# NMR Applications Biological Science



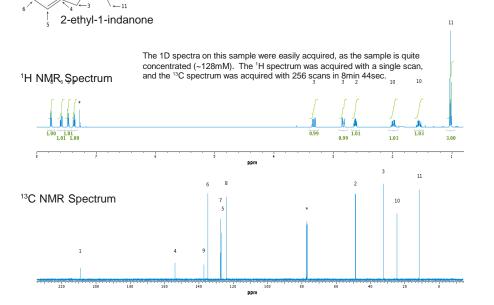
http://nmr.vuw.ac.nz





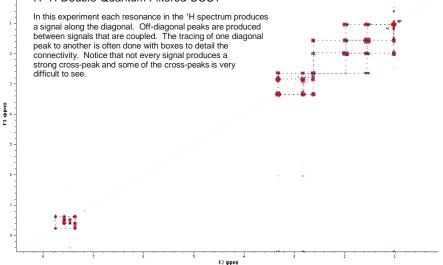
#### **Chemical structure analyses**

A sample of 2% 2-ethyl-1-indanone in CDCI was used to acquire all these examples.



#### <sup>1</sup>H-<sup>1</sup>H Double-Quantum Filtered COSY

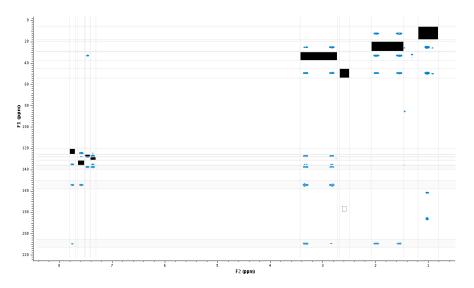
77



	<sup>1</sup> H- <sup>13</sup> C Gradient HSQC				•	•	
١.						÷	÷
			÷				1
1			÷		÷		÷
							1.1
				•	1	1	1
Í.							1
		:	1	1	1	1	1.1
		:	1	1	1	1	1.1
							1.1
	In this experiment each nearest neighbor <sup>1</sup> H- <sup>13</sup> C pair produces a	1	1	1	1	1	1
-							
	signal, and the shift for each may be read as the coordinate of the	1	1	1	1	1	1
			÷	1	÷	÷	
	signal. This gHSQC was run with a multiplicity filter that makes	1	1	1	1	1	1
	the methylene peaks negative, which is why they are red in this		÷	1	÷	÷	
	the methylene peaks negative, which is why they are red in this contour plot.	1	1	1	1	1	1
	•		÷		÷	÷	
				1		1	1
		1	÷.,	1	÷	÷	÷
				1		1	1
			1		1.1	1	
				1		1	1
1	e e e e e e e e e e e e e e e e e e e	1	1.1	1	1.1	1	1
-	· · · · · · · · · · · · · · · · · · ·			1			1
	· · · · · · · · · · · · · · · · · · ·	1	1.1		1.1	1	1
				1	1		1

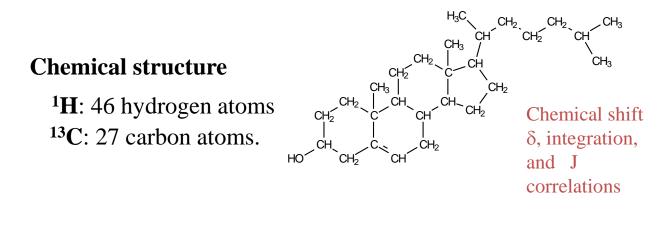
#### <sup>1</sup>H-<sup>13</sup>C Gradient HMBC

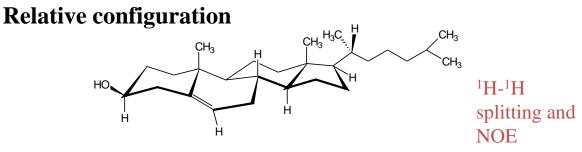
In this experiment signals are produced by <sup>13</sup>C atoms coupled to <sup>1</sup>H that are not directly attached. Typically, the experiment is set up to show couplings between next nearest neighbors (<sup>2</sup>J couplings). The spectrum is deciphered below with intersecting boxes, the black fields have no signal as they would are where a nearest neighbor (1J) coupling would exist. Notice that the quaternary carbons, which produced no signal in the HSQC above, do show up here and are highlighted in gray.



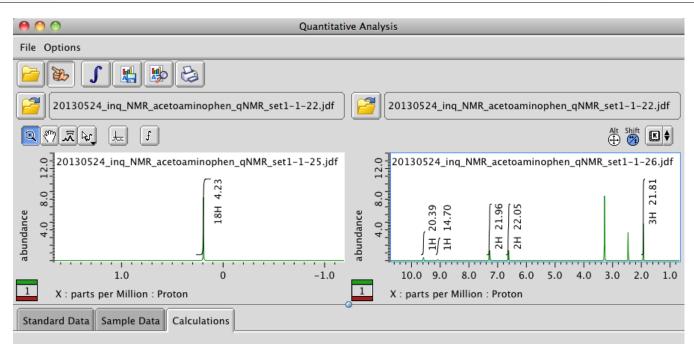
### **Stereo Chemistry**

Because NOE can reveal 1H spins that are in proximity in 3D space, it is often used to assist research on the stereochemistry of organic compounds





## **Quantitative Analyses - qNMR**



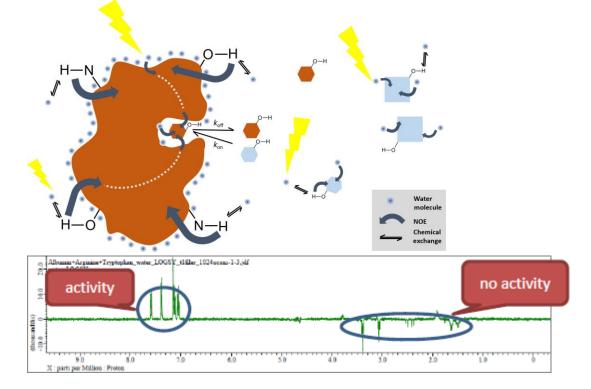
Molarity : C' = C \* I'/I \* H/H' \* T'/T \* d'/d Purity : P' = C' \* M' / (100 \* V')

No	. Po	sition	Group	Integral(I')	Protons(H')	Molarity(C')	Purity(P')	Avg. Calc.		
	1 1.93	2[ppm]		37.07[abn]	3	21.81[mmol/L]	98.39[%]			
	2 6.62	26[ppm]		24.98[abn]	2	22.05[mmol/L]	99.48[%]	<b>V</b>		
	3 7.28	87[ppm]		24.89[abn]	2	21.96[mmol/L]	99.10[%]	<b>Ø</b>		
	4 9.07	78[ppm]		8.33[abn]	1	14.70[mmol/L]	66.32[%]			
	5 9.58	33[ppm]		11.55[abn]	1	20.39[mmol/L]	91.99[%]			
	S	Supp	oort	s inter	nal an	d exteri	n <mark>al st</mark> a	ndar	d methods	
								9		
	Gain Scale 19.8 Avg. Molarity 21.94[mmol/L] Avg. Purity 98.99[%]									

4 <u>Quantitative Analyses – qNMR, Adolfo Botana, Jeol Inc.</u>

### **Saturation Transfer Differences**

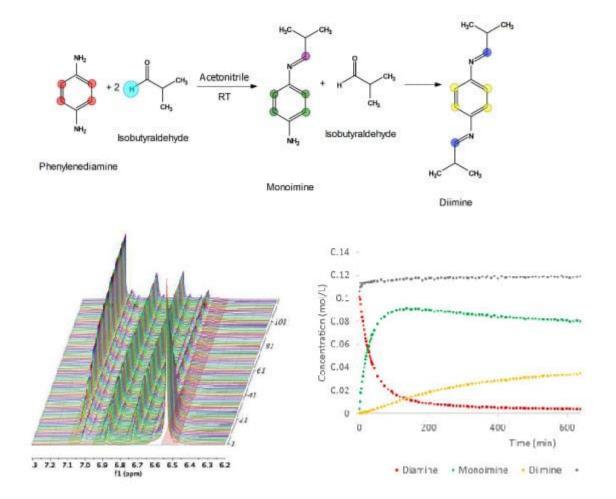
WaterLOGSY pulse sequence is a sensitive ligand-observed for detection of interaction between macromolecules, such as a ligand and a protein and DNA or RNA fragments.



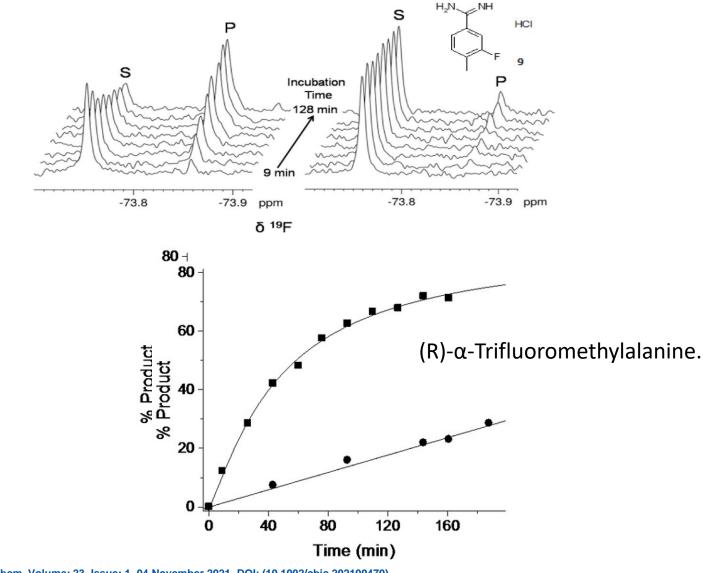
<u>NMR waterLOGSY as An Assay in Drug Development Programmes for Detecting Protein-Ligand Interactions</u> <u>WaterLOGSY as a method for primary NMR screening: Practical aspects and range of applicability</u> The discovery of novel antitrypanosomal 4-phenyl-6-(pyridin-3-yl)pyrimidines

Solutions for Innovation JEOL

#### **Reaction Monitoring and Kinetic analyses**

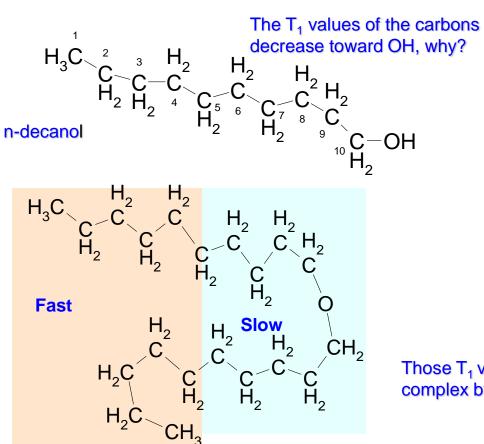


#### 19F NMR for the Monitoring of Protease Digestion of Peptides



ChemBioChem, Volume: 23, Issue: 1, 04 November 2021, DOI: (10.1002/cbic.202100470) https://chemistry-europe.onlinelibrary.wiley.com/doi/10.1002/cbic.202100470

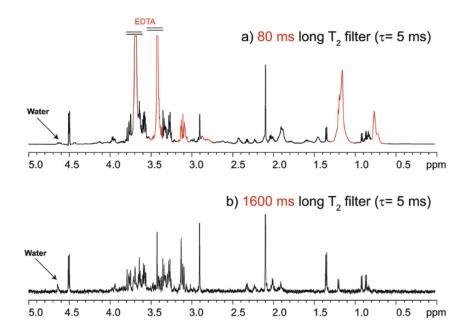
#### **Structural Information from T**<sub>1</sub>



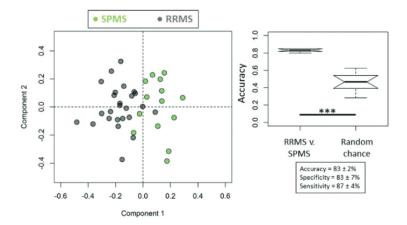
Carbon	T <sub>1</sub> /sec
1	3.1
2	2.2
3	1.6
4	1.1
5	0.84
6	0.84
7	0.84
8	0.77
9	0.77
10	0.65

Those T<sub>1</sub> values prove the two molecular complex by hydrogen bound

#### **Biological samples analysis**



**Fig. 5** Wasted pulse sequences allow the use of  $T_2$  filters of a length impossible to use achieve with presat-CPMG. This allows the introduction of  $T_2$  encoding to distinguish between different metabolite populations. Compare (b), in which a 1600 ms long filter has been made possible by Wasted-II, with (a) in which an 80 ms filter has been used (also using Wasted-II). Note that the suppression of the water signal is excellent even when using these long filters. The sample is human blood with non-deuterated EDTA.

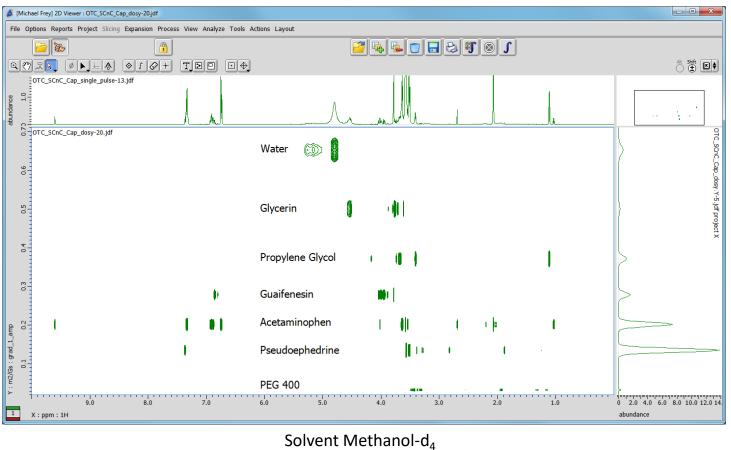


**Fig. 6** OPLS-DA results from blood plasma Wasted-II <sup>1</sup>H NMR data discriminating SP from RR multiple sclerosis patients. Left, a representative scores plots illustrating separation between SPMS and RRMS plasma spectra in the multivariate models, and right, the accuracy of the cross-validated ensemble of OPLS-DA models is significantly better than random chance. Kolmogorov–Smirnov test *p*-values <0.001 are represented by \*\*\*.

https://doi.org/10.1039/C9AN01005J

### **DOSY NMR of paracetamol tablet**

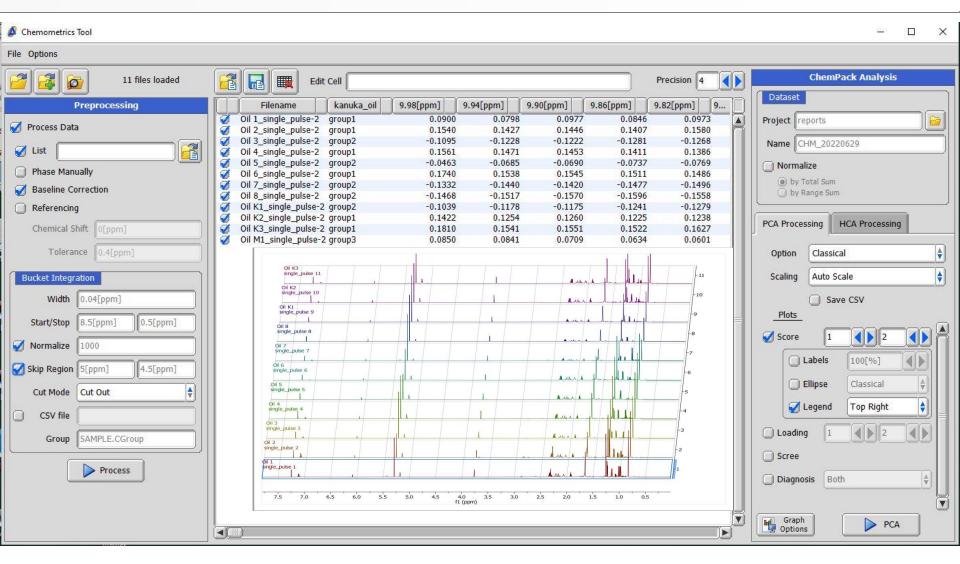
#### Practical Introduction to DOSY



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https://nmr.chemistry.manchester.ac.uk/?q=node/432

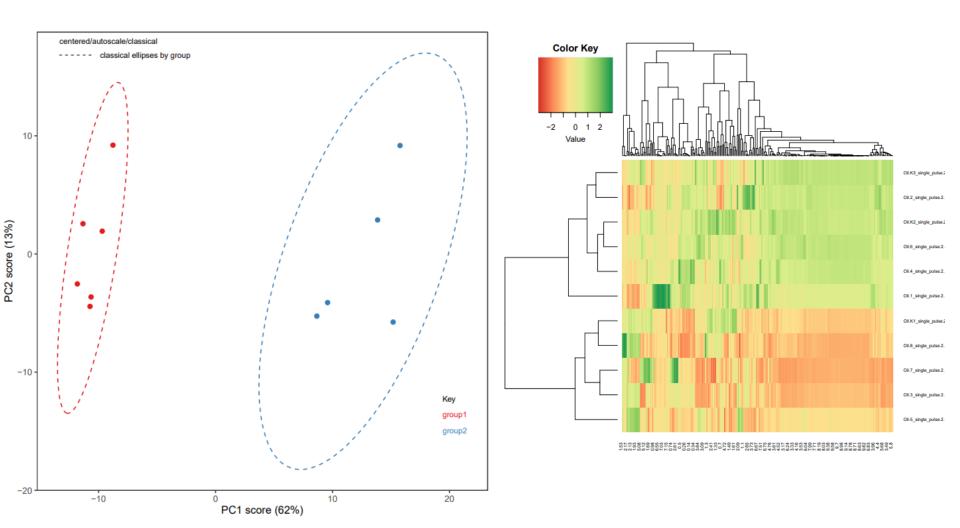
### **Metabolomics**



http://nmr.vuw.ac.nz/nmr/wp-content/uploads/presentations/Metabolomics.pdf

http://nmr.vuw.ac.nz/wunmr/wp-content/uploads/webinars/NMR\_chemometrics\_Jeol.pdf

### **Chemometrics Tool in Delta**

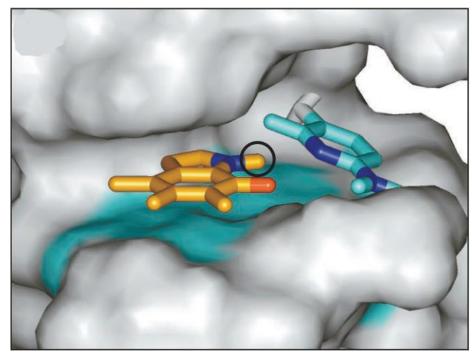


PCA- Principal Component Analyses

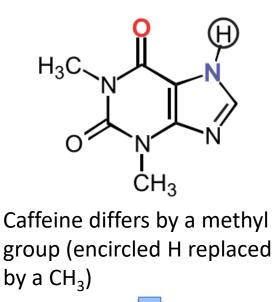
#### HCA- Hierarchical Cluster Analyses

http://nmr.vuw.ac.nz/nmr/wp-content/uploads/presentations/Metabolomics.pdf http://nmr.vuw.ac.nz/wunmr/wp-content/uploads/webinars/NMR chemometrics Jeol.pdf

## Molecular investigation of the interaction targetaptamer: where does the binding event takes place ?



Stacking and hydrogen bond interaction ! RNA structural interactions in a ligand binding site proved by NMR spectroscopy

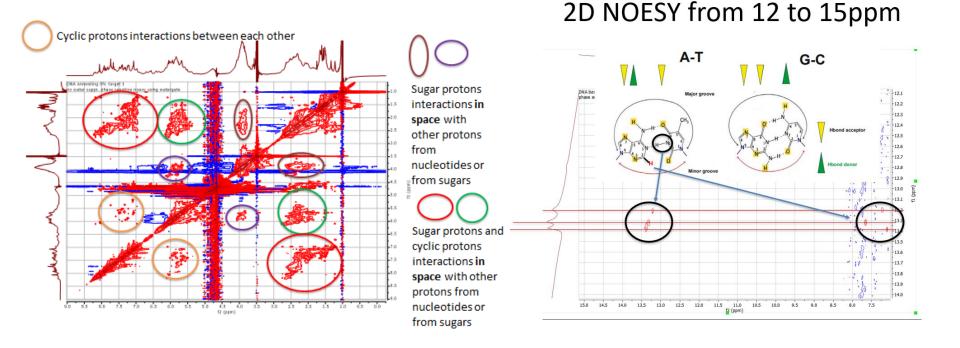


Displays affinity for theophylline 10,000 times that of caffeine

Hermann, T. and D. J. Patel (2000). "Adaptive Recognition by Nucleic Acid Aptamers." <u>Science **287**(5454): 820-825.</u> Zimmermann, G. R., et al. (1997). "Interlocking structural motifs mediate molecular discrimination by a theophylline-binding RNA." <u>Nature Structural Biology **4**(8): 644-649.</u>

### **Noesy-Nuclear Overhauser Effect**

http://nmr.vuw.ac.nz/wunmr/wp-content/uploads/applications/Aptemer\_NMR.pdf



Unraveling the binding mode of a methamphetamine aptamer: a spec-troscopic and calorimetric investigation Clement Sester,†,‡ Jordan AJ McCone, II Ian Vorster,‡ Joanne E Harvey, II and Justin M Hodgkiss\*,†,‡

http://nmr.vuw.ac.nz/wunmr/wp-content/uploads/applications/Encapsulating%20an%20amino%20acid%20in%20a%20DNA%20fold.pdf http://nmr.vuw.ac.nz/wunmr/wp-content/uploads/applications/Aptemer\_NMR.pdf http://nmr.vuw.ac.nz/wunmr/wp-content/uploads/webinars/NMR\_chemometrics\_Jeol.pdf

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