

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 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: 20260905T133318+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 [Kravitz](#) .

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.

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

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.

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.

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

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

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.