BIOMATERIALS

Forces in Biomolecular Systems SFB 863

Analyzing Conformational Dynamics of Proteins using single particle cryo EM

David Haselbach

Max-Planck-Institut für biophysikalische Chemie, Göttingen

Abstract:

Several technological breakthroughs made single particle cryo EM recently the major tool to investigate the structure of macromolecular complexes. Still, its full potential has not been fully reached. In contrast to the other main methods of structural biology, the signals from every individual molecule can be easily distinguished in cryo EM images. With this, an ensemble of different structures, visualizing several conformations of a molecule, can be calculated from a single dataset. So far there is no systematic method to visualize the conformational space a molecule samples.

I will present an approach based on principal component analysis to visualize the full range of conformational movement of a molecule. I will demonstrate this on several examples. Most strikingly I will show the first high resolution structure of the complete human 26S proteasome in complex with a chemotherapeutic. Employing the mentioned conformational sorting scheme we could show that drug binding significantly reduces conformational flexibility of the full molecule.

Friday, May 13th, 2015, 13:00

Room PH 127

Contact: Matthias Rief, matthias.rief@mytum.de, phone: 089-289-12471