GIPAW: Applications to Organic Materials

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Oxygen-17 NMR

$^{17}$O MAS Glutamic Acid · HCl
Oxygen-17 NMR

$^{17}$O MAS Glutamic Acid . HCl
Oxygen-17 NMR

$^{17}$O MAS Glutamic Acid . HCl

<table>
<thead>
<tr>
<th>Site</th>
<th>Calculation</th>
<th>Experiment</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>$\delta_{\text{iso}}$(ppm)</td>
<td>$C_Q$(MHz)</td>
</tr>
<tr>
<td>O1</td>
<td>177.6</td>
<td>7.72</td>
</tr>
<tr>
<td>O2</td>
<td>316.9</td>
<td>8.61</td>
</tr>
<tr>
<td>O3</td>
<td>311.0</td>
<td>8.90</td>
</tr>
<tr>
<td>O4</td>
<td>198.0</td>
<td>8.13</td>
</tr>
</tbody>
</table>

Ray Dupree (Warwick)
Glutamic Acid Polymorphs

- We find correlations between NMR parameters and hydrogen-bond strength
  

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**Chemical Shift**

- 

**Quadrupolar Coupling**

- 

**Asymmetry**

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**Extended to wide range of amino-acids**

*Combined first-principles computational and experimental multinuclear solid-state NMR investigation of amino acids*

Gervais, C; Dupree, R; Pike, KJ; Bonhomme, C; Profeta, M; Pickard, CJ; Mauri, F, J. Phys. Chem. A, 109 (31), 6960 -6969, 2005.
Oxygen-17 NMR Future Perspectives

Transmembrane proteins

$^{17}$O-[Ala12]-WALP23 synthetic peptide

- Chemical shift decreases ~1200ppm/Å with C=O bond length

WALP23 in DSPC Vesicle

$\delta_{iso}=311\pm1$ppm   C=O 1.217Å

WALP23 in Hydrated DSPC Vesicle

$\delta_{iso}=315\pm1$ppm   C=O 1.223Å

Solid-State $^{17}$O NMR as a Probe for Structural Studies of Proteins in Biomembranes

V. Lemaitre, M.R.R. de Planque, A.P. Howes, M.E. Smith, R. Dupree, A. Watts

J. Am. Chem. Soc.; 2004; 126(47); 15320
J-Resolved Solid-State NMR

Maltose
sugar used in brewing

Cross-peaks when J-coupling between spins: - C-H “bonds”

MAS-J-HMQC

Steven Brown (Warwick)
J-Resolved Solid-State NMR

X - first principles
molecule only

H axis

C axis

13C axis

1H axis

GIPAW: Zurich 2009 Jonathan R. Yates
J-Resolved Solid-State NMR

Molecule to solid variation due to intermolecular interactions (weak hydrogen bonds)

Maltose

anhydrous α–maltose: H4’ proton

crystal structure

δiso(¹H; cryst) = 3.66 ppm

isolated molecule

δiso(¹H; mol) = 1.76 ppm

Δδiso(¹H; mol to crys) = 1.90 ppm
Intermolecular “Weak” Hydrogen bonds

Correlation between a large calculated $\Delta\delta_{\text{iso}}(^1\text{H}; \text{mol to crys})$ and a short H…O intermolecular distance (<2.7) and a CHO bond angle greater than 130 degrees

Uracil

Isolate H-bonding from ring currents

<table>
<thead>
<tr>
<th>Doner</th>
<th>$\Delta \delta$ (Mol-Xal)</th>
</tr>
</thead>
<tbody>
<tr>
<td>N-H</td>
<td>5.1</td>
</tr>
<tr>
<td>N-H</td>
<td>5.4</td>
</tr>
<tr>
<td>C-H</td>
<td>2.0</td>
</tr>
<tr>
<td>C-H</td>
<td>2.2</td>
</tr>
</tbody>
</table>

\(J. \text{ Am. Chem. Soc.} \ 130 \quad 945 \ (2008)\)
NMR Crystallography

Regulatory requirement to identify polymorphic forms of new pharmaceuticals

4-Methyl-2-nitroacetanilide (MNA)

Two molecules in Asymmetric Unit

Testosterone

Robin K. Harris, Sian A. Joyce, Chris J. Pickard, Sylvian Cadars and Lyndon Emsley

Phys. Chem. Chem. Phys., 2006, 8, 137
recent progress has been made in the application of diffraction of new materials and in the pharmaceutical industry. The development using the Xplor-NIH MM package calculations and experiments before and after structure optimization. The structure of fairly large systematic deviations from the reference structure. For constraints obtained from comparison with back calculated PSD systems, a group of structures has a standard deviation of 0.14 Å, and it the best overall agreement with the experimental constraints. This resulted in the group of 16 structures shown in Figure 1a having molecular modeling (MM) with experimental proton spin diffusion determination of the three-dimensional structure of a powdered inorganic networks, -alanine (L-alanine), and we determined the crystal structure to within 0.13 Å of the known structure. The validity was obtained from 2D correlation experiments to this method allows for a fully solid-state treatment of the system this method is found to provide remarkably accurate predictions of solid-state NMR chemical shifts. This value of this approach here between this code and other quantum chemical approaches have never been used to determine structures. Indeed, for example, we note that, in addition to the position and orientation space is very large, and calculation times are currently prohibitive. DFT methods are currently not capable of determining complex systems, isotopically enriched biological states. Structural characterization of crystalline powders represents a surprising since (i) these groups are not protonated and so are not state NMR chemical shifts.

The PSD constrained structure was determined by fitting the experimental chemical shifts, keeping the slope fixed to 1. We used a standard molecular modeling force field including potentials generated on the fly and a 2 Monkhorst–Pack k-point grid. The reference shielding was calculated using the same energy expansion during the molecular modeling optimization. They parameters as those used for the geometry optimization. They

Comparison between the structure of

![Flow chart for NMR crystallography.](image)

**Scheme 1** outlines the protocol for powder NMR crystallography using combined NMR refinement, and (b) the 16 structures refined using the plane wave DFT/NMR chemical shift approach described here. The figure shows one diffraction (orange) and (a) the 16 structures obtained from the MM/PSD-
Guanosine

\[ 2h J_{N7b,N1a} = 6.2 \pm 0.4 \text{ Hz (expt)} \]
\[ 6.5 \text{ Hz (calc)} \]

\[ 2h J_{N7a,N1b} = 7.4 \pm 0.4 \text{ Hz (expt)} \]
\[ 7.7 \text{ Hz (calc)} \]


self-assembles into ribbons

molecular electronics (FET)

Predictions

\[ 2h J_{O6a,N2b} = 5.7 \text{ Hz} \]
\[ ^1 J_{O6a,C1a} = 22.0 \text{ Hz} \]
\textbf{\(^{17}\text{O} - ^{15}\text{N}\) J-couplings}

Observing \(^{15}\text{N}\) spin-echo

\begin{align*}
2hJ_{\text{NO}} & \quad \text{Expt} \quad \text{Calc} \\
\text{N1-O4:} & \quad 6.7 \pm 0.4 \text{ Hz} \quad 6.1 \text{ Hz} \\
\text{N3-O4:} & \quad 4.8 \pm 0.5 \text{ Hz} \quad 4.6 \text{ Hz}
\end{align*}

\(2J_{\text{NN}}\)

\begin{align*}
\text{N1-N3:} & \quad 2.7 \pm 0.1 \text{ Hz} \quad 2.7 \text{ Hz}
\end{align*}

Observing \(^{17}\text{O}\) spin-echo

\begin{align*}
2J_{\text{ON}} & \\
\text{O4-N1/3:} & \quad 5.1 \pm 0.5 \text{ Hz} \quad 5.4 \text{ Hz}
\end{align*}

\textit{J. Am. Chem. Soc. 131 1820 (2009)}
Intra-molecular H-bonds

Steven Brown (Warwick)

![Intra-molecular H-bonds](image)

<table>
<thead>
<tr>
<th>Pyrrole (A)</th>
<th>Triazole (B)</th>
</tr>
</thead>
<tbody>
<tr>
<td>$^{2h}J_{N9N1}$</td>
<td>$^{1}J_{N9N1'}$</td>
</tr>
<tr>
<td>Calculation[7]</td>
<td>8.1</td>
</tr>
<tr>
<td>Experiment[6]</td>
<td>8.0±0.3</td>
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Effect of Crystal Lattice

full crystal

isolated molecule
Intra-molecular H-bonds

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<th>$^{1}J_{N9N1'}$</th>
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<tr>
<td>Solid-state</td>
<td>8.1</td>
<td>-9.8</td>
<td>J computed for a perfect crystal of (A)</td>
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<tr>
<td>Electrostatic</td>
<td>0.5</td>
<td>0.4</td>
<td>change in J due to effect of crystal lattice (isolated molecule at crystal geometry)</td>
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<tr>
<td>Structural</td>
<td>1.2</td>
<td>0.0</td>
<td>change in J due to subsequent relaxation of isolated molecule</td>
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<td>Molecular</td>
<td>9.8</td>
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# Intra-molecular H-bonds

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<tr>
<th></th>
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<th>Comment</th>
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<tr>
<td>Solution-state</td>
<td>9.0</td>
<td>10.3</td>
<td>Experimental result (note: systematic 0.9 Hz error due to neglect of solvation)</td>
</tr>
</tbody>
</table>