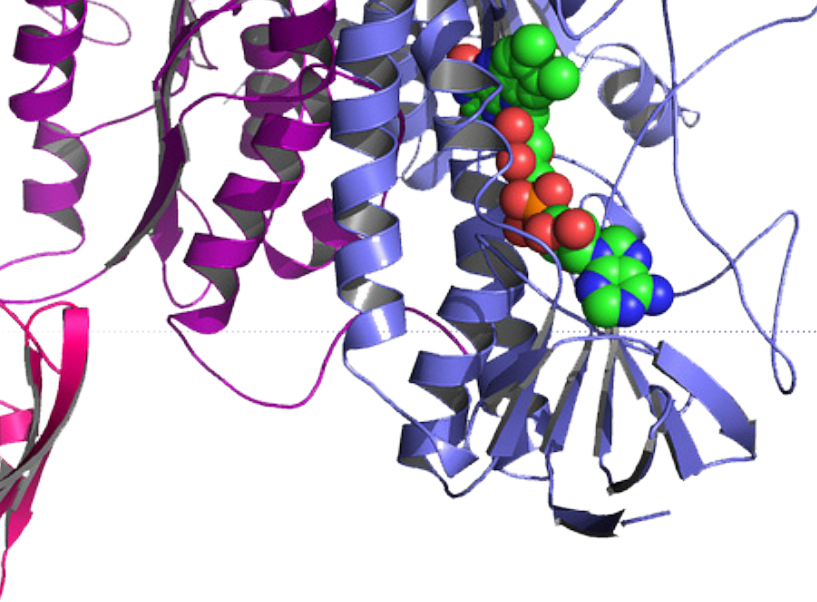


A scientific user facility
for macromolecular
crystallography

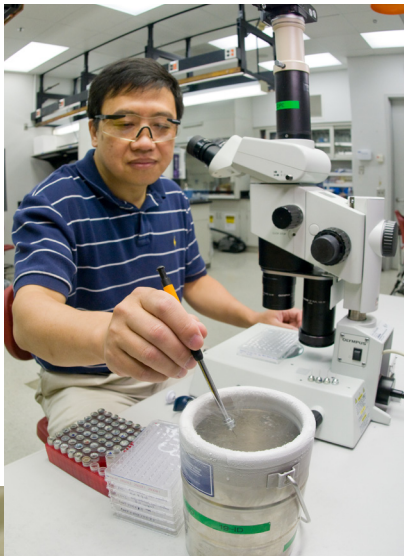
Structural Biology Center

BEAMLINES AT THE
ADVANCED PHOTON SOURCE

The Structural Biology Center enables the atomic-scale study of macromolecular systems using very small crystal samples. It also offers the most efficient data collection and structure determination systems for protein crystallography worldwide. Thanks to recent advances with larger, faster X-ray detectors and automation of laboratory processes for expressing proteins and growing crystals, the time required to solve molecular structures has been greatly reduced. Research that not long ago took months or years may now take only hours. In addition, one need not be a macromolecular crystallographer to take advantage of these facilities; our experienced beamline staff are available to guide even novice users through the entire process.



An optimized approach to synchrotron data collection



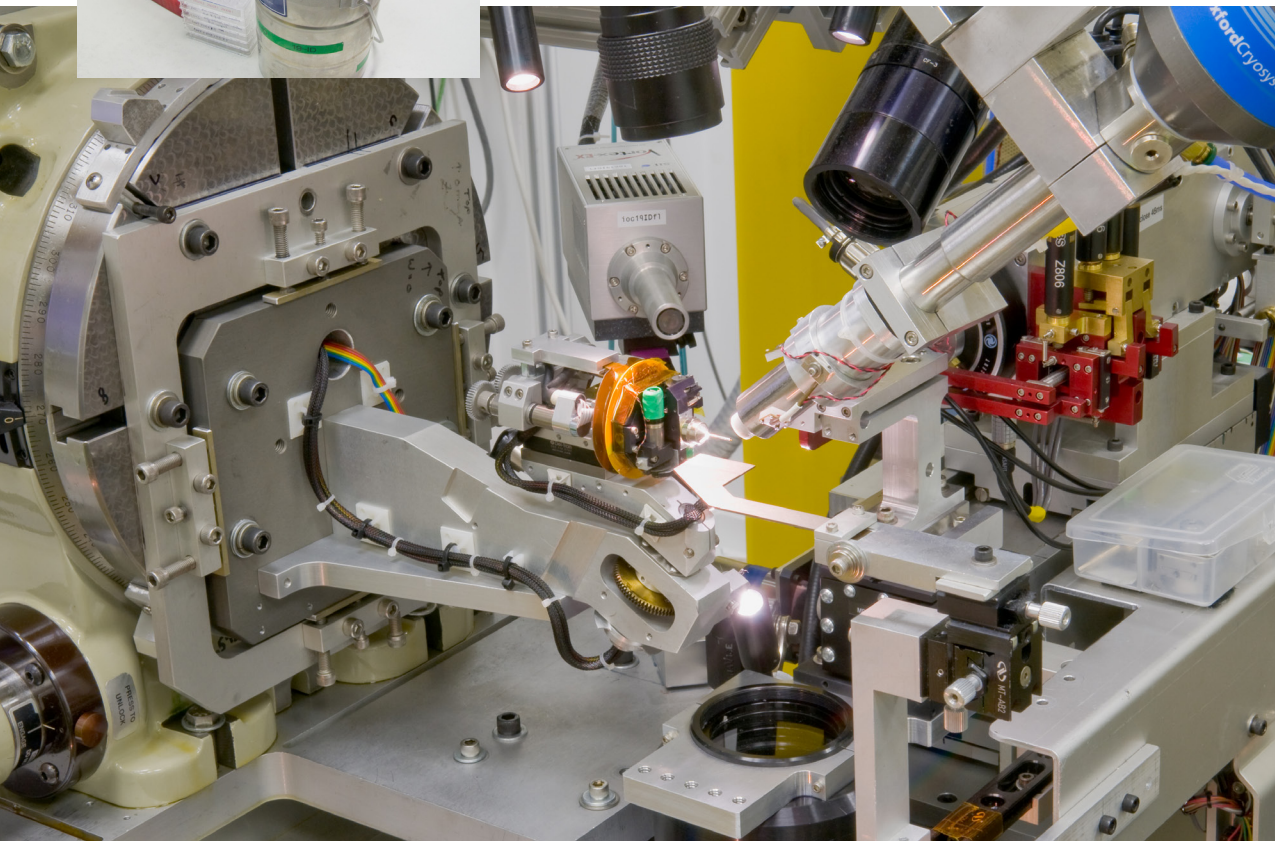
A user at SBC freezes a protein crystal in liquid nitrogen

WHO WE ARE

Supported by the U.S. Department of Energy, the Structural Biology Center (SBC) is a scientific user facility located at Sector 19 of the Advanced Photon Source (APS) at Argonne National Laboratory, southwest of Chicago. A national synchrotron X-ray research facility, the APS provides the brightest X-ray beams available in the Western Hemisphere. In addition, APS has been approved to design facility upgrades, which will further extend the capabilities of this phenomenal source. The SBC offers two experiment stations, the insertion-device beamline, 19-ID, and the bending magnet beamline, 19-BM, which are among the most powerful and focused X-ray sources available for structural biology.

The SBC beamlines are well suited for a wide range of crystallographic experiments involving:

- ▶ Crystals of macromolecular assemblies with very large unit cells
- ▶ Multi- or Single Wavelength Anomalous Diffraction (MAD/SAD) phasing
- ▶ Crystals of membrane proteins
- ▶ Small, weakly diffracting crystals
- ▶ Ultra high-resolution crystallography
- ▶ Helium and nitrogen cryocrystallography



The sample environment at beamline 19-ID

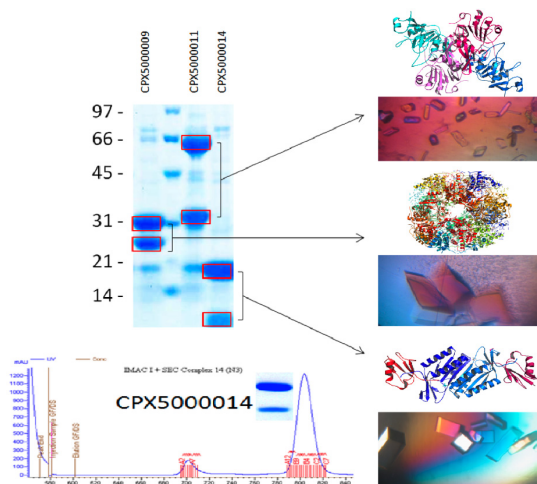
A highly productive resource for structural biologists

CAPABILITIES

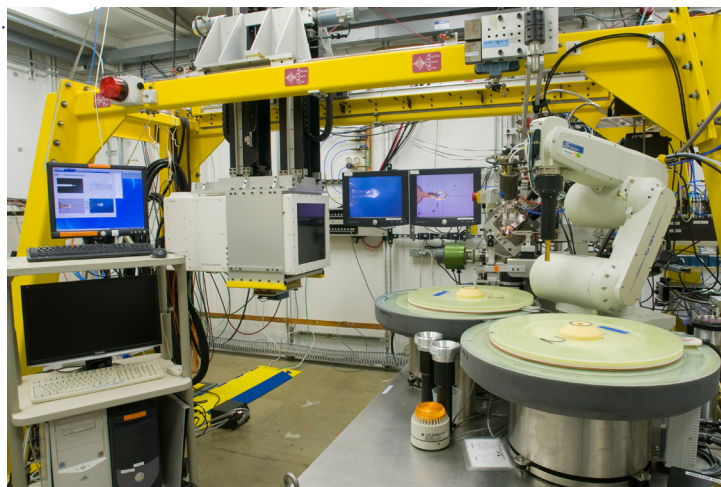
The SBC philosophy for synchrotron data collection is that the optimal product is not just a diffraction data set, but also an interpretable electron density map and a macromolecular structure. SBC output is enhanced by:

- ▶ On-axis sample viewing optics;
- ▶ An improved sample environment, including back-lit paddles;
- ▶ Easy access to minibeams (5, 10, and 20 μm) and variable beam sizes (25–250 μm);
- ▶ The integration of computing/data storage resources to accelerate data analysis and archiving;
- ▶ Near real-time interpretation of data, optimization of experimental parameters, and structure solution;
- ▶ The full integration of synchrotron hardware, detectors, crystal mounting robot, beamline software (SBCcollect, SBCserver), and crystallographic software packages (HKL3000, CCP4, SOLVE/RESOLVE, PHENIX, ARP/wARP, and COOT).

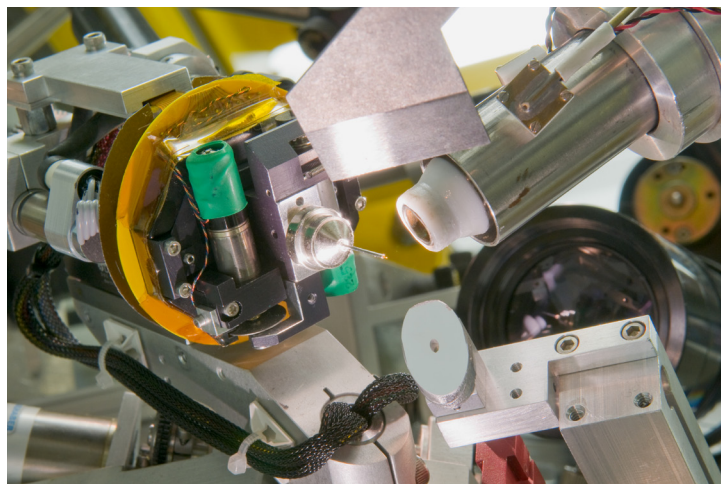
Advanced software developments include loop auto-centering, extrapolation of radiation damage effects, and semi-automated structure determination using SAD/MAD approaches for macromolecular complexes. Diffraction from crystals is recorded on large, fast, and efficient state-of-the-art charge-coupled device (CCD) area detectors. Images are processed by high-performance, integrated computing systems.



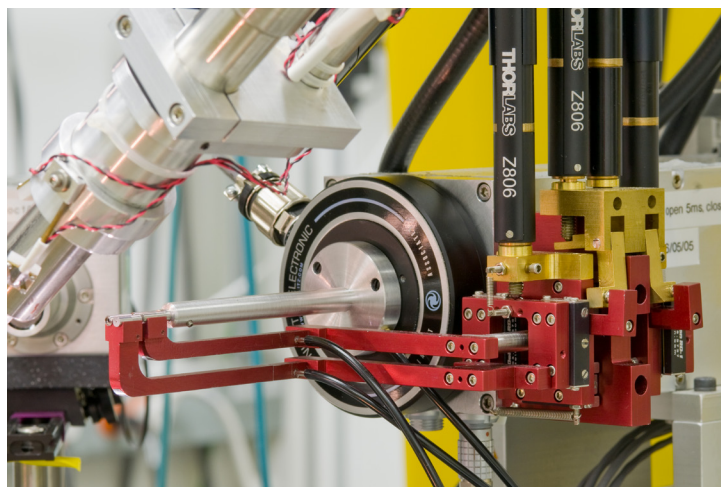
Proteins overexpressed, purified, and crystallized in preparation for data collection at SBC



Inside the experiment station of beamline 19-ID

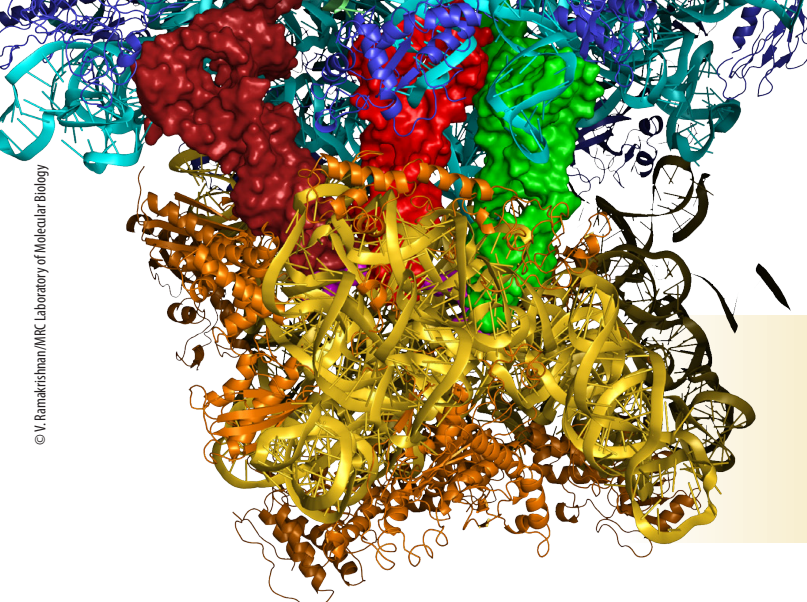


A close-up view of sample environment

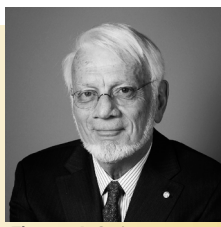


The mini-beam apparatus on beamline 19-ID

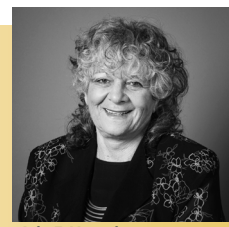
© V. Ramakrishnan/MRC Laboratory of Molecular Biology



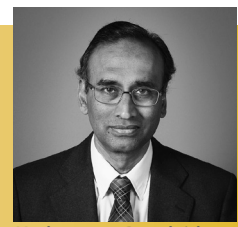
Data collected at SBC beamlines contributed to the 2009 Nobel Prize in Chemistry for studies of the structure and function of the ribosome



Thomas A. Steitz



Ada E. Yonath



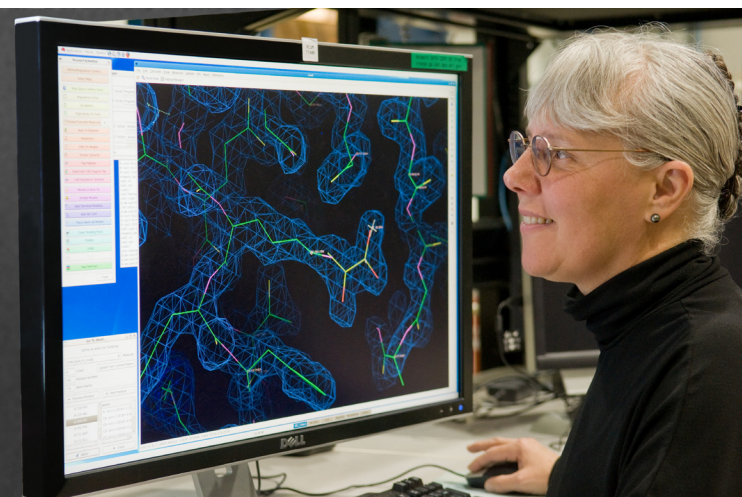
Venkatraman Ramakrishnan

© The Nobel Foundation. Photos: Ulla Moenjan.

USER HIGHLIGHTS

Research at the SBC has revealed how proteins are synthesized inside the cell (ribosome, above), how we see light (rhodopsin), how cells communicate (integrin), and how cells differentiate (gene regulatory factors). Other findings have shed insight into the origins of diseases, including cancer, diabetes, and osteoporosis, and human pathogens such as *Staphylococcus aureus* and *Bacillus anthracis*.

- ▶ Data collected at SBC beamlines contributed to the 2009 Nobel Prize in Chemistry for studies of the structure and function of the ribosome.
- ▶ The SBC has enabled the structure determination of highly challenging macromolecules (including bacterial and human cytochromes, glucosidases, H5N1 virus RNA polymerase, Ebola virus interferon inhibitor VP35, portal proteins, splicing RNA, virulence factors, and membrane proteins).
- ▶ By early 2010:
 - Beamline 19-ID had contributed to more than 2,000 Protein Data Bank (PDB) deposits.
 - Beamline 19-BM had contributed to more than 750 PDB deposits.
 - Work at the SBC had been featured in well over 1,000 peer-reviewed publications.



An SBC user traces an electron density map, using beamline facilities

www.sbc.anl.gov

FOR MORE INFORMATION Go to www.sbc.anl.gov or contact:

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Image on front cover: "The Crystal Structure of a HK97 Family Phage Portal Protein from *Corynebacterium diphtheriae*"; Protein Data Bank (PDB) deposition 3KDR.

The SBC operates a scientific user program and accepts proposals (regular access, rapid access, and remote access) for beamline time. Constructed and operated by Argonne National Laboratory's Biosciences Division, the SBC is funded by the U.S. Department of Energy Office of Science and Office of Biological and Environmental Research.



Argonne National Laboratory is a U.S. Department of Energy laboratory managed by UChicago Argonne, LLC.