

## Metabolic systems analysis with multi-omics data

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Advances in omics technologies have enabled us to measure a large number and variety of molecular components of cells. This should enormously assist in our understanding of complex biological phenomena and the improvement of more quantitative omics methods will accelerate this understanding. However, effective ways to take advantage of such data have not yet been developed. A need exists for an analytic methodology to extract biological characteristics, as well as for more sophisticated quantification methods to advance our understanding of how organisms achieve highly regulated systems. In our current research, we have developed a new technology termed *in vitro* proteome-assisted multiple reactions monitoring for protein absolute quantification (iMPAQT) to measure the absolute quantities of all human proteins. With the use of iMPAQT, we have measured the absolute quantities of almost all metabolic enzymes in human cells and uncovered the weights of each node in human metabolic networks. In addition, we have developed a new computational method based on biochemical systems theory to integrate the absolute quantities of metabolic enzymes, as well as those of

metabolites measured by metabolomics, experimentally available fluxes and metabolic network structure. It is now possible to estimate each flux, calculate sensitivities of fluxes and metabolite concentrations with respect to the concentration of each enzyme, and simulate metabolite concentrations under some perturbations. In order to extend the combined approach of large scale quantification and computational analysis, in our institute we have set up the Research Center for Transomics Medicine, where proteome, transcriptome, metabolome and other omes can be measured. Furthermore, we are now attempting to integrate multi-omics data and analyze insulin action on metabolism in the liver as a pilot study. We expect that a further development of this approach will lead to comprehensive understanding of how the metabolic network system or various biological systems are regulated and will establish a new leading edge of modern biology.

### Biography

Fumiko Matsuzaki is a Molecular and Systems Biologist with a PhD in Medical Science from Kyushu University, Japan. Her work has involved proteomics, metabolomics and molecular and biochemical approaches to the investigation of cancer metabolism, xenobiotic metabolism and membrane trafficking. Recent developments in omics technologies led her to start computational work with bioinformatics and mathematical approaches to take advantage of omics data. She aims to deliver practical methods to decipher complicated biological systems.

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