

Overview of the uses of synchrotron radiation in protein crystallography

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The pioneering use 25 years ago of hard X-ray synchrotron radiation was in structural biology, by Ken Holmes, Gerd Rosenbaum, and Jean Witz. With the more recent arrival of reliable, well-equipped, and accessible beam lines, much of macromolecular crystallography world-wide is now conducted at synchrotron sources. Certain classes of experiments can be conducted only at a synchrotron: MAD experiments, experiments that demand high time resolution, or microcrystal studies. Others can be conducted much better at a synchrotron : study of crystals with large unit cell dimensions, or of crystals where accurate, high-resolution data are required.

Will all of protein crystallography at synchrotrons become "routine"? What steps remain to be taken in that direction? What experiments are likely to remain laboratory-based? What experiments will remain at the frontier? How can we continue to learn from the other scientific disciplines based at synchrotrons - and they from us?