

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: 20260801T190857+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 171 mentions in open access literature.

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

Parker K, et al. (2026) Diverse reference genomes detect variants in the US winter wheat. *The plant genome*, 19(1), e70160.

Ritter EJ, et al. (2025) The assembly and annotation of two teinturier grapevine varieties, Dakapo and Rubired. *GigaByte (Hong Kong, China)*, 2025, gigabyte149.

Funaguma S, et al. (2025) Retrotrans-genomics identifies aberrant THE1B endogenous retrovirus fusion transcripts in the pathogenesis of sarcoidosis. *Nature communications*, 16(1), 1318.

Karthikeyan SK, et al. (2025) MammOnc-DB, an integrative breast cancer data analysis platform for target discovery. *NPJ breast cancer*, 11(1), 35.

Obinu L, et al. (2025) Colora: a Snakemake workflow for complete chromosome-scale de novo genome assembly. *Bioinformatics (Oxford, England)*, 41(5).

Worden P, et al. (2025) Genomic diversity and tracing of *Paenibacillus* larvae in Australia: implications for American foulbrood outbreak surveillance in low-diversity populations. *Microbial genomics*, 11(5).

Dong X, et al. (2025) Genomic insights into the rapid rise of *Pseudomonas aeruginosa* ST463: A high-risk lineage's adaptive strategy in China. *Virulence*, 16(1), 2497901.

Chung G, et al. (2025) TeloSearchLR: an algorithm to detect novel telomere repeat motifs using long sequencing reads. *G3 (Bethesda, Md.)*, 15(6).

Gr??nig N, et al. (2025) CoExpPhylo - a novel pipeline for biosynthesis gene discovery. *BMC genomics*, 26(1), 807.

Zhao J, et al. (2025) Aberrant alternative splicing in alcoholic hepatitis: regulatory roles of RBPs and sQTLs. *BMC gastroenterology*, 25(1), 728.

Zhang ZF, et al. (2025) Global Distribution Patterns of Dark Matter Fungi in Cold Seep: A Metagenomic Meta-Analysis. *Journal of fungi (Basel, Switzerland)*, 11(12).

Winder JC, et al. (2025) Environmental adaptations in metagenomes revealed by deep learning. *BMC biology*, 23(1), 252.

Malpetti D, et al. (2025) Protocol for interpretable and context-specific single-cell-informed deconvolution of bulk RNA-seq data. *STAR protocols*, 6(1), 103670.

Song Z, et al. (2025) CTG-Initiated Cryptic Peptide Translation Up- and Downstream of a Canonical ATG Start Codon Is Enhanced by TLR Stimulation and Induces Tumor Regression in Mice. *Cancer immunology research*, 13(8), 1246.

Chen L, et al. (2025) Early alternative splicing signatures and RBP networks in MASLD progression to cirrhosis. *BMC medical genomics*, 18(1), 185.

Wang CA, et al. (2025) Risk factors for fluoroquinolone- and macrolide-resistance among swine *Campylobacter coli* using multi-layered chain graphs. *PLoS computational biology*, 21(8), e1012797.

Russ E, et al. (2025) Strict retroelement regulation is frequently lost following cancer transformation and generates a promising reservoir of cancer biomarkers. *Mobile DNA*, 16(1), 37.

Staut J, et al. (2025) A map of integrated cis-regulatory elements enhances gene-regulatory analysis in maize. *Plant communications*, 6(7), 101376.

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.

Luo T, et al. (2025) TcEVdb: a database for T-cell-derived small extracellular vesicles from single-cell transcriptomes. *Database : the journal of biological databases and curation*, 2025.