

# 演講公告

時間：2008/11/12 (三) 下午 2:30~3:30

地點：中央大學 太遙中心 R3-112

演講人：吳明佳 博士

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**講題：An adaptive approach to the prediction of protein secondary structure contents in mutants**

## Abstract

An adaptive approach to the prediction of protein secondary structure contents in mutants from wild-type protein structures is presented. The approach is implemented by the introduction of the local hydrophobicity (LHP) around a residue defined as the sum of hydrophobicity (HP) of residues surrounding the residue within a specified distance. According to the geometrical constraint of native protein structures [1] and the experimental evidence that the dimension of the denatured states of specific globular proteins is compact [2], we assumed the three-stages folding model [3] to investigate the effects of LHP in protein folding. By using time series analysis, we find explicit correlation between HP and LHP, and from which the correlation coefficient between LHP and secondary structure can be defined to estimate the percentage contents of secondary structures from changes of LHPs in mutants. The estimations are qualitatively and quantitatively consistent with those from Circular Dichroism measurements on a number of one-point and two-points mutants of staphylococcal nuclease [4].

(1) M.-C. Wu, M. S. Li, M. Kouza, W.-J. Ma, and C.-K. Hu, Geometrical constraint on native protein structures, manuscript submitted (2008).

(2) C.-Y. Chow, M.-C. Wu, H.-J. Fang, C.-K. Hu, H.-M. Chen, and T.-Y. Tsong, Compact dimension of denatured states of staphylococcal nuclease, *Proteins: Struct. Func. Bioinfo.* 72, 901-909 (2008).

(3) T.-Y. Tsong, C.-K. Hu, and M.-C. Wu, Hydrophobic condensation and modular assembly model of protein folding, *BioSystems* 93, 78-89 (2008).

(4) M.-C. Wu, C.-K. Hu, H.-M. Chen, and T.-Y. Tsong, Local hydrophobicity and protein secondary structure formation: Theoretical model and experimental test, manuscript submitted (2008).

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