

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

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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 2.2×10^4 to $4.3 \times 10^7 \text{ M}^{-1}\text{s}^{-1}$, 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.