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Lecture abstract book

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Intrinsically disordered Microtubule Associated Protein 2c (MAP2c): Function and regulation probed by NMR

Lukáš Žídek
Faculty of Science and CEITEC, Masaryk University, Brno, Czech Republic

Relaxation properties of intrinsically disordered proteins (IDPs) make NMR investigation of IDPs more sensitive than studies of well-folded proteins. On the other hand, limited dispersion of chemical shifts of IDPs represents a challenge for the resonance assignment. High resolution approaches, typically combining high dimensionality and long evolution times with non-uniform sampling and accelerated return to equilibrium, are needed especially for IDPs of large size and repetitive amino-acid sequences.

Microtubule associated protein 2c (MAP2c) is a 50 kDa IDP controlling microtubule dynamics in the developing brain and playing other, so-far poorly understood, physiological roles. NMR spectroscopy was used to characterize structural features of MAP2c [1,2] and to probe intermolecular interactions and posttranslational modifications important for the MAP2c function and its regulation. In particular, phosphorylation kinetics by Ser/Thr and Tyr kinases and interactions with regulatory proteins have been monitored with resolution of individual amino acids [1,3]. Cross-talks between different signaling pathways have been observed, documenting complexity of regulatory mechanisms controlling MAP2c functions.

Acknowledgement:
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NMR Spectroscopy in Biomedicine and Structure-Based Drug Design

Robert Konrat
Department of Structural and Computational Biology, Max F. Perutz Laboratories, University of Vienna, Vienna Biocenter Campus 5, A-1030 Vienna, Austria;

robert.konrat@univie.ac.at

The design of small molecules that bind target proteins with high specificity and affinity is based on the optimization of complementary interactions in the bound state versus the respective unbound solvated states. One crucial interaction in drug design is that between the π-electrons of aromatic ring-systems and aromatic or aliphatic CH containing groups. These so-called CH-π interactions are the most common type of non-covalent interaction in protein-ligand interactions. Here fast and reliable detection methods of bound ligand proton CSPs for the identification and optimization of favorable CH-π interactions between ligand hydrocarbons (CH^{ligand}) and protein aromatic amino acids ($\pi^{protein}$) are presented.

Intrinsically disordered proteins (IDPs) are challenging the established structural biology structure-function paradigm and thus mandate suitable theoretical framework and concepts to properly address the subtle interdependence between protein structure and dynamics. In particular, it is their structural flexibility that allows them to adapt to and interact with different binding partners, making IDPs suited for functioning as hubs between several interaction partners. In contrast to stably folded globular proteins IDPs sample larger conformational spaces comprising loosely folded as well as compact conformational substates. In order to adequately grasp the subtleties of state distributions of IDPs appropriate theoretical and experimental techniques are needed. Nuclear magnetic resonance (NMR) has matured into a powerful experimental method for the characterization of IDPs and their complexes in solution. In combination with novel computational protein sequence analysis tools it can be used to provide a more comprehensive view of IDPs and how they can simultaneously maintain modularity, robustness, and adaptability, which are essential features for the generation of structural and phenotypic variation in biological systems.

What links NMR with molecular chirality?

Piotr Garbacz
Faculty of Chemistry, University of Warsaw, Poland

Tensors describing nuclear interactions like, e.g., spin-spin coupling, in a chiral molecule and its enantiomer are qualitatively the same except for a usually overlooked antisymmetric part. The unique feature of the antisymmetric part is its behavior under symmetry operations – it is a pseudovector. However, the antisymmetric part considered alone does not indicate the handedness of a molecule. To see chirality directly, i.e., purely on the physical basis, one needs to combine the antisymmetric part of a nuclear tensor with a quantity that transforms like a polar vector, e.g., a permanent electric dipole moment of the molecule. As the molecular electric dipole couples with an electric field, utilizing the antisymmetric part to see chirality requires an extension of nuclear resonance beyond magnetic interaction to magnetoelectric phenomena that may be used for direct discrimination of enantiomers.

Acknowledgement:
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^{13}C direct detection NMR reveals interesting insights on intrinsically disordered proteins

Isabella C. Felli
CERM and Department of Chemistry Ugo Schiff, University of Florence, Italy

Intrinsically disordered proteins (IDPs) have recently attracted the attention of the scientific community. They sample many different conformations in rapid interconversion, challenging well accepted concepts, such as the structure-function paradigm, stating that a protein functions thanks to its three dimensional structure. When part of complex multi-domain proteins, intrinsically disordered regions (IDRs) often play a key role in modulating the properties of the protein itself. However they pose serious challenges to most of the currently used methods to achieve atomic level information. Current drug discovery approaches based on seeking the optimal fit between complementary well defined surfaces (lock-and-key paradigm) are also bound to fail if applied to IDPs/IDRs.

NMR spectroscopy represents an excellent tool (if not the unique one) to access atom-resolved information about the structural and dynamic properties of highly flexible IDPs/IDRs. NMR methods should be optimized to overcome critical points deriving from the absence of the 3D structure. The impact on NMR observables deriving from the peculiar structural and dynamic properties of IDPs/IDRs will be discussed highlighting how ^{13}C direct detection contributes to overcoming critical points.

Several examples of particular features or motives that often occur in IDPs/IDRs will be presented, revealing novel structural and dynamic modules that are not yet described in the PDB.

Investigating Thermoresponsive Alignment Media via ^{2}H NMR and Diffusion

Christina M. Thiele, Dominic S. Schirra, Timo Imhof, Jonas Kind
Technische Universität Darmstadt, Darmstadt, Germany
cthiele@thielelab.de

Investigating an anisotropic NMR parameter become increasingly important in organic structure elucidation for the determination of conformation and relative configuration of natural products, synthesized compounds and catalysts.[1] To obtain such anisotropic NMR parameter, suitable alignment media are necessary. The use of lyotropic liquid crystals based on helically chiral polymers is especially intriguing as they additionally allow for enantiodiscrimination.[2] We have recently synthesized several homopolypeptides, which form lyotropic liquid crystals that are suitable for the measurement of anisotropic NMR observables and show excellent enantiodiscrimination. Furthermore, they exhibit thermoresponsive properties.[3]
The intriguing properties of these new thermoresponsive alignment media will be described in this presentation. Furthermore, we will shed light on the processes responsible for the thermoresponsivity by using isotope labelling, 2H NMR[4] and anisotropic diffusion[5].

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NMR and DFT analysis of 3D structure and spin-spin coupling constants in biologically active saccharides

Miloš Hricovíni
Institute of Chemistry, Slovak Academy of Sciences, 845 38 Bratislava, Slovakia
E-mail: Milos.Hricovini@savba.sk

Many oligo- and polysaccharides participate in various important biological processes and the molecular basis of these processes has been subject of a number of NMR and theoretical studies. Highly negatively charged glycosaminoglycans - heparin and heparan sulphate belong to the most studied saccharides. Apart from high-resolution NMR data, theoretical analysis is an important part of our understanding of biological properties of heparin and heparan sulphate oligosaccharides. In the present contribution, the results of NMR analysis and density functional theory (DFT) calculations are discussed. Geometry optimizations, evaluating explicit solvent molecules, were performed by the B3LYP/6-311+G(d,p) methods. The optimized molecular geometries in various heparin oligosaccharides allowed calculations of NMR parameters, such as chemical shifts and coupling constants. Comparison of theoretical and experimental NMR data showed that DFT method using the B3LYP functional and the 6-311+G(d,p) basis set, combined with explicit solvent model, can yield sufficiently accurate structural and NMR data for these oligosaccharides.

Dynamics and proton transport in noncrystalline cellulose functionalized with imidazolium cations

Michał Bielejewski, Jadwiga Tritt-Goc
[1] Institute of Molecular Physics Polish Academy of Sciences, Poznań, Poland
michal.bielejewski@ifmpan.poznan.pl

Proton conductors are one of the key elements of modern power sources like fuel cells which converts the chemical energy of hydrogen and oxygen reaction into electricity cleanly and efficiently. To overcome technical limitations and to create durable, cost-efficient, high-performance, and environmentally neutral materials for membranes used in FCs, we have designed and synthesized a nanocomposite based on cellulosic materials and heterocyclic molecules. The nanocrystalline cellulose was used to prepare the foil functionalized with imidazole molecules via a modified sol-gel technique to obtain a new solid proton conductor [1,2]. The ^{1}H, ^{15}N, and ^{13}C CP-MAS NMR spectroscopy has been used to study the dynamical properties of the cation molecule to determine the mechanism and efficiency of protonic transport in studied membranes [3,2]. This presentation will present the possibility of using ^{13}C NMR spectroscopy as an alternative to ^{15}N NMR spectroscopy.

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Solution structure of a lanthanide-binding DNA aptamer determined using high quality pseudocontact shift restraints

Witold Andrałojć,[a] Julia Wieruszewska,[a] Karol Pasternak[a], Zofia Gdaniec[a]
[a]*Institute of Bioorganic Chemistry, Polish Academy of Sciences, Noskowskiego 12/14, 61-704 Poznan, Poland*
* e-mail: wandralojc@ibch.poznan.pl

NMR spectroscopy is among the primary techniques used for high resolution structural studies of nucleic acid systems. Classical approaches to biomolecular NMR structure determination rely of the measurement of inter-proton distances up to 5-6 Å, through the means of the Nuclear Overhauser Effect (NOE). The local nature of these distance restraints can lead to a poor reproduction of some global structural features of the studied molecule (e. g. the degree of helical bending). Long-range NMR structural restraints derived from the presence of a paramagnetic ion in the studied system can radically change this situation and have already found much success in NMR studies of proteins, beyond just structure determination[1,2]. However, the potential of paramagnetic NMR methods remains largely unrealized for nucleic acids due to lack of general methods to rigidly and site-specifically introduce paramagnetic ions into these systems.
Here we present the high-resolution NMR structure of a lanthanide-binding DNA aptamer and demonstrate that lanthanide ions bound to this system induce large magnitude paramagnetic effects (pseudocontact shifts; PCS), readily interpretable in terms of structural parameters. We propose that the lanthanide binding motif uncovered for this system can be exploited to introduce lanthanide binding sites into a broad range of different DNA and RNA molecules to facilitate their structural and functional NMR studies. The presented structure is also of interest by itself, as it constitutes the first high-resolution structure of a metal-binding aptamer deposited in the PDB, furthering our understanding of high-affinity metal binding by DNA.

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Exploring macrolide binding modes by NMR spectroscopy

Predrag Novak
University of Zagreb, Faculty of Science, Department of Chemistry, Zagreb, Croatia

15- membered macrolides are well-known class of antibacterials widely prescribed to treat upper and lower respiratory tract infections [1]. Azithromycin is a semi-synthetic macrolide antibiotic derived from erythromycin possessing broad spectrum of antibacterial potency and favorable pharmacokinetics. Similar to other macrolide antibiotics it exerts its activity by binding to the bacterial ribosomal 23S rRNA in domain V at the peptidyl transferase region and blocks the exit tunnel which in turn inhibits the bacterial protein synthesis. However, bacterial resistance to marketed antibiotics is growing rapidly and represents one of the major hazards to human health worldwide. Recently discovered conjugates of azithromycin and thiosemicarbazones, the macrozones, represent new class of macrolide derivatives that exhibit promising activities against resistant pathogens [2-3].

Interaction studies of macrolide antibiotics and some selected macrozones with their biological targets will be presented in this talk. NMR experiments such as transferred nuclear Overhauser effect spectroscopy (trNOESY), saturation transfer difference (STD), diffusion and solvent paramagnetic relaxation experiments (PRE) in combination with molecular modelling have been employed to characterize binding modes and epitopes and asses bound conformations [4-6]. These data can serve as a platform for design of novel inhibitors with an improved biological profile.

Acknowledgements:
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Do we know what we eat – food metabolomics?

Dessislava Gerginova[1], Biljana Smit[2], Svetlana Simova[1]
[1]*Institute of Organic Chemistry with Centre of Phytochemistry, Acad. G. Bonchev bl. 9, 1113 Sofia, Bulgaria*
[2]*Department of Science, Institute for Information Technologies, University of Kragujevac, Jovana Cvijića bb, 34000 Kragujevac, Serbia*

Metabolomics aims to profile all chemical compounds present in a system. Numerous chemicals can be monitored simultaneously by using NMR or MS without prior knowledge of which compounds are altered. Investigations in food science include how a food product changes with food processing, to detect adulteration or misbranding or changes in nutritional profile, to understand what flavor compounds contribute to product liking, and to explore how dietary interventions with these food products alter the human metabolome. Data can also be correlated with other information, e.g. sensory evaluation data, genetic analyses or microbiological data to provide additional value.
On the example of a set of samples collected from a certain area a series of problems will be demonstrated indicating deficiencies in the information we get about the origin and composition of an everyday used food product.
Acknowledgements: This work was supported by the National Research Program “Healthy Foods for a Strong Bio-economy and Quality of Life” using the distributed research infrastructure INFRAMAT, Ministry of Education and Science.

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Methods for exploring non-Fourier dimensions - from small molecules to proteins.

Krzysztof Kazimierczuk,
Centre of New Technologies, University of Warsaw

The possibility of adding extra dimensions to spectra made the NMR spectroscopy a powerful analytical tool. Besides commonly used indirect „Fourier dimensions", i.e., those processed with Fourier transform, we often acquire a series of spectra under varying experimental conditions. These can be pulse sequence parameters (e.g. mixing times or diffusion-encoding gradients), environmental conditions (temperature, pH or concentration) or reaction progress.[1]

The resulting stack of n-dimensional spectra may be considered as an n+1-dimensional object. This concept opens the way to new processing methods for exploring non-Fourier dimensions.
Over the last decade, my group has developed several methods based on time-resolved non-uniform sampling (TR-NUS), Radon transform, and non-stationary signal processing. In my presentation, I will recapitulate the theory of these approaches and show their applications in metabolomics[2], reaction monitoring[3], ligand binding[4] and studying protein dynamics[5]. I will also discuss the currently developed concepts of exploring non-Fourier dimensions in protein research, e.g., fast measurements of TOCSY transfer curves.

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Magnetic Resonance Imaging in Biomedical, Pharmaceutical and Geological Sciences

Władysław P. Węglarz
Institute of Nuclear Physics Polish Academy of Sciences, Kraków, Poland

During the last four decades the Magnetic Resonance Imaging (MRI) and Spectroscopy (MRS) become a very powerful diagnostic modality, due to possibility of non-invasive visualisation of the human body. However, besides of the clinical applications, it is also used as a useful research tool in preclinical bio-medicine, for testing new pharmacological or theranostic therapies using animal models of the civilisation diseases and imaging of the structure, functions and metabolisms of the living organisms. It is also used in different branches of material sciences for e.g. characterisation of the properties of new theranostics and contrast agents as well as pharmaceutical, food or porous materials. Such broad range of applications is available due to possibility of obtaining images and localised NMR spectra, dependent on different physico-chemical properties, including nuclear relaxation times, diffusion, perfusion, magnetisation exchange, or presence of specific metabolites, to name a few. In most cases the proton (1H) MRI is utilized, however other nuclei, like ^{19}F, ^{31}P, ^{23}Na or ^{39}K are investigated as well. In the present lecture a few examples of using different MRI/MRS techniques for investigations of the brain structure and metabolism using animal models in vivo and ex vivo[1-3], optimising contrasting properties of the novel theranostic agents for drug delivery[4-6], testing novel pharmaceutical dosage forms properties and in vivo distribution[7] and finally for characterisation of the oil- and gas-bearing porous rocks[8-9] will be presented.

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Recent developments in NMR of quadrupolar nuclei in solids

Trébosc,[1] Lafon,[1] Hung,[2] Gan,[2] Nagashima,[3] Sasaki,[4] Bayzou,[1] Amoureux[1,5]
[1] Lille-France, [2] Tallahassee-US, [3] Tsukuba-Japan, [4] Bruker-Japan, [5] Bruker-France

Over 74% of NMR active nuclei have a spin $I \geq 1$ and are subject to quadrupole interactions. Nevertheless, the observation of these nuclei in solids often remains more challenging than with spin-1/2 nuclei since: (i) the spectral resolution is decreased by the second-order quadrupolar interaction, (ii) the larger size of the density matrix complicates the spin dynamics, and (iii) the quadrupole interactions exceed the rf-field amplitude. We will present recent techniques we introduced to facilitate the observation of these quadrupolar isotopes.
We have analyzed the performances of the recent cosine low-power MQMAS sequence,[1] and showed that for spin-3/2 isotope, this technique is more efficient than STMAS and requires lower rf-field; whereas for spin-5/2 nuclei, this variant is as efficient as the high-power one but requires rf-fields smaller than 20 kHz and hence, can be employed for low-γ nuclei and large diameter rotors.[2] These advantages are obtained without the need for the so-called STMAS specifications, and the sequences have been extended to obtain MQ-HETCOR spectra.
We have also developed efficient pulse sequences to transfer magnetization from protons to quadrupolar nuclei at slow-moderate or fast MAS (ν_R = 10-25 or > 60 kHz).[3-5] For $\nu_R \leq 20$ kHz, the most efficient pulse sequence is *D*-RINEPT using adiabatic pulses. This transfer has been combined with DNP to detect low-γ quadrupolar nuclei with natural abundance near surfaces or sub-surfaces, such as ^{17}O, ^{95}Mo, ^{47,49}Ti, ^{67}Zn.[5] More recently, this transfer has been combined with MQMAS to detect DNP-enhanced high-resolution NMR spectra of quadrupolar nuclei, such as ^{17}O, near surfaces (Fig).[6]
Finally, we have analyzed the *T*-HMQC technique[7] for the indirect detection without t_1 noise of spin-1/2 nuclei subject to large CSA (^{195}Pt), as well as spin-1 (^{14}N) and spin-3/2 (^{35}Cl) quadrupolar nuclei.[8] For spin-3/2 nuclei, this method can provide a resolution enhancement of ca. 4.[9]

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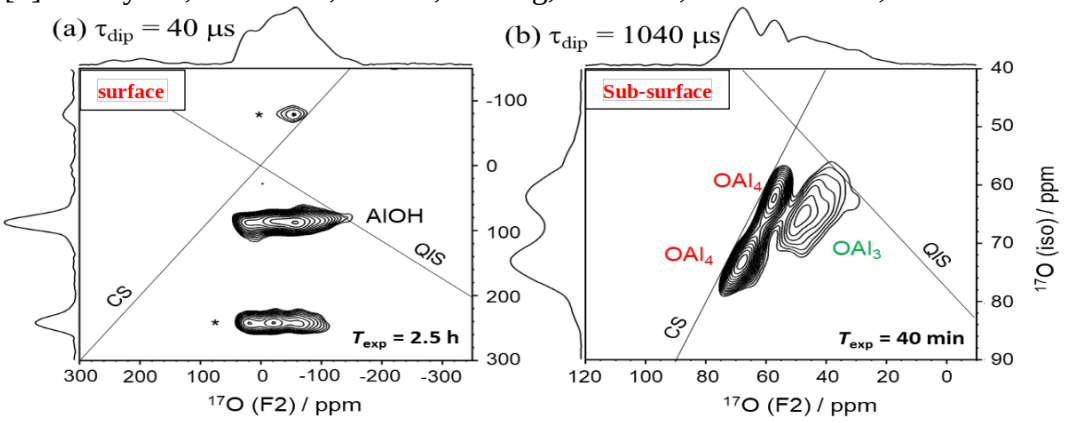

2D DNP-enhanced ^{1}H→^{17}O *D*-RINEPT-MQMAS spectra of γ-Al_2O_3 with τ_{dip} = (a) 40 or (b) 1040 μs.

New salts of teriflunomide (TFM) – Single crystal X-ray and solid state NMR investigation

Piotr Paluch[1,2], Tomasz Pawlak[1], Rafał Dolot[1], Grzegorz Bujacz[3], Marek J.Potrzebowski[1]
[1]Centre of Molecular and Macromolecular Studies, Polish Academy of Sciences
[2]Faculty of Chemistry, Biological and Chemical Research Centre, University of Warsaw
[3]Institute of Molecular and Industrial Biotechnology, Lodz University of Technology

email: ppaluch@cbmm.lodz.pl

New salts of teriflunomide TFM (drug approved for Multiple Sclerosis treatment) with inorganic counterions: lithium (TFM_Li), sodium (TFM_Na), potassium (TFM_K), rubidium (TFM_Rb), caesium (TFM_Cs) and ammonium (TFM_NH4) were prepared and investigated employing solid state NMR Spectroscopy, Powder X-ray Dif- fraction PXRD and Single Crystal X-ray Diffraction (SC XRD). Crystal and molecular structures of three salts: TFM_Na TFM_Cs and TFM_NH4 were determined. Compared to the native TFM, for all crystalline salt structures, a conformational change of the teriflunomide molecule involving about 180-degree rotation of the end group, forming an intramolecular hydrogen bond N–H···O is observed. By applying a complementary multi-technique approach, employing 1D and 2D solid state multinuclear (^{1}H,^{13}C, ^{15}N, ^{19}F, ^{23}Na,^{7}Li, ^{133}Cs) MAS NMR techniques, single and powder X-ray diffraction measurements, as well as the DFT-based GIPAW calculations of NMR chemical shifts for TFM_Na and TFM_Cs allowed to propose structural features of TFM_Li for which it was not possible to obtain adequate material for single crystal X-Ray measurments.

Acknowledgement:
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Amyloid fibrils and intact cells seen by multinuclear solid-state NMR spectroscopy at fast MAS regime

Alons Lends
Latvian Institute of Organic Synthesis, Riga

The solid-state NMR (ssNMR) spectroscopy is a powerful technique to study biological systems at atomic level close to their native state. Recently fast MAS techniques has revolutionized ssNMR spectroscopy, by requiring less 1 mg of sample material. Here we are going to present the application of ssNMR to study amyloid fibrils and intact cells. In the first part of presentation, we are going to explore ^{19}F detection methods with a novel fluorine labelling methods to study amyloid fibrils at fast MAS regime. We manage to achieve an excellent resolution in ^{19}F dimension. This technique will be further explored to obtain unambiguous distance restraints for the 3D structure calculations. Additionally, we will also show the incorporation of selectively ^{2}H labelled amino acids into proteins to apply ^{2}H detection methods for the specific dynamic measurements. In the second part of the talk, we will demonstrate the ^{1}H detection methods to study intact yeast cells. For this sample we manage to achieve a moderate resolution with a good sensitivity. This allowed us to identify the main structural components and dynamics of the cells.

Conformational exchange and proton dynamics – from DNA recognition to enzymatic catalysis by NMR

Rasmus Linser
Technical University Dortmund, Dortmund, Germany

Conformational exchange and proton dynamics – from DNA recognition to enzymatic catalysis by NMR Structural dynamics are the fundament of biomolecular functionality. NMR gives atomic-resolution insights for conformational exchange as well as fluctuations of chemical constitution at an unsurpassed level of detail. Here I will give an overview over some of the current questions we are tackling in our group, reaching from a dynamics-optimized artificial epigenetic reader to micro-crystalline enzymes, touching on the virtues of fast magic-angle spinning and higher-dimensionality, proton-detected experiments.

Improving sensitivity of solid-state NMR of proteins by optimal control methods

Zdeněk Tošner
Charles University in Prague, Prague, Czech Republic

We have recently developed several strategies to improve sensitivity of solid-state NMR experiments of protein samples. Traditional cross-polarization methods used to establish inter-nuclear correlations suffer from radiofrequency field inhomogeneity and lead to volume selection when only part of a sample yields NMR signal. Our tm-SPICE optimal control pulses are designed to compensate for this inhomogeneity and yield sensitivity gains of about 50% for the ^{15}N-^{13}C transfer. A new concept of TROP pulses explores the preservation of equivalent pathways principle in multidimensional experiments known from liquid state NMR. Transferring both x- and y-magnetization components after indirect chemical shift evolution leads to the additional 1.41-fold increase of sensitivity per indirect dimension. This provides an order of magnitude time savings in just-emerging 4-5D proton-detected experiments.

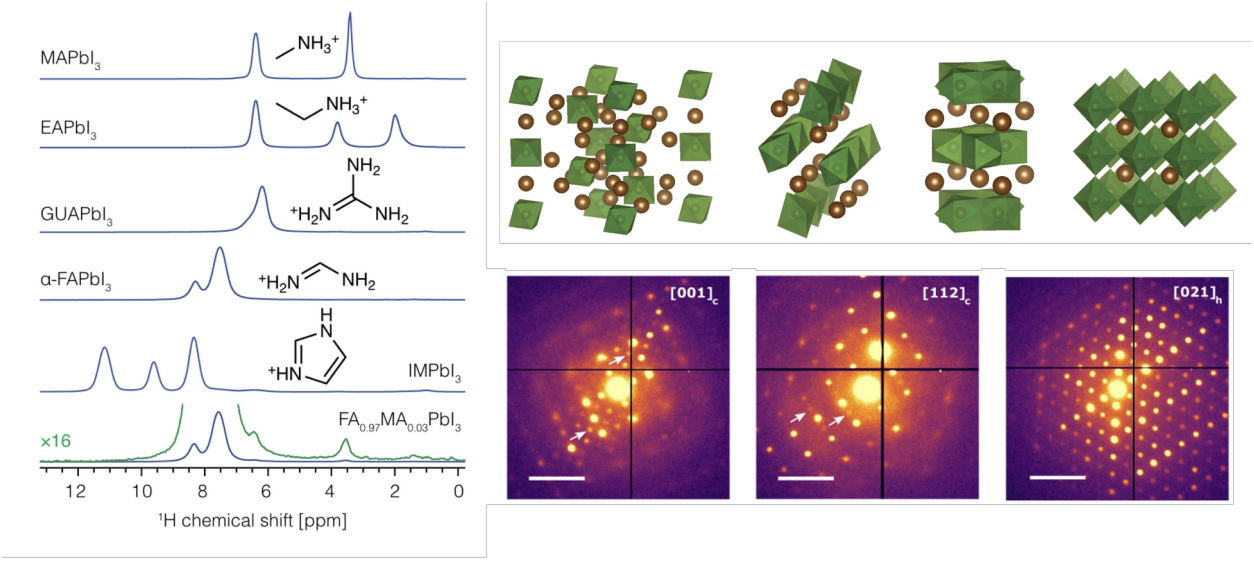
New approaches to determining the atomic-level structure of advanced materials

Dominik J. Kubicki
Department of Physics, University of Warwick
@DominikJKubicki ,http://kubickilab.wordpress.com/

Determining the structure-property relationships at multiple length scales is one of the key tenets of rational design of new materials. While diffraction techniques offer insight into the long-range structure of solids, many properties are determined by local structure, which can be accessed using approaches based on, e.g., total scattering (PDF), XAFS, and magnetic resonance (NMR and ESR).

I will use the example of metal halide perovskites to discuss how we can determine the atomic-level structure of solids in an element-specific manner using solid-state NMR spectroscopy. The range of research problems includes quantifying dopant incorporation, phase segregation, decomposition pathways, passivation mechanisms, and structural dynamics.[1] I will also show how electron diffraction allows us to study structural phenomena inaccessible with X-rays.[2]

I will then discuss my take on studying these multifaceted materials *in situ* and *operando* to elucidate the mechanism of structural transformations in fully assembled optoelectronic devices, especially under illumination. These strategies will be key to elucidating the performance-limiting factors in devices such as solar cells, light emitting diodes, and X-ray detectors.



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NMR assignment of methyl groups using 13C homonuclear transfers, tailored isotope labelling and proton detection with MAS up to 100 kHz

Jan Stanek[1], Piotr Paluch[1,2], Rafał Augustyniak[1], Mai-Liis Org[3], Kalju Vanatalu[3], Ats Kaldma,[3] Ago Samoson[3],
[1]Faculty of Chemistry, Biological and Chemical Research Centre, University of Warsaw
[2]Centre of Molecular and Macromolecular Studies, Polish Academy of Sciences
[3]Tallin University of Technology, Tallinn, Estonia

janstanek@chem.uw.edu.pl

In NMR spectroscopy of proteins, methyl protons play a particular role as sensitive reporters on protein dynamics, allosteric effects and protein-protein interactions, accessible in solution in high-molecular weight systems approaching 1 MDa. However, their systematic resonance assignment presents a challenge, and often requires a labor-intensive mutagenesis approach. Here we address the issue by using solid-state NMR methods, and leverage recent technological advancements in 1H-detection with magic-angle spinning at frequencies up to and beyond 100 kHz [1].

We employ specific 1H-labelling of Ile, Leu, and Val residues, and otherwise an extensive deuteration and uniform 13C-enrichment, to establish correlations between methyl and backbone amide 1H resonances. To this end, we systematically evaluate efficiency of a series of RF schemes which transfer 13C coherence across entire 13C side-chains of methyl-containing residues. Performance of ten methods for recoupling of either isotropic 13C-13C scalar or anisotropic dipolar interactions (five variants of TOBSY, FLOPSY, DIPSI, WALTZ, RFDR and DREAM) is evaluated experimentally at two magic-angle spinning (55 and 94.5 kHz) and magnetic field conditions (18.8 and 23.5 T).

Model isotopically-labelled compounds and alpha-spectrin SH3 protein are used as convenient reference systems. Results indicate a pivotal role of increased MAS rates for efficiency of multiple-bond 13C transfer even in highly deuterated protein samples. Additionally, spin dynamics simulations in SIMPSON are performed to determine optimal parameters of these RF schemes, up to recently experimentally attained spinning frequencies (200 kHz) and B0 field strengths (30.5 T), and beyond.

We revisit the concept of linearization of 13C side-chains by tailored isotope labelling and show a dramatic sensitivity gain of methyl-to-backbone correlations. We also demonstrate that high-resolution 4D spectroscopy with non-uniform sampling is key to remove ambiguities in simultaneous resonance assignment of methyl proton and carbon chemical shifts. We estimate that a combination of suitable isotope labelling, sensitive 1H-detection, and optimal RF designs for ultra-fast MAS enables methyl resonance assignment in microcrystalline proteins as large as 500 residues [2].

We additionally present the surprising advantages of 2H decoupling for resolution and coherence lifetime of 13C spins in extensively deuterated proteins. In this respect, we revisit the conventional triple-correlation approach (HN-CA/CB/CO) and present ultimate RF designs for backbone resonance assignment with 3D to 5D spectroscopy [1,3], along with recent novel approaches for resonance assignment in nondeuterated proteins [4].

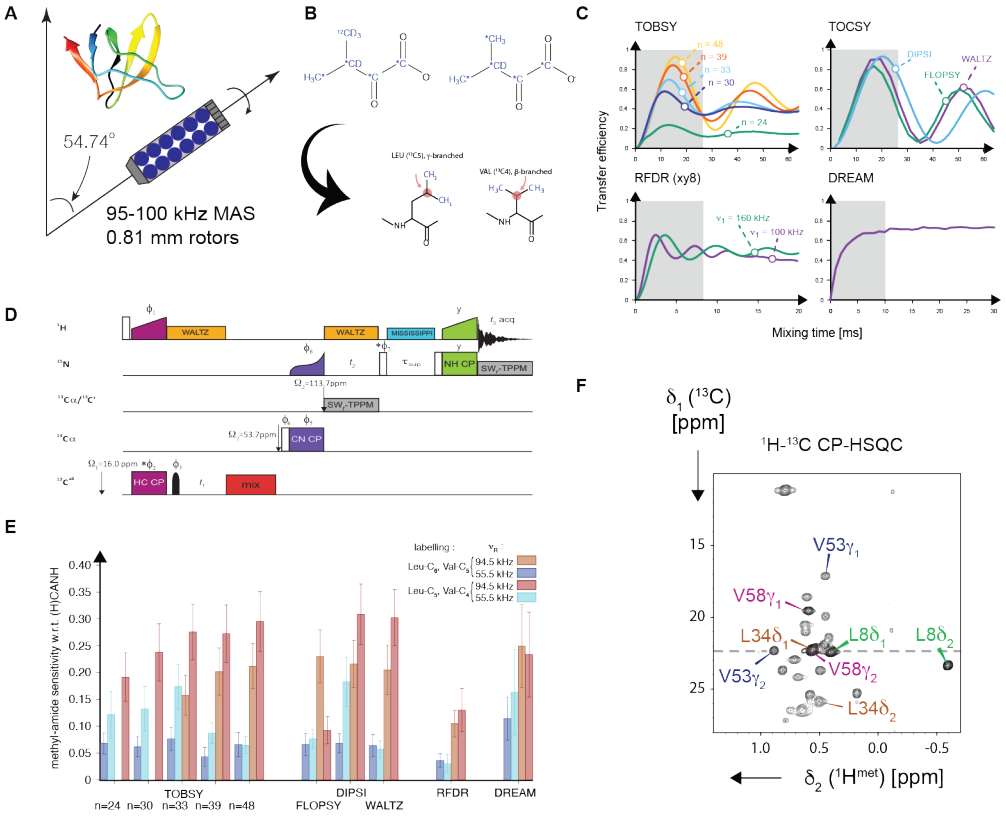

Figure: A combination of (A) ultrafast (95-100 kHz) magic-angle spinning in small (0.81 mm) rotors, (B) suitable precursors for biochemical synthesis of ILV aminoacids, (C) spin dynamics simulations, (D) 3-4D spectroscopy and a careful choice between J- and D-mediated 13C-13C mixing schemes is used in this work for efficient assignment of 1H and 13C chemical shifts of methyl groups (E).

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Probing gas species adsorbed at the surfaces of porous materials using ssNMR and modeling

Luís Mafra
CICECO - Aveiro Institute of Materials, Department of Chemistry, University of Aveiro, 3810-193 Aveiro, Portugal.

Email: lmafra@ua.pt

This presentation highlights the most recent advances from our team in studying the speciation of gas adsorbates (mainly CO2) and trimethylphosphine oxide (TMPO) probe molecules that interact with the surfaces of porous materials. The nature of adsorbate species formed in confined spaces, their location inside the pore structure and the type of adsorbate-adsorbent interactions, determines many properties in catalytic and CO2-adsorbent materials such as gas sorption capacity/kinetics, selectivity, acid strength and cyclic stability. However, an atomic-level understanding of the adsorbate sorption mechanisms in porous media and the interactions involved therein remains elusive, hindering our ability to design improved catalytic and sorbent materials. The lack of advanced spectroscopic studies, tailored to elucidate the structure of adsorbed gas species, has also been a major bottleneck for further progresses in understanding the physical chemistry of gas-solid interfaces. This talk shows examples on the use of solid-state (ss) NMR spectroscopy has a unique site-selective technique to study the structure and the dynamics of CO2 species adsorbed at porous adsorbent materials. Unprecedented atomistic description of the host–guest and guest–guest interactions of TMPO molecules confined within HZSM-5 molecular-sized voids combining ssNMR, DFT and ab initio molecular dynamics (AIMD)-based computational modeling will also be showcased.

NMR crystallography – demanding but gratifying

Marta K. Dudek
Centre of Molecular and Macromolecular Studies, Polish Academy of Sciences, Sienkiewicza 112, 90-363, Lodz, Poland

NMR crystallography is an excellent approach to describe crystal structures of molecules crystallizing in the form of microcrystalline powders. Typically, it consists of advanced solid-state NMR and powder X-Ray diffraction experiments, complemented by quantum chemical calculations to find and validate a structural model of the crystal form of the investigated molecule. This contribution will show the basics of NMR crystallography, its strong and weak points, a variety of its different flavours in which it is currently used, as well as its various applications.

UNIVERSITY OF CAMBRIDGE
Department of Chemistry

NMR SERVICE

CUSTOMISED SOLUTIONS IN MAGNETIC RESONANCE: SPECIAL PROBES FOR MAS AND *IN SITU* NMR ON ENERGY STORAGE MATERIALS

Oliver Pecher[1,2] (o.pecher@nmr-service.de)

[1] NMR Service GmbH, Blumenstr. 70 Haus 3, 99092 Erfurt, DE
[2] University of Cambridge, Yusuf Hamied Department of Chemistry, Lensfield Rd., Cambridge CB2 1EW, UK

The manifold applications of magnetic resonance include the research of new and innovative materials. NMR SERVICE develops and manufactures customised probes and accessories for solid-state NMR/NQR experiments and related methods. We guide you all the way from planning the setup, installing the hardware, supporting your experiments, troubleshooting, and hardware modifications/upgrades.

Here, we will report on recent developments regarding MAS power handling and increased experimental efficiency in solid-state NMR investigations, e.g.

- MAS 3.2 600 WB NMR probe optimised for low-gamma ^{39}K NMR experiments
- Static *in situ/operando* NMR probes to research energy storage materials (Fig. 1)[1,2,3,4]
- Static *in situ/operando* NMR probe to measure coin cells

Furthermore, we will give some insights into our probes/accessories that combine the application of static solid-state NMR with electrochemical[1,2,3,4] and optical measurements (e.g. UV/Vis, IR/RA). Finally, the challenges and some solutions in ^{7}Li and ^{23}Na *in situ* NMR experiments on SiO[5] and Sn[6] anodes as well as hard carbon[7] are briefly discussed.

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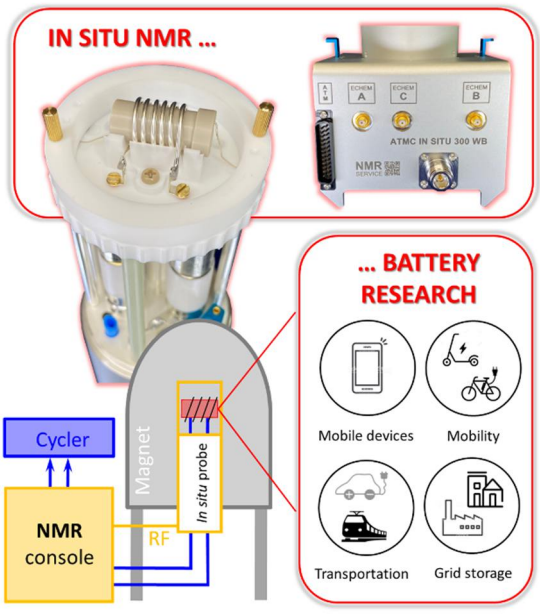

Figure 1. *In situ* NMR applied in battery research. Customised hardware and experimental approaches by NMR SERVICE help to make the experiments happen.