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binding response after 10 s of injection was used to calculate the values in Table 2.

Regeneration, removal of the bound analyte, of the collagen coated matrix was carried out by passing 100 mM HCl over the sensor chip surface for 5 min, followed by HBS buffer flow.

Data analysis. The binding ratio at a specific analyte concentration (υ) was calculated using equation 1, where R is the SPR response, L represents the immobilized collagen, A represents the soluble CBD analyte, and MWt is the molecular weight of the proteins.

$$\upsilon = R(A)\,MWt(L) / R(L)\,MWt(A) \qquad (1)$$

A plot of υ/[A] (binding ratio at a specific analyte concentration divided by that concentration) *verus* analyte concentration, [A], was non-linearly fit to equation 2.

$$\upsilon/[A] = (BR/K_D) / (1 + [A]/K_D) \qquad (2)$$

The apparent dissociation constant (K_D) and the approximate binding ratio (BR) under these assay conditions were then determined. The BR represents the maximum number of adhesin molecules binding to one collagen molecule and is an approximation due to overlapping of the immobilized collagen strands on the matrix.

CD spectra. All CD spectra were collected using a Jasco J720 spectropolarimeter calibrated with a 0.1% (w v^{-1}) 10-camphorsulfonic acid-d solution. Spectra were measured at 25 °C and five scans were averaged. A 0.05 cm path length cell was used for near-UV (250–320 nm) CD and a 1 cm path length cell was used for far-UV (190–250 nm) CD.

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If anyone needed convincing of the importance of the new frontier of structural biology that nuclear magnetic resonance spectroscopy (NMR) has opened up, she or he need go no further than the special *Nature Structural Biology* NMR supplement that accompanies this issue. Although superconducting magnets are of central importance to this field, they are only part of a wide range of materials needed to probe the inner workings of (or to design drugs against) macromolecules in solution (as well as the solid state).

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These notes were compiled by Tracy Smith