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BioSim Talk #12

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WPI PRIMe, Osaka University

January 24th 2025 (Fri)
1.30 – 3.00 pm

Institute for Protein Research
Osaka U. (Suita Campus)
2nd floor conference room (Large)

Massive Replica Exchange Simulations on Fugaku to Sample Protein Kinase-Inhibitor Binding Landscapes

Molecular dynamics (MD) simulations are widely used to understand the molecular mechanisms of disease and aid in drug design. While traditional drug design focused on optimizing binding affinity, there has been a shift toward a kinetic-based approach after recognizing that kinetic parameters such as binding and unbinding rates (k_{on}, k_{off}) and residence time often correlate more strongly with drug efficacy. This change highlights the importance of studying the binding pathway in detail, including a detailed description of interactions and metastable states. In this talk, I will discuss our work using MD simulations to sample the binding energy landscape of protein kinases and their inhibitors. By employing 2D replica exchange (RE) simulations on supercomputer Fugaku, we obtained a wide sampling of the binding energy landscape, providing insights into inhibitor binding. I will present the RE enhanced sampling method and share insights into the effect of inhibitor size and flexibility on binding and their potential implications for drug design.

Link for online participation via Zoom:
Meeting ID: 884 9329 0540
Passcode: 629225
Please inform us if you will be participating online or joining our slack
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