MAS CryoProbe™

Outstanding Sensitivity Enhancement for Solid-State NMR

The MAS CryoProbe enables solid-state NMR experiments with unprecedented signal-to-noise ratios, without the need for sample modification. The signal-to-noise enhancement, measured against a convectional probe of similar rotor size and RF configuration, is **typically larger than 3**, which translates into time savings of **one order of magnitude.**

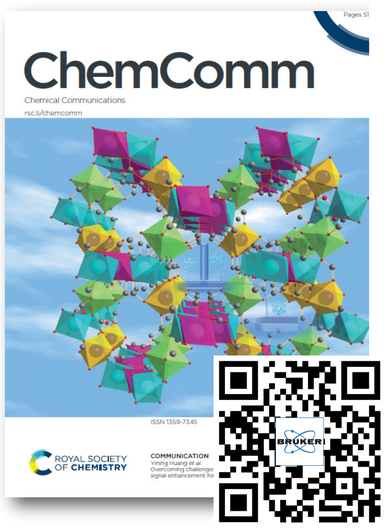
Sample	Experiment	$\varepsilon^{(+)}$	Time saving
Alpha glycine(*)	1D ^{13}C CPMAS	> 3	> 9 x
	1D ^{15}N CPMAS	> 3	> 9 x
U(^{13}C,^{15}N)-Kif5b kinesin bound to microtubules(*)	1D ^{13}C CPMAS	3.1	9 x
	2D ^{13}C^{13}C CORD	2.1	4 x
	2D NCACX	5	25 x
	3D NCACX/NCOCX	7/7.7	~49 x
Crystalline and amorphous Posaconazole, and in ASD preparation(**)	1D ^{13}C CPMAS	~ 5	25 x
	1D ^{15}N CPMAS	~ 6	36 x
Magnesium silicate hydrate phase(***)	1D ^{29}Si DPMAS	>7	>50 x

(*) comparison done against a 3.2 mm Efree probe, (**) comparison done against a 4 mm HCN probe, (***) comparison done against a 7 mm HX probe
(+) Sensitivity enhancement factor, scaled by mass of the sample, number of scans, and magnetic field strength.

Hassan, A. *JMR* **311**, 106680 (2020).

Large biological assemblies: Kinesin bound to microtubules

- The **2D ^{13}C-^{13}C CORD** showed many more cross peaks in the aromatic region of the spectrum, a region frequently devoid of cross peaks. A quick version of the same experiment was recorded in about **1 hour (ns = 1)**, useful to obtain a fast assessment of sample quality and estimation the secondary structure of the protein.
- The 3D NCACX and NCOCX spectra are of very high quality, both with respect to sensitivity and resolution, and required just a fraction of the time: **4-6 days** of measurement time compared to the **15-19 days** on a conventional probe at higher field and applying non-uniform acquisition scheme.



Wanli Zhang., *Chem. Commun*., **59**, 5205, (2023).

Resolving several inequivalent ^{67}Zn sites by 2D MQMAS of microporous MOF (α-Zn-formate)

- The low gyrometric ratio and low natural abundance and quadrupolar nature makes ^{67}Zn-spectroscopy extremely difficult, especially for microporous samples at natural abundance.
- The nature of the sample requires the acquisition of a 2D MQMAS spectrum to resolve the different ^{67}Zn sites, a demanding **experiment time- prohibitive with conventional probes** on such a challenging sample.

Yong Du *at al., Analyst* **148**, 724 (2023)

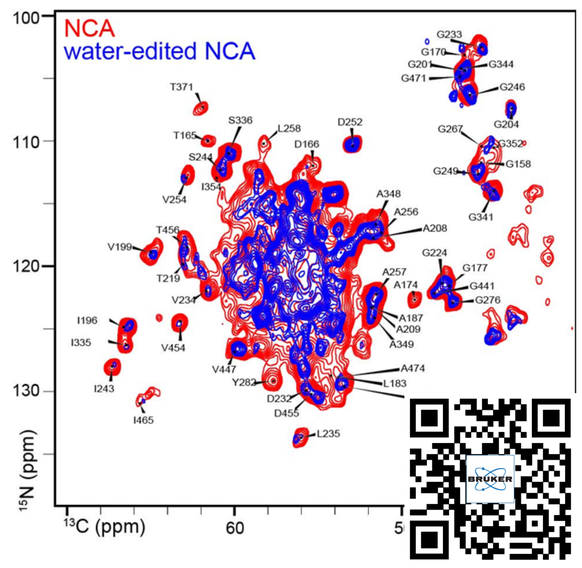
Advanced characterization of APIs in crystalline and amorphous forms, and in ASD formulations.

- Crystalline materials: routine 1D ^{13}C / ^{15}N CP experiments require only 18 minutes / 4 hours, **2D ^{1}H–^{13}C HETCOR** routinely recordable within an hour, trough-bond ^{13}C–^{13}C and trough-space **^{1}H–^{15}N. correlation** experiments become **feasible at natural abundance**.
- **^{1}H-^{13}C and ^{1}H-^{15}N HETCOR experiments** performed at different mixing times highlights the packing of an API when produced into an **amorphous** form, and the interaction of the API with the other components in the **formulate drug**.

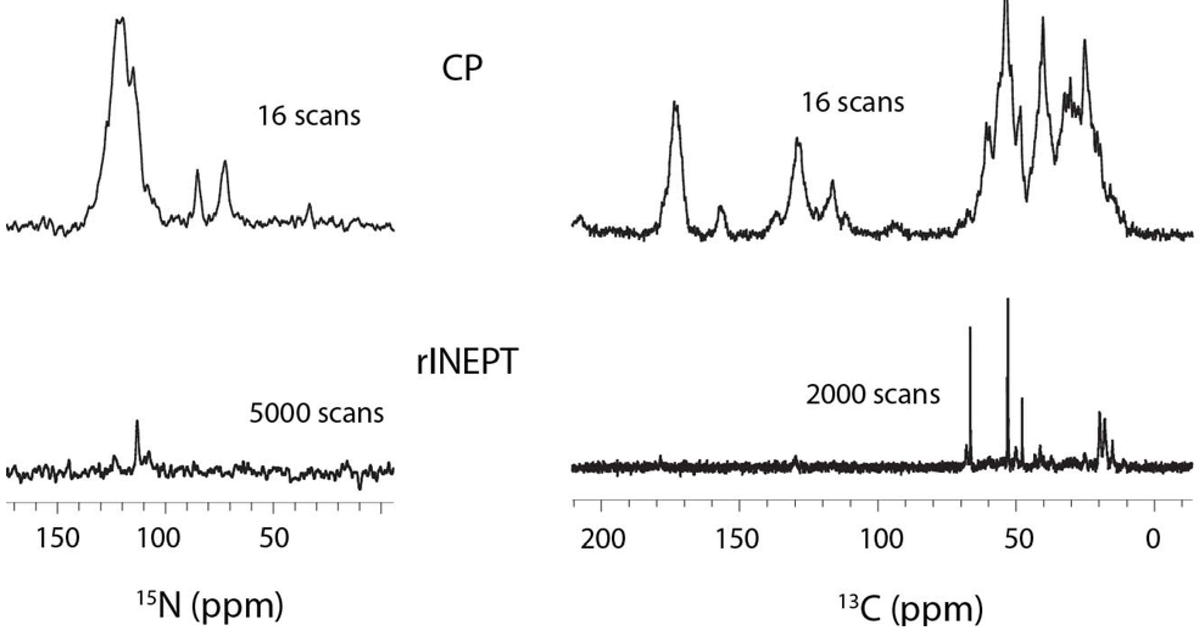
Solid-State NMR MAS CryoProbe Enables Structural Studies of Human Blood Protein Vitronectin Bound to Hydroxyapatite

By using the CryoProbe designed for Magic Angle Spinning (MAS) experiments, the team headed by F. Marassi (Medical College of Wisconsin) was able to acquire three-dimensional solid-state NMR spectra for sequential assignment and characterization of site-specific water-protein interactions. This provides initial insights into the organization of the Vn-HAP complex, which is associated with various pathological settings, including macular degeneration eyes and Alzheimer's disease brains.

- **3D NCACX and 3D NCOCX** spectra were **recorded in about 10 days** with the MAS CryoProbe. On a conventional probe, it would have been impractical to perform this study.
- Thanks to the higher sensitivity, even the small fraction of the protein residues facing the **water interface** could be characterized by NCA and water-edited NCA. Furthermore, it was possible to detect with a J-based transfer rINEPT experiment the weak signals from **dynamic domains of the protein.**



Gopinath, T. *et al., Journa*l of Structural Biology, **216**, 108061(2024).



Find out more and book a demo!

The CryoProbe technology overcomes the sensitivity limitations of Nuclear Magnetic Resonance, enabling the study of complex biomolecular assemblies, metal sites of challenging quadrupolar nuclei, the polymorphism, packing of APIs in different formulations, and much more.

To learn more about MAS CryoProbes and book a demo, visit our website.

Key features of the MAS CryoProbe

- HCN or HX with enhanced sensitivities by a factor of >3
- One order of magnitude faster data acquisition and significantly increased productivity.
- Solid state NMR experiments, with strong RF fields, long spin-lock times and outstanding DCP yields.
- Automatic tuning, matching and magic angle adjustment and lift-assisted sample exchange.
- MAS rates up to 20 kHz with dedicated MAS rotors