

# Protein aggregation might not be related to protein misfolding\*

Chin-Kun Hu

*Institute of Physics of Academia Sinica, Taipei 11529, Taiwan*

<http://proj1.sinica.edu.tw/~statphys/>

Email: [huck@phys.sinica.edu.tw](mailto:huck@phys.sinica.edu.tw)

Key words : protein aggregation, protein misfolding, human disease

Abstract: Ideas and methods of statistical physics have been shown to be useful for understanding some interesting problems in physical systems [1]. After the development of molecular biology, it is of interest to know whether one can use ideas and methods of statistical physics to understand some interesting biological problems from the molecular level. In this talk, I will address the problem of protein aggregation, which is related to many human diseases. Simple models have been found to be useful for understanding the behavior of protein aggregation [2,3,4]. It has been proposed that protein aggregation is due to protein misfolding [5]. However, Figures 1(a) and 2(a) of [3] show that peptide chains aggregate with the conformation of the first excited state of the one chain system rather than the ground state conformation, and Fig. 2(a) is a stable conformation. Figures 2, Fig. 4, Table1, and Table 2 of [4] show that most stable conformation of one chain system is different from the most stable conformation of two-chains system. In such cases, protein aggregation is not due to protein mis-folding [6]. It is of interest to study or review similar problems in other systems.

References.

- [1] For a recent review, see C.-K. Hu: *Chinese J. Phys. (Taipei)* 52, 1-76 (2014).
- [2] W.-J. Ma, and C.-K. Hu: *J. Phys. Soc. Jpn.* 79, 054001 (2010); *J. Phys. Soc. Jpn.* 79, 104002 (2010).
- [3] M. S. Li, N. T. Co, G. Reddy, C. -K. Hu, J. E. Straub, and D. Thirumalai: *Phys. Rev. Lett.* 105, 218101(2010); N. T. Co, C.-K. Hu and M. S. Li, *J. Chem. Phys.* 138, 185101 (2013).
- [4] H.-L. Chiang, C. J. Chen, H. Okumura, C.-K. Hu: *J. Comp. Chem.*, 35, 1430-1437 (2014); H. -L. Chiang, S. T. Ngo, C. -J. Chen, C.-K. Hu, *Plos One*, 8, 65358 (2013).
- [5] C. M. Dobson, *Nature* 426, 884 (2003); F. Chiti and C. M. Dobson, *Annu. Rev. Biochem.* 75, 333 (2006).
- [6] C.-K. Hu: Protein aggregation and human diseases, *Journal of Physics: Conference Series*, 604, 012009 (2015)..

\* talk at Int. Conf. on Computer Simulation in Phys. and beyond 6-10 Sep. 2015, Moscow.