

Figure S1. The first 2D  $^1\text{H}$ - $^1\text{H}$  planes obtained from the first data set (A) and second data set (B) of the 3D  $^{15}\text{N}$ -edited NOESY-HSQC experiment with the pulse scheme shown in Figure 1 in the main text. The experiment was recorded with uniformly  $^{15}\text{N}$ -labeled calmodulin in  $^1\text{H}_2\text{O}$ : $^2\text{H}_2\text{O}$  (90:10) solution (protein concentration 1 mM, 5 mM  $\text{CaCl}_2$ , pH 6.5, 25  $^\circ\text{C}$ ) on a Bruker Avance 500 MHz spectrometer equipped with a cryoprobe.  $128(t_1) \times 512(t_3)$  complex points were collected with spectral widths of 5500 ( $^1\text{H}$ ) and 8012 Hz ( $^1\text{H}$ ) by setting  $t_2 = 0$ . An interscan delay of 1 s with 32 scans per increment was used, resulting in a total experimental time of 2.7 h for each data set. The mixing times were:  $\tau_{\text{mix}} = 80$  ms and  $\tau'_{\text{mix}} = 74$  ms. The scaling factor was 0.99 for the second data set. The two data sets were acquired in an interleaved manner. Figure C is the difference spectrum and  $C = A - B \cdot 0.99$ . Signals in black represent opposite sign with respect to those in red. Artifacts parallel to the strong diagonals can be observed in both A and B. These are suppressed in the difference spectrum C. Relatively strong negative peaks at  $\sim 7.2$  ppm result from some  $\text{NH}_2$  groups in which the protons undergo fast chemical exchange with water protons, giving rise to rapid decays of magnetizations  $\text{H}_z\text{N}_z$  and  $\text{H}_z$ . For these  $\text{NH}_2$  groups,  $R(\text{N}_z)/R(\text{H}_z\text{N}_z) < (R(\text{N}_z)/R(\text{H}_z\text{N}_z))_{\text{AV}}$  and negative residual diagonal peaks are expected.

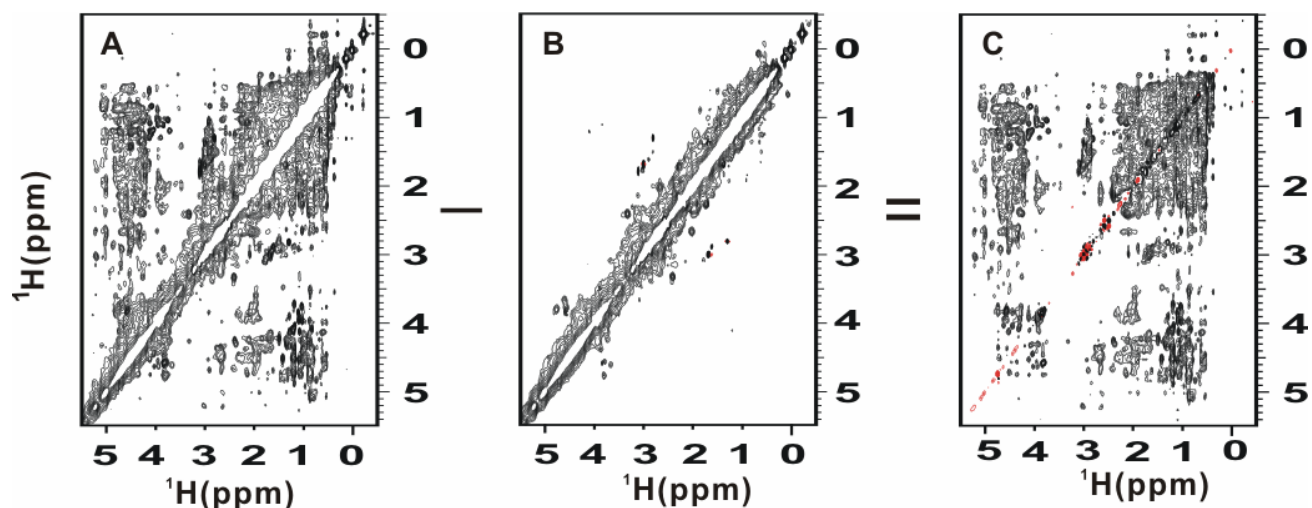


Figure S2. The first 2D  $^1\text{H}$ - $^1\text{H}$  planes obtained from the first data set (A) and second data set (B) of the 3D  $^{13}\text{C}$ -edited NOESY-HSQC experiment. The experiment was recorded with uniformly  $^{13}\text{C}$ -labeled DdCAD-1 (24 kDa) in  $^2\text{H}_2\text{O}$  solution (protein concentration 0.8 mM, 20 mM  $\text{Na}_3\text{PO}_4$ , pH 6.6, 30 °C) on a Bruker Avance 500 MHz spectrometer equipped with a cryoprobe.  $128(t_1) \times 512(t_3)$  complex points were collected with spectral widths of 5500 ( $^1\text{H}$ ) and 8012 Hz ( $^1\text{H}$ ) by setting  $t_2 = 0$ . An interscan delay of 1 s with 8 scans per increment was used, resulting in a total experimental time of 40 minutes for each data set. The mixing times were:  $\tau_{\text{mix}} = 80$  ms and  $\tau'_{\text{mix}} = 64$  ms. The scaling factor was 0.98 for the second data set. The two data sets were acquired in an interleaved manner. Figure C is the difference spectrum and  $C = A - B \cdot 0.98$ . Signals in red represent opposite sign with respect to those in black.