Universität Basel

Research Project

Microfluidic Sample Preparation for High-Resolution Electron Microscopy, Visual Proteomics and Electron Tomography

Third-party funded project

Project title Microfluidic Sample Preparation for High-Resolution Electron Microscopy, Visual Proteomics and Electron Tomography
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Electron microscopy (EM) introduced a fast and lasting change to structural and cellular biology. Direct electron detector cameras and improved image processing algorithms now allow structure determination of large biomolecules by cryogenic EM (cryo-EM) at atomic resolution using a single particle approach. Strategies to study the cellular ultrastructure, such as electron tomography (ET), correlative light and electron microscopy (CLEM), and the lamella milling of eukaryotic cells, opened new windows allowing biologists to study the mechanism of cellular processes at unprecedented precision.
Unfortunately, sample preparation remains a bottleneck, and, surprisingly, EM is rarely used as a bio-analytical tool despite its immense potential to detect proteins on the single-molecule level. Both (i) new single-cell analysis tools and (ii) advanced methods for protein isolation and cryo-EM sample preparation are urgently needed. Here, we aim at (i) the development of a versatile system for the fast protein production, protein isolation, and cryo-EM sample preparation for the structural analysis of sensitive protein complexes, (ii) the development of a new targeted and untargeted single-cell analysis method named ”single-cell visual proteomics,” and (iii) the development of a new strategy for the blotting-free cryopreservation of eukaryotic cells to study cellular structures by ET.

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Follow-up project of 3242170 Fast protein-complex isolation, sample preparation and data processing for high-resolution structural analysis and visual proteomics

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