

Infectious Diseases Labs

A*STAR IDL



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Monday 17th February 2025 9:00 AM to 10:00 AM (SGT)

Venue: Codon A & B, Matrix Level 5

Signaling Networks at the Virus-Host Interface

The successful establishment of viral infection may rely on the virus's ability to sense and adapt to the host signaling landscape. This process may occur through virus-host proteinprotein interactions, many of which are regulated by host-mediated post-translational modifications on viral proteins. For instance, phosphorylation of viral proteins by host kinases may enable them to function as biosensors, allowing the virus to fine-tune its life cycle in coordination with the host response. Here, we annotated human kinase motifs in viral proteins from over 1000 viruses using the Kinase Library algorithm, a computational tool that scores a kinase's preference for each phosphoacceptor (S/T/Y) based on its amino acid context. We integrated these results with over 20,000 viral protein structures generated by AlphaFold and identified putative viral phosphorylation sites and upstream kinase signaling cascades that represent novel virus-host interactions. As a mechanistic case study, we present recent data on SARS-CoV-2 Orf9b and how it acts as a biosensor of innate immune pathway activation. When phosphorylated, we believe it switches its function, possessing multifunctionality during the viral life cycle. By probing virus-host interactions, we seek to pinpoint critical mechanisms by which viruses sense and respond to host signaling, uncovering novel targets for antivirals.

Dr Mehdi Bouhaddou is an Assistant Professor in the Department of Microbiology, Immunology, and Molecular Genetics (MIMG) and co-affiliated with the Institute for Quantitative and Computational Biosciences (QCBio). Dr Bouhaddou directs a Quantitative Systems Biology lab that studies how protein-protein interactions and post-translational modifications impact signaling networks, from systems-level features to basic mechanisms.

He performed his postdoctoral training with Dr Nevan J. Krogan at UC San Francisco (UCSF) in virology, mass spectrometry proteomics, bioinformatics, and network modeling receiving F32 (NCI) and K99 (NIAID) awards. He developed virus-host interaction networks for SARS-CoV-2 and other coronaviruses, and systematically compared the molecular response to emerging SARS-CoV-2 variants to pinpoint variant-specific mechanisms of pathogenesis. Prior to his postdoc, Dr Bouhaddou developed ordinary differential equation (ODE) mathematical models at Roche and during his PhD in Biomedical Sciences with Dr Marc Birtwistle at the Icahn School of Medicine at Mount Sinai. He received his Bachelor's degree from UC Berkeley in Cognitive Neuroscience.

Hosted by: Prof Marco Vignuzzi

