FA5-MS05-O1

SAXS Combined with Crystallography and Computation: Defining Accurate Dynamic Macromolecular Assemblies in Solution. Michal Hammel[a], Greg Hura[a], John Tainer[a]. [a]*Lawrence Berkeley National Laboratory, Berkeley, CA 94720, USA.*
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Crystallography supplies unparalleled structural detail for mechanistic analyses; however, it is restricted to describing low energy conformations of macromolecules within crystal lattices. Small angle X-ray scattering (SAXS) offers complementary information about macromolecular folding, unfolding, aggregation, extended conformations, flexibly linked domains, shape, conformation, and assembly state in solution, albeit at the lower resolution range of about 50 to 10 Å resolution, but without the size limitations inherent in NMR and electron microscopy studies. Examples from data collected at SIBYLS, a dual SAXS and protein crystallography synchrotron beamline, will be drawn upon to demonstrate the complimentary use of SAXS with protein crystallography. I will also describe the recent implementation of a sample loading automation tool for high throughput SAXS data collection. A particular emphasis will be placed on the need for computational development in light of the high throughput nature of SAXS data collection. The utility of high throughput SAXS will discussed in the context of program project SBDR (Structural Cell Biology of DNA Repair Machines) and its potential to contribute to Structural Genomics efforts.

Keywords: SAXS; protein conformational analysis; high throughput

FA5-MS05-O2

Coexisting Lipid Domains. Georg Pabst[a], Beate Boulgaropoulos[a], Bibhu R. Sarangi[b], Peter Laggner[a], Velayudhan A. Raghunathan[b]. [a]*Institute of Biophysics and Nanosystems Research, Austrian Academy of Sciences, A-8010 Graz, Austria.* [b]*Raman Research Institute, Bangalore 560 080, India.*
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Sorting of membrane lipids and proteins into domains of particular composition (rafts) is supposed to be one of the most fundamental processes in cellular functioning. Although domains are known to exist in phospholipid model systems for more than 30 years, there is still plenty to learn from their biophysical properties which could be of physiological relevance. We have, therefore, probed the temperature and composition dependent properties of various coexisting phases using small- and wide-angle x-ray diffraction (SWAXD) in combination with several other complementary techniques. In particular, we have focused on structure and interactions of coexisting fluid-gel domains, found in lipid mixtures containing ceramide, a second messenger for apoptosis (programmed cell death). Additionally, I will also report on the partitioning of cholesterol in coexisting liquid-ordered (L_o) and liquid-disordered (L_d) domains of raft-like mixtures. Our results reveal a preferential partitioning of cholesterol into L_o domains. However, unlike previously assumed also L_d domains contain significant amounts of cholesterol.

Keywords: biological model membranes; phase separation; X-ray diffraction

FA5-MS05-O3

Laboratory SWAXS for Applications in Pharmaceutical Technology. Aden Hodzic[a,b], Manfred Kriechbaum[b,c], Peter Laggner[b,c]. [a]*Research Center Pharmaceutical Engineering GmbH, Inffeldgasse 21/A, 8010 Graz, Austria.* [b]*Hecus X-ray Systems GmbH, Reininghausstrasse 13a, A-8020 Graz, Austria.* [c]*IBN - Institute of Biophysics and Nanosystems Research, Austrian Academy of Sciences, Schmiedlstrasse 6, Graz, Austria.*
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Combined small- and wide-angle X-ray scattering (SWAXS) is becoming an increasingly important technique in pharmaceutical solid-state characterization1). Highly relevant questions of polymorphism in crystalline materials, stability and nanostructure of amorphous states, inner surface in controlled-release formulations, and stability and ageing of controlled release formulations can be addressed by this technique. The information to be gained by SAXS expands largely the scope of conventional powder diffraction techniques. A particular advantage lies in the simultaneous observation of nano-scale (SAXS) and atomic scale (WAXS). With the development of high-brilliance laboratory SWAXS systems (Hecus S3MICROpix) the times for analysis have been greatly reduced, and hence the method can be applied to quality screening and process analytical technology (PAT). Examples will be presented for technologically relevant systems, such as polymorphic forms of active ingredients (carbamazepine), lactose-based inhaler powders, controlled-release microsopheres (EDLA), and amorphous fomulations. The results show, that an analysis in terms of robust SAXS parameters, such as inner surface, total absolute scattering power, and Porod exponent, can provide highly valuable technological information.

[1] Laggner, P., M. Kriechbaum, M. Rappolt, G. Pabst, H. Amenitsch, A. Johs, K. Lohner, D. Zweytick, R. Koschuch, and P. Abuja. **2005**, *Solid State Characterization of Pharmaceuticals*. Eds. A. and M. Zakrzewski. Assa International, Danbury, chapter 12.

FA5-MS05-O4

GISAXS for Single-Crystal-Like Silicate Films Formed at the Air-Water Interface. U-Ser Jeng[a], Ying-Huang Lai[a,b], Je-Wei Chang[b], Yi-Jiun Chen [b], Hsiang-Wei Cheng[b], Wei-Ting Hsu[b], Chih-Chang Weng[b], Chun-Jen Su[a], Chiu-Hun Su[a], Kuei-Fen Liao[a]. [a]*National Synchrotron Radiation Research Center,*