

# Resource Summary Report

Generated by [PRECISE-TBI](#) on Sep 18, 2026

## Trim Galore

RRID:SCR\_011847

Type: Tool

---

### Proper Citation

Trim Galore (RRID:SCR\_011847)

---

### Resource Information

**URL:** [http://www.bioinformatics.babraham.ac.uk/projects/trim\\_galore/](http://www.bioinformatics.babraham.ac.uk/projects/trim_galore/)

**Proper Citation:** Trim Galore (RRID:SCR\_011847)

**Description:** Software tool to automate quality and adapter trimming as well as quality control, with some added functionality to remove biased methylation positions for RRBS sequence files for directional, non-directional or paired-end sequencing. Wrapper around Cutadapt and FastQC to consistently apply adapter and quality trimming to FastQ files, with extra functionality for Reduced Representation Bisulfite Sequencing data.

**Abbreviations:** Trim Galore!

**Synonyms:** TrimGalore

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

**Keywords:** Automate, quality, adapter, trimming, remove, biased, methylation, position, RRBS, reduced, representation, bisulfite, data, sequence, wrapper, bio.tools

**Availability:** Free, Available for download, Freely available

**Resource Name:** Trim Galore

**Resource ID:** SCR\_011847

**Alternate IDs:** biotools:trim\_galore, OMICS\_01096, SCR\_016946

**Alternate URLs:** <https://github.com/FelixKrueger/TrimGalore>, [https://bio.tools/trim\\_galore](https://bio.tools/trim_galore), <https://sources.debian.org/src/trim-galore/>

**License:** GNU General Public License v3.0

**Record Creation Time:** 20220129T080307+0000

**Record Last Update:** 20260912T200100+0000

---

## Ratings and Alerts

- Used for sequencing service by the Human Islet Research Network community. Contact(s): [Golnaz Vahedi](#), [Klaus Kaestner](#) - Human Islets Research Network <https://hirnetwork.org/>

No alerts have been found for Trim Galore.

---

## Data and Source Information

**Source:** [SciCrunch Registry](#)

---

## Usage and Citation Metrics

We found 7582 mentions in open access literature.

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

Zeng TB, et al. (2026) SETDB1 enables development beyond cleavage stages by extinguishing the MERVL-driven two-cell totipotency transcriptional program in the mouse embryo. *eLife*, 15.

Gauthier J, et al. (2026) B cell-intrinsic IL-2 signaling regulates inflammation by promoting IL-10 expression in CD25+ age-associated B cells. *Immunity*, 59(2), 354.

Liu H, et al. (2026) C9orf72 hexanucleotide repeat RNA drives transcriptional dysregulation through genome-wide DNA:RNA hybrid G-quadruplexes. *Neuron*, 114(6), 1045.

Tao H, et al. (2026) NSD1-Mediated PPAR $\gamma$  Methylation Enhances PTEN Activity to Suppress Glycolysis and Tumor Progression in Endometrial Cancer. *Cancer research*, 86(10), 2464.

Zink A, et al. (2026) Pluripotent stem-cell-based screening uncovers sildenafil as a mitochondrial disease therapy. *Cell*, 189(6), 1656.

Kamimae-Lanning AN, et al. (2026) Metabolite-induced DNA damage drives stochastic stem cell loss and clonal hematopoiesis. *Cell stem cell*, 33(4), 642.

Torigata K, et al. (2026) Human iPSC cardiomyocyte patch transplantation modifies extracellular matrix and fibroblast behavior after myocardial infarction. *iScience*, 29(4), 115341.

Zhang Y, et al. (2026) Co-occurrence of transcriptionally distinct persister cell states underpins neoadjuvant therapy resistance in triple-negative breast cancer. *Genome medicine*, 18(1).

Liu Q, et al. (2026) Structural variation drives praziquantel response and host adaptation in *Schistosoma japonicum*. *iScience*, 29(6), 116118.

Friske JD, et al. (2026) A Conserved Enhancer Locus in Extrachromosomal DNA and Homogeneously Staining Regions Activates MYC Transcription in Group 3 Medulloblastoma. *Cancer research*, 86(13), 3160.

Guillon M, et al. (2026) MECP2 mutations rewire human ESC fate and bias cortical lineage commitment. *Stem cell reports*, 21(5), 102895.

Reed KSM, et al. (2026) Genome reorganization and its functional impact during breast cancer progression. *eLife*, 14.

Dong YP, et al. (2026) Early replication fragile sites are associated with cancer-related CNVs and SNVs in human embryonic stem cells. *Stem cell reports*, 21(7), 102968.

Zhang J, et al. (2026) RNA exonuclease REXO4 resolves m6A-marked R-loops and suppresses anti-tumor immunity. *Molecular cell*.

Wang H, et al. (2026) ZNF296 Drives Immune Evasion in Epithelial Cancers by Repressing Immune Stimulatory Genes. *Cancer research*, 86(1), 116.

Bready D, et al. (2026) A developmentally regulated long-range enhancer-promoter contact mediates human neural development. *bioRxiv : the preprint server for biology*.

Cai S, et al. (2026) Condensation of an H3K9me3 methyltransferase complex promotes heritable gene silencing and heterochromatin formation. *Cell reports*, 45(4), 117152.

Wang Z, et al. (2026) Transcriptomics and functional genomics implicate WNT3 in hemispheric lateralization of speech production. *iScience*, 29(2), 114692.

Yao B, et al. (2026) Divergent tumor immunity determined by bacteria-cancer cell engagement. *Cell*, 189(6), 1748.

Song SJ, et al. (2026) Arid1a deficiency promotes metabolic dysfunction-associated steatohepatitis and hepatocellular carcinoma by disrupting the FXR-gut microbiota-bile acid axis. *Cancer letters*, 652, 218567.