Strategies and stories for the small-scale crystallization laboratory

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Automation has made it possible to generate massive amounts of crystallization data. How can academic laboratories benefit from this to establish a best-practice procedure for small-scale throughput facilities?

The crystallization facility at Uppsala University processes 800 SBS-format plates per year, of which 73% are for the in-house structural biology groups. Our automation consists of two crystallization robots (Mosquito, Oryx), a desktop imaging system (CrystalMation), and a liquid-handling robot (Scorpion). Most of our groups work on structure-based drug design, which means dealing with (often insoluble) compounds intended for cocrystallization or soaking. In this lecture I will share experiences from our crystallization facility regarding:

- recommendations for how many and which screens to stock for initial screening
- examples of false positives and negatives with UV detection of protein crystals
- how to recognize leads worth optimizing
- matrix microseeding as a first-choice optimization method
- real-life horror stories and successes

Our experiences may be useful for other small-scale facilities hoping to gain the most crystallization information about their targets for the least amount of materials, time and effort.

Microseed matrix screening for optimization in protein crystallization: what have we learned? A. D'Arcy, T. Bergfors, S. W. Cowan-Jacob & M. Marsh (2014). *Acta Cryst.* F**70**, 1117-1126.