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# A direct comparison between membrane adsorber and packed column chromatography performance

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## Abstract

The purpose of this work was to compare side by side the performance of packed bed and membrane chromatography adsorption processes for protein purification. The comparison was performed using anion exchange media with the same ligand immobilized on the adsorbing surface, namely the strong Q quaternary ammonium group, R-CH<sub>2</sub>-N<sup>+</sup>-(CH<sub>3</sub>)<sub>3</sub>, and bovine serum albumin (BSA) as a model protein. In addition, the stationary phase volume was held constant for each geometry (3 mL) and runs were executed using the same mobile phase superficial velocity. As expected, the packed bed column showed higher equilibrium binding of BSA at 66.9 mg/mL versus 43.04 mg/mL for the membrane adsorber. Dynamic binding capacities were also higher in the packed bed; for example, at 97.5 cm/h, a capacity of 62.8 mg/mL was measured for the packed bed versus 20.7 mg/mL for the membrane adsorber. The higher equilibrium and dynamic capacities of the packed bed are likely due to the higher surface area per unit volume of the resin. However, the maximum productivity for the membrane adsorber was 111 mg/(mL h) a value that was 3.3 times higher than the one of the packed column. The bed utilization – defined as the ratio of the dynamic binding capacity at 10% breakthrough to the saturation binding capacity - was also higher for the packed column at long residence times and lower at short residence times confirming the better performance of membrane chromatography at high flow rates.

## Keywords

Chromatography; Membrane adsorber; Packed column; Binding capacity; Productivity.

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## 40 1. Introduction

41  
42 Packed bed chromatography is by far the most common technique used for high resolution  
43 separations of proteins, both as an analytical tool and as a process unit operation [1]. In a  
44 conventional process the column is operated in a capture mode, using highly porous resins with  
45 different functionalities according to the mode of operation. Among all chromatographic  
46 techniques, ion exchange has been the most widely employed method for protein purification  
47 since the development of cellulosic ion exchangers in the 1950s [2].

48 Membrane chromatography is a relatively new technique developed with the purpose of  
49 operating at higher flow rates and at reduced process time relative to bead-based column  
50 chromatography. Higher flow rates are possible with membranes because the resulting  
51 pressure drop is significantly lower than in traditional packed-column chromatography  
52 processes, and because solute transport in membrane devices is primarily by convection to the  
53 membrane internal surface, rather than the much slower intraparticle diffusion that is rate  
54 controlling in chromatography beads [1, 3-4]. In addition, since membrane adsorbers are  
55 generally less costly to manufacture, they can potentially be used as single-use devices that  
56 eliminate the difficulties and costs often associated with packing a chromatographic column,  
57 and the cleaning and validation steps required of multi-use columns [5].

58 One significant drawback associated with the use of membrane adsorbers in a capture mode is  
59 that their binding product capacities are generally lower than those of column chromatography  
60 resins. As a result, the industrial application of membrane adsorbers has been largely limited to  
61 flowthrough polishing applications in biopharmaceutical production processes in which small  
62 concentrations of impurities bind to the chromatography media, while product flows through  
63 [3-16]. Indeed, with the development of novel membrane materials with higher binding  
64 capacities the use of membrane adsorbers for product capture is of increasing interest [17-21].  
65 Among those, cation exchange membranes made by porous polyacrylate hydrogels on a  
66 polypropylene support have been used for monoclonal antibody capture obtaining IgG dynamic  
67 binding capacities higher than 60 mg/mL at 10% breakthrough [6-7]. Comparable binding  
68 capacities were reported for high capacity multimodal cation exchanger membranes prepared  
69 by immobilizing poly(glycidyl methacrylate) tentacles on cellulosic membranes [8]. More recent  
70 work reports novel membranes with improved material structure: the use of polymer brushes  
71 and membrane based on electrospun nanofibers and nonwovens are the strategies that have  
72 been mostly employed [22-24]. These improved structures have resulted in high binding  
73 capacities. In addition, recent work has looked at the behavior of membrane adsorbers in  
74 different flow configurations [25-26] and has focused on developing interesting novel module  
75 designs that have resulted in improved performance [27-28].

76 The comparison of performance for different types of chromatographic supports has been  
77 considered by several authors, but most papers have reported results of experiments targeted  
78 to a specific application with columns of different volumes or experiments in which the  
79 operating conditions were not chosen with the aim of direct comparison. Ribero *et al.*  
80 investigated the performance of different chromatographic supports to be used for purification  
81 of recombinant Factor IX. They tested two different anion exchange resins, a membrane  
82 adsorber and a monolithic column and chose to continue with the monolith due to its higher  
83 binding capacity for the target molecule [29], based on their goal of finding the best material

84 for the purification of Factor IX. The higher value of the dynamic binding capacity was the main  
85 criteria of choice among different stationary phases together with the resolution and  
86 selectivity. However, the comparison did not keep column volume and superficial velocity  
87 constant among options.

88 Liu *et al.* tested commercial cation exchanger membranes and compared them to monoliths  
89 and packed columns for antibody capture with interesting results. Ultimately, they chose to  
90 operate with the protein A column for capture, despite the fact that the cation exchanger  
91 membrane adsorber, operated in overloaded isocratic mode, was more effective in the removal  
92 of host cell proteins and high molecular weight impurities [30]. Although Bhut *et al.* considered  
93 stationary phases of the same volume and the same weak anion exchange functionality, they  
94 presented newly designed membranes that were not commercially available with high binding  
95 capacity and compared them with standard materials: a regenerated cellulose membrane and  
96 an agarose resin [31]. However, superficial velocities between devices were not held constant.  
97 Similarly, in a pioneering work, Kubota *et al.* performed a very thoughtful comparison between  
98 hollow fiber membranes and a packed bed column of the same volume and the similar ion-  
99 exchange functionality; however, they did not operate the two supports at the same superficial  
100 velocity, which is an aspect that is often disregarded [32].

101 Comparisons between packed bed and membrane chromatography are rare in the literature  
102 and they are often undertaken to highlight the high throughput of novel membrane materials.  
103 The majority of the works that report such comparisons generally consider binding capacity as  
104 the major performance parameter for evaluation of the different options without looking at  
105 other chromatographic performance parameters such as resolution, productivity, or bed  
106 utilization.

107 Because of the numerous advantages that membrane chromatography potentially offers, this  
108 study aims to more directly compare properties and performance of the membrane and more  
109 traditional column geometries. The work presented in this paper considers porosity, binding  
110 capacity, mass transfer rate, bed utilization and productivity between the two geometries more  
111 fully than has been done in previous studies [29-32]. To do this, a side-by-side comparison of  
112 each geometry, using a membrane adsorber and chromatography resin that are commercially  
113 available, have the same strong anion exchange functionality, are readily scalable, and have  
114 identical bed volumes, 3 mL, was performed. Bovine serum albumin (BSA) is used as a model  
115 protein and the columns were operated in non-competitive conditions at the same superficial  
116 velocity to properly evaluate the transport phenomena limitations of the chromatographic  
117 supports. Comparison was also performed by looking at performance parameters with respect  
118 to residence time, even though due to the different bed geometries and packing characteristics  
119 it was not possible to operate the packed column at the same low residence times, i.e. high  
120 flow rates, of the membrane adsorbers.

121

122

## 123 **2. Experimental**

124

### 125 **2.1 Materials**

126 The membrane adsorber used during the experiments was an anion exchange Sartobind® Q  
127 Nano 3 mL, produced by Sartorius Stedim Biotech GmbH. This is a radial flow module consisting

128 of 30 membrane layers. The volume of the membrane bed is 3 mL and the membrane surface  
129 area available for flow is 110 cm<sup>2</sup>. Liquid flows around the bed, then radially through the  
130 membrane layers into a central channel and finally through the outlet channel. The membranes  
131 present in the module have a base matrix of stabilized and reinforced cellulose with an  
132 immobilized quaternary ammonium group. This adsorber is a strong anion exchanger and has a  
133 long-term pH stability range from 2-12. The average membrane pore diameter is 3-5 μm. The  
134 module can be operated at a maximum pressure of 4 bar, the recommended flow rate is 10-15  
135 mL/min, and the BSA binding capacity reported by the vendor is 29 mg/mL (conditions  
136 unspecified).

137 Q Sepharose™ Fast Flow resin, produced by GE Healthcare Life Sciences, was used as adsorbent  
138 for column experiments. This anion exchange resin has a matrix comprised of Sepharose™ (6%  
139 cross-linked agarose) and, like the Sartobind® Q Nano, the strong quaternary ammonium  
140 ligand. Beads are spherical with a diameter ranging from 45 to 165 μm and an average size of  
141 90 μm as reported by the vendor. They can be used at superficial velocities up to 700 cm/h. The  
142 exclusion limit for globular proteins is 4 MDa, but the size distribution of intraparticle and  
143 interparticle pores is unknown. Beads are stable from pH 2 to 12 and they are resistant to all  
144 commonly used aqueous buffers (e.g. 1 M NaOH, 8 M urea, 8 M guanidine hydrochloride). A  
145 summary of the properties for each of the chromatographic media is given in Table 1.  
146 All solution components, NaCl (USP/FCC/EP/BP grades), NaOH (NF/FCC grades), Tris (molecular  
147 biology grade), and HCl (reagent grade) for pH adjustment for Tris, used in these experiments  
148 were purchased from ThermoFisher Scientific. Lysozyme, molecular weight (MW) of 14388 Da  
149 and isoelectric point (pI) of 11.0 [33] was purchased from ThermoFisher Scientific [34]. Bovine  
150 Serum Albumin (BSA), MW 66430 and pI 4.7, was purchased from Sigma-Aldrich with a purity ≥  
151 96% [35]. BSA and lysozyme solutions were filtered with 0.21 μm cellulose nitrate membrane  
152 filters (Whatman) before experiments. The filter material was hydrophilic as to minimize non-  
153 specific protein adsorption.

154

## 155 **2.2 Equipment**

156 The characterizations of the chromatographic devices tested was performed on an  
157 ÄKTAexplorer 100, manufactured by GE Healthcare Life Sciences and controlled by UNICORN™  
158 software. Experimental runs were carried out in parallel with both the Sartobind® Q Nano 3 mL  
159 module and with a column packed with Q Sepharose™ Fast Flow resin with a total bed volume  
160 of 3 mL.

161 For experiments that required a packed column, Q Sepharose™ Fast Flow resin was flow packed  
162 in an Econoline® Column from Sorbent Technologies Inc. The external tube is made of  
163 borosilicate glass with an inner diameter of 1 cm and an adjustable bed height from 0 to 12.5  
164 cm. The pressure limit for the column is 80 bar.

165

## 166 **2.3 Methods**

### 167 **2.3.1 Column packing**

168 Resin was packed under flow with high purity water at a flow rate of 5 mL/min. To calculate the  
169 amount of resin slurry required for a bed volume of 3 mL, equal to the volume of the  
170 membrane unit, a packing factor of 1.1 was used. The resulting bed had a height of 3.8 cm,  
171 corresponding to a volume of 2.98 mL.

172 To assess the quality of packing, a pulse injection of a 2 M NaCl solution was made on the  
173 column equilibrated with 0.5 M NaCl to calculate the height equivalent of a theoretical plate  
174 (HETP) and the asymmetry factor of the packed column. Following the pulse injection,  
175 additional 0.5 M NaCl was fed to the column at 2 mL/min, which corresponds to a superficial  
176 velocity of 153 cm/h, to move the 2 M NaCl pulse through the column. Analysis of the  
177 conductivity peak from the column resulted in a reduced HETP value ( $=\text{HETP}/d_p$ , where  $d_p$  is the  
178 resin diameter) of 3.31 and an asymmetry value of 1.68.

179

### 180 **2.3.2 Porosity determination**

181 The porosities of the chromatographic media were determined by statistical moment analysis  
182 on experimental data obtained using lysozyme as a tracer [36-37]. Lysozyme has an isoelectric  
183 point of 11 [33] and therefore at pH 8 does not bind to the positively charged groups of the  
184 chromatographic supports; in addition, 0.25 M NaCl was added to the lysozyme solution to  
185 further prevent binding to the media. After equilibrating the membrane adsorber or the packed  
186 column with 50 mM Tris, 0.25 M NaCl, pH 8, a solution of 2.5 mg/mL lysozyme in equilibration  
187 buffer was injected using a 100  $\mu\text{L}$  loop. Lysozyme in the column effluent was monitored by UV  
188 absorbance at 280 nm. For the membrane adsorber, injections were performed both with and  
189 without the membrane adsorber attached to the AKTAexplorer system. For the packed column,  
190 injections were performed both with a packed column attached to the AKTA system and an  
191 unpacked column with the plungers set to 0 mL.

192 Lysozyme injections were performed for each system setup (with membrane adsorber, without  
193 membrane adsorber, with packed column, and with unpacked column) at five different  
194 superficial flow velocities; lysozyme retention volume values were calculated as the averages of  
195 the results at each of the five superficial velocities. The superficial velocities were held constant  
196 between the experiments with the membrane capsule and those with the packed column. The  
197 experiments with the membrane unit were performed at 5, 7.5, 10, 12.5 and 15 mL/min, the  
198 latter being the operational flow rate recommended by the manufacturer. The superficial  
199 velocity corresponding to each of these flow rates was determined as an integral average of the  
200 radial velocity from the outer radius to the inner radius of the membrane bed, and the resulting  
201 formula is reported in eq. (1):

202

$$203 \quad u_{MA} = \frac{F}{2\pi L(R_{ext} - R_{int})} \ln \left( \frac{R_{ext}}{R_{int}} \right) \quad (1)$$

204

205 where  $F$  is the volumetric flow rate,  $L$  is the length of the membrane bed, and  $R_{ext}$  and  $R_{int}$  are  
206 the outer and inner radii of the membrane bed, respectively. The resulting superficial velocity  
207 values were also used for the packed column experiments, but in this case, the corresponding  
208 volumetric flow rate was calculated from the definition of superficial velocity in a packed  
209 column:

210

$$211 \quad u_{PB} = \frac{F}{\pi R_{col}^2} \quad (2)$$

212

213 where  $R_{col}$  is the inner radius of the column. Volumetric flow rates and superficial velocity  
214 values used in the porosity measurements are summarized in Table 2.

215 After each experiment, the chromatographic media, membrane adsorber or packed column,  
216 was regenerated with 2 M NaCl and sanitized with 1 M NaOH. During these steps, no UV  
217 absorbance peaks were observed, demonstrating that lysozyme in fact did not bind to the  
218 chromatographic media.  
219 Once retention volumes for lysozyme were measured, the porosity of the membrane adsorber  
220 (designated MA in the equations below) was determined as follows. The total void volume of  
221 the membrane adsorber, including both membrane pores and other membrane volume  
222 contributions, was calculated by subtracting the retention volume of lysozyme with no module  
223 connected from the retention volume of lysozyme with a module connected:

$$225 \quad V_{\text{total voids, MA}} = V_{\text{sys with MA}} - V_{\text{sys without MA}} \quad (3)$$

226  
227 For the membrane adsorbers, the resulting void volume not only includes the membrane pores,  
228 but also includes the voids related to the various flow channels within the membrane module  
229 housing and the liquid distributors in the module. To determine the membrane module dead  
230 volume, the membrane adsorber was broken open and its internal dimensions were measured  
231 with a gauge. The volume of these additional contributions was then subtracted from the total  
232 void volume calculated with Eq. (3) to obtain the volume of the membrane pores.

$$234 \quad V_{\text{pores}} = V_{\text{total voids, MA}} - V_{\text{module}} \quad (4)$$

235  
236 The porosity is then calculated as the ratio of  $V_{\text{pores}}$  to the reported volume of the membrane  
237 adsorber, 3 mL.

238 The procedure is similar for the packed bed, with column voids – both interparticle and  
239 intraparticle - calculated as:

$$241 \quad V_{\text{total voids, PB}} = V_{\text{sys with packed column}} - V_{\text{sys with empty column}} \quad (5)$$

242  
243 And again, the porosity is calculated as the ratio of  $V_{\text{total voids, PB}}$  to the total volume of the  
244 packed bed, 3 mL.

### 246 **2.3.3 Adsorption isotherm determination**

247 Adsorption isotherms for BSA on the solids supports were measured with two different  
248 procedures, in batch mode for Q Sepharose™ Fast Flow resin and with the AKTAexplorer system  
249 for the Sartobind® Q Nano membrane adsorber. Batch measurements were not possible for the  
250 membranes because at the time of this study, they were only available as part of a module and  
251 not as loose membrane sheets.

252 Adsorption isotherms for BSA in 50 mM Tris, pH 8.0 on Q Sepharose™ Fast Flow resin were  
253 measured in batch experiments at room temperature. First, a kinetic study was performed to  
254 determine the time necessary for the BSA in solution to reach the equilibrium with the  
255 adsorbent. Based on this study, a time of 180 minutes was shown to be sufficient. The isotherm  
256 was obtained using 12 mL Poly-Prep (Biorad) columns as the adsorption vessels, filled with 140  
257  $\mu\text{L}$  of resin slurry. BSA concentration in the feed ranged from 0.008 to 9.21 mg/mL. Fresh resin  
258 was loaded to the vessels and washed four times with 50 mM Tris at pH 8; during each wash,

259 the containers were placed for 10 min on an orbital shaker. Then buffer supernatants were  
260 removed. Successively, BSA solutions were loaded to the vessels, and they were incubated on  
261 the orbital shaker for 180 min at room temperature. BSA concentration was measured with UV  
262 absorbance readings at 280 nm and the mass of BSA adsorbed on the resin was calculated as  
263 the difference in the mass of BSA in the loading solution and the mass of BSA measured in the  
264 supernatant sample. The value was divided by the volume (mL) of solid resin to determine the  
265 value of the binding capacity,  $q$ , the mass (in mg) of BSA bound per unit volume (in mL) of resin.  
266  $q$  is plotted against the final equilibrium concentration of BSA in Tris buffer.  
267 The adsorption isotherm for BSA on Sartobind® Q Nano membranes was measured in  
268 breakthrough experiments performed using BSA, at different concentration values, in 50 mM  
269 Tris, pH 9.0. Specifically, BSA solutions with concentrations ranging from 0.023 to 2.01 mg/mL  
270 were fed to the membrane adsorber at a fixed flow rate of 10 mL/min. Feeding continued until  
271 saturation was achieved, as determined by a UV trace that asymptotically flattened out.  
272 Following the breakthrough run, BSA was eluted from the membrane adsorber using 2M NaCl.  
273 The amount of BSA recovered in the eluate was quantified by UV absorbance. This value was  
274 divided by the volume of the membrane adsorber to determine the BSA binding capacity. Upon  
275 completion of elution with 2M NaCl, the membrane was re-equilibrated and used again for  
276 another concentration of BSA.

277

#### 278 **2.3.4. Dynamic characterization**

279 Breakthrough studies were conducted on the membrane adsorber and packed bed column to  
280 determine the dynamic binding capacity at 10% breakthrough ( $DBC_{10\%}$ ) using solutions of 1  
281 mg/mL BSA in 50 mM Tris, pH 8. These solutions were loaded to the column until, when the  
282 concentration of BSA, based on UV absorbance at 280 nm, plateaued. Experiments for each  
283 geometry were performed at 5 different flow rates in order to study the influence of the  
284 superficial velocity on dynamic binding capacity. The superficial velocities used are the same for  
285 both the membrane adsorber and packed bed and are equal to those used for porosity  
286 measurements (see Table 2). Upon completion of each breakthrough run, BSA was eluted from  
287 the relevant stationary phase using 0.5 M NaCl; the chromatographic media was then  
288 regenerated with 1 M NaOH for membranes and 2 M NaCl for the packed bed column, and then  
289 equilibrated with 50 mM Tris, pH 8 prior to the next experiment.

290 The  $DBC_{10\%}$  value was determined by first calculating, from a mass balance, the amount of BSA  
291 that was bound to the media at 10% breakthrough:

292

$$293 \quad m_{\text{ads},10\%} = c_0 V_{\text{loaded},10\%} - c_0 V_{\text{sys}} \quad (6)$$

294

295 where  $m_{\text{ads},10\%}$  is the mass of BSA adsorbed,  $c_0$  is the concentration of BSA in the feed,  $V_{\text{loaded},10\%}$   
296 is the volume of BSA solution loaded at 10% breakthrough, and  $V_{\text{sys}}$  is the total system dead  
297 volume that was determined in a separate tracer experiment [38]. The last term of the  
298 equation introduces an approximation, since the concentration of biomolecule is considered  
299 uniform over the entire system and equal to the feed concentration, while, downstream of the  
300 column and, in particular, between the column outlet and the UV detector where the  
301 concentration is measured, it is lower. However, an estimate of the volume downstream of the



302 chromatographic column shows that the volume between the outlet and UV detector is only  
303 approximately 3% of the total dead volume; therefore the assumption that the concentration of  
304 BSA over the entire dead volume is equal to the concentration of BSA in the feed does not give  
305 rise to a significant error.

306  $DBC_{10\%}$  was then calculated by dividing  $m_{ads,10\%}$  by the volume of the stationary phase.  
307 For a more exhaustive comparison, process parameters such as bed utilization and productivity  
308 of the two different chromatographic processes have been evaluated. Bed utilization is defined  
309 as the amount of protein adsorbed at a given breakthrough point, with respect to the amount  
310 of protein adsorbed at complete saturation [39]; in particular, bed utilization at 10%  
311 breakthrough can be written as:

312

$$313 \quad \text{Bed Utilization} = \frac{DBC_{10\%}}{DBC_{100\%}} \quad (7)$$

314

315 Productivity,  $P$ , is defined as the mass of the target biomolecule recovered in the elution step  
316 per unit volume of media per unit time of the complete chromatographic cycle; that is the sum  
317 of the equilibration, adsorption (load), washing, elution and regeneration times. In symbols:

318

$$319 \quad P = \frac{m_{eluted\ product}}{V_{media} t_{chromatographic\ cycle}} \quad (8)$$

320

321

### 322 **3. Results and Discussion**

323

#### 324 **3.1 Porosity**

325 For the Sartobind® Q Nano module, the porosity determined using the lysozyme tracer  
326 procedure previously described was 58%. For the Econoline® column packed with Q  
327 Sepharose™ Fast Flow resin, the resulting porosity was 64%. This value includes both intra-  
328 particle and inter-particle pores. As expected, the porosity of the packed bed is greater than  
329 that of the membrane adsorber given its higher specific surface area.

330 In addition to estimating porosity using lysozyme as a tracer, a similar procedure using 2 M NaCl  
331 as a tracer in a packed column equilibrated with 0.5 M NaCl was executed. Interestingly, the  
332 resulting packed column porosity determined with NaCl was 80%, significantly higher than the  
333 porosity measured by the lysozyme method. If it is assumed that the interparticle porosity of  
334 the bed is 0.36, the theoretical value for a bed of randomly packed hard spheres, the resulting  
335 intraparticle porosity values using lysozyme and NaCl as a tracer are 0.69 and 0.44, respectively.  
336 The value calculated using NaCl is in agreement with what has been reported previously for  
337 Sepharose FF resins [40-41], while the value for lysozyme is significantly lower. This suggests  
338 that a portion of resin pores is not accessible to lysozyme. The difference in porosity values  
339 using lysozyme and NaCl was not expected, given that the exclusion limit for Q Sepharose FF

340 resin is 4 MDa for globular proteins, while the molecular weight of lysozyme is only 14.4 kDa.  
341 However, the pore size distribution of the resin is unknown, therefore it is likely that this  
342 distribution is sufficiently broad to determine the difference observed. In addition, it is possible  
343 that the NaCl method for porosity determination overestimates porosity due to some binding  
344 interactions of NaCl to the anion exchange resin.

345

### 346 **3.2 Adsorption isotherms**

347 The equilibrium binding capacity of BSA on both stationary phases can be well represented by  
348 the Langmuir isotherm model:

349

$$350 \quad q_{eq} = \frac{c_{eq} q_{max}}{c_{eq} + K_d} \quad (9)$$

351

352 In which the symbols  $q_{eq}$  and  $c_{eq}$  indicate the equilibrium values of the protein concentration on  
353 the surface and in the liquid solution, respectively,  $q_{max}$  indicates the maximum adsorption  
354 capacity, and  $K_d$  is the dissociation constant.

355 The equilibrium isotherm for BSA adsorption onto Q Sepharose™ Fast Flow resin is reported in  
356 Figure 1 as a function of the protein concentration in solution at equilibrium. The experimental  
357 results have been fitted using the Langmuir adsorption isotherm expression in Equation (9),  
358 which gives a maximum equilibrium binding capacity  $q_{max}$ , of 66.9 mg/mL and a dissociation  
359 constant,  $K_d$ , of 0.0836 mg/mL.

360 As discussed in the Experimental section, §2.3.3, the adsorption isotherm for the membrane  
361 was obtained in breakthrough experiments since the only format available for membranes was  
362 the Sartobind® Q Nano commercial unit. The data are shown in Figure 2, and are fitted to the  
363 Langmuir isotherm with a maximum binding capacity of 43.04 mg/mL and a dissociation  
364 constant,  $K_d$ , of 0.011 mg/mL.

365 Although the two supports are functionalized with a quaternary ammonium ligand, the  
366 dissociation constants differ by a factor of 7.6. This could be ascribed to the different base  
367 materials, the different immobilization chemistry, the possible use of spacers or brushes in the  
368 membrane adsorbents, and differences in the chemistry of the ligand itself. Similar or even  
369 higher differences have been observed by Hahn *et al.* in a comparison of different commercial  
370 protein A resins [42], suggesting that even chromatography media with the “same” chemistry  
371 might have significantly different  $K_d$  values. For both supports, the membrane and resin, the  
372 dissociation constant is extremely low, comparable to those observed in affinity  
373 chromatography processes [42-45]; a  $K_d$  of the same order of magnitude was reported by Tao  
374 *et al.* for BSA dissolved in 50 mM Tris pH 8.2 on DEAE-Sephadex ion exchange resin [46]. This  
375 means that BSA dissolved in Tris buffer at a pH close to 8 has a very high affinity for adsorbents  
376 that contain positively charged amine groups.

377 As expected, the maximum binding capacity of BSA onto the Q Sepharose™ FF resin is higher  
378 than on the Sartobind® Q Nano membrane, despite the fact that the isotherm data for the  
379 membrane were measured at a slightly higher pH (pH = 9) than the isotherm data for the resin  
380 (pH = 8). It is also worth noting that the ratio of the maximum binding capacity of the resin  
381 (66.9 mg/mL) with respect to the membrane (43.04 mg/mL) equals 1.55 and this value is lower  
382 than the ratio of the average ligand density of the two supports that equals 1.68 (0.21

383 mmol/mL vs. 0.13 mmol/mL), which indicates a slightly better level of ligand accessibility for  
384 the membrane adsorbers.

385

### 386 **3.3 Dynamic characterization**

387 The effect of flow rate on dynamic binding capacity was investigated for the two stationary  
388 phases in experiments performed by feeding 1 mg/mL BSA solutions. For the membrane  
389 adsorber, the breakthrough curves at different flow rates overlap very well from the onset to  
390 complete breakthrough as can be observed in Figure 3. This suggests that the dynamic binding  
391 capacity is independent of flow rate, thus confirming the dominant convective mass transport  
392 in the membrane adsorber [1, 3-4]. Conversely, for the packed column, breakthrough curves at  
393 different flow rates deviate significantly from one another; specifically, as the flow rate  
394 increases the curves broaden and the steepest curve corresponds to the lowest flow rate as  
395 illustrated in Figure 3. This is the behavior expected when intraparticle diffusion limits solute  
396 mass transfer as is the case with the packed bed.

397 It is worth noting that the breakthrough curves for the membrane device show a consistent  
398 “kink” starting at a volume of just more than 100 mL. In the Sartobind® Q Nano capsules used  
399 in this study, the membrane is wound to form a cylinder, with flow from the exterior of the  
400 cylinder through the layers of membrane, to the interior. The kink in the breakthrough curve  
401 shows up as the membrane adsorber nears complete saturation with BSA. Notably,  
402 breakthrough curves for the packed bed do not show similar behavior. A possible explanation  
403 is that as the BSA front moves to the interior of the membrane capsule, it may encounter an  
404 irregularity in the winding of the membrane that causes dispersion of the front and results in  
405 the kink.

406 The behavior of the dynamic binding capacity with respect to flowrate is better illustrated by  
407 plotting the dynamic binding capacity at 10% breakthrough as a function of the superficial  
408 velocity and of residence time for both supports. These plots are shown in Figure 4. As  
409 expected, the  $DBC_{10\%}$  of the membrane adsorber remains constant, and it is almost 70% of the  
410 binding capacity obtained at saturation (data not shown), which corresponds to the bed  
411 utilization as defined in Eq. 7. Conversely, the  $DBC_{10\%}$  of the packed column decreases at  
412 increasing flow rate as the breakthrough curves broaden. This result confirms that, in the range  
413 of flow rates tested, the membrane adsorber is not affected by solute mass transfer and kinetic  
414 limitations, thus this device can be used up to 300 cm/h without any decrease in binding  
415 capacity. Similar conclusions can be drawn from the behavior of  $DBC_{10\%}$  as a function of  
416 residence time shown in Figure 4b. In this plot the  $DBC_{10\%}$  of the two media— both actual values  
417 and values that have been extrapolated to the residence times that were out of the operating  
418 range of the device tested – are shown. The values for the membrane adsorbers were obtained  
419 by averaging the  $DBC_{10\%}$  values at all flow rates ( $DBC_{10\%}=20.619 \pm 0.177$ ), whereas the data for  
420 the packed column were fitted with an exponential trendline using the function implemented in  
421 Microsoft Excel 2010 with a value of  $R^2 = 0.9971$ . It is interesting to note that at residence times  
422 lower than 0.5 minutes the  $DBC_{10\%}$  of the membrane adsorber is larger than that of the packed  
423 column. Mass transfer limitations in membrane adsorbers are much less important than in  
424 conventional chromatographic columns where the loss in  $DBC_{10\%}$  under the range of flow rates  
425 considered in this study is nearly 50%; this is in agreement with data from previous studies that  
426 measured the effect of flow rate on the DBC of antibodies on protein A resins [42,47].

427 Although values of dynamic binding capacity are higher for the bead-based chromatographic  
428 process, these values taken alone do not represent a complete evaluation of the process  
429 performance, which also requires consideration of buffer consumption, number of cycles for  
430 resin and/or membrane adsorber replacement, bed utilization and productivity. Even though a  
431 complete process evaluation was not the purpose of this work, data from the breakthrough  
432 studies was used to evaluate membrane and packed column bed utilization and productivity as  
433 simple tools to properly compare the two supports.

434 Since chromatographic processes are often operated at 10% breakthrough, bed utilization is an  
435 interesting parameter to compare the two different stationary phases. The results obtained for  
436 our experimental systems confirm that at low values of the residence time, i.e. at higher flow  
437 rates, bed utilization is higher for the membrane adsorber, as shown in Figure 5. In this figure  
438 bed utilization was plotted as a function of the residence time. Indeed, at low residence times  
439 the convective media outperforms the packed bed column, while at higher residence times the  
440 column binding capacity can be fully exploited and bed utilization becomes higher for the resin  
441 (Figure 5).

442 Since the two stationary phases were characterized in complete bind and elute studies, it is  
443 worth to compare the elution peaks obtained at different flow rates for both configurations.  
444 From the elution data reported in Figure 6, it can be observed that the profiles obtained with  
445 the membrane adsorber do not depend on flow rate, while the dependence on flow rate for the  
446 elution from the packed column shows only a small amount of tailing. However, the packed  
447 column peaks are not completely defined due to the high concentration of BSA recovered that  
448 was above the detection limit of the UV detector of the FPLC as can be noticed from their  
449 profiles (Figure 6).

450 Finally, the data from the breakthrough studies was used to estimate membrane and packed  
451 column productivity. Following each breakthrough run, BSA was eluted from the membrane  
452 adsorber and packed column. The amount of BSA eluted was divided by the cycle time, which  
453 was the sum of the time needed for all the chromatographic steps, namely equilibration, load,  
454 wash and elution, and a bed volume of 3 mL for each geometry. The results are plotted for the  
455 two stationary phases as a function of linear velocity as reported in Figure 7. The productivity of  
456 the membrane adsorber shows a linear dependence on the superficial velocity, since the  
457 dynamic binding capacity at 10% breakthrough is independent of flow rate in the range  
458 inspected. The productivity with the packed column slightly increases with superficial velocity,  
459 indicating that when the flow rate increases, the advantage related to the reduction of cycle  
460 duration overcomes the disadvantage related to  $DBC_{10\%}$  decrease, but it is always lower than  
461 the productivity achieved with the membrane adsorber. The difference between the two  
462 technologies is greater at higher superficial velocities. The Sartobind® Q Nano capsule achieves  
463 a higher productivity than the column even if its binding capacity is lower because the  
464 membrane bed has a bigger cross section than the resin bed, thus the volumetric flow rate at a  
465 given superficial velocity with the module is higher and the cycle duration is lower. The  
466 maximum productivity with the membrane adsorber is 3.3 times higher than the maximum  
467 productivity obtained with the packed column. It is necessary to point out that the  
468 experimental protocols with the packed column were not optimized for the washing and  
469 elution steps and cycle duration can be reduced. However, even if the duration of the washing  
470 and elution steps in the cycles with the column were considered equal to that in the cycles with

471 the membrane module, the maximum productivity with the Sartobind® membrane module  
472 would be 3 times higher than the maximum productivity with the column.

473  
474

#### 475 **4. Conclusions**

476

477 Despite the development of new membranes with improved binding capacity, packed bed  
478 chromatography in bind-and-elute mode continues to be the dominant mode of purification,  
479 with the use of membrane adsorbers for bioprocessing relegated to flow through mode for  
480 polishing steps. While membrane chromatography, in which solute mass transfer is dominated  
481 by convection, is a fast process, packed bed chromatography has a higher binding capacity. In  
482 this work a direct comparison between the two chromatographic geometries was executed  
483 using an integrated approach that combines theory and experiments.

484 The performance of membrane adsorbers and packed bed columns has been experimentally  
485 studied in detail using the same bench-scale chromatography system. The results obtained  
486 using BSA as a model protein have been used to compare the two geometries in terms of  
487 binding capacity – both equilibrium and dynamic, productivity and bed utilization. As expected  
488 the maximum equilibrium binding capacity of the packed column is higher than that of the  
489 membrane adsorber, reflecting the greater surface area per unit volume in the packed bed.  
490 Likewise, the packed bed showed higher dynamic binding capacity values at 10% breakthrough  
491 over all superficial velocities studied. However, the percent difference in  $DBC_{10\%}$  between the  
492 packed bed and membrane was significantly reduced at the higher superficial velocities. This  
493 results because the  $DBC_{10\%}$  values for the membrane were independent of superficial velocity  
494 due to convective solute transport, while  $DBC_{10\%}$  for the packed bed decreased significantly due  
495 to intraparticle mass transfer limitations.

496 The advantage of not having intraparticle transport limitations in the membrane device become  
497 more apparent when performance parameters like bed utilization and productivity are  
498 calculated. Bed utilization is significantly higher for the membrane device, even when solute  
499 fluid residence times are lower. Further, the productivity of the membrane adsorber is at least  
500 3 times higher and this represents the true advantage of membrane chromatography, which  
501 can be successfully operated at high flow rates. Indeed, the obtained results confirm the  
502 potential of membrane adsorbers in bind-and-elute mode and the methodology employed  
503 might be used as a guide for process characterization of novel chromatographic membranes  
504 and improved membrane adsorber modules.

505

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507

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#### 513 **References**

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- 515 [1] R. Ghosh, Protein separation using membrane chromatography: opportunities and challenges, *J.*  
516 *Chromatogr. A* 952 (2002) 13-27. [https://doi.org/10.1016/S0021-9673\(02\)00057-2](https://doi.org/10.1016/S0021-9673(02)00057-2)
- 517 [2] G. Choudary, C. Horvath, Ion-exchange chromatography, *Methods Enzymol.* 270 (1996) 47-82.
- 518 [3] C. Boi, Membrane adsorbers as purification tools for monoclonal antibodies purification, *J.*  
519 *Chromatogr. B* 848 (2007) 19-27.
- 520 [4] V. Orr, L. Zhong, M. Moo-Young, C.P. Chou, Recent advances in bioprocessing application of  
521 membrane chromatography, *Biotechnol. Advances* 31 (2013) 450–465.
- 522 [5] U. Gottschalk, Disposables in downstream processing, *Adv. Biochem. Eng. Biotechnol.* 115 (2010)  
523 171–183.
- 524 [6] H.L. Knudsen, R.L. Fahrner, Y. Xu, L.A. Norling, G.S. Blank Membrane ion-exchange chromatography  
525 for process-scale antibody purification, *J. Chromatogr. A* 907 (2001) 145–154.
- 526 [7] U. Gottschalk, L. Giovannoni, M. Ventani, Antibody purification using membrane adsorbers,  
527 *BioPharm Int.* 21 (2008) 48-52.
- 528 [8] J. Weaver, S.M. Husson, L. Murphy, S.R. Wickramasinghe, Anion Exchange Membrane Adsorbers for  
529 Flow-Through Polishing Steps: Part I. Clearance of Minute Virus of Mice, *Biotechnol. Bioeng.* 110  
530 (2013) 491-499.
- 531 [9] J. Weaver, S.M. Husson, L. Murphy, S.R. Wickramasinghe, Anion Exchange Membrane Adsorbers for  
532 Flow-Through Polishing Steps: Part II. Virus, Host Cell Protein, DNA Clearance, and Antibody  
533 Recovery, *Biotechnol. Bioeng.* 110 (2013) 500-510.
- 534 [10] M. Phillips, J. Cormier, J. Ferrence, C. Dowd, R. Kiss, H. Lutz, J. Carter, Performance of a membrane  
535 adsorber for trace impurity removal in biotechnology manufacturing, *J. Chromatogr. A* 1078 (2005)  
536 74-82.
- 537 [11] J.X. Zhou, T. Tressel, Basic concepts in Q membrane chromatography for large scale antibody  
538 production, *Biotechnol. Prog.* 22(2006) 341–349.
- 539 [12] M. Kuczewski, N. Fraud, R. Faber, G. Zarbis-Papastoitsis, Development of a polishing step using a  
540 hydrophobic interaction membrane adsorber with a PER.C6-derived recombinant antibody,  
541 *Biotechnol. Bioeng.* 105 (2010) 296–305.
- 542 [13] R. Chen, J. John, A. Lavrentieva, S. Müller, M. Tomala, Y. Zhao, R. Zweigerdt, S. Beutel, B. Hitzmann,  
543 C. Kasper, U. Martin, U. Rinas, F. Stahl, T. Scheper, Cytokine production using membrane adsorbers:  
544 human basic fibroblast growth factor produced by *Escherichia coli*, *Eng. Life Sci* 12 (2012) 29–38.  
545 <https://doi.org/10.1002/elsc.201100045>
- 546 [14] M. Woo, N.Z. Khan, J. Royce, U. Mehta, B. Gagnon, S. Ramaswamy S, N. Soice, M. Morelli, K.-S.  
547 Cheng, A novel primary amine-based anion exchange membrane adsorber, *J. Chromatogr A* 1218  
548 (2011) 5386–5392. <https://doi.org/10.1016/j.chroma.2011.03.068>
- 549 [15] W. Riordan, S. Heilmann, K. Brorson, K. Seshadri, Y. He, M. Etzel, Design of salt-tolerant membrane  
550 adsorbers for viral clearance, *Biotechnol. Bioeng.* 103 (2009) 920–929.  
551 <https://doi.org/10.1002/bit.22314>
- 552 [16] W.T. Riordan, S.M. Heilman, K. Brorson, K. Seshadri, M.R. Etzel, Salt tolerant membrane  
553 adsorbers for robust impurity clearance, *Biotechnol. Prog.* 25 (2009) 1695–1702.
- 554 [17] Y. Hou, M. Brower, D. Pollard, D. Kanani, R. Jacquemart, B. Kachuik, J. Stout, Advective hydrogel  
555 membrane chromatography for monoclonal antibody purification in bioprocessing, *Biotechnol.*  
556 *Prog.* 31 (2015) 974-982.
- 557 [18] M. Kuczewski, E. Schirmer, B. Lain, G.A. Zarbis-Papastoitsis, Single-use purification process for the  
558 production of a monoclonal antibody produced in a PER.C6 human cell line, *Biotechnol. J.* 6 (2011)  
559 56–65.
- 560 [19] B. Bhut, S. Wickramasinghe, S. Husson, Preparation of high-capacity, weak anion-exchange  
561 membranes for protein separations using surface initiated atom transfer radical polymerization, *J.*  
562 *Memb. Sci.*, 325 (2008) 176-183.

- 563 [20] J. Wang, E.W. Jenkins, J.R. Robinson, A. Wilson, S.M. Husson, A new multimodal membrane  
564 adsorber for monoclonal antibody purifications, *J. Memb. Sci.* 492 (2015) 137–146.
- 565 [21] M. Heller, R. Wimbish, P.V. Gurgel, B. Pourdeyhimi, R.G. Carbonell, Reducing diffusion limitations in  
566 ion exchange grafted membranes using high surface area nonwovens, *J. Memb. Sci.* 514 (2016) 53-  
567 64.
- 568 [22] M.X. Hu, X. Li, J. N. Li, J.J. Huang, G.R. Ren, Multilayer affinity adsorption of albumin on polymer  
569 brushes modified membranes in a continuous-flow system, *J. Chromatogr. A*, 1538 (2018) 94–103.  
570 <https://doi.org/10.1016/j.chroma.2018.01.031>
- 571 [23] J. Ye, X. Wang, J. Chu, D. Yao, Y. Zhang, J. Meng, Electrospun poly(styrene-co-maleic anhydride)  
572 nanofibrous membrane: A versatile platform for mixed mode membrane adsorbers *Appl. Surf. Sci.*  
573 484 (2019) 62–71. <https://doi.org/10.1016/j.apsusc.2019.04.106>
- 574 [24] I.S. Ng, C.P. Song, C.W. Ooi, B.T. Tey, Y.H. Lee, Y.K. Chang, Purification of lysozyme from chicken egg  
575 white using nanofiber membrane immobilized with Reactive Orange 4 dye, *Int. J. Biol. Macromol.*  
576 134 (2019) 458–468. <https://doi.org/10.1016/j.ijbiomac.2019.05.054>
- 577 [25] L. Voswinkel, M.R. Etzel, U. Kulozik, Adsorption of beta-lactoglobulin in anion exchange membrane  
578 chromatography versus the contacting mode and temperature, *LWT - Food Sci. Technol.* 79 (2017)  
579 78-83. <http://dx.doi.org/10.1016/j.lwt.2017.01.016>
- 580 [26] G. Gieseler, I. Pepelanova, A. Meyer, L. Villain, S. Beutel, U. Rinas, T. Scheper, Considerations on the  
581 flow configuration of membrane chromatography devices for the purification of human basic  
582 fibroblast growth factor from crude lysates, *Eng. Life Sci.* 16 (2016) 697–705.  
583 <https://doi.org/10.1002/elsc.201600006>
- 584 [27] P. Madadkar, Q.Wu, R. Ghosh, A laterally-fed membrane chromatography module, *J. Membr. Sci.*  
585 487 (2015)173–179. <http://dx.doi.org/10.1016/j.memsci.2015.03.056>
- 586 [28] G. Chen, U. Umatheva, L. Alforque, H. Shirataki, S. Ogawa, C. Kato, R. Ghosh, An annular-flow,  
587 hollow-fiber membrane chromatography device for fast, high-resolution protein separation at low  
588 pressure. *J. Membr. Sci.* 590 (2019) 117305-117312.  
589 <https://doi.org/10.1016/j.memsci.2019.117305>
- 590 [29] D.A. Ribeiro, D.F. Passos, H.C. Ferraz, L.R. Castilho, Anion-exchange purification of recombinant  
591 factor IX from cell culture supernatant using different chromatography supports, *J. Chromatogr. B*  
592 938 (2013) 111–118.
- 593 [30] H.F. Liu, B. McCooey, T. Duarte, D.E. Myers, T. Hudson, A. Amanullah, R. van Reis, B.D. Kelley,  
594 Exploration of overloaded cation exchange chromatography for monoclonal antibody purification, *J.*  
595 *Chromatogr. A* 1218 (2011) 6943–6952.
- 596 [31] B.V. Bhut, K.A. Christensen, S.M. Husson, Membrane chromatography: Protein purification from *E.*  
597 *coli* lysate using newly designed and commercial anion-exchange stationary phases, *J. Chromatogr.*  
598 *A*, 1217 (2010) 4946–4957.
- 599 [32] N. Kubota, S. Miura, K. Saito, K. Sugita, K. Watanabe, T. Sugo, Comparison of protein adsorption by  
600 anion-exchange interaction onto porous hollow-fiber membrane and gel bead-packed bed, *J.*  
601 *Memb. Sci.* 117 (1996) 135-142.
- 602 [33] G. Alderton, W.H. Ward, H.L. Fevold, Isolation of lysozyme from egg white, *J. Biol. Chem.* 157  
603 (1945) 43-58
- 604 [34] Thermofisher Scientific, Lysozyme properties  
605 <https://www.thermofisher.com/order/catalog/product/89833> consulted on 08/08/2019.
- 606 [35] Sigma-Aldrich, Bovine Serum Albumin properties  
607 [https://www.sigmaaldrich.com/content/dam/sigma-](https://www.sigmaaldrich.com/content/dam/sigma-aldrich/docs/Sigma/Product_Information_Sheet/a2153pis.pdf)  
608 [aldrich/docs/Sigma/Product\\_Information\\_Sheet/a2153pis.pdf](https://www.sigmaaldrich.com/content/dam/sigma-aldrich/docs/Sigma/Product_Information_Sheet/a2153pis.pdf) consulted on 08/08/2019.
- 609 [36] G. Guiochon, A. Felinger, D.G. Shiradzi, A.M. Katti, *Fundamentals of preparative and nonlinear*  
610 *chromatography*, second ed., Elsevier Inc., San Diego, California, 2006.

- 611 [37] M.O. Herigstad, S. Dimartino, C. Boi, G.C. Sarti, Experimental characterization of the transport  
612 phenomena, adsorption, and elution in a protein A affinity monolithic medium, *J. Chromatogr. A*,  
613 1407 (2015) 130-138.
- 614 [38] C. Boi, S. Dimartino, G.C. Sarti, Modeling and simulation of affinity membrane adsorption, *J.*  
615 *Chromatogr. A*, 1162 (2007) 24-33.
- 616 [39] S. Dimartino, O.M. Herigstad, C. Boi, E. Lalli, G. Sarti, Experimental and Theoretical Analysis to  
617 Assess the Use of Monolithic Columns in Process Chromatography, *Chem. Eng. Trans.* 49 (2016) 25-  
618 30.
- 619 [40] P. DePhillips, A.M. Lenhoff, Pore size distributions of cation-exchange adsorbents determined by  
620 inverse size-exclusion chromatography, *J. Chromatogr. A* 883 (2000) 39–54.
- 621 [41] V. Natarajan, S. Cramer, A methodology for the characterization of ion-exchange resins, *Sep. Sci.*  
622 *Technol.* 35 (2000) 1717-1742.
- 623 [42] R. Hahn, R. Schlegel, A. Jungbauer, Comparison of protein A affinity sorbents, *J. Chromatogr. B*, 790  
624 (2003) 35-51.
- 625 [43] H. Bak, O.R.T. Thomas, J. Abildskov, Lumped parameter model for prediction of initial breakthrough  
626 profiles for the chromatographic capture of antibodies from a complex feedstock, *J. Chromatogr. B*,  
627 848 (2007) 131-141.
- 628 [44] C. Boi, S. Dimartino, G.C. Sarti, Performance of a new protein A affinity membrane for the primary  
629 recovery of antibodies, *Biotechnol. Prog.* 24 (2008) 640-647.
- 630 [45] H. Yang, P. Gurgel, R.G. Carbonell, Purification of human immunoglobulin G via Fc-specific small  
631 peptide ligand affinity chromatography, *J. Chromatogr. A*, 1216 (2009) 910-918.
- 632 [46] Z. Tao, C. Yu, H. Zhang, Y. He, Comparative study of adsorption isotherms of BSA on DEAE and CM-  
633 Dextran- type ion exchangers, *React. Funct. Polym.* 32 (1997) 257-262.
- 634 [47] K. Swinnen, A. Krul, I. Van Goidsenhoven, N. Van Tichelt, A. Roosen, K. Van Houdt, Performance  
635 comparison of protein A affinity resins for the purification of monoclonal antibodies, *J. Chromatogr.*  
636 *B* 848 (2007) 97-107.
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638

## Figure Captions

639

640 **Figure 1:** Equilibrium adsorption isotherm of BSA on Q Sepharose Fast Flow resin.

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642

643 **Figure 2:** Equilibrium adsorption isotherm of BSA on Sartobind® Q Nano membranes.

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646 **Figure 3:** Effect of flow rate on breakthrough curves of BSA solutions on membrane adsorber (a) and  
647 packed column (b).

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649

650 **Figure 4:** Effect of superficial velocity (a) and residence time (b) on dynamic binding capacity of BSA  
651 solutions for the two chromatographic media.

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654 **Figure 5:** Comparison of bed utilization values between membrane adsorbers and packed column as a  
655 function of residence time.

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658 **Figure 6:** Elution profiles at different flow rates obtained in experiments at 100% breakthrough for the  
659 membrane adsorber (a) and the packed column (b)

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661 **Figure 7:** Productivity obtained in experiments at 10% breakthrough as a function of linear velocity:  
662 comparison between membrane adsorbers and packed column.

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