

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 resource, software toolkit

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: 20260905T133103+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 77 mentions in open access literature.

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

Wang K, et al. (2026) Rapid and precise amplicon-based genome sequencing to preparedness and response chikungunya virus outbreaks. *Emerging microbes & infections*, 15(1), 2660424.

Kartashov MY, et al. (2026) Expanding diversity of tick-borne phleboviruses (Phlebovirus mukawaense, Mudanjiang phlebovirus, Gomselga Virus, and Onega tick phlebovirus) in Russia. *PloS one*, 21(6), e0349564.

Bourke BP, et al. (2026) Diverse novel and avian-associated viruses in the ileal viromes of Northern Mockingbird (*Mimus polyglottos*). *Archives of virology*, 171(4).

Avadhanula V, et al. (2026) Evolutionary dynamics of Respiratory Syncytial Virus in pre-pandemic, pandemic, and post-pandemic periods in Houston, Texas, USA. *bioRxiv : the preprint server for biology*.

Ba?i? A, et al. (2026) Occurrence and molecular characterization of *Giardia duodenalis* in domestic and wild mesocarnivores in Bosnia and Herzegovina. *International journal for parasitology. Parasites and wildlife*, 29, 101197.

Loeanurit N, et al. (2026) Chlorinated bis-4-hydroxycoumarins suppress flavivirus replication by inhibiting dengue virus type 2 translation and replication. *Scientific reports*, 16(1), 5300.

Malago S, et al. (2026) Introduction of a European Central-South-Eastern West Nile Virus Lineage 2 Strain in Italy in 2023: Evidence from the First Locally Acquired Neuroinvasive Case in the Calabria Region. *International journal of molecular sciences*, 27(4).

Taboada B, et al. (2026) Post-Pandemic Genomic Diversity and Lineage Turnover of Influenza Viruses in Mexico During 2022-2023. *Viruses*, 18(6).

Kartashov MY, et al. (2026) First Report of Orthonairovirus songlingense in *Haemaphysalis concinna* Ticks from Russia. *Viruses*, 18(6).

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.

Griffon AF, et al. (2025) Development of a competition assay to assess the in vitro fitness of dengue virus serotypes using an optimized serotype-specific qRT-PCR. *PloS one*, 20(12), e0339033.

Bessi re P, et al. (2025) Seroprevalence and genetic diversity of feline immunodeficiency virus in outdoor cats in France. *Veterinary research*, 57(1), 6.

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

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

Torres-Hern ndez 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.

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

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

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.

 u tra 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.

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