

HIV Protease Structural Database

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The HIV Protease Database (HIVdb) is an archive of experimentally determined 3-D structures of Human Immunodeficiency Virus Type 1 (HIV-1), Human Immunodeficiency Virus Type 2 (HIV-2), and Simian Immunodeficiency Virus (SIV) proteases and their complexes with inhibitors or products of substrate cleavage. It serves a global community of researchers, educators and students. HIVdb is one of the first databases of macromolecular structures outside of Protein Data Bank (PDB). The origin of the HIVdb was the fact that the race to create efficient inhibitors that could be used as agents against HIV infection has already resulted in six such FDA-approved drugs. HIVdb includes both primary structural data and derived information for a single enzyme. For that reason, it serves as an example of a special subset of structure-derived databases that can exist on their own, as well as coexist with the larger structural database and its tools. Information regarding one particular enzyme can show in detail how the structure adopts different ligands, changes interactions, and conformationally adjusts to binding under different conditions. For proteins that serve as drug design targets, it is important to study these interactions fully and in as many complexes as possible. By a careful analysis of the wild type as well as drug resistant mutants of HIV-1 PR, there is a real chance of overcoming the problem of resistance.

HIVdb is a repository for those structures of HIV protease that have never been released or deposited to PDB. Together with the official PDB data, HIVDB provided a unique source of information in a statistical sense. The Database contains 207 structures; 148 taken from PDB, and 59 that are unique entries in HIVdb. Query tools in terms of the creation of ensembles for statistical analysis were designed. We present a new form, location, tools and data form of the HIV Protease database. The new tools utilize a standard PDB user interface, but provide extra capabilities connected exclusively with this one protein and its ligands. We present also a strategy of design of specific subset or sub database of the PDB with an aim to point out statistical dimension of the problem related to a single protein structure. We are currently annotating the ligands in order to include their chemical properties. This approach puts the emphasis for large scale database and scalability.

HIVdb is currently found at two places - the project that was originated and completed under NIGMS support is located as an archive at National Cancer Institute at Frederick at <http://home2.ncifcrf.gov/HIVdb/>. The new HIVdb portal is located at the National Institute of Standards and Technology at <http://srdata.nist.gov/hivdb> and will be updated and developed with increasing number of solved structures.