Flexible Access and Highly Automated Beamline for Macromolecular Crystallography (AMX)

AMX at NSLS-II

- Will provide structural biologists with ready access to an advanced facility for precise structure determinations at unprecedented rates
- Will optimally exploit unique source characteristics and deliver a very high flux in a suitably small focused beam
- Will be highly automated to support remote access and extensive experimental studies

Examples of Science Areas & Impact

- STRUCTURAL BIOLOGY: Atomic structures of large protein and nucleic acid complexes, including membrane proteins, are prerequisites to gaining insights into their function, and interactions, thus creating molecular movies
- BIOCHEMISTRY: Structural analysis of all intermediates in entire enzymatic cycles and pathways will expand our understanding of cellular and microbiological processes
- PHYSIOLOGY AND MEDICINE: Crystallographic studies of the interactions of drugs with their targets are essential in the development of improved and new pharmacologically effective compounds

Beamline Capabilities

TECHNIQUE: macromolecular crystallography
Source: canted U20 In-vacuum undulator
ENERGY RANGE / RESOLUTION: 5-20 keV; \( \Delta E/E \sim 5 \times 10^{-4} \)
SPATIAL RESOLUTION: beam size from 6x5 to 300 \( \mu \text{m}^2 \) (diffraction resolution to < 1 Å)

Ribbon diagram of the gating ring of the human BK channel Ca-activation apparatus. This channel encodes negative feedback regulation of membrane voltage and Ca-signaling, which plays a central role in numerous physiological processes.


Spokesperson: Dieter Schneider, Brookhaven National Laboratory