Resource Summary Report

Generated by FDI Lab - SciCrunch.org on Apr 27, 2025

DDBJ Sequence Read Archive

RRID:SCR_001370
Type: Tool

Proper Citation

DDBJ Sequence Read Archive (RRID:SCR_001370)

Resource Information

URL: http://trace.ddbj.nig.ac.jp/dra/

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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.

Abbreviations: DRA

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

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

Resource Name: DDBJ Sequence Read Archive

Resource ID: SCR_001370

Alternate IDs: OMICS_01027, nlx_152515

Record Creation Time: 20220129T080207+0000

Record Last Update: 20250426T055438+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 66 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Ishiguro H, et al. (2024) Reduced chondroitin sulfate content prevents diabetic neuropathy through transforming growth factor-? 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.

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.

Ishihara T, et al. (2022) Presence of H3K4me3 on Paternally Expressed Genes of the Paternal Genome From Sperm to Implantation. Frontiers in cell and developmental biology, 10, 838684.

Koganebuchi K, et al. (2021) An analysis of the demographic history of the risk allele R4810K in RNF213 of moyamoya disease. Annals of human genetics, 85(5), 166.

Cho K, et al. (2021) Altered microbiota by a high-fat diet accelerates lethal myeloid hematopoiesis associated with systemic SOCS3 deficiency. iScience, 24(10), 103117.

Yokotani N, et al. (2021) Transcriptome analysis of Clavibacter michiganensis subsp. michiganensis-infected tomatoes: a role of salicylic acid in the host response. BMC plant biology, 21(1), 476.

Tsay JJ, et al. (2021) Lower Airway Dysbiosis Affects Lung Cancer Progression. Cancer discovery, 11(2), 293.

Nakamura A, et al. (2020) Asperuloside Improves Obesity and Type 2 Diabetes through Modulation of Gut Microbiota and Metabolic Signaling. iScience, 23(9), 101522.

Yamada T, et al. (2020) Systematic Analysis of Targets of Pumilio-Mediated mRNA Decay Reveals that PUM1 Repression by DNA Damage Activates Translesion Synthesis. Cell reports, 31(5), 107542.

Hitachi K, et al. (2019) Data describing the effects of depletion of Myoparr, myogenin, Ddx17, and hnRNPK in differentiating C2C12 cells. Data in brief, 25, 104172.