Structural Biology of HIV-1 entry

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The Division of Structural Biology at the DHVI brings together a diverse range of expertise, including X-ray crystallography, cryo-electron microscopy (cryo-EM), negative stain EM, small angle X-ray scattering (SAXS), molecular dynamics, biophysics and biochemistry, to understand HIV-1 entry. In this project we will analyze available structural data using computational tools including molecular dynamics simulations to explore and expand the range of structural space beyond the experimentally determined structures, with the goal of discovering new intermediates along the HIV-1 entry pathway. We will follow a hypothesis-driven approach to decipher how the HIV-1 Envelope (Env) undergoes entry. This project will involve development of methods for analyses of structural data, as well as collaborations with biologists to validate the results of the computational analyses.

Special Features

- Opportunity to be involved in structural biology projects involving cryo-EM.