Resource Summary Report

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Stanford University HIV Drug Resistance Database

RRID:SCR_006631
Type: Tool

Proper Citation

Stanford University HIV Drug Resistance Database (RRID:SCR_006631)

Resource Information

URL: http://hivdb.stanford.edu/

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Description: The Stanford University HIV Drug Resistance Database is a curated public database designed to represent, store, and analyze the different forms of data underlying HIVs drug resistance. HIVDB has three main types of content: (1) Database queries and references, (2) Interactive programs, and (3) Educational resources. Database queries are designed primarily for researchers studying HIV drug resistance. The interactive programs and educational resources are designed for both researchers and those wishing to learn more about HIV drug resistance. 1.DATABASE QUERY AND REFERENCE PAGES Genotype-Treatment Correlations This Genotype-Treatment section of the database links to 15 interactive query pages that explore the relationship between treatment with HIV-1 antiretroviral drugs (ARVs) and mutations in HIV reverse transcriptase (RT), protease, and integrase. There are five types of interactive query pages: Treatment Profiles (Protease and RT inhibitors) Mutation Profiles (Protease and RT mutations) Detailed Treatment Queries (Protease, RT, and integrase inhibitors) Detailed Mutation Queries (Protease, RT, and integrase mutations) Mutation Prevalence According to Subtype and Treatment Genotype-Phenotype Correlations The main page of the Genotype-Phenotype Correlations section links to four interactive query pages: three dynamically updated data summaries and one regularly updated downloadable dataset. Drug Resistance Positions Query for levels of resistance associated with known drug resistance mutations Detailed Phenotype Queries Queries for levels of resistance associated with individual mutations or mutation combinations at all positions of protease, RT, and integrase Patterns of Drug Resistance Mutations Downloadable Reference Dataset Genotype-Clinical Correlations This part of the database has two main sections: Clinical Trials Datasets Summaries of Clinical Studies References This part of the database has two main sections: one with summaries of the data from each of the references in HIVDB and one in which every primate immunodeficiency virus sequence in GenBank is annotated according to its presence or absence in HIVDB. Studies in HIVDB GenBank => HIVDB New Submissions Approximately every three months, the New Submissions section lists the studies that

have been entered into HIVDB. The study title links to the introductory page of the study in the References section. Database Statistics (http://hivdb.stanford.edu/pages/HIVdbStatistics.html) 2. INTERACTIVE PROGRAMS HIVDB has seven main interactive programs. 1. HIVdb Program Mutation List Analysis Sequence Analysis HIVdb Output Sierra Web Service Release Notes Algorithm Specification Interface (ASI) 2. HIValg Program 3. HIVseq Program 4. Calibrated Population Resistance (CPR) tool 5. Mutation ARV Evidence Listing (MARVEL) 6. ART-AiDE 7. Rega HIV-1 Subtyping tool Three programs in the HIV Drug Resistance Database share a common code base: HIVseq, HIVdb, and HIValg. HIVseq accepts user-submitted protease, RT, and integrase sequences, compares them to the consensus subtype B reference sequence, and uses the differences as query parameters for interrogating the HIV Drug Resistance database (Shafer, D Jung, & B Betts, Nat Med 2000; Rhee SY et al. AIDS 2006). The query result provides users with the prevalence of protease, RT and integrase mutations according to subtype and PI, nucleoside RT inhibitor (NRTI), non-nucleoside RT inhibitor (NNRTI), and integrase inhibitor (INI) exposure. This allows users to detect unusual sequence results immediately so that the person doing the sequencing can check the primary sequence output while it is still on the desktop. In addition, unexpected associations between sequences or isolates can be discovered by immediately retrieving data on isolates sharing one or more mutations with the sequence. There are three ways in which the HIVdb program can be used: (i) entering a list of protease and RT mutations, (ii) entering a complete sequence containing protease, RT, and/or integrase, and (iii) using a Web Service. HIVdb is an expert system that accepts user-submitted HIV-1 pol sequences and returns inferred levels of resistance to 20 FDA-approved ARV drugs including 8 PIs, 7 NRTIs, 4 NNRTIs, and - with this update - one INI. In the HIVdb system, each HIV-1 drug resistance mutation is assigned a drug penalty score and a comment; the total score for a drug is derived by adding the scores of each mutation associated with resistance to that drug. Using the total drug score, the program reports one of the following levels of inferred drug resistance: susceptible, potential low-level resistance, low-level resistance, intermediate resistance, and high-level resistance. HIValg is designed for users interested in comparing the results of different algorithms or who are interested in comparing and evaluating existing and newly developed algorithms. The ability to develop new algorithms that can be run on the HIV Drug Resistance Database depends on the Algorithm Specific Interface (ASI) compiler (Shafer & Betts JCM 2003). Submission of Sequences and Mutations For each of the three programs, sequences can be entered using either the Sequence Analysis Form or the Mutation List form. 3. EDUCATIONAL RESOURCES HIVDB contains several regularly updated sections summarizing data linking RT, protease, and integrase mutations and antiretroviral drugs (ARVs). These sections include (i) tabular summaries of the major mutations associated with each ARV class, (ii) detailed summaries of the major, minor, and accessory mutations associated with each ARV, (iii) the comments used by the HIVdb program, (iv) the scores used by the HIVdb program, (v) clinical studies in which baseline drug resistance mutations have been correlated with the virological response (clinical outcome) to a specific ARV, (vi) mutations that can be used for drug resistance surveillance, and (vii) a two-page PDF handout. 1. Drug Resistance Summaries Tabular Drug Resistance Summaries by ARV Class Detailed Drug Resistance Summaries by ARV Drug Resistance Mutation Comments Used by the HIVdb Program Drug Resistance Mutation Scores Used by the HIVdb Program Genotype-Clinical Outcome Correlation Studies 2. Surveillance Drug-Resistance Mutation List Section 3. PDF Handout Grant Support 1. National Institute for Allergy and Infectious Diseases (NIAID, NIH): Online HIV Drug Resistance Database (PI: Robert W. Shafer, MD, 1R01AI68581-01A1), 04/01/06 -

3/31/11 2. National Institute for Allergy and Infectious Diseases (NIAID, NIH) supplement to the grant Identification of Multidrug-Resistant HIV-1 Isolates (PI: Robert W. Shafer, MD, AI46148-01): Supplement provided 1999-2005. 3. NIH/NIGMS Program Project on AIDS Structural Biology Program Project: Targeting Ensembles of Drug Resistant Protease Variants (PI: Celia Schiffer, PhD, University of Massachusetts): 2002-2007 4. University-wide AIDS Research Program (CR03-ST-524). Community collaborative award: Optimizing Clinical HIV Genotypic Resistance Interpretation: Principal Investigators: Robert W. Shafer, MD and W. Jeffrey Fessel MD (Kaiser Permanente Medical Care Program): 2004-2005 5. Stanford University Bio-X Interdisciplinary Initiative: HIV Gene Sequence Analysis for Drug Resistance Studies: A Pharmacogenetic Challenge Principal Investigators: Robert W. Shafer, MD and Daphne Koller, Ph.D. (Computer Science): 2000-2002

Synonyms: HIVDB

Resource Type: bibliography, data or information resource, data repository, data set, database, narrative resource, service resource, storage service resource, training material

Keywords: drug resistance, drug-resistance mutations, antiretroviral, antiretroviral drugs, cd4 counts, clinical, genotypes, hiv, hiv-1, hiv-2, ini, integrase inhibitors, integrase mutations, lentivirus pol, mutation, nnrti, non-human primate, nrti, phenotype, pi, plasma hiv-1 rna levels, protease inhibitors, protease mutations, publications, references, rt inhibitors, rt mutations, treatment, data set, FASEB list

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Resource ID: SCR_006631

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Record Creation Time: 20220129T080237+0000

Record Last Update: 20260821T193813+0000

Ratings and Alerts

No rating or validation information has been found for Stanford University HIV Drug Resistance Database.

No alerts have been found for Stanford University HIV Drug Resistance Database.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 487 mentions in open access literature.

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

Shafer RW, et al. (2026) Optimizing HIV-1 Genotypic Resistance Testing for Low- and Middle-Income Countries: High-Impact HIV-1 Mutations Across WHO-Defined Scenarios. Viruses, 18(6).

Tchiakpe E, et al. (2026) HIV-1 Resistance to Dolutegravir in Benin: The Need to Improve and Strengthen Therapeutic Patient Education Strategies to Achieve the Third Objective 95 of UNAIDS 95-95-95 Target. Case reports in infectious diseases, 2026, 9324746.

Ye X, et al. (2026) Comparative effectiveness and safety of integrase strand transfer inhibitor (INSTI)-based versus non-INSTI-based antiretroviral regimens in treatment-naïve people with HIV: A real-world retrospective cohort study. Medicine, 105(21), e48891.

Melnychuk S, et al. (2026) Notable transmitted HIV drug resistance among people who inject drugs in Pakistan. The Journal of antimicrobial chemotherapy, 81(1).

Curto C, et al. (2026) Late diagnosis of paediatric HIV infection in high-income countries: Lessons from the HIV Perinatal Virtual Clinic. HIV medicine, 27(3), 477.

Srinivasan P, et al. (2026) Preclinical evaluation of long-acting cabotegravir and rilpivirine for HIV post-exposure prophylaxis in a macaque model. EBioMedicine, 123, 106067.

El Khalili O, et al. (2026) Development of a Next-Generation Sequencing Protocol for Assessing Lenacapavir Resistance in HIV-1 Capsid. Journal of medical virology, 98(1), e70773.

van Kampen J, et al. (2026) Two cases of possible transmitted HIV drug resistance to all currently available integrase inhibitors, the Netherlands, 2025. Euro surveillance : bulletin Europeen sur les maladies transmissibles = European communicable disease bulletin, 31(8).

Collercandy N, et al. (2026) HIV epidemic and needs beyond fast-track cities: a transmission network analysis to study the dynamics of HIV clusters in a French region near Paris. Microbiology spectrum, 14(6), e0254225.

Farquhar H, et al. (2026) Protein language model embeddings improve HIV drug resistance prediction: a comprehensive benchmark with attention-based interpretability. Bioinformatics (Oxford, England), 42(5).

Fan X, et al. (2026) Pretreatment drug resistance profiles and transmission dynamics of HIV-1 among adults aged ?50 in Hebei Province, China. Frontiers in cellular and infection microbiology, 16, 1823851.

Tadenfok C, et al. (2026) Efficacy of dolutegravir-based therapy in achieving virological suppression in PLHIV in low- and middle-income countries: real-world evidence from a large clinical cohort in Cameroon. BMC infectious diseases, 26(1).

Saladini F, et al. (2026) HIV-1 Sub-subtype A6 Remains Susceptible to Second-Generation Integrase Inhibitors With Limited Emergence of Resistance in Vitro. Open forum infectious diseases, 13(5), ofag230.

Wulan WN, et al. (2026) Protocol for the identification of recent HIV infection in newly diagnosed individuals. STAR protocols, 7(2), 104504.

Duan Y, et al. (2026) Acquired HIV-1 Drug Resistance and Molecular Transmission Networks in Zhongwei, Ningxia, China. Viruses, 18(6).

García-Moncada E, et al. (2026) Amplicon-Based Multiregion Genomic Characterization of HIV-1 in a Tertiary-Care Hospital in Mexico: Antiretroviral Resistance Mutations and Subtype Diversity. International journal of molecular sciences, 27(12).

Luz AL, et al. (2026) HIV-1 integrase resistance in the context of antiretroviral therapy in paediatric patients ? Northeast Brazil. The Brazilian journal of infectious diseases : an official publication of the Brazilian Society of Infectious Diseases, 30(2), 105788.

Mbogo LW, et al. (2026) HIV viral non-suppression and drug resistance among persons who inject drugs on dolutegravir antiretroviral therapy in Kenya. medRxiv : the preprint server for health sciences.

Tchiakpe E, et al. (2026) HIV-1 genetic diversity and reverse transcriptase resistance mutations in Benin before dolutegravir era, West Africa. PloS one, 21(5), e0348800.

Lunkuse S, et al. (2025) Diagnostic Accuracy of Next-Generation Sequencing: Prevalence of HIV-1 Drug Resistance and Associated Factors Among Adults on Integrase Inhibitors with Virologic Failure. Viruses, 17(12).