

# Resource Summary Report

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## VICUNA

RRID:SCR\_006302

Type: Tool

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### Proper Citation

VICUNA (RRID:SCR\_006302)

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### Resource Information

**URL:** <http://www.broadinstitute.org/scientific-community/science/projects/viral-genomics/vicuna>

**Proper Citation:** VICUNA (RRID:SCR\_006302)

**Description:** A de novo assembly program targeting populations with high mutation rates.

**Abbreviations:** VICUNA

**Resource Type:** software resource

**Defining Citation:** [PMID:22974120](#)

**Keywords:** c++, bio.tools

**Resource Name:** VICUNA

**Resource ID:** SCR\_006302

**Alternate IDs:** biotools:vicuna, OMICS\_02162

**Alternate URLs:** <https://bio.tools/vicuna>

**Record Creation Time:** 20220129T080235+0000

**Record Last Update:** 20260912T195637+0000

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### Ratings and Alerts

No rating or validation information has been found for VICUNA.

No alerts have been found for VICUNA.

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### Data and Source Information

## Usage and Citation Metrics

We found 26 mentions in open access literature.

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

Hansen D, et al. (2025) Impact of HIV-1 capsid polymorphisms on viral infectivity and susceptibility to lenacapavir. *mBio*, 16(5), e0018725.

Zaim Bin Ahmad MS, et al. (2025) Large-scale moral machine experiment on large language models. *PloS one*, 20(5), e0322776.

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

Kim KA, et al. (2023) Next-generation sequencing analysis of hepatitis C virus resistance-associated substitutions in direct-acting antiviral failure in South Korea. *Clinical and molecular hepatology*, 29(2), 496.

Tully DC, et al. (2023) Validation of Dried Blood Spots for Capturing Hepatitis C Virus Diversity for Genomic Surveillance. *medRxiv : the preprint server for health sciences*.

Castruita JAS, et al. (2023) SARS-CoV-2 spike mRNA vaccine sequences circulate in blood up to 28 days after COVID-19 vaccination. *APMIS : acta pathologica, microbiologica, et immunologica Scandinavica*, 131(3), 128.

Hochstatter KR, et al. (2021) Hepatitis C Virus Transmission Clusters in Public Health and Correctional Settings, Wisconsin, USA, 2016-2017. *Emerging infectious diseases*, 27(2), 480.

Collins DR, et al. (2021) Functional impairment of HIV-specific CD8+ T cells precedes aborted spontaneous control of viremia. *Immunity*, 54(10), 2372.

Gaube G, et al. (2020) Characterization of HIV-1 diversity in various compartments at the time of primary infection by ultradeep sequencing. *Scientific reports*, 10(1), 2409.

Manso CF, et al. (2020) Technical Validation of a Hepatitis C Virus Whole Genome Sequencing Assay for Detection of Genotype and Antiviral Resistance in the Clinical Pathway. *Frontiers in microbiology*, 11, 576572.

Singer JB, et al. (2019) Interpreting Viral Deep Sequencing Data with GLUE. *Viruses*, 11(4).

Ansari MA, et al. (2017) Genome-to-genome analysis highlights the effect of the human innate and adaptive immune systems on the hepatitis C virus. *Nature genetics*, 49(5), 666.

Jagdagsuren D, et al. (2017) The second molecular epidemiological study of HIV infection in Mongolia between 2010 and 2016. *PloS one*, 12(12), e0189605.

Vrancken B, et al. (2016) Quantifying Next Generation Sequencing Sample Pre-Processing Bias in HIV-1 Complete Genome Sequencing. *Viruses*, 8(1).

Rose R, et al. (2016) Challenges in the analysis of viral metagenomes. *Virus evolution*, 2(2), vew022.

Bull RA, et al. (2016) A method for near full-length amplification and sequencing for six hepatitis C virus genotypes. *BMC genomics*, 17, 247.

Simmonds TJ, et al. (2016) Characterization of a venom gland-associated rhabdovirus in the parasitoid wasp *Diachasmimorpha longicaudata*. *Journal of insect physiology*, 91-92, 48.

Swadling L, et al. (2016) Highly-Immunogenic Virally-Vectored T-cell Vaccines Cannot Overcome Subversion of the T-cell Response by HCV during Chronic Infection. *Vaccines*, 4(3).

Salazar-Gonzalez JF, et al. (2016) Use of Dried Blood Spots to Elucidate Full-Length Transmitted/Founder HIV-1 Genomes. *Pathogens & immunity*, 1(1), 129.

Marascio N, et al. (2016) Detection of Natural Resistance-Associated Substitutions by Ion Semiconductor Technology in HCV1b Positive, Direct-Acting Antiviral Agents-Naïve Patients. *International journal of molecular sciences*, 17(9).