

Protein Microcrystallography – the first 1 μ m beam structure

Pat Edwards

M.R.C. Laboratory of Molecular Biology, Cambridge, UK

Microcrystallography beam-lines have allowed many important structures to be solved from difficult protein crystals, previously impossible to measure. The technology developed on ID13, translated to the MX beam-line ID23-2, allowed large screenings and routine measurements with tiny crystals. With access to both these beam-lines through long term proposals, we have been able to solve several GPCR structures, including the first structure of a beta 1 adrenergic receptor; an important pharmacological target. More recently, we have been involved with ID13 to develop scanning methods using micrometre beam sizes. Last year we published the first structure performed with a focussed synchrotron radiation beam of 1 μ m. The experiment showed that a high-resolution diffraction pattern can be obtained from a 20 μ m³ crystal volume, and that despite the high radiation dose it was possible to obtain an excellent high resolution map without significant radiation damage. Thus these results show further new opportunities for solving structures from much smaller crystals than previously anticipated.