# Resource Summary Report

Generated by NIF on Apr 16, 2025

# 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

**Funding:**

**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:** 20250410T070328+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 465 mentions in open access literature.

**Listed below are recent publications.** The full list is available at NIF.

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).

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

Mendeville MS, et al. (2025) Integrating genetic subtypes with PET scan monitoring to predict outcome in diffuse large B-cell lymphoma. Nature communications, 16(1), 109.

Gilbert A, et al. (2024) Radiosensitizing Effect of PARP Inhibition on Chondrosarcoma and Chondrocyte Cells Is Dependent on Radiation LET. Biomolecules, 14(9).

Hakim MS, et al. (2024) Sequence analysis of the Spike, RNA-dependent RNA polymerase, and protease genes reveals a distinct evolutionary pattern of SARS-CoV-2 variants circulating in Yogyakarta and Central Java provinces, Indonesia. Virus genes, 60(2), 105.

Fuhrmann L, et al. (2024) V-pipe 3.0: a sustainable pipeline for within-sample viral genetic diversity estimation. GigaScience, 13.

Cattaneo D, et al. (2024) Value and limitations of targeted next-generation sequencing in idiopathic hypereosinophilia: an integrative diagnostic tool in challenging cases. Clinical and experimental medicine, 24(1), 165.

Deboutte W, et al. (2024) Known and novel viruses in Belgian honey bees: yearly differences, spatial clustering, and associations with overwintering loss. Microbiology spectrum, 12(7), e0358123.

Marti A, et al. (2024) Fitness adaptations of Japanese encephalitis virus in pigs following vector-free serial passaging. PLoS pathogens, 20(8), e1012059.

Phumiphanjarphak W, et al. (2024) Entourage: all-in-one sequence analysis software for genome assembly, virus detection, virus discovery, and intrasample variation profiling. BMC bioinformatics, 25(1), 222.

Liu Y, et al. (2024) Crykey: Rapid identification of SARS-CoV-2 cryptic mutations in wastewater. Nature communications, 15(1), 4545.

He Y, et al. (2024) Expanding plant genome editing scope and profiles with CRISPR-FrCas9 systems targeting palindromic TA sites. Plant biotechnology journal, 22(9), 2488.

Rahman N, et al. (2024) Mobilisation and analyses of publicly available SARS-CoV-2 data for pandemic responses. Microbial genomics, 10(2).

Wang D, et al. (2024) Substantial viral diversity in bats and rodents from East Africa: insights into evolution, recombination, and cocirculation. Microbiome, 12(1), 72.

Xie L, et al. (2024) An ovalbumin fusion strategy to increase recombinant protein secretion in chicken eggs. Journal of biological engineering, 18(1), 5.

Banga J, et al. (2024) Severe Acute Respiratory Syndrome Coronavirus 2 Household Transmission During the Omicron Era in Massachusetts: A Prospective, Case-Ascertained Study Using Genomic Epidemiology. Open forum infectious diseases, 11(11), ofae591.

Pyöriä L, et al. (2024) Intra-host genomic diversity and integration landscape of human tissue-resident DNA virome. Nucleic acids research, 52(21), 13073.

Ferreira Sa Antunes T, et al. (2024) Intra-Host Citrus Tristeza Virus Populations during Prolonged Infection Initiated by a Well-Defined Sequence Variant in Nicotiana benthamiana. Viruses, 16(9).

Lim JH, et al. (2024) Bronchial washing fluid sequencing is useful in the diagnosis of lung cancer with necrotic tumor. Translational oncology, 50, 102134.

Manuto L, et al. (2024) Immune System Deficiencies Do Not Alter SARS-CoV-2 Evolutionary Rate but Favour the Emergence of Mutations by Extending Viral Persistence. Viruses, 16(3).