

Resource Summary Report

Generated by [NIF](#) on Sep 2, 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: data or information resource, disease-related portal, portal, topical 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: 20260829T182739+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 71 mentions in open access literature.

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

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

Jiang H, et al. (2025) Using Phylogenetic Analysis to Detect National and International Dimensions of Hepatitis C Virus 1b Transmission Clusters - China, 1989-2021. China CDC weekly, 7(13), 435.

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.

Zhang M, et al. (2024) Transmission network of Hepatitis C virus subtype 2a in Huazhou County, Shaanxi Province, China. BMC infectious diseases, 24(1), 1048.

Dietz J, et al. (2024) Rare HCV subtypes and retreatment outcomes in a cohort of European DAA-experienced patients. JHEP reports : innovation in hepatology, 6(7), 101072.

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).

Xu R, et al. (2022) The evolutionary dynamics and epidemiological history of hepatitis C virus genotype 6, including unique strains from the Li community of Hainan Island, China. Virus evolution, 8(1), veac012.

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

Deng X, et al. (2022) Transmission networks of hepatitis C virus among HIV/HCV-coinfected patients in Guangdong, China. Virology journal, 19(1), 117.

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

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.

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.