Prediction and Dissection of Widely-Varying Association Rate Constants of Actin-Binding Proteins

Kenneth H. Zhou¹, Xiaodong Pang², Sanbo Qin², and Huan-Xiang Zhou²*

¹Lawton Chiles High School, Tallahassee, FL 32312
²Department of Physics and Institute of Molecular Biophysics, Florida State University, Tallahassee, FL 32306

Actin polymerization and depolymerization are essential for cell motility and are regulated by a class of proteins called actin-binding proteins. The widely-varying rate constants ($k_a$) of the actin-binding proteins associating with G-actin, from $2.2 \times 10^4$ to $4.3 \times 10^7$ M$^{-1}$s$^{-1}$, appear to be tuned for the regulatory roles. Here we applied our previously developed transient-complex theory to study the association of seven actin-binding proteins with G-actin. We found that the 1000-fold $k_a$ variations among the actin-binding proteins can mostly be attributed to disparate inter-protein electrostatic interactions. The association mechanisms also showed variations, resulting from the different shapes and degrees of tightness of the interfaces formed by the seven actin-binding proteins with G-actin. This study demonstrates the various ways that actin-binding proteins use physical properties to tune their association rate constants to ranges suitable for distinct regulatory functions.