Exciting cryoEM projects for Master/Dipl. Students are available in a newly established Lab at MPI IBP, Frankfurt!

We use Electron Microscopes to determine the 3D-structure of macromolecular complexes – with a special focus on membrane proteins.

CryoEM a method to image membrane proteins in solution!

Our main method is electron cryo-microscopy (cryoEM). In cryoEM protein samples can be imaged in solution at low temperatures. To stabilise the sample prior to imaging it is flash cooled to the temperature of liquid nitrogen – a process happening so quickly that ice crystals cannot form, preserving the sample in amorphous (glasslike) buffer.

When I started in cryoEM as a Dipl. Student (~10 years ago at the JGU Mainz) this method was still in its infancy – Today, after several groundbreaking revolutions, cryoEM is rivaling with X-ray crystallography and was selected as “Method of the year 2015” by Nature Methods.

Unlike other methods for 3D-structural charactization, in cryoEM individual particles can be directly seen - which enables us to also analyse heterogeneous samples and to trace conformational changes.

Visualizing the dynamics of a membrane protein!

We utilise the power of cryoEM to obtain precise snapshots of active membrane proteins and to learn about the individual steps during an ATP-hydrolysis or transport cycle (for example). To do this we image mixed populations of the protein and dissect the conformations computationally.

Also, we are characterising complexes, that are formed, between neuronal surface receptors (sortilins) and messenger molecules. The ir specific interaction triggers intracellular signalling, which directly controls neuronal development and synaptic plasticity. These complexes can only be purified in minute amounts, which makes them inaccessible for X-ray crystallography or NMR studies.

If you would like to join a young and ambitious team, to see proteins and determine their 3D-structure please inquire!

![Division of labor in transhydrogenase](image.png)

Artistic representation of the members of the sortilin family ... accurate structures have to be determined.

The conformational spectrum of two ABC transporters. Moeller et al. 2015 STRUCTURE

If interested please contact Arne Möller directly!
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