NUS National University of Singapore | Department of Biological Sciences, Faculty of Science

ON-SITE BIOLOGY COLLOQUIUM

Friday, 21 Aug 2026 | 4 pm | S3 05-02 Conference Room 1

Hosted by Dr Lin Qingsong

Map to Block S3

Structural proteomics to uncover protein structures and interactions

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Proteins are complex molecules that adopt a large variety of structural conformations and interact with each other in protein-protein interactomes. Cross-linking mass spectrometry (XL-MS) utilizes cross-linkers as "molecular rulers" to reveal distance proximities of interacting proteins at the residue-to-residue level. XL-MS has emerged to be a powerful technique that reveals both protein structural features and protein interactomes. Our recent work has expanded the coverage and applications of XL-MS. First, commonly used cross-linkers mainly target lysines which comprise 7% of protein amino acids. We recently developed bi-functional photo-activatable (BFPA) cross-linkers, which can theoretically react any to any amino acid. Second, we used cross-linkers with different spacer arms lengths to reveal a key interacting residue of Dengue NS3 with co-factor NS2B by XL-MS. Cross-link data guided molecular dynamics simulations revealed a possible compact conformation of the Dengue NS3 with NS2B cofactor complex. Third, we combined cross-linking with quantitative proteomics and XL-MS to reveal the extended protein interactome with BET inhibitor, JQ-1, across two different cancer cell lines. Our work has extended the coverage of XL-MS at the protein residue level, revealed new viral protein structural interactions and identified the drug-binding associated protein interactome.

About the Speaker

*Ser Zheng is a Senior Scientist and Platform Lead (Structural Proteomics and Interactome) at Institute of Molecular and Cell Biology (IMCB), A*STAR Singapore. He obtained his PhD from Weill Cornell Medicine, USA. Zheng's research expertise in structural proteomics and interactomics developed new cross-linker tools and methods and revealed protein structural features and transient interactomes. Zheng has authored numerous publications, filed patents, presented his research at international conferences and won early career grants. Zheng's research aims to develop cross-linking mass spectrometry and interactome technologies to uncover aberrant protein folding of intrinsically disordered proteins and RNA-protein interactions in human disease and therapeutics.*