

Resource Summary Report

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The HIV Positive Selection Mutation Database

RRID:SCR_007957

Type: Tool

Proper Citation

The HIV Positive Selection Mutation Database (RRID:SCR_007957)

Resource Information

URL: <http://www.ncbi.nlm.nih.gov/pmc/articles/PMC1669717/>

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Description: This is a dataset of clinical HIV sequences, including a method of decoding the evolutionary pathways by which HIV evolves drug resistance. "Fitness landscape" describing how HIV proteins can evolve, is shown as a kinetic network. Drug resistance is a major problem in the treatment of AIDS, due to the very high mutation rate of human immunodeficiency virus (HIV) and subsequent rapid development of resistance to new drugs. Identification of mutations associated with drug resistance is critical for both individualized treatment selection and new drug design. We have performed an automated mutation analysis of HIV Type 1 (HIV-1) protease and reverse transcriptase (RT) from approximately 50,000 AIDS patient plasma samples sequenced by Specialty Laboratories Inc. from 1999 to mid-2002. This dataset provides a nearly complete mutagenesis of HIV protease and enables the calculation of statistically significant Ka/Ks values for each individual amino acid mutation in protease and RT. Positive selection (i.e., $Ka/Ks > 1$ indicating increased reproductive fitness) detected 19 of 23 known drug-resistant mutation positions in protease and 20 of 34 such positions in RT. We also discovered 163 new amino acid mutations in HIV protease and RT that are strong candidates for drug resistance or fitness. Our results match available independent data on protease mutations associated with specific drug treatments and mutations with positive reproductive fitness, with high statistical significance (the P values for the observed matches to occur by random chance are $1e-5.2$ and $1e-16.6$, respectively). Our data indicate that positive selection mapping is an analysis that can yield powerful insights from high-throughput sequencing of rapidly mutating pathogens. This database has been made possible by the generous contribution of HIV sequence chromatograms by Specialty Laboratories, Inc.

Synonyms: The HIV Positive Selection Mutation Database

Resource Type: data or information resource, database

Defining Citation: [PMID:17108357](#)

Resource Name: The HIV Positive Selection Mutation Database

Resource ID: SCR_007957

Alternate IDs: nif-0000-03551

Record Creation Time: 20220129T080244+0000

Record Last Update: 20260821T193831+0000

Ratings and Alerts

No rating or validation information has been found for The HIV Positive Selection Mutation Database.

No alerts have been found for The HIV Positive Selection Mutation Database.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We have not found any literature mentions for this resource.