



Contribution ID: 559

Type: Oral Presentation

Structure and Affinity of Protein Complexes in Infectious Diseases

Monday, 4 July 2016 14:00 (40 minutes)

**Abstract content (Max 300 words)
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Special chars**

Humans are protected against infections by a highly sophisticated and multi-tiered immune system. For microorganisms to successfully initiate an infection in humans they need to interfere with critical elements in signaling and metabolic pathways of the host to locally carve a niche for their survival. For this purpose the pathogens release dedicated molecules that selectively interact with central receptors and regulators of the host. We are investigating how virulence factors bind to host receptors to understand how they block or modify their function at the molecular level. This often provides a unique view to understanding critical host regulation pathways revealing unexpected entry points that may be exploited in drug development or in fundamentally understanding underlying processes. We combine X-ray crystallography with biophysical techniques such as isothermal titration calorimetry (ITC), surface plasmon resonance (SPR) spectroscopy and microscale- thermophoresis, as well as biomolecular techniques such as site-directed mutagenesis to obtain a comprehensive picture of individual molecular pathogen-host interactions.

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Primary author: Prof. SCHUBERT, Wolf-Dieter (University of the Western Cape)

Presenter: Prof. SCHUBERT, Wolf-Dieter (University of the Western Cape)

Session Classification: Winter School: The Biophysics of Cells and Macromolecules

Track Classification: Track F - Applied Physics