
Colloquium

Relaxation Optimized SAIL Method for Studying Structures and Dynamics of Large Proteins and Protein Complexes

Masatsune Kainosho

Tokyo Metropolitan University & Nagoya University, Japan

The Stereo-Array Isotope Labeling (SAIL) method has been successfully applied for structure determinations of proteins as large as 50 kDa, which are unamenable to conventional NMR methods.⁽¹⁾ In view of the recent trend of integrative structural biology research, the major role of NMR spectroscopy has shifted from structure determinations to elucidations of the dynamics and interactions of biologically interesting large protein complexes. The relaxation optimized SAIL approach will facilitate various investigations of protein dynamics with wider amplitudes and time-scale ranges for large protein complexes. Our recent results along this line will be presented.^(2,3)

References:

- 1) Kainosho M, Torizawa T, Iwashita Y, Terauchi T, Ono A M, Güntert P (2006), Nature, 440: 52-57.
- 2) Miyanoiri Y, Takeda M, Okuma K, Ono, AM, Terauchi T, Kainosho M (2013), J Biomol NMR, 57, 237-49.
- 3) Yang C-J, Takeda M, Jee JG, Kainosho M, Biochemistry, Biochemistry, in press, DOI: 10.1021/acs.biochem.5b00820

Wednesday, Dec 2nd 2015

4:00 PM (Tea/Coffee at 3:45 PM)

Seminar Hall, TCIS