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New bio-solid-state-NMR methods within the DynamicsCenter: “Exact-Solid-State-Distances and “Dipolar Order-Parameters”

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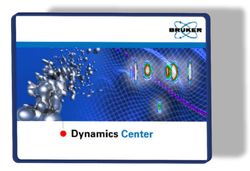

Dipolar Order-Parameters

Detection of slow timescale molecular motion

- The dipolar coupling between H and N is measured via rotor synchronized recoupling.
- Molecular motion scales the effective dipolar coupling.
- The site-specific coupling is transformed into order parameters as dynamics information.
- In solid-state NMR dynamics are not overshaded by the correlation time and thus, slow dynamics are detectable

Easy to use semi automated workflow

- Can use series of 2D and series of 3D
- Able to import peaklist from BMRB, CCPNmr, XEASY, SPARKY and TopSpin.
- fully automated peak-picking available.
- PDB import, shiftlist import in BMRB and SPARKY.
- Interactive user interface including live refitting and peak-list adjustment.
- Order parameters plottable on 3D structure.
- Different exports including excel, PDF and PNG.

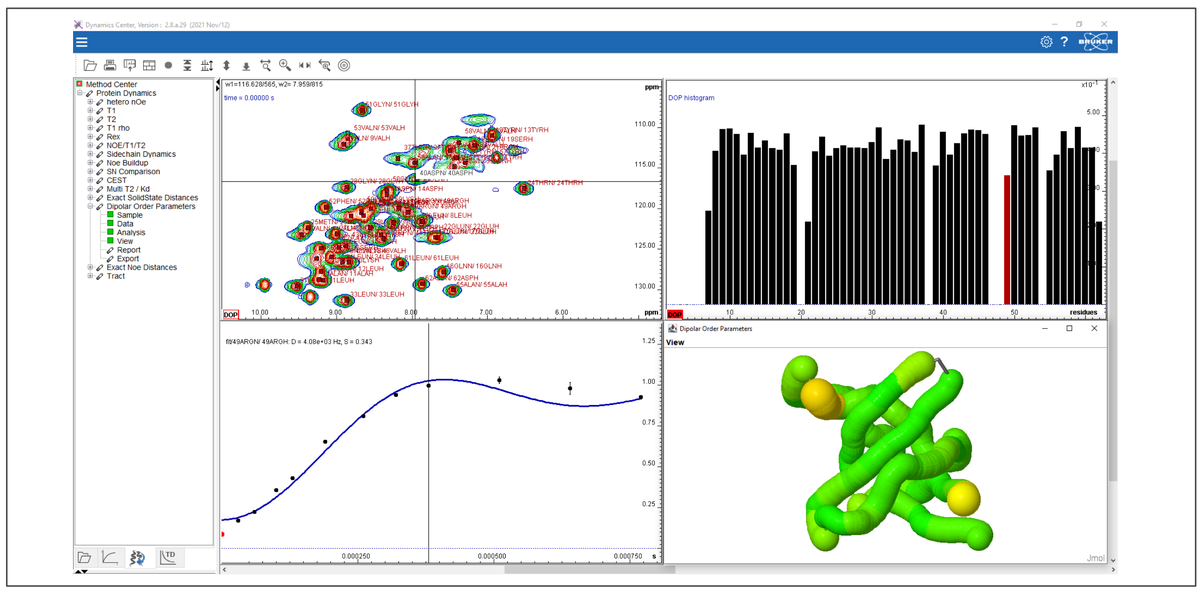

Fig. 1 Dipolar order parameters by series of 2D REDOR spectra. Order parameters represented as bar plot and on the protein structure.

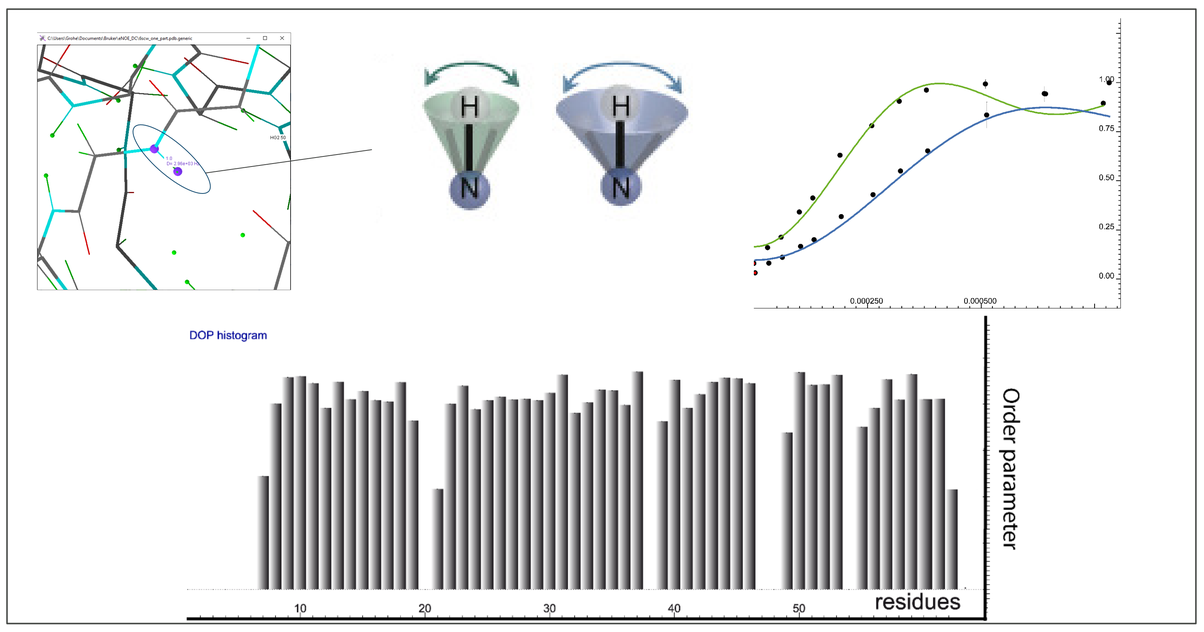

Fig. 2 Dipolar Order parameters by REDOR are a measure of the amplitude of protein motion.

https://www.bruker.com/protected/en/services/software-downloads/nmr.html

Exact solid-sate Distances

Determination of precise interproton distances for proteins in the solid state

- 1H-1H distance determination in solid-state NMR suffers from sources of error which are mainly side-specific magnetization loss during mixing, side-specific H to X transfer efficiency (in terms of 3D) and side-specific spin diffusion/dipolar truncation.
- All of the above-mentioned errors are taken into account by the new DynamicsCenter toolkit.
- Different CP transfer efficiency and polarization-loss during mixing are minimized by an automated normalizations procedure.
- Correction for spin-diffusion and dipolar truncation is done using a preliminary structural model.

Detection of slow timescale molecular motion

- Imports buildup data al series of 2D or 3D.
- Imports structure in pdb format.
- Imports peaklists in CCPNmr, SPARKY, XEASY, BMRG and TOPSPIN format.
- Imports shift-lists in Sparky and BMRB format. Performs an automated 3D-RFDR assignment using the shiftlist together with the pdb structure.
- Interactive user interface including correlation plot results table and structure display (Fig 3).
- Exports exact distance restraints in CYANA, ARIA and CNS format.
- Excel, PDF and PNG export.

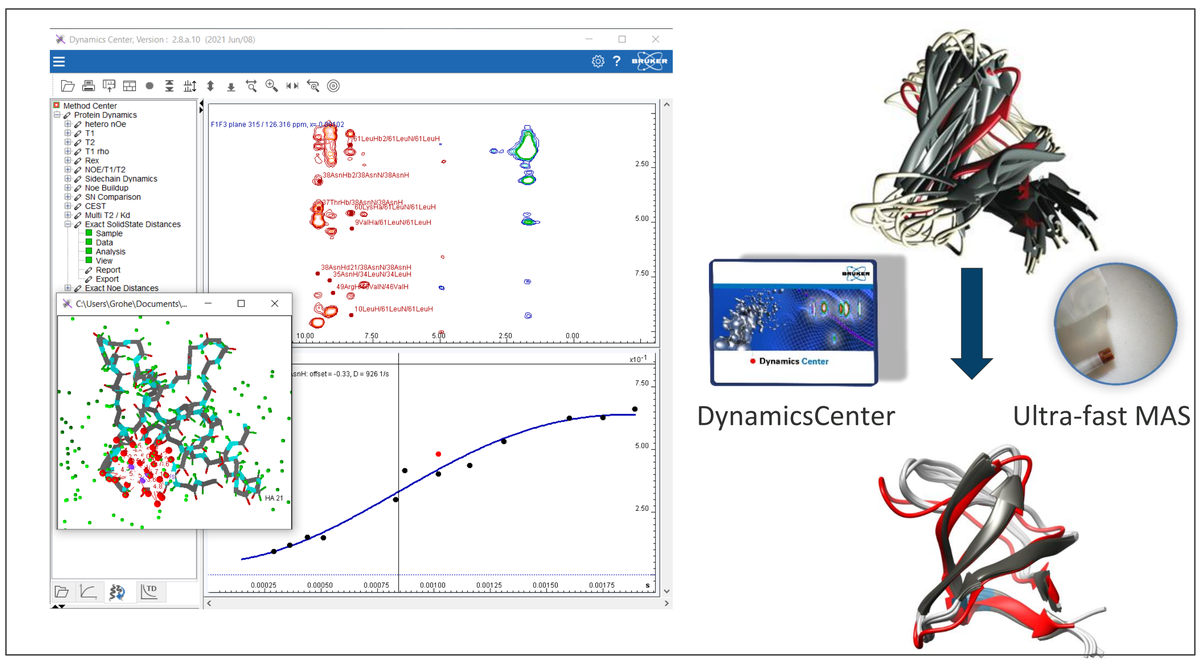

Fig. 3 Screenshot from the “exact solid-state distances” module of the DynamicsCenter. Precise distances can be used for determination of dynamics and to improve protein structures tremendously.

Conclusion

- The DynamicsCenter makes determination of relevant protein motion and precise protein structure for solid protein easy and fast.
- The obtained information about structure and dynamics is highly relevant for biochemistry and pharma.

Citations:

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4. Jain, M.G. et al. Selective 1H–1H Distance Restraints in Fully Protonated Proteins by Very Fast Magic-Angle Spinning Solid-State NMR. *J. Phys. Chem. Lett.* **8**, 2399-2405 (2017).

5. Haller, J.D., Schanda, P. Amplitudes and time scales of picosecond-to-microsecond motion in proteins studied by solid-state NMR: a critical evaluation of experimental approaches and application to crystalline ubiquitin. *J Biomol NMR* **57**, 263–280 (2013). https://doi.org/10.1007/s10858-013-9787-x