X-RAY CRYSTALLOGRAPHY SHARED SERVICE

CIBR: Center for Innovative Biomedical Resources

CORE INSTRUMENTATION

Alchemist DT screen maker (Rigaku)

• This instrument is a liquid-handling robot that can automatically aliquot reagents for crystallization optimization trials.

Gryphon LCP Drop Setter (Art Robbins)

• Combines an automated syringe dispenser and the pipetting head into one compact crystallization robot capable of highly accurate, precise and rapid automated plate set up. It is accurate to as low as 25 nL volumes and scaled up from there.

Minstrel DT UV automated microscope (Rigaku)

 Allows automated imaging of crystallization experiments with uV fluorescence imaging. The image takes advantage of tryptophan fluorescence to determine whether a position in the plate has protein (i.e. and not salt) crystals. The results are stored on a file server that allows remote access. This allows the investigator to see the results of their crystallization experiment from anywhere in the world.

X-ray Diffraction System

- Our Rigaku-MSC Micromax 7 generator has recently been upgraded with a VariMax-HF optical system. With the system, the beam is 50% smaller and 14.5x brighter.
- Raxis-4++ image plate detector
- Oxford cryosystems cryocooling system

Robotic Crystallization and Documentation



MISSION

The X-ray Crystallography Shared Service provides the expertise, training and equipment to help determine important proteins structures as part of the UMGCCC mission to understand the molecular basis of cancer-causing cellular defects. The X-ray Crystallography Shared Service will be most valuable in helping the UMB research community understand underlying causes of diseases and develop novel therapeutic interventions.

CORE SERVICES

The facility makes state-ofthe-art robotic crystallization and automated documentation of crystallization experiments available to UMGCCC researchers.

Members of the X-ray Crystallography Shared Service are available to consult with investigators regarding sample preparation, yields, and quality.

Data collection and structure solution can also be carried out by the core for a fee.

We are also willing to consult with investigators who want to perform the structure determination themselves.



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CONTACT



Eric J. Sundberg, PhD Professor of Medicine Co-Director, Basic Science Division Institute of Human Virology University of Maryland School of Medicine esundberg@ihv.umaryland.edu

Recent Data – S100B Inhibitors



Biochemistry. 2014; 53(42): 6628

LOCATION 725 West Lombard Street Room N362 Baltimore, MD 21201 410-706-7468

