

Resource Summary Report

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HIV Sequence Database

RRID:SCR_002906

Type: Tool

Proper Citation

HIV Sequence Database (RRID:SCR_002906)

Resource Information

URL: <http://hiv-web.lanl.gov/>

Proper Citation: HIV Sequence Database (RRID:SCR_002906)

Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on January 4, 2023. HIV Sequence Database is a database of annotated HIV sequences, plus a variety of tools and information for researchers studying HIV and SIV. The main aim of this website is to provide easy access to our sequence database, alignments, and the tools and interfaces we have produced. The HIV Sequence Database focuses on five primary goals: * Collecting HIV and SIV sequence data (all sequences since 1987) * Curating and annotating this data, and making it available to the scientific community * Computer analysis of HIV and related sequences * Production of software for the analysis of (sequence) data * The data and analyses on this site and published in a yearly printed publication, the HIV sequence Compendium, which is available free of charge.

Abbreviations: HIV Sequence Database

Resource Type: analysis service resource, data analysis service, data or information resource, database, production service resource, service resource

Keywords: drug resistance, genetics, mutation, vaccine, human immunodeficiency virus, siv, sequence, alignment, simian immunodeficiency virus, FASEB list

Related Condition: Human immunodeficiency virus, Simian immunodeficiency virus

Funding: NIAID

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: HIV Sequence Database

Resource ID: SCR_002906

Alternate IDs: nif-0000-02967

Record Creation Time: 20220129T080216+0000

Record Last Update: 20260829T182117+0000

Ratings and Alerts

No rating or validation information has been found for HIV Sequence Database.

No alerts have been found for HIV Sequence Database.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 110 mentions in open access literature.

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

Maphumulo NF, et al. (2024) HIV-1 envelope facilitates the development of protease inhibitor resistance through acquiring mutations associated with viral entry and immune escape. *Frontiers in microbiology*, 15, 1388729.

Lu X, et al. (2023) Recombinant characteristics of three novel HIV-1 second-generation recombinant forms composed of CRF01_AE and CRF07_BC isolated in Hebei province, China. *Archives of virology*, 168(4), 111.

Yang X, et al. (2022) Genetic characterization of a novel HIV?1 CRF01_AE/ CRF07_BC recombinant form found among men who have sex with men in Baoding City, Hebei Province, China. *Archives of virology*, 167(11), 2395.

Zhang Y, et al. (2022) Using molecular network analysis to explore the characteristics of HIV-1 transmission in a China-Myanmar border area. *PloS one*, 17(5), e0268143.

Lai A, et al. (2021) Early-Transmitted Variants and Their Evolution in a HIV-1 Positive Couple: NGS and Phylogenetic Analyses. *Viruses*, 13(3).

Bello G, et al. (2020) Increasing prevalence and local transmission of non-B HIV-1 subtypes in the French Antilles and French Guiana between 1995 and 2018. *Virus evolution*, 6(2), veaa081.

F Löchel H, et al. (2020) Comparative analyses of error handling strategies for next-generation sequencing in precision medicine. *Scientific reports*, 10(1), 5750.

Fokam J, et al. (2020) Pre-treatment drug resistance and HIV-1 genetic diversity in the rural and urban settings of Northwest-Cameroon. *PloS one*, 15(7), e0235958.

Kiros M, et al. (2020) Increased HIV-1 pretreatment drug resistance with consistent clade homogeneity among ART-naive HIV-1 infected individuals in Ethiopia. *Retrovirology*,

17(1), 33.

Tchiakpe E, et al. (2020) Moderate rate of transmitted resistance mutations to antiretrovirals and genetic diversity in newly HIV-1 patients diagnosed in Benin. BMC research notes, 13(1), 314.

Long S, et al. (2020) Maximizing viral detection with SIV droplet digital PCR (ddPCR) assays. PloS one, 15(5), e0233085.

Long S, et al. (2020) Development and optimization of a simian immunodeficiency virus (SIV) droplet digital PCR (ddPCR) assay. PloS one, 15(10), e0240447.

Jia D, et al. (2019) Two-year cross-sectional studies reveal that single, young MSMs in Shenzhen, China are at high risk for HIV infection. Virology journal, 16(1), 83.

Wirten M, et al. (2019) New HIV-1 circulating recombinant form 94: from phylogenetic detection of a large transmission cluster to prevention in the age of geosocial-networking apps in France, 2013 to 2017. Euro surveillance : bulletin Europeen sur les maladies transmissibles = European communicable disease bulletin, 24(39).

Bendenoun M, et al. (2018) What Is the most Important for Elite Control: Genetic Background of Patient, Genetic Background of Partner, both or neither? Description of Complete Natural History within a Couple of MSM. EBioMedicine, 27, 51.

Kmiec D, et al. (2018) SIVcol Nef counteracts SERINC5 by promoting its proteasomal degradation but does not efficiently enhance HIV-1 replication in human CD4+ T cells and lymphoid tissue. PLoS pathogens, 14(8), e1007269.

Li WY, et al. (2018) Molecular epidemiology of HIV-1 infection among men who have sex with men in Taiwan from 2013 to 2015. PloS one, 13(12), e0202622.

Chen M, et al. (2018) HIV-1 genetic transmission networks among men who have sex with men in Kunming, China. PloS one, 13(4), e0196548.

Wu ZL, et al. (2018) Dynamic Characteristics and HIV Infection of Men who have Sex with Men from 2011 to 2017 in Yinchuan, Ningxia, China. Current HIV research, 16(5), 364.

Wu Y, et al. (2017) Characterization of a novel HIV-1 unique recombinant form between CRF07_BC and CRF55_01B in men who have sex with men in Guangzhou, China. PloS one, 12(4), e0175770.