

Internship proposal (project period: Feb. to May, 2015)

Systems biology of signal transduction networks based on shotgun proteomics technology

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Research project

Signal transduction systems coordinate complex cellular information to regulate biological events such as cell proliferation and differentiation. Previous in-depth cell signaling analyses under a variety of experimental conditions revealed many of the key molecules and related events leading to each biological effect. Although the widespread association of signaling molecules contributes essentially to cellular regulation, their network-wide behavior is mostly yet to be analyzed. Current shotgun proteomics technology based on high-resolution nanoflow liquid chromatography-tandem mass spectrometry system enables us to detect thousands of signaling molecules in a comprehensive and unbiased manner. We mainly focus on proteomics-based computational analyses of disease-related signaling networks to understand and regulate aberrant cellular responses from a systems perspective.

Recent publications

1. Kozuka-Hata H, Nasu-Nishimura Y, Koyama-Nasu R, Ao-Kondo H, Tsumoto K, Akiyama T, and Oyama M. Phosphoproteome of human glioblastoma initiating cells reveals novel signaling regulators encoded by the transcriptome. *PLoS One*, 7: e43398 (2012).
2. Kozuka-Hata H, Tasaki S, and Oyama M. Phosphoproteomics-based systems analysis of signal transduction networks. *Front. Physiol.*, 2: 113 (2011).
3. Oyama M, Nagashima T, Suzuki T, Kozuka-Hata H, Yumoto N, Shiraishi Y, Ikeda K, Kuroki Y, Gotoh N, Ishida T, Inoue S, Kitano H, and Okada-Hatakeyama M. Integrated quantitative analysis of the phosphoproteome and transcriptome in tamoxifen-resistant breast cancer. *J. Biol. Chem.*, 286: 818-829 (2011).
4. Tasaki S, Nagasaki M, Kozuka-Hata H, Semba K, Gotoh N, Hattori S, Inoue J, Yamamoto T, Miyano S, Sugano S, and Oyama M. Phosphoproteomics-based modeling defines the regulatory mechanism underlying aberrant EGFR signaling. *PLoS One*, 5: e13926 (2010).
5. Oyama M, Kozuka-Hata H, Tasaki S, Semba K, Hattori S, Sugano S, Inoue J, and Yamamoto T. Temporal perturbation of tyrosine-phosphoproteome dynamics reveals the system-wide regulatory networks. *Mol. Cell. Proteomics*, 8: 226-231 (2009).