Resource Summary Report

Generated by NIF on Aug 15, 2026

NGmerge

RRID:SCR_024483
Type: Tool

Proper Citation

NGmerge (RRID:SCR_024483)

Resource Information

URL: https://github.com/harvardinformatics/NGmerge

Proper Citation: NGmerge (RRID:SCR_024483)

Description: Software tool for merging paired-end reads via novel empirically derived models of sequencing errors. Used for merging paired-end reads and removing adapters. Corrects errors and ambiguous bases and assigns quality scores for merged bases that accurately reflect the error rates.

Resource Type: software application, software resource

Defining Citation: PMID:30572828

Keywords: merging paired-end reads, sequencing errors, removing adapters, correct errors, correct ambiguous bases, assign quality scores for merged bases, error rates,

Availability: Free, Available for download, Freely available

Resource Name: NGmerge

Resource ID: SCR_024483

License: MIT license

Record Creation Time: 20231002T161336+0000

Record Last Update: 20260815T042848+0000

Ratings and Alerts

No rating or validation information has been found for NGmerge.

No alerts have been found for NGmerge.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 32 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF .

Krishna A, et al. (2026) Mutational scanning reveals oncogenic CTNNB1 mutations have diverse effects on signaling. Nature genetics, 58(2), 366.

Singh US, et al. (2026) Early hominin arrival in Southeast Asia triggered the evolution of major human malaria vectors. Scientific reports, 16(1).

Rahat MTI, et al. (2026) Identification of bacterial key genes and therapeutic targets in hypertensive patients with type 2 diabetes through bioinformatics analysis. Scientific reports, 16(1), 6431.

Ortega R, et al. (2026) PARP1 and PARP2 are dispensable for DNA repair by microhomology-mediated end-joining at double-ended DSBs. Nucleic acids research, 54(1).

Alsolami S, et al. (2026) Stable bioreactor control reveals acidic pH-driven metabolic reprogramming and mitochondrial dysfunction in human lymphoblastoid cells. Communications biology, 9(1).

Alsolami S, et al. (2026) A single small molecule-based human embryo model reveals V-ATPase requirement??in mammalian blastocyst cavitation. Cell research, 36(7), 475.

F Sousa J, et al. (2026) Comparative multi-omic analysis reveals conserved and derived mechanisms of fin and limb regeneration. Nature communications, 17(1).

Freund MM, et al. (2026) Pioneer-factor activity requires stable chromatin occupancy mediated by both sequence-specific binding and disordered protein domains. Science advances, 12(25), eaef2244.

Chang HC, et al. (2025) Asparagine deprivation enhances T cell antitumour response in patients via ROS-mediated metabolic and signal adaptations. Nature metabolism, 7(5), 918.

Ortega R, et al. (2025) PARP1 and PARP2 are dispensable for DNA repair by microhomology-mediated end-joining during mitosis. bioRxiv : the preprint server for biology.

Zhang Y, et al. (2025) A BRN2:MYC transcriptional axis regulates interconversion between therapy-resistant and tumorigenic phenotypes in melanoma. Cell reports, 44(12), 116675.

Shakya SB, et al. (2025) Convergent evolution of noncoding elements associated with short tarsus length in birds. BMC biology, 23(1), 52.

Hurtado JE, et al. (2025) Nickase fidelity drives EvolvR-mediated diversification in mammalian cells. Nature communications, 16(1), 3723.

Sin SYW, et al. (2024) Genetic Basis and Evolution of Structural Color Polymorphism in an Australian Songbird. Molecular biology and evolution, 41(3).

Strizki JM, et al. (2024) Molnupiravir maintains antiviral activity against SARS-CoV-2 variants and exhibits a high barrier to the development of resistance. Antimicrobial agents and chemotherapy, 68(1), e0095323.

Lu Z, et al. (2024) BIT: Bayesian Identification of Transcriptional Regulators from Epigenomics-Based Query Region Sets. bioRxiv : the preprint server for biology.

Connor R, et al. (2024) Recommendations for Uniform Variant Calling of SARS-CoV-2 Genome Sequence across Bioinformatic Workflows. Viruses, 16(3).

Mermet-Meillon F, et al. (2024) Protein destabilization underlies pathogenic missense mutations in ARID1B. Nature structural & molecular biology, 31(7), 1018.

Hunt M, et al. (2024) Addressing pandemic-wide systematic errors in the SARS-CoV-2 phylogeny. bioRxiv : the preprint server for biology.

Spilsberg B, et al. (2024) Development and application of a whole genome amplicon sequencing method for infectious salmon anemia virus (ISAV). Frontiers in microbiology, 15, 1392607.