

Resource Summary Report

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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 resource, software toolkit

Defining Citation: [PMID:19906712](#)

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

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: 20260821T194259+0000

Ratings and Alerts

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

No alerts have been found for sra-toolkit.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 271 mentions in open access literature.

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

Ulmke PA, et al. (2026) Identification of novel genes with enriched expression in human intermediate progenitors reveals a key role for CDKN3 in cortical development. Stem cell reports, 103012.

Lee M, et al. (2026) LINE-1 Locus Transcription Nucleates Oncogenic Chromatin Architecture. Cancer discovery, 16(4), 800.

Lei W, et al. (2026) TEDD: a comprehensive database for translation efficiency dynamics. Nucleic acids research, 54(D1), D511.

Bustos ML, et al. (2026) Impact of non-standardized reporting on reproducibility, usability, and integration in nasopharyngeal metagenomic research: a systematic review. Frontiers in microbiology, 17, 1707004.

Dai J, et al. (2026) Functional germline variants together with somatic mutations alter the integrity of cancer hallmark regulatory networks. Genome medicine, 18(1).

Pallais JP, et al. (2026) Complement 3a Receptor mediates high fat diet induced hypothalamic accumulation of lipid associated microglia to regulate neuroinflammation and obesity. bioRxiv : the preprint server for biology.

Sauerborn E, et al. (2026) Resolving plasmid-encoded carbapenem resistance dynamics and reservoirs in a hospital setting through nanopore sequencing. Microbial genomics, 12(2).

Ramiro-Martínez P, et al. (2026) Plasmid mutation rates scale with copy number. Proceedings of the National Academy of Sciences of the United States of America, 123(4), e2526088123.

Gorczyca M, et al. (2026) Phenotyping transcription factors-related genotypes in *Y. lipolytica* across a range of industrially relevant process parameters and chemical stress conditions. Microbial cell factories, 25(1).

White RT, et al. (2026) Decentralized nanopore genomics reveals diverse *Klebsiella pneumoniae* and no evidence of patient-patient transmission in a New Zealand hospital. Microbial genomics, 12(4).

Arboleda-Baena C, et al. (2026) HVRLocator: a computationally efficient tool for identifying hypervariable regions in large 16S rRNA datasets. *GigaScience*, 15.

Chen R, et al. (2026) Genomic and epidemiologic evidence for attenuated virulence in *Salmonella* Montevideo associated with cattle and beef products in the United States. *Frontiers in microbiology*, 17, 1837237.

Rocha AAD, et al. (2026) Conserved gene clusters in entomopathogenic filamentous fungi. *Genetics and molecular biology*, 49(1), e20250168.

Soni J, et al. (2026) Intracellular microbial shifts during COVID-19 infection and longitudinal recovery revealed by single-cell RNA sequencing. *iScience*, 29(7), 116344.

Ji Y, et al. (2026) Unveiling Global Diversity of Patescibacteriota and Functional Interactions with Host Microbes. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 13(11), e09416.

Engl T, et al. (2026) Catabolism of acetosyringone and co-metabolic transformation of 2,4,6-trichlorophenol by a novel FAD-dependent monooxygenase. *mSystems*, 11(2), e0124225.

Barrett CF, et al. (2026) Mycoheterotrophy and plastid genome evolution in the early-diverging epidendroid orchid tribe Nervilieae: independent transitions in *Epipogium* and *Stereosandra*. *AoB PLANTS*, 18(1), plag002.

Hunt M, et al. (2026) Addressing pandemic-wide systematic errors in the SARS-CoV-2 phylogeny. *Nature methods*, 23(3), 653.

Wang Z, et al. (2026) Host-Filtered Blood Nucleic Acids for Pathogen Detection: Shared Background, Sparse Signal, and Methodological Limits. *Pathogens* (Basel, Switzerland), 15(1).

Kon T, et al. (2026) Genomic consequences of domestication and the diversification of body coloration and morphology in ornamental medaka strains. *Molecular biology and evolution*, 43(2).