

Resource Summary Report

Generated by [kravitz2](#) on Jul 31, 2026

DDBJ Sequence Read Archive

RRID:SCR_001370

Type: Tool

Proper Citation

DDBJ Sequence Read Archive (RRID:SCR_001370)

Resource Information

URL: <https://www.ddbj.nig.ac.jp/dra/index-e.html>

Proper Citation: DDBJ Sequence Read Archive (RRID:SCR_001370)

Description: Archive database for output data generated by next-generation sequencing machines including Roche 454 GS System, Illumina Genome Analyzer, Applied Biosystems SOLiD System, and others. DRA is a member of the International Nucleotide Sequence Database Collaboration (INSDC) and archiving the data in a close collaboration with NCBI Sequence Read Archive (SRA) and EBI Sequence Read Archive (ERA). Please submit the trace data from conventional capillary sequencers to DDBJ Trace Archive., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Abbreviations: DRA

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

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

Keywords: sequence, next-generation sequencing, sequence read, FASEB list

Funding: Japanese Ministry of Education Culture Sports Science and Technology MEXT

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: DDBJ Sequence Read Archive

Resource ID: SCR_001370

Alternate IDs: r3d100013696, OMICS_01027, nlx_152515

Alternate URLs: <http://trace.ddbj.nig.ac.jp/dra/>

Record Creation Time: 20220129T080207+0000

Ratings and Alerts

No rating or validation information has been found for DDBJ Sequence Read Archive.

No alerts have been found for DDBJ Sequence Read Archive.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 74 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Ozaki S, et al. (2025) Plasma protein increase as a chronological aging factor in healthy toy poodles. Scientific reports, 15(1), 42087.

Kunigo K, et al. (2025) Targeted long-read methylation analysis using hybridization capture suitable for clinical specimens. Cell reports methods, 5(11), 101215.

Yoshida K, et al. (2025) Role of ferroptosis-related GPX4 signaling in the fusion of human trophoblast cells. Scientific reports, 15(1), 39515.

Saito M, et al. (2025) Deletion of the Mis12C-Binding Domain of CENP-C Promotes Chromosomal Aneuploidy in Cutaneous Squamous Cell Carcinoma. Cancer science, 116(12), 3532.

Kumagai N, et al. (2025) Identification of an innexin required for termination of the asexual state in planarian reproductive switching. PLoS genetics, 21(11), e1011944.

Iguchi E, et al. (2025) Epithelial Regnase-1 inhibits colorectal tumor growth by regulating IL-17 signaling via degradation of NFKBIZ mRNA. Proceedings of the National Academy of Sciences of the United States of America, 122(23), e2500820122.

Kong F, et al. (2025) MEF2D regulates T-cell function via CD70-CD27 signaling and promotes immune evasion in hepatocellular carcinoma. Journal of immunology (Baltimore, Md. : 1950), 214(11), 3162.

Ishiguro H, et al. (2024) Reduced chondroitin sulfate content prevents diabetic neuropathy through transforming growth factor- β signaling suppression. iScience, 27(4), 109528.

Deycmar S, et al. (2024) Epigenetic MLH1 silencing concurs with mismatch repair deficiency in sporadic, naturally occurring colorectal cancer in rhesus macaques. Journal of translational medicine, 22(1), 292.

Tsukimi T, et al. (2024) Genetic mutation in Escherichia coli genome during adaptation to the murine intestine is optimized for the host diet. *mSystems*, 9(2), e0112323.

Saygin C, et al. (2024) Acute Lymphoblastic Leukemia with Myeloid Mutations Is a High-Risk Disease Associated with Clonal Hematopoiesis. *Blood cancer discovery*, 5(3), 164.

Martínez-Quintanilla J, et al. (2024) Precision Oncology and Systemic Targeted Therapy in Pseudomyxoma Peritonei. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 30(18), 4082.

Tsay JJ, et al. (2024) Lung Microbial and Host Genomic Signatures as Predictors of Prognosis in Early-Stage Adenocarcinoma. *Cancer epidemiology, biomarkers & prevention : a publication of the American Association for Cancer Research, cosponsored by the American Society of Preventive Oncology*, 33(11), 1433.

Ji MT, et al. (2024) Limited WKY chromosomal regions confer increases in anxiety and fear memory in a F344 congenic rat strain. *Physiological genomics*, 56(4), 327.

Guo X, et al. (2024) Hypoxia-Induced Neuronal Activity in Glioma Patients Polarizes Microglia by Potentiating RNA m6A Demethylation. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 30(6), 1160.

Guo X, et al. (2024) Neuronal Activity Promotes Glioma Progression by Inducing Proneural-to-Mesenchymal Transition in Glioma Stem Cells. *Cancer research*, 84(3), 372.

Salari K, et al. (2023) Development and Multicenter Case-Control Validation of Urinary Comprehensive Genomic Profiling for Urothelial Carcinoma Diagnosis, Surveillance, and Risk-Prediction. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 29(18), 3668.

Nagai M, et al. (2023) High body temperature increases gut microbiota-dependent host resistance to influenza A virus and SARS-CoV-2 infection. *Nature communications*, 14(1), 3863.

Smits WK, et al. (2023) Elevated enhancer-oncogene contacts and higher oncogene expression levels by recurrent CTCF inactivating mutations in acute T cell leukemia. *Cell reports*, 42(4), 112373.

Ishihara S, et al. (2022) Rap1 prevents colitogenic Th17 cell expansion and facilitates Treg cell differentiation and distal TCR signaling. *Communications biology*, 5(1), 206.