

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

Genotyping

RRID:SCR_016645

Type: Tool

Proper Citation

Genotyping (RRID:SCR_016645)

Resource Information

URL: <https://www.ncbi.nlm.nih.gov/projects/genotyping/formpage.cgi>

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Description: Web tool to identify the genotype of a viral sequence. A window is slid along the query sequence and each window is compared by BLAST to each of the reference sequences for a particular virus.

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

Keywords: identify, genotype, viral, sequence, bio.tools

Availability: Free, Freely available

Resource Name: Genotyping

Resource ID: SCR_016645

Alternate IDs: biotools:ncbi_genotyping

Alternate URLs: https://bio.tools/ncbi_genotyping

Record Creation Time: 20220129T080331+0000

Record Last Update: 20260905T132812+0000

Ratings and Alerts

No rating or validation information has been found for Genotyping.

No alerts have been found for Genotyping.

Data and Source Information

Usage and Citation Metrics

We found 40 mentions in open access literature.

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

Odallo VB, et al. (2026) Molecular characterization of hepatitis B virus genotypes A and D among inmates and blood donors in Northeastern Kenya. PloS one, 21(2), e0336726.

Balinda SN, et al. (2026) Evolutionary dynamics of HIV-1 recombinants: analysis of contemporary and historical viral populations in East Africa. Virology journal, 23(1).

Chambal LM, et al. (2026) Local insights into hepatitis B Virus: genotype distribution and clinical profiles among HIV/HBV co-infected patients in Maputo, Mozambique. BMC infectious diseases, 26(1).

Mullins JI, et al. (2025) Long-Read Deep Sequencing Reveals High Rates of Multilineage Transmission and Rapid Viral Population Changes in Acute HIV Infection. bioRxiv : the preprint server for biology.

Dumaidi K, et al. (2025) Sero-Molecular Markers and Genetic Diversity of Hepatitis B Virus Isolated From Hemodialysis Patients From Jenin District, West Bank, Palestine. The Canadian journal of infectious diseases & medical microbiology = Journal canadien des maladies infectieuses et de la microbiologie medicale, 2025, 6981644.

Das R, et al. (2025) Emergence of HCV genotype 6 and its new variants among intravenous drug users in Manipur, a north-eastern state of India. Therapeutic advances in infectious disease, 12, 20499361251351302.

Jose-Abrego A, et al. (2025) Hepatitis C Virus Resistance-Associated Substitutions in Mexico. Viruses, 17(2).

Klutsch S, et al. (2025) Fatal Hepatitis B Reactivation in Absence of Antibody to Hepatitis B Core Antigen in a Lymphoma Patient. Journal of medical virology, 97(7), e70480.

Koul M, et al. (2025) VITALdb: to select the best viroinformatics tools for a desired virus or application. Briefings in bioinformatics, 26(2).

Wasitthankasem R, et al. (2024) Historical drivers of HCV Subtypes 1b and 3a in Thailand and 6f in Phetchabun, an HCV endemic area of the country. Virus evolution, 10(1), veae079.

Potter BI, et al. (2024) Contemporary and historical human migration patterns shape hepatitis B virus diversity. Virus evolution, 10(1), veae009.

Teiti I, et al. (2024) Towards elimination of chronic viral hepatitis in French Polynesia: results from a national population-based survey. The Lancet regional health. Western Pacific, 45, 101035.

Wieczorek L, et al. (2023) Evolution of HIV-1 envelope towards reduced neutralization sensitivity, as demonstrated by contemporary HIV-1 subtype B from the United States. *PLoS pathogens*, 19(12), e1011780.

Sarker MS, et al. (2023) High Diversity and Transmission Dynamics of HIV-1 Non-C Subtypes in Bangladesh. *Tropical medicine and infectious disease*, 8(9).

Li M, et al. (2023) Development and clinical validation of a one-step pentaplex real-time reverse transcription PCR assay for detection of hepatitis virus B, C, E, *Treponema pallidum*, and a human housekeeping gene. *BMC infectious diseases*, 23(1), 358.

Jose-Abrego A, et al. (2023) High Frequency of Antiviral Resistance Mutations in HBV Genotypes A2 and H: Multidrug Resistance Strains in Mexico. *Journal of clinical and translational hepatology*, 11(5), 1023.

Lai MW, et al. (2022) Absence of chronicity in infants born to immunized mothers with occult HBV infection in Taiwan. *Journal of hepatology*, 77(1), 63.

Sahibzada KI, et al. (2022) Hepatitis C virus transmission cluster among injection drug users in Pakistan. *PloS one*, 17(7), e0270910.

Liu M, et al. (2022) Pretreatment drug resistance in people living with HIV: A large retrospective cohort study in Chongqing, China. *HIV medicine*, 23 Suppl 1(Suppl 1), 95.

Lai X, et al. (2022) Effect of mutations across reverse transcriptase region on HBV replication and progression of liver diseases in Chinese patients. *Journal of clinical laboratory analysis*, 36(7), e24530.