Resource Summary Report

Generated by dkNET on Apr 15, 2025

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

Proper Citation: NCBI Sequence Read Archive (SRA) (RRID:SCR_004891)

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, service resource, data repository, database, 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

Record Creation Time: 20220129T080227+0000

Record Last Update: 20250412T054923+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 6130 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

Zhao C, et al. (2025) Temperature-dependent lifespan extension is achieved in miR-80-deleted Caenorhabditis elegans by NLP-45 to modulate endoplasmic reticulum unfolded protein responses. Aging cell, 24(1), e14345.

Wang J, et al. (2025) Characteristic alterations of gut microbiota and serum metabolites in patients with chronic tinnitus: a multi-omics analysis. Microbiology spectrum, 13(1), e0187824.

Zhao Y, et al. (2025) ITS amplicon sequencing revealed that rare taxa of tea rhizosphere fungi are closely related to the environment and provide feedback on tea tree diseases. Microbiology spectrum, 13(1), e0188924.

Islam MSU, et al. (2025) Genome-wide identification and characterization of cation-proton antiporter (CPA) gene family in rice (Oryza sativa L.) and their expression profiles in response to phytohormones. PloS one, 20(1), e0317008.

Shaikh K, et al. (2025) ZFAND6 promotes TRAF2-dependent mitophagy to restrain cGAS-STING signaling. iScience, 28(1), 111544.

Oliveira BPN, et al. (2025) Evaluation of Probiotic Effects on the Growth Performance and Microbiome of Nile Tilapia (Oreochromis niloticus) in a High-Density Biofloc System. Aquaculture nutrition, 2025, 5868806.

Neha SA, et al. (2025) Impacts of host phylogeny, diet, and geography on the gut microbiome of rodents. PloS one, 20(1), e0316101.

Liao Y, et al. (2025) Functions of thyroid hormone signaling in regulating melanophore, iridophore, erythrophore, and pigment pattern formation in spotted scat (Scatophagus argus). BMC genomics, 26(1), 79.

Antwerpen M, et al. (2025) Archival and Newly Isolated Historical Bacillus anthracis Strains Populate the Deeper Phylogeny of the A.Br.075(Sterne) Clade. Pathogens (Basel, Switzerland), 14(1).

Jacobs E, et al. (2025) A method for authenticating the fidelity of Cryptococcus neoformans knockout collections. bioRxiv : the preprint server for biology.

Zhang M, et al. (2025) Macrophage Notch1 signaling modulates regulatory T cells via the TGFB axis in early MASLD. JHEP reports : innovation in hepatology, 7(1), 101242.

Liu J, et al. (2025) Subtilisin-like protease 4 regulates cold tolerance through cell wall modification in rice. Scientific reports, 15(1), 426.

Guan JL, et al. (2025) High-dose dual therapy for Helicobacter pylori eradication inducing less impact on the gut microbiota. Gut pathogens, 17(1), 7.

Li YR, et al. (2025) Allogeneic CD33-directed CAR-NKT cells for the treatment of bone marrow-resident myeloid malignancies. Nature communications, 16(1), 1248.

Bongiovanni D, et al. (2025) Impact of urbanization on antimicrobial resistance in soil microbial communities. Scientific reports, 15(1), 633.

Sawaswong V, et al. (2025) Diversity and antimicrobial resistance profiles of Mycobacterium avium complex clinical isolates in Thailand based on whole genome comparative analysis. Scientific reports, 15(1), 772.

Mougari S, et al. (2025) Intranasally administrated fusion-inhibitory lipopeptides block SARS-CoV-2 infection in mice and enable long-term protective immunity. Communications biology, 8(1), 57.

Marotta J, et al. (2025) The BfmRS stress response protects Acinetobacter baumannii against defects in outer membrane lipoprotein biogenesis. Journal of bacteriology, 207(1), e0033224.

Luo Y, et al. (2025) Characterization and functional analysis of conserved non-coding sequences among poaceae: insights into gene regulation and phenotypic variation in maize. BMC genomics, 26(1), 46.

Yu X, et al. (2025) Super pan-genome reveals extensive genomic variations associated with phenotypic divergence in Actinidia. Molecular horticulture, 5(1), 4.