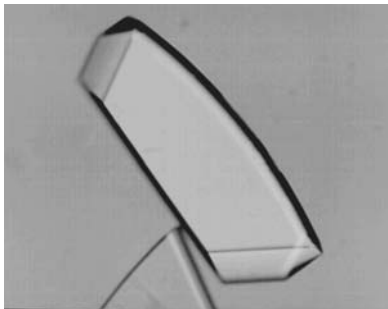


## PICTURE GALLERY



*Crystallization Cold Room with Stereo Zoom Microscopes*



*Typical protein crystal (G. Zhou)*

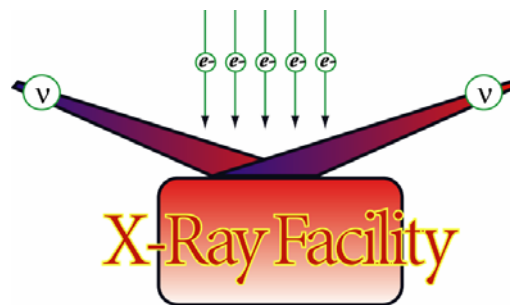


*Data Collection & Processing Computers*

## CONTACT



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X - Ray Crystallography Facility

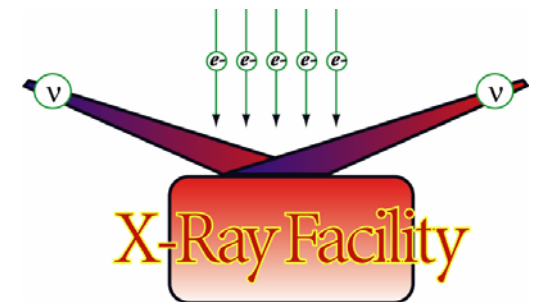
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**X-RAY FACILITY**  
KASHA LABORATORY  
INSTITUTE OF  
MOLECULAR BIOPHYSICS

*Macromolecular X-Ray  
Crystallography Facility  
Florida State University  
Tallahassee, FL 32306*



# X- RAY FACILITY

## INSTITUTE OF MOLECULAR BIOPHYSICS (IMB)

### INSTRUMENTS & SERVICES

The X- Ray Facility established in 1993 is located on the fourth floor of Kasha Laboratory Building (KLB 410-413), [Institute of Molecular Biophysics](#). It is a multi user macromolecular x-ray crystallography facility occupying 1100 ft<sup>2</sup> and equipped with three copper rotating anode generators (Rigaku H2R and Elliott GX-20). It has one R-Axis IIc image plate (IP) detector and one Mar165 charge-coupled device (CCD) detector. The generators are coupled to Osmic confocal (Blue or Purple) Max Flux or Supper mirror systems and Oxford Cryo Stream cryo coolers. Auto-mated data collection and detector control are handled by dedicated Linux or Windows NT computers. X-ray diffraction data can be collected at variety of temperatures including cryo temperatures. Researchers from the [Structural Biology \(SB\)](#) Program at the Florida State University and the State University Systems use the facility to collect x-ray diffraction data from single crystals of biological macromolecules. Shared computer resources in several platforms (HP-Alpha, Linux, NT and Win2000) are available for data manipulation & modeling. Popular software packages like HKL 2000, Mosflm, CNS, 'O', CCP4, Rsref, TNT, and ShelX running under different operating systems are available. Data archiving using DDS-3, DDS-4, DVD±R & ±RW, and CD-R & RW media is supported

The facility provides the following services:

1. Single crystal (capillary or loop mounted) x-ray diffraction data collection from proteins,

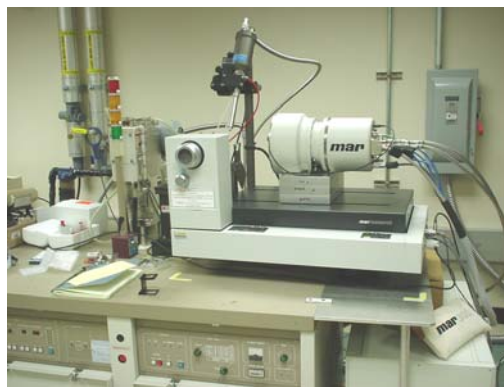
nucleic acids, and other macromolecules using automated image plate or CCD detector.

2. Macromolecular data collection at temperatures ranging from 80 to 400 K using gaseous nitrogen stream including cryo data collection using cryo loops.

3. Low- and high-resolution data collection using large sample detector distances (w/ Helium path) and non-zero 2-theta angles.

4. Preliminary data processing (indexing, merging and scaling) of single crystal data sets using popular data processing software.

5. Fiber diffraction data collection from fibrous proteins & viruses using standalone image plate or x-ray film with double mirror focusing system.



*MarCCD165 detector w/ Osmic Purple confocal mirrors on Rigaku generator (Courtesy: Mar-USA)*

### DATA COLLECTION PROCEDURE

The Facility does not charge a fee for data collection and processing for the [members](#) of the Structural Biology (SB) Program.

New users are requested to contact one of the SB faculty members or the Director of

IMB to schedule their initial meeting. Subsequent to the selection, the users can contact the facility director [Thayumanasamy Somasundaram](#) [Soma] either by phone: (850) 644-6448 or by e-mail [soma@sb.fsu.edu](mailto:soma@sb.fsu.edu) for further assistance. Depending on the schedule and availability of a particular instrument, the users will be assigned a time slot. The current and allotted schedules are posted daily in XRF website: <http://www.sb.fsu.edu/~xray>. The users are required to share the cost of consumables like cryogen, cryo accessories, magnetic and optical media.

E-mail: [soma@sb.fsu.edu](mailto:soma@sb.fsu.edu)

URL: <http://www.sb.fsu.edu/~xray>

Phone: 850 644-6448 | 850 645-1333

Location: KLB 410-414



*R-Axis IIc IP detector w/ Blue Osmic confocal Max-Flux mirror system (Rigaku/MS)*