presence of metallic copper, and to cuprite in the orange tesserae. These phases are responsible for both the colour and opacity of the samples. In this context, in addition to the redox conditions in kilns, the relationships between the precipitation of the above phases and differing amounts of copper and lead in the samples were also discussed.

Lastly, the similarity of the present results with those already reported in the literature indicates routine glass production processes, notwithstanding their different age and provenance.

Keywords: archaeometry. XAS, glass

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Using 2D detectors for x-ray imaging

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The unique properties of newer generation solid state 2D detectors - like the combination of high dynamic range, low background and high spatial resolution with no point spread broadening - offer the possibility for new imaging applications.

In this contribution we will show examples of non-destructive X-ray imaging applications with a PIXcel^{3D} detector that is based on the Medipix2 technology. Examples include imaging techniques based on transmission geometry, Bragg diffraction (X-ray topography) and non-coherent scattering effects. These imaging applications allow to combine traditional X-ray analysis with micro-structural investigations of the samples and the correlation with macroscopic material properties. Examples of organic samples and semiconductor materials will be shown.

Keywords: imaging

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Macromolecular crystallization: robotics, procedures and Innovations

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At the time of crystallization experiments the structure of a macromolecule is not known and hence an optimum strategy cannot be established. At the LMB, scientists can undertake initial experiments using a wide variety of conditions and robust automated procedures [1]. The procedures are straightforward, enabling LMB scientists to operate independently. We are continuously developing methods, like the Pi sampling [2] and devices to increase the chance of crystallization and crystal optimization. There are now different MRC crystallization plates that can be used on commercially available robots [3]. Also, we have created screens like MORPHEUS [4] to complete the formulation of commercial kits.

[1] D. Stock *et al. Prog. Biophys. Mol. Biol.* **2005**, *88*, 311-327. [2] F. Gorrec *et al. Acta D,* **2011**, *67*, 463-470. [3] F. Gorrec *et al. Poster presentation (www.swissci.com)*. [4] F. Gorrec, *J. Appl. Cryst.* **2009**, *42*, 1035-1042.

Keywords: macromolecular crystallization, screen, automation

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Utilization of desiccant for enhancing protein crystallization

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The vapor diffusion (hanging or sitting drop) technique is widely used in protein crystallization screens. In conventional vapor diffusion crystallization screens the concentration of protein usually increases from $0.5C_p$ (C_p: the initial protein concentration before mixing with the reservoir solution) to ~C_p. This limited concentration range reduces the probability of the solution being in the nucleation zone. If the protein concentration range is increased, we may expect to see a higher crystallization success rate.

Based on the above consideration, we proposed a new method to increase the concentration range in protein crystallization by using desiccant instead of the reservoir solution in the vapor diffusion technique[1]. Fig. 1 illustrates the difference in the arrangement of crystallization cells between the conventional and modified vapor diffusion methods.

Thirteen proteins were tested using the modified and conventional sitting drop methods. It was found that the improvement by using the modified method is strikingly significant. With consideration of the following features we recommend this modified method for practical protein crystallization screens. (1) Conditions under which drops remain clear in the conventional vapor diffusion method may yield crystals in the modified method. (2) The modified method can produce crystals from solutions with lower initial protein concentrations, which consumes less protein. It is always very difficult to produce protein samples at concentrations sufficient for crystallization trials. Using the modified method, we did not need to worry as much about the concentration of the protein during sample preparation. (3) The involved modification is very simple and efficient and can be applied without the need for large changes to the standard vapor diffusion protocol. The modification can also be integrated into automated systems. (4) Finally, the modified method reduces the cost of screening because no reservoir solution is necessary.

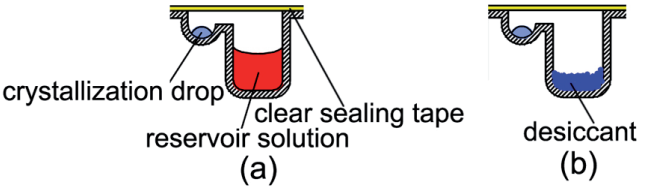

Figure 1. Schematic illustration of the difference in the arrangement of crystallization cells between the conventional and modified vapor diffusion methods. (a) The arrangement of crystallization cells in the conventional vapor diffusion method (sitting drop method). (b) The arrangement of crystallization cells in the modified vapor diffusion method[1].

[1] Q.Q. Lu, D.C. Yin, R.Q. Chen, S.X. Xie, Y.M. Liu, X.F. Zhang, L. Zhu, Z.T. Liu, P. Shang, *J. Appl. Cryst.* **2010,** *43*, 1021-1026.

Keywords: protein, crystallization, methodology

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Fields and crystals: what can we learn about quality?

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