

**W0393**

**New Tools for Crystal Handling and Mounting in the High-Throughput Era.** R.E. Thorne, Y. Kalinin, A. Bartnik, A. Stewart, J. Kmetko, Z. Stum, R. Gillilan, Cornell U., Ithaca, NY, USA.

Given the enormous investments in high-throughput expression/crystallization technology and in X-ray hardware, it thus makes little sense that the quantity and quality of diffraction data should in any way be limited by the few-dollar tools used to retrieve and mount crystals. A simple mounting technology<sup>1</sup> based on microfabricated films wrapped around cylindrical pins resolves the problems of current methods for both macromolecular and small molecule crystallography. Crystals are retrieved via a convenient, scoop-like action. Mounting of small (<50 micron) crystals is straightforward, and complete data sets with minimal background can be obtained from sub-10 micron protein crystals. Excess surrounding liquid is minimized, reducing background scatter, improving flash cooling and simplifying cryoprotection. Rapid automated alignment in the X-ray beam can be performed without optical observation of the crystal. Glass capillaries are eliminated using a related room-temperature data collection technology<sup>2</sup>. Crystals can be rapidly screened prior to cryoprotection and flash cooling, and both room and low temperature data can easily be collected using the same crystal.

<sup>1</sup>Thorne, R. E., *et al.* (2003). *J. Appl. Cryst.* 36, 1455-1460.

<sup>2</sup>Kalinin, Y. *et al.* (2005). *J. Appl. Cryst.* (in press).