

Resource Summary Report

Generated by [nidm-terms](#) on Jul 29, 2026

LoFreq

RRID:SCR_013054

Type: Tool

Proper Citation

LoFreq (RRID:SCR_013054)

Resource Information

URL: <http://sourceforge.net/projects/lofreq/>

Proper Citation: LoFreq (RRID:SCR_013054)

Description: A fast and sensitive variant-caller for inferring single-nucleotide variants (SNVs) from high-throughput sequencing data.

Abbreviations: LoFreq

Synonyms: LoFreq - Sensitive variant-calling from sequencing data

Resource Type: software resource

Defining Citation: [PMID:23066108](#), [DOI:10.1093/nar/gks918](#)

Availability: Free, Freely available

Resource Name: LoFreq

Resource ID: SCR_013054

Alternate IDs: OMICS_00063

Old URLs: <https://sources.debian.org/src/lofreq/>

License: GNU General Public License, v2

Record Creation Time: 20220129T080314+0000

Record Last Update: 20260725T190743+0000

Ratings and Alerts

No rating or validation information has been found for LoFreq.

No alerts have been found for LoFreq.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 523 mentions in open access literature.

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

Ye F, et al. (2025) Characteristics and filtering of low-frequency artificial short deletion variations based on nanopore sequencing. GigaScience, 14.

Walker MR, et al. (2025) Temporal dynamics of viral fitness and the adaptive immune response in HCV infection. eLife, 13.

Brumage L, et al. (2025) In vivo functional screens reveal KEAP1 loss as a driver of chemoresistance in small cell lung cancer. Science advances, 11(17), eadq7084.

Prasad AN, et al. (2025) Remdesivir, mAb114, REGN-EB3, and ZMapp partially rescue nonhuman primates infected with a low passage Kikwit variant of Ebola virus. Nature communications, 16(1), 3824.

Sibale LL, et al. (2025) Within-host genetic diversity of pneumococcal serotype 3 during one-year prolonged carriage in a healthy adult. Nature communications, 16(1), 8920.

Dantas ACS, et al. (2025) Analysis of the prevalence, spread, and mutation patterns of SARS-CoV-2 variants: data from COVID-19 testing expansion strategy study in salvador, Northeast Brazil. Scientific reports, 15(1), 31866.

Cavalli L, et al. (2025) SARS-CoV-2 Intra-host Variation Shows Evidence of Transmission and Convergent Evolution in a University Surveillance Cohort. bioRxiv : the preprint server for biology.

Jin K, et al. (2025) Lethal clinical outcome and chemotherapy and immunotherapy resistance in patients with urothelial carcinoma with MDM2 amplification or overexpression. Journal for immunotherapy of cancer, 13(1).

Paul S, et al. (2025) Cooperation between the Hippo and MAPK pathway activation drives acquired resistance to TEAD inhibition. Nature communications, 16(1), 1743.

Xu J, et al. (2025) Development of SARS-CoV-2 as a viral vector: A novel intranasal bivalent vaccine for SARS-CoV-2 and RSV. Science advances, 11(39), eadx7487.

Manara MC, et al. (2025) Genomic profiling of a collection of patient-derived xenografts and cell lines identified ixabepilone as an active drug against chemo-resistant osteosarcoma. Journal of experimental & clinical cancer research : CR, 44(1), 195.

Feinberg MA, et al. (2025) Interaction of West Nile virus NS5 with orthoflavivirus SLA RNAs and their effects on viral replication and inhibition. *Journal of virology*, 99(9), e0202324.

Skelly DA, et al. (2025) Mapping the genetic landscape establishing a tumor immune microenvironment favorable for anti-PD-1 response. *Cell reports*, 44(5), 115698.

Joos M, et al. (2025) EPS inhibitor treatment of *Salmonella* impacts evolution without selecting for resistance to biofilm inhibition. *NPJ biofilms and microbiomes*, 11(1), 73.

Li L, et al. (2025) MGVS-seq: a sensitive and culture-independent method for detecting microbial genetic variation. *Frontiers in microbiology*, 16, 1603255.

van Bree JWM, et al. (2025) Effect of increased CpG and UpA dinucleotides in the West Nile virus genome on virus transmission by *Culex* mosquitoes and pathogenesis in a vertebrate host. *Journal of virology*, 99(10), e0110225.

Wang S, et al. (2025) TMBquant: an explainable AI-powered caller advancing tumor mutation burden quantification across heterogeneous samples. *Briefings in bioinformatics*, 26(5).

Mo J, et al. (2025) Passage of human-origin influenza A virus in swine tracheal epithelial cells selects for adaptive mutations in the hemagglutinin gene. *PloS one*, 20(8), e0327096.

Moreno GK, et al. (2025) Geospatial and demographic patterns of SARS-CoV-2 spread in Massachusetts from over 130,000 genomes. *medRxiv : the preprint server for health sciences*.

Fuchs J, et al. (2025) SARS-CoV-2 infection dynamics in a MHC-I-mismatched lung transplant recipient. *Nature communications*, 16(1), 8292.