s7.m4.p3 **Development Of A Crystallisation Screen for Organic Compounds.** C. Keats, K. Prout, and D. Watkin, *Chemical Crystallography Laboratory, University of Oxford, 9 Parks Road, Oxford, OX1 3PD, UK.* G. Tranter and R. W. Lancaster, *Glaxo Wellcome Medicines Research Centre, Gunnels Wood Road, Stevenage, Hertfordshire, SG1 2NY, UK.*
Keywords: crystallisation, polymorphism.

Molecular structure determination by X-ray diffraction has the potential to become a routine analytical tool. Single crystal analysis has been revolutionised by CCD diffractometers, which can collect analytical quality data in a few hours, and powder diffraction is gaining importance through new methods of ab-initio structure solution. Eventually, both techniques will be limited by the availability of suitable crystalline material. For single crystal work, a sample size of a few tenths of a mm is adequate. Well-crystallised material is needed even for powder diffraction. It has been shown that usually sample quality rather than instrument capability is the factor limiting the diffraction data resolution.

The growth of crystals for either technique is not well characterised, and though some systems have been intensely studied, there are no generally applicable rules or guidelines. Solution crystallisation is the easiest technique to implement into a screening process; the modifying factors are the properties of the solvent of evaporation and the interaction of the crystallisation molecule with the solvent molecules.

A crystallisation screen for small organic compounds has been developed, comprising of sixty organic solvents (selected by cluster analysis of physical properties). The primary aim of the screen was to obtain good quality crystals for single-crystal X-ray diffraction. The secondary aim was to screen compounds for polymorphism.

The results of the systematic crystallisation of the polymorphic systems barbital, sulphapyridine and flufenamic acid are presented. The techniques used were a solvent evaporation screen and a precipitant-solvent evaporation matrix. The crystal structure is presented for an unreported polymorph of barbital, [C2/c, cell parameters a = 12.750(2) Å, b = 16.936(2) Å, c = 10.180(1) Å, β = 120.60(1) °]. It is suspected that this polymorph is the "disappearing" barbital III[1,2,3], melting point 181 °C. The crystal structure of flufenamic acid II[4] polymorph [$P2_1/c$, cell parameters a = 11.242(1) Å, b = 10.408(1) Å, c = 11.849(1) Å, β = 112.83(1) °] is also presented.

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s7.m4.p4 **Effects of Equilibration Control on Protein Crystallization**. T.L. Bray, L.J. DeLucas, *University of Alabama at Birmingham, Center for Biophysical Sciences and Engineering, HPB 309A, 1530 3rd Avenue South, Birmingham, AL 35294-0010, USA.*
Keywords: dynamic, control, protein.

Obtaining large, high quality protein crystals continues to be the rate limiting step in the determination of three-dimensional protein structures. While significant advances have been made in recent years to better understand and control some aspects of protein crystallization, instruments or devices capable of controlling protein crystallization that are both effective and user-friendly have not been readily available. Our laboratory has been actively developing methods and custom systems for dynamically controlling protein crystallization processes for several years using vapor diffusion and temperature methods of crystal growth. We have recently designed new systems which utilize the capabilities of earlier breadboard systems with enhancements to the original designs and used them to crystallize over 10 proteins from commercial and internal sources. We have used these systems to demonstrate conclusively that controlling the equilibration of protein solutions has dramatic, systematic effects on crystallization results. For each protein, slowing the rate of solvent evaporation from the protein solution produces smaller populations of larger crystals than obtained at faster evaporation rates. These devices are simple to use, yet provide significant control over the evaporation of solvent from protein solutions, allowing for improvements in crystallization results. The results from these studies will be presented, along with strategies for optimizing crystallization using methods for controlling the evaporation of water from protein solutions.