

# Resource Summary Report

Generated by [FDI Lab - SciCrunch.org](#) on Apr 15, 2025

## sra-toolkit

RRID:SCR\_024350

Type: Tool

### Proper Citation

sra-toolkit (RRID:SCR\_024350)

### Resource Information

**URL:** <https://github.com/ncbi/sra-tools/>

**Proper Citation:** sra-toolkit (RRID:SCR\_024350)

**Description:** Software collection of tools and libraries for using data in the INSDC Sequence Read Archives.Used for long term storage of the next-generation sequence traces.

**Synonyms:** NCBI SRA Toolkit

**Resource Type:** software toolkit, software resource

**Defining Citation:** [PMID:19906712](#)

**Keywords:** using data in the INSDC Sequence Read Archives, long term storage of the next-generation sequence traces,

**Funding:**

**Availability:** Free, Available for download, Freely available,

**Resource Name:** sra-toolkit

**Resource ID:** SCR\_024350

**Alternate IDs:** OMICS\_03771

**Old URLs:** <https://sources.debian.org/src/sra-toolkit/>

**Record Creation Time:** 20230830T050217+0000

**Record Last Update:** 20250412T060654+0000

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## Ratings and Alerts

No rating or validation information has been found for sra-toolkit.

No alerts have been found for sra-toolkit.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 67 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [FDI Lab - SciCrunch.org](#).

Napoletano S, et al. (2025) Integrative analysis of miRNA expression data reveals a minimal signature for tumour cells classification. Computational and structural biotechnology journal, 27, 233.

Zhang J, et al. (2025) Histone methyltransferases MLL2 and SETD1A/B play distinct roles in H3K4me3 deposition during the transition from totipotency to pluripotency. The EMBO journal, 44(2), 437.

Rishik S, et al. (2025) miRNATissueAtlas 2025: an update to the uniformly processed and annotated human and mouse non-coding RNA tissue atlas. Nucleic acids research, 53(D1), D129.

Rakibova Y, et al. (2024) Nucleoid-associated proteins shape the global protein occupancy and transcriptional landscape of a clinical isolate of *Vibrio cholerae*. bioRxiv : the preprint server for biology.

Alfonso P, et al. (2024) Unveiling the hidden viromes across the animal tree of life: insights from a taxonomic classification pipeline applied to invertebrates of 31 metazoan phyla. mSystems, 9(5), e0012424.

Santana LS, et al. (2024) Benchmarking tools for transcription factor prioritization. Computational and structural biotechnology journal, 23, 2190.

Jespersen MG, et al. (2024) Pangenome evaluation of gene essentiality in *Streptococcus pyogenes*. Microbiology spectrum, 12(8), e0324023.

Banerjee G, et al. (2024) Protocol for the construction and functional profiling of metagenome-assembled genomes for microbiome analyses. STAR protocols, 5(3), 103167.

Pruvost O, et al. (2024) Genetic Signatures of Contrasted Outbreak Histories of "Candidatus *Liberibacter asiaticus*", the Bacterium That Causes Citrus Huanglongbing, in Three

Outermost Regions of the European Union. *Evolutionary applications*, 17(12), e70053.

Hosaka AJ, et al. (2024) A de novo genome assembly of *Solanum bulbocastanum* Dun., a Mexican diploid species reproductively isolated from the A-genome species, including cultivated potatoes. *G3 (Bethesda, Md.)*, 14(6).

Xu P, et al. (2024) Cancer marker TNFRSF1A: From single-cell heterogeneity of renal cell carcinoma to functional validation. *Oncology letters*, 28(3), 425.

Lee SG, et al. (2024) Variant- and vaccination-specific alternative splicing profiles in SARS-CoV-2 infections. *iScience*, 27(3), 109177.

Liu Z, et al. (2024) CDS-DB, an omnibus for patient-derived gene expression signatures induced by cancer treatment. *Nucleic acids research*, 52(D1), D1163.

Homma H, et al. (2024) Dynamic molecular network analysis of iPSC-Purkinje cells differentiation delineates roles of ISG15 in SCA1 at the earliest stage. *Communications biology*, 7(1), 413.

Toga K, et al. (2024) Genome-Wide Search for Gene Mutations Likely Conferring Insecticide Resistance in the Common Bed Bug, *Cimex lectularius*. *Insects*, 15(10).

Sachslehner AP, et al. (2024) The Evolution of Transglutaminases Underlies the Origin and Loss of Cornified Skin Appendages in Vertebrates. *Molecular biology and evolution*, 41(6).

Varambally S, et al. (2024) MammOnc-DB, an integrative breast cancer data analysis platform for target discovery. *Research square*.

Peñas-Utrilla D, et al. (2024) Mining genomic repositories to further our knowledge of the extent of SARS-CoV-2 co-infections. *Microbial genomics*, 10(1).

Martin MA, et al. (2024) Influenza A genomic diversity during human infections underscores the strength of genetic drift and the existence of tight transmission bottlenecks. *Virus evolution*, 10(1), veae042.

Le Clercq LS, et al. (2024) Phenotypic correlates between clock genes and phenology among populations of Diederik cuckoo, *Chrysococcyx caprius*. *Ecology and evolution*, 14(8), e70117.