

The Structural Biology Program

The Structural Biology Program at Brookhaven Lab's National Synchrotron Light Source II (NSLS-II) enables discovery-class research on fundamental biological questions. Researchers can use the program's world-class instruments to investigate the atomic building blocks of a wide range of biological samples using state-of-the-art x-ray scattering and diffraction techniques.

The program's scientific focus is to investigate the molecular structure and function of complex biomolecules using extremely small crystals and molecules in solution.

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National Synchrotron Light Source II

A U.S. Department of Energy
Office of Science User Facility

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Structural Biology

at the National Synchrotron Light Source II

Investigating and understanding
biology through molecular
characterization and structure

To Become a User:
www.bnl.gov/ps/userguide

Beam time at NSLS-II is available at no charge to researchers and it is granted through a peer-review proposal process. Proprietary access is also available at a full cost-recovery rate.

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beamlines

16-ID
LiX

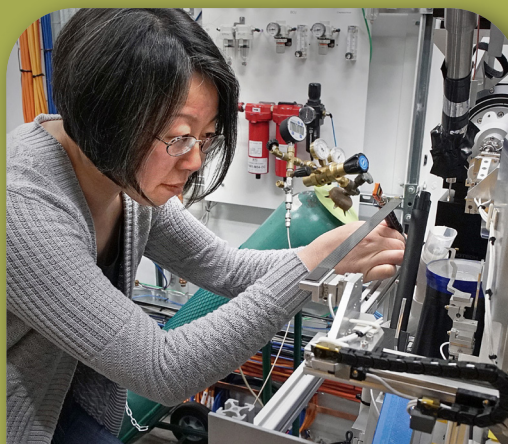
Life Science X-ray Scattering

The Life Science X-ray Scattering (LiX) beamline is specifically designed for life science applications beyond crystallography. Using x-ray scattering and imaging techniques, LiX's diverse user community studies complex proteins and macromolecules in solution. Researchers can choose from a broad range of x-ray-based techniques to investigate the properties of proteins and macromolecules *in vivo*.

17-BM
XFP

Biological X-ray Footprinting and Spectroscopy

The Biological X-ray Footprinting and Spectroscopy (XFP) beamline is designed for studying the dynamics and structure of biological macromolecules in solution. XFP provides researchers with a versatile setup and intense broadband x-rays for investigating the interactions of biological macromolecules *in vivo*. The beamline is operated by the Case Western Reserve University Center for Synchrotron Biosciences.



Highly Automated Macro- molecular Crystallography

17-ID-1
AMX

The Highly Automated Macromolecular Crystallography (AMX) beamline is designed to meet the needs of bioscience researchers by revealing the structures and functions of protein complexes. AMX offers researchers a fast and efficient way to quickly discover the best crystals among available specimens and then to investigate them with high precision using state-of-the-art detector systems.

Frontier Microfocusing Macro- molecular Crystallography

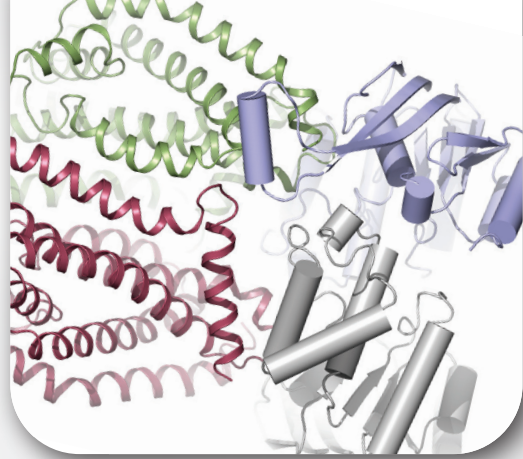
17-ID-2
FMX

The Frontier Microfocusing Macromolecular Crystallography (FMX) beamline is optimized to solve bio-crystallographic challenges by offering researchers access to its unmatched micron-sized x-ray beam and high photon flux. Researchers can benefit from the fast sample exchange and temperature-controlled sample environment at FMX.

Biological Microdiffraction Facility

19-ID
NYX

The Biological Microdiffraction Facility (NYX) beamline offers hard x-ray macromolecular crystallography with high energy resolution for the finer examination of proteins and complex biological molecules. The beamline is developed and operated by the New York Structural Biology Center.



Scientists Reveal Unexpected Structure For O-antigen Transporters

Scientists revealed an unexpected channel-forming structure for an O-antigen transporter, called Wzm-Wzt. This transporter protein is found in the cell membranes of highly abundant gram-negative bacteria, and transports polysaccharides through the outer cell membranes. Using advanced x-ray diffraction measurements, the scientists found that the transporter's channel-forming structure is unique and stands in contrast to classical mechanisms that are usually used by this kind of ABC transporter.

Reference: *Nature*, 553, 361–365 (2018)

Scientists Develop New Structure- Function Model for Protein Complex in Cellular Autophagy

Scientists unlocked the function and structure of a yeast protein complex called Snx4-Atg20, which is needed for autophagy—an essential cell function. Autophagy is a form of cell self-cleaning where a protein captures unused cellular material in vesicles and degrades the captured contents. In this study, scientists used small-angle x-ray scattering (SAXS) to map the shape of the complex and reported a detailed investigation of its structure and function.

Reference: *PNAS*, E10112–E10121 (2017)