Applications of anomalous scattering in protein crystallography

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The anomalous scattering effect has been known since many years and it has been used in the past, in combination with isomorphous replacement, to solve the ambiguity of the phase problem [1-3]. Only recently it has become a very powerful and general tool in the structural determination of macromolecular structures [4-6]. This is mainly due to the combination of two factors: the availability of synchrotron radiation and the techniques of molecular biology. In fact, the magnitude of the real (f') and imaginary (f'') components of anomalous dispersion for a heavy element strongly depends on the wavelength used in the experiment. Consequently, the measurement of diffraction data at three (or even two or one) appropriate wavelengths can allow the complete determination of a crystal structure, given an appropriate anomalous scatterer is present in the crystal. This technique is known as MAD (Multiple Anomalous Dispersion) or SAD (Single Anomalous Dispersion).

Two examples will be used to illustrate the effectiveness of the technique. The first demonstrate that the presence of one Zn$^{2+}$ ion in a protein of about 16 kDa can produce interpretable electron density maps. The second example shows how anomalous diffraction data combined with the phases of a well-refined structure have been used to detect the presence of a specific atomic species.