

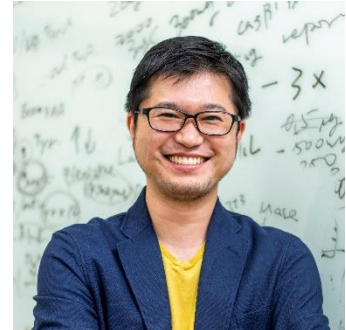
Advanced Tricks in Ribosome Profiling

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Abstract

Ribosome profiling, which is based on deep sequencing of ribosome footprints, has served as a powerful tool for elucidating the regulatory mechanism of protein synthesis.

Translation regulation plays a pivotal role in the diversification of gene expression and the response to intra- and extracellular environmental cues. Ribosome profiling (or Ribo-Seq) serves as a sensitive, quantitative, comprehensive, and data-rich technique to survey ribosome traversal across the cellular transcriptome. However, the current method has substantial issues, such as a large quantity of input material, sample scalability, and data calibration. To overcome these issues, we recently developed several new derivatives of ribosome profiling. I will present the unpublished advances of the techniques.

Biography

Shintaro Iwasaki is a Chief Scientist (PI) in the Cluster for Pioneering Research, RIKEN, Japan. He is also a Visiting Associate Professor at The University of Tokyo, Japan. He obtained PhD from The University of Tokyo, working on the complex assembly and the function of small RNAs in the laboratory of Dr. Yukihide Tomari. As a post-doctoral fellow with Dr. Nicholas Ingolia at the University of California, Berkeley, he studied the unique mechanism of rocaglates, and translation inhibitors. As an independent investigator, Dr. Iwasaki is dedicated to uncovering the fundamental processes that govern protein synthesis, employing cutting-edge techniques of next-generation deep sequencing and traditional biochemistry. Since its launch in 2016, Iwasaki laboratory has served as a regional hub for RNA research, sharing his expertise in ribosome profiling. He was awarded the Young Investigator Award, The Japanese Biochemical Society, 2023; Samuro Kakiuchi Memorial Research Award for Young Scientists, The Japanese Biochemical Society/Gushinkai, 2021; and The Young Scientists' Prize, The Minister of Education, Culture, Sports, Science and Technology, Japan, 2019.