Seminar

“IRTG Soft Matter Science”

Tuning Interactions in Protein Solutions towards to Controlled Protein Crystallization

Prof. Fajun Zhang

Institut für Angewandte Physik, Universität Tübingen, Auf der Morgenstelle 10, 72076 Tübingen,Germany

Tuesday, April 12, 14h15

“Hörsaal Makromolekulare Chemie”,

Stefan-Meier-Str. 31, Freiburg

You are welcome to meet Pr. F. Zhang, do not hesitate to contact Christelle Vergnat (softmattergraduate@physik.uni-freiburg.de)

Tuning Interactions in Protein Solutions towards to Controlled Protein Crystallization

Fajun Zhang,[1,*] Marcell Wolf,[1] Felix Roogen-Runge,[1] Maximilian W. A. Skoda,[2] Robert M. J. Jacobs,[3] and Frank Schreiber[1]

[1]*Institut für Angewandte Physik, Universität Tübingen, Auf der Morgenstelle 10, 72076 Tübingen,Germany*
[2]*ISIS, Rutherford Appleton Laboratory, Chilton, Didcot, OX11 0OX, United Kingdom*
[3]*Department of Chemistry, Chemistry Research Laboratory, University of Oxford, Mansfield Road, OX1 3TA, United Kingdom*
**e-mail: fajun.zhang@uni-tuebingen.de*

Non-specific protein-protein interactions in aqueous solution play a crucial role on protein crystallization and the protein-aggregation related diseases, such as cataracts, and sickle cell anemia. The challenge of a comprehensive understanding is to tune and control the phase behavior in protein solutions. We have studied the phase behavior of model globular proteins in solution in the presence of multivalent counterions. It has been shown that negatively charged globular proteins at neutral pH in the presence of multivalent counterions undergo a "reentrant condensation (RC)" phase behavior [1,2], i.e. a phase-separated regime occurs in between two critical salt concentrations, c* < c**, giving a meta-stable liquid-liquid phase separation (LLPS). This reentrant phase behavior corresponds to an effective charge inversion of proteins as confirmed by zeta-potential measurements and supported by Monte Carlo simulations [1,2]. Crystallization from the condensed regime follows different mechanisms. Close to c*, crystals grow following a classic nucleation and growth mechanism; close to c**, the crystallization follows a two-step mechanism, i.e, crystals growth follows a meta-stable LLPS [3]. X-ray diffraction analyses on the high quality single crystals provide direct evidence of the crystal structure and cation binding sites [3]. Our discovery of the RC and LLPS induced by multivalent metal ions provides a new way to tune protein interactions with predictable phase behavior as well as controlling protein crystallization.

[1] Zhang, F.; Skoda, M. W. A.; Jacobs, R. M. J.; Zorn, S.; Martin, R. A.; Martin, C. M.; Clark, G. F.; Weggler, S.; Hildebrandt, A.; Kohlbacher, O.; Schreiber, F. *Phys. Rev. Lett.* **2008**, 101, 148101.

[2] Zhang, F.; Weggler, S.; Ziller, M.; Ianeselli, L.; Heck, B. S.; Hildebrandt, A.; Kohlbacher, O.; Skoda, M. W. A.; Jacobs, R. M. J.; Schreiber, F. *Proteins: Structure, Function, and Bioinformatics* **2010**, 78, 3450-3457.

[3] Zhang, F., Zocher, G., Sauter, A., Stehle, T. & Schreiber, F. J. Appl. Cryst. **2011** Accepted.