Hepatitis C virus enzyme sites revealed

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U.S. researchers say the crystal structure of one of the hepatitis C viral proteins might offer new opportunities for antiviral drug design.

Charles Rice and colleagues at Rockefeller University say the viral genome encodes a single polyprotein, which cleaves into proteins including the NS2-3 protease.

The crystal structure of the protease catalytic domain reveals a novel structure: it is actually a dimer composed of two identical proteins that each contributes amino acids to two equivalent active sites.

The researchers say concentration and dimerization of NS2-3 may be a limiting factor in the viral life cycle because the protease is essential for viral replication. Therefore, details of the structure might help in the search for small-molecule inhibitors directed against the active site.

The disease affects an estimated 170 million people worldwide, often leading to cirrhosis and liver cancer.

The study is detailed in this week's issue of the journal Nature.