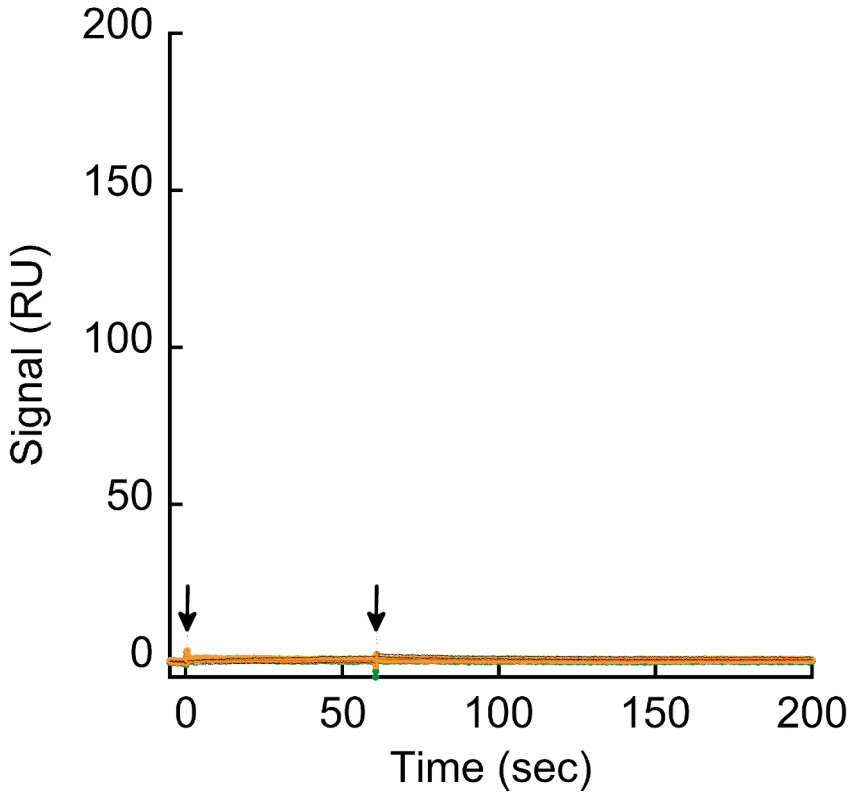


**Figure S1, reference to Figure 1.** Negative control binding experiments using the MHC-like molecule MULT-1. SPR binding sensograms collected using immobilized m04ED (WT) with increasing concentrations of MULT-1 flow-through, as outlined in Experimental Procedures. The start of the injection (association) and wash out (dissociation) phases are indicated with vertical arrows. Unlike full-length $D^d$ (Figure 1b), this MHC-like molecule, lacking the $\alpha_3$ domain, bound petide and $\beta_2$-microglobulin shows a flat binding profile (after correction of non-specific refracive index chages using a mock surface without m04ED) that is typically of a lack of specific binding to the m04ED surface.

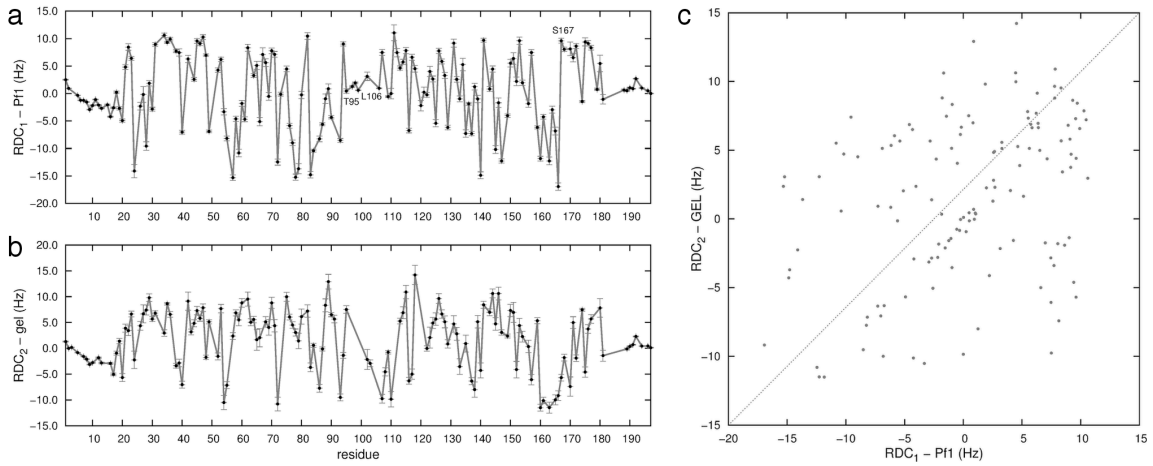


**Figure S2, reference to Table 2.** $^{15}$N-$^{1}$H backbone RDC values measured in two alignment media for m04ED (Figure 1c). Values measured in **(a)** bacteriophage Pf1 and **(b)** positively charged gels, correspond to approximate alignment tensor magnitudes and Rhombicities of -8.3 Hz/0.19 and -7.0 Hz/0.40 respectively, as estimated using the histogram method (Clore et al., 1998). The RDC splittings were measured for well-resolved peaks in the 2D TROSY-HSQC spectrum using a quantitative ARTSY experiment (Fitzkee and Bax, 2010). Error bars report experimental uncertainties as propagated from the spectral peak-to-noise ratio. Key residues defining the central flexible loop region and kinked C-terminal helix are indicated. **(c)** Correlation diagram between the two RDC datasets, showing a linear correlation coefficient of 0.36 (Tolman and Ruan, 2006), indicating the datasets are nearly independent.

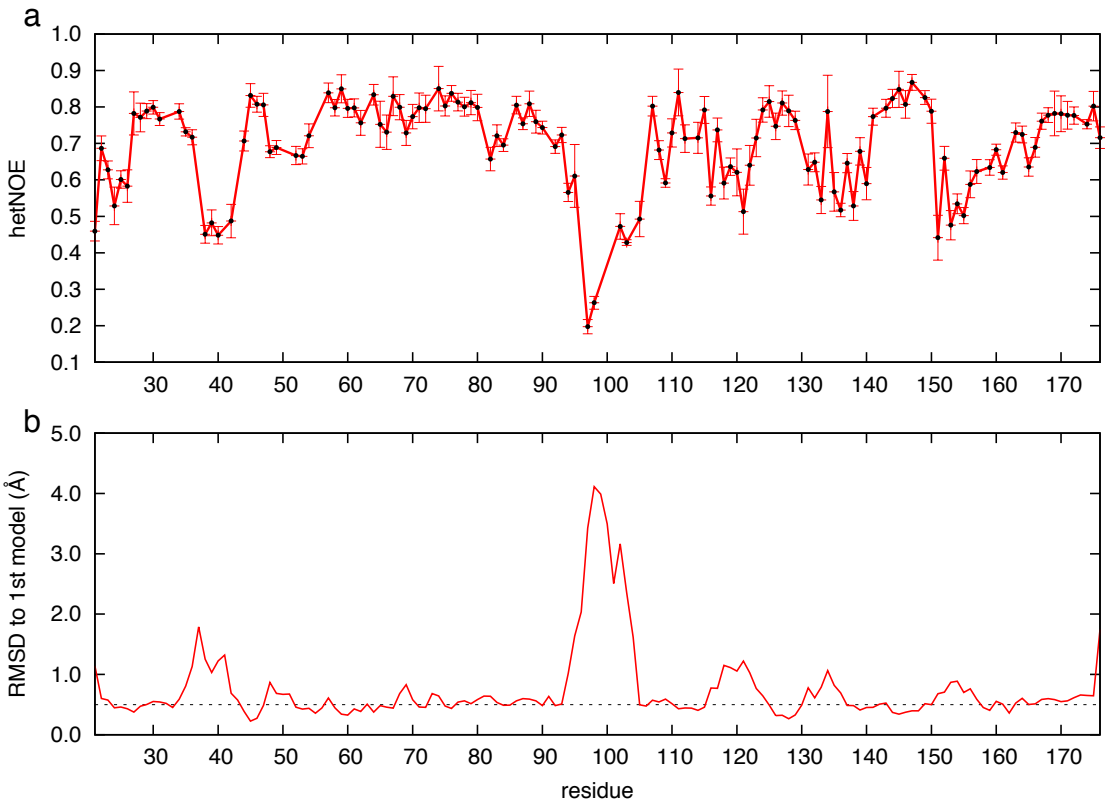


**Figure S3, reference to Figure 3.** Structural convergence in the final CS-Rosetta ensemble shown in Figure 3c. **(a)** Experimental $^{15}$N-{$^{1}$H} NOE values from Figure 2a plotted only for m04ED core residues 21-176 included in the Rosetta structure calculations. Errors are propagated from the spectral peak-to-noise ratios. **(b)** Average backbone heavy atom RMSD values computed over the 10 lowest-energy models from the final CS-Rosetta calculations (Table 1, #7 and Figure 3c).

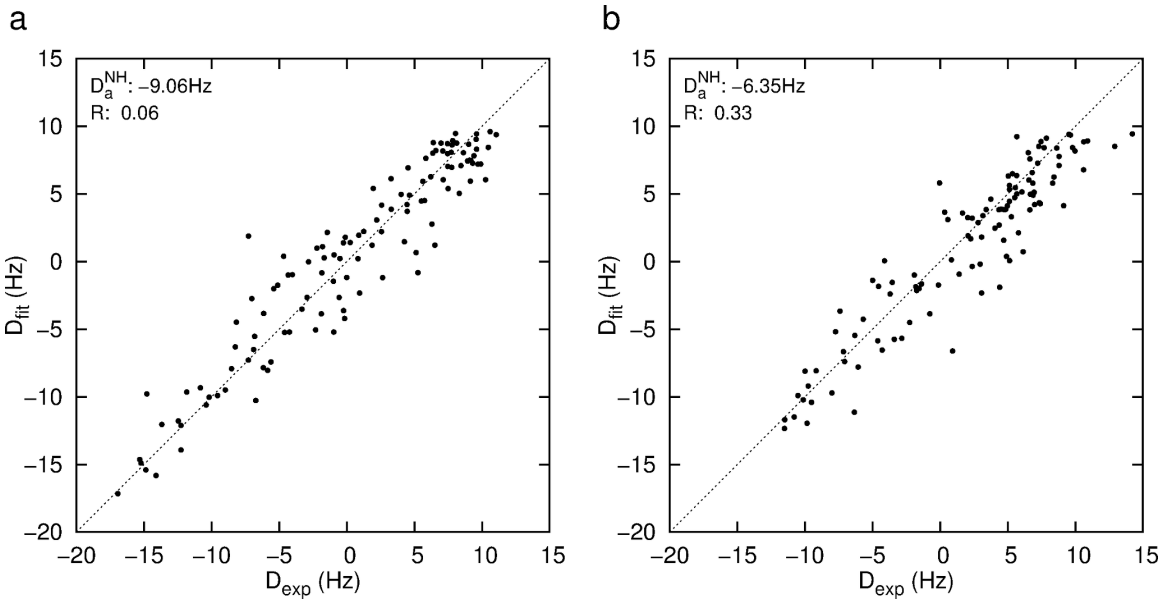


**Figure S4, reference to Figure 3, Table 2.** Structure fits to the RDC experimental data, shown for the top-ranking model from the final NMR ensemble of Figure 3c. The final RDC quality (Q) factors (Cornilescu et al., 1998) for the Pf1 **(a)** and gel **(b)** datasets are 0.29 and 0.41 respectively (Pearson's linear correlation coefficients ($R_P$) of 95% and 90%). The structure-based fitted alignment tensor magnitudes and rhombicities are indicated in each plot.

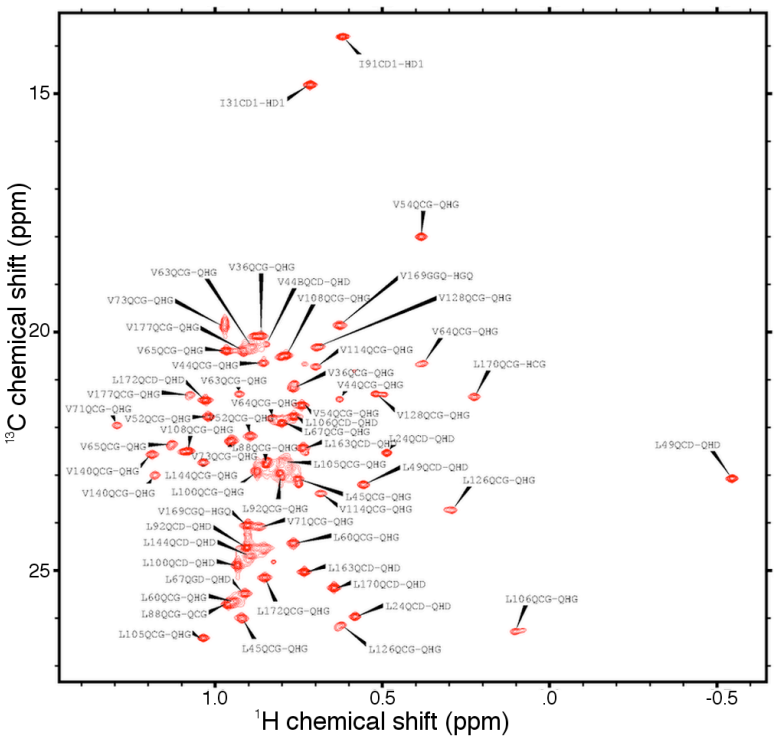


**Figure S5, reference to Figure 1.** Methyl region of a $^{1}$H-$^{13}$C HMQC spectrum recorded at 900 MHz using an ILV methyl $^{13}$C-labeled sample of m04ED (Figure 1c). The complete resonance assignments of 2 Ile $C^{\delta 1}$, 16 Leu $C^{\delta 1}$, $C^{\delta 2}$ and 15 Val $C^{\gamma 1}$, $C^{\gamma 2}$ are indicated.