ABSTRACT

Structural biology with focus on the determination of the protein structure has attracted extensive scientific interest, and various techniques have been developed. $^{13}$C isotope edited FTIR spectroscopy is a developing technique to address the structure of peptide in residue level with quick response. $^1$ On the other hand, the amphiphilic interface structures (e.g., cell membrane) have been shown to affect peptides/proteins structure. $^2$ The air-water interface has been used to mimic the amphiphilic interface and Langmuir trough techniques accurately control and monitor the interaction and distance between peptides/proteins at the air-water interface. $^2$ In addition, Infrared Reflection-Absorption Spectroscopy (IRRAS) is used to determine the orientation of peptides/proteins at the interface. $^2$ Thus, the our group anticipates that the orientation of a $^{13}$C labeled residue in a peptide can be determined selectively, apart from other residues, by IRRAS. With both conformation and orientation determined, the three-dimensional structure of peptides can be evaluated at physiological conditions. In this thesis, a peptide with sequence of YAAAA(KAAAA)$^4$ (referred as Pep25 hereafter) was used as a model peptide of $\alpha$-helix to spread at the air-water interface, because we have determined the conformation of Pep25 in residue level by the $^{13}$C isotope-edited FTIR. $^3$ Langmuir monolayer trough techniques together with IRRAS show that Pep25 does not form typical Langmuir monolayer at the interface. Potential plans to make Pep25 to form stable monolayer are also discussed in this thesis.

REFERENCES