4 Joint AIC - SILS Conference



Contribution ID: 158

Type: Commercial Communication

Peeping into the cell with Cryo-Electron Tomography

Tuesday, 13 September 2022 12:45 (30 minutes)

In recent years, single-particle cryo-EM has emerged as a mainstream structural biology technique which can determine the 3D structure of proteins and protein complexes at atomic resolution. However, single particle cryo-EM is limited to highly purified and isolated proteins that are averaged to determine their 3D structure and lacks a connection to the cellular context. Here, cryo-electron-tomography fills the gap by visualizing proteins within their functional cellular environments Cryo-electron tomography (cryo-ET) is evolving into the method of choice for elucidating biological structures in their native environment. Together with subtomogram averaging (STA), it offers a unique way of imaging biological complexes in a near to native state and at subna-nometer resolution. Cryo-electron tomography (cryo-ET) provides unprecedented insights into the inner workings of cells, but clear, reliable results depend on high-quality cryo-lamella preparation. In this presentation we will introduce to you the 3 platform that Thermo Fisher Scientific developed to further Cryo-ET: notably the Aquilos, the Hydra and the Arcits. The Thermo Scientific Arctis Cryo-Plasma Focused Ion Beam (Cryo-PFIB) is specifically designed for automated, high-throughput production of cryo-lamellae from vitrified cells. Its Autoloader system provides a unique, direct connection between cryo-FIB-SEM sample preparation and cryo-transmission electron microscopy (cryo-TEM) within the tomography workflow.

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Presenter: MALETTA, Max (Thermo Fisher Scientific) **Session Classification:** Commercial Presentations