

Keynotes



Jonas RIES studied physics in Bremen and Konstanz and completed his PhD in Biophysics at the TU Dresden in the group of Petra Schwille, where he developed new methods to measure dynamics in artificial and cellular membranes. As a Postdoctoral Fellow at the ETH Zurich in the group of Vahid Sandoghdar he established single-molecule localization based super resolution microscopy and developed an efficient and simple labeling scheme for this method. In 2012 he joined the EMBL in Heidelberg as a group leader. The Ries group develops super resolution microscopy technologies to visualize the structure and dynamics of protein machines on the nanoscale in fixed and living cells. One main focus of the group is to use these techniques to investigate the dynamic structural organization of the machinery that drives clathrin-mediated endocytosis.

SUPERRESOLUTION MICROSCOPY FOR STRUCTURAL CELL BIOLOGY

J. RIES

European molecular biology laboratory (EMBL) - heidelberg (Germany)

Superresolution microscopy, such as single-molecule localization microscopy (SMLM), is becoming a key technique for structural cell biology, ideally complementing electron microscopy.

I will discuss projects in my group in which we contributed to this aim to develop technologies to image the structure and dynamics of molecular machines in cells. We a) pushed the 3D resolution in multi-color towards the nanometer scale, b) increased throughput and imaging speed of the notoriously slow SMLM, c) developed reference standards for quality control and for counting of protein copy numbers in complexes and d) developed software to extract specific and quantitative information from SMLM data for biological interpretation.

I will then show, how these new technologies enabled us to gain mechanistic insights into the structural organization of a complex protein machine, namely the machinery involved in clathrin-mediated endocytosis. We developed a high-throughput superresolution microscope to reconstruct the nanoscale structural organization of 23 endocytic proteins from over 100,000 endocytic sites in yeast. This allowed us to visualize where individual proteins are localized within the machinery throughout the endocytic process and resulted in a model of how the force is produced to pull in the membrane and form a vesicle. In mammalian cells, we could address a long-standing question how the clathrin coat is formed and the membranes are deformed during vesicle formation.