Early events of protein folding studied by cryo-stopped-flow method

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Early events of protein folding have been extensively studied by jump methods (temperature jump and concentration jump). Results show that the earliest events such as α-helix formation are finished very rapidly, rapider than μs.

We have developed cryo-stopped-flow method for investigating the early events of protein folding. Results obtained up to now are summarized as follows;

1) α-helix formation are too rapid to be detected by cryo-stopped-flow method , consistent with the temperature-jump results.
2) All proteins so far measured formed intermediate which is rich in α-helix. The fraction of the experimentally observed α-helix is proportional to the fraction of α-helix calculated by Helix2 program.
3) A mutant of src SH3, A45G, forms α-helix-rich equilibrium intermediate at acidic PH. This equilibrium intermediate is the same as the transiently obtained intermediate as far as CD and radius of gyration are concerned.

For our studies, BL-15A and the circumstances are essential. Time-resolved study is very important to protein folding. We do hope the new more powerful beam-line will be constructed for our study.