

PROTEIN POWDER DIFFRACTION AT THE ESRF

Jon Wright, Irene Margiolaki, Yves Watier
ESRF, 6 Rue Jules Horowitz, BP 220, 38043 Grenoble, France

We can use x-ray diffraction to see how the atoms and molecules fit together inside crystalline materials. For single crystal diffraction experiments we need crystals which are "large enough" to be able to measure all the diffraction spots in 3D. Currently there is a range of crystallite sizes which are "too small" to be studied as single crystals. From a few unit cells (~50 nm) up to around ~10 microns we can only record x-ray diffraction data by powder methods. This crystal size problem is being tackled from two directions; lowering the size of the smallest crystals for 'single crystal' methods, and raising the level of structural detail that can be extracted from powder data [1].

By using micro-focused x-ray beams the crystallite sizes can be reduced. Eventually the experiments may be limited by radiation damage and only a few shots can be recorded per particle. Also, it becomes very difficult to have only a single crystallite in the beam. Software developments [2] for multi-crystal diffraction experiments offer us the possibility to process data for tens or hundreds of crystallites and to get 'single crystal' data from a much wider range of samples.

Using multiple 1D powder patterns, where the peak positions are slightly shifted, can help to alleviate the peak overlap problem. This effect was used to determine the crystal structure of the SH3 domain of Ponsin by molecular replacement from powder data [3]. Those data were sufficiently good for interpretable electron density maps to be used in order to rebuild the parts of the structure that were different from the search model. Without a search model we must overcome the crystallographic phase problem. Powder data could be used for low resolution phasing [4] of some small proteins with heavy atoms by the single isomorphous replacement method. Those data in [3,4] were all collected at room temperature, but further improvements are possible when protein samples can be successfully frozen [5].

[1] I. Margiolaki and J. P. Wright, *Acta Cryst.* (2008). A64, 169-180

[2] <http://fable.wiki.sourceforge.net/> and <http://www.totalcryst.dk/>

[3] I. Margiolaki, J. P. Wright, M. Wilmanns, A. N. Fitch, N. Pinotsis. *J. Am. Chem. Soc.* (2007) 129 11865-11871.

[4] J. P. Wright, C. Besnard, I. Margiolaki, S. Basso, F. Camus, A. N. Fitch, G. C. Fox, P. Pattison and M. Schiltz. *J. Appl. Cryst.* (2008). 41, 329-339

[5] Y. Watier, I. Margiolaki, J. Wright, L. Knight, A. Fitch, M. Norrman and G. Schluckebier. *Acta Cryst.* (2008). A64, C312