

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: 20260919T195044+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 [nidm-terms](#).

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.

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.

Yue L, et al. (2026) Transcriptome and proteome combined analysis of wool fiber diameter regulation mechanism. *Animal bioscience*, 39(2), 250378.

Kang M, et al. (2026) NGSMHC: a simple bioinformatics tool for comprehensively typing major histocompatibility complex genes in non-human species using next-generation sequencing data. *Animal bioscience*, 39(2), 250468.

- Li J, et al. (2026) FNDC4 Drives Metastasis and Immune Evasion in Pancreatic Cancer. *Cancer research*, 86(2), 349.
- 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.
- Vivek AT, et al. (2026) Integrative multi-omics analysis widens annotation and functional insights into long non-coding RNAs of *Arabidopsis thaliana*. *Biology direct*, 21(1), 14.
- 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.
- Chen T, et al. (2026) Synovial Fluid-derived *Micrococcus Luteus* G18 Exacerbates Osteoarthritis Progression by Promoting Chondrocyte Degradation via TLR2/JNK/AP-1 Signaling Pathway. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 13(6), e14220.
- Xue Y, et al. (2026) The PbrMADS1-PbrMYB169 complex has uniquely emerged to regulate lignification of stone cells in pear. *Journal of integrative plant biology*, 68(1), 239.
- van Heule M, et al. (2026) Beyond nocardioform: Transcriptionally active microbes and host responses in equine mucoid placentitis. *Equine veterinary journal*, 58(2), 601.
- Hu Y, et al. (2026) The impact of land-use intensity on the community dynamics of colonial volvocine algae in the Yangtze River Basin. *Microbiology spectrum*, 14(2), e0217425.
- Tyagi S, et al. (2026) Comparative transcriptome analysis reveals ABI3/VP1-WRKY25-STR1 regulatory module linking specialized metabolism with root system development and stress response in *Rauvolfia serpentina*. *BMC genomics*, 27(1), 219.
- Pang S, et al. (2026) LRRK2R1627P mutation amplifies environmental risk factors induced chronic inflammation and α -synuclein aggregation in the gut of rats. *NPJ Parkinson's disease*, 12(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).
- Cuevas-Sierra A, et al. (2026) Disease-specific crosstalk of Alistipes with lipoprotein profiles in overweight individuals at high cardiometabolic risk. *Scientific reports*, 16(1).