Removing Irradiation Problems Associated with a High-Flux Synchrotron Radiation Circular Dichroism Beamline

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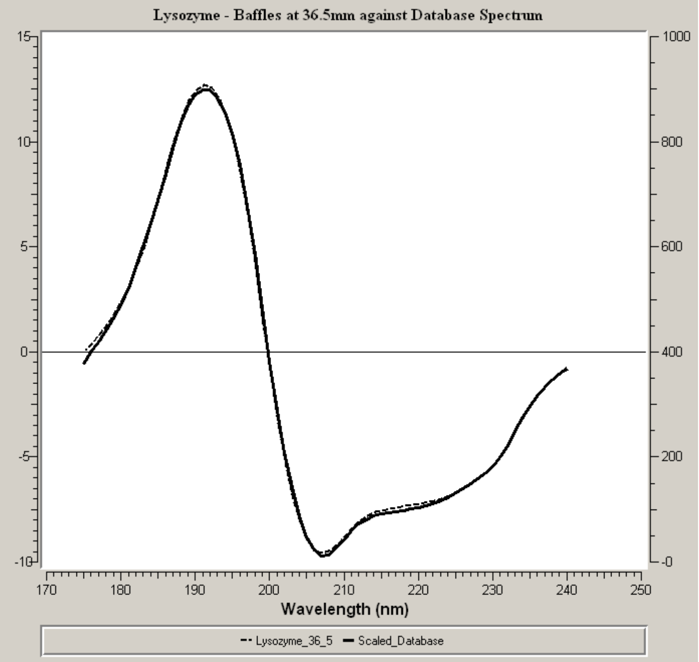
The Synchrotron Radiation Circular Dichroism (SRCD) beamline CD12 has been shown to have a high enough flux at low wavelengths sufficient to cause notable irradiation problems with protein samples while their spectral data were being collected. The experiments reported here have been focused on ways to circumvent this problem through limiting the beam flux. Initial methods were through usage of attenuation cells placed beam-side of the sample cell, which proved reasonably successful in reducing the high flux problem but also reduced the ability to obtain data to low wavelengths, the key benefit of the SRCD technique. Further approaches were to limit the beam cross-sectional area hitting the sample either by closing slits near to the sample or baffles near to the monochromator (see the figure below). Here is shown that such methods result in apparent complete removal of this protein denaturation problem over the course of collecting three/four successive spectra. Through eliminating this denaturation problem multiple SRCD scans for protein samples can be collected, vital both for good practice, and for statistically valid results.



SP175 Database spectrum of Lysozyme (scaled) [solid line] against

Baffle-attenuated Lysozyme (average of four runs) [dotted line]