

# Resource Summary Report

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## 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 processing software, web application, software application, data analysis software, software resource, sequence analysis software

**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:** 20260815T042712+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 [dkNET](#) .

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.