

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 [ASWG](#) .

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.

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

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.

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).

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.

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.

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

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).

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

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.

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.

Verbinnen G, et al. (2026) The diversity of insecticide target site mutations in *Apis mellifera*. *BMC genomics*, 27(1).

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

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.

Bechi Genzano C, et al. (2026) Modeling immune responses to autologous and allogeneic human stem cell-derived islet grafts in vivo. *JCI insight*, 11(11).

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.

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).