# Dynamics of folded and partial unfolded proteins observed by solution inelastic neutron scattering

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Protein has biological function under the physiological condition, which is usually in a solution. So far most inelastic neutron scattering experiments with biological samples are limited in the hydrated powder condition due to the strong solvent scattering. But recently solution inelastic neutron scattering experiments have emerged in the literature, which is even now challenging work [1].

We performed solution scattering experiment with AGNES using Staphylococcal nuclease (SNase) of native and truncated mutant. The energy resolution of ANGNES is 120 $\mu$eV. Truncated mutant is SNase without C-terminal 13 residues, which is in the partial unfolded state under the physiological condition.

Figures are the scattering profiles of two samples at 280 K and 300 K. Under the temperatures the native SNase is in the folded state. Elastic incoherent structure factor (EISF) of the folded state hardly decreases upon heating from 280 K to 300 K. This indicates that the folded structure is thermally stable in these temperatures. On the other hand, EISF of the partial unfolded state notably decreases upon the heating. The difference of EISF between two temperatures suggests that conformational entropy of the unfolded protein at 300 K is significantly larger than that at 280 K.

The quantitative analysis of solution inelastic neutron scattering will make it possible to characterize the dynamical properties of protein structure and give important insight into the protein folding problem.

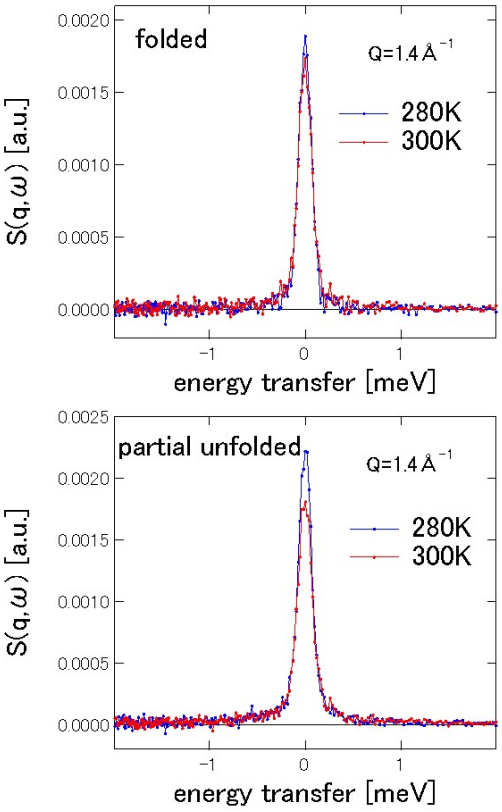


Fig. 1. Solution inelastic neutron scattering spectra of SNase in folded and partial-unfolded states.

[1] J. Fitter et al. : "Chem.Phys. ", 292, 405 (2003).