

Resource Summary Report

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

FLASH

RRID:SCR_005531

Type: Tool

Proper Citation

FLASH (RRID:SCR_005531)

Resource Information

URL: <http://ccb.jhu.edu/software/FLASH/>

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Description: Open source software tool to merge paired-end reads from next-generation sequencing experiments. Designed to merge pairs of reads when original DNA fragments are shorter than twice length of reads. Can improve genome assemblies and transcriptome assembly by merging RNA-seq data.

Abbreviations: FLASH

Synonyms: Fast Length Adjustment of SHort reads, Fast Length Adjustment of Short reads

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

Defining Citation: [PMID:21903629](#)

Keywords: bio.tools

Funding: NHGRI R01 HG006677;
NIGMS R01 GM083873;
NLM R01 LM006845

Availability: Free, Available for download, Freely available

Resource Name: FLASH

Resource ID: SCR_005531

Alternate IDs: biotools:flash, OMICS_01047

Alternate URLs: <https://sourceforge.net/projects/flashpage/files/>, <https://bio.tools/flash>, <https://sources.debian.org/src/flash/>

Record Creation Time: 20220129T080230+0000

Record Last Update: 20260912T195627+0000

Ratings and Alerts

No rating or validation information has been found for FLASH.

No alerts have been found for FLASH.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2461 mentions in open access literature.

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

Chen N, et al. (2026) The potential of *Protaetia brevitarsis* as a functional food that enhances immune function and gut microbiota in mice. *iScience*, 29(4), 114939.

Kong JY, et al. (2026) Cross-site oral and esophageal microbiome signatures define diagnostic patterns and reveal mechanistic drivers of ESCC. *iScience*, 29(8), 116667.

Swift SZ, et al. (2026) Integration of Short- and Long-Read RNA Sequencing Enables the Discovery of Circular RNAs. *Cancer research*, 86(5), 1300.

Schmelzer L, et al. (2026) Linking STRs/SNPs and DNA methylation using massively parallel sequencing for potential forensic applications. *International journal of legal medicine*, 140(2), 621.

Xu Y, et al. (2026) Comprehensive 16s rRNA sequencing and metabolomics to investigate the effect of anticancer bioactive peptides combined with oxaliplatin on gastric cancer. *Scientific reports*, 16(1), 4314.

Wang J, et al. (2026) Gut microbiota-metabolite interactions in cisplatin-induced acute kidney injury in rats. *BMC microbiology*, 26(1).

Gao J-H, et al. (2026) Inhibition of PFKFB3 in macrophages ameliorates intestinal inflammation by modulating gut microbiota in DSS-induced colitis. *mSystems*, 11(1), e0063225.

Yu Z, et al. (2026) Responses of Restored Vegetation Communities, Soil Properties, and Microbial Composition to Different Fertilization Treatments in an Alpine Mining Area. *Plants (Basel, Switzerland)*, 15(4).

Liu Y, et al. (2026) Microbial Differences in Rhizospheric and Ednophytic Microbiota in Healthy Chinese Yam Roots and Those Affected by Yam End Black Disease. *Biology*, 15(4).

Chen Q, et al. (2026) Relationship Between *Histomonas meleagridis* Infection and Cecal Intestinal Microbiota of Chickens. *Veterinary sciences*, 13(2).

Godoy-Lozano EE, et al. (2026) Enrichment hydrocarbon-degrading bacterial communities from the southern Gulf of Mexico in long-term stored sediments. *Biodegradation*, 37(2).

Han X, et al. (2026) Effects of arbuscular mycorrhizal fungus on the functional bacteria assembly in promoting plant growth and nutrient acquisition in karst soil. *BMC microbiology*, 26(1).

Li Y, et al. (2026) Metabolomic and metagenomic insights into WFBG-mediated regulation of gut microbiota and metabolism in broilers. *Applied and environmental microbiology*, 92(1), e0189025.

Wang X, et al. (2026) Longitudinal study of mammary microbiota dynamics and mastitis prevention in Holstein cows by dry-off strategy. *Frontiers in veterinary science*, 13, 1751837.

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).

Anil , et al. (2026) Microbial zonation and functional roles in the gut of white grub (*Maladera insanabilis*) larvae. *Scientific reports*, 16(1).

Yuan J, et al. (2026) *Bacillus amyloliquefaciens* regulates oxidative damage through ssc-miR-10390 by targeting WT1 in the intestine of piglets. *Animal microbiome*, 8(1).

Pavlovskaya M, et al. (2026) Phytoplankton dynamics shape bacterioplankton community structure and metabolism during the austral summer-autumn transition in the Western Antarctic Peninsula. *FEMS microbiology ecology*, 102(6).

Sui J, et al. (2026) Soil-Nutrient Depletion and Microbial Community Restructuring in Continuous Celery Cropping: Opposing Responses of Bacteria and Fungi. *Biology*, 15(10).

Yuan Z, et al. (2026) Enoki mushroom residue-based biochar loaded with *Bacillus megaterium* YZS-M06 improves coastal sandy soil and promotes *Ipomoea pes-caprae* growth. *Bioresources and bioprocessing*, 13(1).