

# **Synchrotron Radiation Circular Dichroism Spectroscopy and Protein Crystallography: Complementary Methods in Structural Genomics**

**B. Wallace**

*Crystallography, Birkbeck College, University of London, London, United Kingdom*

Circular Dichroism (CD) spectroscopy is a well-established technique that can provide valuable information that is complementary to X-ray crystallography. While CD spectroscopy is no substitute for X-ray data in terms of resolution, it can provide both dynamic and static structural information on molecules in solution, and information that is useful for the validation of crystal structures. Synchrotron Radiation Circular Dichroism (SRCD) extends conventional CD spectroscopy (using lab-based instruments) because the high flux of the synchrotron enables measurement of data to lower wavelengths (resulting in higher information content) and in the presence of absorbing components (buffers, salts, and detergents). The lower wavelength data mean that not only can it provide more accurate information on secondary structure, but also information on fold motifs can be discerned from the spectra. The ability to measure the spectra of proteins in the presence of absorbing components means that it can examine proteins both under crystallisation and physiological conditions, thus enabling the validation of the biological relevance of crystal environments. CD spectroscopy may also be useful as an aid to rational crystallisation.

SRCD has a number of emerging applications in structural and functional genomics, including the identification of novel folds as an aid to target selection, providing information for rescue of higher hanging fruit, and the ability to examine membrane proteins, a class of proteins often by-passed by structural genomics programmes; For functional genomics, it enables high throughput screening for binding of potential ligands as a means of identifying enzyme activity, and identification of mutations associated with disease states as a means of identifying biological systems activity.

In summary, SRCD can be a useful technique in conjunction with protein crystallography and other biophysical techniques in a wide-range of structural and functional studies.