

Resource Summary Report

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FASTX-Toolkit

RRID:SCR_005534

Type: Tool

Proper Citation

FASTX-Toolkit (RRID:SCR_005534)

Resource Information

URL: http://hannonlab.cshl.edu/fastx_toolkit/

Proper Citation: FASTX-Toolkit (RRID:SCR_005534)

Description: Software tool as collection of command line tools for Short-Reads FASTA/FASTQ files preprocessing.

Synonyms: FASTQ/A short-reads pre-processing tools

Resource Type: software toolkit, software resource, software application, data processing software

Keywords: Short reads, FASTA file, FASTQ file, preprocessing, command line tools, bio.tools

Resource Name: FASTX-Toolkit

Resource ID: SCR_005534

Alternate IDs: SCR_019035, SCR_015042, biotools:fastx-toolkit, OMICS_01045

Alternate URLs: https://github.com/agordon/fastx_toolkit, <https://bio.tools/fastx-toolkit>

License: Affero GPL (AGPL)

Record Creation Time: 20220129T080230+0000

Record Last Update: 20260808T190305+0000

Ratings and Alerts

No rating or validation information has been found for FASTX-Toolkit.

No alerts have been found for FASTX-Toolkit.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2864 mentions in open access literature.

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

Tomassi AH, et al. (2026) Precision RNAi in Tomato Using Synthetic Trans-Acting Small Interfering RNAs Derived From Minimal Precursors. *Plant biotechnology journal*, 24(3), 1269.

Choubey P, et al. (2026) Cohesin complex cooperates with PU.1 at super-enhancers to regulate the differentiation and identity of conventional dendritic cells. *Cell reports*, 45(5), 117331.

Kaur H, et al. (2026) Dynamicity of Topoisomerase 1 binding at super-enhancers regulates TLR-responsive gene expression program in macrophages. *Cell reports*, 45(7), 117604.

Yinda CK, et al. (2026) Spatio-temporal dynamics of Hendra virus in Australia reveal stable maintenance of diverse viral clades among Pteropus bats. *Nature microbiology*, 11(4), 851.

Bronnec P, et al. (2026) SpeckSeq enables high-throughput functional stratification of MEFV variants in autoinflammatory diseases. *The Journal of experimental medicine*, 223(2).

Solbach MD, et al. (2026) Legacies of consecutive summer droughts on soil-borne plant parasitic protists (Oomycota: Stramenopila and Phytomyxea: Rhizaria) and protistan consumers (Cercozoa: Rhizaria) along an experimental plant diversity gradient. *The New phytologist*, 249(4), 2010.

Mullick A, et al. (2026) AAV Assembled Capsids Are Produced in Cells Blocked From Cell Cycle Progression. *Biotechnology and bioengineering*, 123(2), 273.

Brosnan CA, et al. (2026) Foliar-applied double-stranded RNA is mobile, transfers to plant pathogens, and triggers RNAi. *Nucleic acids research*, 54(1).

Calderón L, et al. (2026) In vivo CRISPR/Cas9 screens identify new regulators of B cell activation and plasma cell differentiation. *The Journal of experimental medicine*, 223(3).

Allaby RG, et al. (2026) Early colonization before inundation consistent with northern glacial refugia in Southern Doggerland revealed by sedimentary ancient DNA. *Proceedings of the National Academy of Sciences of the United States of America*, 123(11), e2508402123.

Feng Z, et al. (2026) DNA polymorphisms and N6-methyladenosine RNA methylation influencing microRNA expression and regulatory activity in plants. *BMC plant biology*,

26(1).

Kashiyama Y, et al. (2026) Transient molecular chimerism for exploiting xenogeneic organelles. *Nature communications*, 17(1).

Cheng J, et al. (2026) RNA-Binding Proteins Alter Redox Gene Splicing in Biliary Atresia: Insights from Expression Profiling. *ACS omega*, 11(15), 23328.

Hwang RW, et al. (2026) Accelerated reprogramming of hiPSCs into functional brain endothelial-like cells using multiplexed CRISPR activation. *Scientific reports*, 16(1).

Downing T, et al. (2026) Using pangenome variation graphs to improve mutation detection in a large DNA virus. *Microbial genomics*, 12(5).

Zhang X, et al. (2026) Ovoid cell is an inducible small-sized morphotype that enhances proliferation and antifungal drug tolerance in the human fungal pathogen *Cryptococcus neoformans*. *PLoS pathogens*, 22(6), e1014302.

Gilbride C, et al. (2026) A stable subgenomic reporter coronavirus enables transcriptional profiling of bystander cells. *The Journal of general virology*, 107(6).

Black KA, et al. (2026) Resolution of a T1-Like Bacteriophage Outbreak by Receptor Engineering. *Molecular biotechnology*, 68(3), 1411.

Chang Q, et al. (2026) Integrative RNA-seq and iRIP-seq analysis links SNRPA overexpression to transcriptomic and splicing alterations in hepatocellular carcinoma cells. *Frontiers in oncology*, 16, 1800728.

Müller J, et al. (2026) GLYATL1 is associated with metabolic and epigenetic changes and with endocrine resistance in luminal breast cancer. *Clinical epigenetics*, 18(1).