Announcement

GCC[1] BioSAXS Workshop

Tuesday, January 25, 2011

The Woodlands, TX • 9am to 4pm CST

No registration fee • Public event • Lunch is provided

In a continuing effort to further the current understanding of Small Angle X-ray Scattering (SAXS) as used for the elucidation of biological macromolecular structure, Rigaku Americas Corporation and the Gulf Coast Consortium SAXNS Group are pleased to co-sponsor a day-long complementary workshop, on Tuesday, January 25, 2011 (lunch will be provided), focused on the latest developments in BioSAXS technologies and applications.

Program

Morning (Lectures): 9am – noon

- BioSAXS hardware review
  - Katsunari Sasaki, Ph.D. (RAC)
- BioSAXS sample prep and data collection
  - Angela Criswell, Ph.D. (RAC)
- BioSAXS data processing and interpretation
  - Tom Grant (Hauptman-Woodward Institute)
- Gulf Coast Consortium SAXNS Group
  - Highlight of current BioSAXS projects
  - Proposed regional BioSAXS facility

Lunch: noon – 1pm

Afternoon: 1pm – 4pm

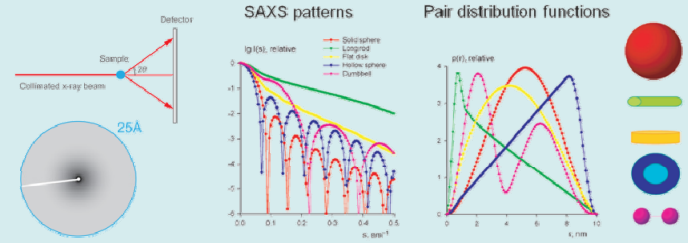
- ATSAS 2.4 workshop[2]
  - Bring your laptops to install/run ATSAS

[1]Gulf Coast Consortia (GCC) is a collaborative alliance for quantitative biomedical sciences research and training, including University of Texas Medical Branch at Galveston, University of Texas Health Science Center at Houston, Baylor College of Medicine, Rice University, University of Texas M.D. Anderson Cancer Center and the University of Houston. The GCC mission is to provide an effective infrastructure to support interdisciplinary training programs in multiple areas of quantitative life sciences, facilitate effective use of shared major equipment and facilities, and catalyze interactions to support and create dynamic programs of research across the GCC institutions.

[2]software for BioSAXS analysis: **www.embl-hamburg.de/biosaxs/software.html** (*J. Appl. Cryst.* (2003). **36**: 1277-1282).

Small Angle X-ray Scattering

SAXS is a powerful technique as applied to structural biology (BioSAXS) and is a complimentary to both macromolecular crystallography and NMR spectroscopy. The scattering distribution in a BioSAXS experiment is a measure of the pair distribution function and thus gives information about the distribution of intra-molecular distances with a molecule or molecular assembly.



BioSAXS measurements provide low resolution isotropic X-ray scattering as compared to the high resolution diffraction measured from a crystal. The low angle X-ray scattering from a protein in solution can provide information about the low resolution structural characteristics, including:

- Calculation of generalized structural parameters
- Determination of molecular shape
- Differentiation of mono-disperse and aggregated solutions
- Differentiation of folded and unfolded protein solutions
- Characterization of oligomeric states

This type of information can be useful in the crystallization stage of a protein structural project as well as during the structure analysis stage. The determination of whether a solution is mono-disperse or aggregated or whether a protein is folded or unfolded can help accelerate the crystallization step by eliminating samples that will never crystallize.

At the structure analysis stage, the low resolution molecular shapes can be used to confirm the initial structure envelope or in the case of large molecular complexes, the shape can be used to model the complex structure from the structures of individual molecules or domains.

RSVP: www.surveymonkey.com/s/biosaxs

Sponsored by: Gulf Coast Consortia for Quantitative Biomedical Sciences

Rigaku

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BioSAXS Workshop signup form: www.surveymonkey.com/s/biosaxs