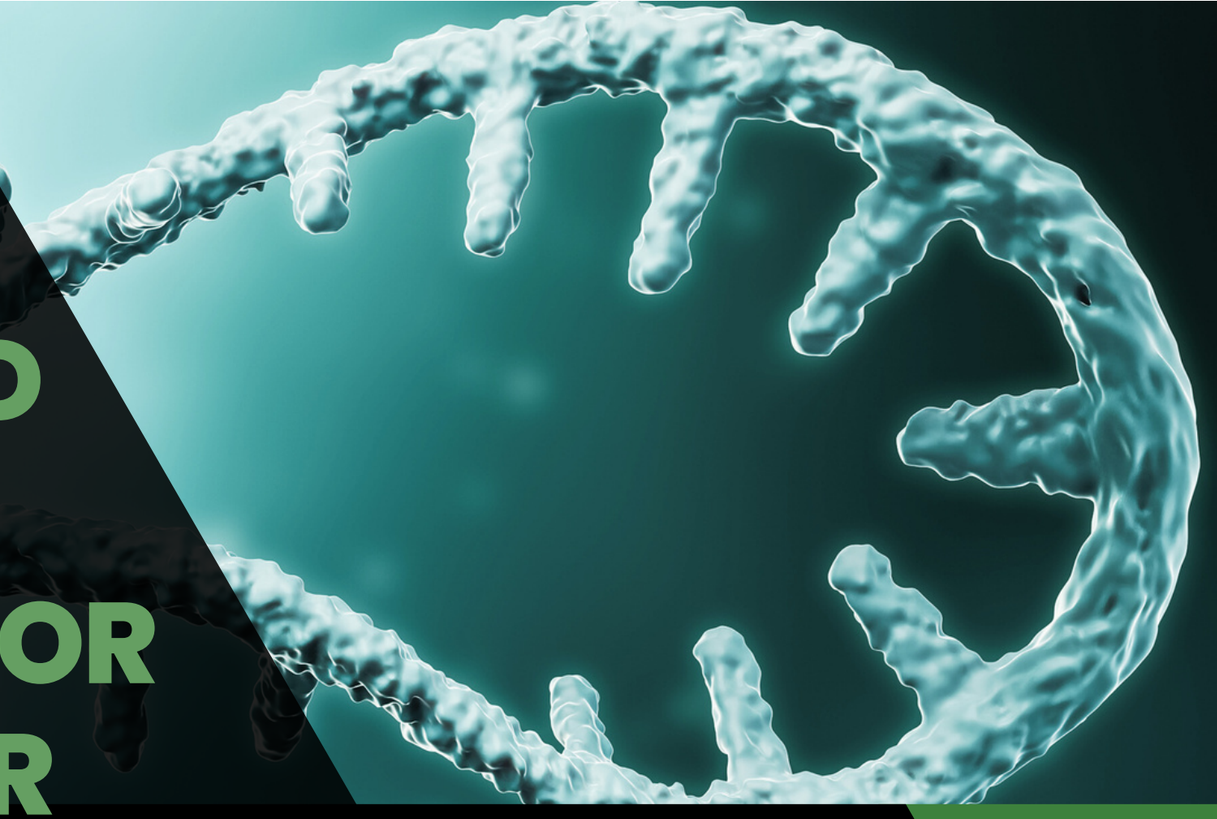
SINGAPORE RNA SEMINAR SERIES

GENETICALLY ENCODED AND IMMUNO-PROXIMITY LABELING FOR MAPPING SUBCELLULAR BIOMOLECULES



Thursday 23 January 2025
3.00pm (SGT, GMT+8)

Via Zoom

About the speaker

Peng Zou is currently a vice dean and an associate professor with tenure at the College of Chemistry and Molecular Engineering of Peking University. He is jointly appointed as a principal investigator at the PKU-IDG/McGovern Institute for Brain Research and the PKU-Tsinghua Center for Life Sciences. Peng received his B.S. degree in Chemistry with a double major in Physics from PKU in 2007, and his PhD in Biological Chemistry from MIT in 2012. Following his postdoc training at Harvard University, Peng joined the faculty at PKU in 2015 and was promoted to a tenured associate professor in 2021. His lab focuses on inventing chemical tools for the spatiotemporally resolved mapping of biomolecules and biophysical signaling that underlie neuronal functions. This mainly follows three lines of efforts: free radical-based chemical probes for profiling proteins and RNAs in neurons, optical reporters for neural activities, and directed evolution platforms that drive technological advancements in the above two fronts. Peng is the recipient of the Life Chemistry Young Investigator Award from Chinese Chemistry Society in 2023, C&EN's Talented 12 Award from American Chemical Society in 2019, the OKeanos-CAPA Young Investigator Award at the Chemical and Biology Interface in 2020. Since 2024, he is an associate editor of ACS Bioconjugate Chemistry.

Dr. Peng Zou
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About the seminar

Over the past decade, proximity labeling methods have emerged as powerful tools for mapping biomolecules in their native context. These methods often capitalize on the in situ generation of highly reactive intermediates for covalently tagging biomolecules located within nanometers to sub-micrometers from the source of labeling. In this talk, I will present a toolbox of genetically encoded photocatalytic proximity labeling methods (CAP-seq and CAP-MS) and immuno-proximity labeling method (iPL). CAP-seq and CAP-MS profile subcellular RNAs and proteins in both membrane-bound and membrane-less organelles, allowing temporally resolved mapping of stress granule components during the assembly stage. As a complement to genetically encoded proximity labeling, iPL allows tagging biomolecules that are proximal to endogenous baits, without the need for genetically engineering the sample. We applied iPL to profile the AIS proteome and its dynamic changes during neuronal maturation. Together, these methods portray a high-resolution map of the subcellular transcriptome and proteome, which provide a rich source for understanding cellular physiology.

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