NCBI Sequence Read Archive (SRA)

RRID:SCR_004891
Type: Tool

Proper Citation

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Resource Information


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Description: Repository of raw sequencing data from next generation of sequencing platforms including including Roche 454 GS System, Illumina Genome Analyzer, Applied Biosystems SOLiD System, Helicos Heliscope, Complete Genomics, and Pacific Biosciences SMRT. In addition to raw sequence data, SRA now stores alignment information in form of read placements on reference sequence. Data submissions are welcome. Archive of high throughput sequencing data, part of international partnership of archives (INSDC) at NCBI, European Bioinformatics Institute and DNA Database of Japan. Data submitted to any of this three organizations are shared among them.

Abbreviations: SRA

Synonyms: Sequence Read Archive, NCBI SRA, SRA,

Resource Type: storage service resource, database, service resource, data or information resource, data repository

Defining Citation: PMID:22009675, PMID:21062823

Keywords: sequence, blast, next-generation sequence, alignment, read placement, reference sequence, roche 454 gs system, illumina genome analyzer, applied biosystems solid system, helicos heliscope, complete genomics, pacific biosciences smrt, high-throughput sequencing, data analysis service, gold standard

Funding Agency: NLM
Availability: Free, Available for download, Freely available

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Resource ID: SCR_004891

Alternate IDs: nlx_86174, OMICS_01031

Ratings and Alerts

No rating or validation information has been found for NCBI Sequence Read Archive (SRA).

No alerts have been found for NCBI Sequence Read Archive (SRA).

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 4898 mentions in open access literature.

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


Block AM, et al. (2023) Mycobacterium tuberculosis Requires the Outer Membrane Lipid Phthiocerol Dimycocerosate for Starvation-Induced Antibiotic Tolerance. mSystems, 8(1), e0069922.


Laamarti M, et al. (2023) Afro-TB dataset as a large scale genomic data of Mycobacterium tuberculosis in Africa. Scientific data, 10(1), 212.
Lorenzetti APR, et al. (2023) A Genome-Scale Atlas Reveals Complex Interplay of Transcription and Translation in an Archaeon. mSystems, 8(2), e0081622.


Ji M, et al. (2023) Tundra Soil Viruses Mediate Responses of Microbial Communities to Climate Warming. mBio, 14(2), e0300922.

Flemington EK, et al. (2023) SpliceTools, a suite of downstream RNA splicing analysis tools to investigate mechanisms and impact of alternative splicing. Nucleic acids research, 51(7), e42.

Jiang RX, et al. (2023) Environmental Factors Affect the Bacterial Community in Diaphorina citri, an Important Vector of "Candidatus Liberibacter asiaticus". Microbiology spectrum, 11(2), e0529822.


