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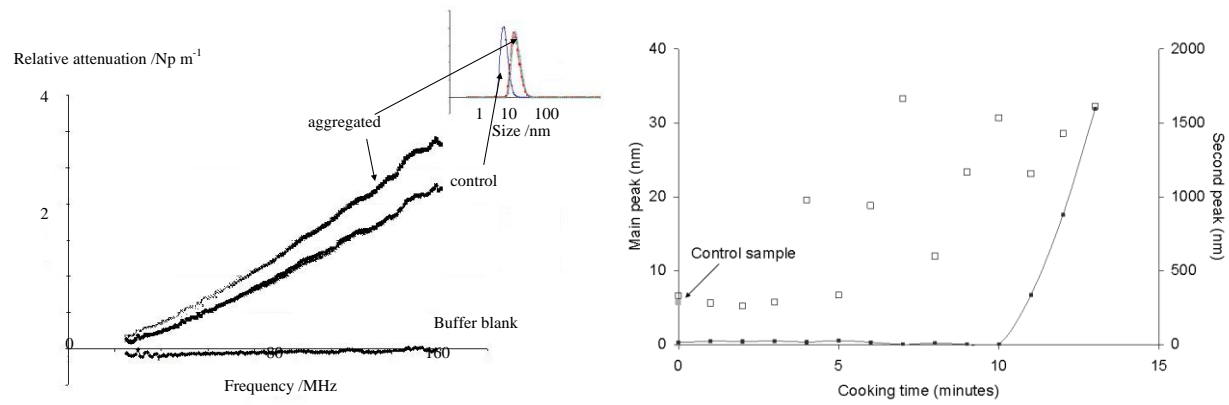
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Abstract: The ability of ultrasound spectroscopy to characterise protein denaturation at relatively high concentrations and under conditions found in foods, is examined. Measurement of longitudinal sound velocity against concentration and frequency (20-160 MHz) for the bovine serum albumin monomer at pH 7.0 gave a frequency independent value for molecular compressibility of at 25 °C, corresponding to a sound velocity for the BSA molecule of 1920 ms⁻¹. At 160 MHz, the longitudinal sound attenuation in BSA molecules is ~5200 Npm⁻¹, a factor of 10 higher than in water. The excess attenuation of the solution over water was nearly 90 Npm⁻¹ at the highest measured volume fraction of 0.03 (or 3% v/v). Concentration-dependent ultrasound velocity (20 - 160 MHz) and attenuation (2 - 120 MHz) spectra were obtained over time for heated bovine serum albumin (BSA) solutions up to 40 mg/mL at neutral pH and at 25 °C. An acoustic scattering model was used which considered the solute molecules as scatterers of ultrasound, to determine the molecules' sound velocity, compressibility, and attenuation properties. Mild heat treatment caused the molecule to organise into dimers and trimers, without change in sound velocity; implying that there is little or no change in secondary structure. Changes in attenuation spectra correlated with estimated molecular weight as determined through DLS and SEC measurements. During oligomerisation, the BSA molecules continue to behave acoustically as monomers.

Under severe heat treatment, BSA rapidly suffered irreversible denaturation and gelation occurred which affected both ultrasound attenuation spectra and the velocity of sound, consistent with significant molecular conformation changes and/or molecule-molecule interactions.

*Graphical Abstract



Ultrasound spectroscopy (velocity and attenuation 2-160 MHz) measurements can follow all stages in the denaturation of bovine serum albumin, from dimerisation through to severe denaturation. Velocity and attenuation relate to different features of the molecule. Velocity is sensitive to changes in conformation, secondary structure, and any significant changes in elastic or shear properties, attenuation is affected by relaxation processes and possibly aggregation.

For Food Hydrocolloids: Investigation of bovine serum albumin denaturation

1 **Investigation of bovine serum albumin denaturation using**
2 **ultrasonic spectroscopy**

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14

15 *Abstract*

16 The ability of ultrasound spectroscopy to characterise protein denaturation at relatively high
17 concentrations and under conditions found in foods, is examined. Measurement of
18 longitudinal sound velocity against concentration and frequency (20-160 MHz) for the bovine
19 serum albumin monomer at pH 7.0 gave a frequency independent value for molecular
20 compressibility of $\kappa' = 2.05 \times 10^{-10} \text{ Pa}^{-1}$ at 25 °C, corresponding to a sound velocity for the
21 BSA molecule of 1920 ms^{-1} . At 160 MHz, the longitudinal sound attenuation in BSA

22 molecules is $\sim 5200 \text{ Npm}^{-1}$, a factor of 10 higher than in water. The excess attenuation of the
23 solution over water was nearly 90 Npm^{-1} at the highest measured volume fraction of 0.03 (or
24 3% v/v). Concentration-dependent ultrasound velocity (20 - 160 MHz) and attenuation (2 -
25 120 MHz) spectra were obtained over time for heated bovine serum albumin (BSA) solutions
26 up to 40 mg/mL at neutral pH and at 25 °C. An acoustic scattering model was used which
27 considered the solute molecules as scatterers of ultrasound, to determine the molecules'
28 sound velocity, compressibility, and attenuation properties. Mild heat treatment caused the
29 molecule to organise into dimers and trimers, without change in sound velocity; implying that
30 there is little or no change in secondary structure. Changes in attenuation spectra correlated
31 with estimated molecular weight as determined through DLS and SEC measurements. During
32 oligomerisation, the BSA molecules continue to behave acoustically as monomers.

33 Under severe heat treatment, BSA rapidly suffered irreversible denaturation and gelation
34 occurred which affected both ultrasound attenuation spectra and the velocity of sound,
35 consistent with significant molecular conformation changes and/or molecule-molecule
36 interactions.

37 *Keywords:* ultrasound spectroscopy; compressibility; bovine serum albumin; aggregation;
38 gelation; protein-protein interactions; protein-solvent interactions.

39 **1. Introduction**

40 Ultrasound spectroscopy is increasingly used to investigate the properties of biomolecules,
41 for example functional properties such as storage modulus arising from protein-protein
42 interactions in high protein concentration solutions (Saluja, Badkar, Zeng, Nema, & Kalonia,
43 2007) and for folding studies (El Kadi, et al., 2006). In this work we measure for the first
44 time both velocity spectra (20 – 160 MHz) and attenuation spectra (2 – 160 MHz). Velocity

45 and attenuation relate to different features of the molecule. Velocity is sensitive to changes in
46 conformation, secondary structure, and any significant changes in elastic or shear properties,
47 attenuation is affected by relaxation processes and possibly aggregation. Ultrasound velocity
48 has the unique property that it is affected by the adiabatic compressibility of the molecule and
49 hence is sensitive to molecular transitions that alter compressibility. An example of such a
50 transition is crystallization, to which ultrasound velocity is very sensitive, primarily due to
51 adiabatic compressibility (or bulk modulus) change associated with the phase change (Povey,
52 Awad, Huo, & Ding, 2007). Ultrasound has the further advantage that it can be used for bulk
53 measurement in optically opaque, concentrated or multiple scattering media and is therefore a
54 complementary technique to light scattering and circular dichroism. Unlike circular
55 dichroism however, ultrasound does not provide specific information about secondary and
56 tertiary structure, but does respond to changes in molar free energy (Chalikian, 2008). The
57 key advantage of ultrasound in this work is its ability to provide information at all stages in
58 the aggregation of the protein BSA, from dimerisation through to gelation, offering a method
59 for characterising proteins under the conditions in which they are used in foods.

60 In this work we use a method previously reported in this journal (Aparenten, Buttner, Mignot,
61 Pascal, & Povey, 2000) for obtaining molecular compressibility of BSA from ultrasound
62 measurements of velocity and attenuation. Our previous study was carried out at a single
63 frequency and only velocity was measured. As in the previous study, here it is assumed that
64 the protein molecule is a particle that scatters ultrasound according to classical scattering
65 theory.

66 A number of mechanisms, other than that of scattering, have been proposed for the features in
67 the absorption spectra of protein solutions including BSA (Kessler & Dunn, 1969; Hussey &
68 Edmonds, 1971; Holmes & Challis, 1996). These include changes in conformation, proton

69 transfer reactions, solvation effects and other relaxation effects. Models have been developed
70 to estimate the contribution of the proposed mechanisms to the attenuation. In particular,
71 relaxation models are used to identify the relaxation frequencies (Holmes & Challis, 1996).
72 Some workers have fitted a small number of relaxations in their experimental frequency
73 range, whilst others fit a continuous range of relaxation frequencies.

74 (Bryant & McClements, 1999) proposed that the overall attenuation of ultrasound by a
75 protein solution (α_{soln}) be divided into molecular relaxation (α_{MR}) and scattering contributions
76 (α_{s}). This presupposes that the relaxation contribution can be identified prior to separating out
77 the scattering contribution. Holmes and Challis (1996) found that at a temperature of 37 °C,
78 higher than that used in this study, a large frequency squared dependent term needed to be
79 subtracted from their data, before a two frequency relaxation model could be fitted to their
80 data. Whilst they suggest this subtracted term is due to another high frequency relaxation,
81 our data suggest that the subtracted term could be, at least in part, due to scattering of sound
82 by the BSA molecule. In this paper we analyse the attenuation data entirely in the context of
83 the scattering model, without attempting to separate the relaxation contribution.

84 **1.1 Scattering model**

85 The straightforward classical model of sound propagation relates the velocity of sound v to
86 the elastic modulus M and density of a material ρ through

$$87 \quad v = \sqrt{M/\rho} \quad (1)$$

88 The elastic modulus depends on the type of wave propagating and the material through which
89 it propagates. In this work we measure only the longitudinal propagation mode (also called
90 the compressional mode) which is a pressure wave. Other modes include shear and surface
91 modes. The shear mode requires a significant shear modulus, G , in order to propagate. In

92 solid materials the elastic modulus governing longitudinal wave propagation is related to the
93 bulk modulus K_B given by

$$94 \quad M = K_B + 4G/3 \quad (2)$$

95 In fluids such as the protein solutions which form most of the subject of this paper, the elastic
96 modulus is given by the bulk modulus which is related to the adiabatic compressibility κ
97 through

$$98 \quad M = K_B = 1/\kappa \quad (3)$$

99 The classical model is formally correct but cannot predict the effects of scattering by small
100 particles. In contrast, the scattering model approach considers each molecule or dispersed
101 phase particle as a scattering object, which has the effect of removing energy from the
102 forward transmitted sound wave (usually an incident plane wave) and scattering it in all
103 directions (Povey, 1997). Such scattering may affect both longitudinal wave attenuation
104 (through the wave amplitude) and velocity (through a change in phase of the wave). These
105 ultrasound propagation parameters depend on the properties of the continuous and dispersed
106 phase materials, and the concentration of the dispersed matter (Challis, Povey, Mather, &
107 Holmes, 2005; Povey, 1997).

108 In the present work, the systems were measured in the long wavelength region, in which the
109 wavelength of the sound wave is much larger than the scatterer (molecule) radius. In this
110 case, the scattering model shows that the wave number (K_{soln} , not to be confused with the
111 bulk modulus K_B) of the solution can be written in terms of the solvent (water) wave number
112 ($K = \frac{\omega}{v} + i\alpha$, where ω is radial frequency, v is sound velocity, $i = \sqrt{-1}$ and α is attenuation
113 coefficient). At the concentrations used in this study, the second order (in concentration)
114 multiple scattering term, is negligible, and the attenuation and velocity vary linearly with the

115 concentration (ϕ) expressed as the product of partial molar volume (Table 1 and Table 2) and
 116 the mole fraction as a fraction of the mean molar volume of the solution (Povey, 1997):

$$117 \quad (\alpha_{\text{soln}} - \alpha_{\text{solv}} - \alpha_{\text{MR}}) = C_{\alpha}\phi + O(\phi^2) \quad (4)$$

$$118 \quad \frac{1}{v_{\text{soln}}^2} - \frac{1}{v_{\text{solv}}^2} = C_v\phi + O(\phi^2) \quad (5)$$

119 Here subscripts $_{\text{soln}}$ and $_{\text{solv}}$ refer to the properties of the protein solution and to the solvent
 120 containing buffer. The scattering model shows that the concentration dependence is obtained
 121 as a volume fraction, rather than other concentration measures often used such as weight
 122 fraction. This means that the partial molar volume (Table 1) has a significant impact on sound
 123 velocity. Attenuation and inverse square velocity show a linear dependence in volume
 124 fraction when measured relative to the same parameter in the pure solvent. The parameters
 125 C_{α} and C_v define the respective gradients of the excess parameters with volume fraction.
 126 Note in relation to those data analyses that extrapolate linearly to infinite dilution, scattering
 127 theory predicts the inverse square velocity of sound to depend linearly on volume
 128 concentration (Equation 5).

129 According to the scattering model, the gradient C_v obtained from the velocity measurements
 130 relates to the real parts of the coefficients given above, which are a fractional compressibility
 131 difference $\Delta\kappa/\kappa$, a fractional density difference $\Delta\rho/\rho$ and a thermal contribution Y .

$$132 \quad C_v = \left(1/v^2\right)\{(\Delta\kappa/\kappa) + (\Delta\rho/\rho) + Y\} \quad (6)$$

133 Each of the terms is independent of frequency in the long wavelength region. Thus it is
 134 expected that the velocity gradient parameter should be independent of frequency. For the
 135 thermal term, the frequency independence only applies when the thermal wavelength is also

136 long, so that if the velocity gradient is indeed independent of frequency, the validity of this
137 limit is confirmed. Rearranging the expression leads to the compressibility of the molecules.

$$138 \quad \kappa' = \kappa \left[1 + v^2 C_v - (\Delta\rho/\rho) - Y \right] \quad (7)$$

139 where the factor Y arises from thermal scattering (Povey, 1997).

140 The molar compressibility and hence the sound velocity will be affected by changes in partial
141 molar volume, heat capacity, solvation and the pressure of the applied acoustic field.
142 Because the acoustic field has frequency and duration, relaxation effects will certainly be
143 present. The pressure may have an effect because an acoustic field is a pressure fluctuation
144 with amplitude of approximately 20 kPa for a typical 100 W m^{-2} , 1 MHz pulse in water at
145 $25 \text{ }^\circ\text{C}$ (Povey & McClements, 1988; Povey, 1997). No attempt has been made in this work to
146 unravel in detail the relative contributions of these effects during oligomerisation and
147 denaturation of the studied protein, although we studied the frequency dependence of both
148 sound velocity and attenuation. Determined compressibility includes both intrinsic and
149 hydration terms.

150 **2. Materials and Methods**

151 **2.1 Protein solutions**

152 The water used in all experiments is MilliQ water (Millipore, Ma, USA) , prepared by ion
153 exchange, used because it gives much more reproducible results than triple distilled water in
154 ultrasound experiments.

155 Bovine serum albumin (BSA- Product number A2153, Fraction V, Sigma-Aldrich Company
156 Ltd, Gillingham, UK) is a widely used globular protein with a molecular weight of 66500 Da
157 (Murayama & Tomida, 2004). 40 g/l solutions of BSA were prepared by the slow dissolution

158 of the freeze-dried protein in 0.1 M potassium phosphate buffer (pH 9.6) and then stored at
159 4 °C, prior to use. Just before measurement, samples were buffered at pH 7.0.

160 Concentrations are quoted as mass of protein in volume of solution and later converted to
161 volume fraction by using the solution density measurements. Solutions were degassed in an
162 ultrasonic bath. For the cross platform and oligomerisation studies 5 g/l solutions of BSA
163 were finally prepared in 20 mM potassium phosphate buffered to pH 7.0.

164 **2.2 Oligomerisation experiments**

165 Samples were prepared in 10 ml aliquots and heated in a water bath at 70 °C +/- 0.02 °C for
166 60, 120, and 180 min. After heating, the samples were allowed to cool to room temperature.
167 The control sample was maintained at room temperature. Sub-samples were removed after
168 heating and were analysed by dynamic light scattering (DLS) and size exclusion
169 chromatography (SEC). The remaining sample was analysed by ultrasound spectrometry.

170 **2.3 Gelation experiments**

171 The BSA solutions were heated in a thermostat-controlled oil-bath (refrigerated and heating
172 circulator from Jubalo, F25-MC, accuracy +/- 0.02 °C) so that the time-temperature profiles
173 could be controlled and registered. The solutions were sealed in A4 cans and maintained at
174 25 °C during 10 min for the equilibrium time. They were then heated up to 80 °C over a
175 period of 25 min, maintained at 80 °C during a few minutes (0, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11,
176 12, 13, 14, 15 or 16 minutes), and finally cooled down to 25 °C during 25 minutes. In-can
177 temperature was measured in two positions and logged together with the bath temperature
178 using type T thermocouples. Measurements of the storage modulus (G') and of the loss
179 modulus (G'') were performed using a Bohlin C-VOR rheometer from Bohlin Instruments.

180 The measuring system used was C14, cup and vane tool (vane diameter of 14 mm and gap
181 width of 0.15 mm), which has a stress range of 1–750 Pa, with a strain sensitivity of $\sim 10^{-4}$.
182 After pre-shearing, 4 drops of silicone oil AS4 (Fluka, from Sigma-Aldrich) were added to
183 avoid evaporation. The temperature was set to 80 °C, and G' and G'' were measured during
184 2 hours. More severe heat treatments were applied using a computer controlled steam retort
185 (Figure 1).

186 **2.4 Instrumentation**

187 **2.4.1 Ultrasound velocity and attenuation**

188 Ultrasound velocity and attenuation measurements were made using the ICHOS II instrument
189 (PAA Ltd, Farnborough, UK). The system is based on the “pitch and catch” method, with a
190 longitudinal transmitted pulse passed through the sample to a receiver; in the frequency range
191 1-200 MHz, operating in the near field. In practice, this operating frequency range is
192 significantly reduced by signal to noise considerations. The sample cell is made of stainless
193 steel and requires a sample volume of 7-11 ml, with a path length for the ultrasound signal of
194 11.2 mm at 25 °C. The cell temperature is maintained by a water jacket and homogeneity is
195 assisted by a magnetic stirrer. The sample temperature in all experiments was
196 $25\text{ °C} \pm 0.2\text{ °C}$.

197 The instrument measures the intensity of the ultrasound signal received after transmission
198 through the sample, and the time of flight of that signal in the sample. For instrument details,
199 please refer to the manufacturer’s documentation. Measurements are calibrated against a
200 reference sample, in this case, pure water because of the high accuracy data available. The
201 velocity of longitudinal sound in pure water is obtained by the “148-point” equation of
202 Bilaniuk & Wong, (1993, 1996), which defines its temperature dependence up to fifth order.

203 The measured temperature was 24.8 °C, and the velocity in water is therefore 1496.2 ms⁻¹
204 and independent of frequency.

205 The velocity in the sample is determined by calibrating the time of flight against that
206 measured in pure water at each frequency. Similarly, for attenuation, the intensity measured
207 in the sample is calibrated against that measured in water.

208 The measurements were found to be accurate over the range 20-160 MHz. Outside this
209 range, the intensity in water (and sample) was too low. Velocity measurements were carried
210 out in the ICHOS II spectrometer with an accuracy of $\pm 0.2 \text{ m s}^{-1}$. The main determinant of
211 the accuracy of ultrasound velocity measurements is temperature control ($\pm 200 \text{ mK}$) because
212 the temperature coefficient of the velocity of sound in water at ambient temperature and
213 pressure is $3 \text{ ms}^{-1}\text{°C}^{-1}$. Relative to velocity, ultrasound attenuation is much less sensitive to
214 temperature variation.

215 Data were also obtained using a Malvern Ultrasizer ultrasound spectrometer. This operates
216 by producing a quasi-static longitudinal standing wave in a chamber holding at least 500 ml
217 of sample, within which transducers, operating between 2 MHz and 120 MHz, move. The
218 transducers are moved to obtain optimal signal to noise ratio and hence accuracy, within
219 given frequency bands. This contrasts with the PAA instrument whose transducers operate at
220 a fixed path length and which operate in pulsed mode. The Ultrasizer produces absolute
221 attenuation spectra, whereas the PAA system operates in a comparative mode with water.

222 **2.4.2 Dynamic light scattering**

223 A Malvern Zetasizer Nano was used at both NPL and Leeds to follow the size of the BSA
224 and its aggregated states. There are some issues with interpretation of data for the highly
225 aggregated forms of BSA as the light scattering technique relies on particles undergoing

226 Brownian motion. In particular, once a gel network forms in which diffusion is arrested,
227 sizing can no longer be carried out. The refractive index used for the BSA is 1.45 (the protein
228 refractive index) and a value of 0.00 for the absorption (at the laser wavelength of 633 nm).
229 For the phosphate buffer (the dispersant), the viscosity measured was 1.04 cP with 1.3357 for
230 the refractive index.

231 **2.4.3 Density and partial molar volume**

232 The method to obtain the volume fraction for the ultrasound measurements was as described
233 in Apenten et al. (2000) with partial molar volume determined according to the method of
234 Atkins (Atkins & de Paula, 2002). Measurements of density (Table 1) were made using a
235 vibrating tube densitometer (Anton Paar, Gratz, Austria) for solutions of various
236 concentrations.

237 **2.4.2 Size Exclusion Chromatography**

238 For all SEC measurements the HPLC (Jasco) was operated using Borwin (Version 1)
239 software. Control and heat-treated BSA measurement samples were injected (10 μ l) onto a
240 BioSep-SEC-S2000 (Phenomenex) column equilibrated in 1 x PBS [10 mM phosphate
241 buffer, 2.7 mM KCl, 137 mM NaCl, pH 7.4] running buffer at room temperature. The
242 injector was washed twice between injections. The column method run time was 10 minutes
243 at room temperature, under isocratic conditions where the mobile phase was 1 x PBS pH 7.4
244 at a flow rate of 1 ml min⁻¹. Eluted protein was monitored at multiple wavelengths using a
245 Multiwavelength detector (Jasco MD-2010 Plus). The column was calibrated using a set of
246 protein standards covering a range of known molecular weights (Blue Dextran (2000
247 kDa), Thyroglobulin (Bovine) (669 kDa), IgG (Bovine) (150 kDa), Serum Albumin (Bovine)
248 66kDa, Ovalbumin (Chicken) 44 kDa, Lysozyme (Chicken) 14.5 kDa .

249 The procedure followed was a modification of the methods of Whitaker (1963) and Andrews
250 (1964). Void volume (V_o) was determined by recording the elution volume (retention time)
251 of Blue Dextran at 280 nm. The elution volume (V_e) of each protein in the M_w marker mixture
252 was determined at 280 nm by observing the retention time recorded by the instrument
253 software.

254 A standard curve was created by plotting the \log_{10} of the M_w vs. V_e/V_o for each protein in the
255 mixture. V_e/V_o values were calculated for the unknown samples and the standard curve used
256 to determine the estimated M_w .

257 **3 Results**

258 **3.1 Determination of Acoustic Parameters**

259 As indicated by Equation 3 above, it is necessary to measure the dependence of the velocity
260 of longitudinal sound on the volume fraction of the protein in solution, in order to determine
261 the molecular compressibility. Studies of concentration dependence were carried out on BSA
262 solutions and density measurements as previously reported in Apenten et al (2000) were used.
263 The partial molar volume, effective molecular density, and effective molecular radius for
264 BSA were obtained from these data using a molecular weight of 66500 Da (Murayama &
265 Tomida, 2004) and are given in Table 2. These data were then used to calculate volume
266 fraction.

267 Velocity measurements taken in the ICHOS II, over the range 20-160 MHz and a
268 concentration range up to 40 mg ml⁻¹ showed no frequency dependence. The concentrations
269 were converted to volume fraction using the partial molar volume, and a single mean value of

270 velocity taken for each concentration. Figure 2 shows the inverse of the velocity relative to
271 water plotted against volume fraction, following the method of Equation 5.

272 A linear relationship is clearly suitable for this experimental data. Hence, it is appropriate to
273 neglect the multiple scattering contribution to velocity at these concentrations. The gradient
274 of the straight-line fit is the parameter C_v (Equation 6). If thermal contributions are neglected
275 initially and we assume that molecular relaxation is insignificant, the velocity gradient C_v
276 relates only to the compressibility and density difference between water containing buffer and
277 the BSA molecules in solution. Since the density of the BSA molecules has been determined
278 from the solution density measurements (Table 2), the compressibility of the BSA molecules
279 can be found (Equation 7): this is the molar adiabatic compressibility for BSA and lumps
280 together the intrinsic compressibility of the protein chain, the compressibility of any cavities
281 within the protein structure arising from its tertiary structure and solvent interactions with the
282 protein which are also a function of solvent accessible surface (– see discussion below). Its
283 value of $\kappa' = 2.05 \times 10^{-10} \text{ Pa}^{-1}$ (corresponding to a longitudinal sound velocity for the
284 hydrated BSA molecule of 1920 ms^{-1}) and our previously obtained value for BSA of 1.2×10^{-10}
285 Pa^{-1} compare with the value for water of $4.48 \times 10^{-10} \text{ Pa}^{-1}$. Our previous work indicated that
286 the compressibility was very sensitive to pH and to the thermal history of the protein; the
287 experiments reported here were carried out isothermally, whereas our earlier experiments
288 involved scanning the temperature at $20 \text{ }^\circ\text{C h}^{-1}$. Our value ($\kappa' = 2.05 \times 10^{-10} \text{ Pa}^{-1}$) for the
289 adiabatic compressibility of the hydrated molecule between 0 mg ml^{-1} and 40 mg ml^{-1} can be
290 compared with the value of $0.89 \times 10^{-10} \text{ Pa}^{-1}$ given by Chalikian (1996) for the ‘apparent
291 specific adiabatic compressibility’ (The hydrated value, not the intrinsic value) for BSA at a
292 single concentration of 3 mg ml^{-1} . The Chalikian (1996) method involved subtracting the
293 velocity of sound in the solvent from that in the 3 mg ml^{-1} solution, this is called the velocity

294 increment. On the other hand, our method plots the inverse square velocity against
295 concentration over the entire concentration range (Figure 2), a much more accurate
296 procedure. The scattering theory calculation estimates the contribution of thermal scattering
297 to the compressibility of 4%, much less than the estimate made in our earlier work by the
298 frequency independent, temperature scanning method. The compressibility value determined
299 by this method is the property of the scatterer of sound, which is the BSA molecule and any
300 modified water surrounding it (hydration layer). Scattering theory does not independently
301 provide a method for identifying the contribution of hydration and intrinsic compressibility
302 terms, but does identify the likely effect of thermal scattering in the compressibility
303 calculation. Given the nature of the temperature dependence of the compressibility (Figure 3
304 in Apenten et al. (2000)), the thermal scattering contribution may have a big relative impact
305 on compressibility close to the melting temperatures (T_{m1} and T_{m2}) because here the
306 compressibility is small and the thermal contribution may therefore be a large proportion of
307 the total compressibility. Comparison of the two sets of the experiments indicates that there
308 may be a significant time dependent and hysteresis component in the compressibility. As
309 discussed below, we can also expect the entropic contribution from the hydrophobic groups
310 coming in contact with water as the molecule unfolds to have an impact on compressibility.

311 Holmes and Challis' (1996) data indicate that at the relaxation peak of 20 MHz;
312 approximately half of the attenuation relative to water is due to relaxation processes at 37 °C.
313 The attenuation data for the BSA solution at 25 °C is shown in Figure 3. We have not
314 attempted to separate out the contributions of relaxation and scattering, due to the complexity
315 of the problem. The attenuation for the molecules is determined from Equation 4, through a
316 plot of attenuation against concentration of BSA, where we have combined together
317 relaxation contribution and scattering contributions. It is notable that the attenuation of the

318 molecules is very large compared with water. At 160 MHz, the attenuation in water is
319 $\sim 560 \text{ Npm}^{-1}$, but for the BSA molecules, it is $\sim 5200 \text{ Npm}^{-1}$, almost a factor of 10 higher. The
320 excess attenuation of the solution over water was nearly 90 Npm^{-1} at the highest
321 concentration, which corresponded to a volume fraction of 0.03 (or 3% v/v).

322 **3.2 Oligomerisation (Protein-protein interaction)**

323 The BSA samples were heated in such a way that all stages of the
324 oligomerisation/aggregation process of the protein could be studied. The ICHOS II
325 instrument had the advantage that it requires only a few millilitres of sample. Figure 4
326 contains data from three replicated experiments and shows that aggregation can be
327 reproducibly induced in BSA at 60°C increasing the particle size from approximately 8 nm
328 to approximately 21 nm within one hour, according to DLS measurements (insert in Figure
329 4). Further treatment up to 3 h appears to have no further effect on particle size, although the
330 higher resolution SEC data measured at 70°C (Figure 5, Figure 6) indicates that the amount
331 of monomer and dimer continue to decrease with an increase of the trimer; nevertheless, only
332 the monomer, dimer and trimer are present in significant quantities. It is unlikely that
333 significant denaturation is occurring in these experiments because no change in the velocity
334 of sound was seen, consistent with studies in HSA (Mitra, Sinha, & Pal, 2007) and an
335 unchanging molecular conformation.

336 **3.3 Heat denaturation of BSA**

337 This part of the study presented a challenge due to the large quantities of protein (500 ml)
338 required by the Malvern Ultrasizer. The Ultrasizer was nevertheless included because it
339 gives absolute attenuation values, useable as a reference. Thus, it was necessary to heat large
340 quantities and this was achieved using canning techniques for which a typical heating curve is

341 shown in Figure 1. The resultant attenuation spectra and DLS data are shown in Figure 7,
342 Figure 8, together with an estimate of the relative proportions of monomer, dimer and trimer
343 in the 20 nm peak (Table 4). It is clear that aggregation of the BSA is manifested in these
344 data, showing an increase in attenuation with heating. Little change in the main peak in the
345 DLS data is seen, in comparison with the control sample for the first three minutes. After
346 four minutes the size of the main peak begins to increase and becomes more scattered with a
347 distinct increasing trend in size. The secondary peak appears after ten minutes then rapidly
348 rises for the rest of the experiment. Associated changes in the velocity of sound and density
349 (not shown) are too small to explain the changes in the attenuation spectra. However,
350 significant changes in the velocity of sound occurred at the point where it became impossible
351 to carry out attenuation spectroscopy and DLS measurements, probably due to the
352 introduction of a frame modulus to the elastic modulus, in addition to compressibility, arising
353 from gelation (see later discussion). On heating at 80 °C for 100 s, the initial BSA solution
354 becomes yellow and translucent, then more cloudy. After 1000 s at 80 °C, the sample
355 becomes gel like, and becomes stiffer with heating time.

356 The storage modulus G' increases with heating time and approaches G'' at roughly two
357 minutes (Figure 9). The DLS data (Figure 8) indicates the appearance of large aggregates
358 after 10 minutes. Between 100 and 300 seconds, G' increased rapidly signifying that
359 aggregates were forming in solution, then after ten minutes gelation occurred, coinciding with
360 the rapid rise in the secondary DLS peak in Figure 8. Then G' kept on increasing with the
361 time of cooking, indicating that gelation continued to develop (Baier, Decker, &
362 McClements, 2004). The fact that G' continues to increase throughout 2 hours shows that the
363 gel formation was not completed and that the structure of the gel was still evolving. Neither
364 DLS nor attenuation spectroscopy could be performed after roughly ten minutes at 80 °C, in

365 the case of the Ultrasizer; this was because the transducer movement broke up the gel
366 structure. Whilst this problem does not present in the case of the ICHOS II instrument,
367 measurements were only carried out on samples that did not gel. No measurements were
368 possible on the BSA sample heated at 105 °C because it was not possible to insert the solid
369 sample into the ultrasound measurement cells, which are designed to take liquids.

370 The DLS data (Figure 8) indicates that dimerisation and trimerisation (Table 4) dominates the
371 first 4 minutes of ‘cooking’, followed by the rapid increase in large aggregates. However, it
372 was not possible to resolve dimers from trimers based on the DLS data. Attenuation shows
373 an increasing trend with cooking time, presumably as it responds (Figure 10) to the
374 aggregation process.

375 **4 Discussion**

376 **4.1 Relaxation**

377 BSA has been the subject of significant attention in ultrasound studies (Kessler & Dunn,
378 1969; Zana & Lang, 1970; Hussey & Edmonds, 1971; Lang, Tondre, & Zana, 1971;
379 Kremkau & Cowgill, 1985; Barnes, Evans & Lewis, 1985; Kremkau, 1988; Bryant &
380 McClements, 1999), presumably because the quantities required to make accurate attenuation
381 measurements necessitated a readily available protein. At lower frequencies than our range
382 (Barnes et al. (1985, 1986, 1988), some absorption peaks indicate conformational changes
383 and proton transfer at amino groups.

384 In the frequency range of the experiments reported in this work, most absorption was
385 previously attributed to proton transfer equilibria (Kessler and Dunn (1969), Dunn & Kessler,
386 (1970), Barnes et al.(1985) Choi, Bae & Takagi (1990), Holmes and Challis (1996)) These

387 workers carried out a variety of relaxation frequency fitting. In contrast, in our work no
388 absorption peaks were observed. We analyse the attenuation spectra as a scattering
389 phenomenon, where relaxation effects are lumped together in the apparent attenuation
390 properties of the solute (i.e. in the frequency squared dependence of the attenuation
391 coefficient).

392 Mitra, Sinha & Pal (2007), recently reported measurements in the temperature range 20 °C to
393 70 °C, on human serum albumin (HSA) using a range of techniques including ultrasound,
394 which suggest a rapid loss in α -helicity beyond 55 °C but no observable change in secondary
395 and tertiary structure below this temperature.

396 It is apparent from these studies, that relaxation processes make a significant contribution to
397 the molecular attenuation of sound, in addition to scattering effects. The separation of the
398 contributions of relaxation and scattering is non-trivial and is the subject of current studies in
399 our laboratory. Whilst, in the case of ultrasound attenuation, we have not separated out the
400 relaxation contribution and have studied the ultrasonic data in the context of scattering by the
401 molecules, we have shown above that in the case of BSA, the dependence of the velocity of
402 sound is accurately explained by a scattering model (Figure 2).

403 **4.1 Denaturation**

404 When the BSA solution is heated, the protein molecules unfold, the compact structural form
405 of the molecule is disrupted. The globular proteins undergo conformational changes that
406 allow hydrophobic groups or groups containing sulfhydryls, to be exposed. Protein
407 aggregation and gel formation occur when the protein surface activity is sufficient. According
408 to Clark, Kavanagh & Ross-Murphy (2001), heat-induced gelation of BSA is considered a
409 multistage process that involves three main stages. The first step is the initial protein

410 unfolding under heating which leads to a more reactive structural form. Sometimes
411 dimerisation happens. The second step is the formation of linear fibril aggregates via
412 disulfide and hydrophobic bonding. The aggregates form by nucleation and growth. The third
413 step is a random cross-linking of the fibrils via non-covalent interaction. The association of
414 the fibrils follow a random poly-condensation process that generates many species. The BSA
415 gels show a strong inter-fibril connection. The visual observation of the samples after heating
416 gives an idea of the nucleation and growth of the aggregates, because the more the samples
417 were heated, the more it was possible to see bigger particles. The random poly-condensation
418 of the fibrils can also explain a big variation in the size distribution of particles even if
419 globally the size of the BSA particles increases with heating.

420 Boye, Kalab, Alli, & C.Y. (2000) on the other hand showed that a BSA gel is made of a
421 network of small BSA aggregates of different shapes and sizes in the nanometre scale. These
422 aggregates form through both disulfide and hydrophobic bonding. When native BSA
423 molecules are dispersed in phosphate buffer at neutral pH, they do not form gels because the
424 attractive interactions, which are principally van der Waals, hydrogen bonding, and
425 hydrophobic interactions, are weaker than the repulsive interactions, which are mostly
426 electrostatic, hydration and configurational entropy (Baier, Decker & McClements, 2004).
427 This point of view is more in accord with our results than the linear fibril view of Clark,
428 Kavanagh and Ross-Murphy, although we cannot exclude the formation of linear fibrils in the
429 final stages of gel formation.

430 The heat- or pressure-induced unfolding (denaturation) process is commonly treated as a two-
431 state model or transition comprising a native (N) and unfolded (U) state $N \leftrightarrow U$. This model
432 particularly applies to the unfolding of small monomeric globular proteins (Privalov, 1979),
433 for which intermediate states are neglected since they are considered so sparsely populated.

434 The main driving forces for folding are the entropic contributions of free water and changes
435 in entropy due to release/binding of water molecules, affecting the hydrophobic core of
436 globular proteins. At ambient and physiological temperatures, unfolding carries a significant
437 entropic cost, particularly due to the presentation of hydrophobic side chains to the solvent.

438 In order to understand how denaturation of the BSA molecule may impact its acoustic
439 properties it is necessary to locate them in the preceding model of oligomerisation and
440 denaturation.

441 Sound velocity is determined for the solution by the molar compressibility, which includes
442 contributions from the intrinsic compressibility of the molecule and the modified
443 compressibility of the water surrounding the molecule (commonly known as the hydration
444 layer). Thermodynamically, the compressibility is related to free energy since isothermal
445 compressibility is the pressure gradient of the chemical potential (Chalikian, 2008). Whilst
446 the intrinsic compressibility is affected primarily by secondary structure, the hydration
447 contribution is determined largely by the solvent-accessible area of the molecule. Since we
448 measure *adiabatic compressibility* in acoustic experiments, an additional thermal term will be
449 present.

450 A number of workers have reported studies of protein denaturation processes using
451 ultrasound velocity and absorption techniques (Kremkau, 1987; Wang, Tolkach & Kulozik,
452 2006). A detailed discussion of the relationship between solvent accessible area, intrinsic
453 compressibility, and hydration compressibility is to be found in Apenten et al (2000) and
454 Chalikian (2008). Molecular compressibility is likely to change in step with structural
455 changes associated with denaturation of the molecule, although the free energy difference
456 between folded and unfolded states of BSA is relatively small, since enthalpic and entropic
457 terms are approximately equal but opposite in sign, so folding in itself is unlikely to

458 contribute significantly to changes in compressibility. Our observation that the velocity of
459 sound in the BSA molecule hardly changes during the initial stages of denaturation is
460 consistent with small changes in free energy, solvent accessible area and secondary structure.

461 On the other hand, the attenuation of the molecule is not so directly related to free energy and
462 solvent accessible area. Rather it is controlled by scattering and relaxation, which appears
463 much more sensitive to denaturation. The ultrasound scattering model developed from our
464 data indicates that particle size changes associated with oligomerisation (dimers, trimers, etc)
465 are well below the size range where changes will impact on the ultrasound attenuation. We
466 expect therefore, but cannot prove since we were unable to separate the effects of scattering
467 and relaxation, that the attenuation changes we observe during oligomerisation arise due to
468 relaxation effects,.

469 Time- and frequency-independence of the sound velocity and density indicates that the
470 compressibility of the weakly heated treated molecules is constant, consistent with an
471 absence of significant changes to the primary, secondary and tertiary structure of the
472 molecule.

473 Significant changes in the velocity of sound (not shown) were observed once gelation
474 occurred, together with significant changes in elastic modulus (Figure 9). This may be
475 expected since gelation arising from denaturation will add an additional term to the material
476 compressibility due to the introduction of shear (G) and frame (an additional compressional
477 modulus arising from molecule-molecule interactions in the solid state) moduli to elastic
478 modulus governing the propagation of compressional ultrasound waves. Referring to
479 Equations 1 and 2, Figure 9 and the determined value for the bulk modulus of water of $2.23 \times$
480 10^9 Pa, the shear modulus in the most denatured samples does not exceed 100 Pa, far too
481 small a value to be measurable through the longitudinal wave velocity. This leaves

482 contributions from the frame modulus and/or changes in molecular structure as possible
483 explanations for the changing velocity of sound under conditions of severe denaturation.

484 **5 Conclusions**

485 In the experiments described above, conditions were adjusted so that the initial stages of
486 dimerisation and trimerisation could be studied. Less severe heat treatment caused the
487 molecule to form dimers and trimers, detected by the ICHOS II system through changes in
488 attenuation spectra consistent with DLS and SEC observed particle size increase. In this
489 case, no velocity changes were observed; this is consistent with little or no molecular
490 conformation change.

491 BSA was then 'cooked', the protein underwent all the stages of oligomerisation, aggregation,
492 denaturation and gelation described above. Irreversible denaturation and gelation of the
493 protein affected both ultrasound attenuation spectra and the velocity of sound, consistent with
494 significant molecular conformation change and/or molecule-molecule interaction.

495 Ultrasound measurements are sensitive to all stages in the aggregation and denaturation of
496 BSA, responding to changes in the tertiary and quaternary structure. Aggregation led to
497 measurable changes in ultrasound spectra correlating with DLS sizes. During
498 oligomerisation, the BSA molecules continue to behave acoustically as individual particles,
499 exhibiting little change in their compressibility. It is only when significant denaturation
500 occurs that molecular compressibility may change significantly. The burst-rf, pulsed-wave
501 ICHOS II system was much more sensitive to protein aggregation than the quasi-continuous-
502 wave Ultrasizer system for reasons which are still unclear.

503 In this study we set out to elucidate a theory which allowed quantitative interpretation of
504 ultrasound data in terms of particle properties such as size and compressibility. This proved

505 difficult because (a) proteins both scatter sound and exhibit relaxation and (b) the interaction
506 between the protein and water is a complicated one involving solvent accessible area, cavities
507 and entropic hydrophobic interactions during folding, unfolding and oligomerisation. A
508 significant question is why ultrasound attenuation detects dimers and trimers in a region
509 where scattering predicts that it is insensitive to particle size? This is likely to be because
510 oligomerisation changes molecular relaxation, without altering the acoustic scattering cross-
511 section significantly.

512 In summary, concentration dependent ultrasound velocity spectroscopy, together with
513 densitometry uniquely measures a key parameter which is characteristic of protein structure,
514 the molecular adiabatic compressibility. This can be related to solvent accessible surface area,
515 hence providing insight into protein-solvent interactions. A novel aspect of our study is the
516 demonstration that ultrasound attenuation spectroscopy is sensitive to protein-protein
517 interactions such as dimerisation, trimerisation and stages of denaturation including gelation.
518 Together, velocity and attenuation spectroscopy reveal details of protein-protein and protein-
519 solvent interactions at the relatively high protein concentrations found in foods. This can give
520 a unique insight into the relationship between protein structure and function in foods and
521 many other protein containing systems, including biological systems. Future work in this area
522 requires the separate identification of relaxation and scattering contributions to acoustic
523 propagation and comparison between the measured molecular adiabatic compressibility and
524 that determined from molecular modelling.

525

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631 **Tables**

632 Table 1 Calculation of partial molar volume for BSA.

633 Table 2 Partial molar volume, density and radius of BSA molecules in solution, derived from
634 the solution density measurements in this work and by Chalikian (1996), including the used
635 relationships between molecule radius, partial molar volume, molecular density and
636 molecular weight.

637 Table 3 Properties of water and BSA solute molecules used in calculations

638 Table 4 Monomer and oligomer data for BSA (Figure 8). Gravimetric data in the first row is
639 taken from Table 2 and is computed on the assumption that only monomers exist. These data
640 were obtained before heating. The DLS diameters are taken from the measured peaks in
641 Figure 8. In the final row, the composition of material in the 20 nm peak is then estimated
642 assuming it is composed of monomer, dimer and trimer.

643 **Figure Captions**

644 Figure 1 Representative temperature-time plot for the BSA denaturation studies. Solid line –
645 retort temperature; dashed line – in-can temperature.

646 Figure 2 Inverse square velocity of sound plotted against partial molar volume fraction of
647 BSA.

648 Figure 3 Attenuation relative to water, of BSA solution plotted versus frequency measured in
649 the ICHOS instrument, of BSA solution (dotted line) heated at 60 °C for 1h and control (solid
650 line) for 10 g/L at pH 7

651 Figure 4 Attenuation relative to water plotted against frequency for BSA in aggregated and
652 monomer forms. Inset is the DLS plot of volume % versus size. The standard error of the
653 attenuation measurements is $\pm 0.2 \text{ Np m}^{-1}$ and data are plotted for three replicated
654 experiments.

655 Figure 5 SEC retention time versus absorbance for BSA heated to 70 °C for 60 min (closed
656 circles), 120 min (plus signs) and 180 min (inverted triangles), together with the unheated
657 control sample (squares).

658 Figure 6 % total peak area plotted against heating time for the data of Figure 5. Peak 1
659 represents the trimer species. Peak 2 represents the dimer species and peak 3 represents the
660 monomer species.

661 Figure 7 Total attenuation spectra for 40 g/l, pH 7 BSA solutions for ‘cooking times’ of 0 min
662 ■, 2 min □, 4 min ▲, 6 min X, 8 min ○ and 10 min ●.

663 Figure 8 DLS particle size distributions for 0 min (solid line), 4 min (dashed line), 8 min
664 (dotted line) and 12 min (dotted-dashed line); for the system of Figure 7.

665 Figure 9 Plot of G' and G'' for BSA heated at 80 °C.

666 Figure 10 Total attenuation of BSA solution plotted versus cooking time at 80 °C for 40g/l at
667 pH 7 and 115MHz.

Figure 1

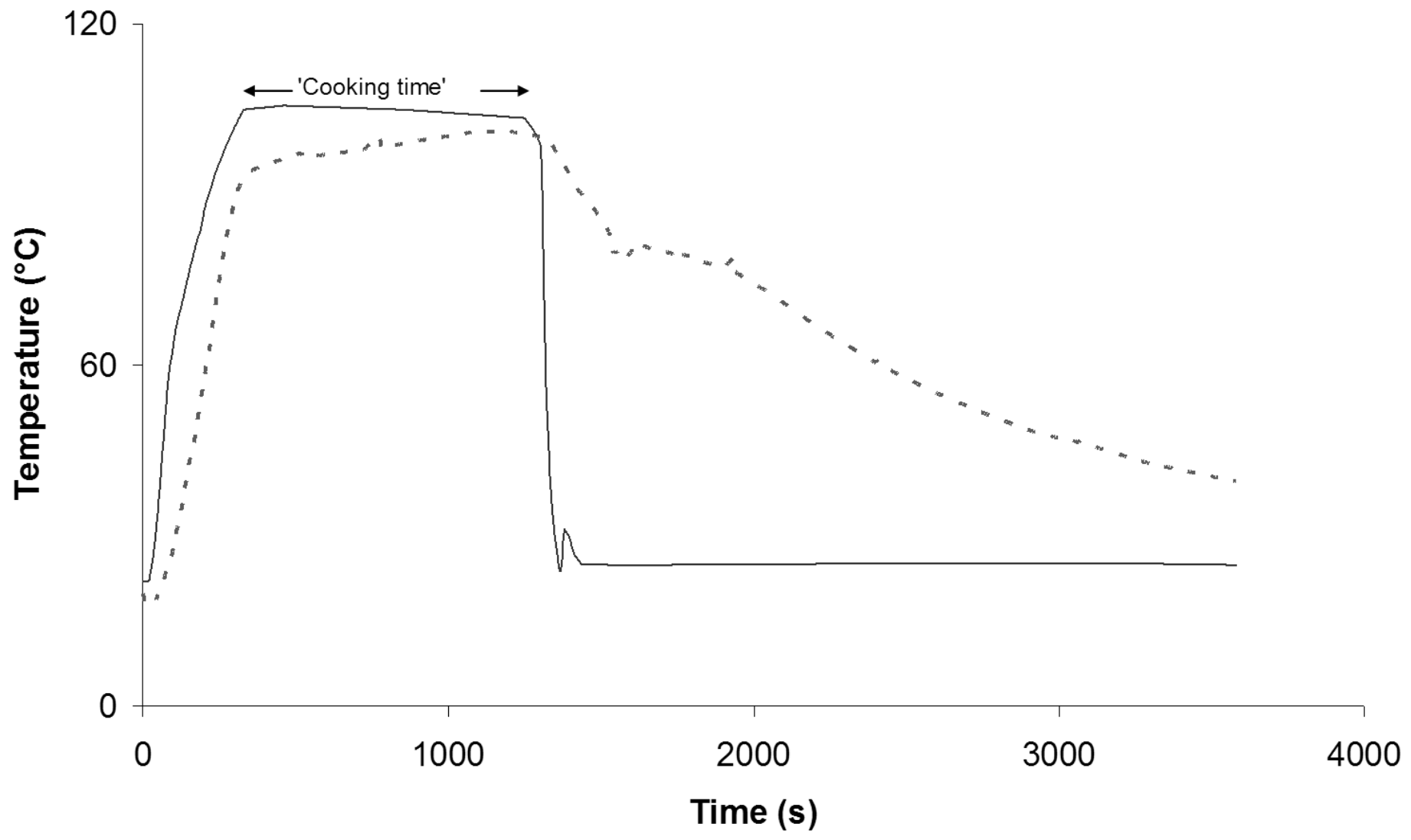


Figure 2

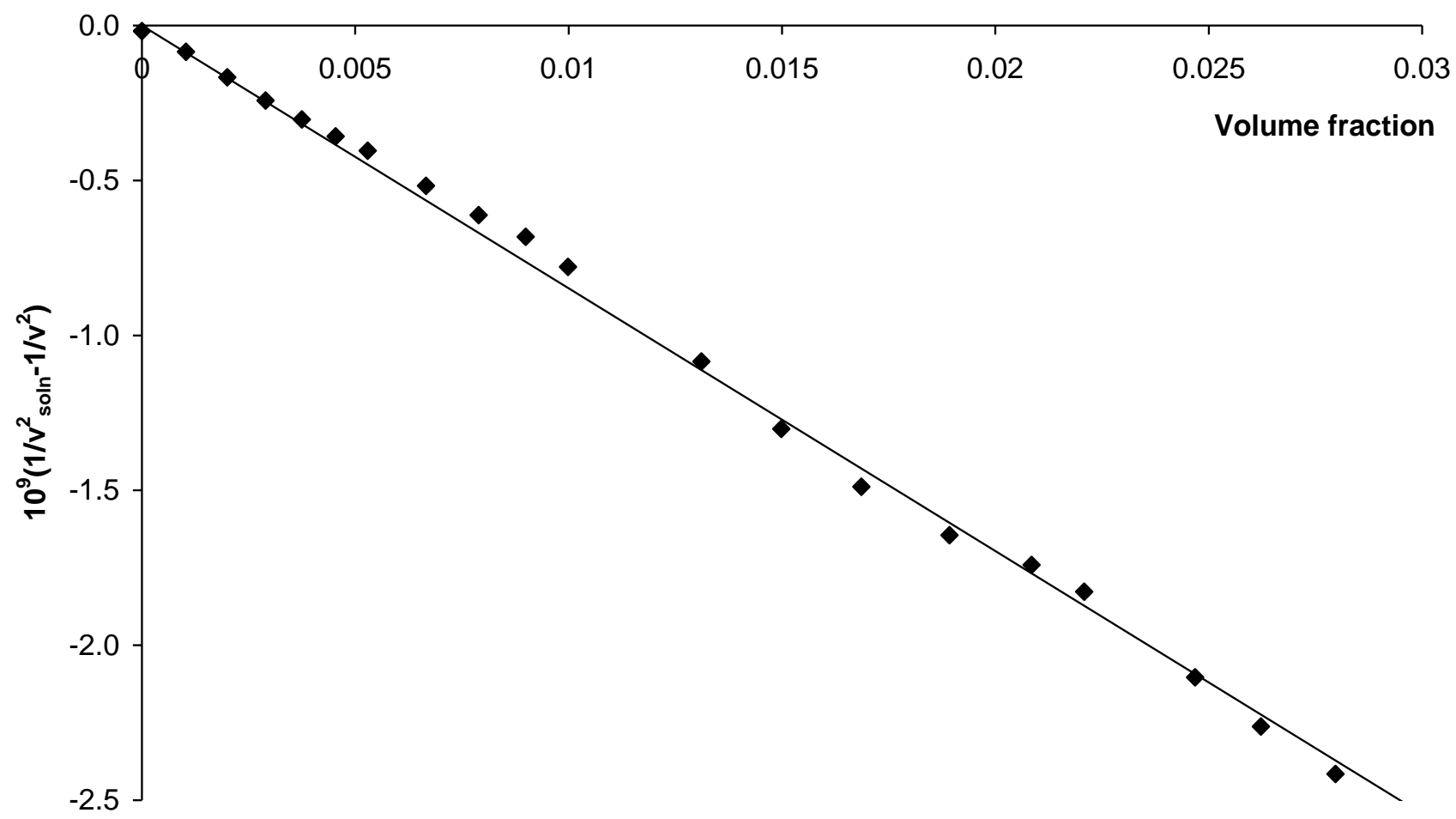


Figure 3

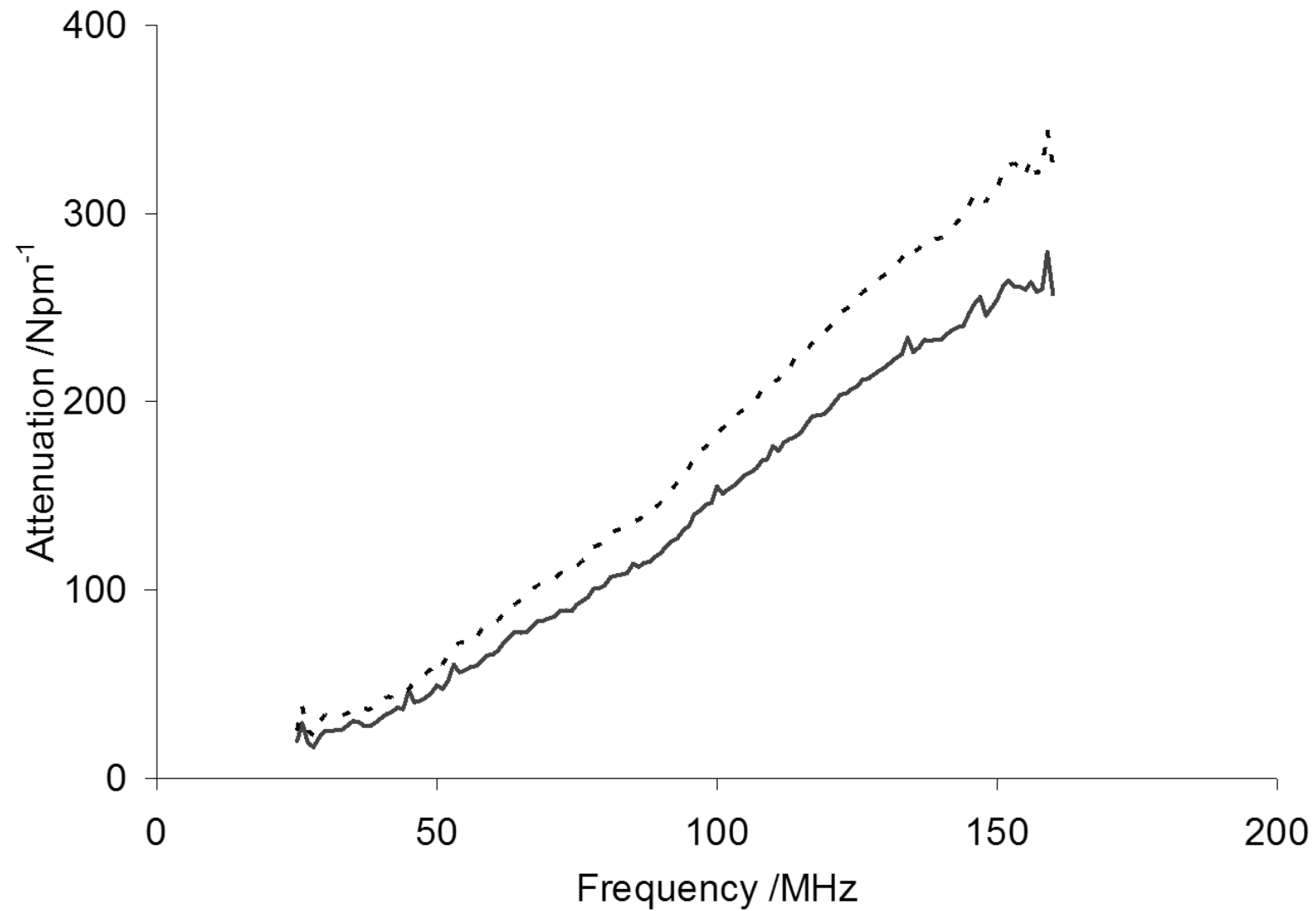


Figure 4

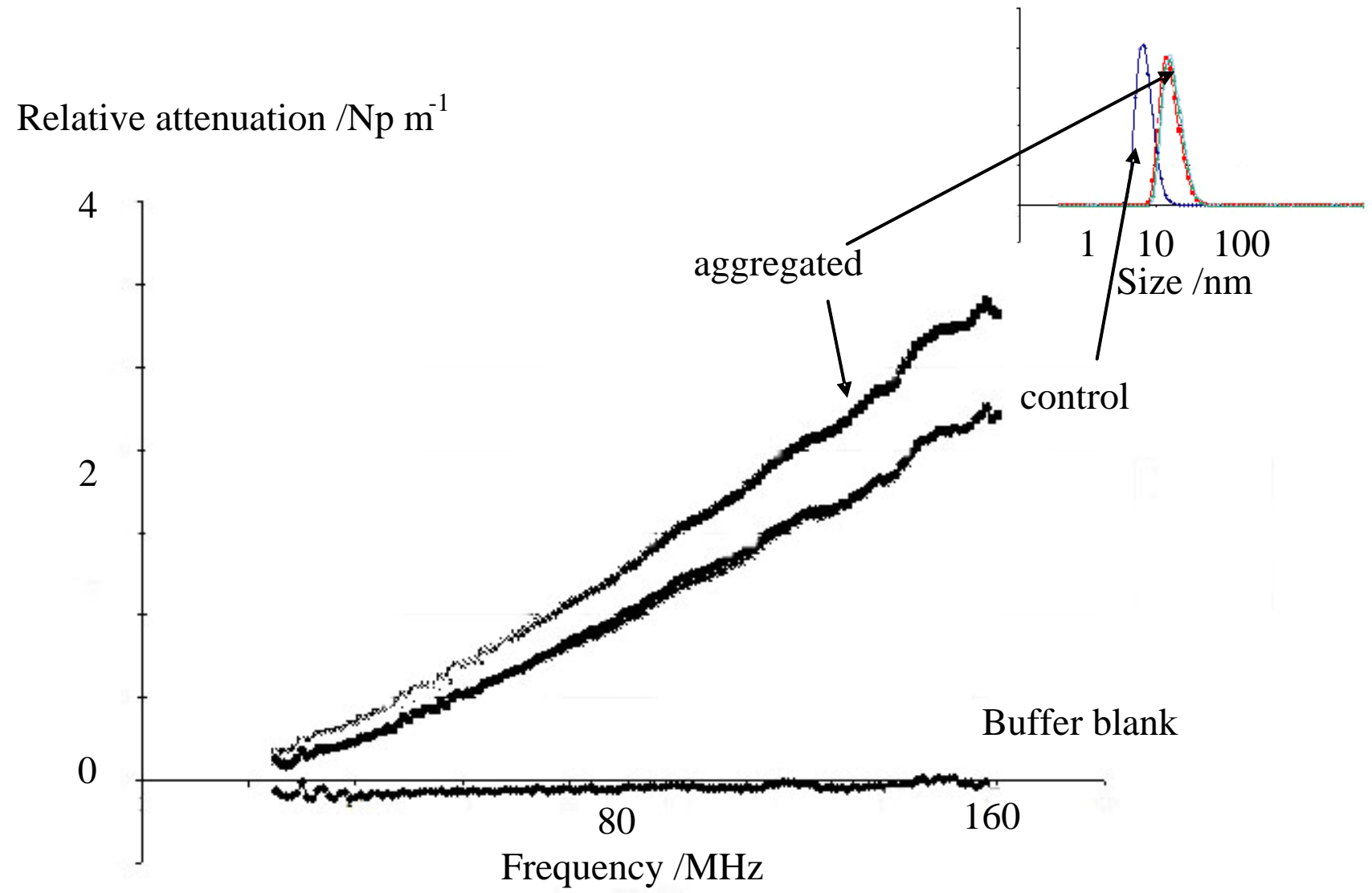


Figure 5

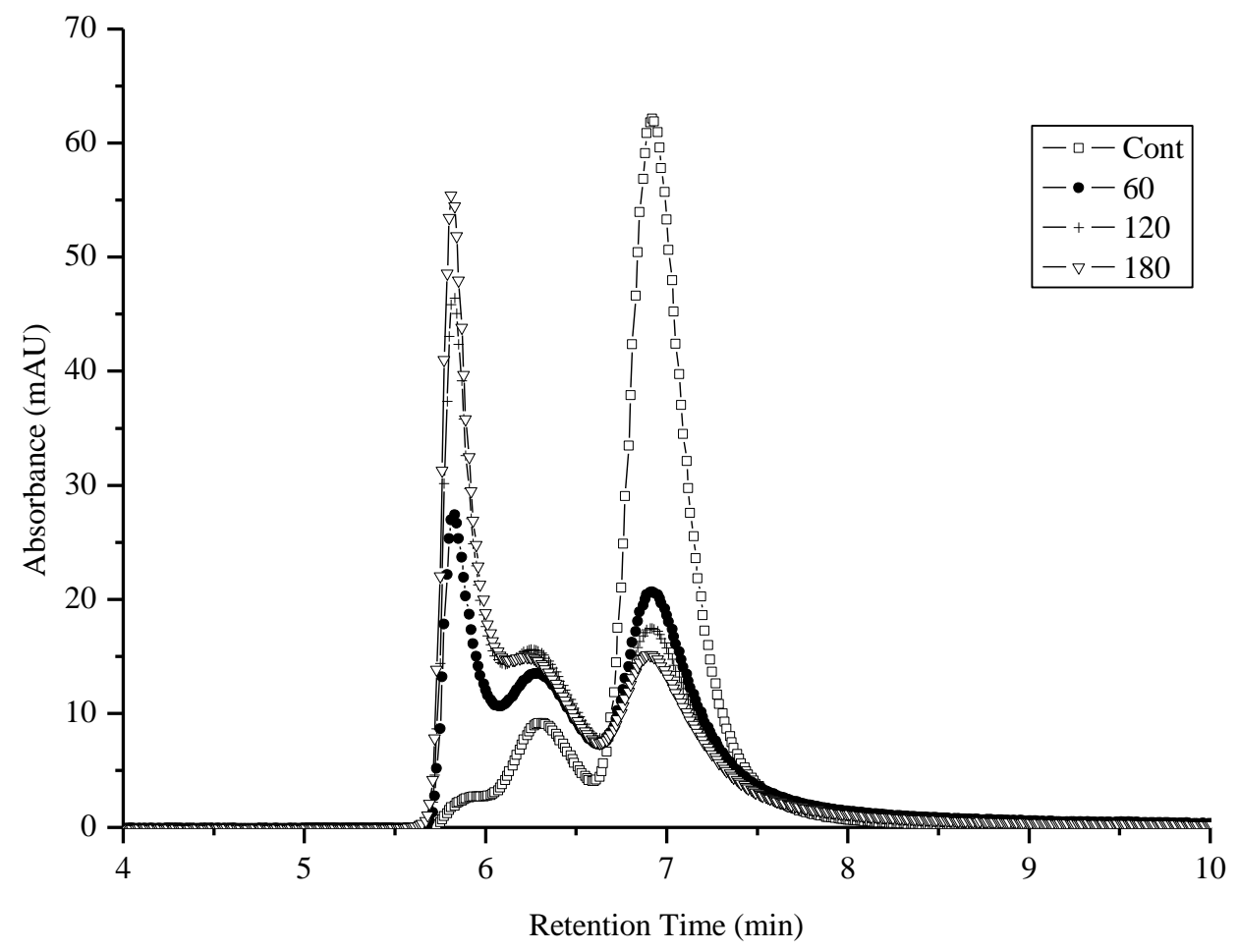
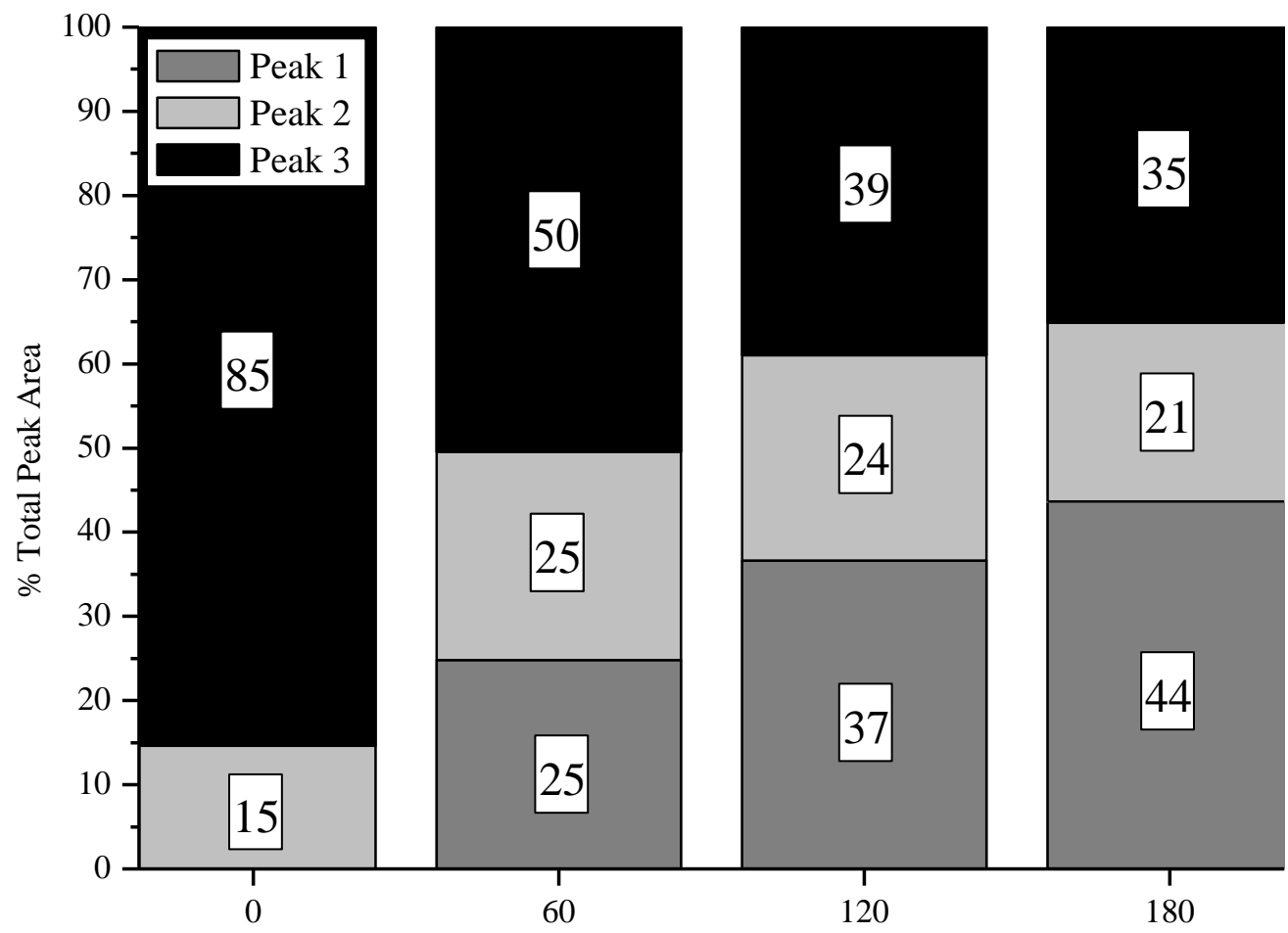


Figure 6



Abscissa values are the heating periods in minutes

Figure 7

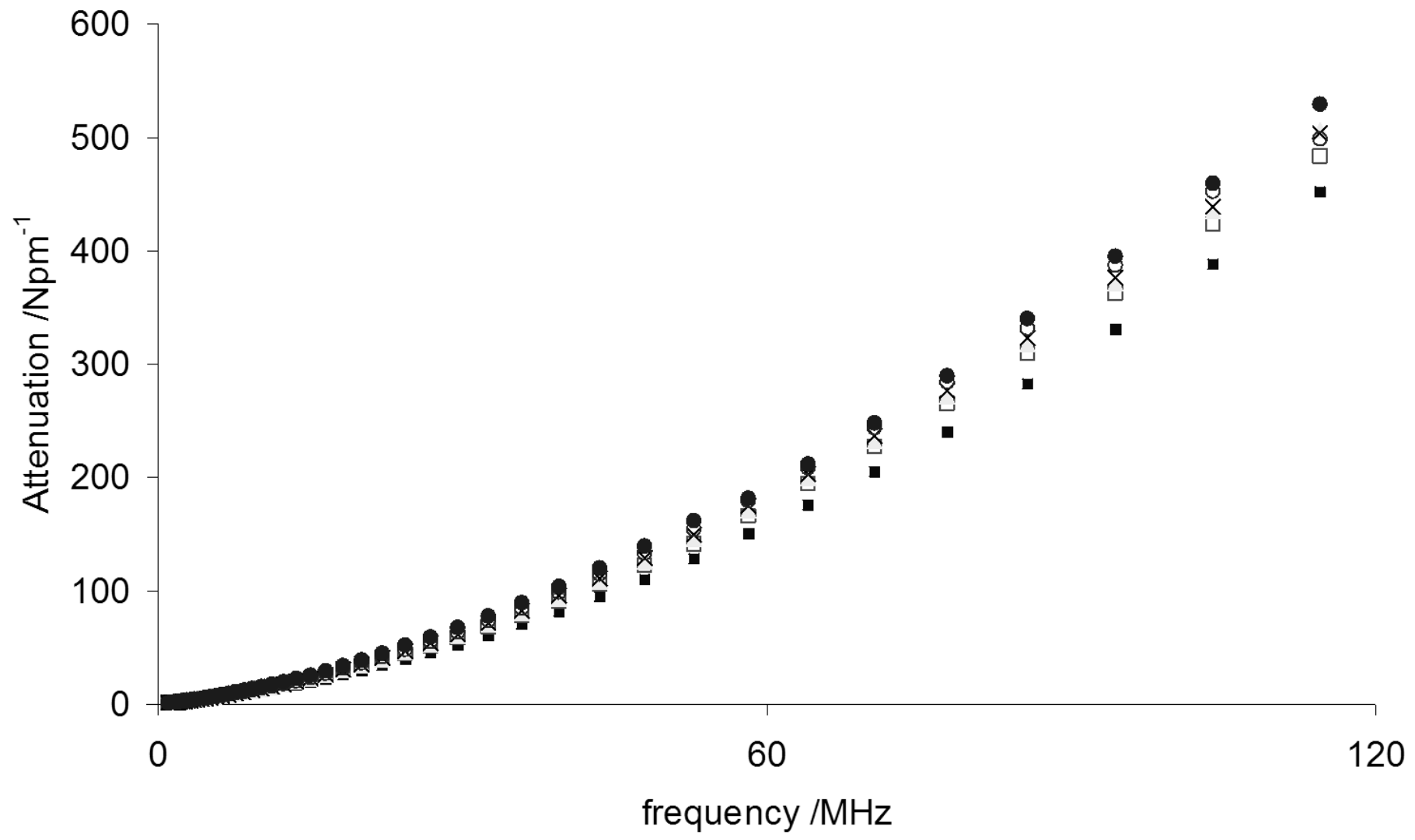


Figure 8

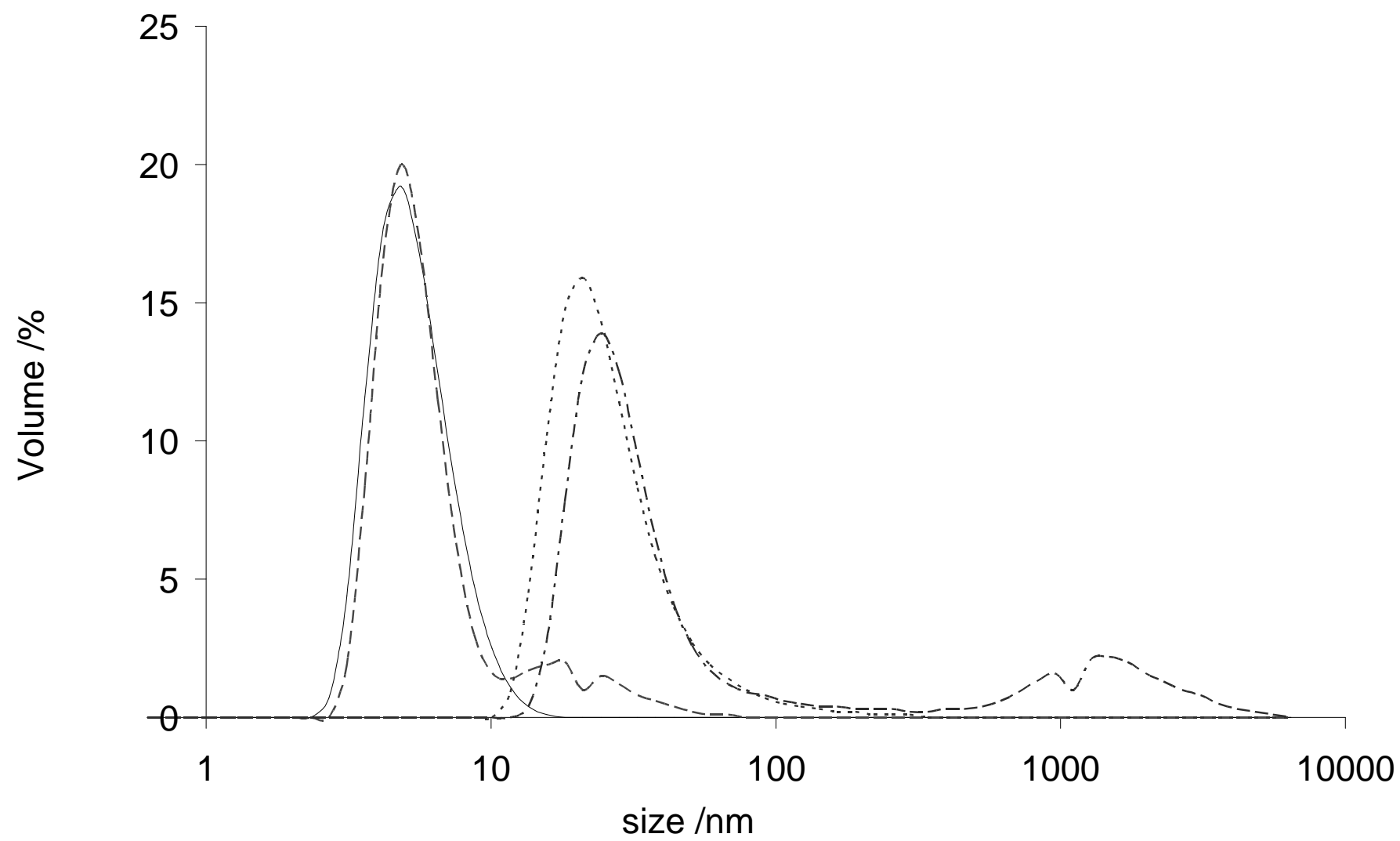


Figure 9

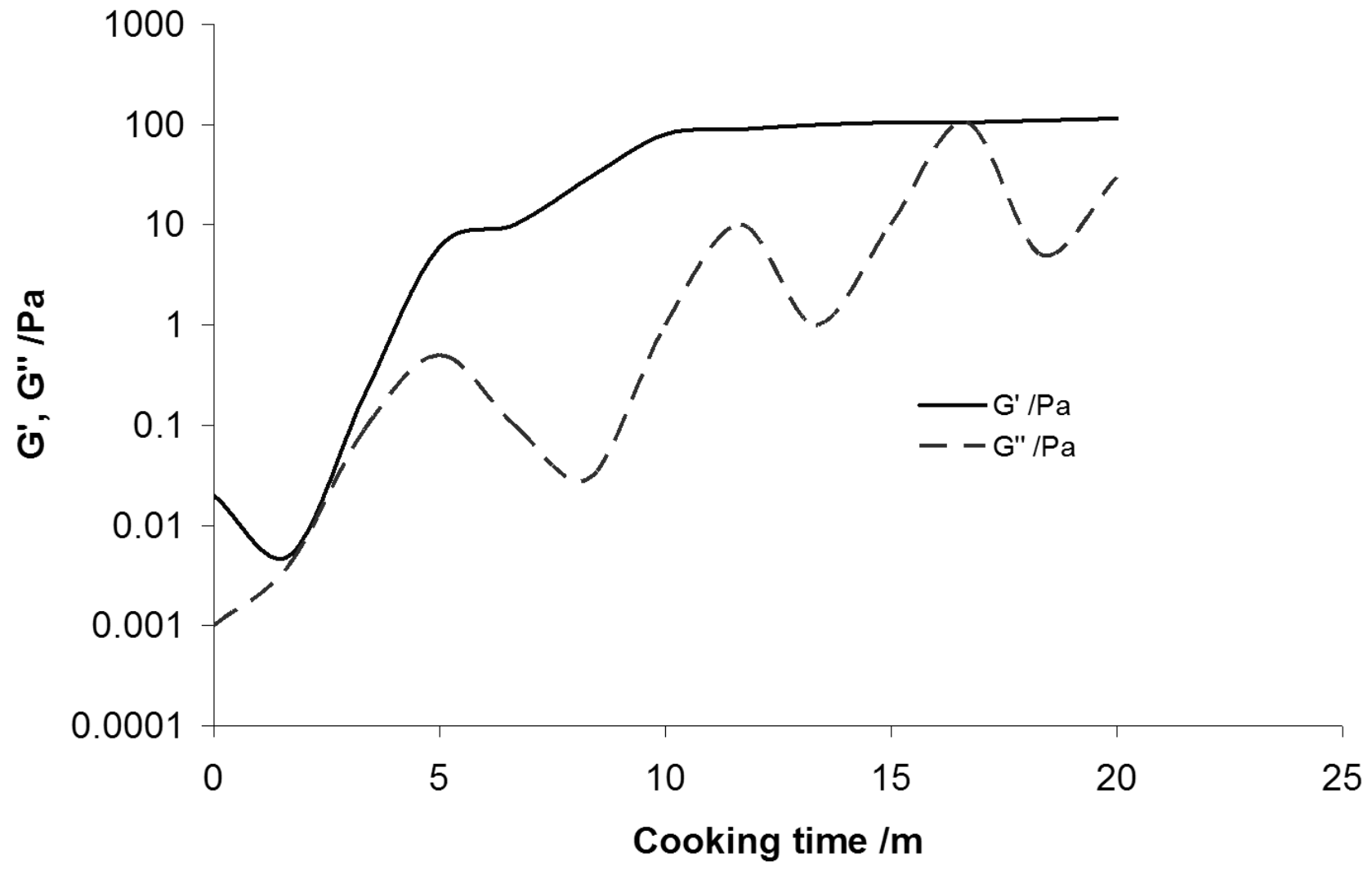


Figure 10

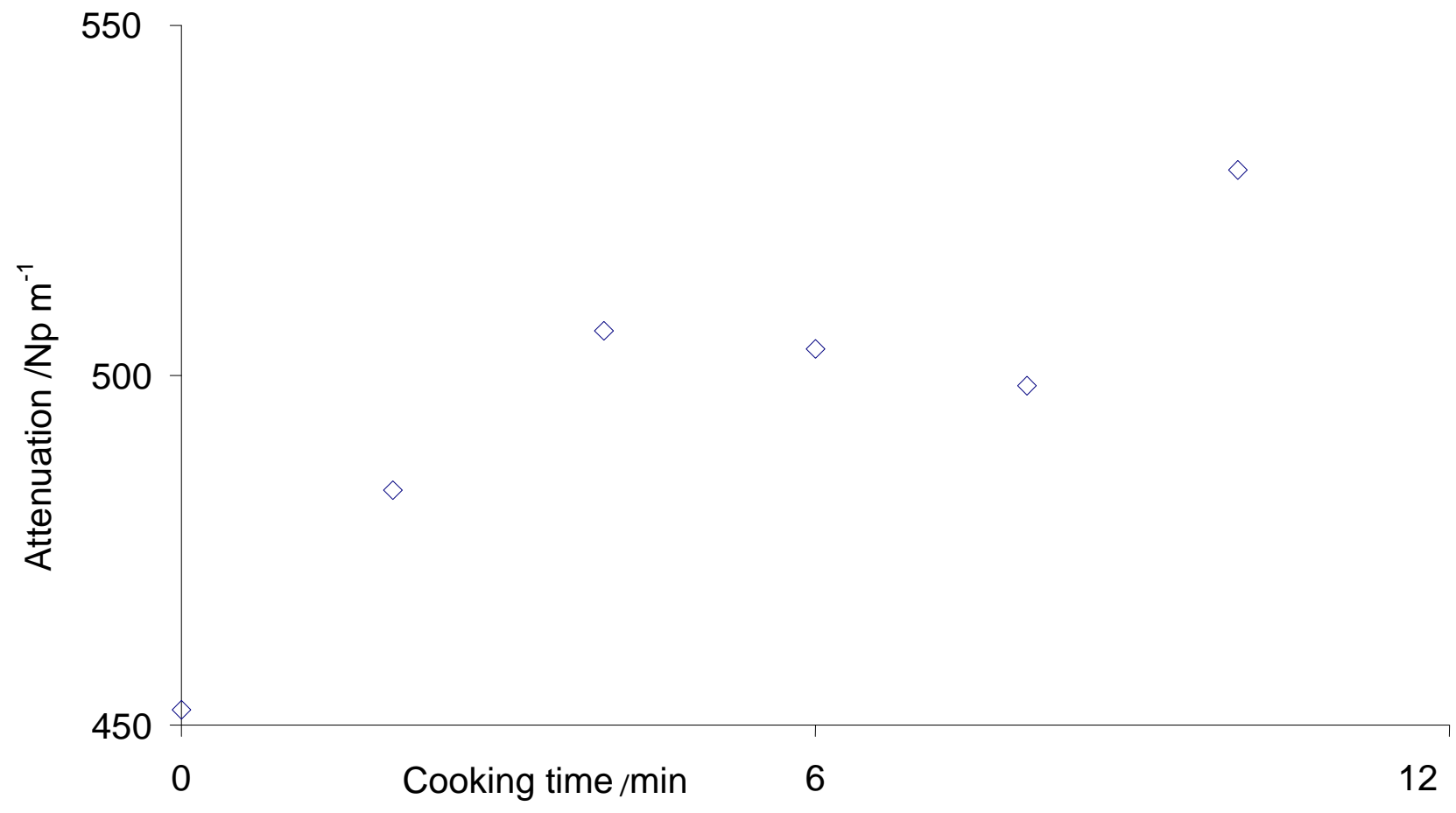


Table 1

$c / \text{mg mL}^{-1}$	$\rho / \text{kg m}^{-3}$	V / mL	m_{BSA}
0	1002.8	997.2	0
10	1005.1	1005.0	0.000151
20	1007.9	1012.2	0.000304
30	1010.5	1019.9	0.000460
40	1012.6	1028.1	0.000618

Table 2

Property	Value	
	This work	Chalikian (1996)
Partial molar volume \tilde{V}_{BSA}	49823 mL mole ⁻¹	49980 mL mole ⁻¹
Density ρ_{BSA}	1334.7 kg m ⁻³	1361 kg m ⁻³
Radius of molecule r	2.7 nm	2.7 nm
Molecular weight MW	66500 kDa	68000 kDa
	$\frac{4}{3}\pi r^3(6.022 \times 10^{23}) = \tilde{V}_{BSA}$	
	$\frac{4}{3}\pi r^3(6.022 \times 10^{23}) \times \rho_{BSA} = MW \times 1.660 \times 10^{-24}$	

Table 3

Property	Water	BSA solute
Ultrasound velocity / m s^{-1}	1496.2	
Density / kg m^{-3}	997.0	1334.7
Thermal expansivity / K^{-1}	0.00011	0.00042
Viscosity / Pa s	0.0009	
Specific heat capacity / $\text{J kg}^{-1} \text{K}^{-1}$	4178	1900 ^a
Thermal conductivity / $\text{W m}^{-1} \text{K}^{-1}$	0.591	0.17 ^a
Attenuation exponent p	2	
Attenuation factor / $\text{Np m}^{-1} \text{MHz}^{-p}$	0.022	

a Bryant & McClements (1999)

Table 4

	diameter	volume	Volumi	Monomeric	dimeric	trimeric
	/nm	/nm³	nosity	units	units	units
Gravimetric	5.4	82.44	3.25	1		
DLS monomeric	8	268.08		1		
dimeric	10.07	536.16		2		
trimeric	11.53	804.24		3		
DLS aggregate	20	4188.79		15.625	7.81	5.21

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14 November 2010

Dear Editor,

I am pleased to submit an extensively revised version of our paper entitled
"Investigation of bovine serum albumin denaturation using ultrasonic spectroscopy"
for consideration for publication in Food Hydrocolloids.

Best wishes,

Malcolm Povey

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Author's reply to reviewers comments.

We are very grateful to the reviewers for their careful reading of our manuscript and their valuable comments. Our replies (In blue italics) follow each comment below. We have provided a word manuscript using 'track changes' to mark our changes.

Reviewers' comments:

Reviewer #1: In this work, the authors report ultrasonic properties of BSA solutions (pH 7) before and after various heating steps. They characterize the resultant aggregation by dynamic light scattering and chromatography and the properties of gels forms by small deformation rheological measurements. As the authors describe, various authors have used ultrasonic methods to characterize the effects of thermal treatments on proteins. My biggest difficulty in this work was deciphering the important and novel findings. In general a shorter and more focused paper would be helpful.

What is the major distinction between the current work and the Apenten paper by some of the main authors? Are there any numbers to compare between papers? In general wherever possible provide direct numerical comparisons with data from other studies. What types of figures have been reported for protein density, ultrasonic velocity and compressibility?

The major distinctions between the current work and the Apenten work are that we measured (a) over a wide frequency range (2-160 MHz) rather than at one frequency (2.25 MHz); (b) isothermally rather than by scanning temperature at 20 C hr⁻¹; (c) both velocity and attenuation.

We have added a detailed comparison of data from our previous work and other studies, quoting data where available.(Table 2 and)

P14, last sentence: I am not clear why protein folding thermodynamics would lead to differences between the analytical methods. Also there really hasn't been much discussion of protein denaturation to this point.

We have omitted this since it overly complicates the argument.

P15, first sentence: I don't see anything in Figure 4 that could support a statement on the reproducibility of the experiment nor on the kinetics of aggregation. Further down that page the authors state that the ICHOS technique is sensitive to oligomerization. Is it not equally possible that the changes seen are due to denaturation?

We have added the standard error and the number of experimental replicates to Figure 4 to indicate the reproducibility of our experiments. No statements are made regarding the kinetics of aggregation, except to note that aggregation appears to be largely complete after 1h heat treatment. This is based on the fact that little measurable change in SEC or ultrasound data can be seen after that time, up to a further two hours of measurement. This has been clarified in the paragraph. It is possible that denaturation contributes to the measured changes, however, there is

no accompanying change in the velocity of sound which would be expected if denaturation was occurring.

Again on P14 Table 4 is referenced for the first time to state that the ICHOS method cannot distinguish the proportions of the oligomers. I don't follow what is being listed in the table, how the numbers were calculated, or how it supports the conclusion

We agree that the presence here of Table 4 is misleading. It is an estimate of the proportions of oligomers obtained for the experiment conducted at 70 °C and is based solely on DLS data.

Overall the first paragraph on P15 took me a long time to read and understand and would probably benefit from a rewrite.

This paragraph has been rewritten.

I found Figure 9 hard to follow and unhelpful. Surely the position of the median size within each peak is less important than the population of the peak.

This Figure has been removed from the paper.

In the chromatography data, how were the peaks deconvoluted? Is it certain that the three peaks correspond to monomers, dimers and trimers?

The column was calibrated using a set of protein standards covering a range of known molecular weights (Blue Dextran (2000 kDa), Thyroglobulin (Bovine) (669 kDa), IgG (Bovine) (150 kDa), Serum Albumin (Bovine) 66kDa, Ovalbumin (Chicken) 44 kDa, Lysozyme (Chicken) 14.5 kDa . The procedure followed was a modification of the methods of Whitaker [19] and Andrews [20].

Whitaker, J.R., Determination of Molecular Weights of Proteins by Gel Filtration of Sephadex. Anal Chem, 1963. 35(12): p. 1950-3.

Andrews, P., Estimation of the molecular weights of proteins by Sephadex gel-filtration. Biochem J, 1964. 91(2): p. 222-33.

Void volume (V₀) was determined by recording the elution volume (retention time) of Blue Dextran at 280 nm. The elution volume (V_e) of each protein in the Mw marker mixture was determined at 280 nm by observing the retention time recorded by the instrument software.

A standard curve was created by plotting the Log₁₀ of the Mw vs. V_e/V₀ for each protein in the mixture. V_e/V₀ values were calculated for the unknown samples and the standard curve used to determine the estimated Mw.

This detail has been added to the manuscript

Was there any effort made to degas the gels and viscous solutions?

No, however, the headspace was degassed using steam during the canning process, and prior to heating.

I found Figure 10 unnecessary and the relevant observations could easily be conveyed in the text.

This Figure has been removed from the paper.

P19, Does the Clark, Kavanaugh and Ross-Murphy paper state that linear fibril formation is a general phenomenon in protein gelation? (I don't have a copy in front of me but I don't remember that). Seems to contradict the Boye ref in the next paragraph.

Clark, Kavanaugh and Ross-Murphy indeed say as quoted "network building appears to involve three main stages: initial protein unfolding, linear fibrillar aggregation, and random cross-linking of the fibrils" It does indeed appear to contradict Boye et al whose point of view is more consistent with our data. However, we were unable to make detailed measurements on the final stiff gel. We have added a comment to this effect.

The first complete sentence on P20 would seem to be a better fit with the start of the denaturation section before the discussion of aggregation mechanisms. The second complete sentence on that page introduces surface activity. This is the first mention of surface activity and appears to make no sense in context. The whole protein denaturation section seems to contain a lot of detail not really germane to the manuscript.

We have shortened the discussion according to this referees comments.

The first sentence on P21 seems to suggest that ultrasonic attenuation changes depends on free energy differences. Is ultrasonic velocity directly related to free energy?

Isothermal compressibility is given by the pressure gradient of the chemical potential which is related to the Gibbs Free Energy. The ultrasound velocity depends on the adiabatic compressibility which contains thermal terms as well and upon density. So it is not simply related to the free energy, although it can be argued that it is 'directly' related because there is a relationship. A comment along these lines has been incorporated into the paper.

In many cases the axis labels in the figures reproduces incorrectly.

The publisher's pdf converter inaccurately converts our word documents to pdf. We have attended to this problem.

Check the abbreviation for cooking time in Figure 11 and 12

Corrected to min.

Is the oscillation in the G'' data real (Figure 11).

The wiggles in the data are well within instrumental error. However, we do not have an explanation for these.

Reviewer #2: The manuscript was presented in a clear and organised manner. However, there are several points that needed to be clarified.

General comments and corrections

1. Please number each line of the manuscript for the ease of reviewing

We have done this.

2. Please elaborate the novelty of present investigation, with the aid of suitable citations. It was not clearly reveal in the introduction sections.

3. Please explain clearly the key advantages of using ultrasound spectroscopy in characterizing BSA denaturation. Indicate clearly in the introduction and / or results and discussion
4. Please explain the rationale and reason of not using circular dichroism (CD), and probably compared with the results of previous work with the current results, in the results and discussion

Points 2 to 4 above have been addressed in a modified introduction.

Specific corrections

1. Figure 1, 3, 7, 9, 11: Please provide a better quality figure to indicate the y-axis clearly.

This was caused by a fault in the word to pdf conversion during document submission and has now been corrected.

2. Section 2.4.2: Please explain the reason of using multiple wavelength detector in Size Exclusion Chromatography. Please provide valid citation, if this is a validated method. Usually, SEC was detected using RI or MALS detector.

2. This has been done in the reply to the first referee.

Reviewer #3: The work by Povey et al. reported ultrasonic spectroscopic study on the denaturation and gelation of bovine serum albumin. The study provided a new insight into the structure change, molecular interaction, and molecule-solvent interaction during denaturation and gelation of proteins. The reviewer would recommend the publication of the paper after the following points have been considered during revision:

- 1) The structure of the paper can be better balanced. For example, the theoretical background and instrumentation of ultrasonic spectroscopy should be shortened, and only the essential equations necessary for the discussion of data presented. More significantly, the authors reviewed extensively and in details the previous works on contribution of molecular relaxation to ultrasonic attenuation. This was just for the purpose of demonstrating that even without separating out the relaxation contribution their data could be described by scattering model. Such a detailed review of molecular relaxation therefore seems not absolutely relevant, and can be briefed.

The discussion has been extensively revised.

- 2) In page 16, the authors stated G' and G'' crossed at roughly two minutes. There however seemed to be no a real crossover between G' and G'' from Figure 11; they just approached each other. Considering this and the DLS data that showed no large scale aggregation before 10 mins, I would prefer to think that gelation did not occurred until 10 mins. The author however argued that the gel started to form between 100s and 300s.

The text has been altered in accordance with the above comment.

- 3) Most of the equations were not displayed correctly in the pdf file.

This was due to a problem in the pdf converter which has been addressed. The original was a word document.

- 4) The axes and axis labels of most of the figures, particularly in Figure 1, 3, 7, 9 and 11, need to be made clear.

This was also a problem caused by the pdf converter, which has been addressed.

5) In Figure 5, Please give the wavelength at which the absorption was measured.

The wavelength was 280 nm, more detail is given in the reply to the first referee.