

Resource Summary Report

Generated by [Kravitz](#) on Sep 17, 2026

AfterQC

RRID:SCR_016390

Type: Tool

Proper Citation

AfterQC (RRID:SCR_016390)

Resource Information

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

Proper Citation: AfterQC (RRID:SCR_016390)

Description: Software that performs automatic filtering, trimming, error removing, and quality control for fastq data.

Synonyms: After QC

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

Defining Citation: [PMID:28361673](#)

Keywords: fastq, qc, editing, filtering, trimming, dna, rna, seq, sequence, sequencing, poly, pair-end, python

Availability: Free, Available for download

Resource Name: AfterQC

Resource ID: SCR_016390

License: MIT License

Record Creation Time: 20220129T080330+0000

Record Last Update: 20260912T200104+0000

Ratings and Alerts

No rating or validation information has been found for AfterQC.

No alerts have been found for AfterQC.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 15 mentions in open access literature.

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

Pang C, et al. (2026) Translating transcriptomics analysis into diagnostic workflows: clinical variant identification and interpretation in hypothesis-driven and hypothesis-free approaches. *EBioMedicine*, 128, 106313.

Feng X, et al. (2024) In vivo CRISPR screens identify Mga as an immunotherapy target in triple-negative breast cancer. *Proceedings of the National Academy of Sciences of the United States of America*, 121(39), e2406325121.

Lan Q, et al. (2024) Mesenchyme instructs growth while epithelium directs branching in the mouse mammary gland. *eLife*, 13.

Sulic AM, et al. (2023) Transcriptomic landscape of early hair follicle and epidermal development. *Cell reports*, 42(6), 112643.

MacPherson RA, et al. (2023) Genetic and genomic analyses of *Drosophila melanogaster* models of chromatin modification disorders. *Genetics*, 224(4).

Gaeta NC, et al. (2022) Genomic features of a multidrug-resistant and mercury-tolerant environmental *Escherichia coli* recovered after a mining dam disaster in South America. *The Science of the total environment*, 823, 153590.

Darnaud M, et al. (2021) A standardized gnotobiotic mouse model harboring a minimal 15-member mouse gut microbiota recapitulates SOPF/SPF phenotypes. *Nature communications*, 12(1), 6686.

Siconelli MJL, et al. (2021) Evidence for current circulation of an ancient West Nile virus strain (NY99) in Brazil. *Revista da Sociedade Brasileira de Medicina Tropical*, 54.

Afzal M, et al. (2020) Legume genomics and transcriptomics: From classic breeding to modern technologies. *Saudi journal of biological sciences*, 27(1), 543.

Dos Santos Bezerra R, et al. (2020) Detection of Influenza A(H3N2) Virus RNA in Donated Blood. *Emerging infectious diseases*, 26(7), 1621.

Feodorova VA, et al. (2020) Data of de novo genome assembly of the *Chlamydia psittaci* strain isolated from the livestock in Volga Region, Russian Federation. *Data in brief*, 29, 105190.

de Laval B, et al. (2020) C/EBP β -Dependent Epigenetic Memory Induces Trained Immunity in Hematopoietic Stem Cells. *Cell stem cell*, 26(5), 657.

Sandberg TE, et al. (2020) Synthetic cross-phyla gene replacement and evolutionary assimilation of major enzymes. *Nature ecology & evolution*, 4(10), 1402.

Biggs LC, et al. (2018) Hair follicle dermal condensation forms via Fgf20 primed cell cycle exit, cell motility, and aggregation. *eLife*, 7.

Chen S, et al. (2017) AfterQC: automatic filtering, trimming, error removing and quality control for fastq data. *BMC bioinformatics*, 18(Suppl 3), 80.