

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>

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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, software application, software resource, data processing software

Defining Citation: [PMID:30423086](#)

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

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

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: 20260807T042859+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 [NIF](#) .

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).

Chen P, et al. (2026) Metabolomic and Transcriptomic Profiling of Two Closely Related Species within the Genus *Oldenlandia*. *Scientific data*, 13(1).

Ning H, et al. (2026) Fermentation-driven function enhancement of faba bean (poly)phenols: Bioactivity augmentation and intestinal flora modulation. *Food chemistry: X*, 33, 103563.

Daguia-Wenam P-T, et al. (2026) The P protein T25M substitution is involved in the quasispecies and virulence of Newcastle disease virus. *Microbiology spectrum*, 14(3), e0063925.

Li G, et al. (2026) Rhizosphere bacterial characteristics reveal the invasive advantage of *Sphagneticola trilobata* compared to the greening grass *Axonopus compressus*. *BMC microbiology*, 26(1).

Wu D, et al. (2026) TROP2 confers resistance to oxidative stress-induced cancer cell death through YAP/HMOX1 signaling. *Journal of translational medicine*, 24(1).

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.

Singh NK, et al. (2026) Chloroplast genome sequencing in winged bean (*Psophocarpus tetragonolobus* L.) and comparative analysis with other legumes. *BMC plant biology*, 26(1), 264.

Yang W, et al. (2026) Multi-omics reveals co-regulation of hepatic bile acid metabolism in laying hens by host genetics and the cecal *Anaerostipes*. *Poultry science*, 105(3), 106388.

Wang X, et al. (2026) Multi-omics integration unveils fungal succession and volatile metabolite dynamics in spontaneous fermentation of Beibinghong icewine: Identifying yeast strains critical for flavor development. *Food chemistry: X*, 33, 103442.

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

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).

Zhang X, et al. (2026) Molecular mechanism of gallium nitrate in inhibiting bacterial biofilm formation through pykF modulation. PloS one, 21(3), e0337557.

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).

Yang G, et al. (2026) The Whole Transcriptome Sequencing Profile of Serum-Derived Exosomes and Potential Pathophysiology of Age-Related Hearing Loss. Diagnostics (Basel, Switzerland), 16(2).

Maqbool M, et al. (2026) Exploration of the genomic diversity of third-generation cephalosporin-resistant *Escherichia coli* in Australian clinical settings. Microbial genomics, 12(1).

Zhang X, et al. (2026) Epidemiological and genomic profiles of NDM-1-Producing ST25-KL2 carbapenem-resistant *Klebsiella pneumoniae* among pediatric patients in Hangzhou, China. BMC microbiology, 26(1).

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

Hong Y-P, et al. (2026) Epidemiology and genomics of azithromycin-resistant extensively drug-resistant *Salmonella enterica* serovar Typhimurium in Taiwan. Antimicrobial agents and chemotherapy, 70(4), e0133425.

Guo X, et al. (2026) Macrophage-Derived CuET Vesicles Synergistically Enhance Paclitaxel Efficacy by Inhibiting Tumor Growth and Boosting Immunity in Breast Cancer. International journal of nanomedicine, 21, 570540.