

Enabling Access to Biomolecular Crystallization Capabilities with Robotics and Advanced Imaging

Sarah Bowman (sbowman@hwi.buffalo.edu), HWI, **Sarah Bowman**, Hauptman-Woodward Medical Research Institute, **Tiffany Wright**, Hauptman-Woodward Medical Research Institute, **Elizabeth Snell**, Hauptman-Woodward Medical Research Institute, **Miranda Lynch**, Hauptman-Woodward Medical Research Institute, **Gabrielle Budziszewski**, Hauptman-Woodward Medical Research Institute

Structural biology is the scientific arena focused on generating three-dimensional models of biomolecules. There are a number of techniques for structure determination, including X-ray crystallography and cryoelectron microscopy. X-ray crystallography methods have contributed over 85% of all experimental 3D structural models available in the Protein Data Bank, the major repository of biomolecular structures. X-ray crystallography relies on production of high-quality macromolecular crystals that diffract; the generation of crystals is the primary bottleneck of the method.

In this poster, we will describe the National High-Throughput Crystallization (HTX) Center at Hauptman-Woodward Medical Research Institute in Buffalo, NY. The HTX Center has been in operation as a high-throughput crystallization screening facility for over 20 years, and provides a combination of robotics for high-throughput sample handling with advanced imaging to detect crystals. Multiple imaging modes coupled with rapid automated image analysis empower identification of crystallization lead conditions for X-ray crystallography experiments. We operate in a fee-for-service capacity and have a user base that includes academic institutions, non-profit research institutes, government agencies, and industry. For non-proprietary crystallization services, we are subsidized by federal funding from the National Institutes of Health (R24GM141256) which designates the HTX Center as a National Resource and enables broad access to the facility.

The HTX Center offers an efficient and economical means for crystallization that has proven extremely successful at identifying crystallization conditions to break the bottleneck for X-ray crystallography methods. The centralized approach with standardized methodology and quality controls provides a robust, rigorous, and reproducible means to target crystallization with resources not typically available to individual laboratories. We will discuss challenges and successes of providing crystallization resources to the user community.