HIGH BRIGHTNESS X-RAY SCATTERING FOR LIFE SCIENCES (LiX)

BROOKHAVEN NATIONAL LABORATORY

NATIONAL SYNCHROTRON LIGHT SOURCE II

SCIENTIFIC SCOPE

The LiX beamline is part of the Advanced Beamlines for Biological Investigations using X-rays (ABBIX) project funded by National Institute of Health. It will provide state-of-the-art capabilities in 3 scientific areas: (1) high throughput (> 1 sample/buffer pair per minute) biomolecular solution scattering and time-resolved solution scattering based on microfluidic flow mixers, (2) diffraction from single- and multi-layered lipid membranes, and (3) scattering-based scanning probe imaging and tomography of biological tissues. The design and construction of the LiX beamline is currently under way, with the start of operations scheduled in 2015.

BEAMLINE CHARACTERISTICS

TECHNIQUES:

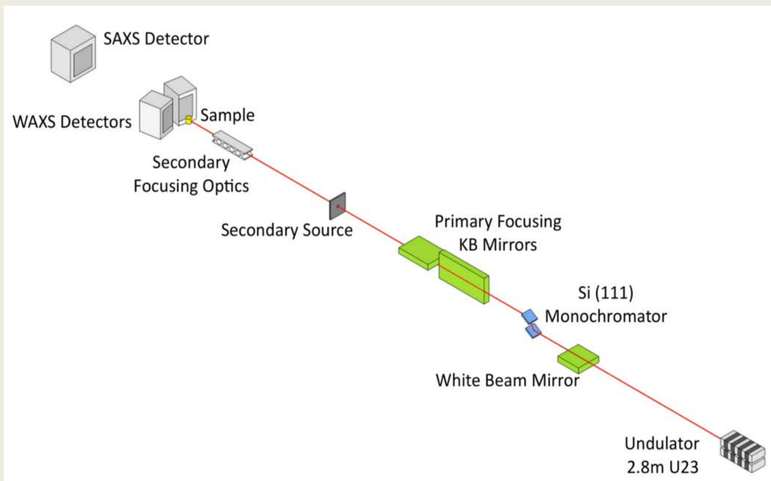
- Solution scattering
- Scattering-based scanning imaging
- Scattering and diffraction from membrane structures

ENDSTATION DETAILS:

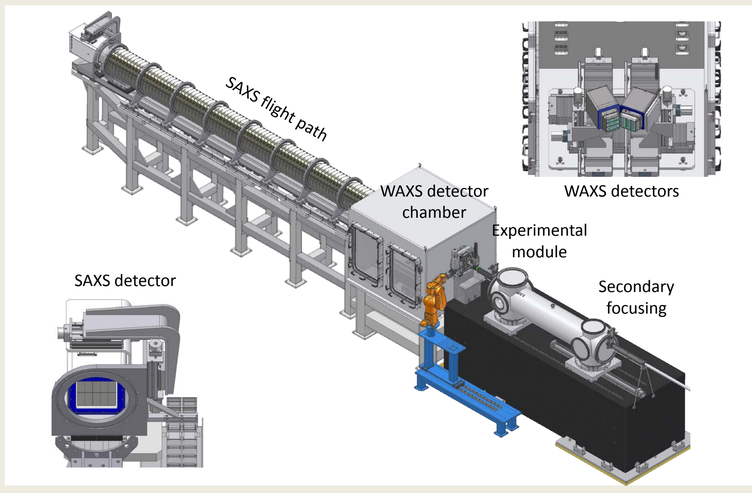
- 6-axis robot
- Automatic handling of protein solution samples, optionally with HPLC
- Pilatus3 detectors for SAXS/WAXS, with continuously variable camera lengths
- On-axis microscope and scanning stage

LiX at NSLS-II:

- Will enable time-resolved solution scattering with resolution down to 10µs; the range of time scales can be varied by selecting from a set of mixing cells
- Will support imaging of biological tissues using scattering intensity as the contrast mechanism, at down to 1µm resolution; coherent diffraction imaging will also be possible
- Will provide new tools for studying membrane structures



Optical layout of the LiX beamline. The secondary source helps to improve beam stability and is imaged to the sample position by Be refractive lenses.



Layout of the LiX experimental station. Several interchangeable experimental modules will be constructed, each dedicated to a sets of supported measurements.

Overview

PORT: 16-ID
SOURCE: undulator (IVU23)
ENERGY RANGE: 2.1 – 18 keV
ENERGY RESOLUTION: $\Delta E/E = 10^{-4}$
SPATIAL RESOLUTION: 1 µm
CONSTRUCTION PROJECT: ABBIX
BEAMLINE STATUS: Under construction
AVAILABLE TO USERS: Spring 2016

Beamline Team

STAFF

Lin Yang: lead beamline scientist
Shirish Chodankar: beamline scientist
Vito Graziano: science associate
Jon DiFabio: mechanical engineer
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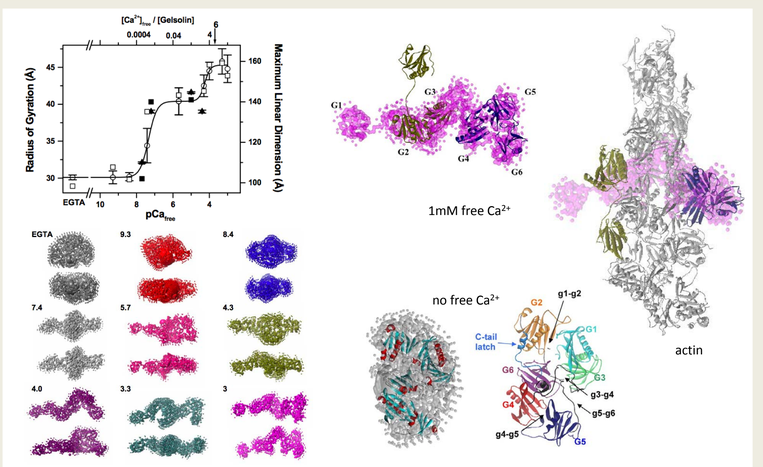
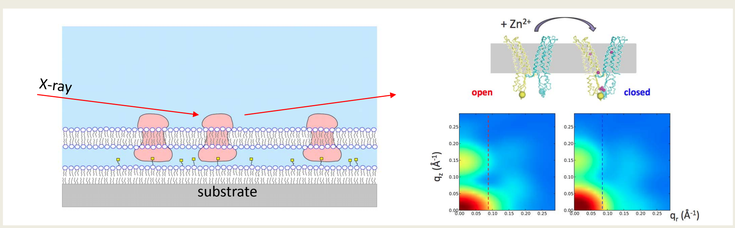
SCIENTIFIC APPLICATIONS

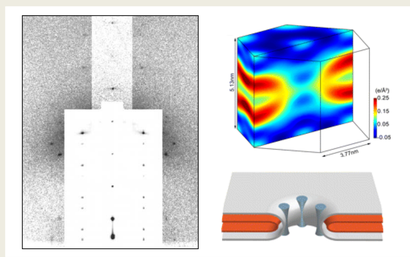


Structure changes of gelsolin induced by Ca^{2+} concentration [Ashish et.al., J. Biol. Chem., 2007]. Basic geometric parameters of the protein molecule can be extracted from solution scattering data. Low-resolution shape models can also be obtained. These models can then be used together with other structural information (e.g. the rigid crystal structure) to under stand how the molecule function under native conditions.

LiX will support different variation of solution scattering measurements, to help how the structure of proteins can be affected by interaction with ligands or other proteins, and how these changes occur as a function of time.

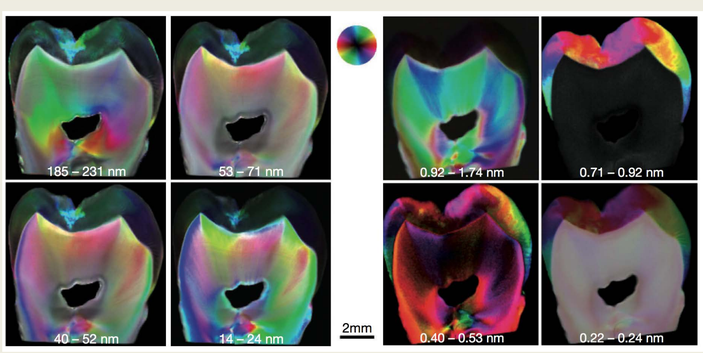


Membrane proteins can be embedded into substrate-supported lipid bilayer and measured by gracing incidence x-ray scattering. The calculated scattering intensity from based on the structure of zinc transporter YiiP is shown on the right.



Small peptides can be incorporated multilayered lipid membranes. Under appropriate conditions, they form periodic structures that diffract x-rays. The structure of the lipid-peptide assemblies can therefore be solved [Qian et.al., PNAS, 2008]. At LiX, these experiments can be performed near the K-edge of phosphorous for MAD phasing.

Conventional solution scattering is not well suited to study membrane proteins. LiX will support measurements on lipid membrane structures to help understand the structure of membrane proteins and how they interact with the membrane itself.



Abundance (intensity) / orientation (color) maps of tooth sections at various length scales [Muller et.al., Euro J Nanomed 2010]. At LiX, maps of this kind can be produced at a spatial resolution of 1µm.

The scattering intensity from biological tissues can be used as a contrast mechanism to construct maps of the underlying structure. These false color images can be correlated with those obtained in other types of microscopy to reveal new information. Each pixel in the map can also be examined following classical SAXS data analysis methods.