Resource Summary Report

Generated by NIF on Apr 8, 2025

VICUNA

RRID:SCR_006302
Type: Tool

Proper Citation

VICUNA (RRID:SCR_006302)

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

Funding:

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: 20250214T183042+0000

Ratings and Alerts

No rating or validation information has been found for VICUNA.

No alerts have been found for VICUNA.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 24 mentions in open access literature.

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

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, 2016-20171. 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).

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

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.

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.

Mordecai GJ, et al. (2016) Diversity in a honey bee pathogen: first report of a third master variant of the Deformed Wing Virus quasispecies. The ISME journal, 10(5), 1264.

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).

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.

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).

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.

Thomson E, et al. (2016) Comparison of Next-Generation Sequencing Technologies for Comprehensive Assessment of Full-Length Hepatitis C Viral Genomes. Journal of clinical microbiology, 54(10), 2470.