Resource Summary Report

Generated by dkNET on Apr 22, 2025

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

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

Funding:

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: 20250422T055942+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

Source: SciCrunch Registry

Usage and Citation Metrics

We found 27 mentions in open access literature.

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

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.

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.

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).

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.

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.

Nishizawa T, et al. (2021) Identification and a full genome analysis of novel camel hepatitis E virus strains obtained from Bactrian camels in Mongolia. Virus research, 299, 198355.

Lorenzi JCC, et al. (2021) Neutralizing Activity of Broadly Neutralizing anti-HIV-1 Antibodies against Primary African Isolates. Journal of virology, 95(5).

Chen X, et al. (2021) A CRISPR-Cas12b-Based Platform for Ultrasensitive, Rapid, and Highly Specific Detection of Hepatitis B Virus Genotypes B and C in Clinical Application. Frontiers in bioengineering and biotechnology, 9, 743322.

Campos KR, et al. (2020) Provirus Mutations of Human T-Lymphotropic Virus 1 and 2 (HTLV-1 and HTLV-2) in HIV-1-Coinfected Individuals. mSphere, 5(5).

Takahashi M, et al. (2020) Prevalence and genotype/subtype distribution of hepatitis E virus (HEV) among wild boars in Japan: Identification of a genotype 5 HEV strain. Virus research, 287, 198106.

Koyaweda GW, et al. (2020) Detection of circulating hepatitis B virus immune escape and polymerase mutants among HBV-positive patients attending Institut Pasteur de Bangui, Central African Republic. International journal of infectious diseases : IJID : official publication of the International Society for Infectious Diseases, 90, 138.

Tamandjou Tchuem CR, et al. (2020) Hepatitis B virus drug resistance mutations in HIV/HBV co-infected children in Windhoek, Namibia. PloS one, 15(9), e0238839.

Fu Y, et al. (2020) Mutational characterization of HBV reverse transcriptase gene and the genotype-phenotype correlation of antiviral resistance among Chinese chronic hepatitis B patients. Emerging microbes & infections, 9(1), 2381.

Fu Y, et al. (2019) Characterization and Clinical Significance of Natural Variability in Hepatitis B Virus Reverse Transcriptase in Treatment-Naive Chinese Patients by Sanger Sequencing and Next-Generation Sequencing. Journal of clinical microbiology, 57(8).

Smole?-Dzirba J, et al. (2019) Transmission patterns of HIV-1 non-R5 strains in Poland. Scientific reports, 9(1), 4970.

Soldi GFR, et al. (2019) Major drug resistance mutations to HIV-1 protease inhibitors (PI) among patients exposed to PI class failing antiretroviral therapy in São Paulo State, Brazil. PloS one, 14(10), e0223210.