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BioSim Talk #8

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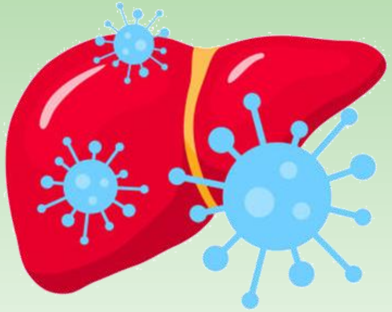
14th November 2025 (Friday)

4.00 – 5.30 pm

Institute for Protein Research
University of Osaka (Suita Campus)
4th floor seminar room



Predicting Viral-Host Protein Interactions: Lessons from AlphaFold Successes and Failures

Despite AlphaFold's breakthrough capacity to accurately predict protein 3D structures from sequence alone, viral protein structure determination remains challenging. Many viral proteins perform multiple roles linked to distinct conformations that vary throughout the viral replication cycle, while others contain highly disordered regions that increase flexibility and resist structural characterization. Hepatitis E virus (HEV) represents a significant global public health challenge, causing approximately 20 million infections annually and contributing to up to 70,000 deaths. The HEV genome encodes three Open Reading Frames (ORFs): a replication polyprotein, a structural capsid protein (ORF2), and a largely disordered protein (ORF3). Together, these proteins orchestrate viral genome replication, provide structural features, evade host defense mechanisms, and mediate cell entry. We extensively applied AlphaFold and related methods, including Boltz, to characterize interactions between the HEV capsid protein (ORF2), ORF3, and cellular receptors. I will discuss the methodological insights gained from this work: how to interpret AlphaFold metrics, strategies to improve structural modeling of virus-host complexes, and how to identify biologically meaningful predictions, and provide practical guidance for integrating structure prediction tools with molecular dynamics.

Link for online participation via Zoom:
Meeting ID: 852 5482 1603
Passcode: 106993

Please inform us if you will be participating online or joining our Slack channel
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