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| Seminar by |
| **Prof. Masayuki Oda,**  **Kyoto Prefectural University**  京都府立大学　織田昌幸　教授 |
| **Monday, March 9, 2015** |

**Time : 16:00 - 17:30**

**Location : Lab 1, Level C, C016**

**Title : Thermodynamic and kinetic analyses for understanding conformational flexibility and function of protein**

Protein fluctuation is closely correlated with its function, and the protein structure in solution should be visualized with consideration of the fluctuation in addition to the most stable or averaged structure determined using conventional methods such as X-ray and NMR. Thermodynamic and kinetic analyses for proteins in solution could provide information on the protein fluctuation. Differential scanning calorimetry (DSC) and isothermal titration calorimetry (ITC) could mainly determine the thermodynamics of protein folding and interaction, respectively. The thermodynamic parameter, entropy, is in correlation with the conformational flexibility of protein. The surface plasmon resonance (SPR) biosensor, Biacore, could determine the binding kinetics such as association and dissociation rates. In this seminar, I first introduce the recently developed methods of calorimetry and SPR biosensor, and next show the application of these methods, together with X-ray and NMR, for the catalytic antibody and the DNA-binding protein [1, 2].

1, Oda *et al*., Thermodynamics and structural basis for transition-state stabilization in antibody-catalyzed hydrolysis. J. Mol. Biol. 369, 198-209, 2007.

2, Inaba *et al*., Thermodynamic effects of multiple protein conformations on stability and DNA binding. Arch. Biochem. Biophys. 537, 225-232, 2013.