Supporting Information for the manuscript

Impact of Magnetic field strength on Resolution and Sensitivity of Proton Resonances in Biological Solids

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Figure S1: to be continued



Figure S1: Simulated MAS dependent ¹H spectral intensities for all value and leucine methyl groups of the α -spectrin SH3 domain. Simulations have been carried out using the program SIMPSON. As an input, the exact geometry of the protein has been employed (PDB ID: 2NUZ).



Figure S2: Simulated methyl proton lineshapes for the α -spectrin SH3 domain at different static magnetic fields.



Figure S3: HSQC type pulse scheme to quantify residue specific magnetization transfer efficiencies.



Figure S4: Carbon line widths for the microcrystalline methyl protonated α -spectrin SH3 domain sample. HSQC spectra were obtained at a MAS frequency of 90 kHz MAS and a B₀ field of 500 MHz and 1 GHz, respectively. Data were acquired using an acquisition time of 20 ms and 35 ms in the proton and carbon dimension, respectively. Data were processed using the apodization function QSINE= 2 (squared sine bell) in Topspin.



Figure S5: Residue specific 1 H-T₂' decay curves obtained at a B₀ field of 1 GHz and a MAS frequency of 90 kHz. Experimental data are fit using a bi-exponential function.



Figure S6: 1D traces from HC correlation experiments recorded employing 500 MHz (red) and 1 GHz (black), respectively. 2D spectra are represented in Figure 1.



Figure S7: Bulk proton T_1 measurements in two magnetic fields. ~ 1.5 times of the T_1 values were set as the recycle delay in the correlation experiments.