SFB 960-/BZR – Kolloquium

15. Oktober 2018, 14.00 Uhr
Neubau Biologie DE._2.121 SONDERTERMIN

Prof. Dr. Matthias Wilmanns

EMBL Hamburg
Head of the Hamburg Unit of the
European Molecular Biology Laboratory

Structural investigation of the holo complex of a mycobacterial type VII secretion system

Export (secretion) as well as import of proteins and metabolites to/from the infected host is essential for both viability and virulence of pathogenic bacteria. Mycobacteria such as Mycobacterium tuberculosis (Mtb) have a special type of secretion system categorized as Type 7 (T7SS) that is not found in most other bacteria. Mtb possesses five T7SS's, named ESX-1 to ESX-5. Aiming to unravel the molecular mechanism of T7SS-mediated secretion, we have selected the ESX-5 system, which critically contributes to Mtb pathogenicity. We recently published an initial overall structural model at about 13 Å using negative stain electron microscopy of the ESX-5 core complex comprising 6 x 4 different subunits and an overall molecular weight of 1,8 MDa [1]. The model revealed the overall dimensions of ESX-5, indicating that it would be confined to the inner mycobacterial membrane, an approximate inner pore diameter, hexameric symmetry and a cytoscolic receptor component EccC with remarkable flexibility and a tentacle-like structure. Here, an update will be presented on a considerable improved more high-resolution structural ESX-5 holo complex model by a divide-and-conquer approach. This includes the use of X-ray crystallography on single domains of the complex, cryo-electron microscopy, small angle X-ray scattering, mass spectrometry-based cross-linking, and integrative modeling on both the holo-complex and single domains.

[1] Beckham et al. (2017) Structure of the mycobacterial ESX-5 type VII secretion system membrane complex by single-particle analysis. Nat Microbiol.

Host: Prof. Reinhard Sterner
Institute for Biophysics and physical Biochemistry
reinhard.sterner@ur.de