

Supplementary Information

**Accessing Methyl Groups in Proteins via  $^1\text{H}$ -detected MAS Solid-state NMR Spectroscopy Employing Random Protonation**

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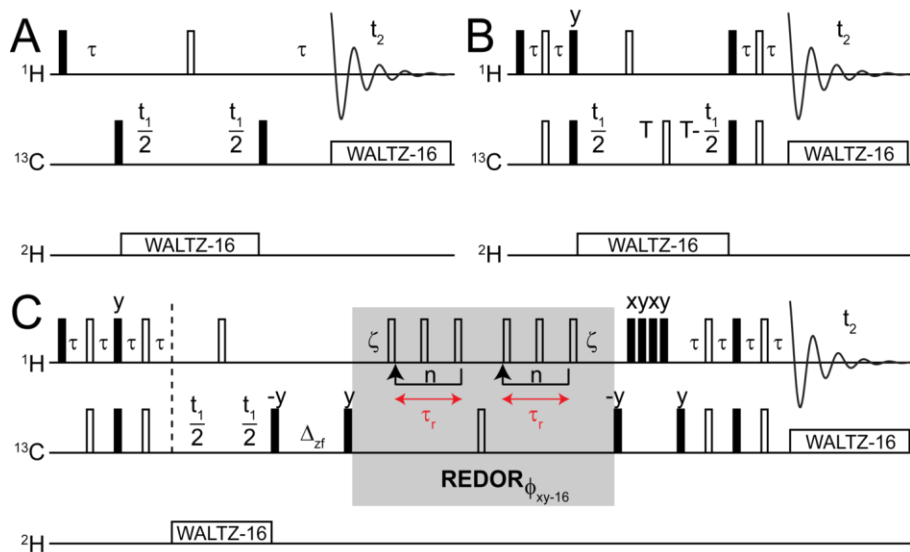


Figure S1.  $^1\text{H}$ -detected pulse sequences for  $^1\text{H}$ ,  $^{13}\text{C}$  correlation spectroscopy and determination of  $^1\text{H}$ ,  $^{13}\text{C}$  dipolar coupling tensors. (A) 2D  $^1\text{H}$ ,  $^{13}\text{C}$  HMQC pulse sequence with  $\tau = 1/2J_{HC} = 3.13 \text{ ms}^{-1}$ . (B) 2D constant-time HSQC experiment, setting the constant-time delay  $T = 1/J_{C,C} = 28.6 \text{ ms}$  and  $\tau = 1/4J_{HC} = 1.79 \text{ ms}^2$ . (C)  $^1\text{H}$ ,  $^{13}\text{C}$  REDOR pulse sequence<sup>3</sup>. The  $^1\text{H}$   $\pi$  pulses during the REDOR period followed the  $xy$ -16 phase cycling scheme<sup>4</sup>. The INEPT transfer delay was set to  $\tau = 1/4J_{HC} = 1.92 \text{ ms}$ .

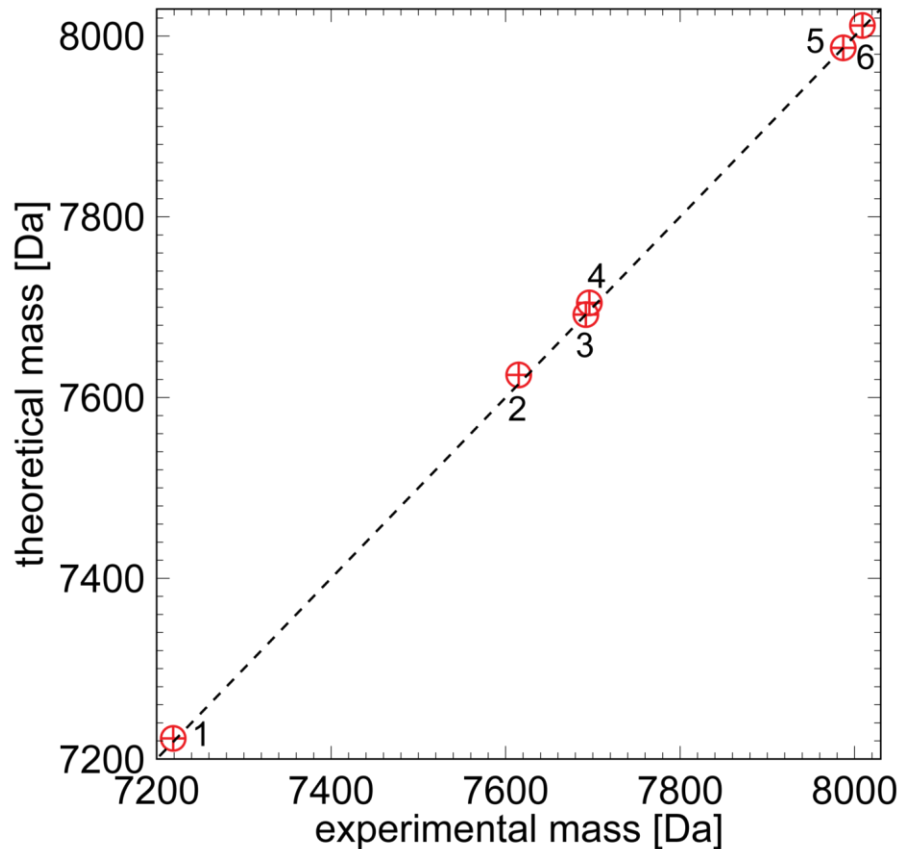


Figure S2. Linear correlation of the experimental to the theoretical mass for differently labelled samples of the SH3 domain of  $\alpha$ -spectrin. The samples employed are from left to right: (1) unlabelled, (2) u-[ $^1\text{H}, ^{13}\text{C}, ^{15}\text{N}$ ], (3) u-[ $^2\text{H}, ^{15}\text{N}$ ], (4) Leu/Val  $^{13}\text{CHD}_2$  otherwise u-[ $^2\text{H}, ^{12}\text{C}, ^{15}\text{N}$ ], (5) 5% GlcRAP, (6) u-[ $^2\text{H}, ^{13}\text{C}, ^{15}\text{N}$ ]. The correlation coefficient  $R^2$  was equal to 0.9998. We yielded an excellent agreement between experimental and theoretical masses, further validating the *in silico* models employed here.

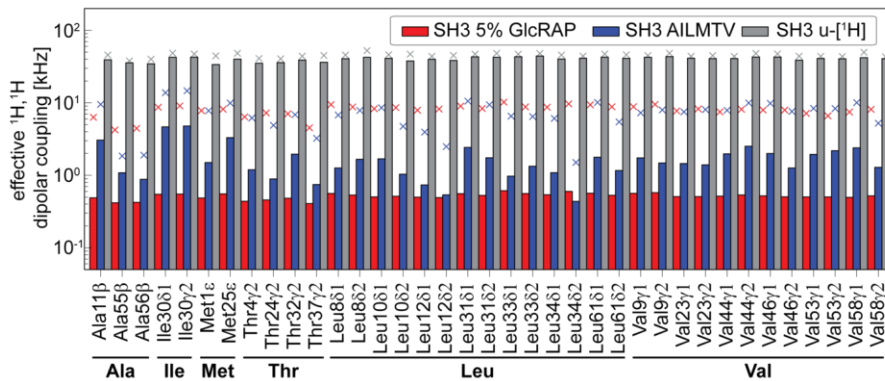


Figure S3. *In silico* calculated  $^1\text{H}, ^1\text{H}$  effective dipolar coupling for methyl groups based on the 1  $\mu\text{s}$  MD relaxed crystal structure of the SH3 domain of  $\alpha$ -spectrin (note the logarithmic y-scale). Here, calculations were carried out for the structures according to the 5% GlcRAP labelling scheme (red bars), the selective Ala $\beta$ /Ile $\gamma_{2,\delta 1}$ /Met $\epsilon$ /Thr $\gamma_2$ /Leu $\delta_{1,\delta 2}$ /Val $\gamma_{1,\gamma 2}$  (AILMTV)  $^{13}\text{CHD}_2$  methyl labelling scheme (blue) and for the uniformly protonated structure (grey). Crosses depict the upper  $2\sigma$  confidence interval. We note, that for the AILMTV labelling scheme we assumed the  $^{13}\text{CHD}_2$  isotopomer for all methyl groups. The composition of methyl groups in the SH3 domain is as follows (occurrence is given in parentheses): Ala (3), Ile (1), Leu (7), Met (2), Thr (4), Val (6).

## References

- 1 Asami, S., Schmieder, P. & Reif, B. High Resolution  $^1\text{H}$ -Detected Solid-State NMR Spectroscopy of Protein Aliphatic Resonances: Access to Tertiary Structure Information. *J. Am. Chem. Soc.* **132**, 15133-15135 (2010).
- 2 Vuister, G. W. & Bax, A. Resolution Enhancement and Spectral Editing of Uniformly C-13-Enriched Proteins by Homonuclear Broad-Band C-13 Decoupling. *J. Magn. Reson.* **98**, 428-435 (1992).
- 3 Schanda, P., Huber, M., Boisbouvier, J., Meier, B. H. & Ernst, M. Solid-State NMR Measurements of Asymmetric Dipolar Couplings Provide Insight into Protein Side-Chain Motion. *Angew. Chem., Int. Ed.* **50**, 11005-11009 (2011).
- 4 Gullion, T. & Schaefer, J. Elimination of Resonance Offset Effects in Rotational-Echo, Double-Resonance Nmr. *J. Magn. Reson.* **92**, 439-442 (1991).