

Resource Summary Report

Generated by [nidm-terms](#) on Jul 29, 2026

HCV Databases

RRID:SCR_002863

Type: Tool

Proper Citation

HCV Databases (RRID:SCR_002863)

Resource Information

URL: <http://hcv.lanl.gov/>

Proper Citation: HCV Databases (RRID:SCR_002863)

Description: The Hepatitis C Virus (HCV) Database Project strives to present HCV-associated genetic and immunologic data in a user-friendly way, by providing access to the central database via web-accessible search interfaces and supplying a number of analysis tools.

Abbreviations: HCV Databases

Synonyms: Hepatitis C Virus Database, Hepatitis C Virus Database Project, HCV Database, Hepatitis C Virus Databases, Hepatitis C Virus (HCV) Database Project

Resource Type: disease-related portal, data or information resource, topical portal, portal

Keywords: hcv, hepatitis c virus, hepatitis c, database, data analysis service, sequence, immunology, annotation, FASEB list

Related Condition: Hepatitis C

Funding: NIAID

Availability: Free, Freely available

Resource Name: HCV Databases

Resource ID: SCR_002863

Alternate IDs: nif-0000-02944

Record Creation Time: 20220129T080215+0000

Record Last Update: 20260729T044041+0000

Ratings and Alerts

No rating or validation information has been found for HCV Databases.

No alerts have been found for HCV Databases.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 66 mentions in open access literature.

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

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

Melnychuk S, et al. (2025) Joint HIV and hepatitis C virus phylogenetic analyses signal network overlap among women engaged in sex work and men who purchase sex. International journal of STD & AIDS, 36(7), 542.

Maggiorella MT, et al. (2023) Epidemiological and molecular characterization of HBV and HCV infections in HIV-1-infected inmate population in Italy: a 2017-2019 multicenter cross-sectional study. Scientific reports, 13(1), 14908.

Ramos D, et al. (2023) Looking at the Molecular Target of NS5A Inhibitors throughout a Population Highly Affected with Hepatitis C Virus. Pathogens (Basel, Switzerland), 12(6).

Mukherjee S, et al. (2022) Selective Depletion of ZAP-Binding CpG Motifs in HCV Evolution. Pathogens (Basel, Switzerland), 12(1).

Qi M, et al. (2021) Complete genome analysis identifies recombinant events and positive selection sites of hepatitis C virus from mainland China during 2010-2019. Virus research, 296, 198354.

Cheng XD, et al. (2021) The genotype analysis of the hepatitis C virus in Heilongjiang Province, China. Medicine, 100(18), e25203.

Choi S, et al. (2021) A Healthcare-Associated Outbreak of HCV Genotype 2a at a Clinic in Seoul. Osong public health and research perspectives, 12(1), 3.

Aibekova L, et al. (2020) Transmission of HIV and HCV within Former Soviet Union Countries. Canadian journal of gastroenterology & hepatology, 2020, 9701920.

Brasher NA, et al. (2020) B cell immunodominance in primary hepatitis C virus infection. Journal of hepatology, 72(4), 670.

Qiu HT, et al. (2019) Paralogues From the Expanded Tlr11 Gene Family in Mudskipper (*Boleophthalmus pectinirostris*) Are Under Positive Selection and Respond Differently to

LPS/Poly(I:C) Challenge. *Frontiers in immunology*, 10, 343.

Xia Y, et al. (2019) Differential escape of HCV from CD8⁺ T cell selection pressure between China and Germany depends on the presenting HLA class I molecule. *Journal of viral hepatitis*, 26(1), 73.

Quadeer AA, et al. (2018) Co-evolution networks of HIV/HCV are modular with direct association to structure and function. *PLoS computational biology*, 14(9), e1006409.

von Delft A, et al. (2018) The generation of a simian adenoviral vectored HCV vaccine encoding genetically conserved gene segments to target multiple HCV genotypes. *Vaccine*, 36(2), 313.

Jaubert C, et al. (2018) RNA synthesis is modulated by G-quadruplex formation in Hepatitis C virus negative RNA strand. *Scientific reports*, 8(1), 8120.

Nguyen TT, et al. (2018) Confirmation of HCV viremia using HCV RNA and core antigen testing on dried blood spot in HIV infected peoples who inject drugs in Vietnam. *BMC infectious diseases*, 18(1), 622.

Stelzl E, et al. (2017) First identification of a recombinant form of hepatitis C virus in Austrian patients by full-genome next generation sequencing. *PloS one*, 12(7), e0181273.

Eltahla AA, et al. (2017) Dynamic evolution of hepatitis C virus resistance-associated substitutions in the absence of antiviral treatment. *Scientific reports*, 7, 41719.

Muñoz de Rueda P, et al. (2017) The antigenic variability of HCV in viral HLA-Ag binding is related to the activation of the host immune response. *Scientific reports*, 7(1), 15513.

Mokhtari C, et al. (2016) Characterization of Samples Identified as Hepatitis C Virus Genotype 1 without Subtype by Abbott RealTime HCV Genotype II Assay Using the New Abbott HCV Genotype Plus RUO Test. *Journal of clinical microbiology*, 54(2), 296.