

## Taking the Edge Off: The softer side of in-house SAD phasing

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The phase problem in macromolecular crystallography has been mitigated dramatically in recent years by advances in methodology and instrumentation. SAD phasing has now become the primary *de novo* phasing method. A search of the PDB of structures released in 2006 reveals the number of structures solved by SAD phasing exceeds those solved by MAD for the first time. A number of these examples of successful S-SAD and Se-SAD phasing used Cr radiation ( $\lambda = 2.29 \text{ \AA}$ ), which can double the anomalous signal of sulfur and selenium compared to Cu radiation.

This report reviews recent results from phasing with the enhanced anomalous signal provided by Cr radiation to demonstrate this longer wavelength can be used to solve *de novo* structures. Selenium, as the heavy atom, with Cr radiation can provide sufficient anomalous scattering for routine phasing. Cr radiation opens a new path to extracting the weak anomalous signal from sulfur to phase native protein data. With the addition of Cr radiation to the crystallographer's toolkit, in-house X-ray sources can routinely provide at least two wavelength options. The combination of diffraction data collected using both Cu ( $\lambda = 1.54 \text{ \AA}$ ) and Cr radiation can improve the electron density tremendously. Anomalous scattering from sulfur can also assist in molecular replacement solutions. Finally, the data collected with Cr radiation can be used to refine a structure. Ultimately, this makes it possible to solve a protein structure with a single data set.

This in-house phasing approach we describe has been given the label “**know before you go**” by John Rose and B.C. Wang at the University of Georgia. This method improves the efficiency of the solution of macromolecular crystal structures and usage of the synchrotron beam time.