

Resource Summary Report

Generated by [SPARC SAWG](#) on Aug 10, 2026

Hypermur

RRID:SCR_014933

Type: Tool

Proper Citation

Hypermur (RRID:SCR_014933)

Resource Information

URL: <https://www.hiv.lanl.gov/content/sequence/HYPERMUT/hypermur.html>

Proper Citation: Hypermur (RRID:SCR_014933)

Description: Web application for the analysis and detection of APOBEC-induced hypermutations. The first sequence in the input alignment will be used as the reference sequence, and each of the other sequences will be used as a query sequence.

Synonyms: Hypermur 2.0

Resource Type: data analysis software, data processing software, software application, sequence analysis software, web application, software resource

Defining Citation: [PMID:10869039](#)

Keywords: mutation, hypermutation, sequence, sequence analysis software genome, web application

Resource Name: Hypermur

Resource ID: SCR_014933

Record Creation Time: 20220129T080323+0000

Record Last Update: 20260810T040635+0000

Ratings and Alerts

No rating or validation information has been found for Hypermur.

No alerts have been found for Hypermur.

Data and Source Information

Usage and Citation Metrics

We found 130 mentions in open access literature.

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

Charre C, et al. (2026) Post-treatment SIV control is associated with specific features of viral persistence before and after treatment interruption. *Nature communications*, 17(1).

Williamson C, et al. (2026) Influence of the broadly neutralizing antibody VRC01 on HIV breakthrough virus populations in antibody-mediated prevention trials. *Nature communications*, 17(1).

Vadaq N, et al. (2026) Longitudinal plasma proteomic signatures of elite and viremic spontaneous HIV controllers. *Nature communications*, 17(1), 1173.

Tyers L, et al. (2025) HIV-1 Rebound Virus Consists of a Small Number of Lineages That Entered the Reservoir Close to ART Initiation. *bioRxiv : the preprint server for biology*.

Kagan RM, et al. (2025) HIV-1 Drug Resistance Trends in the Era of Modern Antiretrovirals: 2018-2024. *Open forum infectious diseases*, 12(8), ofaf446.

Zhao W, et al. (2025) DHX15 inhibits mouse APOBEC3 deamination. *PLoS pathogens*, 21(4), e1013045.

Guang A, et al. (2025) T-shaped alignments integrating HIV-1 near full-length genome and partial pol sequences can improve phylogenetic inference of transmission clusters. *PLoS computational biology*, 21(11), e1013676.

Hardy J, et al. (2025) Aberrant strand transfer events across multiple stages of reverse transcription shape the heterogeneous landscape of the HIV-1 reservoir. *Communications biology*, 8(1), 1703.

Pasternak AO, et al. (2025) Long-term effect of temporary ART initiated during primary HIV-1 infection on viral persistence. *Nature communications*, 16(1), 6989.

Shahid A, et al. (2025) A simple phylogenetic approach to analyze hypermutated HIV proviruses reveals insights into their dynamics and persistence during antiretroviral therapy. *Virus evolution*, 11(1), veae094.

Capoferri AA, et al. (2025) In vivo detection of antisense HIV-1 transcripts in untreated and ART-treated individuals. *Life science alliance*, 8(9).

Lu D, et al. (2025) Near extinction of the HBV quasispecies driven by the hard selective sweep in chronic hepatitis B. *mBio*, 16(8), e0111325.

Gai Y, et al. (2024) Design of Vif-Derived Peptide Inhibitors with Anti-HIV-1 Activity by Interrupting Vif-CBF?? Interaction. *Viruses*, 16(4).

Vela LC, et al. (2024) Profound reduction of HIV-1 reservoir cells over 3 decades of antiretroviral therapy started in early infancy. *JCI insight*, 10(1).

Lee GQ, et al. (2024) HIV-1 subtype A1, D, and recombinant proviral genome landscapes during long-term suppressive therapy. *Nature communications*, 15(1), 5480.

Shichijo T, et al. (2024) Vulnerability to APOBEC3G linked to the pathogenicity of deltaretroviruses. *Proceedings of the National Academy of Sciences of the United States of America*, 121(13), e2309925121.

Julg B, et al. (2024) Safety and antiviral effect of a triple combination of HIV-1 broadly neutralizing antibodies: a phase 1/2a trial. *Nature medicine*, 30(12), 3534.

Capoferri AA, et al. (2024) HIV-1 control in vivo is related to the number but not the fraction of infected cells with viral unspliced RNA. *bioRxiv : the preprint server for biology*.

Li X, et al. (2024) The emergence and circulation of human immunodeficiency virus (HIV)-1 subtype C. *Journal of medical microbiology*, 73(5).

Abdullahi A, et al. (2024) A detailed characterization of drug resistance during darunavir/ritonavir monotherapy highlights a high barrier to the emergence of resistance mutations in protease but identifies alternative pathways of resistance. *The Journal of antimicrobial chemotherapy*, 79(2), 339.