

## **Estimating Protein Fold using Wide-angle Solution Scattering Data**

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The secondary and tertiary structure motifs of protein folds have characteristic distributions of inter-atomic distances that produce features buried within the x-ray scattering pattern from a protein in solution. We have demonstrated that wide-angle x-ray solution (WAXS) scattering contains rich details of the secondary, tertiary and quaternary structure of multiple classes of proteins. Uses to date include the observation of ligand-induced structural changes and the monitoring of fold stages during chemical and radiation-induced protein denaturation.

WAXS scattering patterns obtained at high flux third generation synchrotron beam lines are not only sensitive to protein conformation states, but the scattering patterns generated can be quantitatively compared to data calculated from detailed structural models derived from crystallographic data. This method can be applied to almost any protein in solution including membrane proteins, large protein complexes and proteins with substantially disordered regions. As such, WAXS has the potential for being a sensitive, global method for detecting ligand-induced structural changes in proteins, narrowly categorizing proteins based on their scattering homology to known folds and elucidating the differences between crystal structures and aqueous conformations.

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