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Structural study of hNck2 SH3 domain protein by X-ray solution scattering III. Structure of hNck2 SH3 domain at pH 2.

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Introduction

In the series of reports, we have shown that hNck2 SH3 domain protein takes native β-structured state at pH 6 at low concentration of the protein, but takes dimer at the concentration higher than 1 mg/mL [1], and at low pH, the protein takes mainly monomer even at 3 mg/mL [2]. In this report, we show the acid-induced conformation is not compact. As this state has α-helix, in 12%, it is not randomly coiled, suggesting this state is similar to C state which Yamada *et al* proposed [3].

Experimental

X-ray scattering experiments were done at the beamline of 6A with the same set-up with [2]. Concentration of hNck2 SH3 domain was 3 to 4 mg/mL. At these concentration, the protein forms dimer at pH 6. Experiments were done at 12℃.

Results and Discussion

In Fig. 1, CD values at 222 nm are shown as a function of pH. At low pH, CD decreased drastically, showing the increase of α-helix. At pH 2, content of α-helix is 12 %.

Fig. 2 shows the normalized Kratky plots of hNck2 SH3 domain at various pH. As clearly seen in the figure, there appeared no peaks at acidic pH. This indicates that the protein at this condition was not compact globule state. *Rg* values at acidic pH were even a little higher than those at neutral pH [2]. This also suggests the protein takes non-compact, α-helix-rich, but probably more elongated structure at acidic pH. Results of the structural analysis will be presented in the next report [4].

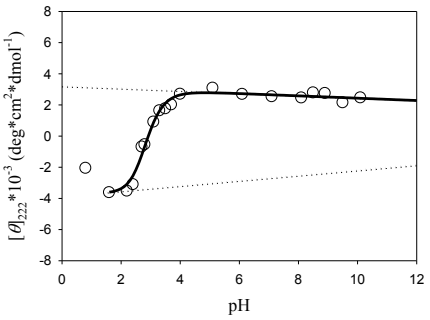

Fig. 1 $[\theta]_{222}$ dependence of pH induced-α-helix forming transition of hNck2 SH3 domain at 12℃.

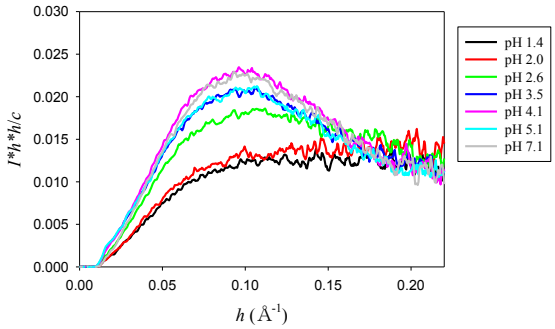

Fig. 2 Normalized Kratky plots of hNck2 SH3 domain at various pH.

References

[1] Matsumura *et al*. (2012) This proceedings, I.
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