

Resource Summary Report

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iVar

RRID:SCR_024045

Type: Tool

Proper Citation

iVar (RRID:SCR_024045)

Resource Information

URL: <https://github.com/andersen-lab/ivar>

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Description: Software package for viral amplicon based sequencing. Additional tools for metagenomic sequencing are actively being incorporated into iVar. Contains intersection of functionality from multiple tools that are required to call iSNVs and consensus sequences from viral sequencing data across multiple replicates. Following functions are implemented in iVar: trimming of primers and low-quality bases; consensus calling; variant calling both iSNVs and insertions/deletions; identifying mismatches to primer sequences and excluding the corresponding reads from alignment files.

Synonyms: ivar

Resource Type: software toolkit, software resource

Defining Citation: [PMID:30621750](#)

Keywords: call iSNVs from viral sequencing data, viral amplicon based sequencing, call iSNVs and consensus sequences from viral sequencing data, call iSNVs

Availability: Free, Available for download, Freely available,

Resource Name: iVar

Resource ID: SCR_024045

Alternate URLs: <https://sources.debian.org/src/ivar/>, <https://andersen-lab.github.io/ivar/html/>

License: GPL-3.0 license

Record Creation Time: 20230824T050211+0000

Record Last Update: 20260729T044601+0000

Ratings and Alerts

No rating or validation information has been found for iVar.

No alerts have been found for iVar.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 66 mentions in open access literature.

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

Edwards CT, et al. (2025) Passive infusion of an S2-Stem broadly neutralizing antibody protects against SARS-CoV-2 infection and lower airway inflammation in rhesus macaques. PLoS pathogens, 21(1), e1012456.

Phumiphanjarphak W, et al. (2025) Discovery of diverse anellovirus sequences in Thai human sequencing data. Microbiology spectrum, 13(10), e0086625.

Torres-Hernández D, et al. (2025) Epidemiology and severity risk factors of dengue virus infection during the 2023-2024 outbreak in Colombia. PLoS neglected tropical diseases, 19(12), e0013115.

Hinzke T, et al. (2025) RNA virus genomes from centuries- to millennia-old Adélie penguin mummies. bioRxiv : the preprint server for biology.

Sankhe S, et al. (2025) Genomic Insights into Neglected Orthobunyaviruses: Molecular Characterization and Phylogenetic Analysis. Viruses, 17(3).

Tar buck NN, et al. (2025) Persistence of SARS-CoV-2 Alpha Variant in White-Tailed Deer, Ohio, USA. Emerging infectious diseases, 31(7), 1319.

Soriano-Tordera C, et al. (2025) Identification and characterization of novel bat coronaviruses in Spain. PLoS pathogens, 21(8), e1013371.

Lambisia AW, et al. (2025) Genomic and clinical epidemiology of SARS-CoV-2 in coastal Kenya: insights into variant circulation, reinfection, and multiple lineage importations during a post-pandemic wave. BMC global and public health, 3(1), 80.

Labiod N, et al. (2025) Case series of Oropouche fever among travellers returning from Cuba to Spain, 2024. Euro surveillance : bulletin Européen sur les maladies transmissibles = European communicable disease bulletin, 30(41).

Ling-Hu T, et al. (2025) The impact of remdesivir on SARS-CoV-2 evolution in vivo. JCI insight, 10(4).

Žuštra A, et al. (2025) Longitudinal dynamics of the nasopharyngeal microbiome in response to SARS-CoV-2 Omicron variant and HIV infection in Kenyan women and their children. *mSystems*, 10(5), e0156824.

Ellegaard KM, et al. (2025) SARS-CoV-2 sequencing artifacts associated with targeted PCR enrichment and read mapping. *PloS one*, 20(10), e0334009.

Goya S, et al. (2025) Distinct Evolutionary Signatures of Human Parainfluenza Viruses 2 and 4 Reveal Host Antagonism Divergence and Phylogenetic Discordance. *Molecular biology and evolution*, 42(10).

Gliši? D, et al. (2025) Endemic Circulation of Cluster 19 African Swine Fever Virus in Serbia and Bosnia and Herzegovina. *Veterinary sciences*, 12(11).

Avadhanula V, et al. (2024) Inter and intra-host diversity of RSV in hematopoietic stem cell transplant adults with normal and delayed viral clearance. *Virus evolution*, 10(1), vead086.

Mostefai F, et al. (2024) Refining SARS-CoV-2 intra-host variation by leveraging large-scale sequencing data. *NAR genomics and bioinformatics*, 6(4), lqae145.

Edwards CT, et al. (2024) Passive infusion of an S2-Stem broadly neutralizing antibody protects against SARS-CoV-2 infection and lower airway inflammation in rhesus macaques. *bioRxiv : the preprint server for biology*.

Jimenez-Vasquez V, et al. (2024) Dispersion of SARS-CoV-2 lineage BA.5.1.25 and its descendants in Peru during two COVID-19 waves in 2022. *Genomics & informatics*, 22(1), 5.

Spilsberg B, et al. (2024) Development and application of a whole genome amplicon sequencing method for infectious salmon anemia virus (ISAV). *Frontiers in microbiology*, 15, 1392607.

Nooruzzaman M, et al. (2024) Emergence of transmissible SARS-CoV-2 variants with decreased sensitivity to antivirals in immunocompromised patients with persistent infections. *Nature communications*, 15(1), 7999.