Resource Summary Report

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Fastaq

RRID:SCR_016091
Type: Tool

Proper Citation

Fastaq (RRID:SCR_016091)

Resource Information

URL: https://github.com/sanger-pathogens/Fastaq

Proper Citation: Fastaq (RRID:SCR_016091)

Description: Software application for diverse collection of scripts that perform useful and common FASTA/FASTQ manipulation tasks, such as filtering, merging, splitting, sorting, trimming, search/replace, etc. Input and output files can be gzipped (format is automatically detected) and individual Fastaq commands can be piped together.

Resource Type: software toolkit, software resource

Keywords: diverse, script, collect, filter, merge, split, sort, trim, search, replace, file, single-letter code, nucleotide, sequence, peptide, amino acid, text-based, format

Funding:

Availability: Free, Available for download, Freely available

Resource Name: Fastaq

Resource ID: SCR_016091

Alternate IDs: OMICS_19987

Alternate URLs: https://sources.debian.org/src/fastaq/

License: Open Source Licence

Record Creation Time: 20220129T080328+0000

Record Last Update: 20250412T060001+0000

Ratings and Alerts

No rating or validation information has been found for Fastaq.

No alerts have been found for Fastaq.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 25 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Mosti F, et al. (2025) Multi-modal investigation reveals pathogenic features of diverse DDX3X missense mutations. PLoS genetics, 21(1), e1011555.

Yang H, et al. (2024) SEMA6B induces macrophage-mediated inflammation and hepatocyte apoptosis in hepatitis B virus-related acute-on-chronic liver failure. Theranostics, 14(13), 5200.

Robic A, et al. (2024) Innovative construction of the first reliable catalogue of bovine circular RNAs. RNA biology, 21(1), 52.

Ullah S, et al. (2024) Molecular characterization and antibiotic susceptibility of Shiga toxin-producing Escherichia coli (STEC) isolated from raw milk of dairy bovines in Khyber Pakhtunkhwa, Pakistan. PloS one, 19(9), e0307830.

Krüger A, et al. (2023) Human mitochondria require mtRF1 for translation termination at non-canonical stop codons. Nature communications, 14(1), 30.

Dicks J, et al. (2023) NCTC3000: a century of bacterial strain collecting leads to a rich genomic data resource. Microbial genomics, 9(5).

Ruis C, et al. (2023) Mutational spectra are associated with bacterial niche. Nature communications, 14(1), 7091.

Chung The H, et al. (2023) Multidrug resistance plasmids underlie clonal expansions and international spread of Salmonella enterica serotype 1,4,[5],12:i:- ST34 in Southeast Asia. Communications biology, 6(1), 1007.

Wong JLC, et al. (2022) Recurrent emergence of Klebsiella pneumoniae carbapenem

resistance mediated by an inhibitory ompK36 mRNA secondary structure. Proceedings of the National Academy of Sciences of the United States of America, 119(38), e2203593119.

Beale MA, et al. (2021) Global phylogeny of Treponema pallidum lineages reveals recent expansion and spread of contemporary syphilis. Nature microbiology, 6(12), 1549.

Horesh G, et al. (2021) A comprehensive and high-quality collection of Escherichia coli genomes and their genes. Microbial genomics, 7(2).

Charalampous T, et al. (2021) Evaluating the potential for respiratory metagenomics to improve treatment of secondary infection and detection of nosocomial transmission on expanded COVID-19 intensive care units. Genome medicine, 13(1), 182.

Blackwell GA, et al. (2021) Exploring bacterial diversity via a curated and searchable snapshot of archived DNA sequences. PLoS biology, 19(11), e3001421.

Rodrigues RA, et al. (2021) Genomic and temporal analyses of Mycobacterium bovis in southern Brazil. Microbial genomics, 7(5).

Tracey A, et al. (2020) Nearly Complete Genome Sequence of Brugia malayi Strain FR3. Microbiology resource announcements, 9(24).

Beale MA, et al. (2019) Genomic epidemiology of syphilis reveals independent emergence of macrolide resistance across multiple circulating lineages. Nature communications, 10(1), 3255.

Taylor MS, et al. (2018) Dissection of affinity captured LINE-1 macromolecular complexes. eLife, 7.

Page AJ, et al. (2018) PlasmidTron: assembling the cause of phenotypes and genotypes from NGS data. Microbial genomics, 4(3).

Page AJ, et al. (2018) Rapid multi-locus sequence typing direct from uncorrected long reads using Krocus. PeerJ, 6, e5233.

Aspeling-Jones H, et al. (2018) An expanded global inventory of allelic variation in the most extremely polymorphic region of Plasmodium falciparum merozoite surface protein 1 provided by short read sequence data. Malaria journal, 17(1), 345.