About the author

Following a BS and an MS in Chemical Engineering at Nagoya University, Japan, and a PhD in Chemical Engineering at Northwestern University, USA, Kazuyuki Shimizu started his career in 1981 as a research associate at Nagoya University, Japan, and was promoted to associate professor in 1990. He then moved to the Kyushu Institute of Technology, Department of Bioscience and Bioinformatics as a professor in 1991. In 2000, he became an adjunct professor at the Institute of Advanced Biosciences (IAB), Keio University, Japan. Kazuyuki was appointed an associate member of the Science Council of Japan from 2006 to 2011.

He has been working on such topics as:

1. Metabolic flux analysis based on the ^{13}C labeling technique (^{13}C–MFA), where metabolic flux distribution is located on top of omics data, and the rigorous metabolic fluxes obtained by this method are used to analyze metabolic regulation of cells;

2. Integration of the different levels of hierarchical omics information, such as transcriptomics, proteomics, metabolomics, and fluxomics data, where it is critical to understand cell metabolism as a whole cell system; and

3. Systems biology, modeling of the main metabolic pathways of a cell using enzymatic reactions together with metabolic regulation based on global regulator (transcription factor), where metabolic pathway genes relationships may lead to the development of virtual microbes.

He recognizes the importance of uncovering the metabolic regulation mechanism of a cell system, based on both experimental (wet) and computational (dry) approaches. He has also organized a UK–Japan collaboration project on microbial systems biology toward developing virtual microbes.

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