

X-ray Absorption Spectroscopy in the Era of Synchrotron-based Crystallography: Is It obsolete?

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Until recently, x-ray absorption spectroscopy (XAS) was the method of choice for determining the structure of the metal sites in proteins. However, recent dramatic advances in the methodology for protein crystallization and in the capabilities of synchrotron-based crystallographic measurements have led to an explosion in the number of protein crystal structures that are available. In this context, it is appropriate to ask what role remains for x-ray absorption spectroscopy as a tool for structural biology. The future prospects for x-ray absorption spectroscopy, particularly as third-generation synchrotron sources become available, will be discussed. Dramatic improvements in both sensitivity and resolution are likely. These improvements, coupled with an improved appreciation of both the strengths and the weaknesses of XAS, suggest that XAS will continue to play a critical role in structural biology.