

Resource Summary Report

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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: data or information resource, data repository, database, service resource, 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 95 mentions in open access literature.

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

Isoyama S, et al. (2026) Cooperative Roles of Class IA PI3K Isoforms in Translocation-Related Sarcoma Cell Survival and Proliferation. Cancer research communications, 6(4), 976.

Amolo KO, et al. (2026) Comprehensive analysis of plasma exosomal and non-exosomal microRNA profiles identifies potential early indicators of carcass traits in Japanese Black cattle. BMC genomics, 27(1).

Kiryu Y, et al. (2026) AlleleMiner: a long-read pipeline for gene-wise de novo allele phasing and variant detection in diploid citrus cultivars. DNA research : an international journal for rapid publication of reports on genes and genomes, 33(2).

Jeong S-Y, et al. (2026) Intrinsic temporal structure and lagged environmental effects shape the dynamics of airborne microscopic eukaryotes. Applied and environmental microbiology, 92(6), e0028626.

Yoshida K, et al. (2026) Dihydroorotate dehydrogenase (DHODH) regulates trophoblast syncytialization through organelle stress-induced cellular senescence. FEBS open bio, 16(6), 1166.

Weinberg F, et al. (2026) Integrative Analysis of Multiomic Pathways Predicts Cancer-Affected Lobes in Lung Cancer. Cancer prevention research (Philadelphia, Pa.), 19(4), 229.

Roels J, et al. (2026) The Hippo Pathway Is Dysregulated in Cancer-Associated Fibroblasts in Anti-PD-L1-Resistant Cancer. Cancer research, 86(11), 2592.

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.

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.

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.

Yang J, et al. (2025) Partially hydrolyzed guar gum attenuates symptoms and modulates the gut microbiota in a model of SARS-CoV-2 infection. *Gut microbiome (Cambridge, England)*, 6, e1.

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.

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.

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.