

Resource Summary Report

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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, sequence analysis software, software resource, data processing software, software application

Defining Citation: [PMID:21903629](#)

Keywords: bio.tools

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

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: 20250430T055346+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 1938 mentions in open access literature.

Listed below are recent publications. The full list is available at [FDI Lab - SciCrunch.org](#).

Jiang Z, et al. (2025) The RodentGPOmics Atlas: a comprehensive database of rodent biology for genomes and pathogens. *Nucleic acids research*, 53(D1), D1144.

Yao Y, et al. (2025) *Bacillus velezensis* A-27 as a potential biocontrol agent against *Meloidogyne incognita* and effects on rhizosphere communities of celery in field. *Scientific reports*, 15(1), 1057.

Li S, et al. (2025) Influences of fluctuating nutrient loadings on nitrate-reducing microorganisms in rivers. *ISME communications*, 5(1), ycae168.

Zhao Y, et al. (2025) Effects of Bile Acids on Growth Performance, Hepatopancreatic Antioxidant Capacity, Intestinal Immune-Related Gene Expression, and Gut Microbiota of *Penaeus vannamei*. *Animals : an open access journal from MDPI*, 15(2).

Wright G, et al. (2025) A microbial natural product fractionation library screen with HRMS/MS dereplication identifies new lipopeptaibiotics against *Candida auris*. *Research square*.

Yang M, et al. (2025) Ningxiang pig-derived *Lactobacillus reuteri* modulates host intramuscular fat deposition via branched-chain amino acid metabolism. *Microbiome*, 13(1), 32.

Yuan Y, et al. (2025) Dietary Taurine Regulation of the Intestinal Microbiome in Chinese Stripe-Necked Turtle (*Mauremys sinensis*). *International journal of molecular sciences*, 26(2).

Zhao MQ, et al. (2025) Profile of intestinal fungal microbiota in acute pancreatitis patients and healthy individuals. *Gut pathogens*, 17(1), 1.

Wang X, et al. (2025) Soil polluted system shapes endophytic fungi communities associated with *Arundo donax*: a field experiment. *PeerJ*, 13, e18789.

Insawake K, et al. (2025) Effects of isoquinoline alkaloids as an alternative to antibiotic on oxidative stress, inflammatory status, and cecal microbiome of broilers under high stocking density. *Poultry science*, 104(1), 104671.

Zhang Q, et al. (2025) Co-housing with Tibetan chickens improved the resistance of Arbor Acres chickens to *Salmonella enterica* serovar Enteritidis infection by altering their gut microbiota composition. *Journal of animal science and biotechnology*, 16(1), 2.

Yin H, et al. (2025) Response of Soil Bacteria to Short-Term Nitrogen Addition in Nutrient-Poor Areas. *Microorganisms*, 13(1).

Lu Z, et al. (2025) Captivity Reduces Diversity and Shifts Composition of the Great Bustard (*Otis tarda dybowskii*) Microbiome. *Ecology and evolution*, 15(1), e70836.

Kalogriopoulos NA, et al. (2025) Synthetic GPCRs for programmable sensing and control of cell behaviour. *Nature*, 637(8044), 230.

Chero-Sandoval L, et al. (2025) Comparative assessment of phenotypic markers in patients with chronic inflammation: Differences on *Bifidobacterium* concerning liver status. *European journal of clinical investigation*, 55(2), e14339.

Liu Q, et al. (2025) *Cyperus esculentus* var. *sativus* Adapts to Multiple Heavy Metal Stresses Through the Assembly of Endophytic Microbial Communities. *Biology*, 14(1).

Lv L, et al. (2025) Seasonal Variations in the Structure and Function of the Gut Flora in Adult Male Rhesus Macaques Reared in Outdoor Colonies. *Microorganisms*, 13(1).

Zhuang Y, et al. (2025) Core microbe *Bifidobacterium* in the hindgut of calves improves the growth phenotype of young hosts by regulating microbial functions and host metabolism. *Microbiome*, 13(1), 13.

Arikan M, et al. (2024) gNOMO2: a comprehensive and modular pipeline for integrated multi-omics analyses of microbiomes. *GigaScience*, 13.

Loo EP, et al. (2024) Sugar transporters spatially organize microbiota colonization along the longitudinal root axis of *Arabidopsis*. *Cell host & microbe*.