**Features of Protein Folding Dynamics Have Been Demonstrated Theoretically**

A protein is an in-line chain of many amino acids, and has unique functions within the organism. It is not until the chain of amino acids has been folded to form an intrinsic structure that the protein fulfills its functions. However, how protein folds into the intrinsic structure with a given amino residues sequence? We are still far from the complete understanding on the principle of protein folding. What we know is that the molecular compaction of a "polymer" represented by polyethylene comprises a "coil-globule transition."

We have used a powerful x-ray synchrotron radiation source to observe the protein folding dynamics of heme oxygenase, which is a protein with a large number of amino acids, and has discovered the fact that proteins also exhibit the same coil-globule transition based on the size dependence on the number of amino acids.

The above findings are expected to help clarify the principles of protein motion, and the prediction of protein structures on the basis of amino-acid sequences.

The research results are to be published in the March 31 issue of "Journal of Molecular Biology."

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