

Resource Summary Report

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[fastp](#)

RRID:SCR_016962

Type: Tool

Proper Citation

fastp (RRID:SCR_016962)

Resource Information

URL: <https://github.com/OpenGene/fastp>

Proper Citation: fastp (RRID:SCR_016962)

Description: Software tool to provide fast all in one preprocessing for FastQ files. Developed in C++ with multithreading supported to afford high performance. Performs quality control, adapter trimming, quality filtering, per read quality pruning and many other operations with a single scan of the FASTQ data.

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

Defining Citation: [PMID:30423086](#)

Keywords: fast, all in one, preprocessing, FastQ, file, data, read, quality, control, adapter, trimming, filtering

Funding: National Science Foundation of China ;
Special Funds for Future Industries of Shenzhen

Availability: Free, Available for download, Freely available

Resource Name: fastp

Resource ID: SCR_016962

License: MIT License

Record Creation Time: 20220129T080332+0000

Record Last Update: 20260912T200019+0000

Ratings and Alerts

No rating or validation information has been found for fastp.

No alerts have been found for fastp.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1745 mentions in open access literature.

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

Li Z, et al. (2026) Mouse chymase mast cell protease-4 facilitates blood feeding of *Aedes aegypti* (Diptera: Culicidae) mosquitoes. *Journal of medical entomology*, 63(1).

Du S, et al. (2026) Characterization and genomic analysis of DSF2: a novel lytic phage infecting multidrug-resistant *Shigella*. *Frontiers in microbiology*, 17, 1740847.

Zhang J, et al. (2026) Gut microbiota dysbiosis drives depression-like behavior in adolescent rats via lysine-regulated mTOR autophagy pathway. *Translational psychiatry*, 16(1).

Chen C, et al. (2026) Consecutive monoculture of sweet potato reduces yield due to deteriorated soil health and disrupted nutrient cycling. *Frontiers in microbiology*, 17, 1747390.

Wei D, et al. (2026) The crayfish-rice coculture model contributes to regulating the soil fertility of rice fields and maintaining the stability of soil microbial community composition and function. *Advanced biotechnology*, 4(2).

Sun J, et al. (2026) A chromosome-level genome assembly of *Rhizopus stolonifer* associated with passion fruit flower rot. *Frontiers in microbiology*, 17, 1757919.

Deng B, et al. (2026) Spatiotemporal dynamics of culturable endophytic microorganisms in *Peucedanum praeruptorum* Dunn and screening for plant growth-promoting strains. *Frontiers in plant science*, 17, 1811872.

Kartashov MY, et al. (2026) Expanding diversity of tick-borne phleboviruses (*Phlebovirus mukawaense*, *Mudanjiang phlebovirus*, *Gomselga Virus*, and *Onega tick phlebovirus*) in Russia. *PloS one*, 21(6), e0349564.

Orcel E, et al. (2026) UMI-guided single locus sequence typing method for phylotyping *Cutibacterium acnes* from skin samples. *Frontiers in cellular and infection microbiology*, 16, 1807759.

Du H, et al. (2026) Niacin promotes motor function recovery after spinal cord injury via Hcar2-dependent microglia immunometabolic regulation. *Clinical and translational medicine*, 16(5), e70683.

Luo C, et al. (2026) Identification of *Campylobacter coli* as a key pathogen in Jinhua piglet diarrhea and its the probiotic control by *Enterococcus faecium*. BMC microbiology, 26(1).

Li J, et al. (2026) Ability of the Chinese herbal residue to alleviate short-distance transportation stress in sheep through the remodeling of the rumen microbiome-metabolism axis. Journal of animal science and biotechnology, 17(1).

Yuan G, et al. (2026) Shading affects the nitrogen cycling process and plant nitrogen uptake by altering the rhizosphere microbial community. Frontiers in plant science, 17, 1780344.

Chu D, et al. (2026) Diet-Driven Divergence in Gut Microbiota Variation Between Two Sympatric Gerbil Species. Ecology and evolution, 16(4), e73367.

Naitchede LHS, et al. (2026) Microbial community characterization in semi-hydroponic systems of Starbor kale (*Brassica oleracea* L.) grown under normal gravity and simulated microgravity. Current research in microbial sciences, 10, 100592.

Xu Y, et al. (2026) The complete chloroplast genome sequence of *Thaumatococcus* *bipinnatifidum*. Mitochondrial DNA. Part B, Resources, 11(1), 150.

Yang Q, et al. (2026) Molecular mechanism of resistance to lonafarnib conferred by mutations in the cysteine-rich region of respiratory syncytial virus fusion glycoprotein and discovery of a lonafarnib-derived antiviral PROTAC. Journal of virology, 100(1), e0148725.

Ali H, et al. (2026) Seasonal shifts in vegetation, soil properties, and microbial communities in Western Himalayan forests. Environmental microbiome, 21(1), 22.

Lorenzo K, et al. (2026) Redundant cytokines license IL-1-driven neutrophil inflammation through MEK/ERK convergence. bioRxiv : the preprint server for biology.

Li P, et al. (2026) Inc015013-CsMYB30-CsJAZ4/6 Module Co-Regulates JA Synthesis and Enhances Cold Hardiness in Tea Plants. International journal of molecular sciences, 27(11).