

Resource Summary Report

Generated by [RRID](#) on Sep 10, 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: 20260905T132731+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 553 mentions in open access literature.

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

Mihindukulasuriya KA, et al. (2026) VICAST: An Integrated Toolkit for Viral Genome Annotation Curation and Low-Frequency Variant Analysis in Passage Studies. bioRxiv : the preprint server for biology.

Baskarane H, et al. (2026) Prevalence and spectrum of homologous recombination repair mutations in patients with metastatic prostate cancer from India. The oncologist, 31(4).

Wagner J, et al. (2026) A complete human pancreatic cancer genome. bioRxiv : the preprint server for biology.

Rouxel C, et al. (2026) Exploration of geographical population structure of Anaplasma phagocytophilum: Insights from 12 newly sequenced European human and bovine genome assemblies. Current research in parasitology & vector-borne diseases, 9, 100393.

González R, et al. (2026) Microbiome composition modulates the lethal outcome of Drosophila A virus infection. Cellular and molecular life sciences : CMLS, 83(1), 61.

Cho AY, et al. (2026) Wild birds drive the introduction, maintenance, and spread of H5N1 clade 2.3.4.4b high pathogenicity avian influenza viruses in Spain, 2021-2022. Virus evolution, 12(1), veag006.

Ortega Del Campo S, et al. (2026) Synergistic antiviral effects of structure-guided peptides and a mutagenic base analog on SARS-CoV-2 replication. Antimicrobial agents and chemotherapy, 70(6), e0188525.

Rosado-Lugo JD, et al. (2026) TXA11114: Discovery of an In Vivo Efficacious Efflux Pump Inhibitor (EPI) That Potentiates Levofloxacin Against Pseudomonas aeruginosa. Antibiotics (Basel, Switzerland), 15(4).

Mkpuma N, et al. (2026) Molecular characterization and phylogeography of equine influenza virus H3N8 detected in donkeys in Nigeria 2022-2023. BMC veterinary research, 22(1).

Braud L, et al. (2026) TERT drives liver tumorigenesis beyond telomere elongation. Life science alliance, 9(9).

Telengech P, et al. (2026) Toward in planta studies of persistent fungal viruses in a model plant. Virus research, 370, 199761.

Castro EM, et al. (2026) A bireporter recombinant SARS-CoV-2 Omicron BA.5 for in vitro and in vivo studies. *bioRxiv : the preprint server for biology*.

Kawai H, et al. (2026) Philadelphia chromosome-positive de novo myelodysplastic syndrome with the p230 BCR::ABL1 fusion gene: a case report. *International journal of hematology*, 123(1), 122.

Tompa M, et al. (2026) Somatic Mutations in Nuclear and Mitochondrial Genes of Mitochondrial Proteins in Primary and Recurrent Glioblastoma. *International journal of molecular sciences*, 27(4).

Oluwasemowo OO, et al. (2026) Impact of Selenium and Vitamin E Deficiency on Zika Virus Pathogenesis and Immune Response in Mice. *Viruses*, 18(2).

de Diego Fuertes M, et al. (2026) Targeted and whole-genome sequencing for drug resistance and genetic relatedness inference of rifampicin-resistant *Mycobacterium tuberculosis*: an in-depth comparison. *ERJ open research*, 12(1).

Kraft T, et al. (2026) Back to the wildtype: SARS-CoV-2 evolution in critically ill patients with severe lung failure. *Infection*, 54(1), 225.

Bucher P, et al. (2026) CAR-adapted PIK3CD base editing enhances T cell anti-tumor potency. *Nature cancer*, 7(2), 368.

Courtney SJ, et al. (2026) Evidence for Powassan virus deletions and defective RNA in field-collected ticks. *Journal of virology*, 100(2), e0135625.

Zhu J, et al. (2026) Engineering hypercompact IscB nucleases for efficient and versatile genome editing in rice. *Genome biology*, 27(1), 49.