Announcement

University of Leeds / Rigaku BioSAXS Workshop

Friday, August 19, 2011

Garstang Building, Biological Sciences • 9am to 5pm

Cost: Free • Lunch is provided • Places limited

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 Astbury Centre for Structural Molecular Biology at the University of Leeds are pleased to co-sponsor a day-long workshop, on Friday, August 19, 2011 (lunch will be provided), focused on the latest developments in BioSAXS technologies and applications.

Program

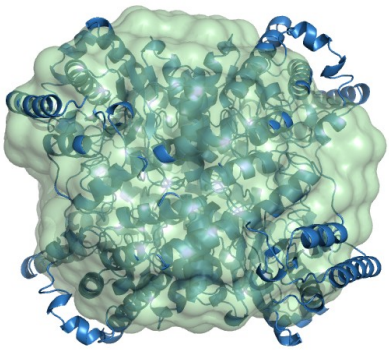
Morning (Lectures):

•BioSAXS sample prep and data collection
Angela Criswell, Ph.D. (Rigaku)
•BioSAXS hardware review
Joseph D. Ferrara, Ph.D. (Rigaku)
•BioSAXS data processing and interpretation
Eddie Snell (Hauptman-Woodward Institute)

Afternoon: (Hands on data handling workshop):

•ATSAS 2.4 workshop
Local computer facilities will used for the ATSAS workshop

Closing Lecture:
Samar Hasnain (University of Liverpool)
• Combining crystallography, scattering and spectroscopy for redox biology



Small Angle X-ray Scattering
SAXS is a powerful technique as applied to structural biology (BioSAXS) and is complementary 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 within 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 generalised structural parameters
- Determination of molecular shape
- Differentiation of mono-disperse and aggregated solutions
- Differentiation of folded and unfolded protein solutions
- Characterisation of oligomeric states

This type of information can be useful in the crystallisation 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 crystallisation step by eliminating samples that will never crystallise.

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

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