# Harnessing SAXS and X-ray crystallography for high-resolution structural studies of macromolecules

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X-ray crystallography remains a dominant approach in high-resolution structural studies. However, because of the nature of the crystallization process and stringent requirements for homogeneity of crystalline matter to be analyzed by X-rays, the method provides a somewhat 'static' representation of a macromolecule under study. In addition, in the absence of any prior structural information and phase estimates, X-ray crystallography alone cannot provide even simplest descriptors about the target molecule structure and may fail to fully inform about structural changes in solution. Here, I will present a summary of our projects that studied enzymes responsible for accurate synthesis of human selenoproteins [1-3]. In all instances, X-ray crystallography and SAXS coupled to size-exclusion chromatography were pivotal for obtaining critical insights and successful completion of studies. Our results highlight the power of a synchronous application of X-ray crystallography and SAXS.

References

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