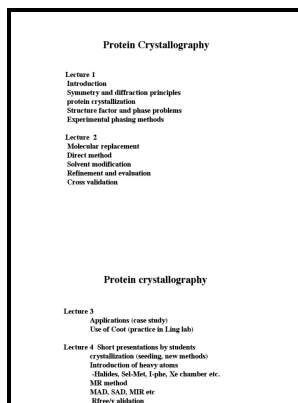


# Application of multiple wavelength anomalous dispersion methods to protein crystallography

## - - Direct Methods



Description: -

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## Protein Crystallography

Our specialists on data collection are able to improve the diffraction quality by using cryo-protectant, anneal and dehydrant. X-ray crystallography is currently the most favored method for structural determination of proteins and other macromolecules. In addition, we can test its purity, stability and assemble state by SDS-PAGE, dynamic light scattering and mass spectrometry upon request.

## Protein Crystallography

Acta Crystallogr D Biol Crystallogr. Acta Crystallogr D Biol Crystallogr. Sometimes I put a little commentary text on the end of the reference, particularly for older work or for papers that I've found especially useful.

## Method of X

Protein purity is checked via SDS-PAGE and western blots. A suite of computer software was written to control the detector and manage all aspects of the data collection. DT Cromer and DA Liberman 1981 , Acta Cryst A37, 267.

## Protein Crystallization

Resins with specific affinity to the tags are used in the case of tagged proteins. Compton form factor JJ Hoyt, D de Fontaine, and WK Warburton 1984 , J. Bijvoet difference Fourier method B-C Wang 1985.

## Method of X

Acta Crystallogr D Biol Crystallogr. In small molecule crystallography a completely different solution is applied.

## Direct Methods

Acta Crystallogr D Biol Crystallogr. A consequence of the wavelength dependence of anomalous dispersion is that the will be significantly perturbed, both in amplitude and in phase, by resonant scattering off an absorption edge. Phase relations based on probability theory have been formulated and these phase relations are applied to suitably chosen clusters of reflections.

**MX : Literature for Crystallographic Theory and Methods**

Sweet, Eds , pp 538-557, Academic Press, New York, 1997. In cases where I can, links to the PubMed or IUCr pages are linked in.

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