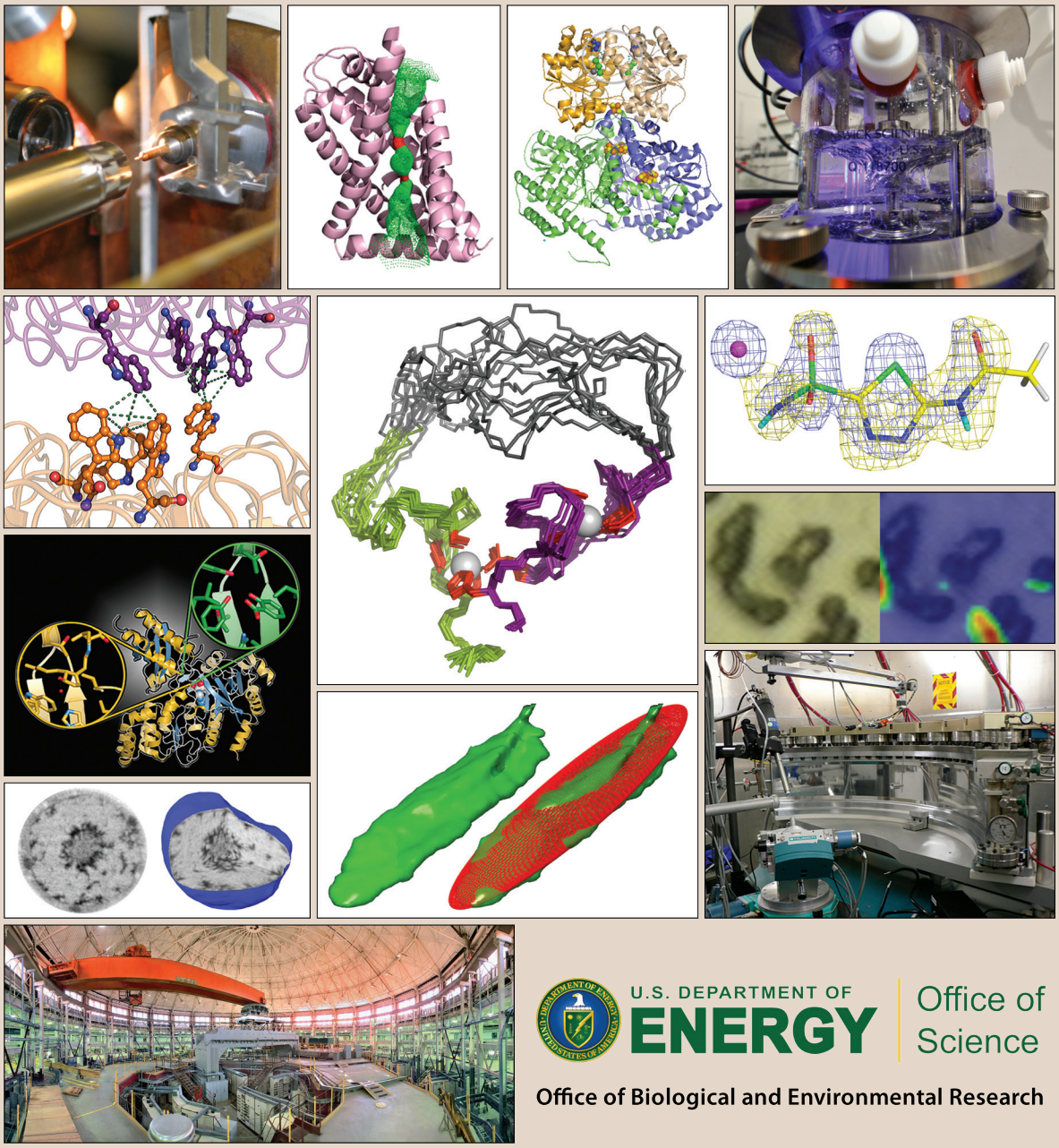
DOE User Facilities

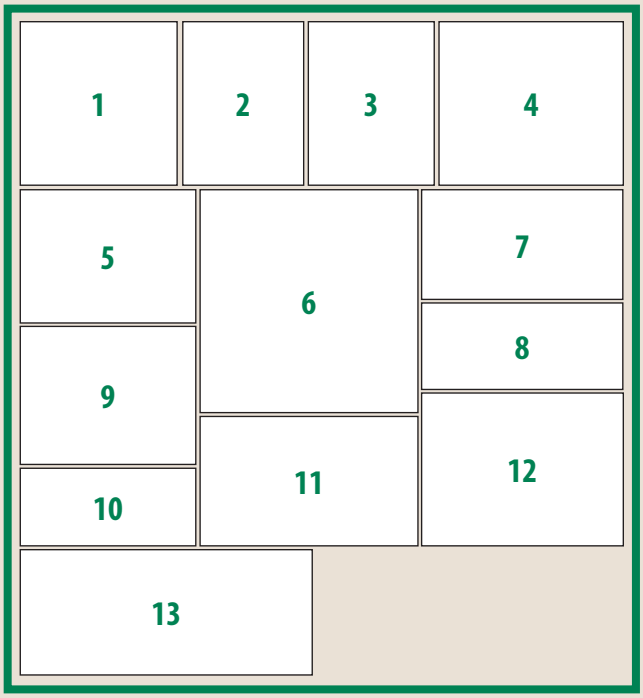
Advanced Technologies for Biology

Synchrotron and Neutron Beam Facilities Accelerating Biological Research



U.S. DEPARTMENT OF ENERGY | Office of Science

Office of Biological and Environmental Research



About the Cover

(1) Robot in action courtesy of SLAC National Accelerator Laboratory (SLAC). **(2)** Structure of a hydrosulfide ion channel protomer courtesy of Brookhaven National Laboratory. **(3)** Structure of a nitrogenase complex courtesy of Lawrence Berkeley National Laboratory (LBNL). **(4)** Bio-deuteration system courtesy of Oak Ridge National Laboratory (ORNL). **(5)** Structure of a plant UVR8 protein courtesy of The Scripps Research Institute. **(6)** Structure of the RNA ligase enzyme 10C courtesy of SLAC. **(7)** Stick representation of acetazolamide bound to its human target enzyme courtesy of Los Alamos National Laboratory (LANL). **(8)** Visual and infrared images of alkane biosynthesis courtesy of LBNL. **(9)** Structures of GH3 protein binding sites in *Arabidopsis thaliana* courtesy of Argonne National Laboratory. (**10)** Tomographic images of mouse olfactory neurons courtesy of LBNL. **(11)** Comparison of small-angle neutron scattering and cryo-electron microscopy models of *Chloroflexus aurantiacus* chlorosomes courtesy of ORNL. **(12)** Large helium-3 filled neutron detector courtesy of LANL. **(13)** Fourier transform infrared microscopy instrumentation at the Advanced Light Source courtesy of LBNL.

Advanced Technologies for Biology

DOE Synchrotron and Neutron Beam Facilities Accelerating Biological Research

genomicscience.energy.gov/userfacilities/structuralbio.shtml

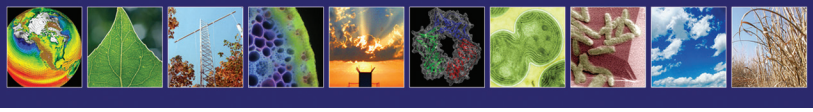
Synchrotron light sources and neutron facilities at the Department of Energy's (DOE) national laboratories enable understanding of the structure of matter down to the atomic or molecular level using approaches not possible with laboratory instrumentation. Synchrotron facilities produce intense beams of photons, from X-rays to infrared to terahertz radiation, while neutron facilities produce beams using particle accelerators or reactors. The beams are directed into experimental stations housing instruments configured for specific biological investigations.

This infrastructure provides user access to beamlines and instrumentation for high-resolution studies of biological organisms and molecules for all areas of research in the life sciences. Users are chosen through a peer-reviewed proposal process managed by each facility. Capabilities of and contact information for each station are described in the following pages. To find out more about what each experimental program offers, contact the facilities directly.

This activity is supported by DOE's Office of Biological and Environmental Research within the Office of Science and is closely coordinated with other federal agencies and private organizations.

Structural Biology Experimental Stations

Office of Biological and Environmental Research



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science.energy.gov/ber/

Structural Biology Center (SBC)

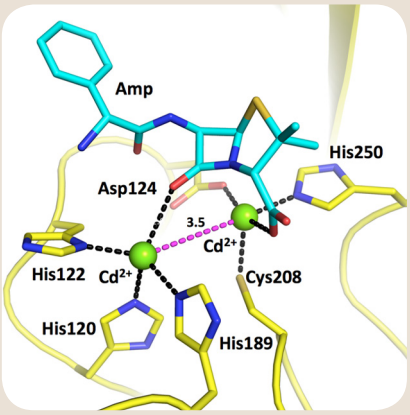
Location: *Advanced Photon Source, Argonne National Laboratory*
Website: *www.sbc.anl.gov*
Principal Investigator: *Andrzej Joachimiak, andrzejj@anl.gov, 630-252-3926*
User Contact: *Stephan Ginell, ginell@anl.gov, 630-252-3972*

SBC is a major protein crystallography research facility that enables the atomic-scale study of macromolecular systems using extremely small (micron-size) crystal samples. SBC's two experimental stations—the insertion-device (ID) beamline and the bending-magnet beamline—are among the most powerful and focused X-ray sources available for structural biology. Output is enhanced by on-axis sample viewing optics; easy access to minibeams (5, 10, and 20 µm) and variable beam sizes (25 to 250 µm); integration of computing and data-storage resources to accelerate data analysis and archiving; near real–time data interpretation, optimization of experimental parameters, and structure solution; and full integration of synchrotron hardware, detectors, crystal mounting robot, beamline software, and crystallographic software packages. These capabilities provide not just diffraction data, but also an interpretable electron density map and a macromolecular structure. For the 19-ID beamline, all these capabilities are available via remote access. SBC's beamlines can be used for a wide range of crystallographic experiments involving:

- Crystals of macromolecular assemblies with very large unit cells
- Crystals of membrane proteins
- Multi- or single-wavelength anomalous diffraction (MAD/SAD) phasing
- Small, weakly diffracting crystals
- Ultrahigh-resolution crystallography
- Cryo-crystallography

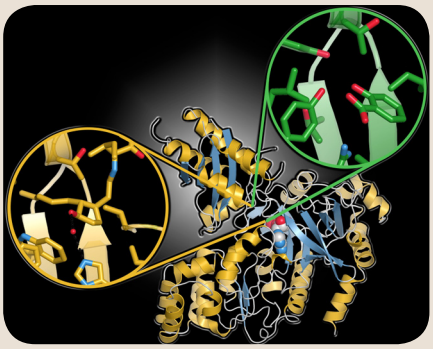
SBC User Highlights

Defeating NDM-1. The New Delhi metallo-beta-lactamase (NDM-1) gene makes multiple pathogenic microorganisms resistant to all known β-lactam antibiotics including carbapenems, which are considered as "last resort" antibiotics. The structural basis for NDM-1's promiscuous activity was revealed via a combination of crystallographic and biochemical studies and theoretical calculations that elucidated a pH-dependent set of pathways. Based on these findings, future active drugs can be predicted. [Kim, Y., et al. 2013. "NDM-1, the Ultimate Promiscuous Enzyme: Substrate Recognition and Catalytic Mechanism," *The FASEB Journal*, DOI: 10.1096/fj.12-224014.]



NDM-1 Structure. *NDM-1 structure in complex with two cadmium ions and antibiotic. Unhydrolyzed ampicillin is depicted in the active site. [Image credit: Argonne National Laboratory]*

Understanding Plant Hormones. Plants respond to developmental cues and environmental stresses by controlling both the level and activity of various hormones. A highly adaptable scaffold enables the evolution of promiscuous activity within the auxin-responsive GH3 enzyme family, leading to diversification of substrate specificity and evolution of metabolic control systems. Newly reported crystal structures provide a glimpse into substrate recognition and control of hormones involved in plant growth, development, and defense, enabling deeper understanding of plant metabolism intricacies. [Westfall, C. S., et al. 2012. "Structural Basis for Prereceptor Modulation of Plant Hormones by GH3 Proteins," *Science* **336**, 1708–11.]



Comparison of GH3 Protein Binding Sites. *In plants, GH3 proteins act as molecular on/off switches that control bioactive plant hormone formation by catalyzing the addition of specific amino acids to jasmonic acid, auxin, and benzoates. X-ray structures of GH3 proteins reveal a common three-dimensional fold but variability in the hormone binding site. This figure shows the variation in the jasmonic acid binding site of* Arabidopsis thaliana *GH3.11/JAR1 (gold) and the salicylic acid binding site of* A. thaliana *GH3.12/PBS3 (green). [Image credit: Argonne National Laboratory]*

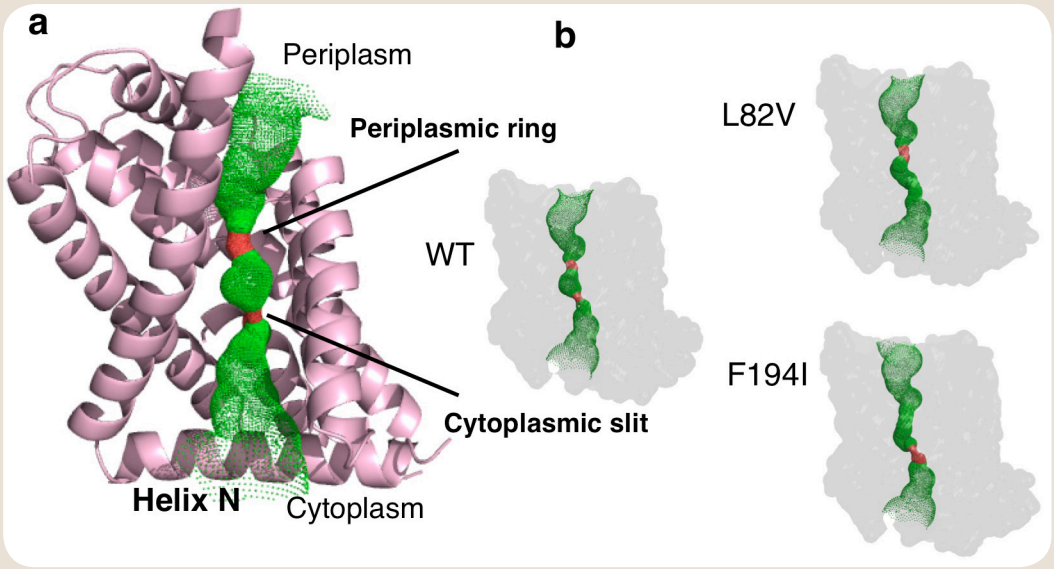
Macromolecular Crystallography Research Resource (PXRR)

Location: *National Synchrotron Light Source, Brookhaven National Laboratory*
Website: *www.px.nsls.bnl.gov*
Principal Investigator: *Robert Sweet, sweet@bnl.gov, 631-344-3401*

PXRR provides facilities and support for macromolecular structure determination by synchrotron X-ray diffraction. Five PXRR beamlines, two of which are high-brightness undulators, enable highly efficient structure determination by every available crystallographic technique. Complementary spectroscopic methods, including optical absorption spectroscopy and Raman spectroscopy, enable simultaneous measurements of the same sample under nearly identical experimental conditions. PXRR also offers a popular mail-in crystallography program, builds new facilities, advances automation, and provides user support for a limited program in small-angle X-ray scattering on macromolecule solutions.

PXRR User Highlight

Understanding the Roles Played by Hydrosulfide Membrane Channel and Its Relatives in Living Systems. The hydrosulfide ion (HS^-), a critical element in the origin of life on Earth, is important in physiology and cellular signaling. The HS^- species is also the terminal product when an anaerobic bacterium derives its oxidative power from sulfate instead of oxygen. A recent study conducted at PXRR beamlines revealed the structure of the hydrosulfide ion channel (HSC), a membrane-pore molecule, elucidating how HS^- is able to escape from pathogenic *Clostridium difficile* cells. In the same protein family, the formate channel (FocA), which has a fold similar to HSC, has been shown to play two other roles related to bioenergy and environmental science. In the first case, hydrogen gas production in *Escherichia coli* depends on the selective decomposition of formate, whose concentration depends on FocA. In the second, when *Euglena* experiences long-term chronic exposure to cadmium ions, it overexpresses a FocA protein. This protein has been proposed as a marker for long-lasting cadmium pollution in water.



Nature of Selectivity Filter in HSC's Ion-Permeation Pathway. **(a)** *Structure of an HSC protomer overlaid with the software-predicted inner pore surface, colored to indicate water permeability (green, permeable; red, impermeable).* **(b)** *Certain mutations, Leu 82Val and Phe194Ile, increase the pore diameter relative to the wild type (WT), as revealed by two more crystal structures. [Image reprinted by permission from Nature Publishing Group: Czyzewski, B. K., and D.-N. Wang. 2012. "Identification and Characterization of a Bacterial Hydrosulphide Ion Channel,"* Nature ***483****, 494–97.]*

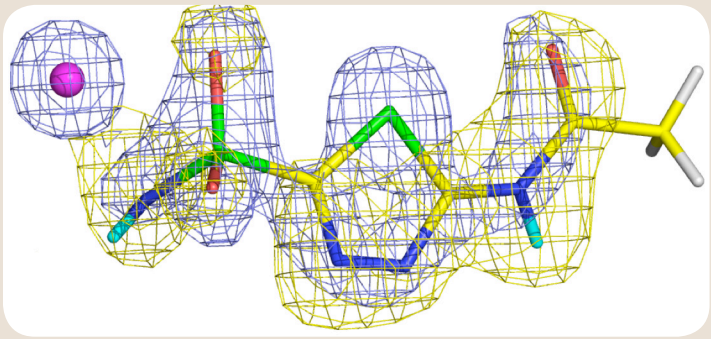
Protein Crystallography Station (PCS)

Location: *Los Alamos Neutron Science Center, Los Alamos National Laboratory*
Website: *lansce.lanl.gov/lujan/instruments/PCS.shtml*
Principal Investigator: *Cliff Unkefer, cju@lanl.gov, 505-665-2560*
User Contact: *Zoë Fisher, zfisher@lanl.gov, 505-665-4105*

PCS is a high-performance neutron beamline that forms the core of a capability for investigating the structure and dynamics of proteins, biological polymers, hydrogen bonding, drug binding, and membranes. Neutron diffraction is a powerful technique for locating hydrogen atoms (which can be hard to detect using X-rays) and thus can provide unique information about how biological macromolecules function and interact with each other and smaller molecules. PCS users have access to neutron beam time, deuteration facilities, technologies for studying protein expression and substrate synthesis with stable isotopes, a purification and crystallization laboratory, and software and support for data reduction and structure analysis. A recently acquired Rigaku HighFlux X-ray system enables users to collect X-ray data at room temperature from the same samples used for neutron diffraction. The PCS beamline exploits the pulsed nature of spallation neutrons and a helium-3 filled detector to collect time-of-flight Laue diffraction patterns. Data collection is efficient and has good signal to noise using all available neutrons [with a wavelength range of about 0.7 to 7.0 angstroms (Å)] in the pulsed white beam.

PCS User Highlights

Neutrons Reveal Atomic Details of Drug Binding. Joint X-ray and neutron crystallography was used to show how human carbonic anhydrase II (HCA II), from an enzyme family found in all life forms, binds acetazolamide (AZM), a clinically used carbonic anhydrase inhibitor. AZM is a sulfonamide drug used to treat a wide range of disorders, such as glaucoma, epilepsy, and altitude sickness. Results of crystallography experiments, which located the hydrogen (H) atoms at the binding site, clearly showed AZM's ionization state and how drug binding displaces key active-site water molecules in HCA. The experiments also revealed H bonding interactions between the drug and enzyme and showed the role of certain waters in drug binding. The results demonstrate that neutron beams provide crucial and specific information that will assist in structure-based drug design applications. [Fisher, S. Z., et al. 2012. "Neutron Diffraction of Acetazolamide-Bound Human Carbonic Anhydrase II Reveals Atomic Details of Drug Binding," *Journal of the American Chemical Society* **134**, 14726–729.]



Complementarity of Neutron and X-Ray Data. *Ball-and-stick figure of AZM and zinc (magenta sphere) in the HCA II active site. Heavier sulfur atoms (red) are clearly visible in the electron density map (blue; contoured at 2.0 σ), while light deuterium atoms (cyan) are visible in the nuclear density map (yellow; contoured at 1.5 σ). [Image credit: Los Alamos National Laboratory]*

Ultrahigh-Resolution Neutron Diffraction of Crambin Protein. About half of all atoms in a protein are H atoms. Unfortunately, H atoms are difficult to visualize in a three-dimensional context, and, for the vast majority of crystal structures, their locations are inferred from the position of their neighboring heavy atoms [carbon (C), nitrogen, oxygen (O), and sulfur]. In a recent study, scientists determined the highest-resolution neutron structure of a protein to date—an ultrahigh resolution of 1.1 Å. The structure was determined from an H/deuterium exchanged crambin crystal. One of the most striking observations was the determination of 94.9% of all H atom positions in the protein, with unambiguous resolution in nuclear density maps. A number of unconventional interactions were clearly defined, including a potential O—H…π interaction between a water molecule and the aromatic ring of residue Y44, as well as a number of potential C—H…O hydrogen bonds. H bonding networks that are unclear in the 0.85 Å ultrahigh-resolution X-ray structure can be resolved by accurate orientation of water molecules. [Chen, J. C.-H., et al. 2012. "Direct Observation of Hydrogen Atom Dynamics and Interactions by Ultrahigh Resolution Neutron Protein Crystallography," *Proceedings of the National Academy of Sciences USA* **109**, 15301–306.]

Structural Molecular Biology (SMB) Center

Location: *Stanford Synchrotron Radiation Lightsource, SLAC National Accelerator Laboratory*

Website: *www-ssrl.slac.stanford.edu/science/smbgroup.html*

Principal Investigators: *Britt Hedman, hedman@slac.stanford.edu, 650-926-3052; Keith Hodgson, hodgson@slac.stanford.edu, 650-926-3153*

User Contact: *Lisa Dunn, lisa@slac.stanford.edu, 650-926-2087*

The SMB Center provides beamline facilities and scientific support for biological studies that use macromolecular crystallography (MC), X-ray absorption spectroscopy (XAS), and small-angle X-ray scattering and diffraction (SAXS) to address and solve challenging problems in structural biology relevant to energy, environmental, and biomedical applications. The SMB Center also works with staff from SLAC's X-ray free-electron laser (Linac Coherent Light Source) to develop innovative new approaches for studying biomolecules, including nanocrystallography and femtosecond time-resolved X-ray spectroscopy.

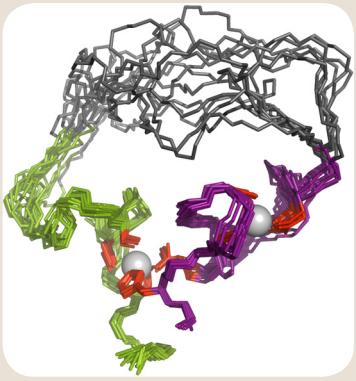
MC determines the three-dimensional (3D) structure of biological molecules at atomic resolution (<1 Å), thereby helping elucidate detailed mechanisms by which macromolecules function in living cells and organisms. The five MC stations provide high-intensity beams for multi- or single-wavelength anomalous diffraction (MAD/SAD) and monochromatic data collection, all with highly automated robotics-based, high-throughput crystal screening and data collection. All MC beamlines provide remote-access control, enabling users to perform measurements from their home labs. A microbeam undulator station with a large-area pixel array detector (PAD) enables studies of micron-sized crystals associated with the most challenging structural biology problems (e.g., large macromolecular complexes with large unit cells, small "micro" crystals, and radiation- and mechanically sensitive samples).

XAS is used to obtain structural and electronic information on metal sites in biomolecules. The foci at the optimized XAS beamlines and instrumentation are on dilute metalloprotein XAS, microbeam imaging XAS, low-Z XAS (for studies of ligands such as sulfur and chlorine), polarized single-crystal XAS, and X-ray emission-based studies. The range of XAS equipment includes advanced solid-state array X-ray fluorescence detector systems, liquid-helium cryostats, and Kirkpatrick-Baez optic micro-XAS instrumentation, as well as a range of sample environments. The SMB Center provides software for flexible data acquisition and on- and off-line data analysis.

SAXS features a state-of-the-art beamline and experimental facilities for solution scattering, lipid membrane diffraction, fiber diffraction, and single-crystal diffraction at scattering angles ranging from microns to a few angstroms. These techniques, enabling structural studies of biological macromolecules and assemblies in physiological or near-physiological conditions, complement high-resolution MC structural techniques. Besides providing automated, high-throughput experimental facilities for equilibrium solution studies, the SAXS beamline maintains premier experimental facilities for time-resolved studies on time scales of milliseconds and longer.

SMB Center User Highlight

Path Toward Efficient Biocatalysts. A major research challenge in enabling large-scale biofuel production is developing enzymes that are highly efficient in converting biomass components into usable fuels. The 3D structures of many enzymes have been resolved, but much less is known about how small changes in their composition can alter structure, produce flexibility, and control catalytic efficiency. New research provides structural evidence for the *in vitro* conversion of a protein with no catalytic function into a highly efficient enzyme that is an effective catalyst for linking RNA molecules. XAS was used to determine the accurate chemical environment around each of the two zinc atoms in the synthesized enzyme's active site, leading to an explanation of why it had developed the catalytic activity.



Structure of an *In Vitro* Synthesized Enzyme. *The 3D nuclear magnetic resonance structure of the RNA ligase enzyme 10C. Active sites are illustrated as zinc atoms in silver surrounded by their coordinating amino acids. [Image reprinted by permission from Nature Publishing Group: Chao, F.-A., et al. 2013. "Structure and Dynamics of a Primordial Catalytic Fold Generated by* In Vitro *Evolution,"* Nature Chemical Biology ***9****, 81–83.]*

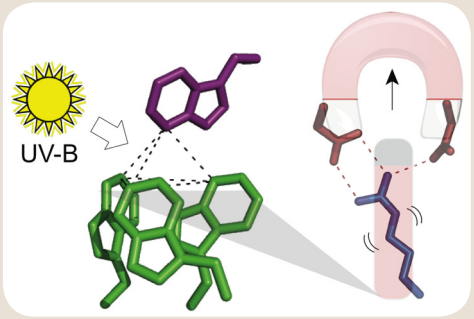
Structurally Integrated Biology for the Life Sciences (SIBYLS) Beamline

Location: *Advanced Light Source, Lawrence Berkeley National Laboratory*
Website: *sibyls.als.lbl.gov*
Principal Investigator: *John Tainer, jatainer@lbl.gov, 510-486-4158*
User Contact: *Jane Tanamachi, jtanamachi@lbl.gov, 510-495-2404*

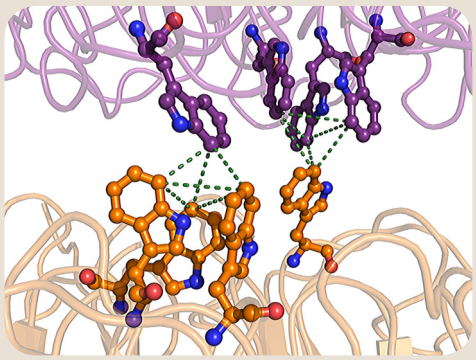
The SIBYLS beamline is a dual endstation synchrotron beamline combining macromolecular crystallography (MX) with small-angle X-ray scattering (SAXS). MX produces high-resolution structural information from biological molecules, and the high-throughput SAXS pipeline enables the same biological systems to be imaged in aqueous solution, closer to their natural state. Combining SAXS results with atomic-resolution structures provides detailed characterizations of mass, radius, conformation, assembly, and shape changes associated with protein folding and functions. SAXS also can resolve ambiguities of crystallography by showing the most likely possible structures.

SIBYLS User Highlight

Revealing the Secrets of an Ultraviolet-Sensing Protein. Ultraviolet (UV) radiation from the sun can damage proteins and DNA inside cells, but plants have evolved some powerful adaptive defenses. A plant photoreceptor known as UVR8 triggers regulatory changes in gene expression in response to UV-B light via an unknown mechanism. SIBYL's crystallographic and SAXS capabilities have enabled researchers to determine UVR8's molecular architecture and its mechanisms for UV-B perception and signal transduction. Beta-propeller subunits form a remarkable, tryptophan-dominated dimer interface stitched together by a complex salt-bridge network. Salt-bridging arginines flank the excitonically coupled cross-dimer tryptophan "pyramid" responsible for UV-B sensing. Photoreception reversibly disrupts salt bridges, triggering dimer dissociation and signal initiation. This ancient UVR8 system, which may have been critical for plants to leave the ocean and thrive on land, is fundamentally different from other known photoreceptors in its use of standard tryptophan side chains instead of specialized chromophores for detecting light. Mutation of a single tryptophan to phenylalanine retunes the photoreceptor to detect UV-C wavelengths. These results establish how UVR8 functions as a photoreceptor without a prosthetic chromophore to promote plant development and survival in sunlight. This research, featured on the March 23, 2012, cover of *Science*, has furthered fundamental understanding of UV sensing in plants. Moreover, the simplicity of UVR8 light-controlled switching may enable this unique photochemistry to be harnessed for new biotechnological applications. [Images above left and at top reprinted by permission from the American Association for the Advancement of Science: Christie, J. M., et al. 2012. "Plant UVR8 Photoreceptor Senses UV-B by Tryptophan-Mediated Disruption of Cross-Dimer Salt Bridges," *Science* **335**, 1492–96.]



Model for UV-B Photoreception by UVR8. *UV-B sensing by the tryptophan pyramid triggers dimer dissociation by disrupting salt bridges.*



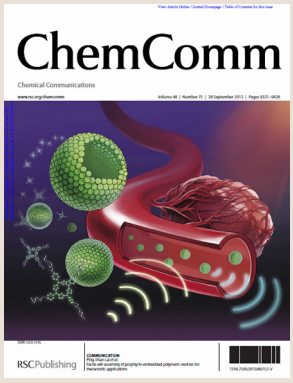
High-Resolution Structure of Plant UVR8 Protein. *Excitation of tryptophan residues (orange and purple sticks) by UV-B radiation results in the donation of electrons from the aromatic clusters to nearby arginine residues, leading to charge neutralization and dimer dissociation. [Image credit: The Scripps Research Institute]*

Center for Structural Molecular Biology (CSMB)

Location: *High Flux Isotope Reactor and Spallation Neutron Source, Oak Ridge National Laboratory*
Website: *www.csmb.ornl.gov*
Principal Investigator: *Paul Langan, langanpa@ornl.gov, 865-576-0666*
User Contact: *csmb@ornl.gov, 865-576-1865*

CSMB is dedicated to developing instrumentation and methods for determining the structure, function, and dynamics of complex biological systems. CSMB's suite of tools includes a small-angle neutron scattering (SANS) facility for studying biological samples under physiological (or physiologically relevant) and industrial processing conditions, small- and wide-angle X-ray scattering instruments, a bio-deuteration laboratory for *in vivo* isotopic labeling, and advanced computational resources for modeling proteins and protein complexes. Deuterium-labeling techniques enable scientists to selectively highlight and map chemically distinct components of larger protein-protein, protein-lipid, or protein–nucleic acid complexes and, moreover, to follow their conformational changes and assembly or disassembly processes in solution on biologically relevant time scales. These capabilities are helping researchers understand how macromolecular systems are formed and interact with other systems in living cells—ultimately bridging the information gap between cellular function and the molecular mechanisms that drive it.

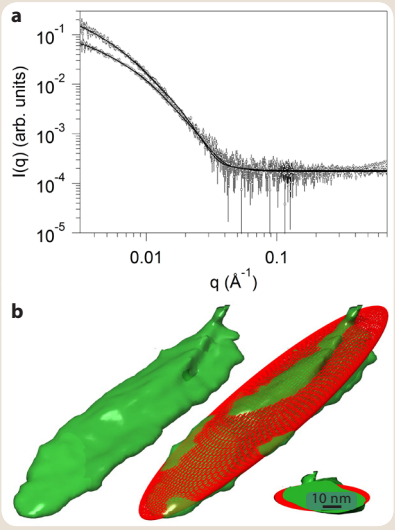
CSMB User Highlights



Polymeric Vesicles for Theranostic Applications. Nanosized vesicles have potential as drug carriers or diagnostic agents because of their ability to entrap and release molecules into their core region in a controlled way. An easy and robust route was developed to fabricate uniform porphysomes consisting of porphyrin-polylactide (PPLA) conjugates that can overcome the obstacles faced with previous systems. The Bio-SANS beamline was used to characterize these new particles and identify the hollow shell structure characteristic of vesicles. These PPLA porphysomes may have potential as a new and stable platform for drug delivery and ultrasonic imaging, especially in cancer theranostics. This research was featured on the Sept. 28, 2012, cover of *Chemical Communications*. [Image reprinted by permission from The Royal Society of Chemistry: Hsu, C.-Y., M.-P. Nieh, and P.-S. Lai. 2012. "Facile Self-Assembly of Porphyrin-Embedded Polymeric Vesicles for Theranostic Applications," *Chemical Communications* **48**, 9343–45.]

Toward Bio-Hybrid Solar Conversion Devices. Chlorosomes make up a highly specialized supramolecular light-harvesting antenna complex found in green photosynthetic bacteria. They are of interest in the development of synthetic devices for solar harvesting and conversion because the organization of bacteriochlorophylls in the chlorosome provides a mechanism for highly efficient light collection and energy funneling to the photosynthetic reaction centers. Researchers investigated sol-gel chemistry as an approach to entrap and stabilize chlorosomes isolated from *Chloroflexus aurantiacus*. The Bio-SANS beamline enabled the characterization of the sol-gel matrix properties, as well as the size, shape, and aggregation state of the entrapped chlorosomes. This approach offers new possibilities for developing artificial solar-harvesting and energy-conversion devices based on naturally occurring photosynthetic systems.

Small-Angle Scattering from Gel-Entrapped Chlorosomes. (a) *SANS intensity profiles from chlorosomes entrapped in different sol-gel formulations and calculated scattering profiles from model ellipsoid forms (solid lines).* **(b)** *Comparison of the* C. aurantiacus *chlorosome reconstructed from the electron density map*[1] *(solid) and the model ellipsoid form (mesh) calculated from fitting the scattering of the sol-gel entrapped chlorosomes. [*[1]*Pšenčik, J., et al. 2009. "Structure of Chlorosomes from the Green Filamentous Bacterium* Chloroflexus aurantiacus*," Journal of Bacteriology* ***191****, 6701–08. Image reprinted by permission from The Royal Society of Chemistry: O'Dell, W. B., et al. 2012. "Sol-Gel Entrapped Light-Harvesting Antennas: Immobilization and Stabilization of Chlorosomes for Energy Harvesting," Journal of Materials Chemistry* ***22****, 22582–591.]*



Advanced Biological and Environmental X-Ray Spectroscopy (ABEX)

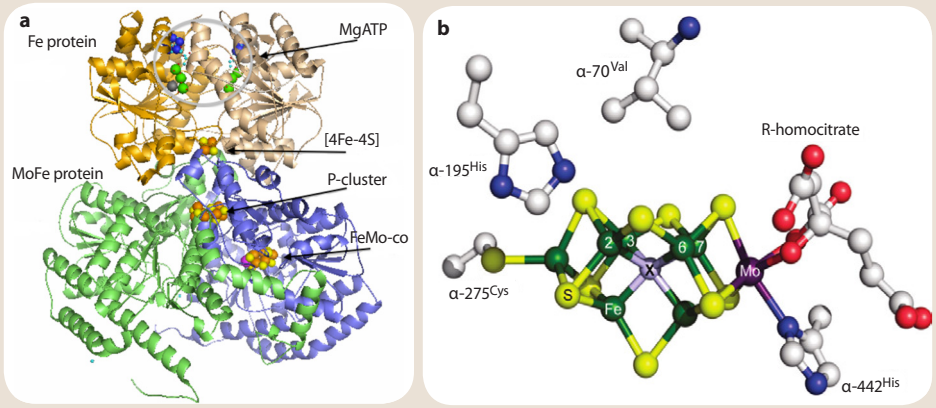
Location: *Advanced Light Source, Lawrence Berkeley National Laboratory*
Website: *abex.lbl.gov*
Principal Investigator: *Stephen Cramer, spcramer@lbl.gov, 510-486-4720*

ABEX is a user resource at the Advanced Light Source (ALS) that enables X-ray spectroscopic characterization of complex biological and environmental systems using soft X-ray absorption spectroscopy (XAS) and X-ray magnetic circular dichroism (XMCD). These spectroscopies exploit the availability of high brightness, circularly polarized soft X-rays at ALS and offer unique advantages in analyzing the detailed electronic and magnetic structure of biological metal sites. ABEX research also develops spectroscopies, such as nuclear resonance vibrational spectroscopy (NRVS), that require high-energy storage rings.

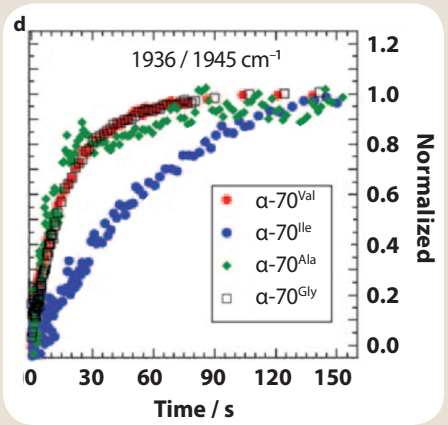
An ABEX instrument development program improves both the sensitivity and ease of use of its endstations for biological and environmental samples. A spectroscopy support laboratory on the ALS mezzanine provides access to electron paramagnetic resonance (EPR), infrared (IR), and resonance Raman instruments, enabling essential control measurements on samples studied by X-ray techniques.

ABEX User Highlight

Revealing the Molecular Underpinnings of a Key Enzyme. As a major component of the biological nitrogen cycle, the bacterial enzyme nitrogenase (N_2ase) converts nitrogen from air into ammonia, thereby making it accessible to plant life. The enzyme achieves this feat at a metal-sulfur cluster called the FeMo cofactor by a mechanism that still is not well understood. Research to better understand how metals and metal clusters interact with nitrogen and reduced nitrogen species is exploiting the soft X-ray region via transition metal L-edge and nitrogen K-edge spectroscopy. Complementary studies have used the stopped-flow IR system in the mezzanine spectroscopy suite to probe time-dependent binding of the carbon monoxide molecule CO to N_2ase.



Molecular Structures. **(a)** *Nitrogenase complex with the Fe protein bound to the MoFe protein.* **(b)** *Close-up of the active site FeMo cofactor.* **(c)** *Comparison of the native enzyme site with a mutant having the larger isoleucine side chain.*



Spectroscopy Results. **(d)** *Comparison of time courses of CO binding observed using 1936 cm^{-1} (α-70^{Val}, α-70^{Ile}, α-70^{Ala}) or 1945 cm^{-1} (α-70^{Gly}). Intensities are normalized at 150 s. [Image credits: Lawrence Berkeley National Laboratory. Images (c) and (d) reprinted by permission from John Wiley and Sons: Yang, Z.-Y., et al. 2011. "Steric Control of the Hi-CO MoFe Nitrogenase Complex Revealed by Stopped-Flow Infrared Spectroscopy,"* Angewandte Chemie International Edition ***50****, 272–75.]*

Berkeley Synchrotron Infrared Structural Biology (BSISB) Program

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Website: *infrared.als.lbl.gov*
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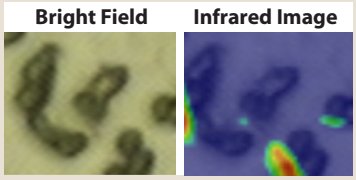
User Contact: *Theresa Pollard, tapollard@lbl.gov, 510-486-6740*

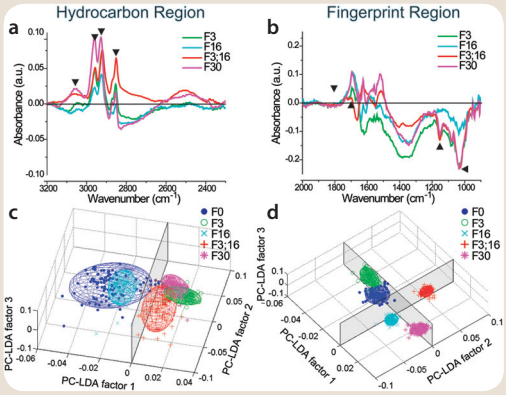
BSISB provides facilities and training support for characterizing cellular chemistry and function by synchrotron radiation–based Fourier transform infrared (SR-FTIR) spectromicroscopy. Other complementary microscopy and spectroscopic imaging methods include fluorescence microscopy and simultaneous optical hyperspectral sample imaging. Aqueous environments hinder SR-FTIR's sensitivity to bacterial activity, but BSISB's integrated *in situ* open-channel microfluidic culturing systems circumvent the water-absorption barrier while allowing cells to maintain their functions. These technological systems enable real-time chemical imaging of bacterial activities in biofilms and facilitate comprehensive understanding of structural and functional dynamics in a wide range of microbial systems. BSISB continues to build new chemical imaging capabilities, advance user-specific microfluidic systems and automation, and develop new software for accelerating data analysis.

BSISB User Highlights

Improving Cyanobacterial Synthesis of Alkanes. Cyanobacteria are important photoautotrophic organisms that can capture carbon dioxide and convert it into a suite of organic compounds such as high-density liquid fuels. Using SR-FTIR as a high-throughput imaging method, researchers tracked metabolic phenotypes of *Synechocystis* 6803, which was engineered for enhanced production of alkanes and free fatty acids. Multivariate SR-FTIR data analysis revealed biochemical shifts in the engineered cells. These results demonstrate the applicability of SR-FTIR spectromicroscopy for rapid metabolic screening and phenotyping of live individual cells.

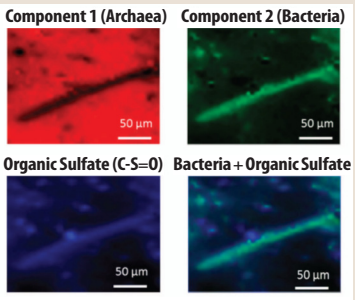


Alkane Biosynthesis. *Comparison of visible and infrared images shows localized production of alkanes adhering to a cyanobacterium's outer cell surface (represented by rainbow-colored speckles; red = maximum).*



Single-Cell Metabolic Fingerprinting of Four Engineered *Synechocystis* 6803 Strains. (a) *and* **(b)** *Mean difference spectrum between engineered strains and F0 control in* **(a)** *hydrocarbon region (3100–2800 cm^{-1}) and* **(b)** *biomolecular fingerprint region.* **(c)** *and* **(d)** *Exploratory three-dimensional analysis of principal components and linear discriminants of strains in the two spectral regions. [Images reprinted by permission from Elsevier: Hu, P., et al. 2013. "Metabolic Phenotyping of the Cyanobacterium* Synechocystis *6803 Engineered for Production of Alkanes and Free Fatty Acids,"* Applied Energy **102**, *850–59.]*

Biochemistry of a Mysterious Microbial Community. Subsurface microbial communities are highly diverse and comprise an enormous fraction of Earth's biomass, but lack of knowledge related to their ecological function makes understanding their ongoing biogeochemical processes difficult. Using SR-FTIR to probe biofilm samples from a cold subsurface sulfur spring, researchers recently determined how bacteria and archaea work together to influence global sulfur and carbon cycles. By revealing the bright spectral signals of alkylic and methyl groups, together with sulfur functional groups, SR-FTIR unambiguously identified the bacteria's sulfur-oxidizing metabolic activity. Archaeal cells, which were the dominant population in this biofilm, showed no such activity, suggesting a thriving mutual metabolism of archaea and bacteria.



Infrared Images of Bacteria in Archaea-Dominated Biofilm. *Relative concentration images (220 µm by 180 µm) of archaea (red) and bacteria (green) recovered by multiple curve resolution analysis and chemical distribution maps of organic sulfate (blue). Merging the relative bacterial concentration image (green) with the organic sulfate distribution map (blue) reveals the co-localization of bacteria and organic sulfate. [Images reprinted by permission from Nature Publishing Group: Probst, A. J., et al. 2013. "Tackling the Minority: Sulfate-Reducing Bacteria in an Archaea-Dominated Subsurface Biofilm,"* The ISME Journal **7**, *635–51.]*

National Center for X-Ray Tomography (NCXT)

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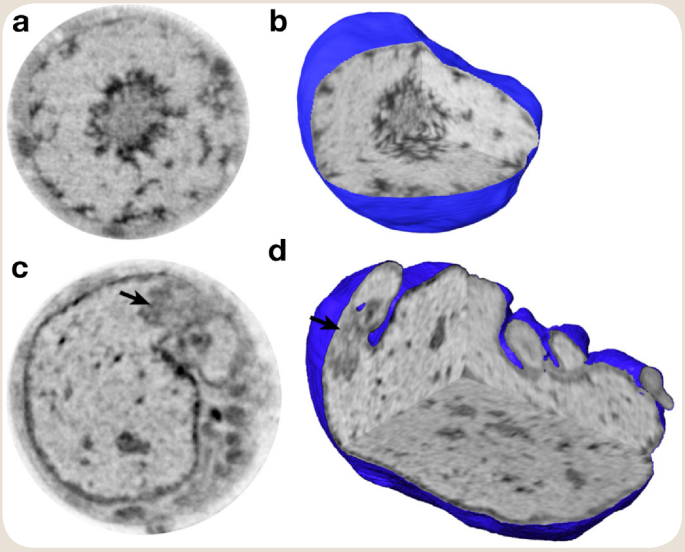
NCXT is leading the development of soft X-ray tomography (SXT) as a technique for imaging fully hydrated biological specimens at high, three-dimensional (3D) spatial resolution. SXT has several distinct advantages over light- and electron-based microscopies and, as a result, can contribute unique insights on cell structure and behavior. Soft X-rays penetrate biological materials much more deeply than electrons, allowing cells up to 15 µm thick to be imaged intact. SXT image contrast is generated by differential X-ray absorption by biomolecules, meaning that cells advantageously do not require exposure to staining or other potentially damaging procedures prior to being imaged. Consequently, SXT produces high-resolution specimen views that are in a close-to-native state.

SXT's utility has been increased dramatically by the concomitant development of high-aperture cryogenic fluorescence tomography (CFT). Cryo-preserved cells, or populations of cells, can now be imaged serially by two disparate tomographic methods. The combination of CFT and SXT allows labeled molecules to be positioned accurately and viewed directly in the context of a high-resolution, quantitative 3D tomographic cell reconstruction.

NCXT User Highlight

Nuclear Architecture and Gene Expression. Gene positioning and regulation of nuclear architecture are thought to influence gene expression. SXT imaging shows that silent olfactory receptor (OR) genes from different chromosomes in mouse olfactory neurons converge in a small number of heterochromatic foci. These foci are OR exclusive and form in a differentiation-dependent manner specific to cell type. OR gene aggregation is developmentally synchronous with the downregulation of the lamin B receptor (LBR) and can be reversed by ectopic LBR expression in mature olfactory neurons. LBR-induced reorganization of nuclear architecture and disruption of OR aggregates perturbs the singularity of OR transcription and disrupts the olfactory neurons' targeting specificity. These observations indicate spatial sequestering of heterochromatinized OR family members as a basis of monogenic and monoallelic gene expression.

SXT Demonstrates Chromatin Decompaction and Nuclear Reorganization upon LBR Expression. (a) *Orthoslice from the tomographic reconstruction of a GFP+ neuron from an OMP-IRES-GFP mouse. Pericentromeric heterochromatin (PH) surrounded by condensed olfactory sensory neuron (OSN)–specific foci can be seen in the nucleus center; only small amounts of heterochromatin are tethered to the nuclear envelope.* **(b)** *Segmented nucleus (blue) seen in a 3D cutaway view with three orthogonal orthoslices shows that the PH is in the nucleus center and the nuclear envelope is not folded.* **(c)** *Orthoslice from an OMP-IRES-tTA; tetO LBR-IRES-GFP mouse. Dark particles surrounding the PH core in the control OSN nucleus are not present in the LBR-expressing nucleus. PH (arrow) is positioned just beneath the highly folded nuclear envelope upon LBR expression. The nuclear envelope is thicker, likely due to LBR presence and recruitment of heterochromatin.* **(d)** *3D cutaway view showing the increased nuclear volume and marked folding of the nuclear envelope. [Images reprinted by permission from Elsevier: Clowney, E. J., et al. 2012. "Nuclear Aggregation of Olfactory Receptor Genes Governs Their Monogenic Expression,"* Cell ***151****, 724–37.]*



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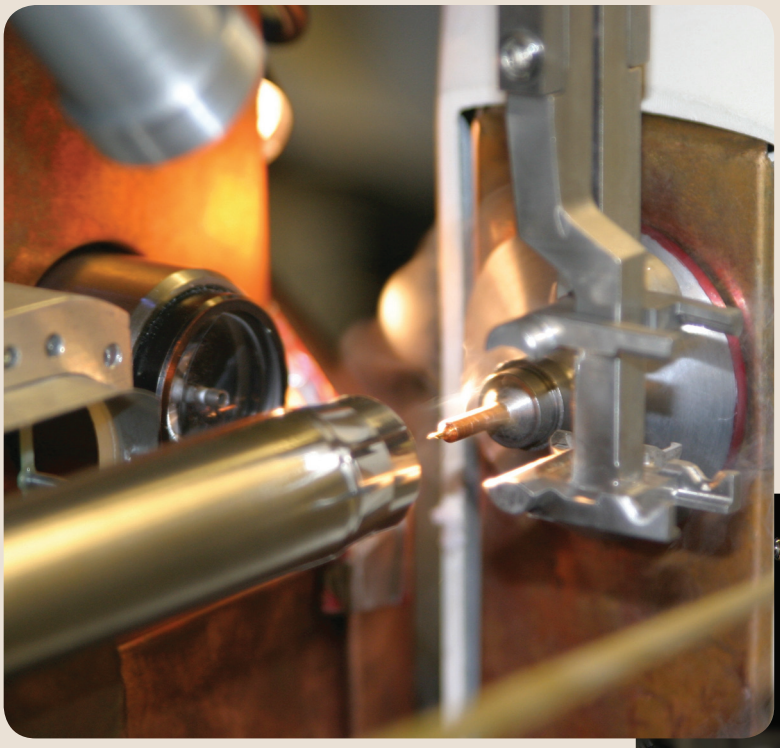
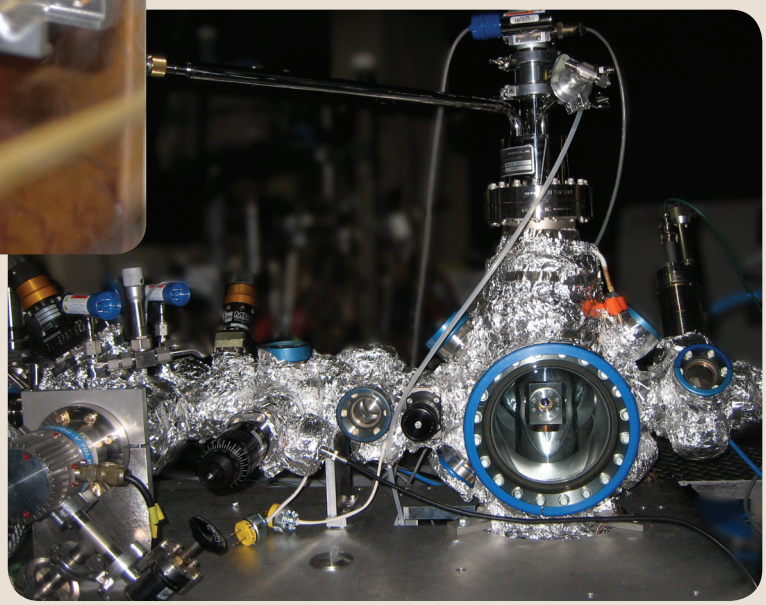


Robot in action at Stanford Synchrotron Radiation Lightsource. [Image credit: SLAC National Accelerator Laboratory]



A helium atmosphere soft X-ray chamber at the Advanced Biological and Environmental X-Ray Spectroscopy experimental station at the Advanced Light Source. [Image credit: Lawrence Berkeley National Laboratory]

March 2013