

# Analysis of Bovine Gamma Globulin Using the ConcentratIR2™

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## INTRODUCTION

Infrared spectroscopy has recently gained recognition as a viable technique for protein structure analysis due to its high information content for biological systems.<sup>1</sup> Specifically, much focus has been placed on the application of infrared spectroscopy to the study of protein unfolding. The process of protein unfolding has been examined extensively by other methods such as fluorescence, circular dichroism, or visible absorption spectroscopy. However, infrared spectroscopy is unique in that it allows analysis of protein unfolding through secondary structure alteration on a timescale unachievable by other techniques, while retaining exceptionally high structural resolution.<sup>1</sup>

ATR (attenuated total reflectance) has proven to be a particularly advantageous infrared technique for analysis of proteins, with its high sampling rate and convenient sample preparation.<sup>2</sup> The [ConcentratIR2™](#) is a multiple reflection ATR accessory capable of analyzing small amounts of liquid on a timescale small enough for effective study of the protein unfolding process.

This work examines the use of the ConcentratIR2™ to analyze small amounts of protein undergoing secondary structural change in response to thermal perturbation.

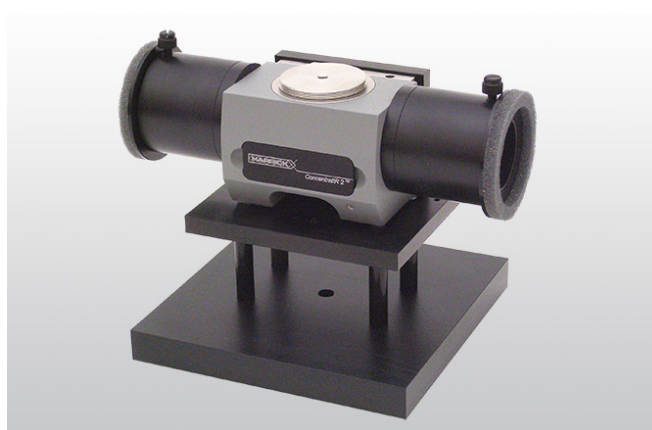


Figure 1. The Harrick ConcentratIR2™ multiple reflection ATR accessory.

## EXPERIMENTAL

This work examines unfolding of BGG protein assay standards. The solution consisted of 750  $\mu\text{g/mL}$  BGG in a 0.9% sodium chloride solution with sodium azide. Measurements were carried out using a commercially available FTIR spectrometer equipped with KBr beamsplitter and MCT detector.

The ConcentratIR2™ was configured with a multiple reflection silicon ATR element. Data were collected over a wavelength range of 4000-650  $\text{cm}^{-1}$ . Parameters for data collection were as follows: aperture was set to 100%, number of scans was 64, gain was set to 8, and resolution to 4  $\text{cm}^{-1}$ . The ConcentratIR2™ was connected to its heated liquid cell that was modulated by a Harrick Temperature Controller. The temperature of the heated cell was held at 100 °C throughout data collection.

Protein samples were injected by syringe through the Luer fittings on the heated cell, with the temperature stable at 100 °C. Enough sample was loaded to ensure the interior of the cell was completely filled. The spectrum was collected immediately upon injection into the cell and subsequently every minute for nine minutes. Two additional spectra were run 20 and 30 minutes

after injection. The fittings of the cell were capped during data collection to prevent evaporation.

## RESULTS AND DISCUSSION

The collected spectra exhibit clear spectral changes in relation to one another, indicating that unfolding of the protein was occurring in response to a significant increase in environmental temperature. Changes in the characteristic amide I band around 1600-1700  $\text{cm}^{-1}$  were of primary focus. The peaks in this region offer the most information regarding the structure of the protein backbone which is the key determinant of protein secondary structure.<sup>3</sup> Within this region, a concomitant increase in wavelength of absorption and intensity of absorption is observed over time. The largest, most dramatic shift in wavelength, a shift from about 1670  $\text{cm}^{-1}$  to 1620  $\text{cm}^{-1}$ , is seen between the time of injection ( $t=0$ ) and one minute after ( $t=1$ ). However, the intensity of absorption changed very little during this period. This suggests that the majority of secondary structure change may have occurred in the moments immediately following exposure of the protein to heat.

As time progresses, the spectra seem to reverse this initial trend- increasing in absorption, yet remaining fairly constant in peak position. The spectra collected every minute from two minutes on show an increase in absorption but a slightly lower increase with each passing minute. Moreover, comparing these to the spectra collected outside this period - namely,  $t=20$  and  $t=30$  - offers insight into protein unfolding in the longer-term. These later spectra are almost identical in peak position and intensity in the amide I region, suggesting that protein conformation is not significantly altered beyond a certain period of time. These results raise the prospect for future studies which could use the ConcentratIR2™ to generate a more detailed profile of the rate of secondary structure change associated with thermally induced protein unfolding.

Changes in base protein conformation brought on by heating result in certain known alterations in secondary structure composition that produce characteristic peaks in the infrared.<sup>4</sup> The amide I band consists of overlapping component bands that reflect particular secondary structures such as alpha

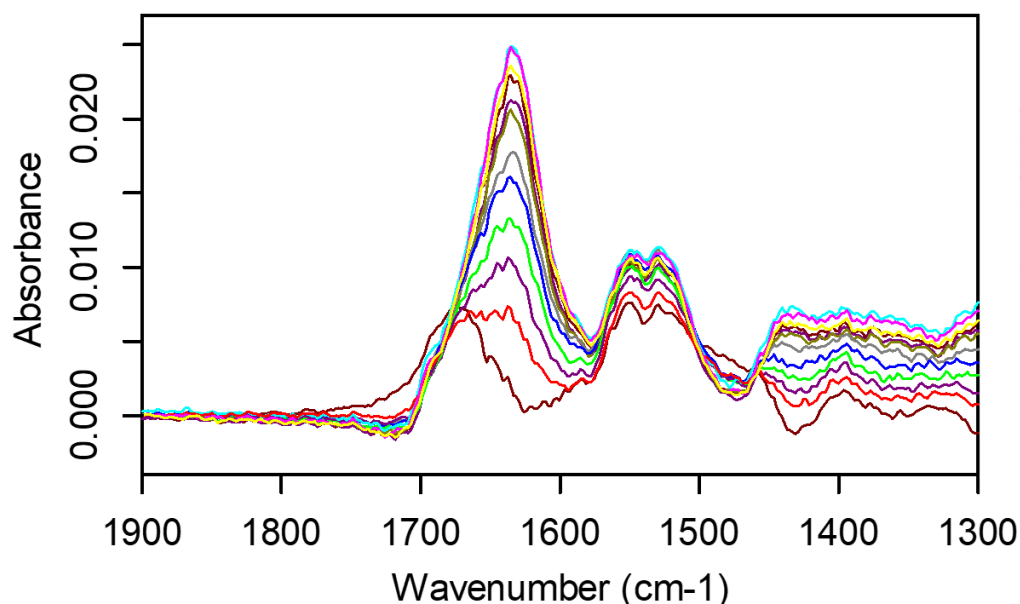


Figure 2. The ATR spectra of BGG at 100°C at 0 (lowest peak), 1, 2, 3, 4, 5, 6, 7, 8, 9, 20, and 30 (highest peak) minutes after injection of sample into cell.

helices, beta sheets, turns, and random structures.<sup>4</sup> Within the amide I region, globular proteins tend to produce prominent bands corresponding to alpha helices and beta sheets in particular.<sup>4</sup> These bands consistently fall at wavenumbers around 1660  $\text{cm}^{-1}$  and 1620-1640  $\text{cm}^{-1}$  for alpha helices and beta sheets, respectively with slight variation possible depending on the specific protein in question.

Examination of the  $t=0$  spectrum reveals a prominent alpha helix peak, spanning from about 1670-1650  $\text{cm}^{-1}$ ; whereas, very little contribution from beta sheets is seen. As described earlier, the most significant change in secondary structure appeared to occur in transition from  $t=0$  to  $t=1$ . Upon this transition, there is an obvious disappearance of the aforementioned alpha helix peak and a concomitant appearance of a prominent beta sheet peak around 1620-1640  $\text{cm}^{-1}$ , signifying a transition in the overall secondary structure composition to primarily beta sheets, agreeing with the findings of another infrared study that also saw a decrease in alpha-helices and increase in betasheets upon thermal perturbation.<sup>5</sup>

This work demonstrates the ease and efficacy with which the ConcentratIR2™ can visualize thermally induced secondary structure change in small amounts of a protein such as BGG. The above findings speak to the high level of structural detail that IR spectroscopy – as opposed to other methods of protein visualization – can achieve, especially in recording minute-to-minute changes in structure associated with protein unfolding.

## REFERENCES

1. Fabian, Heinz. "Protein Folding and Misfolding: Shining Light by Infrared Spectroscopy". (Springer-Verlag, Berlin, 2012), Chap. 1.
2. K.A. Oberg and A.L. Fink, "A New Attenuated Total Reflectance Fourier Transform Infrared Spectroscopy Method for the Study of Proteins in Solution", *Analytical Biochemistry*, 256(1), 92-106 (1998).
3. Andreas Barth. "Infrared Spectroscopy of Proteins", *Biochemica et Biophysica Acta- Bioenergetics*, 1767(9), 1073-1101 (2007).
4. J. Kong and S. Yu, "Fourier Transform Infrared Spectroscopic Analysis of Protein Secondary Structures", *Acta Biochimica et Biophysica Sinica*, 39(8), 549-559 (2007).
5. A. Dong, T.W. Randolph., J.W. Carpenter, "Entrapping intermediates of thermal aggregation in alpha-helical proteins with low concentration of guanidine hydrochloride", *Journal of Biology and Chemistry*, 275(36), 27689 (2000).