



DK Nanocell Colloquium I

Winter Term 2019/20

October 7th 2019 13:30 UG1

Institute of Biophysics, Gruberstrasse 40, Linz

Hue Sun Chan

***Department of Biochemistry, University of Toronto,
Ontario, Canada***

<http://biochemistry.utoronto.ca/person/hue-sun-chan/>

Physics of protein folding, evolution, and phase separation

The Levinthal paradox of protein folding is commonly perceived as stating the impossibility of folding by a completely random search. Often missed, however, is the historical context: The question raised by Levinthal was in response to the experimental discovery of two-state, switch-like cooperative folding in the late 1960s, rather than to the problem of conformational search *per se*. I will discuss the physical implications of this understanding on the notion of a funnel-like energy landscape, and will explore the roles of desolvation, nonnative effects, and enthalpic barriers in cooperative protein folding. How novel folds of proteins may emerge in evolution will be addressed using simple lattice protein models of basic sequence-structure relationship as well as an atomic model of an experimentally observed conformation switch from an all-alpha to an entirely different four-beta+alpha fold. It is important to recognize, however, that not all proteins function as folded structures. Intrinsically disordered proteins (IDPs) perform critical biological functions, especially for the regulation of cellular processes in higher organisms. Remarkably, some IDPs function not only as individual molecules, but also act collectively by undergoing reversible liquid-liquid phase separation in the living cell. The resulting high-IDP phase forms a major component of membraneless organelles such as P granules and nucleolus that, by creating their own IDP-rich compartments, stimulate critical biological functions. To gain physical insight into this newly discovered and fascinating phenomenon, I will outline briefly our effort in using analytical theory to elucidate how biologically functional phase separation of IDPs is governed by their amino acid sequences.

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Monday 07.10.2019

Organising PI: Thomas Renger

UG1 (basement) Institute of Biophysics
Gruberstrasse 40, 4020 Linz

10:00 - 12:30 Morning session

10:00 **Journal Club** Ferdinand Horvath / Thomas Renger

10:45 - 12:30 **Work in progress Seminar and Presentations of master theses (new DK students)** PI

10:45 Ferdinand Horvath DK10: Modeling of conformational transitions of translocon: from structure to function Renger

11:15 Sarah Stainer DK8: Forces and dynamics in protein translocation through the bacterial translocon Hinterdorfer

11:45 Suyash Naik Differential tissue stiffness facilitates the somersault in Hydra Heisenberg

12:00 Herwig Grabmayr DK11: STIM/Orai coupling and CRAC activation Romanin

12:30 - 13:30 *Lunch Break*

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13:30 - 14:30 Afternoon session

13:30 Hue Sun CHAN (University of Toronto, Canada) Physics of protein folding, evolution, and phase separation