

1 **Design of β -lactoglobulin micro- and nanostructures by controlling gelation through**
2 **physical variables**

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13 **Abstract**

14 β -lactoglobulin (β -Lg) is the major protein fraction of bovine whey serum and its principal gelling
15 agent. Its gelation capacity enables conformational changes associated with protein-protein
16 interactions that allow the design of structures with different properties and morphologies. Thus,
17 the aim of this work was to successfully use β -Lg, purified from a commercial whey protein
18 isolate, to develop food-grade micro- (with diameters between 200-300 nm) and nano- (with
19 diameters \leq 100 nm) structures. For this purpose, the phenomena involved in β -Lg gelation
20 were studied under combined effects of concentrations (from 5 to 15 mg mL⁻¹), heating
21 temperature (from 60 to 80 °C) and heating time (from 5 to 25 min) for pH values of 3, 4, 6 and
22 7. The effects of such conditions on β -Lg structures were evaluated and the protein was fully
23 characterized in terms of size polydispersity and charge (by dynamic light scattering – DLS),
24 morphology (by transmission electron microscopy - TEM) and conformational structure (circular
25 dichroism, intrinsic and extrinsic fluorescence). Results have shown that β -Lg nanostructures
26 were formed at pH 3 (with diameters of 12.1 for 22.3) and at 7 (with diameters of 8.9, for 35.3).
27 At pH 4 structures were obtained at macroscale (i.e. \geq 6 μ m) for all β -Lg concentrations when
28 heated at 70 and 80 °C, independent of the time of heating. For pH 6, it was possible to obtain
29 β -Lg structures either at micro- (245.0 to 266.4 nm) or nanoscale (\leq 100 nm) with the lowest
30 PDI values (\leq 0.25), in accordance with TEM analyses, for heating at 80 °C for 15 min. Intrinsic
31 and extrinsic fluorescence data and far-UV circular dichroism spectra measurements revealed
32 conformational changes on β -Lg structure that support these evidences. A strict control of the
33 physical and environmental conditions is crucial for developing β -Lg structures with the desired
34 characteristics, thus calling for the understanding of the mechanisms of protein aggregation and
35 intermolecular interaction when designing β -Lg structures with novel functionalities.

36

37 **Keywords:** Purification; Bio-based structures; Globular proteins; Whey proteins; protein
38 interaction; Aggregation

39 **1. Introduction**

40 Bovine β -lactoglobulin (β -Lg) is a globular protein obtained from milk and the main fraction of
41 whey proteins (ca. 50 % of its protein content), widely used as functional and nutritional
42 ingredient in food, cosmetic and pharmaceutical industry (Pereira et al., 2015; Rodrigues et
43 al., 2015). Whey proteins are obtained from whey, which is a byproduct of cheese production,
44 relatively inexpensive and classified as a GRAS (generally regarded as safe) material
45 (Madalena et al., 2016).

46 The interest in β -Lg from both the scientific community and food and pharmaceutical industries
47 is essentially due to its high nutritional value as a consequence of the rich level of aminoacids,
48 resistance to proteolytic degradation in the stomach, biological (e.g. digestibility, sensory
49 characteristics and high biological value) properties, and gelation capacity – which is
50 particularly important since it allows the formation of structures with different properties and
51 morphologies (Ramos et al., 2012). However, β -Lg at high purity levels, is commercially
52 available only at high cost, therefore obtaining it from cheaper commercial protein solutions is
53 a more feasible alternative to allow a full understanding of the mechanisms behind the protein
54 gelation that lead to structural conformational changes and thus to the formation of different
55 structures (Ramos, Pereira, Rodrigues, et al., 2015; Ramos et al., 2014).

56 Thermally induced gelation usually consists in the unfolding of polypeptide chains of protein in
57 native state with concomitant exposure of initially buried hydrophobic aminoacid residues, and
58 subsequent self-aggregation of protein molecules through physical (electrostatic and
59 hydrophobic) and chemical (disulphide) interactions (Delahaije, Wierenga, Giuseppin, &
60 Gruppen, 2015; Teng, Xu, & Wang, 2015). The extent and behavior of protein aggregation
61 depends on the environmental conditions (e.g. heating temperature, time of heating, pH,
62 protein concentration and ionic strength) (Ramos et al., 2015), and can result in different
63 structures with various sizes, shapes, morphologies and charge.

64 Several researchers have focused their work on understanding the structural gelation of β -Lg
65 but only under limited physical and environmental conditions. For instance, Dombrowski et al.,
66 (2017) showed the formation of soluble β -Lg aggregates with a diameter of 50 nm and
67 displaying an increased surface hydrophobicity for β -Lg at 1.0 % and pH 6.8, when treated at
68 80 °C for 90 min, as compared to native β -Lg. Perez et al. (2014) studied the development β -

69 Lg aggregates as carriers systems, for protein at 1.0 % and pH values ranging from 6.5 to 7.5,
70 upon heat treatment at 85 °C for distinct heating times from 0 to 60 min. The authors reported
71 that β -Lg aggregates were formed at pH 6.5 with increased surface hydrophobicity, thus
72 suggesting a binding ability, being their behavior dependent of production conditions (pH,
73 heating time and/or a combination of those). Despite these studies on β -Lg structures
74 formation and discussions about the structural modifications over distinct conditions, there are
75 limited data about how these conditions affect β -Lg morphology and are related with protein
76 denaturation and aggregation phenomena. In another study, Delahaije et al., (2015) evaluated
77 the kinetics of β -Lg heat-induced aggregation under various conditions (pH, ionic strength,
78 concentration, and temperature), but tested separately. They concluded that electrostatic
79 repulsion between proteins was a crucial factor for β -Lg aggregates' formation and that
80 particle size or aggregates structure was not strongly affected by protein concentration and
81 temperature. Nonetheless, these findings did not consider the effect of various environmental
82 conditions combined, neither their relation with the formation of micro- and nanostructures.

83 In this context, and due to the high cost of commercial β -Lg, a whey protein fractionation
84 process was employed to obtain a β -Lg with a purity level similar to that of commercial protein.
85 Purified β -Lg was extensively characterized and the protein structural (conformational)
86 changes were assessed upon thermal gelation, under combined physical and environmental
87 conditions (various β -Lg concentrations, heating temperatures and times) at distinct pH values
88 (3 to 7), to design food-grade micro- (200 – 300 nm) and nanostructures (\leq 100 nm). The
89 small size of micro- and nanostructures can impart significant changes to physicochemical
90 properties, among them a high surface/volume ratio, smaller pore size and increase in the
91 solubility when compared with macroscale structures formed from the same proteins (Aklakur,
92 Rather, & Kumar, 2016; Monteiro et al., 2016). In this regard, the effects of several conditions
93 on β -Lg structures were evaluated through a complementary set of characterization
94 techniques in order to provide detailed information about the specific conditions that lead to
95 the formation of β -Lg structures at micro- and nanoscale, which hold potential to be used as
96 delivery systems for bioactive compounds.

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98

99 **2. Material and methods**

100 **2.1. Feedstocks and chemicals**

101 Whey Protein Isolate (WPI) powder (Lacprodan DI-9212), kindly supplied by Arla Foods
102 Ingredients (Viby, Denmark), has a β -lg content of ca. 87 %, in a total protein content of 91 %
103 (in dry weight), moisture content of ca. 6 % and vestiges of lactose (max. 0.5 %) and fat (max.
104 0.2 %). β -Lg was obtained as a commercial lyophilized powder from bovine milk (Sigma
105 L0130), containing variants A and B (36.0 kDa) with a purity of 90 % (L0130).
106 Tris(hydroxymethyl)aminomethane, ammonium persulfate (APS), Coomassie Brilliant Blue (R-
107 250), bromophenol blue and tetramethylethylenediamine were purchased from Sigma Aldrich
108 (St. Louis MO, USA). Sodium hydroxide, phosphoric and acetic acids were obtained from
109 Merck (Merck KGaA, Darmstadt, Germany). Hydrochloric acid, glycine and monosodium
110 phosphate were purchased from Panreac (Barcelona, Spain), whereas sodium phosphate
111 dibasic and methanol were obtained from Chem-Lab (Zedelgem, Belgium). Acrylamide was
112 purchased from Bio-Rad (California, USA) and glycerol was obtained from Himedia (Mumbai,
113 India). All other chemicals used in this study were reagent-grade or higher, and were used
114 without further purification.

115

116 **2.2. β -Lg purification method**

117 Purified β -Lg was obtained from WPI by using the salting out method as described by Maté &
118 Krochta (1994) with modifications according with Konrad, Lieske, & Faber (2000). β -Lg was
119 freeze dried to obtain a lyophilized powder. The purity and conformational properties of
120 purified β -Lg were compared with commercial β -Lg lyophilized powder from Sigma. For this
121 purpose, both protein solutions were prepared by dispersing 10 mg mL⁻¹ of β -Lg powder
122 (Jannika Dombrowski, Johler, Warncke, & Kulozik, 2016; Donato, Schmitt, Bovetto, & Rouvet,
123 2009; Kosters, Wierenga, De Vries, & Gruppen, 2011; Schmitt et al., 2009) in 25 mmol L⁻¹
124 sodium phosphate buffer at pH 6. The pH of solutions was adjusted with 0.5 mol L⁻¹ of H₃PO₄
125 or 1 mol L⁻¹ of NaOH, as necessary. The solutions were then stirred continuously with a
126 rotation speed of 400 rpm, for 2 h at room temperature (ca. 25 °C). Afterward, β -Lg solutions
127 were stored at refrigeration temperature (5 °C) overnight to ensure the full rehydration of
128 protein. The β -Lg solutions were then filtered through a 0.2 μ m membrane filter (VWR

129 International, USA) to remove any protein aggregates or impurities. Subsequently, β -Lg
130 morphology, purity, secondary structure and conformational state properties were evaluated
131 for both commercial and purified β -Lg, through dynamic light scattering, SDS-PAGE, turbidity,
132 circular dichroism, intrinsic and extrinsic fluorescence analyses and then comparisons were
133 drawn.

134

135 **2.3. Measurements**

136 **2.3.1. Particle size, polydispersity index, and ζ -potential**

137 Samples of β -Lg were characterized in terms of particle size, polydispersity index (PDI) and ζ -
138 potential by Dynamic Light Scattering (DLS) apparatus (Zetasizer Nano ZS, Malvern
139 Instruments, UK) equipped with He-Ne laser at a wavelength of 633 nm, at 25 °C (Bourbon,
140 Pinheiro, Cerqueira, & Vicente, 2016). Particle size was determined by the method of
141 cumulants fit and was translated into average particle diameters (Z-value) using the Stokes-
142 Einstein relationship (Rodrigues et al., 2015). PDI emerged from cumulants analysis of the
143 measurements and describes the width or the relative variance of the particle diameter
144 distribution. The ζ -potential determines the charge at the surface of the structure and was
145 performed with an angle of 17° (Madalena et al., 2016). Samples (1.5 mL) were poured into
146 disposable sizing cuvettes with a path length of 10 mm for particle size and PDI analyses, and
147 into a folded capillary cell for ζ -potential measurements. All measurements were carried out at
148 25 °C and the results reported as the average \pm standard deviation of at least three replicates.

149

150 **2.3.2. Turbidity**

151 The turbidity of β -Lg solutions (4 mL) prepared at 10 mg mL⁻¹ was evaluated using a double-
152 beam UV/visible spectrophotometer at 500 nm (V-560, Jasco Inc., Tokyo, Japan). The
153 measurements were made at room temperature (ca. 25 °C) according with the procedure
154 reported by Pereira et al., 2015 resorting to a 10 mm path length cuvette, and with 25 mmol L⁻¹
155 sodium phosphate sodium buffer as blank. The measurements were performed in triplicate
156 and experimental values are presented as the average \pm standard deviation.

157

158 **2.3.3. Intrinsic fluorescence**

159 Intrinsic fluorescence measurements of β -Lg dispersions from 5 – 15 mg mL⁻¹ were obtained
160 at ambient temperature (ca. 25 °C) resorting to a spectrofluorimeter (Jasco FP6200, Tokyo,
161 Japan) equipped with a standard thermostated cell holder and a 10 mm path length quartz
162 cuvette (Hellma Analytics, Germany). The excitation wavelength was set at 295 nm to
163 quenching tryptophan (Trp) fluorescence (Madadlou, Flourey, Pezennec, & Dupont, 2018) and
164 the emission spectra were recorded between 300 and 405 nm, and fluorescence intensities
165 were recorded every 2.25 nm. Spectra were baseline-corrected by subtracting blank spectra
166 (i.e. 25 mmol L⁻¹ sodium phosphate buffer) according the procedure adopted by Monteiro et
167 al. (2016) and normalized with unheated β -Lg. The maximum intrinsic fluorescence intensity
168 was given as the average of nine successive measurements.

169

170 **2.3.4. Extrinsic fluorescence**

171 The extrinsic fluorescence of β -Lg dispersions from 5 – 15 mg mL⁻¹ was determined by
172 fluorescence spectroscopy (Jasco FP6200, Tokyo, Japan) using 8-anilino-naphthalene-1-
173 sulfonic acid ammonium salt (ANS) (Sigma-Aldrich, St. Louis, EUA) as the hydrophobic probe,
174 according to the methodology adopted by Wang, Zhong, & Hu (2013) with a few modifications.
175 The β -Lg solutions were incubated at 25 °C prepared ANS solution (at 1.36 mmol L⁻¹ in
176 methanol) for 10 min in the dark before the analysis. The resulting solution was excited at 370
177 nm and emission was collected between 400 and 600 nm at ambient temperature (ca. 25 °C),
178 using a 10 mm path length quartz cuvette. Spectra were baseline-corrected by subtracting
179 blank spectra (i.e. 25 mmol L⁻¹ sodium phosphate buffer and ANS solution). Micro- and
180 nanostructures maximum fluorescence intensity values were normalized by the lowest value
181 corresponding to the unheated β -Lg. The maximum ANS binding fluorescence intensity was
182 given as the average of nine successive measurements.

183

184 **2.3.5. Circular dichroism**

185 The secondary structure content of β -Lg and the effect of heat treatment were evaluated by
186 circular dichroism (CD). CD spectra were obtained resorting to a Jasco J-1500
187 spectropolarimeter (Jasco International Co, Japan). For far-UV experiments, samples in
188 appropriate dilution and spectra were recorded at 25 °C, under constant nitrogen flush, using a

189 quartz cuvette with an optical path length of 1.0 mm (Hellma Analytics, Germany), from 190
190 nm to 260 nm wavelength range with data pitch of 1.0 nm and accumulation of 3 scan,
191 following the procedure used by Bourbon et al., (2016). The CD baseline scan was recorded
192 using a standard solution of 25 mmol L⁻¹ sodium phosphate buffer and then subtracted to
193 scans from β -Lg solutions.

194

195 **2.3.6. Native polyacrylamide gel electrophoresis (Native-PAGE)**

196 In order to compare the integrated intensities of β -Lg bands, samples were analyzed using
197 Native-PAGE or “nondenaturing” gel electrophoresis. Native-PAGE analyses were carried out
198 using the Mini-Protean II dual slab cell system equipped with a PAC 300 power supply (Bio-
199 Rad Laboratories, Hercules, CA, USA) (Bourbon et al., 2016). The resolving and stacking gel
200 contained 12.5 and 3.5 % of polyacrylamide, respectively. Non-reducing loading buffer of
201 tris(hydroxymethyl)aminomethane, 0.5 mol L⁻¹ at pH 6.8, 50 % of glycerol and 0.02 % of
202 bromophenol blue was mixed with β -Lg samples. The gels were stained with Coomassie
203 Brilliant Blue (R-250) solution, maintained overnight in 50 % and 10 % of methanol and acetic
204 acid solutions, respectively. Then, gels were destained with 30 % and 7 % of methanol and
205 acetic acid solutions, respectively (Rodrigues et al., 2015). Standard marker protein
206 PageRuler Unstained Broad Range Protein Ladder (Thermo Scientific) was employed to
207 identify samples by their molecular weight.

208

209 **2.3.7. Fast protein liquid chromatography**

210 β -Lg protein solutions were resolved and quantified by gel filtration chromatography using a
211 Superdex™ 200 10/300 GL column, connected to a fast protein liquid chromatography (FPLC)
212 AKTA-purifier system (GE). β -Lg lyophilized solutions (from Sigma) with concentrations
213 ranging from 5 – 15 mg mL⁻¹ were used to prepare a calibration curve, then 10 mg mL⁻¹ of β -
214 Lg purified samples were analyzed.

215 The protein samples were then centrifuged at 20,000 *g* for 1 h at 25 °C, using a Sorvall
216 centrifuge, and 5 mL of the clarified liquid was carefully collected and filtered through 0.22 μ m
217 filters prior to separation. The eluent was also filtered (0.22 μ m) and degassed under vacuum
218 for 1 h before testing. Samples (100 μ L) were injected into the column and eluted using 0.05

219 mol L⁻¹ of sodium phosphate buffer (pH 7) containing 0.2 g L⁻¹ of sodium azide, as
220 preservative, at a flow rate of 0.5 ml·min⁻¹ under a pressure of 1.5 – 2.0 MPa. Identification
221 (through similarity of retention times – RT) and quantification (by integration of peak area of
222 chromatograms) of the β-Lg present in the eluate was monitored at 280 nm following the
223 procedure previously described by Ramos et al., 2012. All measurements were performed at
224 least in duplicate.

225

226 **2.3.8. Transmission electron microscopy**

227 Transmission electron microscopy (TEM) imaging of β-Lg micro- and nanostructures was
228 conducted on a Zeiss EM 902A (Thornwood, N.Y., USA) microscope at accelerating voltages
229 of 50 and 80 kV. A drop of sample dispersion was deposited onto a carbon support film
230 mounted on a TEM copper grid (Quantifoil, Germany).

231 The excess of solution was removed after 2 min using a filter paper and the grid let for air-
232 drying. The samples were then negatively stained with uranyl acetate (2 % w/w) (Merck,
233 Germany) for 15 s. The grid was finally air dried at room temperature before introducing it in
234 the electron microscope. These conditions were used based in procedures usually adopted by
235 our research group (Monteiro et al., 2016; Bourbon et al., 2015; Pinheiro et al., 2015)

236

237 **2.4. Experimental design**

238 Box-Behnken statistical experimental design was used to evaluate the effect of heating
239 temperature (X_1), β-Lg concentration (X_2) and holding time (X_3) (independent variables), upon
240 particle size (Y_1), polydispersity index (Y_2), intrinsic fluorescence (Y_3) and extrinsic
241 fluorescence (Y_4) intensities (dependent variables), on the development of optimized β-Lg
242 micro- and nanostructures at pH 3, 4, 6 and 7. A 3-factor, 3-level design was used because it
243 was the most appropriated for exploring quadratic response surfaces and constructing second
244 order polynomial models for optimization, thus allowing the use of less experiments. The
245 experimental design encompasses the repetition of center points and the set of points lying at
246 the midpoints of each edge of the multidimensional cube that defines the region of interest.
247 The pH values were selected based on the isoelectric point (pI) of β-Lg (Teng et al., 2015). As
248 shown in Table 1, the independent variables and levels (i.e. low, medium and high) were

249 selected based in previous results from screening experiments. The design matrix was
250 performed in 15 trials following the procedure adopted by Monteiro et al. (2016).

251

252 *«Table 1 to be placed here»*

253

254 **2.5. Development of β -Lg micro- and nanostructures**

255 To study the effects of β -Lg concentration, temperature and time of heating upon the formation
256 of protein micro- and nanostructures at different pH values, the solution pH was adjusted to 3,
257 4, 6 and 7 with 0.5 mol L⁻¹ of H₃PO₄ or 1 mol L⁻¹ of NaOH, as appropriate. Micro- and
258 nanostructures were formed by dispersing 5, 10 and 15 mg mL⁻¹ of β -Lg purified powder in 25
259 mmol L⁻¹ sodium phosphate buffer at pH 3, 4, 6 and 7. The solutions were then stirred
260 continuously with a rotation speed of 400 rpm, for 2 h at room temperature (ca. 25 °C).
261 Afterward, β -Lg solutions were stored at refrigeration temperature (5 °C) overnight to ensure
262 the full rehydration of protein. The β -Lg solutions (5 mL) were then filtered through a 0.2 μ m
263 membrane filter to remove any protein aggregates or impurities and were placed into
264 cylindrical screw-capped glass tubes (100 mm total length and diameter of 20 mm). Heat
265 treatments at different temperatures (i.e. 60 – 80 °C) and times (i.e. 5 - 25 min) were applied
266 through a temperature controlled water bath (MR Hei-Tec + Pt 1000, Heidolph) with samples
267 continuously stirred with magnetic agitation at a rotation speed of 400 rpm. After the heat
268 treatment, the resulting solutions were cooled in ice for 10 min. β -Lg structures were
269 characterized using the techniques described before. Unheated and native β -Lg suspensions
270 were used as control samples.

271

272 **2.6. Statistical analyses**

273 All statistical analyses involving experimental data were performed using Statistica package
274 software version 10.0.228.8 (StatSoft Inc., Tulsa, OK, USA). Statistical significance (at $p \leq$
275 0.05) was determined using ANOVA one-way, followed by Tukey's tests. Unless otherwise
276 stated, all experiments were run at least in triplicate.

277

278 **3. Results and discussion**

279 3.1. β -Lg purification

280 In order to evaluate the purification process, purified β -Lg was extensively characterized in
281 terms of physicochemical properties and the results obtained were compared with the
282 commercial β -Lg at the same conditions. Particle size distribution results of both β -Lg (purified
283 and commercial) are presented in Figure 1, showing a polymodal distribution of unheated β -Lg
284 for both purified and commercial protein with two predominant peaks: peak 1 with maximum
285 between 2 and 10 nm, which is attributed to non-aggregated proteins, and peak 2 associated
286 to native β -Lg aggregates. It is also possible to observe a third peak, but only for purified β -Lg,
287 which can be attributed to strands and clumps of small globular aggregates as result of the
288 purification process. This behavior has been previously reported elsewhere (Rodrigues et al.,
289 2015).

290 In particular for peak 1, measurements revealed a particle size and PDI values of 8.89 ± 0.06
291 nm and of 0.363 ± 0.004 , respectively, for purified β -Lg, and of 6.83 ± 0.16 nm and $0.169 \pm$
292 0.031 , respectively, for commercial β -Lg. Statistically significant differences ($p \leq 0.05$) were
293 obtained between purified and commercial β -Lg for both parameters. These differences may
294 be due to distinct intensities of intrinsic forces (i.e. electrostatic interactions, hydrogen and
295 disulphide bonds, hydration and hydrophobic effects) involved on the stability of the tertiary
296 folds (Ramos et al., 2014). On the other hand, regarding protein turbidity, purified and
297 commercial β -Lg displayed statistically similar values ($p > 0.05$) – 0.0023 ± 0.0003 and 0.0028
298 ± 0.0002 , respectively – suggesting that both proteins are in identical “native” state, i.e. the
299 content of aggregated proteins is very small.

300

301 *«Figure 1 to be placed here»*

302

303 In order to evaluate the protein stability promoted by electrostatic interactions, ζ -potential
304 values were determined. Purified and commercial β -Lg solutions showed a statistically similar
305 ($p > 0.05$) ζ -potential of -9.34 ± 0.71 mV and -7.93 ± 0.99 mV, respectively. These values
306 suggest that β -Lg, in its native state, is a relatively unstable system under the measured
307 conditions. According to Ghalandari, Divsalar, Saboury, & Parivar (2015) and von Staszewski
308 et al. (2012), a colloidal system is considered stable when displaying ζ -potential values above

309 +30 mV or below -30 mV, thus meaning that the charge between particles (i.e. repulsion) is
310 enough to prevent aggregation. The protein conformational changes are widely accessed
311 through intrinsic tryptophan fluorescence measurements (Stănciuc, Aprodu, Răpeanu, &
312 Bahrim, 2012; Vivian & Callis, 2001). This analysis was performed in order to investigate if
313 there is any change in protein structure and dynamics between both β -Lg proteins. The main
314 responsible for β -Lg fluorescence are two tryptophan (Trp) residues (i.e. Trp-19 and Trp-61),
315 being the intrinsic fluorescence of the protein mostly attributed to Trp-19, since it is found in
316 the hydrophobic calyx of β -Lg, while Trp-61 is located in an external loop, close to protein
317 surface (Simion et al., 2015). Figure 2A presents the intrinsic fluorescence intensity results of
318 purified and commercial β -Lg solutions exhibiting both a maximum intensity peak at 333 nm.
319 Typically, β -Lg has a maximum intrinsic fluorescence emission around 335 nm (Diarrassouba,
320 Liang, Remondetto, & Subirade, 2013), so this result corresponds to a blue shift behavior, thus
321 suggesting that chromophoric groups of both samples are more buried in the interior of
322 protein, i.e. hydrophobic groups were protected from the aqueous environment (Perez et al.,
323 2014).

324 The extrinsic fluorescence, by means of the ANS fluorescent probe that binds to hydrophobic
325 sites of proteins, provide information about changes of protein-probe interactions and on
326 variation of the accessible hydrophobic areas (Stănciuc et al., 2012). Figure 2B shows a
327 higher intensity ($p \leq 0.05$) in the peak emission of commercial β -Lg than that of purified β -Lg,
328 thus suggesting that the latter β -Lg was less prone to bind to ANS than commercial ones.
329 Probably, the purification process, which has resulted in a significant higher particle size of β -
330 Lg as mentioned before, led for one hand, to a lower surface-area-to-volume ratio to react with
331 ANS, and for other hand to less change at the conformational level, thus making these
332 hydrophobic groups less exposed to ANS (Perez et al., 2014; Simion et al., 2015). Circular
333 dichroism (CD) spectroscopy provides information on the main secondary structural elements
334 (i.e. α -helix, β -sheet and coil) of proteins, through measurement of polarized light absorbed by
335 peptide bonds (Monteiro et al., 2016). The α -helix structure is characterized by displaying an
336 intense and positive band at 190 nm and negative peaks at 208 and 220 nm, β -sheet by
337 presenting a negative peak with a minimum in the 215 nm region, while random coil structures
338 display a positive peak close to 215 nm and a negative one near to 200 nm (Furtado, Pereira,

339 Vicente, & Cunha, 2018). The values recorded at 190 - 260 nm for purified and commercial β -
340 Lg in native state is depicted in Figure 2C, displaying similar spectra in terms of CD intensity
341 and shape. Average scans exhibited a negative dichroic peak with a minimum at 217 nm (i.e.
342 in the 215 nm region), indicating that the secondary structure of these proteins is rich in β -
343 sheet (Estévez et al., 2017; Fan, Zhang, Yokoyama, & Yi, 2017; Yi, Lam, Yokoyama, Cheng,
344 & Zhong, 2014).

345 Electrophoresis analysis from Figure 2D shows two sets of results, composed by three lanes,
346 where it is possible observe an identical profile for purified and commercial β -Lg. Given that
347 unbound dye is removed by long gel washing gel process, the amount of bound dye is
348 proportional to the protein concentration in the sample (Rodrigues et al., 2015). Both β -Lg
349 samples were characterized by the presence of two high molecular weight bands. The higher
350 molecular weight band with molecular mass between 30 – 40 kDa indicates the presence of β -
351 Lg in dimer form, whereas the lower molecular weight band with molecular mass between 15 –
352 20 kDa corresponds to β -Lg in monomer form, in agreement with previous research on β -Lg
353 (Halder, Chakraborty, Das, & Bose, 2012; Madalena et al., 2016).

354

355 *«Figure 2 to be placed here»*

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357 Fast Protein Liquid Chromatography (FPLC) is the preferential methodology employed for
358 separation and quantification of proteins, essential due to the good resolution and low
359 variability associated to this technique (Ramos et al., 2012). In this regard, FPLC was used to
360 compare both purified and commercial β -Lg in terms of protein content. For this purpose, an
361 appropriate calibration curve ($y = 120.1x + 2.8$) was obtained with $R^2 = 0.999$ using several
362 concentrations of commercial β -Lg, where y is protein content and x is β -Lg concentration.
363 Peak area integration of purified and commercial β -Lg samples at 10 mg mL^{-1} showed
364 statistically similar ($p > 0.05$) concentration values for both proteins, at 123.10 ± 1.90 and
365 $120.70 \pm 0.80 \text{ AU mL}^{-1}$ for purified and commercial proteins, respectively.

366

367 **3.2. Development of micro- and nanostructures**

368 In order to understand the influence of β -Lg concentration and thermal treatment on the
369 formation of micro- and nanostructures, various combined effects (including different
370 concentrations of β -Lg, heating temperatures and times) were carried out to induce protein
371 aggregation. An experimental design, shown in Table 2, was used to evaluate the combined
372 effect of three β -Lg concentrations (5, 10 and 15 mg mL⁻¹), three temperatures (60, 70 and 80
373 °C), and three holding times (5, 15 and 25 min) on the particle size distribution, polydispersity
374 index, and intrinsic and extrinsic fluorescence intensity of β -Lg solutions prepared at four
375 different pH values (3, 4, 6 and 7).

376

377

«Table 2 to be placed here»

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379 These results show that performing the β -Lg gelation process in different combinations of
380 environmental conditions allows obtaining β -Lg structures at nanoscale (i.e. with particle sizes
381 below 50 nm), by changing pH to 3 and 7, independently of the protein concentration (5 - 15
382 mg mL⁻¹), heating temperature (60 – 80 °C) and holding time (5 – 25 min) used. This could be
383 related to the fact that bovine β -Lg at pH values ≤ 3 and ≥ 7 exists as a monomer due to the
384 intermolecular electrostatic repulsions that govern protein interactions at those pH values, thus
385 leading to the formation of low particle size structures under those conditions (Diarrassouba et
386 al., 2013; Ramos et al., 2015). Based on this, we believe that β -Lg structures with small
387 particle sizes (i.e. ≤ 50 nm) can be obtained at pH values far from β -Lg's pI (i.e. 4.6) (Schmitt
388 et al., 2009), since at these conditions the protein is governed by electrostatic repulsions that
389 hamper the aggregation process (Dombrowski et al., 2017).

390 Regarding fluorescence intensity, at pH 3 for all tested conditions and at pH 7 for heating
391 temperatures of 60 °C and 70 °C, β -Lg structures were characterized by relatively low intrinsic
392 and extrinsic fluorescence intensities with maxima recorded at 1.96 and 2.22 (Table 2),
393 respectively. Concerning the structural conformation, the low intrinsic fluorescence intensity
394 obtained suggests that either β -Lg was not completely unfold or the tryptophan residue was
395 not sufficiently exposed, being buried within the native protein structure (Ramos et al., 2015).
396 Regarding extrinsic fluorescence intensity, determined by means of ANS fluorescence probe,
397 it was possible to verify a low accessibility of ANS to hydrophobic areas of β -Lg, translated by

398 a low extrinsic fluorescence intensity emitted (Schmitt et al., 2009). This result corroborates
399 the intrinsic fluorescence observations, thus showing that at these conditions, β -Lg is slightly
400 unfolded, therefore either the tryptophan residues or the hydrophobic groups of β -Lg were less
401 exposed, thus limiting the aggregation process.

402 Within heating treatments at pH 4, it was possible to obtain structures at macroscale (i.e.
403 particles size $\geq 6 \mu\text{m}$) independently of the β -Lg concentration, for heating temperatures of 70
404 and 80 °C (Table 2). Under some combined conditions at 80 °C particles formed a sediment,
405 which indicates that the protein at these conditions is completely unfolded, giving rise to the
406 formation of aggregates. This can be also inferred by the high PDI value (i.e. $\text{PDI} = 1$), and the
407 relatively high extrinsic fluorescence (i.e. ranging from 5.64 to 15.00) (Table 2) obtained,
408 suggesting more hydrophobic sites available for ANS binding are exposed at these conditions
409 (Schmitt et al., 2009). A similar behavior was also observed for intrinsic fluorescence with
410 relatively higher intensity values recorded at this pH for 80 °C, in particular for 15 min holding
411 time (Table 2); thus implying that tryptophan residues, originally buried in the interior of protein
412 chain, are more exposed and so more likely to interact with bioactive molecules (He, Chen, &
413 Moser, 2015).

414 At pH 4, which is relatively close to the pI of β -Lg, the net charge of protein is close to zero,
415 and so the repulsive electrostatic forces weaken and the protein tends to aggregate, thus
416 resulting in higher particle size values (Salgin, Salgin, & Bahadir, 2012). These observations
417 agree with those reported by Leeb et. al (2015), which showed the formation of β -Lg (5 mg
418 mL^{-1}) particle sizes of $1332.1 \pm 56.3 \text{ nm}$ during thermal heating at 80 °C of at pH 5.1. In
419 another study, Schmitt et al. (2009), which obtained large aggregates with sizes above 1 μm
420 for β -Lg (1 mg mL^{-1}) treated at 80 °C for 15 min at pH 4.

421 At pH 6 β -Lg is in a structural transition phase, when the temperature is taken to 80 °C, which
422 is above the β -Lg denaturation temperature – i.e. 76 °C –, it is possible to obtain structures
423 with particle size below and above 100 nm with relatively low PDI values – Table 2. In order to
424 be able to draw conclusions regarding pH 6 on β -Lg physicochemical behavior, a full
425 experiment was performed for these conditions, i.e., pH 6 and heating temperature of 80 °C,
426 and the combined effects of β -Lg concentration and holding time (Figure 3) were evaluated to
427 verify if we were able to produce β -Lg structures with desired properties – i.e. particle sizes

428 within micro- (between 200 and 300 nm) and nano- (≤ 100 nm) scales and with relatively low
429 PDI values (i.e. ≤ 0.25).

430

431 *«Figure 3 to be placed here»*

432

433 In terms of particle size (Figure 3A), β -Lg structures ranged from 65 nm to 267 nm with
434 relatively constant surface charge (between -15.6 and -18.0 mV) ($p > 0.05$) (Figure 3C), as β -
435 Lg concentration or holding time increased. Results showed that β -Lg nanostructures
436 (particles size ≤ 100 nm) can be obtained at 5 mg mL⁻¹ for a heating time up to 25 min, at 10
437 mg mL⁻¹ for a heating time up to 15 min and at 15 mg mL⁻¹ for a holding time of 5 min, without
438 statistically significant differences ($p \leq 0.05$) being found between particles size values.
439 Results also show that large size particles (i.e. microstructures with sizes between 200 and
440 300 nm) can be obtained at 15 mg mL⁻¹ for heating times ≥ 15 min. In fact, the effect of protein
441 concentration and heating time on particles size has been already reported by other authors
442 (Bourbon et al., 2015; Hu, Yu, & Yao, 2007), which pointed to an increase in particles diameter
443 with increased biopolymer concentration and heating time. Furthermore, it is possible to
444 observe that β -Lg solutions present the best PDI values (≤ 0.25) when heated for time periods
445 ≥ 15 min, independently of the β -Lg concentration used (Figure 3B), thus suggesting that the
446 aggregation process originated a relatively monodisperse particle size distribution (Schmitt et
447 al., 2009).

448 According with previously published results, as pH moves away from the protein pI (i.e.
449 between pH 5.2 and 7), β -Lg exhibits an increasing net charge on each molecule and it results
450 in the presence of more dimers (with a molecular weight of approximately 36 700 Da, than
451 monomers (with a molecular weight of 18 277 Da and usually at pH values below 3.0 or above
452 8.0), thus favoring the association and formation of structures with larger particle size (Png et
453 al., 2009). This may be the reason for the higher particle size values observed for β -Lg at pH 6
454 than at pH 3 and 7, when heated at 80 °C – Table 2. This result agrees with a study conducted
455 by Zúñiga et. al (2010), which showed the production of spherical aggregates with an average
456 diameter of 96 nm at pH 6 and linear aggregates with an average diameter of 42 nm at pH 6.8.

457 The changes in the fluorescence intensity of the maximum intrinsic and extrinsic fluorescence
458 spectra (λ_{max}) were used to follow structural changes of the protein induced by protein
459 concentration and heating time at 80 °C. For intrinsic fluorescence an increase of fluorescence
460 intensity at λ_{max} was observed as the heating time increased, particularly for periods ≥ 15 min
461 (Figure 3D). This difference in fluorescence intensity as a function of heating time may be
462 related to changes in the compactness of the protein molecule due to local molecular
463 unfolding, thus increasing the accessibility of buried tryptophan residues (Royer, 2006). This
464 behavior has been also observed by Bourbon et al. (2015) for lactoferrin and lactoferrin-GMP
465 nanohydrogels when heated at 80 °C up to 20 min and by Furtado et al. (2018) for lactoferrin
466 solutions when heated at 90 °C up to 30 min. For extrinsic fluorescence (Figure 3E) it is
467 possible to see that an increase in heating time (from 5 to 25 min) was accompanied by a
468 significant ($p \leq 0.05$) increase in the intensity of ANS fluorescence, independently of the β -Lg
469 concentration used. This increase in extrinsic fluorescence intensity is in line with intrinsic
470 fluorescence results.

471 Taking in consideration the best results obtained before, unheated β -Lg at 5, 10 and 15 mg
472 mL⁻¹ and heated β -Lg at 5, 10 and 15 mg mL⁻¹ at 80 °C for heating times of 15 and 25 min
473 were evaluated by circular dichroism in the far-UV region (190 – 260 nm) – Figure 4. This
474 technique was used to evaluate the influence of selected conditions of heating time in β -Lg
475 secondary structure content in order to establish the best conditions that form structures at
476 micro- (particle size between 200 – 300 nm) and nanoscale (particle size ≤ 100 nm) (Ghorbani
477 Gorji et al., 2015).

478

479 *«Figure 4 to be placed here»*

480

481 The unheated β -Lg CD scans displayed a negative ellipticity minimum near 216 nm,
482 suggesting that its structure is rich in β -sheet, which is consistent with previously reported
483 results (Dave et al., 2013; Delahaije et al., 2016; Gomaa, Nsonzi, Sedman, & Ismail, 2016).
484 Figure 4 also shows an increase in the magnitude of ellipticity as β -Lg concentration
485 increased. This technique is only sensitive to proteins that are fully-dissolved in the solution,
486 so the increase in ellipticity intensity could be due to the fact that more protein is soluble with

487 the increase in β -Lg concentration, consequently more amide chromophores of the peptide
488 bonds can be measured by far-UV CD (Miles & Wallace, 2016). This result is in agreement
489 with that reported by Ioannou et al. (2015), which showed an increase in the magnitude of
490 ellipticity as the concentration of β -Lg increased from 1 mg mL⁻¹ to 40 mg mL⁻¹.

491 Regarding the thermal gelation process, a statistically significant difference ($p \leq 0.05$) is
492 observed in the intensity of the negative peak of heated β -Lg in relation to the unheated β -Lg,
493 independently of protein concentration. This can be related with structural changes due to
494 aggregation phenomena (Jia, Gao, Hao, & Tang, 2017), which is consistent with intrinsic
495 fluorescence data. Native β -Lg is characterized by having most of the hydrophobic amino acid
496 residues buried inside the molecule (Wada, Fujita, & Kitabatake, 2006), so when the protein is
497 subjected to thermal treatment, hydrophobic interactions responsible for maintaining the
498 stability and conformational structure of β -Lg, may be disrupted, thus affecting β -Lg
499 conformational state, resulting in loss of magnitude of the negative chirality of the CD signal
500 (Ramos et al., 2015).

501 Simultaneously, β -Lg aggregation was accompanied by statistically significant differences ($p \leq$
502 0.05) in the red shift of zero-crossing, which suggests the formation of new regular secondary
503 structures during thermal treatment. This result was in agreement with the data reported by
504 Wada et al. (2006), which showed a CD spectra with a decrease of magnitude of the negative
505 ellipticity for β -Lg heated at 80 °C when prepared at 0.5 mg mL⁻¹ and at pH 7.5. These authors
506 also observed a zero-crossing shift to shorter wavelengths, which have been attributed to the
507 increase α -helix structure content in the detriment of β -sheets content.

508 The results shown in Figure 4 also indicate that heating time (15 and 25 min) did not
509 significantly affect ($p > 0.05$) the negative signal intensity, independently of the β -Lg
510 concentration used. These results are in accordance with DLS data, in which protein
511 aggregation is shown to form structures without significance differences of particle size ($p >$
512 0.05), and are also in agreement with the data reported by Delahaije et al. (2016) when β -Lg
513 at 20 mg mL⁻¹ and at pH 7.0 was heated at 80 °C up 30 min, and by Dave et al. (2013) when β -
514 Lg at for 10 mg mL⁻¹ and at pH 2 was heated at 80 °C up to 30 min. Both authors reported that
515 the far-UV CD spectra of β -Lg heated at 80 °C remained approximately constant during
516 heating time.

517

518

«Figure 5 to be placed here»

519

520 The morphology of β -Lg in its native state, and that of micro- and nanostructures was
521 observed by TEM and the respective microphotographs are provided as an insert in Figure 5.
522 Figure 5A indicates that β -Lg in its native state is spherical and heterogeneous, with sizes
523 ranging from 6 to 111.13 nm, which corroborate DLS data for high PDI value (> 0.36). This
524 figure also shows aggregates form a black mass as a result of the negative staining procedure
525 (Zúñiga, Tolkach, Kulozik, & Aguilera, 2010). The particle size of β -Lg microstructures (Figure
526 5B) as measured by TEM is around 140.8 nm, whereas DLS shown size values 245.0 nm. It
527 has been reported that differences between techniques for particle size measurement can be
528 attributed to a sample drying effect for TEM analysis (Bourbon et al., 2016; Machado et al.,
529 2012). However, β -Lg nanostructures (Figure 5C) show a mean particle size of 61.6 nm, which
530 corresponds well with DLS measurements. Micro- (Figure 3B) and nanostructures (Figure 3C)
531 are uniform and homogenous, therefore the low PDI value (≤ 0.22) is well justified by the TEM
532 images. Regarding micro- and nanostructures' shape, images do not reveal a visible and clear
533 limit, but aggregates appear to be spherical and there seem to be clusters present. Clusters
534 can be caused by the negative staining process, in which uranyl ions can be associated to β -
535 Lg (Pinto et al., 2014). These features are consistent with TEM images by Zúñiga et.al (2010)
536 for β -Lg aggregates obtained for protein concentration of 5 % w/v at pH 6, heated at 80 °C
537 during 15 min.

538

539 **4. Conclusions**

540 β -Lg obtained from whey protein isolate was successfully purified and the method proposed is
541 robust and reproducible. Experimental results at pH 3 and 7, independently of protein
542 concentration, heating temperature and holding time, show that it is possible to produce
543 structures with a particle size lower than 100 nm. Tryptophan fluorescence and surface
544 hydrophobicity results suggest that the extent of unfolding and aggregation rate at those
545 conditions are reduced due to the increase of electrostatic repulsion. Conversely, at pH 4
546 unstable structures were obtained, once this pH value is near the protein's pl.

547 Homogeneous and stable β -Lg micro- and nanostructures are formed at pH 6, after gelation
548 process takes place at 80 °C (i.e. above denaturation temperature) during 15 min: using β -Lg
549 at 5 mg mL⁻¹ and 15 mg mL⁻¹ allows obtaining nano- and microscale structures with particles
550 sizes of 70 nm and 250 nm, respectively. Furthermore, intrinsic and extrinsic fluorescence
551 reveled structural changes and suitable environmental conditions to aggregation, while CD
552 spectroscopy showed secondary structure changes with decrease of β -sheet and increase of
553 α -helix contents.

554 The results obtained here represent a significant contribution to enrich the knowledge about
555 the impact of several environmental conditions on β -Lg bio-based delivery systems'
556 characteristics, and point at the possibility to tailor such characteristics as a function of the
557 intended final application, e.g. in the food or pharmaceutical industries.

558

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742 **Figures Caption**

743 **Figure 1.** Typical particle size distribution curve (by intensity) obtained for purified and
744 commercial unheated β -Lg, prepared at 10 mg mL⁻¹ and pH 6.

745 **Figure 2.** Comparison between (•) purified β -Lg and (Δ) commercial β -Lg solutions. (A)
746 Intrinsic fluorescence emission spectra at 295 nm; (B) extrinsic fluorescence emission spectra
747 at 370 nm; (C) Far-UV CD spectra; (D) Native-PAGE. Standard deviation is represented by
748 error bars.

749 **Figure 3.** Values of particle size (A), polydispersity (PDI) (B), surface charge (C), normalized
750 maximum peak of intrinsic fluorescence at 295 nm (D) and normalized maximum peak of
751 extrinsic fluorescence intensity at 370 nm (E) of β -Lg structures formed at pH 6 after heating at
752 80 °C for 5, 10 and 25 min at protein concentrations of 5, 10 and 15 mg mL⁻¹. Each data point
753 is the average of nine successive measurements and the error bars show the standard
754 deviation. Means labeled with the same letter do not statistically differ from each other
755 ($p > 0.05$).

756 **Figure 4.** Far-UV circular dichroism spectra of unheated β -Lg at 5, 10 and 15 mg mL⁻¹ and
757 heated β -Lg at 80 °C for 15 and 25 min for 5, 10 and 15 mg mL⁻¹ at pH 6 (average \pm standard
758 deviation represented by error bars).

759 **Figure 5.** TEM images of β -Lg native state A), β -Lg microstructures B), and β -Lg
760 nanostructures C) (scale bar = 200 nm, magnification = 50.000 x).