Life Sciences Seminar

Structural studies in complex and dynamic environments using cryoelectron tomography

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Host:

Structural analysis of proteins within cells or viruses is usually hindered by the complexity of these environments. Cryo-electron tomography (cryo-ET) and subtomogram averaging are the tools of choice to study structures in their native state, but the resolutions that can be obtained are usually too low for protein secondary structure determination or de novo model building. We have used cryo-ET and subtomogram averaging to study HIV-1 Gag, a multi-domain protein important in virus assembly and maturation. Detailed structural knowledge of Gag interactions within immature HIV-1 was hitherto missing due to the pleomorphic morphology of the virus. In this seminar, I will show a refined cryo-ET and subtomogram averaging workflow that allowed us to obtain an atomic structure of immature capsid (CA, a domain of Gag) in immature HIV-1 particles and provided first insights into the mode-of-action of a new class of HIV-1 inhibitors.
With the advent of methodological improvements, the structural analysis of proteins in even more complex environments comes within reach, such as events involved in actin nucleation and polymerization that drive cell migration or locomotion of actin-exploiting viruses.

Tuesday, January 17, 2017 08:45am - 09:45am
Mondi Seminar Room 2, Central Building

This invitation is valid as a ticket for the ISTA Shuttle from and to Heiligenstadt Station.
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