**Supplementary Materials**

**Lysozyme and BSA separation**

The separation of BSA from lysozyme using MMCF-DEAE showed that a small amount of lysozyme was present in the elution peak as determined through SDS-PAGE analysis (section 3.4, Fig. 9B).

A control experiment using an unmodified MMCF membrane was performed to determine whether the lysozyme retained by MMCF-DEAE resulted from non-specific interaction with the membrane matrix.

The same protocol was used as that described in section 2.12 and an SDS-PAGE analysis was performed (Fig. 1X)

**Fig. 1X:** Coomassie blue stained SDS-PAGE of the fractions collected from the purification of BSA from lysozyme-containing mixtures on unmodified MMCF. Lanes M on either side of the gel correspond to the molecular weight markers. Lane A is the pure BSA control (0.1 mg/mL), lane B the lysozyme control (0.1 mg/mL) and lane AB is a mixture of both. Lanes 1 and 2 are fractions collected during the load step (twentyfold and tenfold diluted respectively). Lane 3-6 correspond to the elution of bound protein.
From Fig. 1X, it can be observed that non-specific protein binding to the membrane matrix was present in the system which strongly indicates that the faint lysozyme band observed in Fig. 9B was a consequence of this interaction.

From a densitometry analysis on Image J, the lysozyme non-specific binding was calculated to be 0.22 mg lysozyme/mL of adsorbent.
**Herring Sperm DNA and BSA separation**

The elution peaks of BSA and fish sperm DNA from the MMCF-DEAE column (see section 3.4) were injected onto a commercial Mono Q 5/50 GL high-resolution Tricorn column (GE Healthcare Life Sciences, Uppsala, Sweden) to assess peak purity. Fractions were diluted to minimise the effect of salt on binding and 4 mL of sample was applied onto the column at 2 mL/min. 20 mM Tris-HCl pH 8.0 was chosen as the running buffer and the elution buffer was comprised of running buffer and 1 M NaCl. A two-step elution was specified at 0.4 M NaCl and 1 M NaCl. Experiments were repeated in triplicate.

**Fig. 2X:** Further analysis of the fractions collected from both elution peaks in section 3.4 to assess peak purity. 4 mL injections were made onto a commercial Mono Q 5/50 GL high-resolution Tricorn column. (A) Chromatography of fractions (tenfold diluted) from the first elution peak. (B) Chromatography of fractions (fifteenfold diluted) from the second elution peak.
It was observed in Fig. 2X that the fractions collected from the first peak were free of DNA contamination and contained 100% pure BSA (Fig. 2XA). Chromatography of the fractions from the second peak (Fig. 2XB) revealed the presence of BSA contamination within the sample. Integration of the peak areas allowed to determine the purity of the fraction which was found to be $81\% \pm 2\%$ herring sperm DNA with a 19% BSA contamination.

The limit of detection of DNA in this experiment can be estimated using Fig. 2X. This figure presents a DNA peak of amplitude ~ 25 mAU which corresponds to ~ 0.001 mg DNA. The UV monitor used, UPC-900, has a detection limit of 0.4 mAU. Therefore, the detection limit of this experiment is more than sixty times below the DNA peak measured in Fig. 2X and is ~ 16 ng of DNA.