Magnetic Resonance
Quotation

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The Business of Science™

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November 10, 2014

Pulsar HC 60 Benchtop NMR Network

Complete Pulsar HC 60 benchtop NMR network provides for high throughput - hands on instruction of introductory and advanced chemistry concepts. The network consists of two Pulsar HC 60 benchtop NMR spectrometers for NMR data collection and two mNova PC NMR workstations for seamless off line NMR processing and analysis.

Item	Qty	Item	Description		Price (US$)
1	2	magnet	1.4T benchtop high resolution magnet module		included
2	2	electronics	NMR electronic module UPS Preconditioning		included
3	2	probe	5mm NMR probe & shims		included
4	2	host workstation	Windows 7 PC host workstation Perpetual Oxford Spinflow NMR software license Perpetual Mestrelab MNova NMR software license		included
5	2	remote workstation	Windows 7 PC remote workstation Perpetual Mestrelab MNova NMR software license		included
		services	Network Installation 12 month warranty		
			Network Total Academic Allowance Network Net Total Transportation **Network Net Total – Delivered & Installed**		$178,600 ($17,860) $160,740 $2,200 **$162,900**

TERMS AND CONDITIONS
This offer is subject to Oxford Instruments Terms and Conditions of Quotation and Sale. Any and all exceptions and exclusions require the written consent of Oxford Instruments.

NMR Performance	Pulsar HC 60 for 1H & 13C / 1D & 2D NMR testing & teaching. Standard 5mm NMR sample tubes. Sample volume = 0.3ml - 0.6ml 1H Frequency = 60.3 MHz 1H Resolution = 0.5 - 0.7 Hz nonspin Experimental - 1D & 2D NMR, T1 & T2 NMR Demonstrations available upon request.
Expiration	Valid for 90 days.

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Payment	20% net 10 days after order 80% net 30 days after delivery
Prices & Currency	Prices are in US Dollars. Import, federal, state and local taxes are not included.
Financing	36 & 60 month lease purchase financing is available upon request.
Shipment	August 2015
INCOTERMS 2010	FCA Factory.
Warranty	12 month warranty commencing with delivery.
Acceptance	The system is accepted with installation including demonstration of published specifications. Any minor faults which have minimal effect on system use will not delay acceptance. All minor faults will be rectified through warranty coverage.
Site of Goods	OIA accepts no responsibility for any effect of site environment on performance of equipment, or for interference or damage to existing equipment caused by operating the product. OIA accepts no responsibility (unless otherwise stated in the contract) for the integration of the goods to be supplied with any other existing equipment.
Transportation, including off loading and site access	In the case where OIA is not contracted to transport or off load the equipment it is the responsibility of the buyer to ensure that only the correct equipment and trained personnel are used. In all cases it is the responsibility of the buyer to ensure that the necessary site access is available to allow the siting of the goods. Information on dimensions and weights is available on request
Spares and Service	OIA guarantees that spare parts and service will be available for the equipment for a minimum of 7 years after last system shipment, provided that parts are available from their original manufacturer. In the event that parts cannot be obtained, OIA will endeavour to offer suitable alternatives or offer upgrades and replacements at preferential rates

Prepared by Marty Marek, Oxford Instrument Benchtop NMR Systems
marty.marek@oxinst.com
773 294 4205

Pulsar™

Delivering NMR to your benchtop

OXFORD INSTRUMENTS

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Pulsar™

NMR for *your* laboratory

The **Pulsar**™ NMR spectrometer from Oxford Instruments delivers affordable, high performance NMR spectroscopy into the laboratory environment.

Benchtop NMR where you want it

Pulsar is a benchtop, cryogen-free NMR spectrometer that offers high performance without the special requirements associated with superconducting magnet instruments.

With a small footprint, **Pulsar** is suited to virtually any laboratory from the teaching or organic synthesis laboratory, to near-line in an industrial production area.

Pulsar in the laboratory environment.

Low Setup and Running Costs

Pulsar works in your laboratory with no need for special Health and Safety requirements. **Pulsar** does not require liquid helium, liquid nitrogen or compressed gasses, and needs only a standard mains electrical supply. So you can concentrate on running samples, not on looking after your instrument.

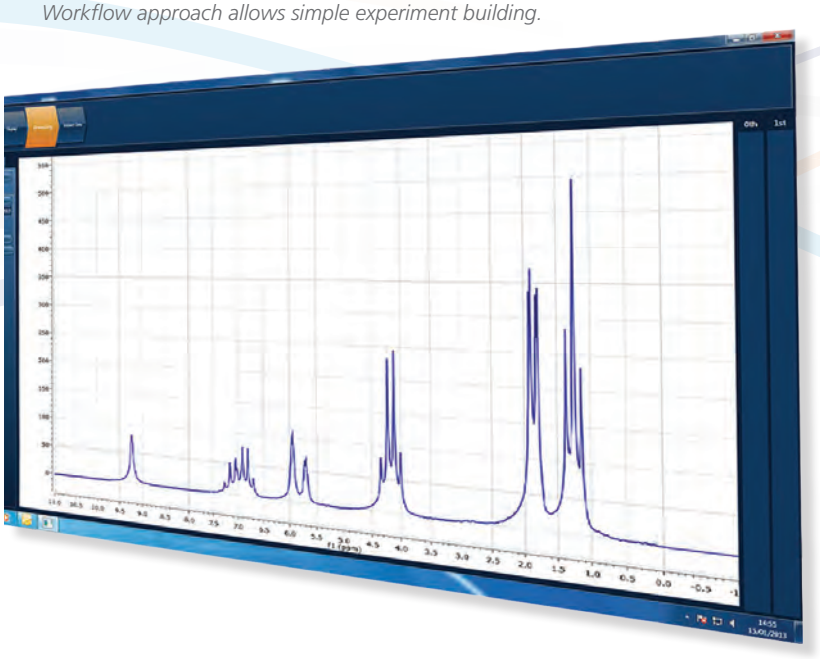
Superior Performance

Pulsar gives you class-leading performance. Incorporating a 1.4 T (60MHz proton resonance) rare-earth permanent magnet with superior homogeneity, **Pulsar** provides outstanding spectral resolution in a benchtop system.

Innovative, Intuitive, Intelligent Software

The **SpinFlow**™ software's graphical user interface enables the user to quickly and easily create routine experiments for simple spectra collection, relaxation measurements or advanced data collection. Instrument control comes from an intuitive, seamless workflow package, and data processing and manipulation is achieved using Mestrelab's powerful, industry-leading Mnova NMR software.

Workflow approach allows simple experiment building.



Cryogen free

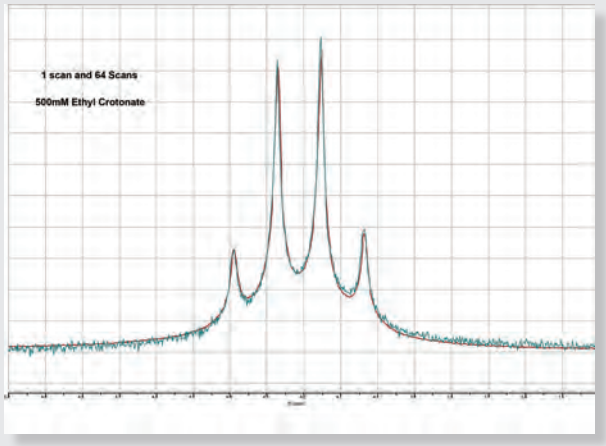
Fast measurements are possible generating routine spectra in seconds, making **Pulsar** the perfect tool to monitor and understand reaction processes (an ideal capability for researchers studying chemical reactions).

Using **Pulsar**

Easy Operation

Pulsar uses standard 5mm NMR tubes, and has a highly efficient automatic shimming routine that optimises the shim in just a few minutes when needed.

For simple proton spectra **Pulsar** has **SoftLock**™ - an advanced software "lock" that guarantees absolute spectral stability without the complexity of an additional traditional lock channel. **SoftLock** is so effective that 2000 scans can be overlaid with no detectable line broadening from misalignment.

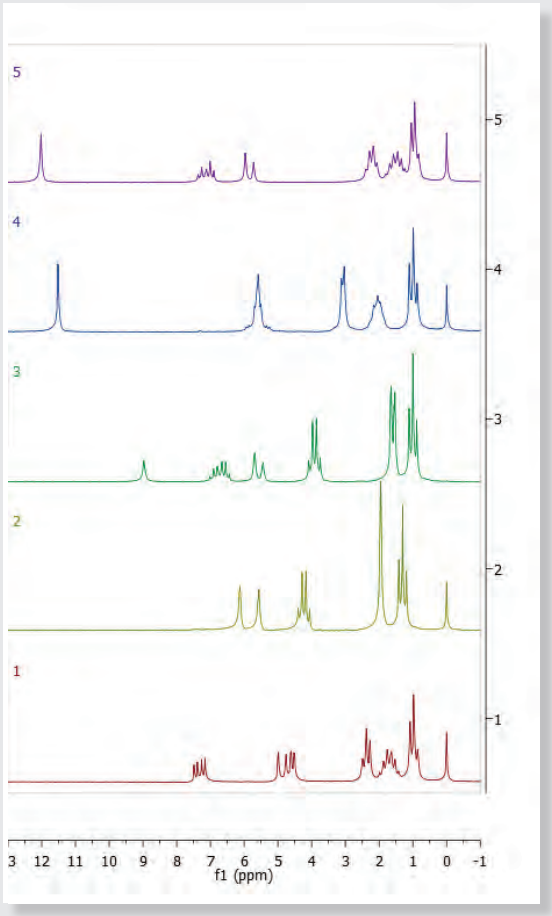


*Operation of **SoftLock** showing overlaid spectra.*

Routine Experiments

NMR spectroscopy is an invaluable analytical technique for chemical analysis. The information from an NMR spectrum complements the information obtained from other types of instrumentation. In many cases it offers unique information about the sample material.

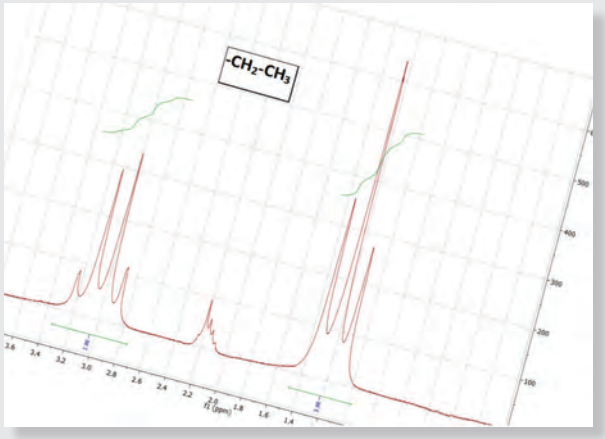
NMR is an excellent technique for the identification of materials and chemical groups. These example spectra (below) show materials with the same molecular formula, $C_6H_{10}O_2$, yet which are chemically different. The NMR spectra differ significantly even in the case of trans-2- and trans-3-hexenoic acids (a pair of structural isomers which consist of the same functional groups and chain lengths).



Spectra of different structural isomers.

The spectral data obtained on **Pulsar** shows clear separation of the multiplets commonly observed in NMR spectra. The example above shows the typical multiplets generated by hydrogen atoms in an ethyl (CH_3CH_2-) group in the molecule.

Integration of the peaks provides a method for determining the number of hydrogen atoms present in each chemical group. The distance between the peaks in these multiplets allows measurement of the coupling constants.

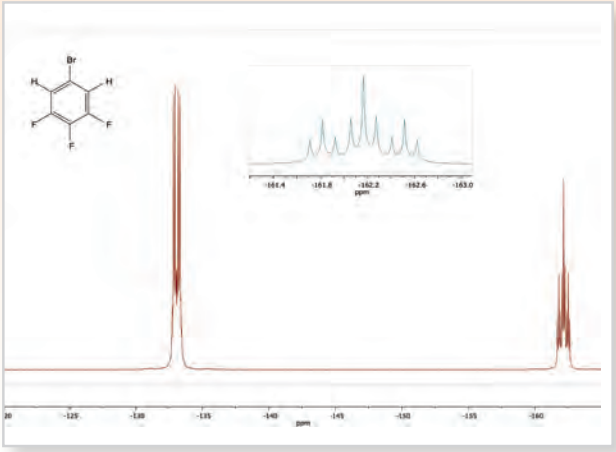


Spectrum showing peak splitting and integration of ethyl resonances.

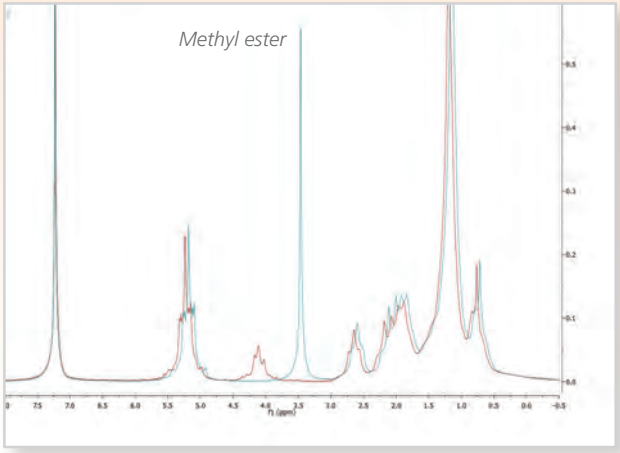
Additional Experiments

In addition to the routine acquisition of ^{1}H NMR spectra, **Pulsar** is capable of performing a variety of experiments. Every **Pulsar** is capable of collecting ^{19}F spectra as well as ^{1}H spectra using the same probe. An example ^{19}F spectrum of 5-bromo-1,2,3-trifluorobenzene is shown below.

Pulsar is also ideal for arrayed experiments. Sequential acquisition of data during a chemical reaction provides a method for monitoring changes in specific functional groups during the reaction. Visual comparison of the spectra at different times of the reaction is straightforward. An example shown (below) is the transesterification of a triglyceride.



19 F spectrum of 5-bromo-1,2,3 trifluorobenzene.

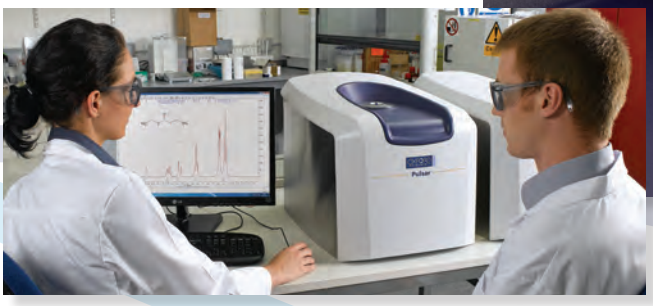


Overlaid spectra of starting material and final product.

NMR Simplified

Instrument performance

Pulsar is designed for a wide range of operators, ranging from novice users to experienced NMR spectroscopists.

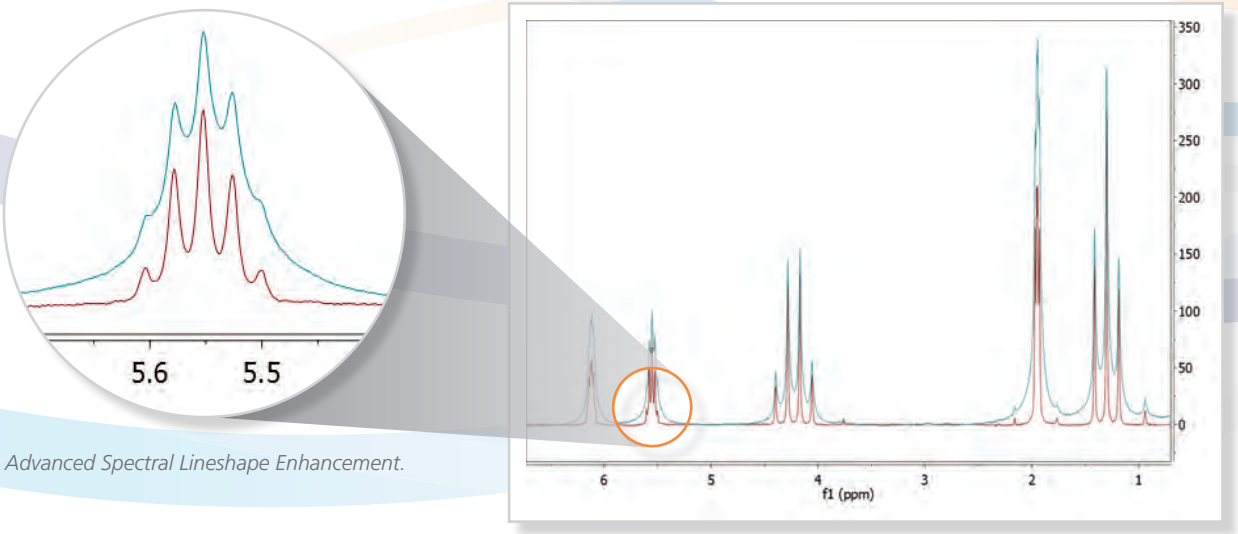


Easy access for sample insertion.

Pulsar utilises standard 5mm sample tubes requiring less than 1ml of sample. The excellent sensitivity of the instrument allows ^{1}H spectra from samples in the millimolar range to be obtained in a short time; a typical sample gives a good quality spectrum within a few seconds. For more demanding samples, multiple scans and signal averaging will yield a more accurate spectrum with less noise.

The resolution of an NMR instrument is dependent on the field homogeneity of its magnet. **Pulsar's** permanent magnet is extremely homogeneous and delivers excellent spectral resolution, leading to increased separation of closely spaced peaks.

For situations where even better resolution is required, the spectral lineshape enhancement routine can be used.



Advanced Spectral Lineshape Enhancement.

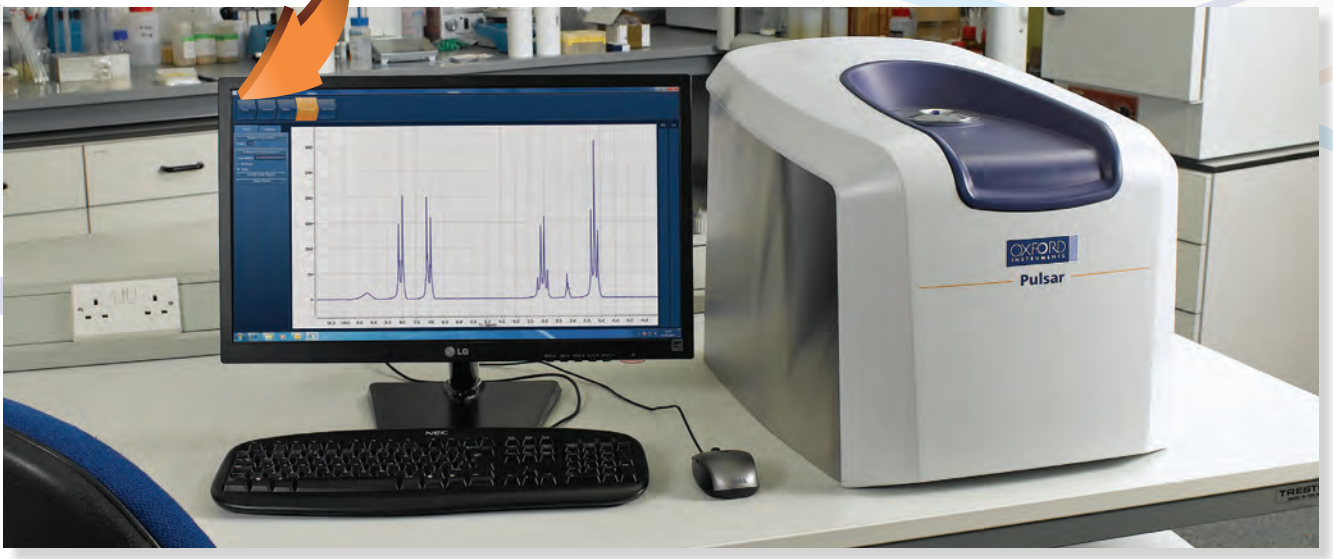
Class leading performance

Software functionality

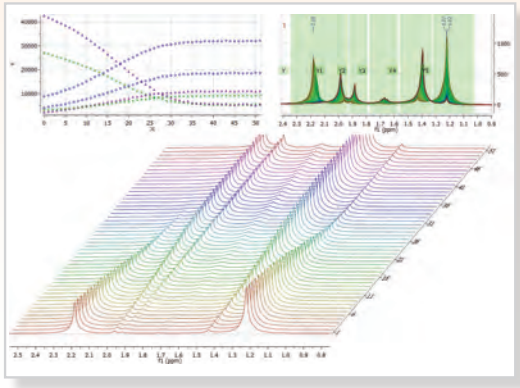
The **Pulsar SpinFlow** instrument control software provides an intuitive user interface. This allows non-expert operation and measurement of sample spectra, as well as catering for the advanced user who may wish to alter experimental parameters. Automated set up routines ensure that the instrument can be optimised for peak performance by all users regardless of their level of experience.

The process of running a sample can be as simple as selecting the experiment and clicking on the 'Acquire' button to collect the spectral data. A complete analysis is summarised by the workflow below.

Workflow approach enhancing productivity.



Once the data collection is complete, the spectrum is available for reporting or further data manipulation. **Pulsar** is packaged with a perpetual license for the powerful Mnova software from Mestrelab. This software has a full suite of routines for processing and analysing NMR data, and has a range of spectral display options including 2D and 3D stacking. This is particularly useful for reaction monitoring experiments.



Stack display allows analysis of time course experiments.

PULSAR

Providing a wide range of service giving total peace of mind

MQC

Oxford Instruments
Worldwide Support and Service

We take great pride in working in close partnership with our customers. Our goal is to provide comprehensive technical support throughout the product's life.

When choosing to work with Oxford Instruments you are safe in the knowledge that you have the backup and support of our skilled product champions and dedicated support engineers throughout the complete lifetime of your instrument. We offer a range of support packages that provide you with the level of service you require.

Our goal is to provide our customers with faultless service and swift expert maintenance on our products to ensure they perform to their highest capabilities.

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MQC benchtop NMR analysers for fast and easy measurement of fat, oil and moisture.

visit **www.oxford-instruments.com/pulsar** for more information or email: **industrial@oxinst.com**

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Delivering NMR to your benchtop

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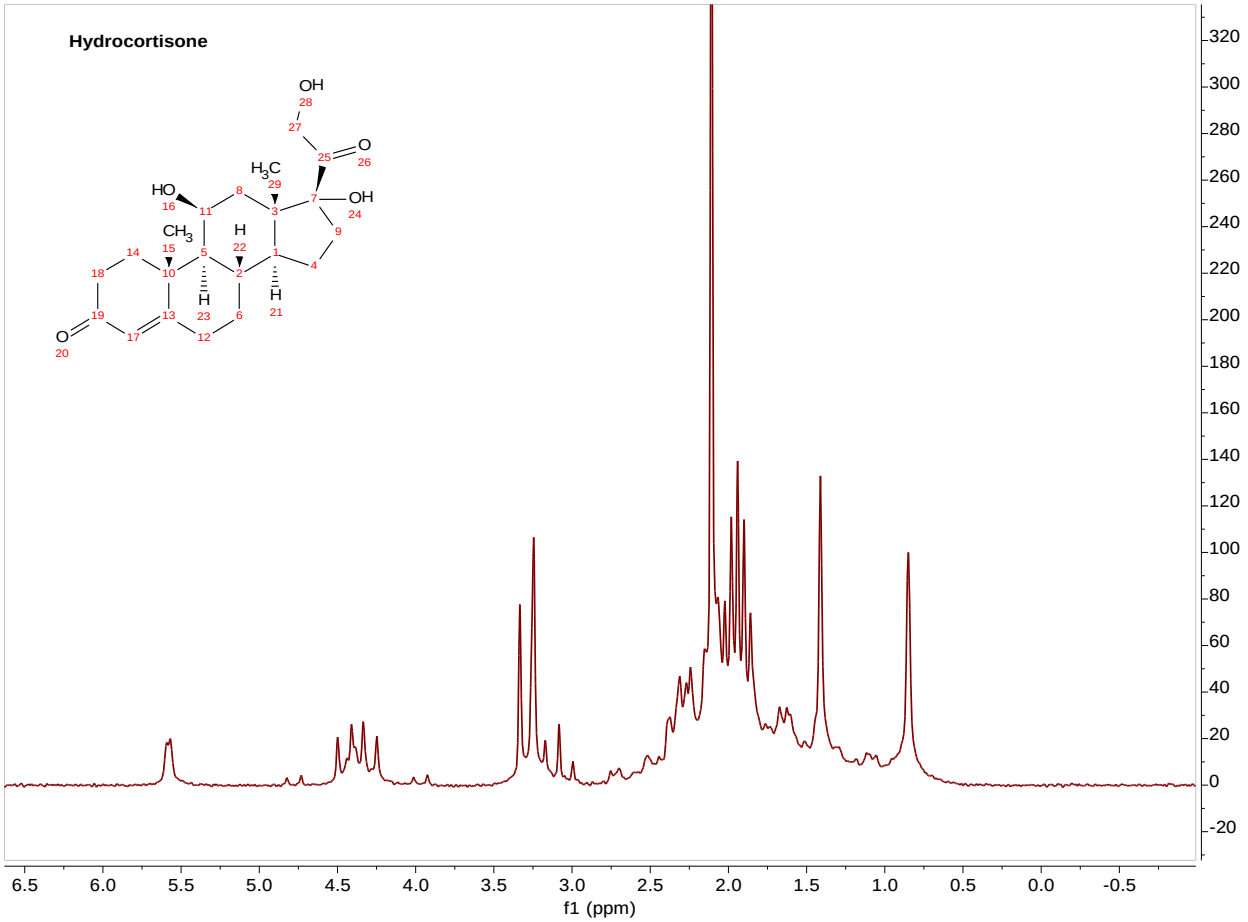

Fig.1: 60MHz ^{1}H-NMR spectrum of hydrocortisone in ACN.

Sample preparation:

- 10 mg of hydrocortisone was dissolved in 0.75mL ACN-d_3.

Measurement parameters:

- 5208 Hz filter;
- 32768 data points;
- Relaxation delay of 15.0s;
- Number of scans 256

Processing:

- Zero filling to 128K data points;
- Phase correction;
- Baseline correction by Whittaker Smoother method;
- Reference to the ACN peak at 1.94 ppm;
- Lorentz-to-Gauss apodization (Exponential -1.0Hz; Gaussian 1.0Hz);

Total measuring time ≈ 85min

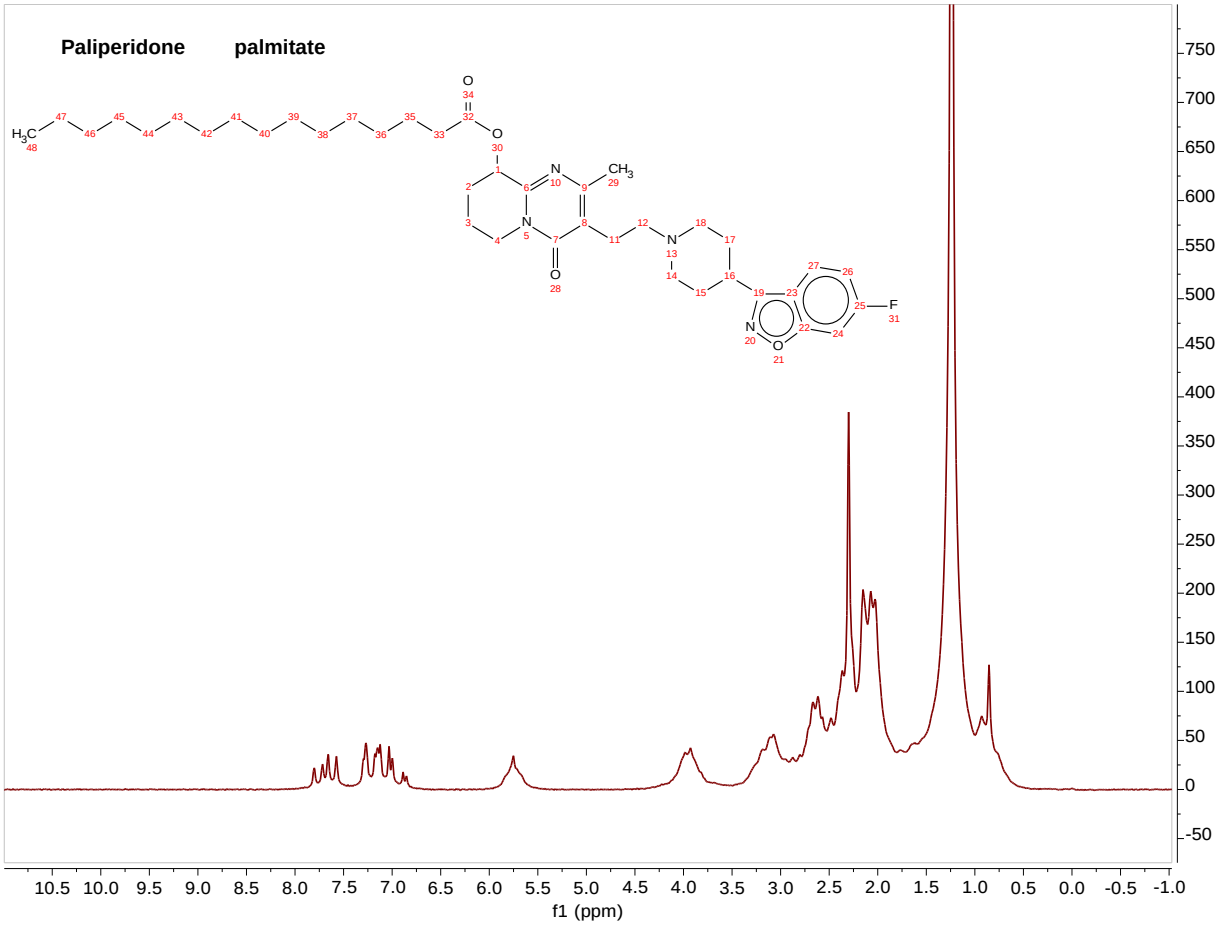

Fig.2: 60MHz ^{1}H-NMR spectrum of paliperidone palmitate in $CDCl_3$.

Sample preparation:

- 50 mg of paliperidone palmitate was dissolved in 0.5mL $CDCl_3$.

Measurement parameters:

- 5000 Hz filter;
- 32768 data points;
- Relaxation delay of 30.0s;
- Number of scans 16

Processing:

- Zero filling to 128K data points;
- Phase correction;
- Baseline correction by Whittaker Smoother method;
- Reference to the TSP peak at 0 ppm;
- Lorentz-to-Gauss apodization (Exponential -1.0Hz; Gaussian 1.0Hz);

Total measuring time ≈10min

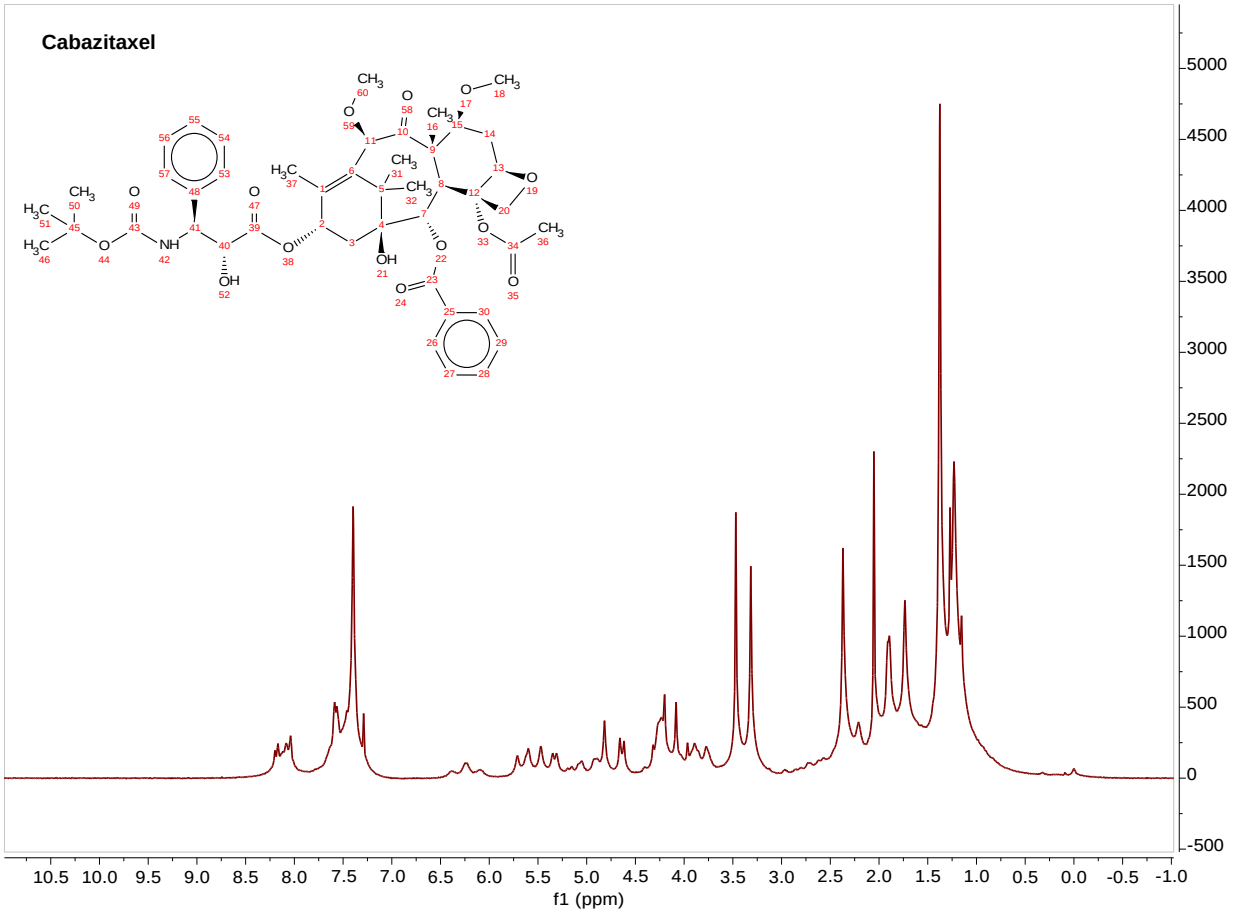

Fig.3: 60MHz ^{1}H-NMR spectrum of cabazitaxel in $CDCl_3$.

Sample preparation:

- 50 mg of cabazitaxel was dissolved in 0.5 mL $CDCl_3$.

Measurement parameters:

- 5000 Hz filter;
- 32768 data points;
- Relaxation delay of 30.0s;
- Number of scans 256

Processing:

- Zero filling to 128K data points;
- Phase correction;
- Baseline correction by Whittaker Smoother method;
- Reference to the TSP peak at 0 ppm;
- Lorentz-to-Gauss apodization (Exponential -1.0Hz; Gaussian 1.0Hz);

Total measuring time ≈150min

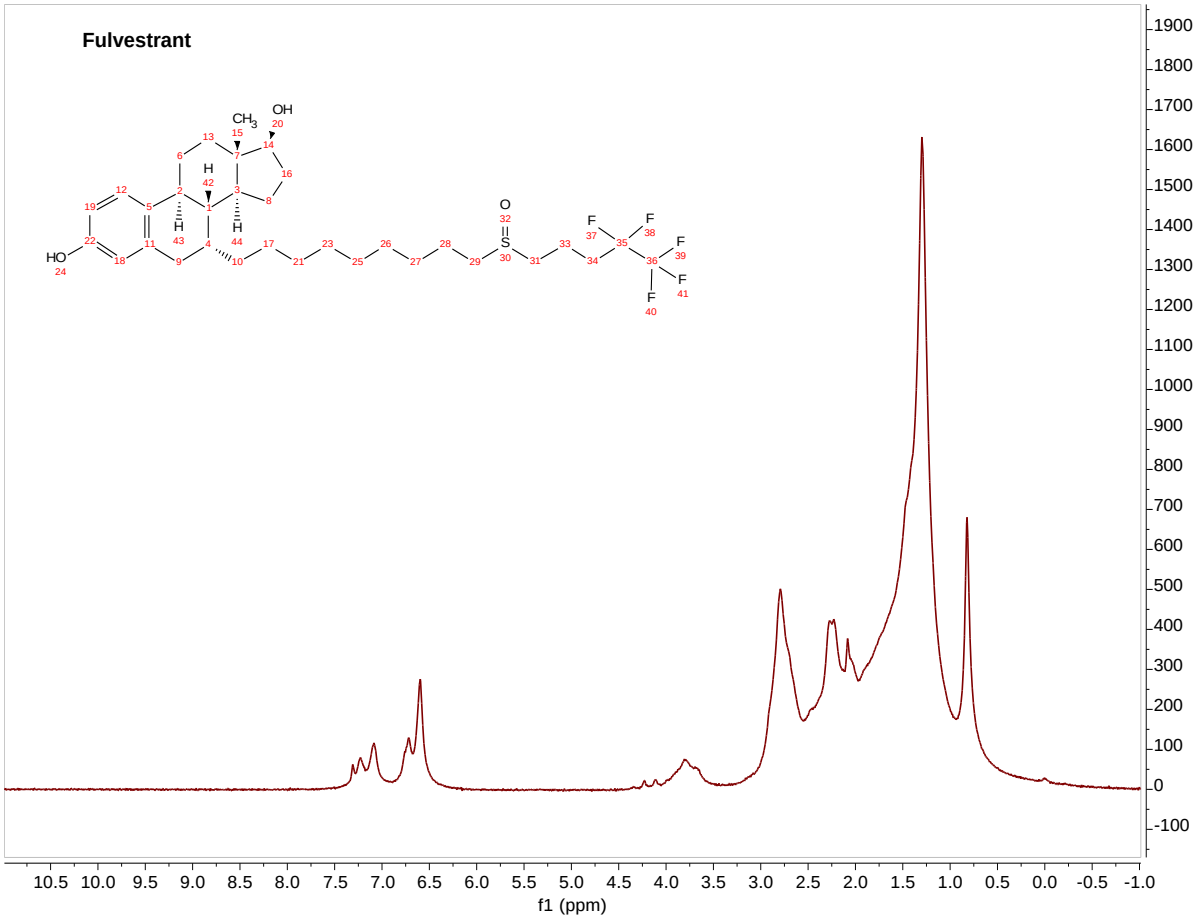

Fig.4: 60MHz ^{1}H-NMR spectrum of fulvestrant in $CDCl_3$.

Sample preparation:

- 35 mg of fulvestrant was dissolved in 0.5 mL $CDCl_3$.

Measurement parameters:

- 5000 Hz filter;
- 32768 data points;
- Relaxation delay of 30.0s;
- Number of scans 64

Processing:

- Zero filling to 128K data points;
- Phase correction;
- Baseline correction by Whittaker Smoother method;
- Reference to the TSP peak at 0 ppm;
- Lorentz-to-Gauss apodization (Exponential -1.0Hz; Gaussian 1.0Hz);

Total measuring time ≈38min

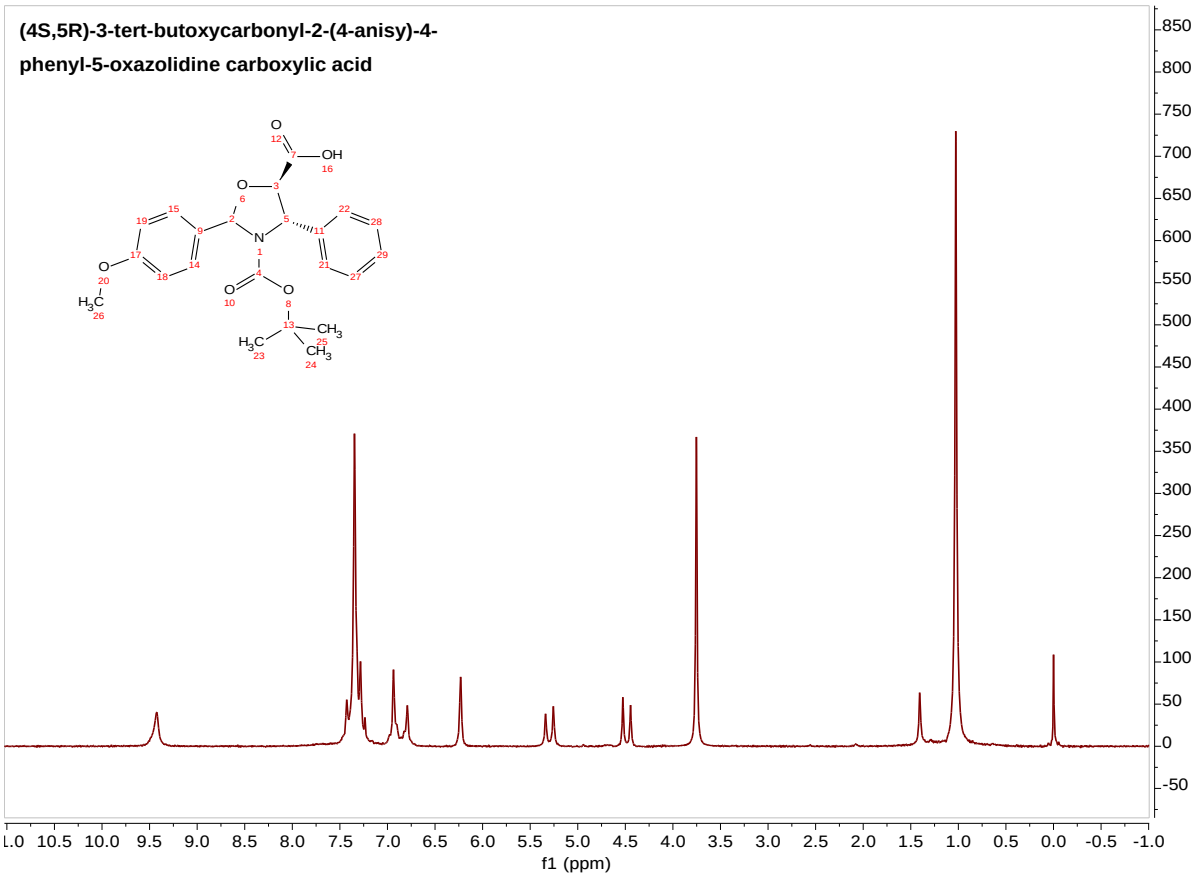

Fig.5: 60MHz ^{1}H-NMR spectrum of (4S, 5R)-3-tert-butoxycarbonyl-2-(4-anisy)-4-phenyl-5-oxazolidine carboxylic acid in $CDCl_3$.

Sample preparation:

- 160 mg of (4S, 5R)-3-tert-butoxycarbonyl-2-(4-anisy)-4-phenyl-5-oxazolidine carboxylic acid was dissolved in 0.5 mL of $CDCl_3$.

Measurement parameters:

- 5000 Hz filter;
- 32768 data points;
- Relaxation delay of 30.0s;
- Number of scans 16

Processing:

- Zero filling to 128K data points;
- Phase correction;
- Baseline correction by Whittaker Smoother method;
- Reference to the TSP peak at 0 ppm;
- Lorentz-to-Gauss apodization (Exponential -1.0Hz; Gaussian 1.0Hz);
- Reference deconvolution to 0.9 Hz.

Total measuring time ≈10min

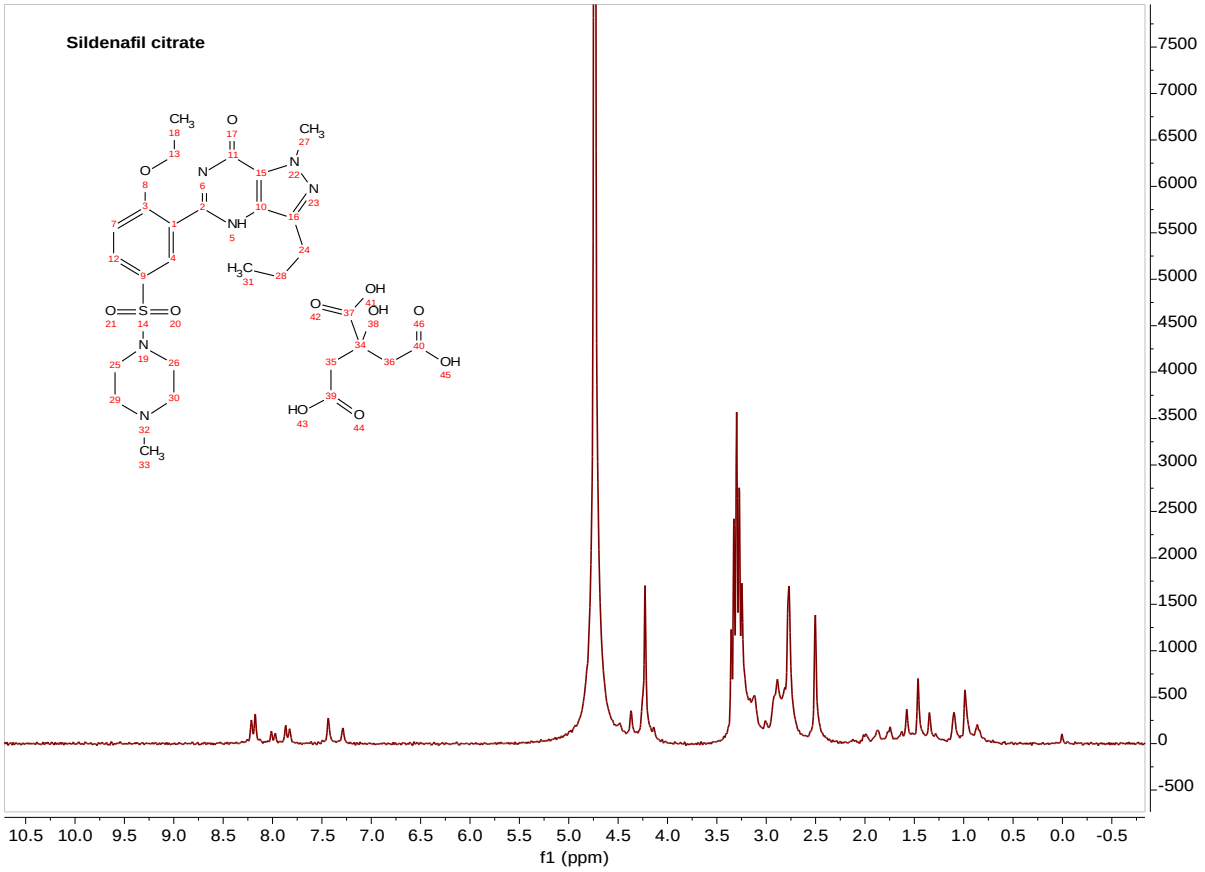

Fig.6: 60MHz ^{1}H-NMR spectrum of sildenafil citrate in methanol-d_4 (around 9 mM).

Sample preparation:

- 9.4 mM of sildenafil citrate solution in CD_3OD.

Measurement parameters:

- 5000 Hz filter;
- 16K data points;
- 30° RF pulse;
- Relaxation delay of 2.0s;
- Number of scans 512.

Processing:

- Zero filling to 128K data points;
- Phase correction;
- Baseline correction by Whittaker Smoother method;
- Reference to the TSP peak at 0 ppm;
- Lorentz-to-Gauss apodization (Exponential -1.0Hz; Gaussian 1.0Hz);

Total measuring time ≈45 min

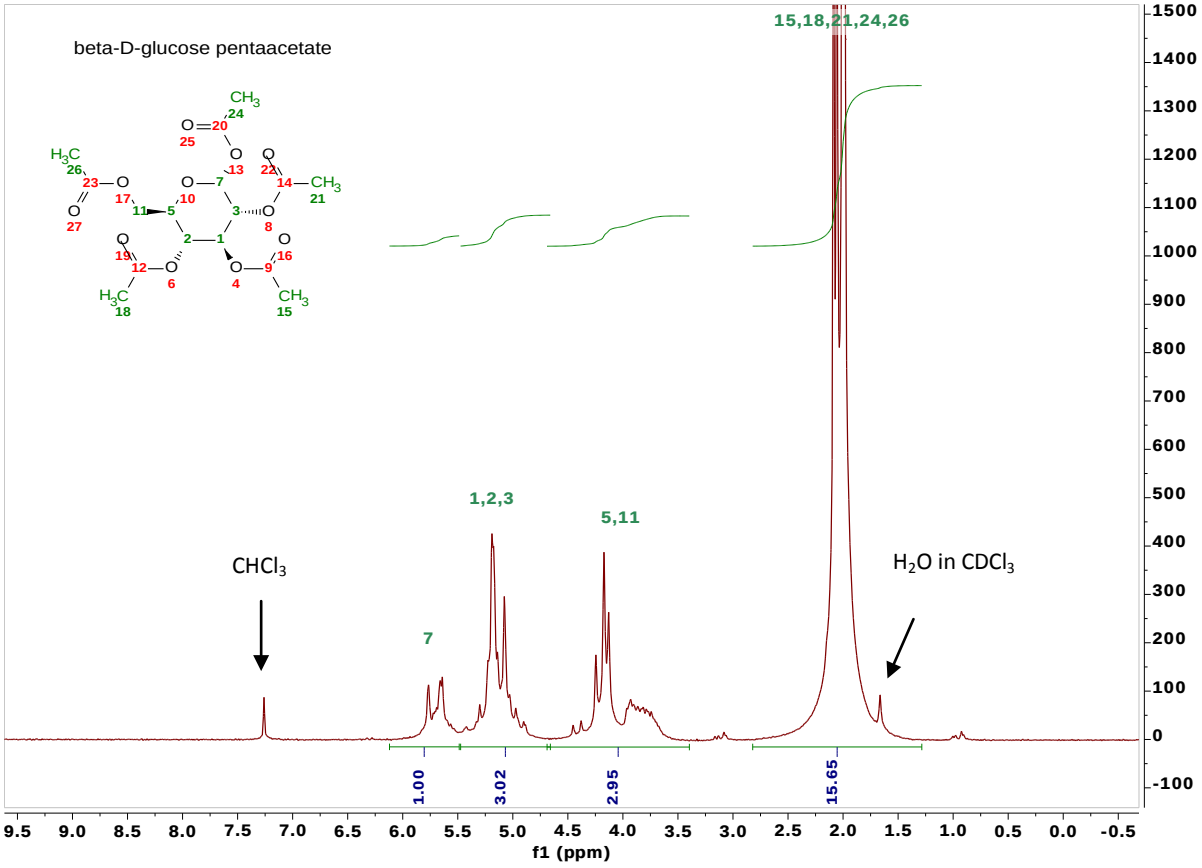

Fig.7: Assigned and integrated 60MHz ^{1}H-NMR spectrum of β-D-glucose pentaacetate.

Sample preparation:

- 78 mg of β-D-glucose pentaacetate was dissolved in 1.0mL of $CDCl_3$ (0.2M).

Measurement parameters:

- 5000 Hz filter;
- 32768 data points;
- Relaxation delay of 30.0s;
- Number of scans 64

Processing:

- Zero filling to 128K data points;
- Phase correction;
- Baseline correction by Whittaker Smoother method;
- Reference to $CHCl_3$ peak at 7.26 ppm;
- Lorentz-to-Gauss apodization (Exponential -0.7Hz; Gaussian 0.7Hz);
- Integration and assignment of all peaks.

Total measuring time ≈38 min

Oxford Instruments

Pulsar 60 Benchtop NMR Spectrometer

5mm 1H nonspin test results acetaminophen, dextromethorphan, d-lactose monohydrate, noscapine and phenacetin

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Introduction

The Oxford Instruments Pulsar HF 60 benchtop NMR spectrometer provides for convenient and reliable analysis of pharmaceutical compounds. In this report, Pulsar's ability to resolve individual proton peaks and integrate them with excellent accuracy and precision.

^{1}H NMR spectra of acetaminophen, dextromethorphan, D-lactose monohydrate, noscapine, and phenacetin were run on the 60 MHz Pulsar benchtop NMR spectrometer under data acquisition and processing conditions as described in this report.

Method

Sample Preparation

The samples were weighed, added to glass vials, and dissolved. Sample concentrations and solvents are shown in Table 1. The samples were transferred to NMR tubes using a glass Pasteur pipette. Where noted in the results, a chemical shift reference compound (TMS or DSS) was also added.

Sample	Solvent	Mass (mg)	Volume (µl)	Concentration (mM)
Acetaminophen	CD_3OD	20	500	265
Phenacetin	CD_3OD	26	500	290
D-lactose monohydrate	D_2O	41	500	227
Dextromethorphan	$CDCl_3$	47	700	247
Noscapine	$CDCl_3$	75	700	259

Table 1: Amounts and concentrations of samples analyzed.

NMR Measurement

All spectra were acquired on a 60MHz (1.45T) Oxford Instruments Pulsar benchtop NMR spectrometer. 1D, ^{1}H spectra were acquired using a pulse - acquire sequence, collecting 32768 data points over a 5208 Hz spectral window. Spectra acquisition time was about 5 seconds, and relaxation delay of 10s. Spectra were collected with 1 scan to demonstrate sensitivity without signal averaging, as well as 64 scans (about 16 minute measurement time) or 128 scans (about 32 minute measurement time) to demonstrate sensitivity improvement with measurement time.

Processing and Analysis

After acquiring a spectrum, the data was transferred to the MNova spectral processing package and the following processing steps applied:

1) Zero filling to 256K data points.
2) Data weighting using a 0.1 Hz exponential function.
3) Phase correction.
4) Baseline correction (3rd order polynomial fit).
5) The chemical shift was set according to the reference used (TMS and DSS at 0ppm, residual $CHCl_3$ at 7.24ppm).
6) Processing included peak integration and calculating signal-to-noise (sensitivity), where noise was measured over a range of 1ppm in a spectral region where no peaks were expected.

Results

Figure1 shows the spectrum of 265mM acetaminophen in methanol-d4. The phenyl ring protons are clearly resolved and the multiplet structure can be seen.

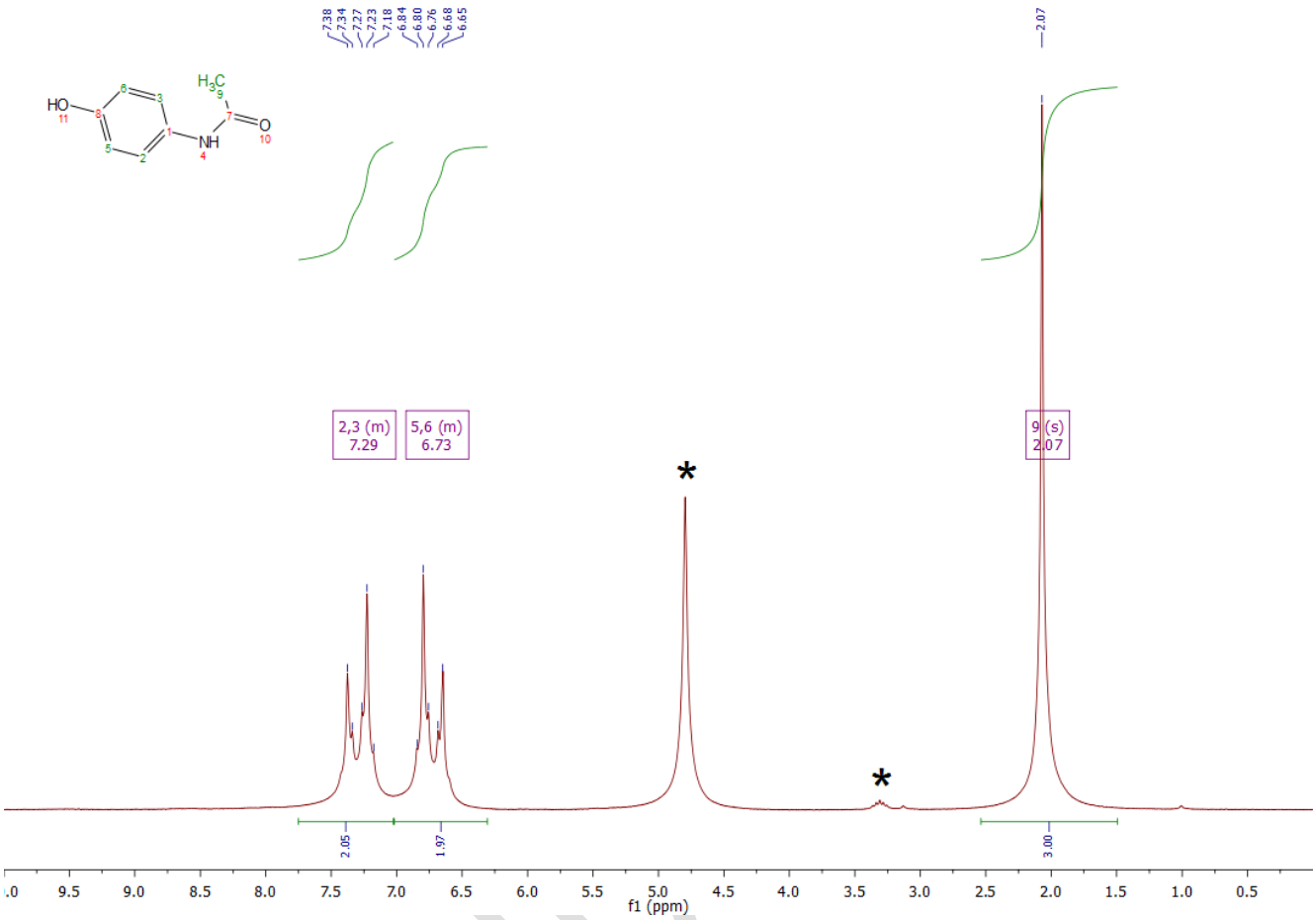

Figure 1: ^{1}H spectrum of 265 mM acetaminophen in methanol-d4 (99.8% D, Sigma-Aldrich). Residual solvent peaks are indicated by asterisks. Peak analysis and assignments are also shown, with atom numbering as indicated in the structure in the upper left-hand corner of the figure. The area of the acetaminophen methyl peak was standardized to 3.00. Chemical shifts were referenced to TMS at 0.00 ppm. The spectrum was acquired with 128 scans. The spectrum was zero-filled to 256k points; 3rd order polynomial baseline correction and a 0.1 Hz exponential function were applied.

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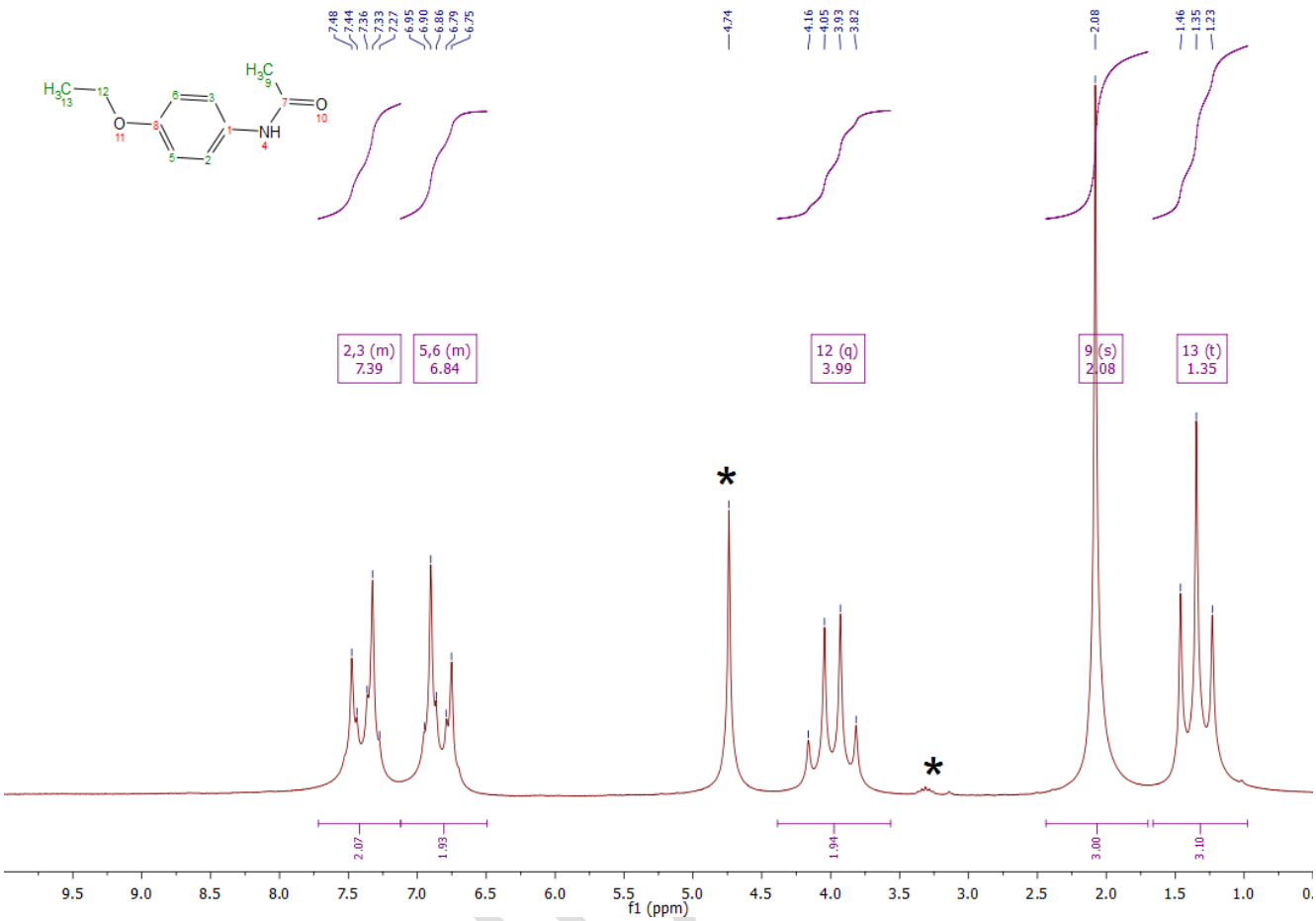

Figure 2: ^{1}H spectrum of 290 mM phenacetin in methanol-d4 (99.8% D, Sigma-Aldrich). Integrals of the sample peaks are shown; the methyl singlet at 2.08 ppm was normalized to an area of 3.00. Peak analysis and assignments are also shown, with atom numbering as indicated in the structure in the upper left-hand corner of the figure. Residual solvent peaks are indicated by asterisks. Chemical shifts were referenced to TMS at 0.00 ppm. The spectrum was zero-filled to 256k points; 3rd order polynomial baseline correction and a 0.1 Hz exponential function were applied.

The spectrum of phenacetin (Figure 2) shows similar resolution and signal-to-noise to that of the acetaminophen spectrum in Figure 1. The resolution of the methyl triplet at 1.35 ppm and methylene quartet at 3.99 ppm allows measurement of the J-coupling constants (6.94 Hz).

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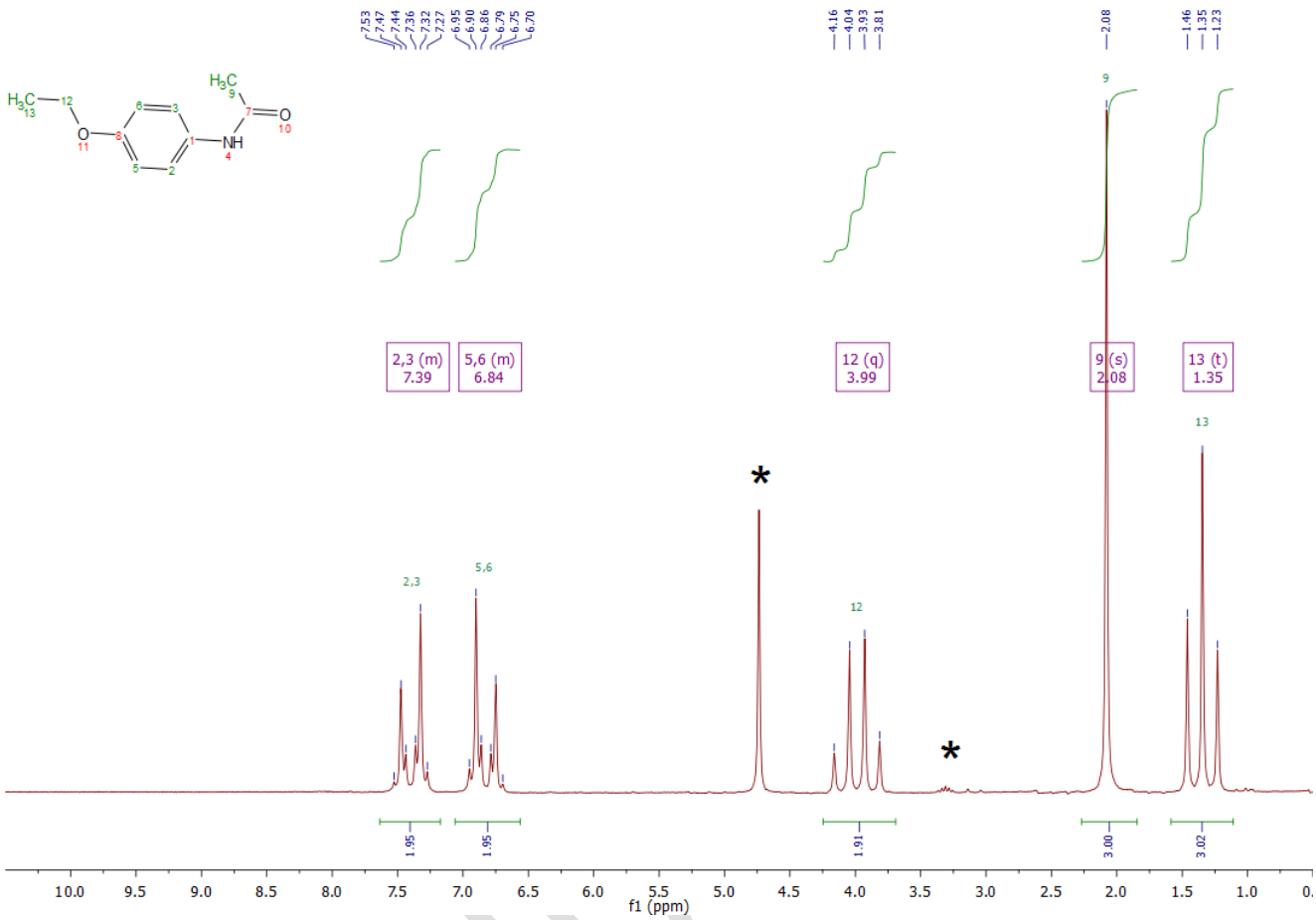

Figure 3: ^{1}H spectrum of 290 mM phenacetin in methanol-d4 as in Figure 2, after the application of reference deconvolution with a target linewidth of 0.50 Hz. Integrals of the sample peaks are shown; the methyl peak at 2.08 ppm was normalized to an area of 3.00. Identical processing parameters were used as in Figure 2, except no exponential function was applied. Asterisks indicate residual solvent peaks.

Taken together, Figures 2 and 3 demonstrate the benefits of using the reference deconvolution algorithm in processing. Figure 2 shows similar resolution to the spectrum of acetaminophen shown in Figure 1. In Figure 3, after application of the algorithm, resolution is greatly enhanced with minimal loss in signal-to-noise ratio. The conservation of peak areas coupled with the enhanced separation allows for easier integration. Increased resolution is easily seen in the separation of the methyl triplet at 1.35 ppm and the methylene quartet at 3.99 ppm, as well as the phenyl ring multiplets between 6.5 ppm and 7.5 ppm

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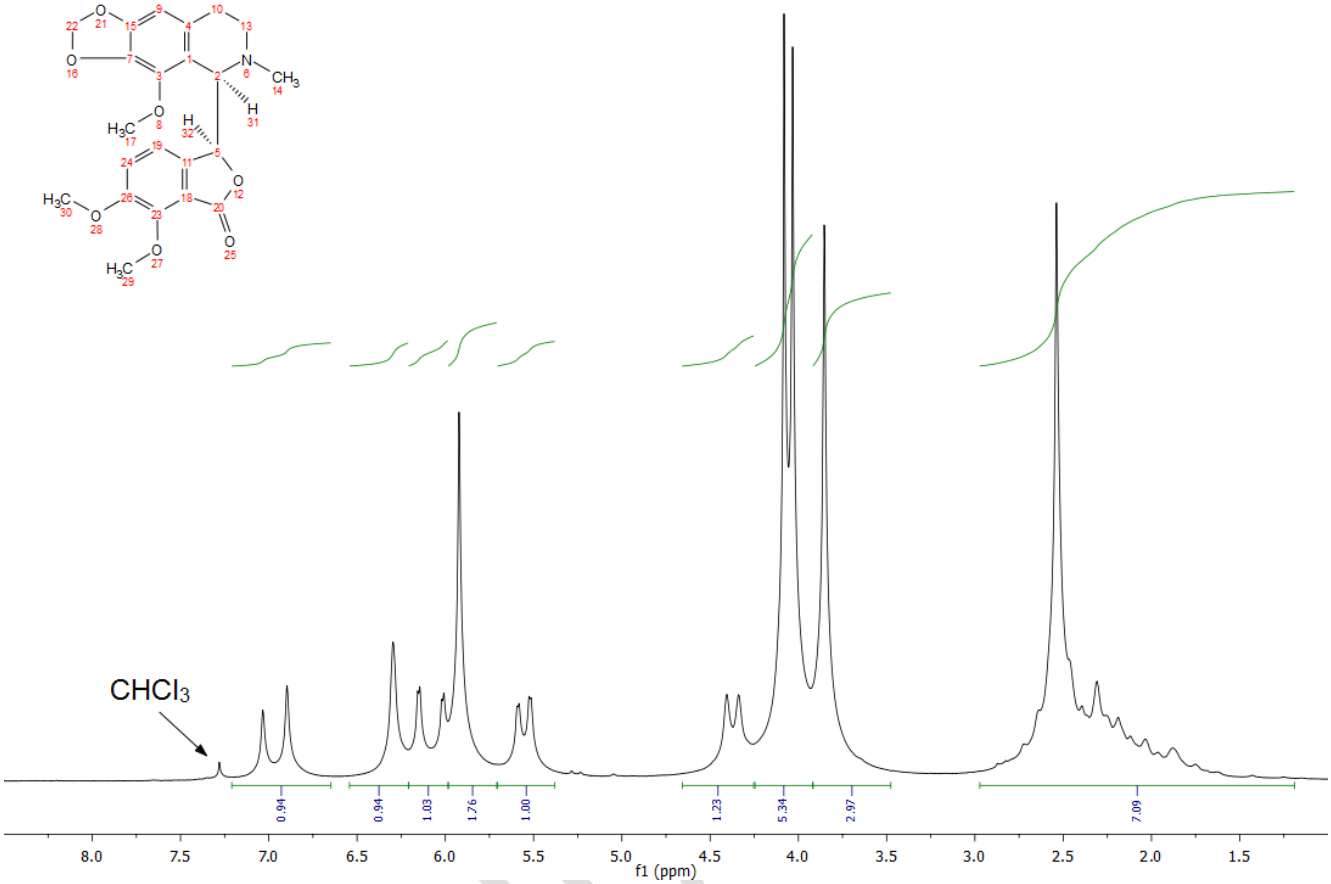

Figure 4: ^{1}H spectrum of 259 mM noscapine in $CDCl_3$ (99.8% D, Sigma-Aldrich). Integrals of the sample peaks are shown; the doublet at approximately 5.5 ppm was normalized to an area of 1.00. Chemical shifts were referenced to TMS at 0 ppm. 128 scans were acquired. The spectrum was zero-filled to 256k points; 3rd order polynomial baseline correction and a 0.1 Hz exponential function were applied.

Figure 4 shows the spectrum of Noscapine with integrals. Peaks due to individual protons are clearly resolved in the aromatic region of the spectrum. The values of the integrals of both the individual peaks and the upfield aliphatic region show excellent agreement with expected values.

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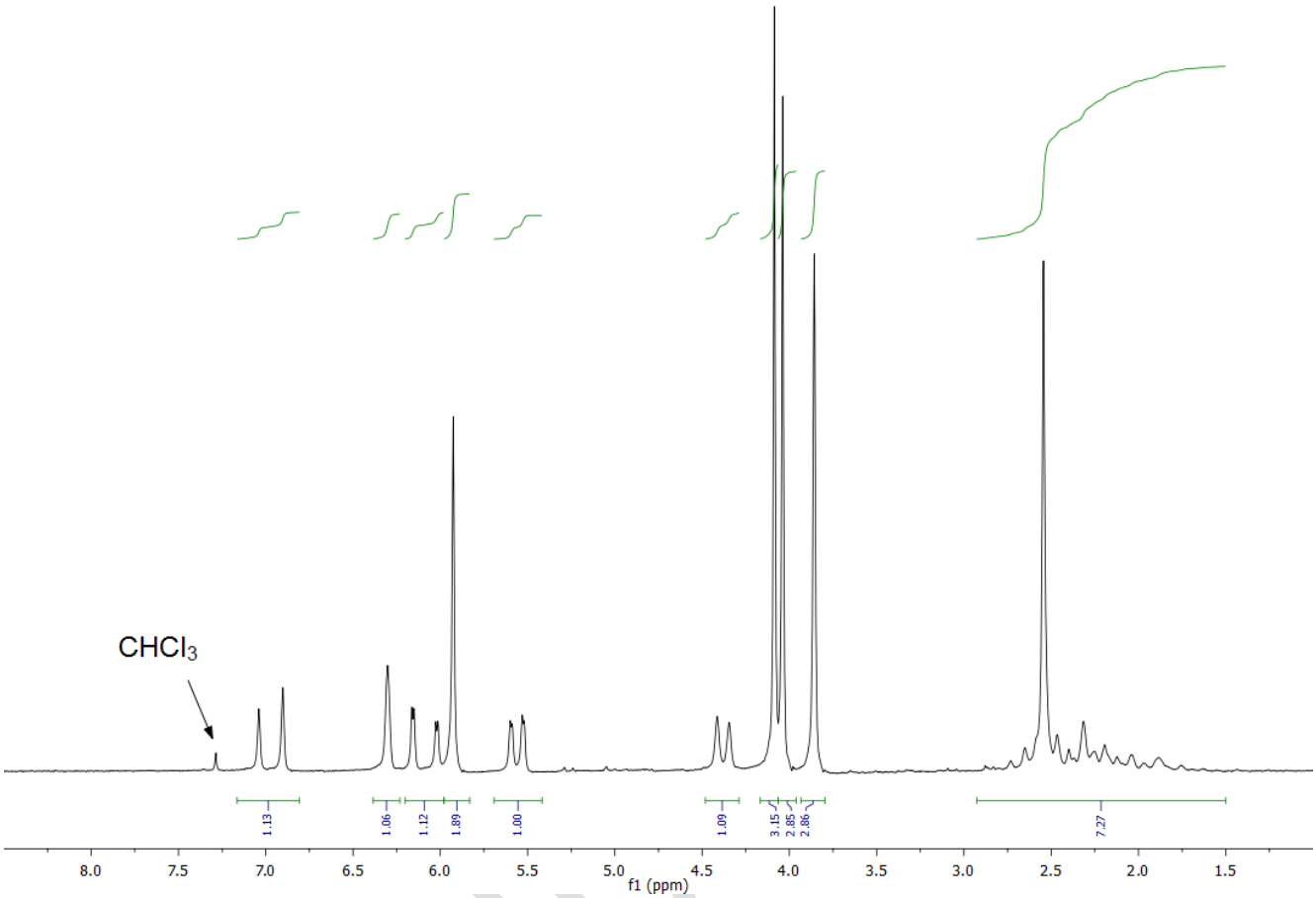

Figure 5: ^{1}H spectrum of 259 mM noscapine in $CDCl_3$ shown in Figure 4 acquired with 64 scans, after the application of reference deconvolution with a target linewidth of 0.50 Hz, using TMS as a reference. Integrals of the sample peaks are shown; the methyl peak at 2.08 ppm was normalized to an area of 3.00. The processing parameters were identical to those used in Figure 2, except no exponential function was applied.

Figure 5 shows the spectrum of noscapine after the application of reference deconvolution, again emphasizing the enhanced resolution possible using this technique. Evaluation of the integrals of the methyl peaks at 4.04 and 4.08 ppm (areas of 3.15 and 2.85 respectively) after reference deconvolution demonstrates the ability to resolve peaks from protons that have similar chemical shifts. Even with minimal processing, as in Figure 4, the spectrum shows good resolution of the aromatic and methyl peaks.

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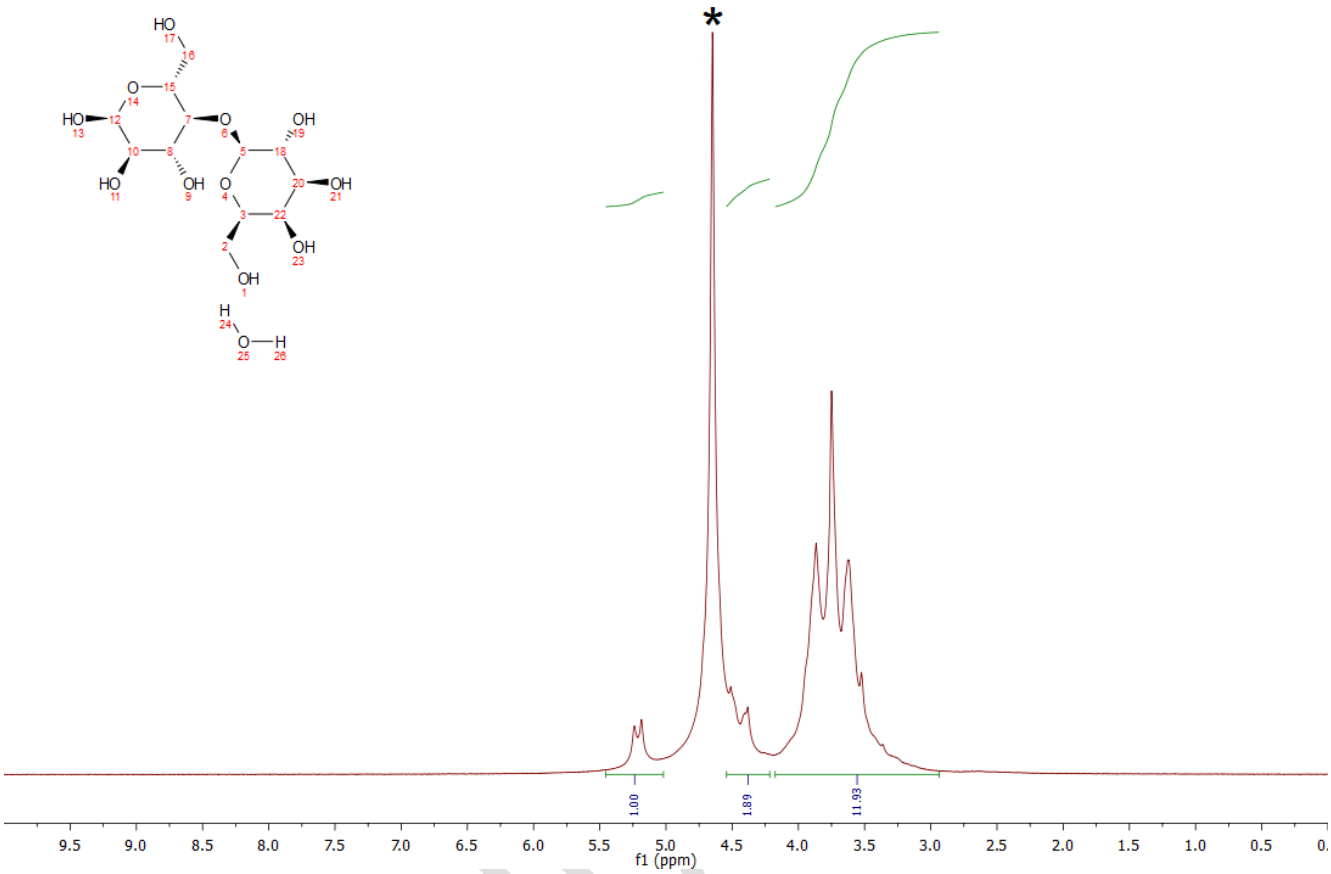

Figure 6: ^{1}H NMR spectrum of D-lactose monohydrate in D_2O. 128 scans were taken for signal averaging. Integrals of spectral regions are shown; the area of the peak at 5.20ppm from the glucose anomeric proton (attached to the carbon labelled as 12 in the inset structure) was normalized to 1. The residual H_2O peak is indicated by an asterisk. Chemical shifts were referenced to DSS at 0 ppm. The spectrum was zero-filled to 256k points; 3rd order polynomial baseline correction and a 0.1 Hz exponential function were applied.

The spectrum of D-lactose monohydrate shows good resolution of the anomeric proton at 5.21 ppm from the water resonance. The sugar backbone region also shows accurate integration, with a ratio of 11.93 to 1 to that of the anomeric proton, compared to an expected ratio of 12:1.

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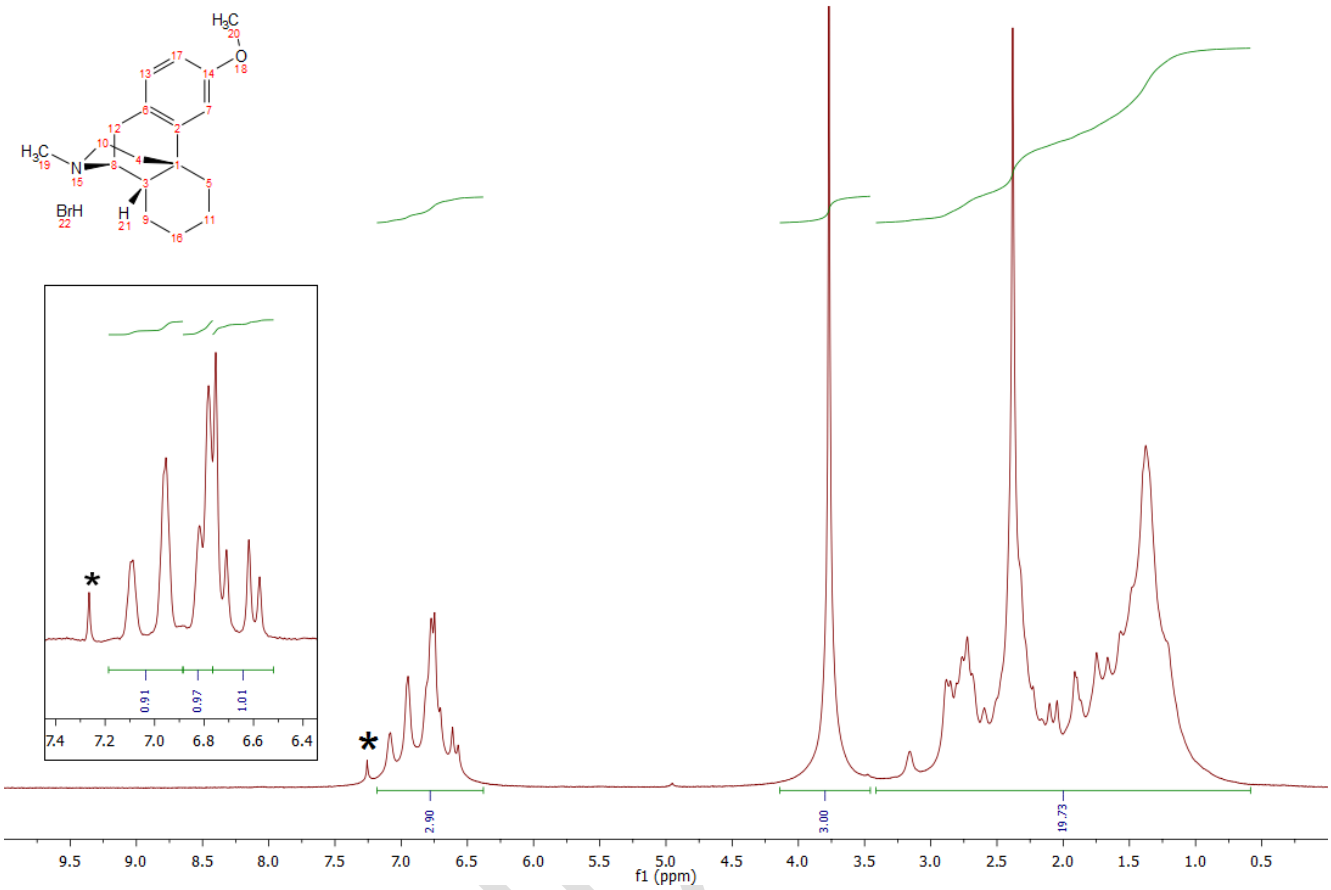

Figure 7: ^{1}H NMR spectrum of 247 mM dextromethorphan in $CDCl_3$ (99.8% D, Sigma-Aldrich). Integrals of the sample regions are shown; the methyl peak at 3.76 ppm was normalized to an area of 3.00. Chemical shifts were referenced to TMS at 0 ppm. The spectrum was zero-filled to 256k points; 3rd order polynomial baseline correction and a 0.1 Hz exponential function were applied. Asterisks indicate the residual $CHCl_3$ solvent peak. The inset spectrum shows an expansion of the aromatic region, after the application of the reference deconvolution algorithm (target linewidth 0.5 Hz), demonstrating resolution of the contributions of individual protons on the aromatic ring.

The spectrum of dextromethorphan (Figure 7) demonstrates good resolution of the aromatic protons, which can be further enhanced by the application of reference deconvolution (see inset). Integration of the various regions shows good accuracy, with a total proton count of 25.63, compared to an expected value of 26.

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Sample	Concentration (mM)	Peak Measured	S/N Ratio (RMS) 1 Scan, 0.1 Hz Exponential	S/N Ratio (RMS) 128 Scans, 0.1 Hz Exponential
Acetaminophen	265	2.07ppm	183.1	2101
Phenacetin	290	2.07ppm	240.4	2623
D-lactose monohydrate	227	3.74ppm	139.8	1350
Dextromethorphan	247	3.76ppm	219.6	2460
Noscapine	259	4.09ppm	268.1	2803

Table 2: Signal to noise ratios of the samples analyzed. The Signal-to-Noise ratios were analyzed on the tallest peak in the spectrum, except in the case of D-lactose monohydrate in D2O, where the tallest peak was that of the residual water. For D-lactose monohydrate, the second-tallest peak, at 3.74ppm, was chosen. Spectra were processed with a 0.1 Hz exponential function, and noise was measured over a 1ppm region in which no signal was expected.

As requested, signal-to-noise ratios were measured. For each sample, the tallest peak in the spectrum was used to determine the signal level, except in the case of D-lactose monohydrate. Because the tallest peak in the D-lactose monohydrate spectrum was largely due to residual water in the solvent, the result would be dependent on the characteristics of the CD_3OD used, and not on the sample itself. As a result, the second-tallest peak (at 3.74ppm) was chosen instead. In addition to the measurements on the spectra shown in the figures, signal-to-noise ratios were measured on single-scan spectra to demonstrate results that can be obtained with these samples on the Pulsar in just a few seconds.

Homonuclear 2D NMR at 60 MHz

An NMR spectrum is produced by performing a discrete Fourier Transform (DFT) on a series of time domain data points measured with a particular gap between each point. It does not matter to the DFT whether the points have been collected in "real time" or if the series of points has been indirectly constructed. This fact is the basis for two dimensional (2D) NMR experiments where one dimension is collected in the usual direct manner and a second dimension is constructed in a stepwise manner.

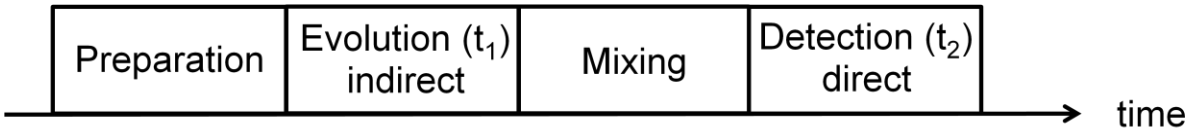

Figure 1: schematic representation of a 2D NMR experiment

The blocks associated with a 2D NMR experiment are shown in figure 1. In the first step the nuclei are exited with RF pulses to generate a non-equilibrium state. This state is allowed to evolve for a time t_1 in step two, before being subjected to further RF manipulation in step three and finally an NMR signal is recorded. This process is repeated N times with the value of t_1 being incremented each step such that the final data is an array of N-nmr signals differing only through the effect of the evolution in step 2. This array can be Fourier transformed with respected to the time t_2 and t_1 to produce a 2D spectrum.

COSY

Correlation Spectroscopy, or COSY as it is commonly referred to, is an NMR experiment that correlates the chemical shifts of spins that share a mutual J-coupling. The J-coupling is the interaction between nuclei that is transmitted through chemical bonds. In general this coupling gets weaker as two nuclear are separated by increasing numbers of bonds and as a result the ^{1}H COSY spectrum correlates hydrogen nuclei on adjacent carbons or, in the case of multiple bond carbons next nearest carbons. The method is most commonly used to determine the underlying structure of the carbon back bone in an organic molecule.

The COSY experiment is demonstrated using ethyl crotonate.

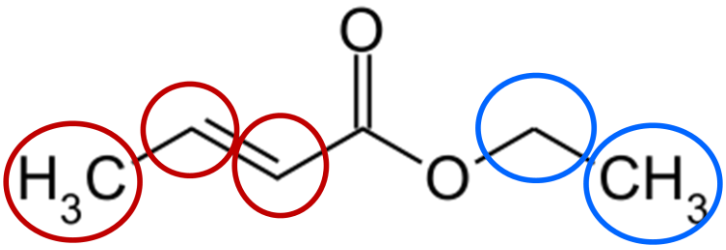

Figure 2: Molecular structure of ethyl crotonate showing groups that share mutual J-coupling. The blue circles are the ethyl group and the red circles are the crotonate group, the peaks related to these groups are highlighted in figure 4.

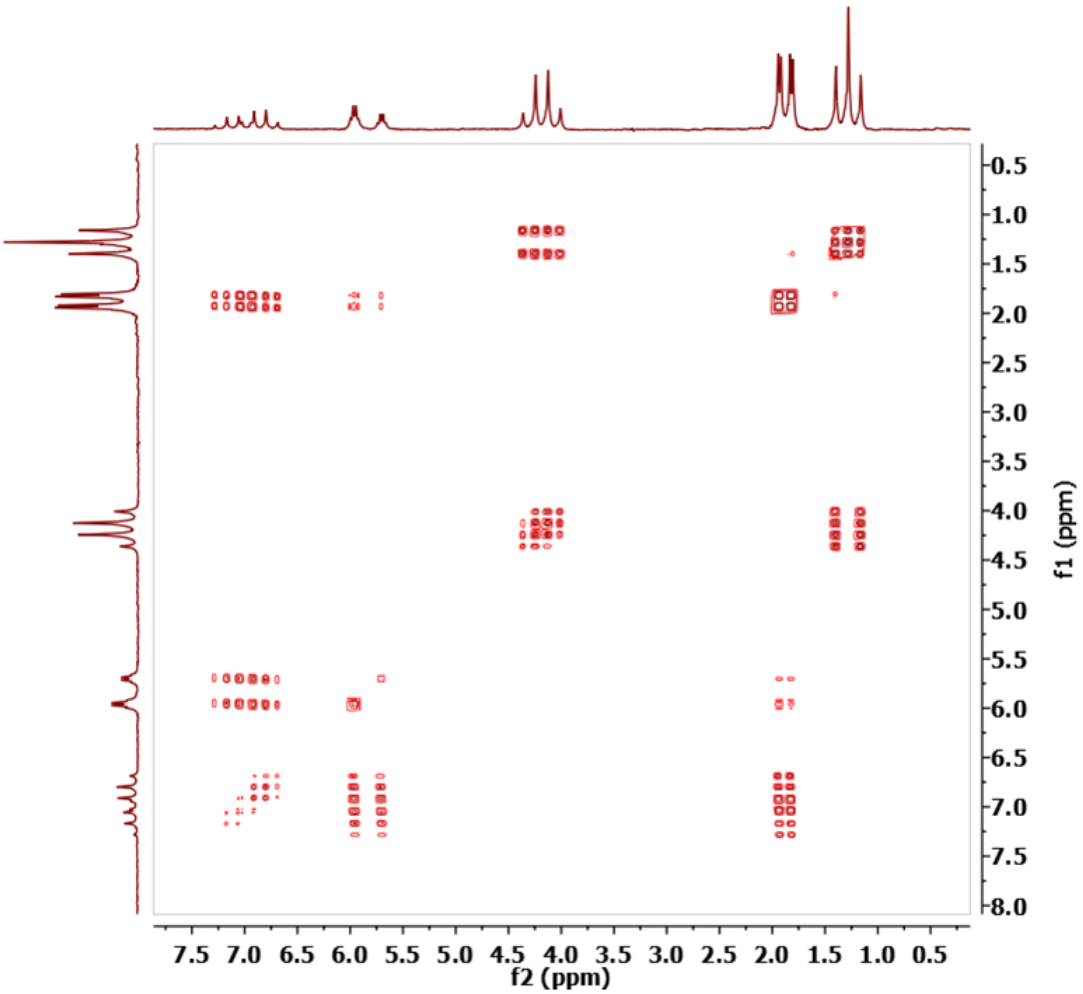

Figure 3: Full COSY spectrum for ethyl crotonate. All peaks in the 1D spectrum show a diagonal peak in the COSY and the cross peaks (off diagonal peaks) show coupling between the particular chemicals shifts,

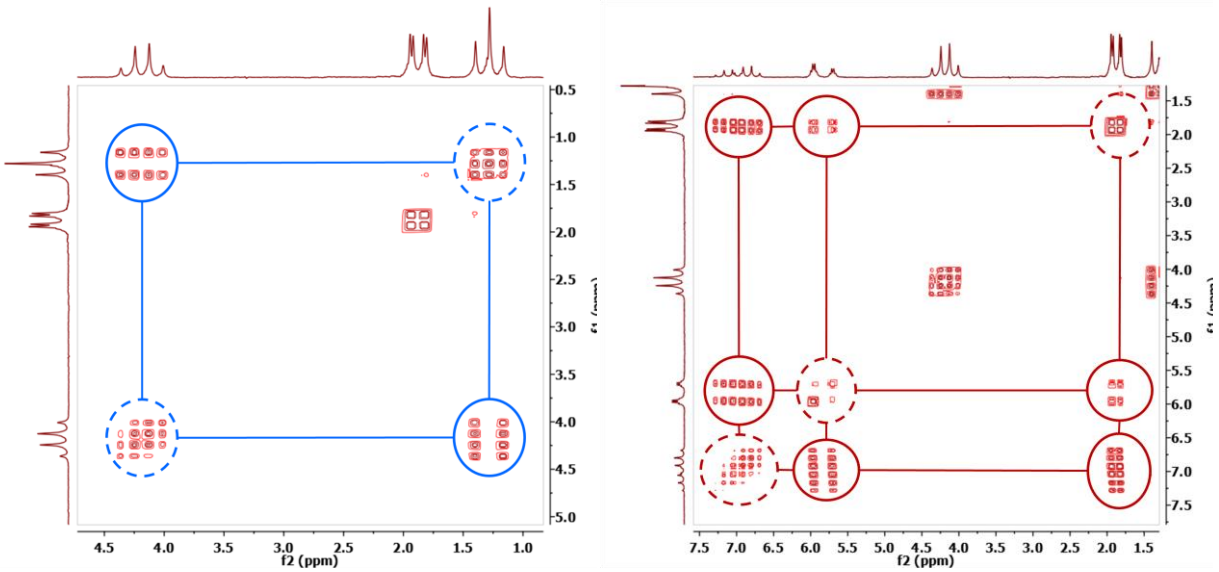

Figure 4: Expanded regions of the COSY spectrum showing the ethyl region of the spectrum (left) and the crotonate region (right). The diagonal peaks are highlighted as dashed circles and the cross peaks are highlighted with full circles.

A COSY spectrum should be symmetrical about a diagonal running from the top right to bottom left (figure 2). All signals that appear in the 1D spectrum will show a peak along this diagonal. The cross-peaks (off diagonal peaks) show which hydrogens share a J-coupling through the correlation between the two chemical shifts. In figure 4 the correlation between the $-CH_3$ and $-CH_2-$ ^1H chemical shifts of in the ethyl group are shown in the right hand plot. The left hand plot shows the correlation network between the two olefinic –CH= and the terminal $–CH_3$ of the crotonate group. In this fragment all the hydrogens are coupled and thus cross peaks are seen between all three chemical shifts.

J-Resolved

The J-resolved experiment is designed to separate the chemical shift from the J-coupling. Unlike the COSY experiments where both dimensions are chemical shift, in the J-resolved experiment the direct observe dimension is chemical shift but the indirect dimension displays the J-coupling.

This experiment is useful for accurately measuring chemical shift in a crowded spectrum with overlapping mulitplets or accurate measurement of coupling constants. The experiment is demonstrated using ethyl crotonate.

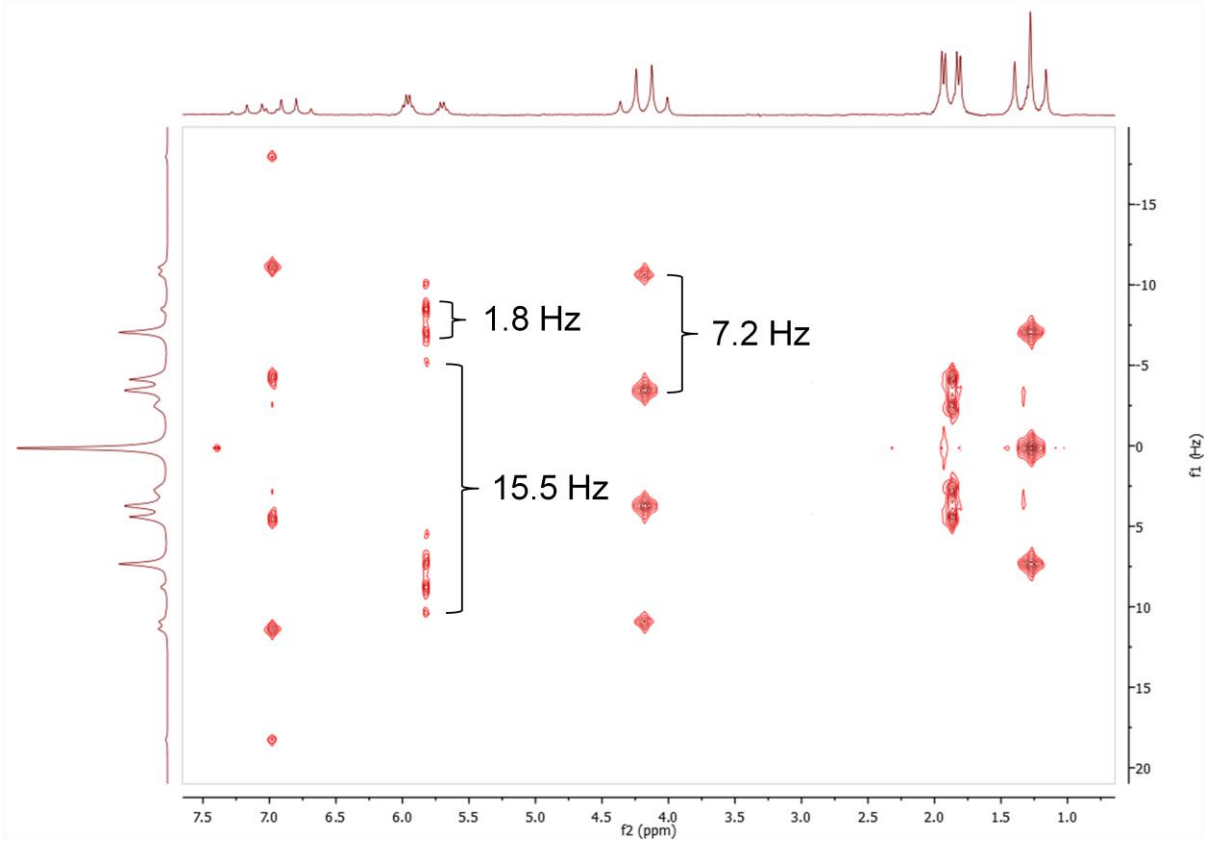

Figure 5: Full J-resolved spectrum of ethyl crotonate. The horizontal axis shows the chemical shift information and the vertical axis shows the J-coupling. Some examples of couplings are highlighted

The J-resolved spectrum in figure 5 shows all the multiplet resonances of the 1D ^1H spectrum of ethyl crotonate resolved in the J-coupling dimension. The splitting patterns are clearly identifiable and the relative coupling constants can be measured.