

Construction of Hierarchical Supramolecular Assembly in Phase-Separated Droplets**Hiroka Sugai**

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**Integrative Approaches to Understanding Antibody Structure and Function****Saeko Yanaka**

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<https://riken-jp.zoom.us/meeting/register/tJYtc--urz4tH9QxKV0yMNPOcOrHmIS7UnWx>**Construction of Hierarchical Supramolecular Assembly in Phase-Separated Droplets**

Biomacromolecular assembly serves as a vital platform for unraveling the complexities of biological phenomena, enhancing our molecular-level understanding of life, while simultaneously contributing to the precise design of functional materials that drive advancements in next-generation nano- and mesoscale technologies. In particular, liquid-liquid phase separation (LLPS)-mediated supramolecular assembly has recently garnered significant attention due to the heightened focus on LLPS-driven biological phenomena. A growing body of research has revealed that biomacromolecules, including nucleic acids and proteins, ubiquitously undergo LLPS in aqueous solutions under specific conditions, giving rise to liquid-like condensates. Our group has focused on supramolecular assemblies composed of chemically defined short oligonucleotides and peptides, particularly their higher-order structures, and has developed unique LLPS-mediated supramolecular assemblies with hierarchical architectures. In this presentation, I will introduce the construction and structural analysis of our hierarchical supramolecular assemblies involving oligonucleotides and peptides in detail.

Integrative Approaches to Understanding Antibody Structure and Function

Antibodies are crucial immune system glycoproteins, recognizing and neutralizing foreign substances via interactions with complement proteins and Fc receptors. Their structure and function arise from the coordinated actions of multiple domains, linked by flexible segments allowing dynamic rearrangement in response to stimuli. Glycosylation significantly impacts effector functions, exhibiting diverse glycoforms.

To elucidate antibody dynamics and interactions, we integrated experimental (NMR, SAXS, high-speed AFM) and theoretical (MD simulation) methods. Experimentally validated MD simulations revealed a dynamic allosteric network within the antibody. This network is sensitive to subtle glycan structural changes, inducing structural alterations at distant sites and modulating effector functions. This mechanistic insight has significant implications for therapeutic antibody design, highlighting the importance of considering both polypeptide and glycan contributions to antibody behavior.