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Using cryo-electron tomography to determine protein structures «*in situ*»

We are studying the structure and assembly of enveloped viruses like HIV and Ebola, as well as protein machineries involved in membrane trafficking within the cell. By combining cryo-electron tomography with computational image processing, we can visualize the structures of proteins assembled on heterogeneous membrane systems *in vitro* with sufficient resolution to determine protein structure *ab initio*. The same methods can be used to determine the structures of assembled protein complexes directly within cells.

Developments in hardware and software are rapidly expanding the capabilities of cryo-electron tomography methods. I will discuss the potential of the technology, and present our most recent data on the structures of HIV-1, Ebola virus and coated membrane vesicles.

Hôte : Groupe des Jeunes Chercheurs de l'IBS