Complementary methods for the study of biomaterials

I. Margiolaki*[1], J. P. Wright[1], Y. Watier[1], I. Collings[1], A. N. Fitch[1],
N. Papageorgiou[2] and B. Canard[2]

[1] *European Synchrotron Radiation Facility (ESRF), Grenoble, France*
[2] *Architecture et Fonction des Macromolécules Biologiques (AFMB), UMR 6098 CNRS, Marseille, France*

*margiolaki@esrf.fr

Studying biological macromolecules in the absence of good quality single crystals is a challenging field attracting considerable scientific interest. Modern developments of X-ray powder diffraction have allowed the structural investigation of a range of proteins establishing the method as a useful complementary tool to traditional approaches [1]. Protein powder specimens consist of a large number of randomly oriented diffracting micro-crystals which are usually formed rapidly by batch crystallization under a variety of conditions. An overview of the most recent developments in this field will be presented including: (a) application of the molecular replacement technique and structure refinements of selected proteins (b) methods for successful cryocooling (c) experimental phasing and extraction of molecular envelopes (Figure) (d) high throughput automated data collection allowing systematic investigations such as screening and phase diagram mapping and (e) application of the method on biologically interesting proteins such as non-structural viral replication proteins coming from emerging viruses [3].

References

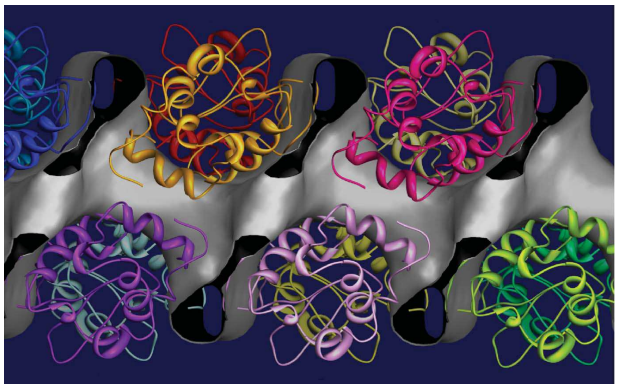

Figure Solvent channels in hen egg white lysozyme crystals. The molecular envelope derived via the single isomorphous replacement method using a gadolinium derivative is represented as grey surface. The figure shows the linear solvent channel which traverses the crystal parallel to the c axis (horizontal display direction). The protein crystal structure, represented as a main-chain ribbon model, is superimposed on this map. [1]

[1] Margiolaki, I. & Wright, J. P., Acta Cryst. (2008). A64, 169-180.
[2] I. Margiolaki et al., J. Am. Chem. Soc. (2007). 129, 11865-11871.
[3] H. Malet et al., J. Virol. (In Press).

Acknowledgments We thank the ESRF for provision of beamtime.