Resource Summary Report

Generated by dkNET on May 8, 2025

SRAdb

RRID:SCR_006524
Type: Tool

Proper Citation

SRAdb (RRID:SCR_006524)

Resource Information

URL: http://www.bioconductor.org/packages/release/bioc/html/SRAdb.html

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Description: Software package to make access to the compilation of metadata from NCBI SRA and tools associated with submission, study, sample, experiment and run much more feasible. This is accomplished by parsing all the NCBI SRA metadata into a SQLite database that can be stored and queried locally. Fulltext search in the package make querying metadata very flexible and powerful. fastq and sra files can be downloaded for doing alignment locally. Beside ftp protocol, the SRAdb has funcitons supporting fastp protocol (ascp from Aspera Connect) for faster downloading large data files over long distance. The SQLite database is updated regularly as new data is added to SRA and can be downloaded at will for the most up-to-date metadata.

Abbreviations: SRAdb

Synonyms: SRAdb - A compilation of metadata from NCBI SRA and tools

Resource Type: software resource

Defining Citation: PMID:23323543

Keywords: bio.tools

Funding:

Availability: Artistic License, v2

Resource Name: SRAdb

Resource ID: SCR_006524

Alternate IDs: biotools:sradb, OMICS_01032

Alternate URLs: https://bio.tools/sradb

Record Creation Time: 20220129T080236+0000

Record Last Update: 20250420T014332+0000

Ratings and Alerts

No rating or validation information has been found for SRAdb.

No alerts have been found for SRAdb.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 18 mentions in open access literature.

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

Jin DM, et al. (2024) Meta-analysis of the human gut microbiome uncovers shared and distinct microbial signatures between diseases. bioRxiv : the preprint server for biology.

Dewar MB, et al. (2024) Defining Transcriptomic Heterogeneity between Left and Right Ventricle-Derived Cardiac Fibroblasts. Cells, 13(4).

Jin D-M, et al. (2024) Meta-analysis of the human gut microbiome uncovers shared and distinct microbial signatures between diseases. mSystems, 9(8), e0029524.

Silva SG, et al. (2023) Natural product biosynthetic potential reflects macroevolutionary diversification within a widely distributed bacterial taxon. mSystems, 8(6), e0064323.

Agostinetto G, et al. (2022) SKIOME Project: a curated collection of skin microbiome datasets enriched with study-related metadata. Database : the journal of biological databases and curation, 2022.

Kasmanas JC, et al. (2021) HumanMetagenomeDB: a public repository of curated and standardized metadata for human metagenomes. Nucleic acids research, 49(D1), D743.

Mukherjee P, et al. (2021) Dual RNA Sequencing Meta-analysis in Plasmodium Infection

Identifies Host-Parasite Interactions. mSystems, 6(2).

Ginno PA, et al. (2020) A genome-scale map of DNA methylation turnover identifies site-specific dependencies of DNMT and TET activity. Nature communications, 11(1), 2680.

Gratton R, et al. (2020) In Vitro Zika Virus Infection of Human Neural Progenitor Cells: Meta-Analysis of RNA-Seq Assays. Microorganisms, 8(2).

Corrêa FB, et al. (2020) TerrestrialMetagenomeDB: a public repository of curated and standardized metadata for terrestrial metagenomes. Nucleic acids research, 48(D1), D626.

Hryckowian AJ, et al. (2020) Bacteroides thetaiotaomicron-Infecting Bacteriophage Isolates Inform Sequence-Based Host Range Predictions. Cell host & microbe, 28(3), 371.

Swamy V, et al. (2019) Eye in a Disk: eyeIntegration Human Pan-Eye and Body Transcriptome Database Version 1.0. Investigative ophthalmology & visual science, 60(8), 3236.

Shi MW, et al. (2019) SAGD: a comprehensive sex-associated gene database from transcriptomes. Nucleic acids research, 47(D1), D835.

Mangul S, et al. (2018) ROP: dumpster diving in RNA-sequencing to find the source of 1 trillion reads across diverse adult human tissues. Genome biology, 19(1), 36.

Ten-Caten F, et al. (2018) Internal RNAs overlapping coding sequences can drive the production of alternative proteins in archaea. RNA biology, 15(8), 1119.

Galeota E, et al. (2017) Ontology-based annotations and semantic relations in large-scale (epi)genomics data. Briefings in bioinformatics, 18(3), 403.

Nellore A, et al. (2016) Human splicing diversity and the extent of unannotated splice junctions across human RNA-seq samples on the Sequence Read Archive. Genome biology, 17(1), 266.

Nayfach S, et al. (2015) Average genome size estimation improves comparative metagenomics and sheds light on the functional ecology of the human microbiome. Genome biology, 16(1), 51.