

Resource Summary Report

Generated by T1D on Jul 29, 2026

HCV Sequence Database

RRID:SCR_006019

Type: Tool

Proper Citation

HCV Sequence Database (RRID:SCR_006019)

Resource Information

URL: <http://hcv.lanl.gov/content/sequence/HCV/ToolsOutline.html>

Proper Citation: HCV Sequence Database (RRID:SCR_006019)

Description: The HCV sequence database collects and annotates sequence data and provides them to the public via a website that contains a user-friendly search interface and a large number of sequence analysis tools, based on the model of the highly regarded Los Alamos HIV database. The hepatitis C virus (HCV) is a significant threat to public health worldwide. The virus is highly variable and evolves rapidly, making it an elusive target for the immune system and for vaccine and drug design. At present, some 30 000 HCV sequences have been published. This central website provides annotated sequences and analysis tools that will be helpful to HCV scientists worldwide. Things you can do: * Find sequences in the database * Download sequences from the database * Retrieve data about the sequences * Analyze sequences * Work with the sequences using our tools * Download ready-made alignments The HCV sequence database was officially launched in September 2003. Since then, its usage has steadily increased and is now at an average of approximately 280 visits per day from distinct IP addresses.

Abbreviations: HCV Sequence Database

Synonyms: Hepatitis C Sequence Database, Hepatitis C Virus Sequence Database, Los Alamos hepatitis C sequence database

Resource Type: service resource, data or information resource, data analysis service, database, production service resource, analysis service resource

Defining Citation: [PMID:15377502](#)

Keywords: hepatitis c virus, sequence, annotation

Related Condition: Hepatitis C

Funding: NIAID

Availability: Public

Resource Name: HCV Sequence Database

Resource ID: SCR_006019

Alternate IDs: nlx_151411

Record Creation Time: 20220129T080233+0000

Record Last Update: 20260729T044130+0000

Ratings and Alerts

No rating or validation information has been found for HCV Sequence Database.

No alerts have been found for HCV Sequence Database.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 19 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#) .

Fahmy AM, et al. (2024) On leveraging self-supervised learning for accurate HCV genotyping. Scientific reports, 14(1), 15463.

Du R, et al. (2022) HCV 6a was expanding and became the predominant subtype among blood donors between 2004 and 2019 in Guangdong, China. Virologica Sinica, 37(5), 765.

Chen X, et al. (2020) Plasma Inflammatory Biomarkers Associated with Advanced Liver Fibrosis in HIV-HCV-Coinfected Individuals. International journal of environmental research and public health, 17(24).

Garc??a-Crespo C, et al. (2020) Dissimilar Conservation Pattern in Hepatitis C Virus Mutant Spectra, Consensus Sequences, and Data Banks. Journal of clinical medicine, 9(11).

Spitz N, et al. (2019) The First Complete Genome Sequences of Hepatitis C Virus Subtype 2b from Latin America: Molecular Characterization and Phylogeographic Analysis. Viruses, 11(11).

Zhang AM, et al. (2019) The distinct epidemic characteristics of HCV co-infection among HIV-1-infected population caused by drug injection and sexual transmission in Yunnan, China. Epidemiology and infection, 147, e261.

- Bhattarai N, et al. (2017) Hepatitis C virus infection inhibits a Src-kinase regulatory phosphatase and reduces T cell activation in vivo. *PLoS pathogens*, 13(2), e1006232.
- Niu Z, et al. (2016) Age and gender distribution of Hepatitis C virus prevalence and genotypes of individuals of physical examination in WuHan, Central China. *SpringerPlus*, 5(1), 1557.
- Yang L, et al. (2016) Evolving Diversity of Hepatitis C Viruses in Yunnan Honghe, China. *International journal of molecular sciences*, 17(3), 403.
- Shaffer JR, et al. (2016) Genome-Wide Association Study Reveals Multiple Loci Influencing Normal Human Facial Morphology. *PLoS genetics*, 12(8), e1006149.
- Qiu P, et al. (2015) HCV genotyping from NGS short reads and its application in genotype detection from HCV mixed infected plasma. *PloS one*, 10(4), e0122082.
- Chen M, et al. (2015) Multiple Introduction and Naturally Occuring Drug Resistance of HCV among HIV-Infected Intravenous Drug Users in Yunnan: An Origin of China's HIV/HCV Epidemics. *PloS one*, 10(11), e0142543.
- Rong X, et al. (2014) Increased prevalence of hepatitis C virus subtype 6a in China: a comparison between 2004-2007 and 2008-2011. *Archives of virology*, 159(12), 3231.
- Dunford L, et al. (2012) Hepatitis C virus in Vietnam: high prevalence of infection in dialysis and multi-transfused patients involving diverse and novel virus variants. *PloS one*, 7(8), e41266.
- Kim Y, et al. (2012) A meta-analysis of the existing knowledge of immunoreactivity against hepatitis C virus (HCV). *PloS one*, 7(5), e38028.
- Lang Kuhs KA, et al. (2012) Induction of intrahepatic HCV NS4B, NS5A and NS5B-specific cellular immune responses following peripheral immunization. *PloS one*, 7(12), e52165.
- Tian D, et al. (2012) Different HCV genotype distributions of HIV-infected individuals in Henan and Guangxi, China. *PloS one*, 7(11), e50343.
- Nakatani SM, et al. (2011) Comparative performance evaluation of hepatitis C virus genotyping based on the 5' untranslated region versus partial sequencing of the NS5B region of brazilian patients with chronic hepatitis C. *Virology journal*, 8, 459.
- Zhang C, et al. (2011) HCV subtype characterization among injection drug users: implication for a crucial role of Zhenjiang in HCV transmission in China. *PloS one*, 6(2), e16817.