

**Src SH3 domain とその変異体 A45G におけるクライオストップ
フロー法によるフォールディング初期過程解析**
**Early events of folding of src SH3 domain and its mutant,
A45G, by cryo-stopped-flow-method**

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It is known that the native structure of various proteins is determined by primary structure (= only amino acid sequence) and there is (are) pathway(s) in their folding mechanism. Usually, protein folding is completed within microseconds to seconds. Especially, early events of the protein folding are performed in nanoseconds to microseconds regions. We have investigated the early events of various proteins folding which changes from denatured state to native state by cryo-stopped-flow method. This method can make unobservable processes in conventional method observe. All the results suggested that all proteins we studied are first formed transient α -helix intermediates before forming their native structures. In the present poster, we show that folding studies of src SH3 domain and its mutant, A45G. We have investigated folding of these two proteins by X-ray solution scattering (compactness), circular dichroism (secondary structure) and tryptophan fluorescence (tertiary structure). These proteins are the center of our folding studies.