

## Microsymposium

**MS61.O03**

*Protein crystallography in the 1970s: starting from scratch in a remote outpost*

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A conversation with Dorothy Hodgkin on a long bus trip, just before I returned to New Zealand in 1970, left me full of determination and optimism. This presentation will recount my experience in starting a protein crystallography lab with only a sealed-source generator and a precession camera for equipment. Crystals had to be large (0.5 - 1.0 mm on edge) and X-ray data, collected at room temperature on a borrowed small-molecule diffractometer, accumulated very slowly. We corrected for absorption and decay and scaled data sets rather crudely. It was very much a do-it-yourself environment. With no CCP4, software had to be borrowed or adapted or written oneself; methods papers in *Acta Cryst.* were like gold as I pored through them trying to understand. Communications with friends, by airmail, were vital. An electron density map for the cysteine protease actinidin, at 2.8 Å, was immediately interpretable thanks to excellent data and phases from more derivatives than were really necessary. An R factor of 42% to 2.0 Å, for a model built in a Richards box, was really quite astonishing. Later FFT-based least squares refinement at the University of York in 1978 was even more astonishing as the R factor rocketed down [1]. No computer graphics, but the difference electron density told the story – in retrospect there was even evidence that the crystals (prepared from kiwifruit bought at the local shop) contained several genetic variants of the protein! It may not have been the most exciting protein in the world (except to me!) but what a way to learn protein crystallography and protein structure.

[1] E. N. Baker, E. J. Dodson, *Acta Cryst.*, 1980, A36, 559-572.

**Keywords:** Early protein crystallography