FAST BIOMOLECULAR NMR WITH FAST MAS (WITHOUT AND WITH DNP)

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For large molecules, ultrafast (100 kHz) spinning narrows spectral resonances better than Brownian motion does for solution NMR, removing a fundamental barrier to the NMR study of large systems with ^{1}H detection. Nonetheless, performing the assignment of all resonances remains a rate-limiting step in protein structural studies, and even the latest optimized protocols fail to perform this step when the protein size exceeds ~20 kDa. We introduce two approaches that address this issue, simultaneous parallel detection[1] and projection spectroscopy of hyperdimensional datasets,[2] allowing to accelerate acquisition and data analysis and at the same time to lift the molecular size barrier of the targets amenable to NMR analysis.

We additionally discuss the applicability of ^{1}H detection methods under cryogenic conditions to perform structural studies with DNP.

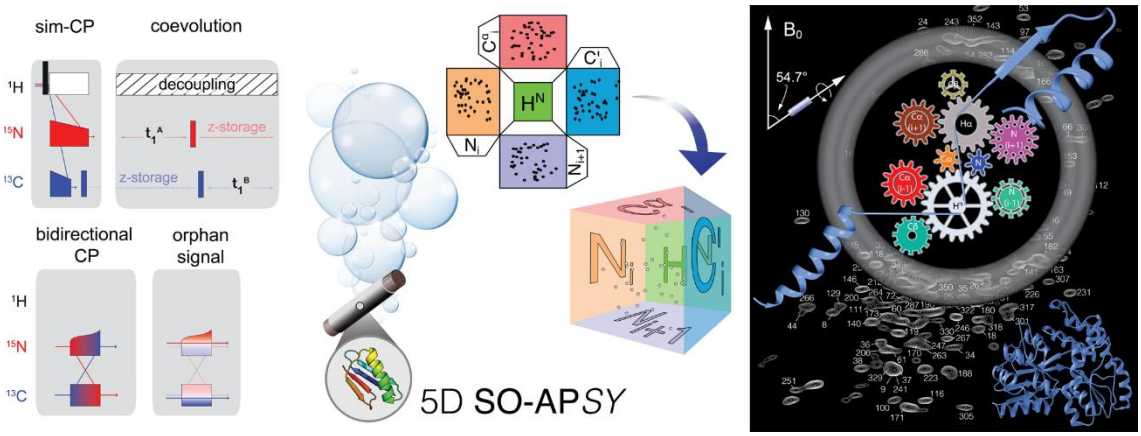

Figure 1. Left: scheme of radiofrequency building blocks for multiple pathway coherence transfers, key for the simultaneous acquisition of a single self-consistent data set composed of multiple ^{1}H-detected 3D spectra. Middle: correlations of five resonance frequencies of nuclear spins within one NMR experiment are now feasible by using projection spectroscopy at 100 kHz MAS. Right: 100 kHz magic-angle spinning NMR allows automatic fingerprinting of large proteins, as demonstrated here on the 42.5 kDa maltose binding protein, the largest protein assigned to date in the solid state.

REFERENCES

[1] H. W. Orton, J. Stanek, T. Schubeis, D. Foucaudeau, C. Oilier, A. W. Draney, T. Le Marcahnd, D. Cala-De Paepe, I. C. Felli, R. Pierattelli, S. Hiller, W. Bermel and G. Pintacuda, *Protein NMR Resonance Assignment without Spectral Analysis: 5D SOlid-State Automated Projection SpectroscopY (SO-APSY)*, *Angew. Chem. Int. Ed.* **2020**, 59, 2380–2384.

[2] J. Stanek, T. Schubeis, P. Paluch., P. Güntert, L. Andreas, and G. Pintacuda, *Automated backbone NMR resonance assignment of large proteins using redundant linking from a single simultaneous acquisition, J. Am. Chem. Soc.* **2020**, 142, 5793–5799.