

Protein Structure and its Folding Rate

Abstract:

First part of the talk gives an overview on protein structure, its spontaneous formation (folding) and on thermodynamic and kinetic aspects of this phenomenon. Universal features of folding are observed near the point of thermodynamic equilibrium between the native and denatured states of the protein. Here the "two-state" transition proceeds without any accumulation of metastable intermediates, and only the transition state ("folding nucleus") is outlined by its essential influence on the folding/unfolding kinetics. In the second part of the talk, a theory of protein folding rates and related phenomena is presented. It refers to the vicinity of equilibrium point. First, it is shown that protein size and stability outline the range of protein folding rates. Then we present methods for calculating folding and unfolding rates of globular proteins from their stabilities and either 3D structures or sequences. And, at last, we show that the same theory outlines the location of the protein-folding nucleus in a reasonable concordance with experiment.

Recommended reading:

1. Finkelstein AV, Ptitsyn OB. *Protein Physics*. Chapters 16-21. Academic Press, An Imprint of Elsevier Science; Amsterdam – Boston – London – New York – Oxford – Paris – San Diego – San Francisco – Singapore – Sydney – Tokyo; 2002; i-xix + 354p.
2. Finkelstein AV, Badretdinov AY. Rate of protein folding near the point of thermodynamic equilibrium between the coil and the most stable chain fold. *Fold Des* 1997;2:115-121.
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6. Ivankov DN, Garbuzynskiy SO, Alm E, Plaxco KW, Baker D, Finkelstein AV. Contact order revisited: Influence of protein size on the folding rate. *Prot Sci* 2003, 12: 2057-2062.
7. Finkelstein AV, Galzitskaya OV. Physics of protein folding. *Physics of*

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9. Ivankov DN, Finkelstein AV. Prediction of protein folding rates from the amino-acid sequence-predicted secondary structure. *Proc Natl Acad Sci USA* 2004, 101:8942-8944.