

Resource Summary Report

Generated by [kravitz2](#) on Jul 31, 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 [kravitz2](#) .

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.

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

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.

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).

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.

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.

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.

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.

Mazzetto E, et al. (2025) Infectivity in full-term placenta of Zika viruses with different lipid profiles. Virus research, 352, 199518.

Rodriguez-Algarra F, et al. (2025) Germline sequence variation within the ribosomal DNA is associated with human complex traits. bioRxiv : the preprint server for biology.

Dos Santos MC, et al. (2025) Does viral circulation in slums have a global impact? The lesson learned from SARS-CoV-2 circulation in Complexo de favelas da Mar??, Rio de Janeiro, Brazil. Frontiers in microbiology, 16, 1483895.

Latorre-Crespo E, et al. (2025) Clinical progression of clonal hematopoiesis is determined by a combination of mutation timing, fitness, and clonal structure. bioRxiv : the preprint server for biology.

Specht I, et al. (2025) JUNIPER: Reconstructing Transmission Events from Next-Generation Sequencing Data at Scale. medRxiv : the preprint server for health sciences.

Leoni G, et al. (2025) PathoSeq-QC: a decision support bioinformatics workflow for robust genomic surveillance. Bioinformatics (Oxford, England), 41(4).