250347.

Yang W, et al. (2026) Intrinsic MicroRNA-10a Restricts Regulatory T Cell Suppressive Function and Intestinal Repair by Coordinating Transcriptional, Metabolic, and Epithelial Repair Pathways. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 13(4), e09953.

Zhang W, et al. (2026) Dynamic change patterns of the human gut microbiota-fluctuation, loss-acquisition, and turnover-and their underlying causes. *ISME communications*, 6(1), ycag046.

Zhang J, et al. (2026) Hypoxia synergizes cGAS-STING activation and AKT1 phosphorylation to drive pulmonary inflammation in one-lung ventilation: therapeutic attenuation by RU.521 and MK2206. *Journal of inflammation (London, England)*, 23(1).

Zhao J, et al. (2026) Lipid metabolic pathways and the roles of candidate transcription factors identified via lipidomic and transcriptomic analyses at various stages of seed development in *Carya illinoensis*. *BMC plant biology*, 26(1).

Zhu K, et al. (2026) Integrated metabolome and microbiome analysis deciphers the effects of resveratrol and ??-hydroxy-??-methylbutyric acid on jejunal function under different protein levels in Tibetan sheep. *Microbiology spectrum*, 14(3), e0284325.

Rassizadeh L, et al. (2026) Extracellular DNA triggers glucosinolate-dependent defence responses against *Frankliniella occidentalis*. *BMC plant biology*, 26(1).

Sun Y, et al. (2026) Physiological and transcriptomic analyses reveal the effects of phytohormones on growth and astaxanthin accumulation in *Haematococcus pluvialis*. *BMC plant biology*, 26(1).

Abagnale V, et al. (2026) Activity and Abundance of Nitrous Oxide Reducing Bacteria in *Platismatia glauca*: An Epiphytic Lichen in the Boreal Spruce Forest. *Environmental microbiology*, 28(3), e70279.

Sun X, et al. (2026) Genome-Wide Association Study Reveals Genetic Loci, Candidate Genes and Favorable Haplotypes for Important Agronomic Traits in *Auricularia cornea*. *Journal of fungi (Basel, Switzerland)*, 12(3).

Yang X, et al. (2026) Comparative Analysis of Nasal and Cloacal Bacterial Communities in Three Sea Turtle Species under Rescue Center Conditions. *Microbial ecology*, 89(1).

Guo X, et al. (2026) DeepISO: deep learning-powered prediction of protein-protein interaction rewiring generated by alternative splicing. *Genome biology*, 27(1).

Yang X, et al. (2026) *Blastocystis* sp. induces neurocognitive deficits in mice via p38 MAPK-mediated downregulation of NR4A1. *Gut microbes*, 18(1), 2659393.

Kang M, et al. (2026) Comparative Analysis of Quorum Sensing-Dependent Transcriptomic Responses in Phytopathogenic *Burkholderia* spp. *The plant pathology journal*, 42(3), 322.

Yu Y, et al. (2026) STAT1 itaconation prevents macrophage cytotoxic mtDNA -induced inflammation in wear particle-induced aseptic loosening. *Cell communication and signaling : CCS*, 24(1).