

25th nanobiofluids seminar

2026 Jun. 1st, 14:00-15:00

Conference Room (Room 134), 1st Floor, Bldg. No.1

<https://www.infront.kyoto-u.ac.jp/en/access/>

[Zoom link](#)

Systems Biology of Insulin Action and Metabolism



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Abstract

1. The "temporal information code" of insulin action: a bottom-up approach

One of the essential elements of signaling networks is to encode information from a wide variety of inputs into a limited set of molecules. We have proposed a "temporal information code" that regulates a variety of physiological functions by encoding input information in temporal patterns of molecular activity, and based on this concept, we are analyzing biological homeostasis by insulin signaling. Taking blood insulin as an example, we will explain how the temporal information of blood insulin is selectively decoded by downstream networks.

2. Transomics of insulin action: a top-down approach

In order to obtain a complete picture of insulin action, we performed transomics measurements integrating metabolomics and transcriptomics, and found that metabolism is regulated by allosteric regulation in the liver of normal mice and by compensatory gene expression in the liver of obese mice. (Top-down approach).

I will talk about approach the principle of homeostasis of living organisms by temporal patterns, using the analysis of systems biology of insulin action using two different approaches.

Biography

Shinya Kuroda is the professor at Department of Biological Sciences, Graduate School of Science, University of Tokyo since 2006. He studied the mechanism of cellular signaling during his PhD course in Osaka University and a post-doc period in Nara Institute of Science and Technology. He learned computation lab at ATR. He became an associate professor at Department of Computer Science, University of Tokyo in 2002, and started his lab of systems biology of cellular signaling of insulin action. He became a full professor at the current position in 2006, and started systems biology of insulin signaling and metabolism. He started the trans-omic analysis of insulin action and metabolism by integrating multi-omic data since 2014.