

## W0353

**Finding Small Protein Crystals with Automated Imaging Systems.** E.J. Hnath<sup>1</sup>, J.A. Adams<sup>2</sup>, K. Opersteny<sup>1</sup>, J.M. Newman<sup>2</sup>, J.W. Pflugrath<sup>1</sup>, <sup>1</sup>Rigaku/MSC, Inc., 9009 New Trails Drive, The Woodlands, TX 77381, <sup>2</sup>RoboDesign International, 5920 Pasteur Ct., Carlsbad CA, 92008.

Imaging systems for the automatic inspection of crystallization trials have matured and have become useful additions to many crystallography laboratories, both high throughput and more traditional labs alike. Recently systems have been developed that allow crystallographers to rely only on the images taken by these systems to score crystallization trials and to determine which crystallization drops may contain 3-dimensional crystals of suitable size for X-ray diffraction experiments.

Detection of small protein crystals is always difficult, whether by using automated crystal imaging systems or by an experienced crystallographer looking under a microscope and making manual adjustments. The use of polarization and variable lighting can make it easier to detect some crystals in digital images taken with automated imaging systems.

Here we present a comparison of images of several protein crystals in different crystallization formats (hanging, sitting and microbatch) and with a range of lighting conditions and polarization. We compare images from a standard manual microscope and the automated Minstrel I imaging system. Our results show that polarization and adjustable lighting can provide excellent quality images that allow detection of even very small protein crystals using automated imaging systems.