s6.m20.p3 **An EU-funded crystallography service at the UK synchrotron.** Elizabeth J.MacLean, Paul R. Raithby, John E.Warren and A. Jane Whittington, *CCLRC Daresbury Laboratory, Warrington, WA4 4AD, UK. E-mail: chemicalcrystallography@dl.ac.uk*

Keywords: Single crystal; Small crystals; Free service

We would like to announce a rolling call for applications from academic scientists who are eligible for EU funding and are interested in trialling a synchrotron chemical crystallography service based at the CCLRC Daresbury Laboratory. [1]

Chemical crystallography experiments using Station 9.8 on the synchrotron at Daresbury have shown that samples which produce little or no diffraction on a sealed tube or rotating anode source can produce very good data sets. We have eight years' experience in chemical crystallography and have produced in excess of 250 refereed papers with sample types including: organic and inorganic materials; minerals; zeolites and other catalysts; organometallic materials; air-sensitive samples; and small polypeptides.

Data will be collected at a wavelength of approximately 0.68 or 0.80 Angstroms, and will normally be collected at 150K. However, it is possible to have the collection done at any temperature between 90 and 600K. We also have facilities available for handling air-sensitive materials in Schlenk tubes.

This service is intended only for samples that have failed on a conventional laboratory source and it will be necessary to state on the application what information, if any, has been observed.

You are eligible to apply to use this service if you are an academic from any of the countries listed below, and your sample has no commercial value. Applications will be peer-reviewed by a panel of academics as and when they are received.

Austria, Belgium, Bulgaria, Cyprus, Czech Republic, Denmark, Estonia, Finland, France, Germany, Greece, Hungary, Ireland, Iceland, Italy, Israel, Latvia, Liechtenstein, Lithuania, Luxemburg, Malta, The Netherlands, Norway, Poland, Portugal, Romania, the Slovak Republic, Slovenia, Spain, Sweden, Switzerland and Turkey.

We are offering two levels of service. Either you send your sample and then: (1) we collect the data and send back the files for structure solution (data only mode); or (2) we also solve and refine the structure and send back the completed files (full structure mode).

If you wish to receive an application form or have any further queries about the service, please contact us at chemicalcrystallography@dl.ac.uk.

[1] http://www.srs.ac.uk/srs/
[2] http://srs.dl.ac.uk/XRD/9.8/

s6.m20.p4 **High-throughput physical characterization of protein solutions using microfluidics.** Morten O.A. Sommer, Jens-Christian Navarro Poulsen and Sine Larsen. *Centre for Crystallographic Studies, Department of Chemistry, University of Copenhagen. E-mail: mortens@fys.ku.dk*

Keywords: High-throughput; Protein crystallization; Microfluidics

Growing diffraction quality crystals from a purified protein solution remains a challenge in structural biology. New crystallization strategies rely on advances in physical characterization of protein solutions and advances in high-throughput technologies; however, to reach the goals of structural biology such as full proteomes high-throughput physical characterization must be developed. This requires an adaptive technology platform allowing integration of both complex biophysical analyses, high-throughput at low cost and low sample consumption. Microfluidic devices have proven useful for conducting a vast amount of biological assays. We report here on the implementation and application of a Multi-Layer Soft Lithography microfluidic device capable of accurately injecting solutions of various physical properties in 100 pL increments into a 5 nL reaction chamber. The low volume consumption and full automation of the device allow high-throughput physical characterization of protein solutions. Using the device we have conducted systematic screens of protein phase behaviour and its dependence on various precipitating agents. Based on the experimentally determined protein phase behaviour crystallization experiments are set up below the precipitation boundary of the protein. Crystallization experiments based on knowledge of protein phase diagrams have proven very successful having significantly more crystal hits when compared to commercially available sparse matrix screens. Our recent experiences with the use of this device for high-throughput physical characterization of protein solutions will be reported.