Structural analysis of GRL-0519 protease inhibitor in complex with a multidrug-resistant HIV-1 protease

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INTRODUCTION

HIV-1 is the most common type of Human Immunodeficiency Virus. It attacks your body's immune system. The virus destroys CD4 cells. These cells help your body fight infections. **HIV-1** can severely damage your immune system and lead to Acquired Immune Deficiency Syndrome (**AIDS**).There is currently no effective cure. Once people get HIV, they have it for life.But with proper medical care, HIV can be controlled. People with HIV who get effective HIV treatment can live long, healthy lives and protect their partners.

Where did HIV come from?
HIV infection in humans came from a type of chimpanzee in central Africa. The chimpanzee version of this virus was probably passed to humans when they came in contact with their infected blood.

Types and Strains of HIV

There are two main types of human immunodeficiency virus - HIV-1 and HIV-2. Both can lead to AIDS. However, they're very different from each other.

HIV-1 is the most common type. When you hear the term "HIV," it's probably HIV-1.
HIV-2 occurs in a much smaller number of people, mostly in West Africa.

HIV constantly makes copies of itself. Some strains multiply faster and can be passed from person to person more easily than others.

Your doctor can treat your HIV better if they know what strain you have. A blood test can tell you. The same test also can tell if certain HIV drugs won't work well for you.

The HIV Life Cycle

EXPERIMENTALS

In order to understand the complete organization of Human Immunodeficiency Virus-1, 3-dimensional structure of its was performed using Computational Biology tool.
Structure of HIV-1 was downloaded from the Protein Data Bank (PDB ID: 4RVI). The analysis include evaluation of hydrogen bonds and secondary structure using PyMOL software.
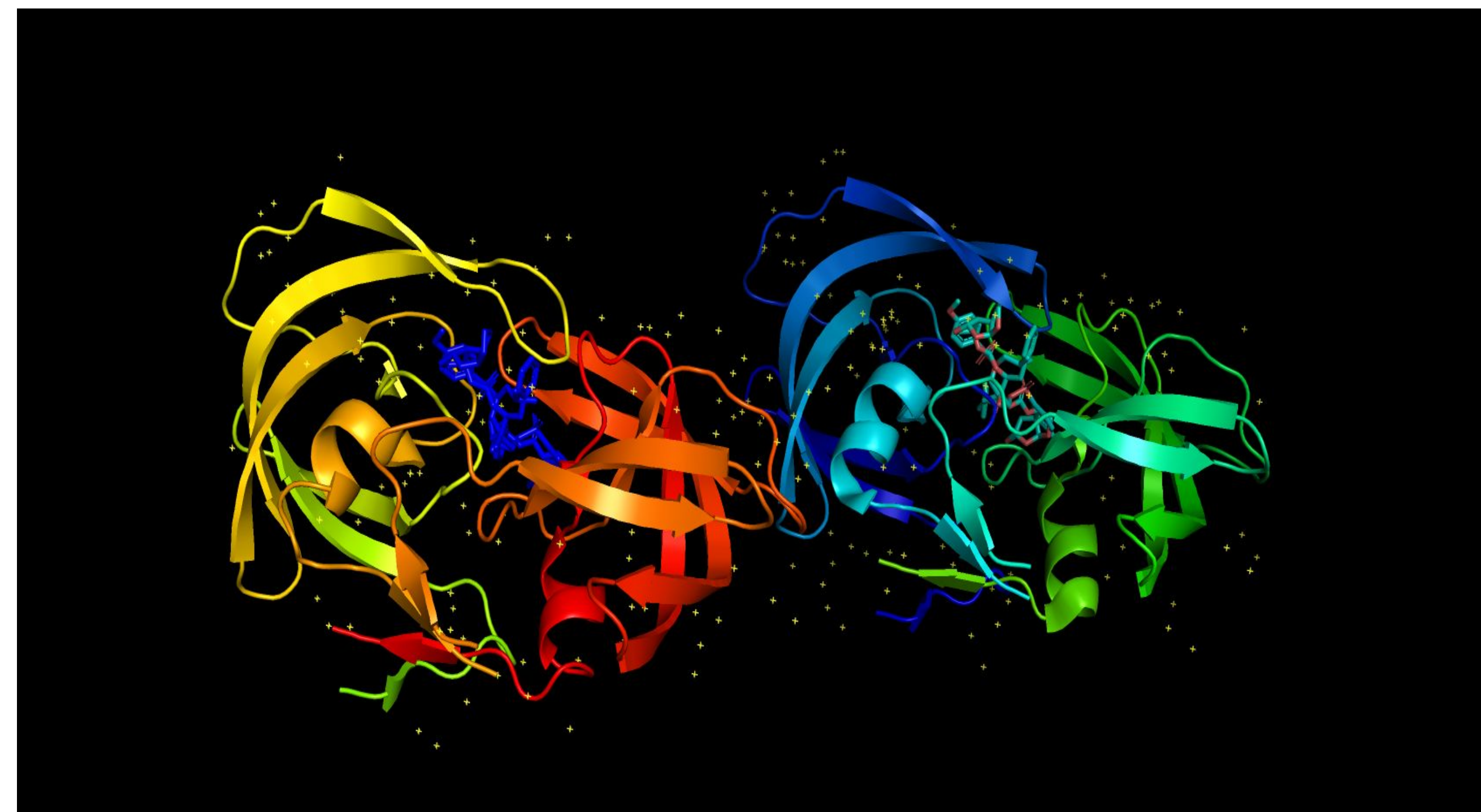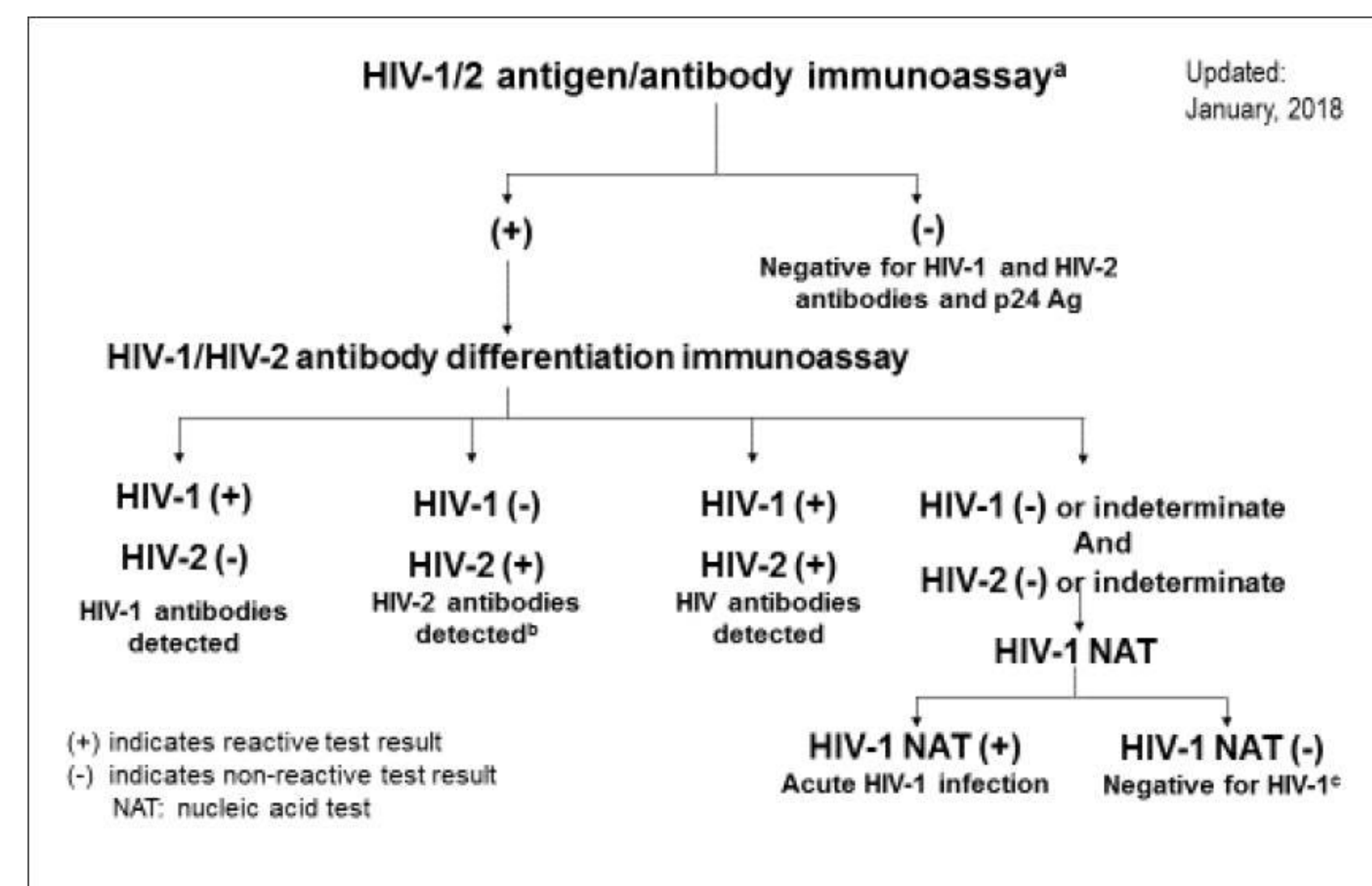

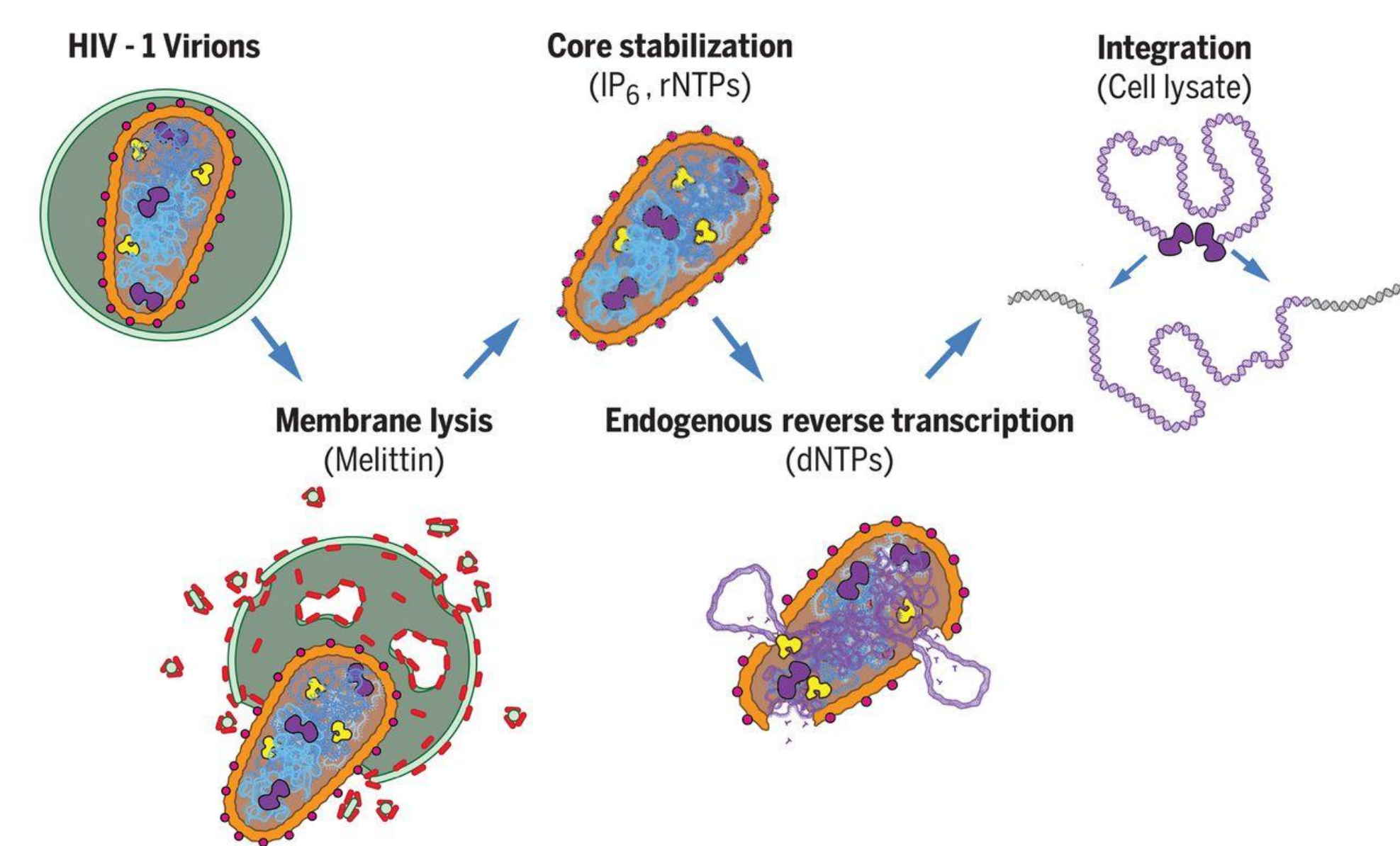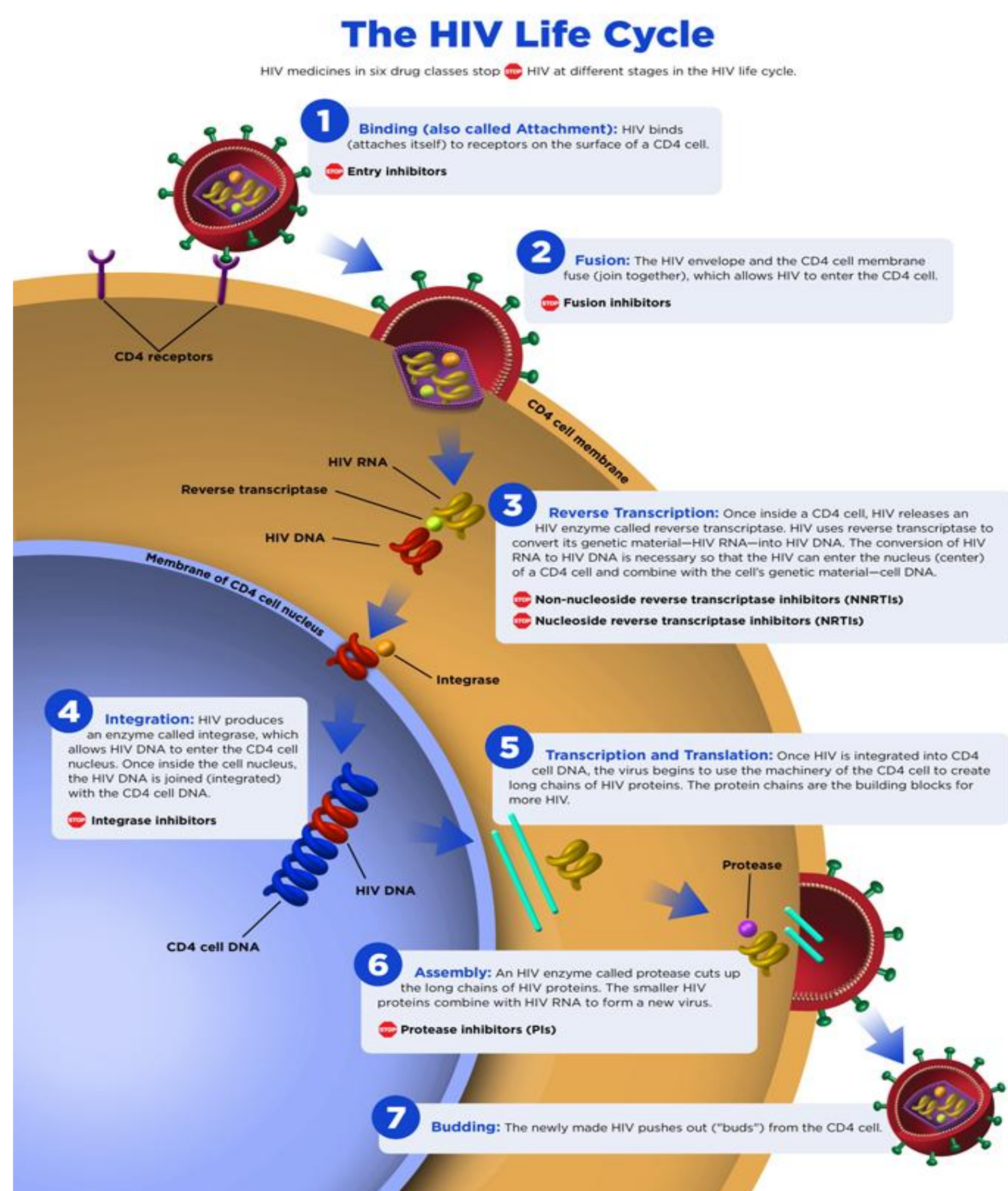**FIGURE-1 HIV infection control and exposure control**

FIGURE-2 Reconstitution and Visualization of HIV-1 capsid dependent replication and integration in vitro

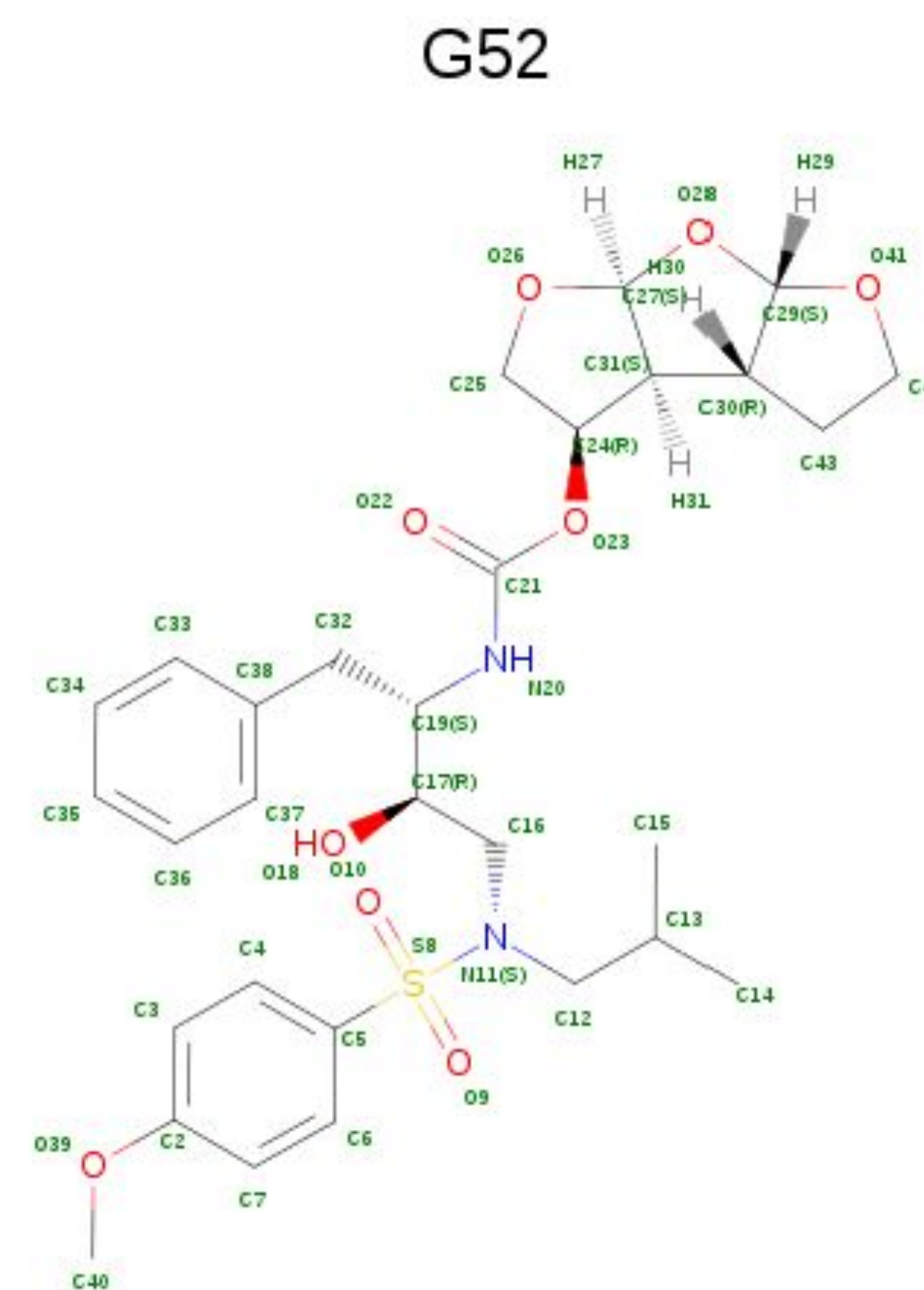**FIGURE-3 The 3 Dimensional structure of GRL0519 multi drug- resistant clinical isolate A02 HIV-1 protease**

FIGURE-4 Bond length and bond angle of the residues in Drug molecule

RESULTS & DISCUSSION

The structure of GRL0519 (PDB ID:4RVI) contains 2 alpha-helices and 2 beta-helices. Followed by the hydrogen bonds which are 26 in number and the average of the bond length of the 22 hydrogen bonds is 2.87Å.

As the hydrogen bond length is less than 3Å, so they are said to be strong.
Each end of the hydrogen bond should be attached to the drug molecule at one end and the other to the water molecule or protein as well which is the primary requirement.

So in this GRL-0519 Protease, there are 7 H-bonds associated with drug and water molecule and 15 H-bonds associated with drug and protein molecule.

FIGURE-5 Summary of the global HIV epidemic

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