

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.