

# **Watching the dancing of molecules by using X-ray solution scattering**

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Proteins, the most diverse biomolecule, undergoes a folding pathway to find a three-dimensional structure that expresses its biological function in a living cell. The failure of protein folding, so-called misfolding, occasionally occurs and this causes the aggregation of proteins, which is directly linked to protein-misfolding diseases such as Alzheimer's disease or Parkinson's disease. In this regard, one of crucial questions in the fields of biochemistry and biophysics is how the unfolded protein can find its native folded structure. Since the dancing movements of unfolded proteins are the essential part of the folding mechanism, it is of importance to directly capture the motion of protein in the folding phase. To study the protein folding in cytochrome c, real-time X-ray scattering has been used and discovered the heterogeneous protein folding that is based on the funnel-like free energy landscape. This study may provide structural insights into the fundamental principle of protein folding and real-time (time-resolved) X-ray scattering can be a robust platform to unravel the protein structure and its motion in the reaction medium.