

# X-ray scattering on soft matter systems – From local order in thin colloid films to high pressure effects on proteins

Martin A. Schroer

*Deutsches Elektronen-Synchrotron (DESY), Notkestr. 85, 22607 Hamburg, Germany*

*Email: [martin.schroer@desy.de](mailto:martin.schroer@desy.de)*

X-ray scattering techniques are excellent tools to resolve the structure of matter from several nanometers size to atomic length scales. Due to their high brilliance third generation synchrotron radiation facilities allow it to study diluted samples in solution employing X-ray beams of only a few hundred nanometers size. A special method to investigate soft matter samples like colloids or even proteins in solution is small angle X-ray scattering (SAXS). This method allows it to determine, for instance, the particle size, shape, and in case of high concentrations the interaction between particles.

In the first part of my talk I will show recent results how SAXS in combination with a nano-focus beam can be employed to resolve the orientational order in dry films made out of binary colloid solution. Therefore, the two-dimensional scattering patterns are analyzed in terms of a X-ray cross-correlation analysis. By this approach angular correlations are detectable within the sample with a spatial resolution of a few microns that are overseen by usual analyzing schemes [1].

In the second part of my talk I will report in detail on the effect of high hydrostatic pressure on concentrated protein solutions as determined by SAXS. It will be shown that pressure, besides unfolding proteins [2], also affects the pair-interaction potential of the protein lysozyme [3]. Especially a nonlinear pressure-dependence of the interaction is revealed for pressures above 2 kbar that persists for different protein concentrations, temperatures, and salt concentrations [3-5]. However, this effect can be modulated when biologically relevant cosolvents (urea, TMAO) are added to the protein solution [6]. Our results point out that the effect of pressure is due to a change of the local structure of the water that moderates the interactions between the protein molecules.

[1] M.A. Schroer *et al.* *in preparation*.

[2] M.A. Schroer, M. Paulus, C. Jeworrek, C. Krywka, S. Schmacke, Y. Zhai, D.C.F. Wieland, Ch.J. Sahle, M. Chimenti, C.A. Royer, B. Garcia-Moreno, M. Tolan, R. Winter. *Biophys. J.* **99**, 3430-3437 (2010).

[3] M.A. Schroer, J. Markgraf, D.C.F. Wieland, Ch.J. Sahle, J. Möller, M. Paulus, M. Tolan, R. Winter. *Phys. Rev. Lett.* **106**, 178102 (2011).

[4] M.A. Schroer, M. Tolan, R. Winter. *Phys. Chem. Chem. Phys.* **14**, 9486-9491 (2012)

[5] J. Möller, M.A. Schroer, M. Erlikamp, S. Grobelny, M. Paulus, S. Tiemeyer, F.J. Wirkert, M. Tolan, R. Winter. *Biophys. J.* **102**, 2641-2648 (2012).

[6] M.A. Schroer, Y. Zhai., D.C.F. Wieland, Ch.J. Sahle, J. Nase, M. Paulus, M. Tolan, R. Winter. *Ang. Chem. Int. Ed.* **50**, 11413-11416 (2011).