FOR5200 SEMINAR Series

GUESTS ARE WELCOME

Digital lecture - For access link please contact the DEEP-DV Office

Boris Bogdanow, PhD

Leibniz-Institute for Molecular Pharmacology (Fan Liu Lab), Berlin

A systems structural perspective on herpesvirus-host protein interactions by cross-linking mass spectrometry

Protein-Protein Interactions (PPIs) facilitate all processes during the viral life cycle. In my work as a post-doctoral researcher at the Leibniz-Institute for Molecular Pharmacology (FMP) in Berlin I seek to understand the structural basis of these interactions at a systematic level. To tackle this, I make use of cross-linking mass spectrometry (XL-MS), a powerful proteomic technique that is able to determine which residues of interacting proteins are in close proximity in their intact cellular environment. I developed XL-MS methods enabling the system-wide charting of protein interaction contact sites in intact extracellular particles and from intact infected cells infected by using Herpesviruses (HCMV, HSV-1) as model systems. We combine these datasets with quantitative proteomics, structural modeling and molecular genetics to yield mechanistic insight into how Herpesviruses target host proteins during their life cycle. For example, we uncovered how the cytomegalovirus tegument protein pp150 recruits PP1 phosphatase and 14-3-3 proteins into extracellular particles and how their interactions affect early and late steps during HCMV biogenesis.

May 2nd
2023
3:00 PM

DEEP-DV

Disrupt - Evade - Exploit
Gene expression and host response programming in DNA virus infection

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