

Resource Summary Report

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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: 20260727T040822+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 23 mentions in open access literature.

Listed below are recent publications. The full list is available at [nidm-terms](#).

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*.

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*.

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

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

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.

Shen C, et al. (2023) MADS8 is indispensable for female reproductive development at high ambient temperatures in cereal crops. *The Plant cell*, 36(1), 65.

Gibson TJ, et al. (2023) Protein-intrinsic properties and context-dependent effects regulate pioneer-factor binding and function. *bioRxiv : the preprint server for biology*.

Filipescu D, et al. (2023) MacroH2A restricts inflammatory gene expression in melanoma cancer-associated fibroblasts by coordinating chromatin looping. *Nature cell biology*, 25(9), 1332.

Sung S, et al. (2023) Distinct characteristics of two types of alternative lengthening of telomeres in mouse embryonic stem cells. *Nucleic acids research*, 51(17), 9122.

Huynh S, et al. (2023) Whole-genome Analyses Reveal Past Population Fluctuations and Low Genetic Diversities of the North Pacific Albatrosses. *Molecular biology and evolution*, 40(7).

Connor R, et al. (2022) Towards increased accuracy and reproducibility in SARS-CoV-2 next generation sequence analysis for public health surveillance. *bioRxiv : the preprint server for biology*.

Rossetti G, et al. (2021) A common genetic variant of a mitochondrial RNA processing enzyme predisposes to insulin resistance. *Science advances*, 7(39), eabi7514.

Mathema B, et al. (2021) Postvaccination SARS-COV-2 among Health Care Workers in New Jersey: A Genomic Epidemiological Study. *Microbiology spectrum*, 9(3), e0188221.

Fonseca TL, et al. (2021) Neonatal thyroxine activation modifies epigenetic programming of the liver. *Nature communications*, 12(1), 4446.