Supplementary Information

Conformational Recognition of an Intrinsically Disordered Protein

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Supplementary Figures

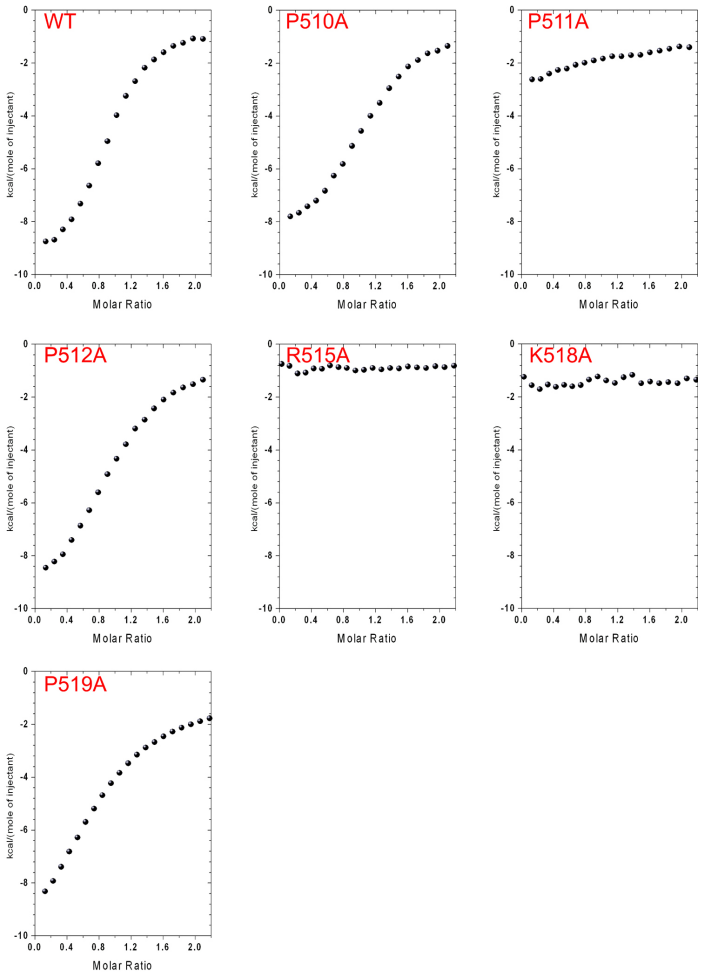

Figure S1. ITC raw data for the interaction between Grb2 SH3 and Gab2$_{503\text{-}524}$ WT and mutants.

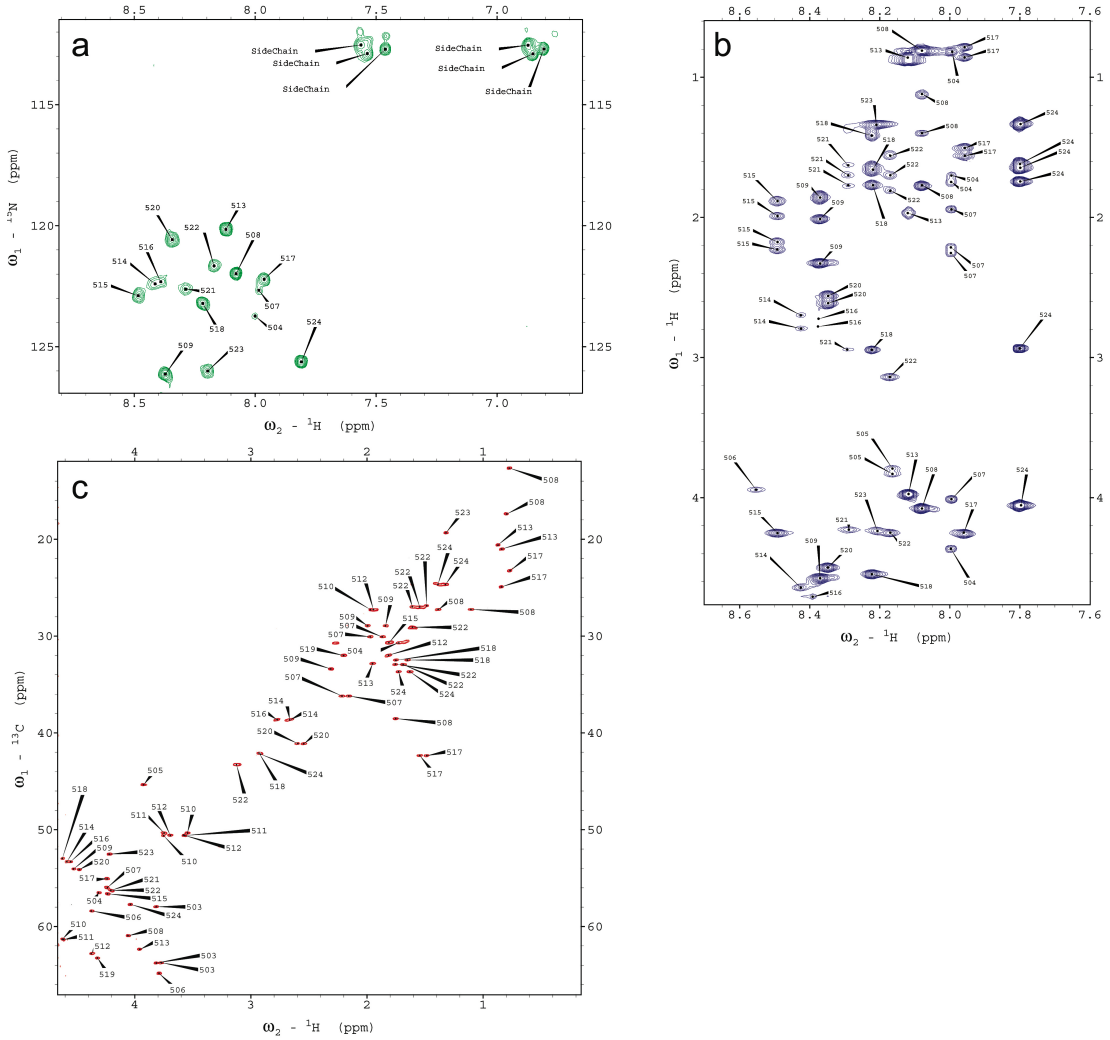

Figure S2. Assigned NMR spectra of $Gab2_{503-524}$ WT sequence measured in 25 mM HEPES at pH 7.5 and 100 mM potassium acetate. The spectra were measured with 800MHz and 600MHz (Bruker Avance III) spectrometer at a temperature of 303K. All NMR spectra were referenced using the NMR signal of the DSS (4,4-dimethyl-4-silapentane-1-sulfonic acid) molecule. A) ^{1}H-^{15}N-HSQC measured using natural abundance of ^{15}N. B) ^{1}H-^{1}H TOCSY measured using 300 ms of mixing time. The HN to aliphatic proton correlations are shown. C) ^{1}H-^{13}C-HSQC measured using natural abundance of ^{13}C.

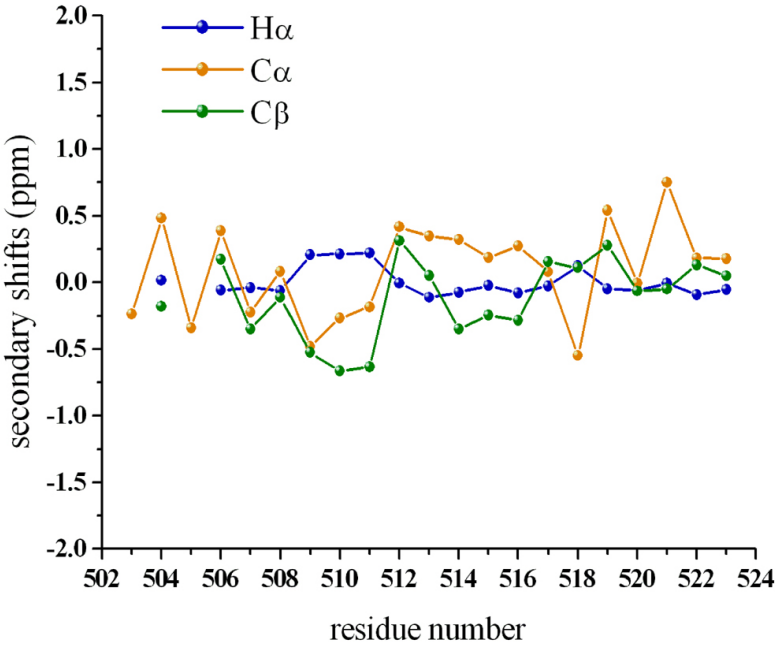

Figure S3. Secondary shifts of the WT Gab2$_{503\text{-}524}$ for Ha (blue), Ca (orange) and Cb (green) resonances at pH 7.5. These are calculated by subtracting random coil values (CamCoil method [15]) from the measured chemical shifts.

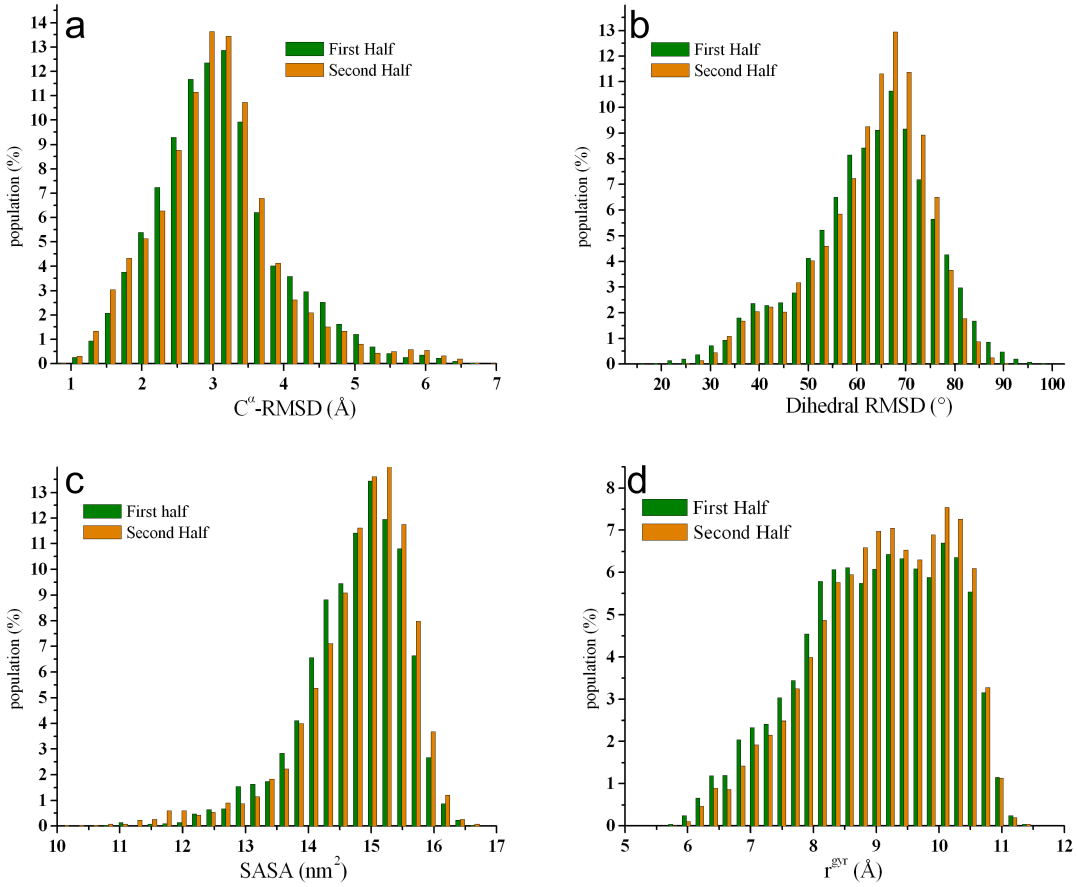

Figure S4. Convergence of the chemical shifts restrained simulations. The wild type sampling is shown. After removing the equilibration phase, the ensemble has been divided in two parts. As a result, the first half (green histograms) of the ensemble is composed of the portions 50 ns to 150 ns of each of the four replicas of the sampling, whereas the second half (orange histograms) is composed of the portions 150 ns to 250 ns. Comparison of the distributions of Ca-RMSD values, dihedral RMSD values, surface accessibility area and gyration radii are reported in panels A, B, C, and D, respectively.

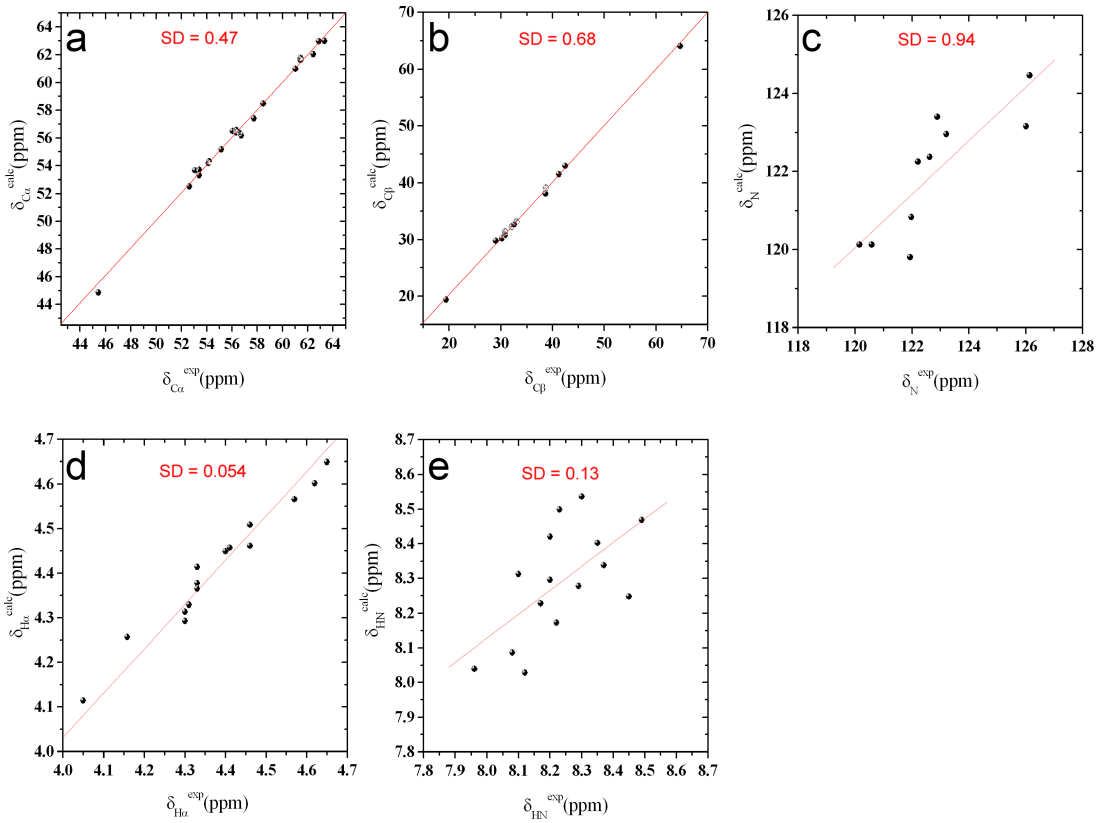

Figure S5. Validation of the chemical-shifts restrained-ensembles. The validation has been made by using the SPARTA+ program (Shen, Y.; Bax, A. *J Biomol NMR* **2010**, *48*, 13) to calculate chemical shifts from the refined ensembles of structures. These, in turn, are compared to the experimental values. As SPARTA+ is based on different principles than the Camshift method (Kohlhoff, K. J. et al. *J Am Chem Soc* **2009**, *131*, 13894), which was here used for performing the structural refinements, the resulting agreement provides an independent validation of the quality of the ensembles. The standard deviations are all significantly lower than the statistical errors of SPARTA+, providing indication of the high accuracy of the structural ensembles. Validations for resonances corresponding to Cα, Cβ, N, Hα and HN atoms are reported in panels A, B, C, D and E, respectively.