

**P033** Recombinant fish growth hormone (rEaGH):  
protein folding and aggregation

**Izabela Zakowska<sup>1</sup>, Chuan-Mei Tsai<sup>2</sup>, Anna Svanidze<sup>1,3</sup>,  
Pei-Hsin Chen<sup>1</sup>, Fang-Hsing Chiang<sup>1</sup>, Hsueh-Liang  
Chu<sup>1</sup>, Chang-You Wu<sup>1</sup> and Chia-Ching Chang<sup>1,2,4\*</sup>**

<sup>1</sup> Department of Biological Science and Technology,  
National Chiao Tung University, HsinChu, 30050, Taiwan

<sup>2</sup> National Nano Device Laboratories, HsinChu, 30078, Taiwan

<sup>3</sup> Institute of Chemistry, Academia Sinica, 128 Sec. 2,  
Academia Rd., Nankang, Taipei, 115, Taiwan

<sup>4</sup> Institute of Physics, Academia Sinica, 128 Sec. 2,  
Academia Rd., Nankang, Taipei, 115, Taiwan

Protein folding may follow a spontaneous or a reaction path dependent process. When the proteins, fail to fold correctly, this failure can result in their aggregation. The aim of this study was to reveal how fast proteins can stabilize themselves during the folding process. We continue the evaluation of the mean collision times versus aggregation fraction for different temperatures. The protein folding stabilizing time parameter ( $\tau_C$ ) from the autocorrelation function (ACF) was determined. We found the protein stabilizing time of rEaGH system is around 48.7  $\mu$ s in 281 K, 48.1  $\mu$ s in 285 K, 47.4  $\mu$ s in 289 K and 45.3  $\mu$ s in 301 K. Three dimensional random walk simulation of diffusion limited aggregation model was used to reveal the mechanism of protein aggregation. These results suggest that spontaneously folding and diffusion-limited aggregation are antagonistic reactions in nature. This study was supported by grants of NSC 95-2811-M-009-009 and NSC 95-2112-M-009-019.