Polymers under Multiple Constraints

Polymer- & Soft-Matter-Seminar

Tuesday, 25th October 2016

at: **5.15pm**

VDP4 1.27, Von-Danckelmann-Platz 4, 06120 Halle

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“Protein folding: non-specific interactions promote highly specific chain organization"

Under suitable conditions, globular proteins can self-assemble spontaneously and reliably. An effective thermodynamic description of this folding reaction was established half a century ago, but a mechanistic understanding is still lacking. This open question has been dubbed "the protein folding problem".

Current efforts to solve the protein folding problem are based on the assumption that highly specific, favorable interactions between and among amino acid side chains are primarily responsible for selecting the native fold. This plausible assumption is grounded in the fact that most residue backbones are chemically equivalent and therefore apparently lacking in discriminatory power. I will challenge this assumption based on three lines of inquiry: (1) Chain collapse is driven mostly by solvent entropy. (2) Chain organization is imposed primarily by the backbone, not the side chains. Of thermodynamic necessity, globular proteins are built on scaffolds of □-helix and □-strands, and the number of available scaffolds is highly limited. (3) Fold selection from the repertoire of available scaffolds emerges largely by eliminating unfavorable interactions rather than by selecting specific favorable interactions.