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Experimental and computational investigations of the interactions between model organic compounds and subsequent membrane fouling

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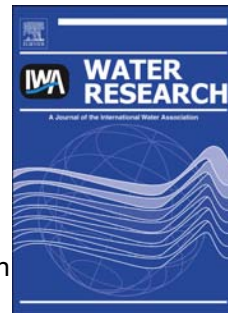
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1 **Experimental and Computational investigations of the Interactions between model**
2 **organic compounds and subsequent membrane fouling**

3

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6

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10

11 **Abstract:**

12

13 The formation of aggregates of sodium alginate and bovine serum albumin (BSA) (as
14 representative biopolymers) with humic acid were detected by Liquid Chromatography (LC)
15 UV₂₅₄ response in the biopolymer region for mixture solutions. BSA interaction with humic
16 acid showed that aggregation occurred both in the presence and absence of calcium,
17 suggesting that multivalent ions did not play a part in the aggregation process. Similar
18 analyses of the alginate interaction with humic acid also showed a positive interaction, but
19 only in the presence of calcium ions. The fouling characteristics for the BSA-humic acid
20 mixture appeared to be significantly greater than the fouling characteristics of the individual
21 solutions, while for the sodium alginate-humic acid mixture, the fouling rate was similar to
22 that of the sodium alginate alone. The effectiveness of hydraulic backwashing, 10-15%
23 reversibility, was observed for the BSA-humic acid mixture, while the % reversibility was
24 20-40% for the sodium alginate-humic acid mixture. Increased humic acid and DOC
25 rejection were observed for both BSA-humic acid and sodium alginate-humic acid solutions
26 compared to the individual solutions, indicating that the biopolymer filter cakes were able to

27 retain humic acids. When compared with BSA-humic acid mixture solution, greater removal
28 of humic acid was observed for alginate-humic mixture, suggesting that sodium alginate may
29 have a greater capacity for associations with humic acid when in the presence of calcium than
30 BSA. Complementary molecular dynamics simulations were designed to provide insights into
31 the specific mechanisms of interaction between BSA and humic acid, as well as between
32 alginate and humic acid. For the BSA-humic acid system; electrostatic, hydrophobic and
33 hydrogen bonding were the dominant types of interactions predicted, whilst divalent ion-
34 mediated bonding was not identified in the simulations, which supported the LC-results.
35 Similarly for the alginate-humic acid system, the interactions predicted were divalent ion-
36 mediated interactions only and this was also supported the LC results. This work suggests
37 that LC-UV₂₅₄ might be used to identify aggregated biopolymers, and that combined with
38 current characterisation techniques, be used to better explain performance variations between
39 water sources.

40

41 *Key words:* organic fouling, microfiltration, liquid chromatography, effluent organic matter,
42 humic acid, biopolymers, molecular dynamics

43

44 1. Introduction

45

46 Membrane filtration in drinking water treatment and wastewater recovery/reuse involves
47 fouling caused by organic matter (Lee et al., 2004). Many studies of organic fouling have
48 focused on one model NOM foulant for the purpose of understanding the fouling mechanism
49 (Schaefer et al., 2000; Lee and Elimelech, 2006). Fouling studies using natural surface waters
50 reported that hydrophilic (non-humic) components of NOM were more significant foulants

51 (Carroll et al., 2000; Gray et al., 2007) than the hydrophobic fraction of NOM (Jucker and
52 Clark, 1994), which consists mainly of organic acids and neutrals.

53

54 However, in recent times, the focus of studies on organic fouling has shifted from the study
55 of single model foulants to mixtures. The interaction between organic compounds has been
56 identified as an important mechanism in membrane fouling (Jermann et al., 2007; Gray et al.,
57 2008; Gray et al., 2011; Henderson et al., 2011). Jermann et al., (2007) investigated the effect
58 of molecular interactions within and between humics and polysaccharide on UF fouling
59 mechanisms at organic concentration levels relevant for Swiss lakes. A similar study was also
60 conducted by Katsoufidou et al., (2010). Their studies highlighted that when a mixture of two
61 or more fouling species was present in water, interplay between organic foulants (foulant-
62 foulant) as well as foulant-membrane interaction were observed.

63

64 Relatively few studies have reported interactions between different organic compounds with
65 respect to fouling by real waters. For example, Gray et al., (2008), in a study of two different
66 surface waters for different membranes, have described the effect of smaller organic acids
67 and proteins on increasing the fouling rate of high molecular weight compounds.
68 Additionally, Kim and Benjamin (2007) have shown that the fouling potential of filtered
69 waters could be similar to that of the original feed water due to the agglomeration of small
70 molecular weight organic compounds that are present in filtered waters. Clearly, the
71 mechanism of organic fouling of low molecular weight compounds is complex. It may
72 involve a range of organic compounds, the predominant foulant may vary with the source of
73 the water and it may be dependent upon the interactions between various components.
74 Therefore, characterization of such organic interactions, including at the molecular level is

75 important for an understanding of membrane fouling and other water treatment processes,
76 such as organic removal via coagulation or ion exchange.

77

78 The aim of this study was to identify possible interactions between organic compounds that
79 are commonly found in natural waters (natural organic matter, NOM) and wastewaters
80 (effluent organic matter, EfOM). Model organic compounds were chosen with structures
81 similar to, or representative of, those considered important in membrane fouling, as well as
82 mixtures of these compounds. More specifically, the compounds used were humic acid,
83 Bovine Serum Albumin (BSA) as an example of a protein and sodium alginate to mimic
84 polysaccharides. Characterizations were performed for solutions in a synthetic background
85 electrolyte of similar composition to that of a municipal wastewater. Liquid chromatography
86 with organic carbon detection (LC-UV₂₅₄-OCD) and LC coupled with a photo-diode array
87 (PDA) detector were used to probe for interactions in the waters themselves. The ability to
88 identify the presence of interactions between various compounds was thus assessed, and
89 complementary molecular dynamics simulations were used to predict the range of specific
90 interactions that may occur at the molecular level. The computational results were then
91 reconciled with the experimental data. In addition, the fouling response of the specific
92 mixtures with a hydrophobic polypropylene membrane was explored, based on the
93 experimental and theoretical findings observed with the presence of interactions between
94 various organic compounds.

95

96 **2. Materials and methods**

97

98 2.1. Organic foulants

99

100 Sodium alginate from brown algae (Sigma-Aldrich), bovine serum albumin (BSA, Sigma-
101 Aldrich), and humic acid (HA) (Fluka) were selected as model organic foulants to represent
102 polysaccharides, proteins, and humic acid found in EfOM. Both sodium alginate and BSA
103 (biopolymers) were chosen to represent the high molecular weight compounds present in
104 surface waters and wastewaters, whereas the smaller humic acid was selected to represent the
105 hydrophobic characteristics of organic matter.

106

107 2.1.1. Feed solution preparation

108

109 Stock solutions (1g/L) were prepared by dissolving each of the foulants in deionized (MilliQ)
110 water. Stock solution of humic acid was adjusted to pH 10 using 5 M sodium hydroxide
111 (NaOH) solution to ensure complete dissolution of the foulants. While raising the pH
112 improved dissolution of the humic acid, a small UV₂₅₄ biopolymer peak was still detected for
113 humic acid solution indicating some residual agglomeration within the humic acid solution.

114

115 Model foulant solutions for organic characterization experiments were prepared from the
116 stock solution. 100ml of each model foulant solution was prepared by diluting the required
117 amount of each foulant stock solution to typically 25 mg/L. In order to investigate the
118 interactions between specific species, a range of mixtures containing one biopolymer (either
119 BSA or alginate) and humic acid were prepared and analysed via LC-PDA. When
120 determining the extent of interaction between BSA or alginate and humic acid via UV₂₅₄ in
121 the biopolymer region, the residual humic acid peak in this region was subtracted from the
122 peak for the mixture solutions.

123

124 The ionic environment for experiments in electrolyte solution consisted of NaCl (0.003 M),
125 CaCl₂ (0.001 M), KCl (0.0004 M) and MgCl₂ (0.0004 M) prepared in deionised water. The
126 solutions were adjusted to pH 7-7.5 with 0.01 M hydrochloric acid. The total ionic strength
127 (circa $I = 0.77 \times 10^{-2}$ M, 420 mg/L) was confirmed by conductivity measurements. The
128 prepared pH, ionic strength and cation concentrations were chosen because of their similarity
129 to a local secondary effluent wastewater. Table 1 summarises the foulant solutions prepared
130 for organic characterization.

131

132 Table 1. Summary of foulant solutions (in electrolyte) prepared for organic characterization

133 2.2. Water quality analyses and characterisation

134

135 Water samples were characterized by pH, conductivity and molecular weight distribution by
136 liquid chromatography (LC). Molecular weight distributions were determined by LC using a
137 photodiode array, (PDA) detector (Method A) as described by Myat et al., 2012, and with LC
138 coupled with UV₂₅₄ (UVD) and organic carbon detector (OCD) (Method B). Analysis by
139 Method B (DOC-Labor) was carried out by the University of New South Wales. This
140 technique was used to confirm the MW of the alginate used in this investigation, as well as
141 providing an analysis of the organic compounds based on molecular weight range and
142 dissolved organic carbon (DOC).

143

144 2.3. Membrane filtration

145

146 Membrane fouling experiments were undertaken using a single hollow fibre membrane
147 filtration apparatus to examine the fouling rate of feed waters. Feed waters were either
148 specific species or a mixture containing one biopolymer (either BSA or alginate) and humic

149 acid . The hydrophobic membrane material was polypropylene with a nominal pore size of
 150 0.2 μm , an outer diameter of 0.50 mm and an inner diameter of 0.25 mm. Tran et al., (2006)
 151 has previously determined the contact angle of this membrane material with a Cahn Dynamic
 152 Contact Angle Analyser, and it was reported to be 160° . Single hollow fibre membranes were
 153 used for filtration using the method described by Myat et al, 2012. This involved confirming
 154 that the clean water permeability of each membrane was within a pre-defined range to ensure
 155 individual membranes had similar filtration characteristics, operating the filtration at a
 156 constant flux of $50 \text{ kg}\cdot\text{m}^{-2}\cdot\text{h}^{-1}$ and backwashing the membrane every 30 minutes of filtration
 157 time.

158

159 The transmembrane pressure (TMP) was recorded with time and the unified membrane
 160 fouling index (UMFI) method developed by Huang et al., 2008 and Nguyen et al., 2011 was
 161 used to assess membrane performance at constant flux. Fouling indices were calculated using
 162 long term filtration data that incorporates backwashing, and from data between filtration and
 163 backwash cycles to assess the effectiveness of hydraulic backwashing. The fouling indices
 164 were based on a resistance-in-series model (Nguyen et al., 2011). Detailed procedures on
 165 analysis or equation derivations can be found in Nguyen et al., 2011. Equation 1 describes the
 166 calculation of specific flux or permeability ($\text{kgm}^{-2}\text{h}^{-1}\text{bar}^{-1}$) in which the resistance due to
 167 fouling increases linearly with the volume or mass of permeate (V) produced (Nguyen et al.,
 168 2011). Membrane performance can be normalized by dividing J by ΔP at any specific mass
 169 by the initial or clean membrane condition as shown in equation (2).

170

$$171 \quad J_s = \frac{J}{\text{TMP}} = \frac{J}{\Delta P} = \frac{1}{\mu(K_{\text{mem}} + k_{\text{foul}}V)} \quad (1)$$

172

$$173 \quad J'_s = \frac{\left(\frac{J}{\Delta P}\right)V}{\left(\frac{J}{\Delta P}\right)_0} = \frac{1}{1 + \left(\frac{K_{total}}{K_{mem}}\right)V} \quad \text{or} \quad \frac{1}{J'_s} = 1 + \left(\frac{K_{total}}{K_{mem}}\right)V \quad (2)$$

174

175 where; J_s = specific flux or permeability ($\text{kgm}^{-2}\text{h}^{-1}\text{bar}^{-1}$)176 J'_s = normalized specific flux177 V = specific mass (kg/m^2)178 K_{mem} = resistance of clean membrane179 k_{total} = total rate constants for resistances

180

181 The inverse of normalized specific flux versus specific mass (kg/m^2) can be used to calculate
 182 different fouling indices for process cycles of filtration and backwashing. Hydraulic
 183 irreversible fouling index (HIFI) can be calculated by using the starting TMP after each
 184 backwash cycle. Increased values of HIFI represent higher rates of irreversible fouling. An
 185 assessment of reversibility after each backwash cycle was also obtained from the modified
 186 method of van den Brink et al., (2009). The analysis was performed by calculating %
 187 reversibility after each backwash cycle by comparing the TMP before backwashing to the
 188 TMP following backwashing as described in equation 3, in which 'n' is equal to the number
 189 of cycles and R represents the inverse of J's value at the time indicated by the subscript.

190

$$191 \quad \% \text{ Reversibility} = \frac{(R_{final})_{n-1} - (R_{start})_n}{(R_{final})_{n-1}} \times 100\% \quad (3)$$

192

193 2.4. Molecular dynamics (MD) modelling

194

195 Molecular dynamics simulations were designed in order to provide insights into the specific
196 mechanisms of interaction between the BSA and humic acid, as well as the alginate-humic
197 acid system. The BSA model used was the solved x-ray diffraction crystal structure as
198 archived in the Protein Data Bank database (Majorek et al., 2012). The humic acid model
199 used was the Temple-Northeastern-Birmingham (TNB) model (Davies et al., 1997). The
200 alginate models used were decamer chains of the three sequences found naturally in algal-
201 sourced alginates. These sequences were poly- α -L-guluronate (GG), poly- β -D-mannuronate
202 (MM) and an alternating guluronate-mannuronate arrangement (GM). The initial construction
203 of the protein-humic acid simulation involved placing six humic acid model molecules
204 around the BSA molecule, at distances further than the non-bonding cut-off (12 Å). This was
205 to ensure that any bonding interactions that occur were not artefacts of the initial simulation
206 state and that they were indicative of actual interactions. The alginate-humic acid simulation
207 was constructed by placing six alginate decamer chains (two of each sequence)
208 approximately 15 Å apart, with six humic acid molecules placed at distances greater than 12
209 Å away from the alginate molecules as well as each other.

210

211 These simulations were constructed using the Visual Molecular Dynamics (VMD) package
212 (Humphrey et al., 1996). These constructs were then solvated, with 15 Å box padding, and
213 ions reflective of the experimental work were randomly added. An initial energy
214 minimization step was used to reduce the energy of water packing and any conflicts via
215 conjugate gradient minimization in the molecular dynamics program-NAMD (Phillips et al.,
216 2005). This minimization involved 10,000 steps for the BSA-TNB system and 20,000 steps
217 for the alginate-TNB system, due to the flexible nature of the alginate chains in use.
218 Simulations were then run under NPT-ensemble conditions, as controlled by a Langevin
219 piston and thermostat in a flexible periodic cell, for 1.5 ns. The electrostatic interactions of

220 the system were calculated via the Particle mesh Ewald method. All non-bonded interactions
221 were subjected to a switching function at 10Å and cut-off at 12Å which was based on the X-
222 PLOR method. The resulting trajectories were analysed for any intermolecular interactions
223 between the species of interest.

224

225 **3. Results and Discussion**

226

227 3.1. Size exclusion chromatography of pure model compounds

228

229 Figs. 1a-c plot the UV₂₅₄ and organic carbon detector response of LC (Method B)
230 chromatograms of the model foulant solutions, the quantified compositions of which are
231 given in Table 4 in supporting information (SI). The response of the single model compound
232 solutions shown in Fig 1a-c, show that all the model substances elicit a response from the
233 organic carbon detector (OCD). Also evident from this figure is that the organic acids elicited
234 responses from the UV₂₅₄ detector, whilst the BSA and alginate did not. The humic acid also
235 displayed a small UV₂₅₄ peak in the biopolymer region (see Fig.7 in Supporting Information)
236 indicative of incomplete dissolution of the humic acid.

237

238 Fig 1. LC-UVD-OCD (Method B) response of pure compounds representative of organic
239 foulants

240

241 When the same solutions were analyzed *via* LC method A, the UV response for sodium
242 alginate was similar to that described above, as no UV absorbance was recorded at the 254
243 nm wavelength. However, for absorbance between 210-220 nm, sodium alginate showed a
244 slight response, possibly due to the uronic acid nature of the monomers from which alginate

245 is constructed. BSA absorbed strongly at UV 210-220 nm, which is characteristic of amino
246 groups (Her et al., 2004). Both UV 210 and 254 absorbance for humic acid showed
247 significant values.

248

249 Her et al., (2007) has previously used the ratio of UV_{210} to UV_{254} absorbances to calculate a
250 UV absorbance ratio index (URI), to distinguish protein-like substances from other NOM
251 components. This previous work demonstrated that URI values were highest for proteins
252 (13.5 for BSA) and lower for other components such as humic and fulvic acids (1.59 for
253 humic acid, 1.88 for fulvic acid). Two BSA peaks were detected (see Fig.8 in SI), at
254 molecular weights of 10 kDa and 22 kDa, which is not uncommon in commercial samples (de
255 Frutos, 1998). The peak corresponding to a molecular weight of 10 kDa was most likely the
256 monomeric species, eliciting a stronger UV absorbance signal than the 22 kDa peak (likely to
257 be the BSA dimer). Therefore, when calculating the URI value for BSA, the maximum
258 absorbance value at 10 kDa was considered for absorbance at both 254 and 210 nm. URIs
259 calculated for each individual foulant compound (both in electrolyte and aqueous
260 environments) are listed in Table 2.

261

262 Table 2. URI values calculated for each individual foulant compound in background
263 electrolyte and aqueous solution

264

265

266 3.2. Specific mixtures by LC (Method A)

267

268 Further investigation into the specific nature of these humic acid/BSA or alginate interactions
269 were carried out by preparing specific mixtures containing two components (humic acid and

270 either alginate or BSA) and analyzing these results by LC (Method A) for any interactions, or
271 lack thereof.

272

273 When BSA was present with humic acid and electrolytes, an additional UV_{254} absorbing
274 biopolymer peak (see Fig.9 in SI) was present. The additional peak at a high MW observed in
275 Fig.9 a) and b) (see SI) appeared at a higher molecular weight than the BSA peak. The value
276 of URI at the high molecular weight biopolymer peak (circa >50 kDa; Fig. 9 in SI) was
277 1.6 ± 0.1 . The calculated URI value for BSA was half of the value of the BSA alone
278 (decreased from 22 ± 2 to 11 ± 2 , circa 10kDa) due to an increase in the UV_{254} signal,
279 suggesting a positive association between BSA and humic acid. To verify whether the
280 additional peak that appeared at 254 nm was the result of divalent cation mediated association
281 between BSA and humic acid, the solution mixture was prepared at the same concentration in
282 deionized water.

283

284 When BSA-humic acid was dissolved in water, the additional UV_{254} absorbing biopolymer
285 peak still appeared (See Fig.10 in SI). The URI value at the high molecular weight
286 biopolymer peak (circa >50 kDa) was 2.2 ± 0.1 . The URI value of BSA was depressed by
287 approximately 80% of its original URI value (decreased from 19 ± 1 to 3.7 ± 0.9) suggesting
288 more numerous associations between BSA and humic acid.

289

290 Regarding the interactions of BSA and humic acid, the reduction in the URI value of the LC
291 peak attributed to the BSA, when compared to the standard BSA-only result, shows a strong
292 association between the protein and the humic acids. These associations were present in both
293 the electrolyte solution as well as deionized water. This suggests that the specific interactions

294 involved in this aggregation are not dependent on ions being present to form. Similar analysis
295 was also undertaken for the alginate-humic acid system, and the results reported in Table 3.

296

297 Table 3. Comparison of absorbance characteristics for mixtures of compounds in background
298 electrolyte and aqueous solution

299

300 .

301

302

303

304 The alginate-humic acid system showed a positive interaction between the alginate and humic
305 acid in electrolyte solution. With this system, considering that alginate has been shown to not
306 absorb UV light at 254 nm, a peak in the UV₂₅₄ chromatogram can be interpreted as an
307 aggregating interaction between the alginate and the humic acid present. Such an increase in
308 absorption at 254nm was recorded for the high molecular weight peak in the alginate-humic
309 acid electrolyte system. However, no UV₂₅₄ significant increase in peak size was recorded,
310 compared to the humic acid alone peak (see Fig. 7 in SI), for the alginate-humic acid system
311 in aqueous environment. This suggests that the alginate-humic acid interactions are ion
312 mediated.

313

314

315

316 The behavior of specific mixtures in solution, as described by the above LC results, indicates
317 that the interaction between the low molecular weight organic acids and the larger
318 biopolymer molecules occurs in the synthetic systems in varying amounts. As previously

319 published studies show (Jermann et al., 2007 and Gray et al., 2011), there can be a change in
320 membrane fouling response, depending on the presence or absence of either a particular
321 component or the interactions between organic compounds. In this study, membrane fouling
322 responses of specific mixtures were tested in order to gain insight into organic fouling of
323 synthetic mixture systems, and to identify if interactions between organic compounds may
324 alter the membrane fouling response.

325

326 3.3. Membrane fouling responses by specific mixtures

327

328 In order to examine the effect of aggregation on membrane fouling, solutions containing the
329 same mixtures as discussed previously were assessed for their membrane fouling potential in
330 an electrolyte environment. In the following experiments, the mixtures containing two
331 foulants had twice as much organic content as the single foulant solutions, as the same
332 individual compound concentrations were maintained for all experiments.

333

334 3.3.1. Fouling studies of BSA, humic acid and BSA-humic acid mixture

335

336 Fig. 2 plots the filtered DOC amount (mg/m^2) versus the resistance (inverse of J 's). This plot
337 is similar to data plots of specific mass (kg/m^2) versus the inverse of J 's (Fig. 3) but allows
338 for the effect of DOC concentration in the mixture to be considered. Fig. 2 clearly shows a
339 greater rate of fouling for the BSA-humic acid mixture compared to the individual organic
340 components. The hydraulic irreversible fouling index (HIFI) results for BSA, humic and
341 BSA-humic mixture are represented in Fig. 3 via the slopes of the data lines.

342

343 Fig. 2. Plot of fouling curves of BSA, humic and BSA-humic mixture solutions

344

345 Fig. 3. Plot of the inverse J 's versus specific mass of BSA, humic and BSA-humic mixture
346 solution (HIFI = slope of lines)

347

348 Due to the relatively small size (150 – 5000 Da) of the humic molecules, it is unlikely that
349 humic acid was retained via size exclusion by the 0.2 μm polypropylene membrane.
350 Therefore, humic acid fouls the membrane by adsorption in/onto the membrane. The
351 estimated HIFI value calculated from Fig. 3 was $2.84 \times 10^{-4} \text{ m}^2/\text{kg}$ after 48 h of filtration time
352 (equivalent to specific mass of $2400 \text{ kg}/\text{m}^2$, total backwash cycles of 82). Approximately
353 25% DOC rejection was observed during 48 h of filtration time, reducing from 7.43 mg/L
354 DOC in the feed to 5.56 mg/L DOC in the permeate. Similarly, the UV_{254} absorbance also
355 decreased from 0.54 to 0.36.

356

357 When the BSA-only solution was filtered by a polypropylene membrane, the fouling trend
358 appeared to be similar to humic acid, although the calculated HIFI value of $1.50 \times 10^{-4} \text{ m}^2/\text{kg}$
359 was approximately 47% lower than the HIFI value of humic acid (see Fig. 3). Although the
360 HIFI value calculated for BSA solution was lower than for humic acid, it is expected that the
361 adsorption of BSA to hydrophobic membranes could occur. Comparison of DOC in the feed
362 and permeate solutions suggested approximately 5% DOC rejection was achieved for the
363 BSA-only solution.

364

365 When the subsequent experiment with the BSA-humic acid mixture was carried out, a change
366 in the fouling trend was observed, with two possible fouling rates evident at different times
367 during the filtration as shown by slope 1 and slope 2 in Fig. 3. The fouling trend of the BSA-
368 humic mixture (mass ratio 1:1) (Fig. 3) showed a slow gradual increase at the beginning of

369 the filtration time, similar to both the humic acid and BSA only runs. The HIFI value
370 calculated up to 1500 kg/m^2 (slope 1 region as labelled in Fig. 3) of the mixture was 7.29×10^{-4}
371 m^2/kg , while the slope 2 region had a HIFI value of $2.05 \times 10^{-3} \text{ m}^2/\text{kg}$. The HIFI value of the
372 slope 2 region was, therefore, significantly greater than the slope 1 region as well as the rates
373 of fouling for humic acid and BSA alone. The higher HIFI values observed for BSA-humic
374 acid mixture indicate the faster accumulation of an irreversible fouling component compared
375 to the individual BSA or humic acid solutions. Furthermore, the fouling curves shown in Fig.
376 2 suggest that the faster rate of fouling for the BSA-humic acid mixture was not a result of a
377 greater DOC concentration alone, as the mixture showed a faster rate of fouling when the
378 DOC concentration was considered.

379

380 Fig. 4. The % permeability reversibility for humic acid (HA), BSA and BSA-humic acid
381 (BSA+HA) system

382

383 The percentage reversible permeability achieved following backwashing of the humic acid,
384 BSA and humic acid-BSA mixture is shown in Fig. 4. BSA showed no recoverable
385 permeability throughout the filtration experiment, while both humic acid and humic acid-
386 BSA mixture displayed a decrease in recoverable permeability initially, while during the
387 latter stages of filtration a slight increase in reversibility was observed. This non-recoverable
388 permeability at the beginning of the process could be due to the adsorption of both humic and
389 BSA to the membrane surface. During the later stages of filtration (i.e., > 40 cycles), filter
390 cake formation could be starting to dominate and therefore, hydraulic backwashing seemed to
391 be more effective. The variation in the % reversibility was maintained between 10-15% after
392 > 40 filtration/backwash cycles. It suggests that the slight increase in reversibility following
393 extended filtration corresponds to filter cake development.

394

395 It is also possible that the influence of both humic acid and BSA fouling may further enhance
396 the smaller MW humic acid to be retained in the filter cake via humic acid-BSA interactions.
397 The removal of humic acid from the BSA-humic mixture solution was approximately 5%
398 higher compared to the individual humic acid solution from UV_{254} measurements (see Fig. 11
399 a) in SI). The overall DOC rejection (%) for the mixture solution was 42% compared to 25%
400 and 5% for the individual humic acid and BSA compounds. Both DOC and UV_{254} data
401 analysis for the permeate solutions is consistent with increased humic acid removal in
402 mixture solutions due to interactions with BSA (protein) compounds. This may cause the
403 increase in HIFI value observed for the BSA-humic acid mixture (Fig. 3) as a result of greater
404 constriction of pores within the filter cake by leading to a more compact structure in the filter
405 cake.

406

407 3.3.2. Fouling studies of sodium alginate and sodium alginate-humic acid mixture

408

409 Filtration of humic acid, sodium alginate and sodium alginate-humic acid solutions in
410 electrolyte were conducted to ascertain the effect and interactions between humic acid and
411 sodium alginate may have on membrane fouling. Fig. 12 in SI plots the fouling curves of
412 sodium alginate, humic acid and sodium alginate-humic mixture. The HIFI results for sodium
413 alginate, humic and sodium alginate-humic mixture are represented in Fig. 5 via the slopes of
414 the data lines.

415

416 Fig. 5. Plot of the inverse of J 's versus specific mass of Alginate, humic and Alginate-humic
417 mixture solution (HIFI = slope of lines)

418

419 The pressure increase in each filtration cycle was very significant during filtration of the
420 alginate solution. The HIFI value calculated for sodium alginate (see Fig. 5) was 3.43×10^{-4}
421 m^2/kg in 48 h of filtration time. Approximately 62% DOC rejection was observed, during 48
422 h filtration time, reducing from 8.73 mg/L DOC in the feed to 3.34 mg/L DOC in the
423 permeate. The fouling trends of sodium alginate-humic acid mixture (mass ratio 1:1) and the
424 sodium alginate solution (Fig. 12 in SI) were similar, but the calculated HIFI value for the
425 mixed solution ($5.51 \times 10^{-4} \text{m}^2/\text{kg}$) was slightly higher (30% increase) than the sodium
426 alginate value.

427

428 From the analysis of the individual filtration cycles for humic acid and sodium alginate, the
429 % reversibility of sodium alginate was maintained between 20-40% over the filtration period.
430 In comparison, the % reversibility for humic acid was only between 5-10% (see Fig. 6).
431 Interestingly, the % reversibility of sodium alginate-humic acid was the similar to that of
432 sodium alginate alone, with the % reversibility being constant at approximately 30% after >
433 40 filtration/backwash cycles (see Fig. 6).

434

435 Fig. 6. The % permeability reversibility for sodium alginate (SA), humic acid (HA) and
436 sodium alginate (SA) + humic acid (HA) systems

437

438 Notably, sodium alginate fouling influences the alginate-humic acid mixture filtered with PP
439 membrane, possibly due to pore constriction by complexing with the humic acid, creating an
440 additional cake resistance. This is strengthened by the fact that the removal of humic acid
441 from the mixture solution was approximately 15% higher compared to the individual humic
442 acid compound. Similarly, the overall DOC rejection (%) for the mixture solution was 72%
443 compared to 25% and 62% for the individual humic acid and sodium alginate compounds,

444 indicating that the sodium alginate filter cake may protect the membrane from humic acid.
445 Both DOC and UV_{254} data analysis for the permeate solutions can be found in the Fig. 11 in
446 SI..

447 Similar findings were reported by Jermann et al., (2007), in which they highlighted the
448 alginate cake, or gel in the presence of calcium, was irreversibly adsorbed onto the membrane
449 by formation of an assorted alginate gel with humic acid incorporated in the presence of
450 calcium ions. Although direct comparison cannot be made due to the comparatively high ratio
451 of $Ca^{2+}: Na^+$ (1:16) used in their feed solutions, interaction between alginate and humic in the
452 presence of calcium was also demonstrated. The filtration performance of sodium alginate
453 could be strongly affected by the added mono-/divalent ions as proposed by van de Ven et al.,
454 (2008). Katsoufidou et al., (2010) also proposed that the fouling mechanism could vary
455 depending on the ratio of calcium ions and alginate/humic acid concentration in the mixture
456 solution. When compared with the BSA-humic acid solution, a greater rejection of humic
457 acid was observed for the alginate-humic mixture suggesting that alginate in the presence of
458 calcium may associate with humic acid to a greater degree than BSA.

459

460 Both LC results and membrane fouling responses for specific mixtures indicate that the
461 interaction between low molecular weight organic acids and larger biopolymers takes place in
462 the synthetic systems. Such interactions might also be possible in more complex mixtures
463 found in natural waters and wastewater effluents. In order to provide insights into the
464 specific interactions that may be forming in solution, molecular dynamics was employed.

465

466

467

468

469 3.4. Molecular dynamics (MD) modelling

470

471 3.4.1. BSA-humic acid interaction by MD

472

473 The hypothesis that the BSA and humic acid were aggregating together in solution, as
474 discussed previously, is supported by the molecular dynamics modeling that was carried out
475 to probe this interaction. The majority of the representative humic acid molecules (TNB
476 model) used in the simulation were observed to interact directly with the BSA model.
477 Regarding the BSA-humic acid system, of the six TNB molecules placed within this
478 simulation, four were identified as binding to the protein within the time frame of the
479 simulation (1.5 ns). Thus, a number of direct interactions between the protein and the TNB
480 molecules were identified.

481

482 The most common type of interaction observed throughout this simulation was hydrophobic,
483 involving both aliphatic and aromatic moieties of the humic acid interacting with
484 hydrophobic regions of the protein surface. For such interactions, involving one of the three
485 humic acid aromatic rings, the hydrophobic region on the protein involved a proline residue.
486 More specifically, the aliphatic part of the pyrrolidine ring associated at angles approaching
487 90° with the plane of the aromatic ring of the humic acid. This interaction shows the
488 characteristics of a 't-stack'-like attractive interaction (Börnsen et al., 1986). The average
489 distance of the aliphatic carbon atom to the center of mass of the aromatic ring was calculated
490 to be $3.84 (\pm 0.02) \text{ \AA}$, which is close to the experimentally determined average value of 3.7 \AA
491 for these types of mixed aliphatic-aromatic π -interactions (Brandl et al., 2001).

492

493 The next most prevalent interaction type identified in the BSA-humic acid system was
494 hydrogen bonding. The dominant functional groups of the humic acid model that hydrogen
495 bonded with the protein surface were the carbonyl (hydrogen bond acceptor), hydroxyl (both
496 acceptor and donor) and amine (donor) moieties. These groups interacted directly with the
497 side chains of a number of different amino residues, the most common being glycine (via the
498 R-NH₂ group), arginine (R-NH₂), serine (R-OH), lysine (R-NH₃⁺), as well as an interaction
499 with a backbone nitrogen atom (R-NH-R').

500

501 Hydrogen bonding was also identified to occur between the BSA and humic models with the
502 TNB model acting as both a hydrogen bond donor as well as an acceptor. These interactions
503 seem quite stable throughout the simulation, with many forming and persisting for several
504 hundred picoseconds of simulation time, until the end of the production run. This is not
505 surprising, given the large number of polar or hydrophilic groups present on the surface of
506 BSA.

507

508

509

510 Another interesting interaction that was identified between the protein and the TNB model
511 was a salt bridge (Fig.13 in SI). Salt bridges may be considered as a special type of hydrogen
512 bond involving a combination of two non-covalent bonds; a neutral R-NH⁺...O-R' hydrogen
513 bond plus an electrostatic cation-anion interaction (Strop et al., 2000). In this regard, it would
514 be expected that the salt bridge interaction would be stronger than a regular hydrogen bond.
515 From the simulation data, the identified salt bridge was the longest lasting interaction,
516 forming at approximately 0.9 ns into the production run and existing unbroken for the
517 remaining 0.6 ns. This suggests that this interaction was energetically favorable and relatively

518 strong compared to the hydrogen bonding that was observed, given that no hydrogen bonds
519 lasted this length of simulation time.

520

521 Interactions between the protein and humic acid model that were not identified during this
522 simulation, yet were expected, were ion-mediated bonding. Given the number and range of
523 ions in this experiment (i.e. Na^+ , K^+ , Ca^{2+} and Mg^{2+}), it was anticipated that an aspect of the
524 interaction would involve ion bridging, especially involving one of the three deprotonated
525 carboxyl groups contained on each of the humic acid models. However, a thorough analysis
526 of the simulation trajectory does not contain any evidence for such cations interacting with
527 the BSA and humic acid model. This initially counterintuitive observation can be reconciled
528 with the experimental results for the BSA and humic acid mixtures in the aqueous
529 environment (i.e. no added ionic strength). As shown previously in Table 4 (see SI), a similar,
530 if not stronger, association was observed between these two species when there were no ions
531 added, compared to the experimental electrolyte environment. This appears to be due to the
532 fact that ions are not directly involved in the interactions of BSA and humic acid. Indeed, a
533 higher ionic strength may actually increase competition between the BSA and surrounding
534 media for the humic acid.

535

536

537 3.4.2. Alginate-humic interaction by MD

538

539 For the alginate-humic acid system, only one type of interaction was observed. This involves
540 water-mediated Ca^{2+} bridging between the deprotonated carboxylate moiety of the TNB
541 molecule and a binding pocket on the alginate (Fig.14in SI). The carboxylate group of the
542 TNB model was directly bound to a Ca^{2+} ion, with an average simulated bond distance of

543 2.14 (± 0.10) Å, for the final 0.5 ns of simulation time. This bonded Ca^{2+} ion was observed to
544 interact with three oxygen atoms (two from hydroxyl moieties and one from a deprotonated
545 carboxylate group) of the alginate via water-mediated hydrogen bonding interactions. The
546 distances between the calcium and the alginate oxygen atoms in these interactions were 4.70
547 (± 1.4) Å (hydroxyl #1), 5.05 (± 1.29) Å (hydroxyl #2) and 4.75 (± 1.76) Å which are typical
548 values for interactions of this type (may range between 4 and 5.5 Å (Jalilehyand et al., 2001)).

549

550

551

552 The type of interactions observed between the components of the BSA-humic acid system are
553 not repeated within the alginate-humic acid simulation. Rather, these interactions are strongly
554 ion-mediated, as the only interactions observed were equivalent to native alginate-alginate
555 bonding mechanisms. This result is not unexpected given that the biopolymer in this
556 simulation, the alginate, is highly negatively charged at a neutral pH with almost complete
557 dissociation of all carboxyl groups. This leads to a relative charge density of one anionic
558 charge per 178 Daltons of mass, compared to BSA which contains one negative charge per
559 4,149 Daltons. Given that the humic acid model is also anionic at the experimental pH, it
560 would be expected that interactions between these two species would be heavily reliant on the
561 ionic environment, in particular the cationic identity and concentrations. This conclusion is
562 supported by the experimental results, whereby there appeared to be little or no complexation
563 between the alginate and humic acid in deionised water (i.e. the URI value increases slightly)
564 yet there was a positive interaction between the two species in the ionic environment (i.e. the
565 URI decreases). The synthetic wastewater systems investigated here, in conjunction with
566 complementary molecular dynamics simulations, have provided strong evidence that
567 interactions between high molecular weight biopolymers and humic acids can occur, and the

568 experimental membrane fouling results demonstrate that these interactions can effect
569 membrane fouling outcomes.

570

571 3.5. Fouling mechanisms

572

573 Based on the hydraulic backwashing analysis and such interactions evidenced for the organic
574 mixtures by both LC results and molecular dynamics (MD) modelling, overall fouling
575 mechanisms were thus proposed. During filtration of BSA-humic acid mixture, enhanced
576 membrane fouling was observed compared to the individual BSA and humic acid systems
577 similar to the findings reported by Madaeni et al., 2006. Madaeni et al., 2006 reported that
578 lower flux decline and higher humic acid rejection were observed for BSA and humic acid
579 system due to the interactions between these compounds. Indeed, the intermolecular
580 interaction between BSA-humic acid system by molecular dynamics simulations and
581 supported by LC analysis demonstrated a range of interactions – including electrostatic,
582 hydrophobic and hydrogen bonding but no ion-mediated interaction. These dominant types of
583 interactions observed are not as strong as ion-mediated interactions. Therefore, it is possible
584 for rearrangement of the BSA and humic acid molecules to occur at low pressures, resulting
585 in a more compact and hydraulically resistant filter cake. Compression of flocculated
586 suspensions are known to be linked to the strength of the networked structure as measured by
587 the compressive yield strength [de Kretser et al, 2003], with weaker intermolecular
588 interactions leading to reduced strength and easier compressibility. Therefore, it is proposed
589 that the resulting formation of a compact fouling cake layer on the membrane surface during
590 filtration/backwashing cycles for BSA-humic acid mixture occurred as filtration progressed
591 over time. This filter cake was not easily hydraulically backwashed as shown by the %
592 reversibility calculated as shown in Fig. 4. It is not immediately obvious why the fouling

593 layer caused by BSA and humic acid system cannot be easily hydraulic backwashed. Hong et
594 al., (2005) suggested that backwash efficiency is closely linked to the structure of the cake
595 layer formed during particle filtration. Therefore, the lower backwashing efficiency may arise
596 from a more densely packed cake layer that prevents fluid flow. Alternatively, weak
597 interactions between foulant entities might lead to uneven filter cake removal during
598 backwashing of hollow fibres, with localized backwashed regions quickly fouling upon
599 filtration as the filter cake rearranges and stabilises.

600

601 Unlike the BSA and humic acid system, the formation of alginate cake or gel with humic acid
602 incorporated occurred only in the presence of divalent Ca^{2+} ions. This is supported by the
603 increased rejection of humic acids during filtration of sodium alginate and humic acid
604 mixture solution. Interestingly, the experimental results showed that the fouling behaviour of
605 the mixture tends to be close to that of sodium alginate alone, suggesting that humic acid
606 does not greatly affect the alginate filter cake structure. Similarly, the reversibility of fouling
607 by backwashing was similar for both the alginate and alginate-humic acid systems. Le-Clech
608 et al., (2006) showed via direct observation the almost complete removal of fouling layer
609 caused by alginate/bentonite solution from a PVDF membrane by backwashing with
610 permeate solution. A similar finding was also reported by Katsoufidou et al., (2010) in which
611 the authors demonstrated fouling reversibility for a sodium alginate and humic acid mixture
612 was greater than for humic acid filtration for a PES membrane. Addition of humic acid to the
613 alginate- Ca^{2+} system may disturb the resultant network, as humic acid competes with alginate
614 to bind with Ca^{2+} . Such interactions will disrupt alginate packing and potentially lead to
615 reduced cross-linking. This may result in a more open and porous filter cake structure.
616 However, the degree of reversibility upon backwashing for the alginate- Ca^{2+} system was

617 already high, and further increases in reversibility were detected when humic acid was added.
618 Further analysis is required to confirm this hypothesis..

619

620

621 3.6. Practical Implications

622

623 The possibility of interactions between large molecular weight biopolymers and smaller
624 organic acids has been demonstrated with potential implications for membrane operations.
625 Increased fouling was demonstrated for protein-humic acid mixtures, while increased humic
626 acid rejection was demonstrated in the presence of polysaccharides and calcium, and proteins.
627 Currently the performance of coagulation in removing these aggregated structures compared
628 to biopolymer compounds and organic acids in isolation is unknown, but it might be
629 speculated, based on their fouling behaviour with hydrophobic membranes, that they may
630 display behaviour different from the isolated compounds.

631

632 However, the detection of biopolymer peaks with LC-UV₂₅₄ is seldom observed for natural
633 waters or wastewater. It might be postulated that this is because of competition between other
634 non-UV absorbing organic species for association with the biopolymers, a lack of available
635 calcium for alginate associations, humic acid associating with smaller molecules or different
636 functional groups on the proteins and polysaccharides than what has been considered (eg.
637 acetylated alginates). Nevertheless, while uncommon, there are examples of biopolymers
638 being detected by LC-UV (Her et al., 2003; Fabris et al., 2007). In the case of Her et al.,
639 (2003) a small UV₂₅₄ peak was observed for a secondary effluent, while Fabris et al., (2007)
640 used LC-UV₂₆₀ for characterization of biopolymers from an algal impacted surface water.
641 The potential for these aggregated structures to form may in part explain why predicting

642 membrane fouling and water quality following coagulation or other pretreatments has been
643 difficult to predict, as the extent of association between species is likely to vary with location
644 and time. Therefore, it may be useful to characterize the biopolymer component of waters
645 using LC-UV (an aggregated component) as well as with LC-Organic Carbon Detector (total
646 biopolymers), to obtain a better understanding of biopolymer behavior in water processes and
647 as a means to better explain the variability between water sources on treatment processes.

648

649 4. Conclusion

650

651 The characterization of the biopolymer fraction into total and aggregated biopolymer
652 components may be useful in explaining variability between water sources in terms of their
653 treatability by coagulation or other pretreatment processes. The formation of aggregates of
654 alginates or BSA as model biopolymer compounds with humic acid was detected by the
655 UV_{254} response in the biopolymer region for mixture solutions. Interestingly, the interaction
656 of BSA with humic acid occurred both in the presence and absence of calcium, suggesting the
657 divalent ions did not play a part in the aggregation process. Similar analyses of the alginate
658 interaction with humic acid also showed a positive interaction, but only in the presence of
659 calcium ions. When molecular dynamics (MD) modelling was employed to provide insights
660 into these organic interactions in solution, the results were complementary to experimental
661 findings. Molecular dynamic simulations of BSA-humic acid system revealed a number of
662 distinct, direct interactions; electrostatic, hydrophobic and hydrogen bonds were the dominant
663 types of interactions predicted. Similarly for the alginate-humic acid system the modelling
664 study strongly suggested that the interaction was water-mediated Ca^{2+} bridging between the
665 deprotonated carboxylate moiety of the humic acid molecule and a binding pocket on the
666 alginate.

667

668 Such a number of distinct, direct interactions between BSA-humic acid mixture led to
669 enhanced membrane fouling compared to alginate-humic acid mixture (i.e. no enhancement
670 of fouling). The dominant types of interactions observed between BSA-humic acid system
671 are expected not to be as strong as ion-mediated interaction; therefore it is possible for both
672 BSA and humic acid molecules to interact through a variety of modes and to rearrange in the
673 cake layer, allowing the creation of a more compact filter cake morphology. This filter cake
674 was not easily hydraulically backwashed possibly due to lower backwashing efficiency for a
675 more densely packed cake layer or because of uneven backwashing for the hollow fibre
676 system and rapid filter cake rearrangement upon recommencing filtration. Unlike the BSA-
677 humic acid mixture, the interaction between alginate and humic acid was divalent ion-
678 mediated only. Therefore, the formation of alginate cake or gel with humic acid incorporated
679 in the presence of divalent Ca^{2+} ions was possible. However, such alginate-humic- Ca^{2+}
680 fouling layer could easily be disturbed after periodic backwashing with deionized water since
681 the % reversibility for this mixture was maintained throughout the experiment. Additionally,
682 the aggregated alginate- Ca^{2+} binding network could be disrupted by adding the humic acid
683 into the mixture, resulting in a more open, porous structure. However, further analysis is
684 required to confirm this hypothesis.

685

686

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688

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693

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- 790

Figure Captions

Fig 1. LC-UVD-OCD (Method B) response of pure compounds representative of organic foulants

Fig. 2. Plot of fouling curves of BSA, humic and BSA-humic mixture solutions

Fig. 3. Plot of the inverse J's versus specific mass of BSA, humic and BSA-humic mixture solution (HIFI = slope of lines)

Fig. 4. The % permeability reversibility for humic acid (HA), BSA and BSA-humic acid (BSA+HA) system

Fig. 5. Plot of the inverse of J's versus specific mass of Alginate, humic and Alginate-humic mixture solution (HIFI = slope of lines)

Fig. 6. The % permeability reversibility for sodium alginate (SA), humic acid (HA) and sodium alginate (SA) + humic acid (HA) systems

Table 1

Summary of foulant solutions (in electrolyte) prepared for organic characterization

Model foulant solutions	pH (± 0.2)	Conductivity ($\pm 5 \mu\text{S}/\text{cm}$)
Sodium alginate	7.6	619
BSA	7.2	620
Humic acid (HA)	7.2	627
BSA + HA	7.0	635
Sodium alginate + HA	7.1	634

Table 2

URI values calculated for each individual foulant compounds in background electrolyte and aqueous solution

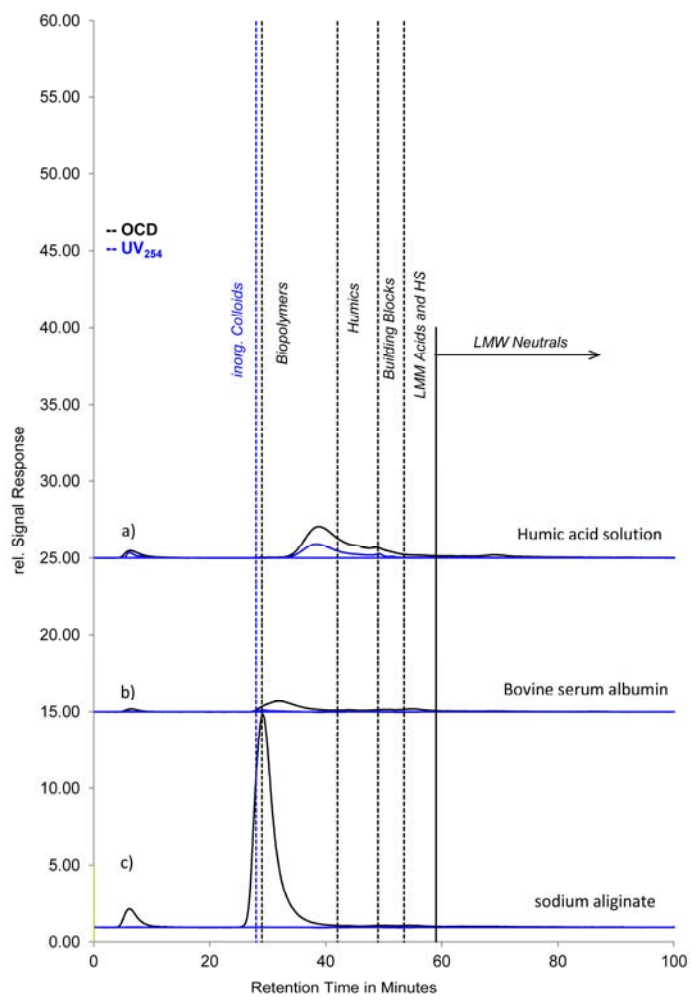
Model foulant substance	URI (aqueous)	URI (electrolyte)
Sodium Alginate	-*	-*
BSA	19±1	22±2
Humic acid (HA)	1.3±0.1	1.4±0.1

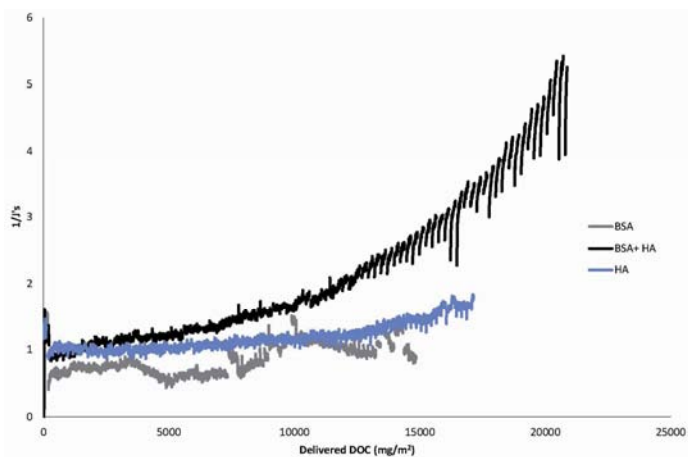
*UV 254nm absorbance 0, therefore a URI value could not be calculated.

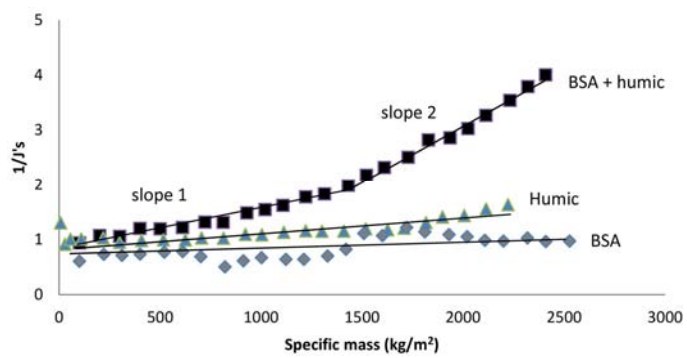
Table 3
Comparison of absorbance characteristics for mixtures of compounds in background electrolyte and aqueous solution

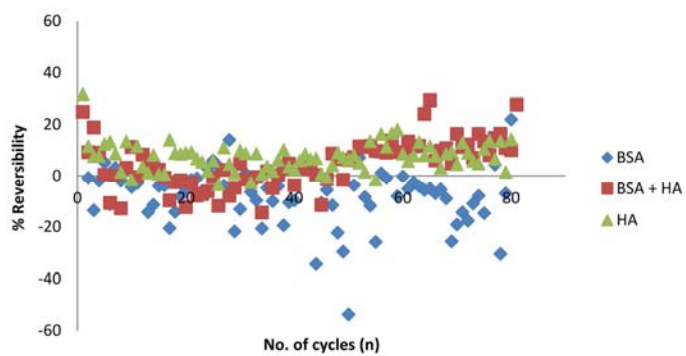
	Aqueous			Electrolyte		
	URI-Humic or Tannic	URI-BSA	URI-biopolymer	URI-Humic or Tannic	URI-BSA	URI-biopolymer
Mixture	5000<MW<150	MW~10kDa	MW>=50 kDa	5000<MW<150	MW~10kDa	MW>=50 kDa
BSA-humic	1.1±0.1	3.7±0.9	2.2±0.1	0.9±0.2	11±2	1.6±0.1
Alg-Humic	1.3±0.1	-		1.4±0.4	-	11.5±0.9

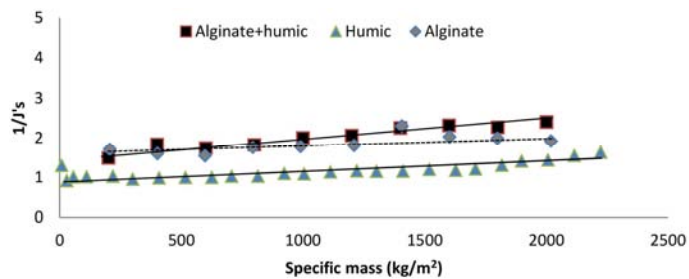
*URI could not be calculated as UV_{254} was zero.

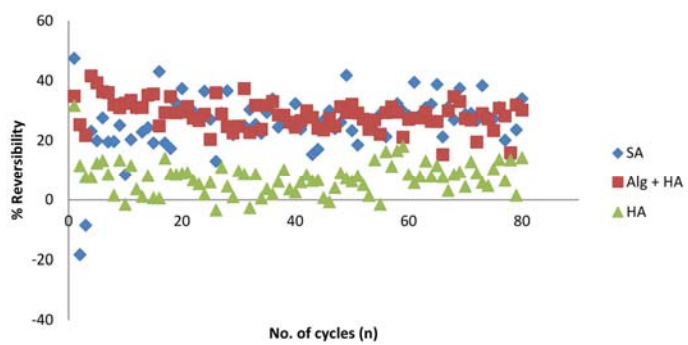












Highlights

- Biopolymers UV254 adsorption indicative of organic acid and biopolymer associations
- Protein-humic acid aggregate due to electrostatic, hydrophobic and hydrogen bonding
- Divalent ion mediated associations between humic acid and polysaccharides
- Protein humic acid associations result in more significant fouling
- Increased rejection of organic acids due to associations with biopolymers

Supplementary Data

Table 4.LC Method B results HA, BSA and Alginate

	Biopolymers	Humic substances	Aromaticity (SUVA – HS)	Building blocks	LMW neutrals	LMW Acids	Inorganic colloids	SUVA
Molecular Weight (Da)	>>20,000	~1,000	~1,000	300-500	<350	<350		
Model substance	ppb-C	ppb-C	L/(mg*m)	ppb-C	ppb-C	ppb-C	m ⁻¹	L/(mg*m)
a) HA	12	826	10.16	306	229	3	0.00	8.86
b) BSA	274	63	1.01	78	55	n.q.	1.31	n.q.
c) Alginate	2732	n.q.	-	497	57	31	0.04	n.q.

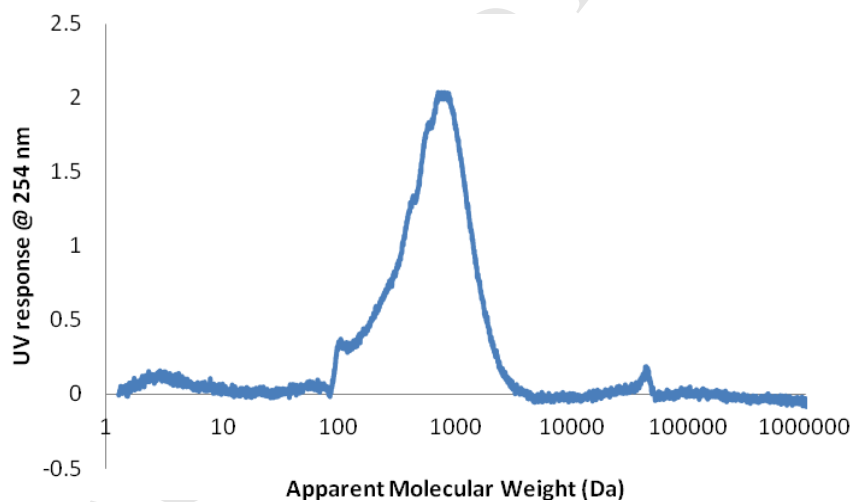


Fig.7. Chromatograms of UV response at 254 nm for humic acid only in deionised solution (Method A)

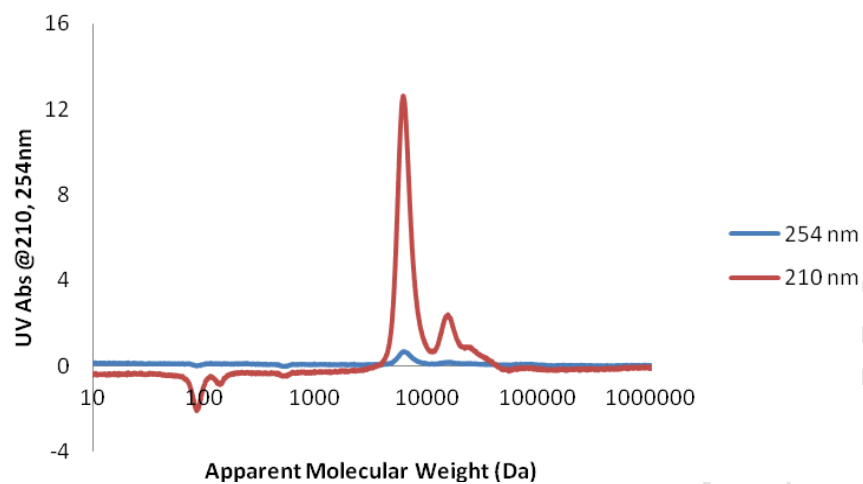
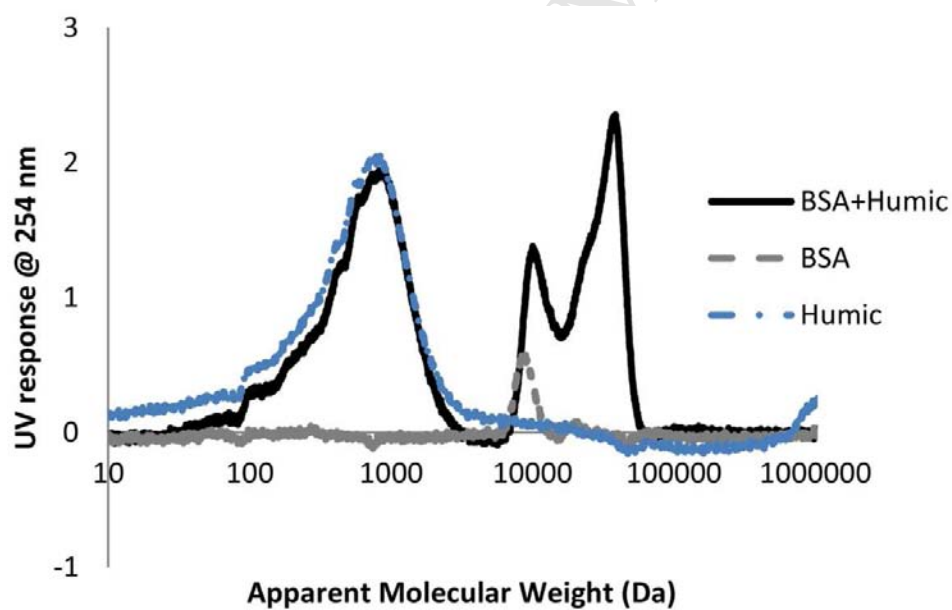


Fig.8. Chromatograms of UV response at 254 nm and 210 nm for BSA only in electrolyte solution (Method A)



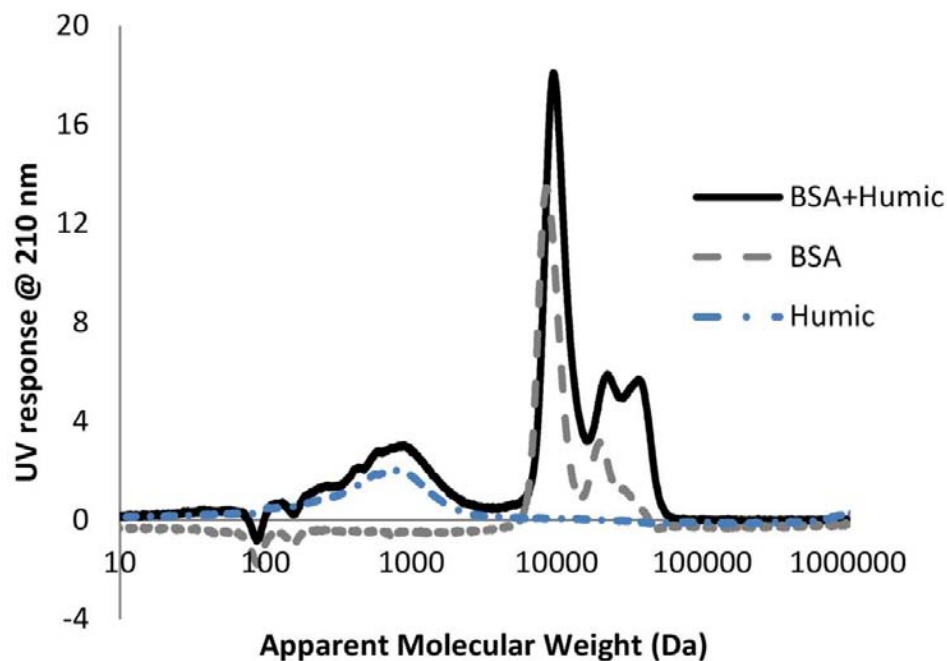
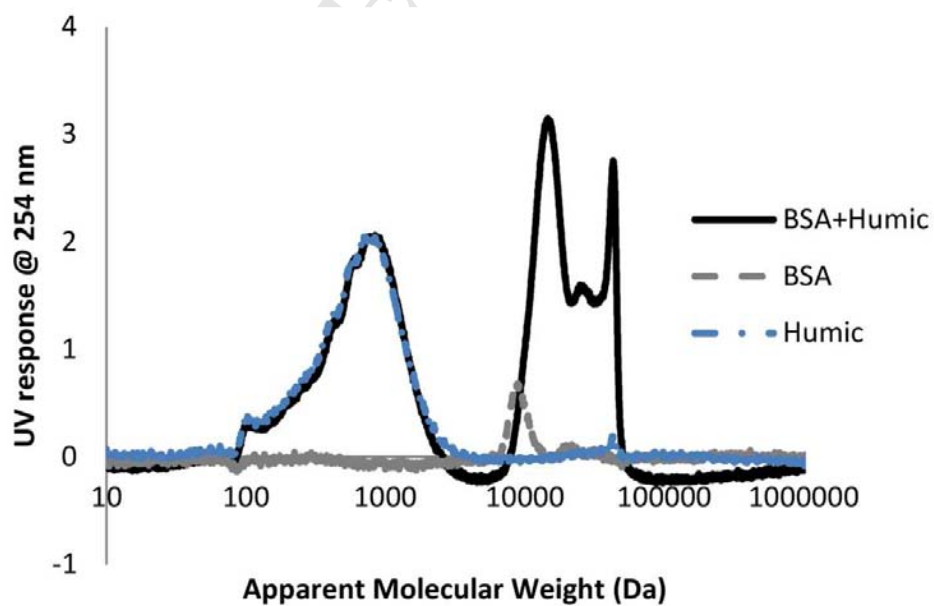


Fig. 9 Chromatograms of UV response at a) 254 nm and b) 210 nm for BSA- humic acid solution in electrolyte (Method A).



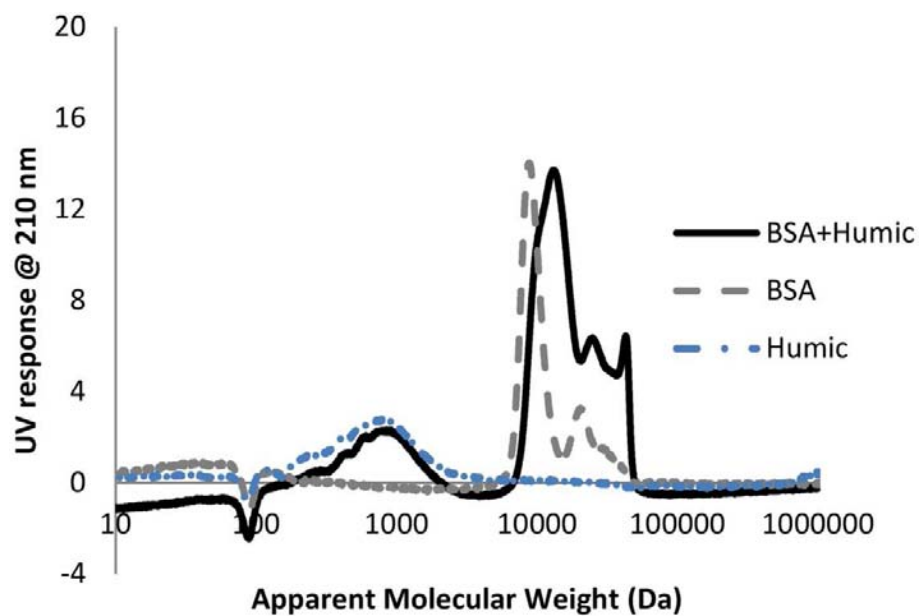
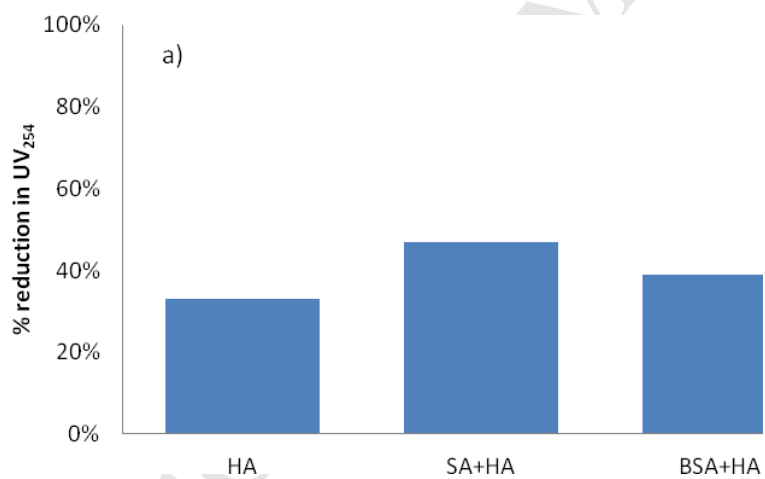


Fig.10 Chromatograms of UV response at a) 254 nm and b) 210 nm for BSA- humic acid solution in water (Method A).



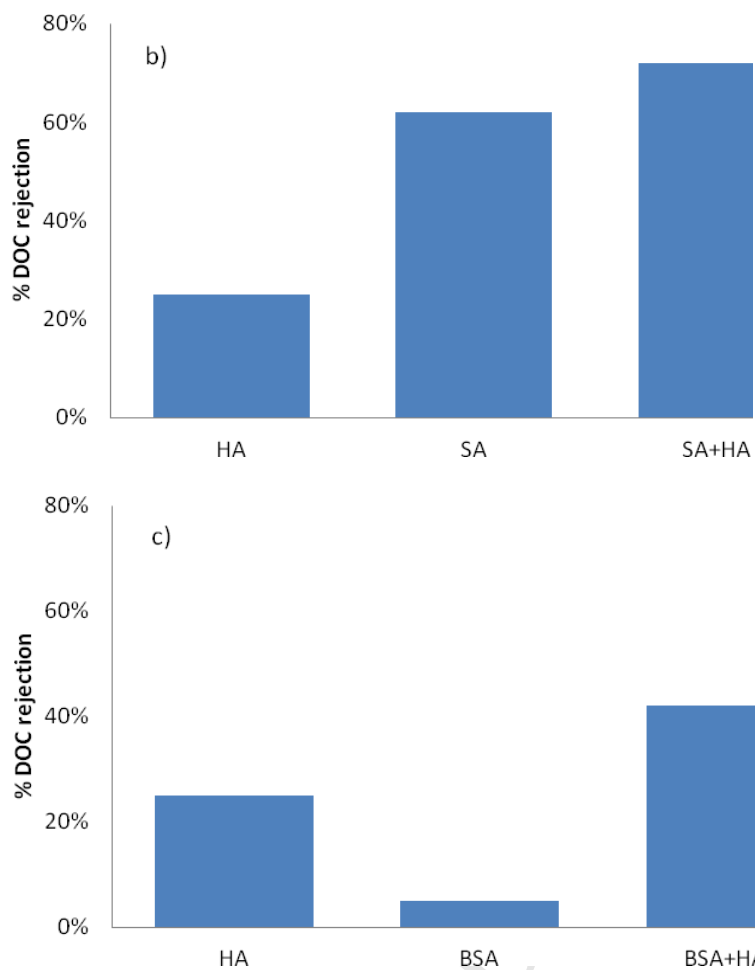


Fig.11 a) % reduction in UV_{254} absorbance in permeate; % rejection in DOC concentration in permeate for b) humic acid (HA), sodium alginate and sodium alginate-humic solutions and c) humic acid (HA), bovine serum albumin (BSA) and BSA-humic solutions

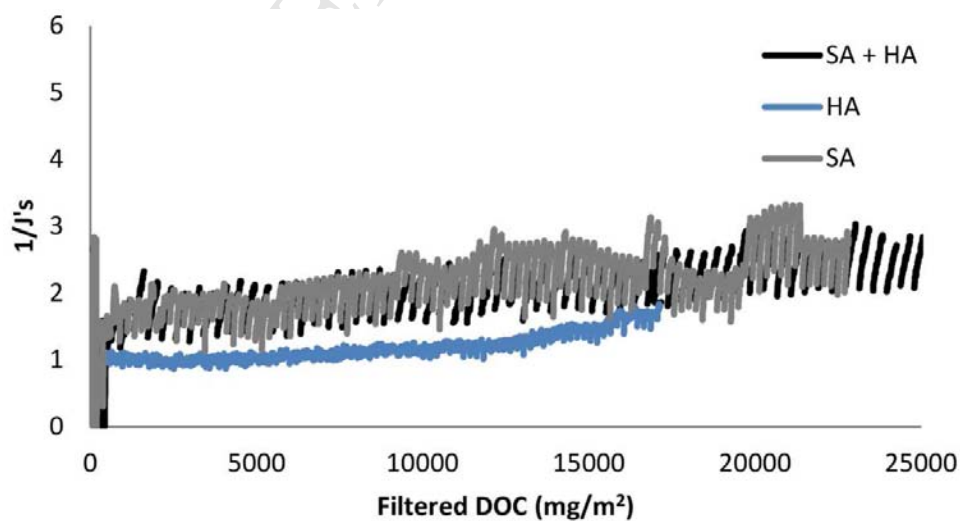


Fig.12 Plot of fouling curves of sodium alginate, humic acid and sodium alginate-humic acid mixture solutions

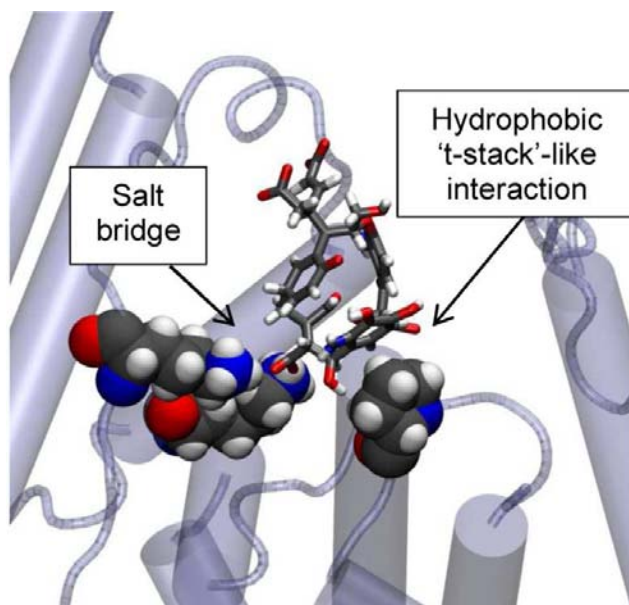


Fig.13. BSA (protein)-humic acid (TNB) attractive interaction, captured in a molecular dynamics simulation. The interacting amino acid residues have been displayed as van der Waals spheres and the TNB model is displayed as tubular (N – blue; O – red, C –black; H – white). A salt bridge interaction may be observed between two -NH_3^+ moieties and a deprotonated carboxylate moiety of the humic acid. A hydrophobic ‘t-stacking’-type interaction may be also observed between the aromatic ring of the humic acid and the aliphatic ring of a proline residue.

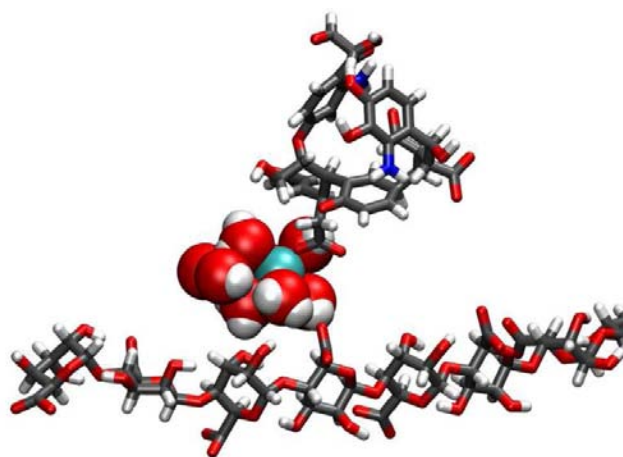


Fig.14. Alginate – humic acid (TNB) attractive interaction, captured during a molecular dynamics simulation. The humic acid molecule (top) and alginate chain (below) is displayed as tubular (N – blue; O – red, C –black; H – white). The Ca^{2+} ion (green) and water molecules are rendered as van der Waals spheres. A direct bond between the carboxylate group of the TNB molecule and a hydrated Ca^{2+} ion can be clearly seen. The interaction between the Ca^{2+} ion and alginate is water-bridged via three hydrogen bonds.