Abstract Submitted
for the SES05 Meeting of
The American Physical Society

Protein-Protein Association: A Transition-State View. HUAN-XIANG ZHOU, Department of Physics and Institute of Molecular Biophysics and School of Computational Science, Florida State University, Tallahassee, FL 32306 — Protein-protein association is central to most protein functions. When two proteins approach each other to form a specific complex, translational and rotational freedom becomes restricted, yet the stabilizing interactions between the partners are formed only when they are close to the bound configuration. This asynchronous decrease in translational/rotational entropy and free energy of interactions leads to a free-energy barrier, which can be identified as the transition state for association [1]. The entropic barrier corresponds to low rate of association, which can be enhanced by favorable electrostatic interactions between the associating proteins. The rate enhancement can be predicted from the electrostatic free energy of interaction in the transition state [2]. The transition-state view of protein-protein association nicely explains the widely-observed disparate dependence of association and dissociation rates on ionic strength, which modulates electrostatic interactions [1, 3]. Once the transition state is reached, the proteins are found to undergo nanosecond-scale conformational adjustment to form the specific complex [4].

[1] H.-X. Zhou (2001). Disparate ionic-strength dependence of on and off rates in protein- protein association. Biopolymers 59, 427-433.

[2] M. Vijayakumar, K.-Y. Wong, G. Schreiber, A. R. Fersht, A. Szabo, and H.-X. Zhou (1998). Electrostatic enhancement of diffusion-controlled protein-protein association: Comparison of theory and experiment on barnase and barstar. J. Mol. Biol. 278, 1015-1024.

[3] H.-X. Zhou (2003). Association and dissociation kinetics of colicin E3 and immunity protein 3: convergence of theory and experiment. Protein Sci. 12, 2379-2382.

[4] X. Huang, F. Dong, and H.-X. Zhou (2005). Electrostatic recognition and induced fit in the k-PVIIA toxin binding to Shaker potassium channel. J. Am. Chem. Soc 127, 6836-6849.

Department of Physics and Institute of Molecular Biophysics and School of Computational Science, Florida Sta

Date submitted: 06 Sep 2005 Electronic form version 1.4