SEMINAR SERIES 2024

SPECIAL SEMINAR 3 DECEMBER, 4:00PM AEDT

Prof. Dr. Mikhail Kudryashev

Max Delbrück Center for Molecular Medicine in the Helmholtz Association, Berlin, Germany

Dr. Mikhail Kudryashev is a structural biologist and biophysicist based in Berlin, with expertise in visualizing macromolecular complexes within their native cellular environments. His lab combines biochemistry, biophysics cryo-electron microscopy and tomography and data science to understand the structure and function of membrane proteins.

He earned his Ph.D. in Biophysics, focusing on advanced imaging techniques, and has since pioneered the use of cryo-electron tomography (cryo-ET) for elucidating the structure and function of large protein assemblies. His work integrates cutting-edge technologies, including cryo-focused ion beam (FIB) milling, AI-driven modeling, and computational biology tools like AlphaFold, to address fundamental questions in molecular and cellular biology.

After two postdoctoral stints in different labs at Biozentrum, The University of Basel, Switzerland (2009-2015), Mikhail became group leader, Max Planck Institute for Biophysics and the Buchmann Institute for Molecular Life Sciences, Goethe University of Frankfurt, Germany (2015). In 2021 he became group leader at the Max Delbrück Centre for Molecular Medicine in the Helmholtz Society, Berlin, Germany and in 2022 received a co-appointment as a W2 Professor for In Situ Structural Biology at the Institute of Medical Physics and Biophysics of Charité – Universitätsmedizin, Berlin, Germany.

Structure of membrane proteins in native membranes by cryo-EM

Subtomogram averaging from cryo-electron tomograms is a powerful method to determine structures of macromolecules in their native state. Outstanding applications to protein lattices, coats and ribosomes provided unique insights into their functions and even revealed interactions with small molecules *in situ.* For other macromolecules, such as membrane proteins, which are present in tomograms in limited numbers, the throughput of data processing and the processing time are key bottlenecks in obtaining high-resolution reconstructions. This is particularly the case for membrane proteins that are typically present in tomograms in moderate amounts.

Dr. Kudryashev will introduce tools that were developed in his lab for *in situ* structural biology with a focus on a large ion channel, RyR1, which is a part of the excitation-contraction coupling in muscle. TomoBEAR is a workflow for processing tomographic data utilizing common cryo-EM tools and original code that allows transparent near-automated tomographic pre-processing, alignment, reconstruction and particle identification followed by structural analysis.

In the second part of the talk, he will show recent results on understanding the molecular architecture of synaptic vesicles. Neurons grown on EM grids and purified synaptic vesicles were imaged by cryo-electron tomography. Individual proteins important for the function of synaptic vesicles, could be identified using this technique.