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

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: 20250517T055711+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 dkNET.

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.

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.

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

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.