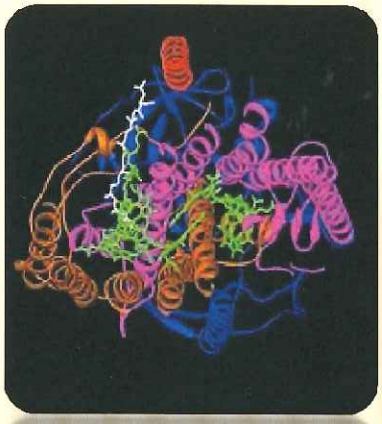
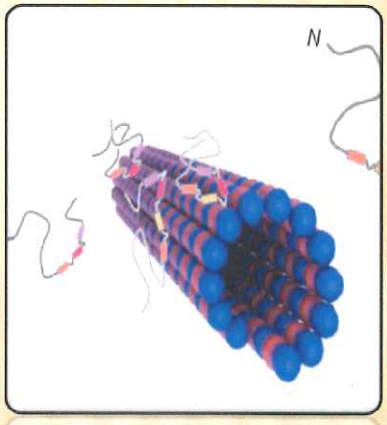
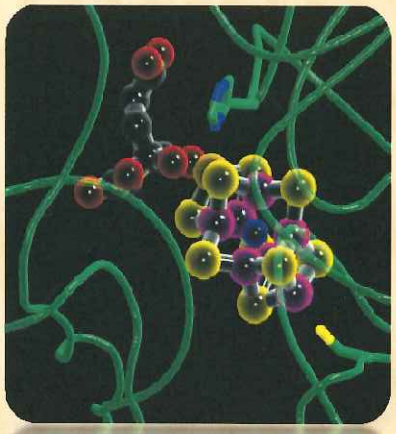
Structural Molecular Biology Center
at the
Stanford Synchrotron Radiation Lightsource







The SMB Center operates 10+ beam lines that provide scientific tools and user support for structure-function paradigm research in biology, bioenergy and biomedicine

The SSRL Structural Molecular Biology Center operates as an integrated resource and has three primary areas (or cores) of technological R&D and scientific focus: **macromolecular crystallography (MC)**, **x-ray absorption spectroscopy (XAS)** and **small angle x-ray scattering/diffraction (SAXS)**. Technological foci in all three areas include development, utilization and improvement of beam lines, detectors and specialized instrumentation, especially to be able to take maximum advantage of the increasingly high x-ray brightness of SSRL's storage ring (SPEAR3). There is vigorous R&D in new methodology and techniques, including enhanced data collection, computing and data management tools to provide "user-friendly, real-time and on-line" data reduction and analysis. The innovations in beam line, instrumentation and methodology developments are guided by a very close coupling to scientific projects aimed at solving forefront problems in SMB in all three core areas. There is significant synergy between the three core areas to address increasingly complex and challenging problems. The SMB program seeks to sustain and enhance the general user program through excellent support, training and dissemination.

The SSRL SMB program is supported by the DOE Office of Biology and Environmental Research and the NIH Center for Research Resources and National Institute of General Medical Science.

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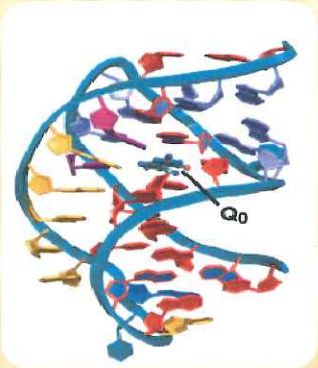
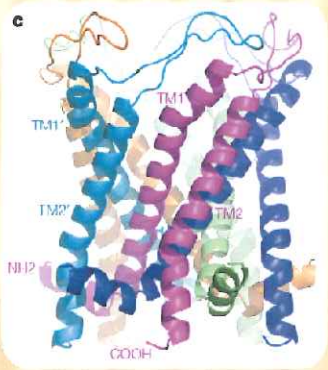
Macromolecular Crystallography

"three-dimensional structural information at the atomic level"

- The SMB Center has 6 MC stations of which 5 are on ID beam lines, providing high-intensity beams for MAD, SAD and monochromatic data collection, while 1 station is used for high throughput crystal screening
- All beam lines are fully automated with robotic sample changers, high-performance large-area CCD detectors, and intuitive data collection software (Blu-Ice)
- The SMB Center is based on a uniform approach with standardized instrumentation and software on all beam lines
- There is full remote access (run the experiment from your home institution) on all MC beam lines
- A high-brightness undulator ID beam line is fully developed for microcrystal diffraction, with a new state-of-the-art Dectris 6M PAD detector that provides advanced capabilities
- The SMB MC staff provide a strong training program for new and more experienced users
- For full information, see http://smb.slac.stanford.edu/public/index.shtml





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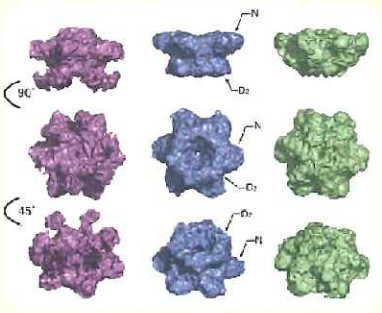
Small Angle X-ray Scattering & Diffraction

"no crystal required"

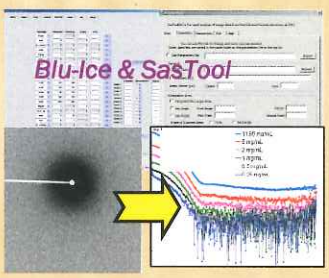


- X-ray scattering from solutions of macromolecules and assemblies provides 3D structures at nanometer resolution, helping interpret atomic resolution structures in the structural physiology context
- The SMB high throughput solution scattering system provides a structural tool for studying molecular interactions, complex structures as well as domain folding properties and structural flexibilities in solution

- Time-resolved instrumentation, down to milliseconds, to investigate molecules at work at tertiary to quaternary structure levels
- Lipid diffraction studies for screening newly synthesized lipids/detergents for membrane protein crystallization
- Fiber diffraction setup for amyloid, filamentous virus and natural fiber studies

- The SMB Center's Beam Line 4-2 is fully dedicated to non-crystalline x-ray scattering and diffraction studies in structural biology
- Fully configurable instrument for 3-3000 Å characteristic lengths
- New-generation CCD and silicon pixel array detectors
- Sample handling devices for high throughput, time-resolved and lipid/fiber studies

- Intuitive experiment control by Blu-Ice; SasTool for rapid data processing
- Structure determination pipeline under development
- Full specifications at http://www-ssrl.slac.stanford.edu/~saxs/



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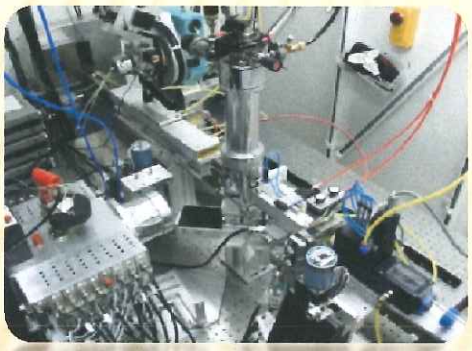
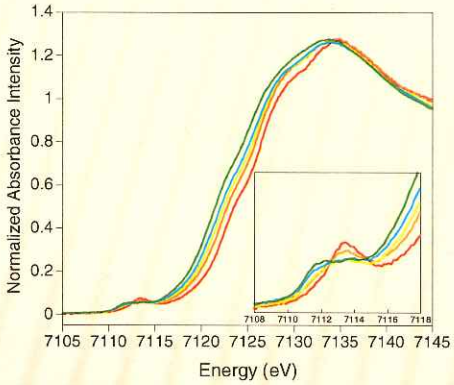
X-ray Absorption Spectroscopy

" electronic & material structure of metal sites"

- Metal ions have key roles in biological structure and function—from being active sites of many enzymes to shuttling electrons in key metabolic pathways, having roles in signaling pathways and being key elements of cancer chemotherapies and disease-related biological malfunctions. Structural information on metal sites in biomolecules can be obtained from x-ray absorption edge and extended fine structure (EXAFS) experiments (collectively called XAS)
- XAS spectromicroscopy provides spatially resolved information about metal distribution and speciation in materials of biological and medical relevance, including tissues





- The SSRL SMB Center has developed one of the largest dedicated and concentrated bioXAS activities in the world with optimized beam lines and specialized instrumentation, including high-performance detector arrays, software and data analysis capabilities for enabling such applications
- The Center provides two dedicated beam lines for solution XAS at metal hard x-ray energies and access to lower-energy beam lines for studies of ligands such as sulfur and chlorine. Separate facilities for microspectroscopy, from micron to mm spatial resolution and over a wide range of metals, are also developed and available
- Specialized instrumentation provides for investigation using XAS in combination with macromolecular crystallography
- For full information, see http://www-ssrl.slac.stanford.edu/smbxas/

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