Molecular Dynamics Analysis of the HIV-1 Protease Enzyme

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The World Health Organization estimates that there are 34 million people living with HIV. In 2010, 2.7 million people were newly infected. HIV protease is an essential protein that cleaves three previral polyproteins necessary for the maturation of the HIV virus. Because the HIV virus mutates at a rapid pace, the effectiveness of many inhibitors is reduced. After many years the controversy over the flap dynamics of HIV-1 protease has never been fully resolved with long time scale full atomistic simulations. This study sought to understand the dynamics of the HIV-1 protease enzyme through the use of long time scale molecular dynamics using the highly efficient DESMOND molecular dynamics package. Simulations were conducted using two forcefields: amber99SB and Charmm27 with two starting structures "closed" (1HVR.pdb) and "semi-open" (1HHP.pdb). Conformational results sampled the "closed," "semi-open," "open" and "wide-open" states. These results shed further light on the dynamics of this important protein.