

G-matrix Fourier Transform (GFT)

Projection NMR Spectroscopy

Theory and Application

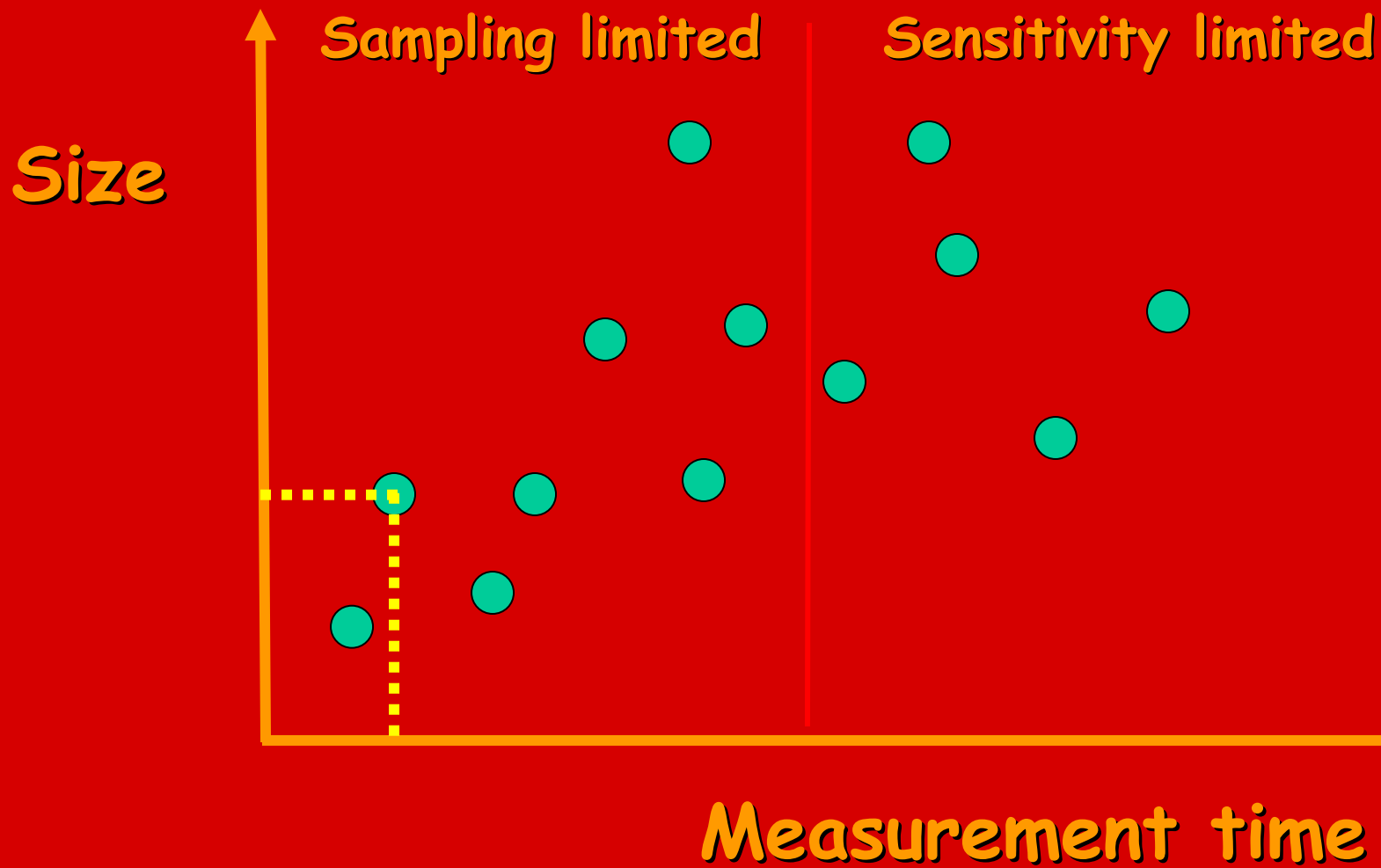
The 'NMR sampling problem':
minimal measurement times scale with
 $\prod n_j$

1 scan *per second*
16 complex points *per dimension* =>

1D	->	1 second
2D	->	~0.5 minutes
3D	->	~0.3 hours
4D	->	~9 hours
5D	->	~12 days
6D	->	~1.1 years

Importance for NMR at highest magnetic fields

- 'Sampling demand' in each indirect dimension scales with the magnetic field strength
=> 4D at 900 versus 600 MHz ^1H resonance frequency is 3.4-times larger
- Sensitivity increases with magnetic field strength



Projection NMR:
a solution of the
NMR sampling problem...
...avoid many dimensions...

Major developments in the 1970-1980s (Richard Ernst and coworkers)

- 'Skewed projections' of homo-nuclear 2D J -spectra were calculated using the 'projection cross-section' theorem to obtain decoupled 1D ^1H NMR spectra;
no joint incrementation of shift evolution periods or phase-sensitive signal detection
- 'Accordion NMR': *joint sampling of chemical shift evolution period and 'mixing time' in EXSY*
-> Reduction in dimensionality

Early 1990s:

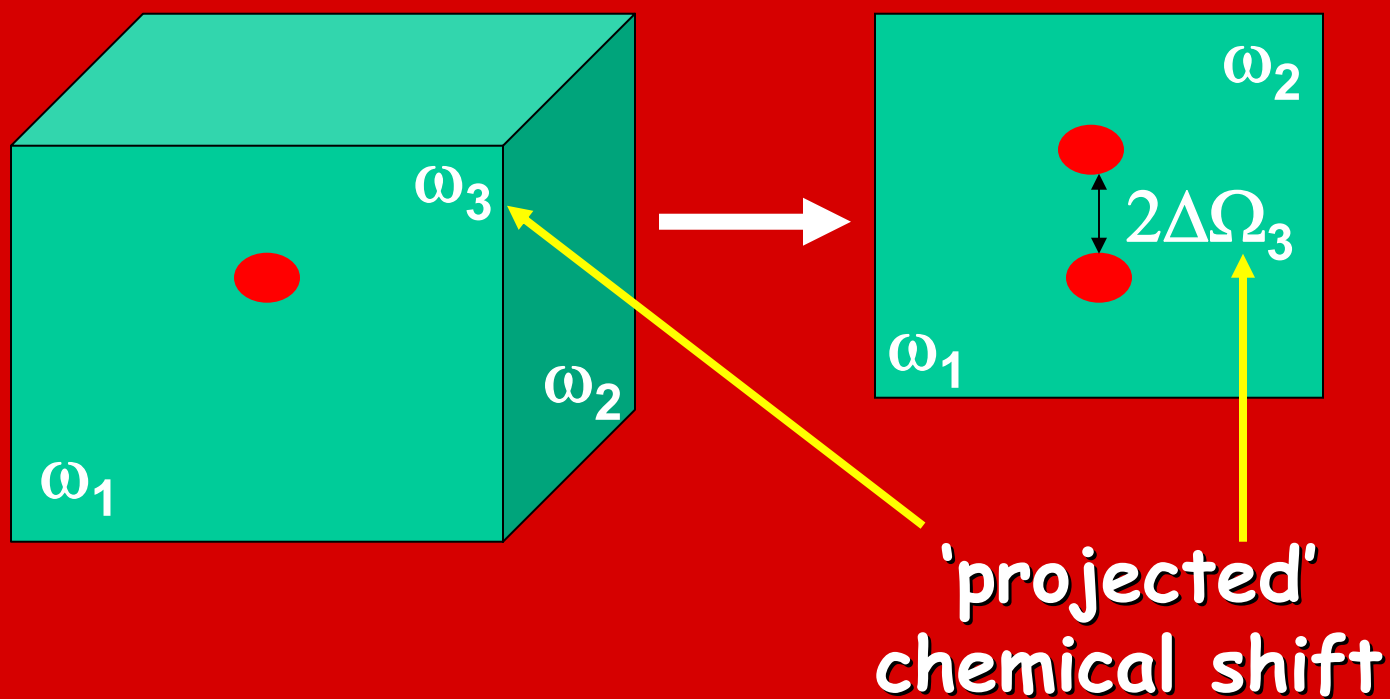
Demand for an approach in which
chemical shifts are jointly
sampled in a phase-sensitive
manner....

Reduced-dimensionality (RD) NMR and its variants:

'Modules' for GFT projection NMR

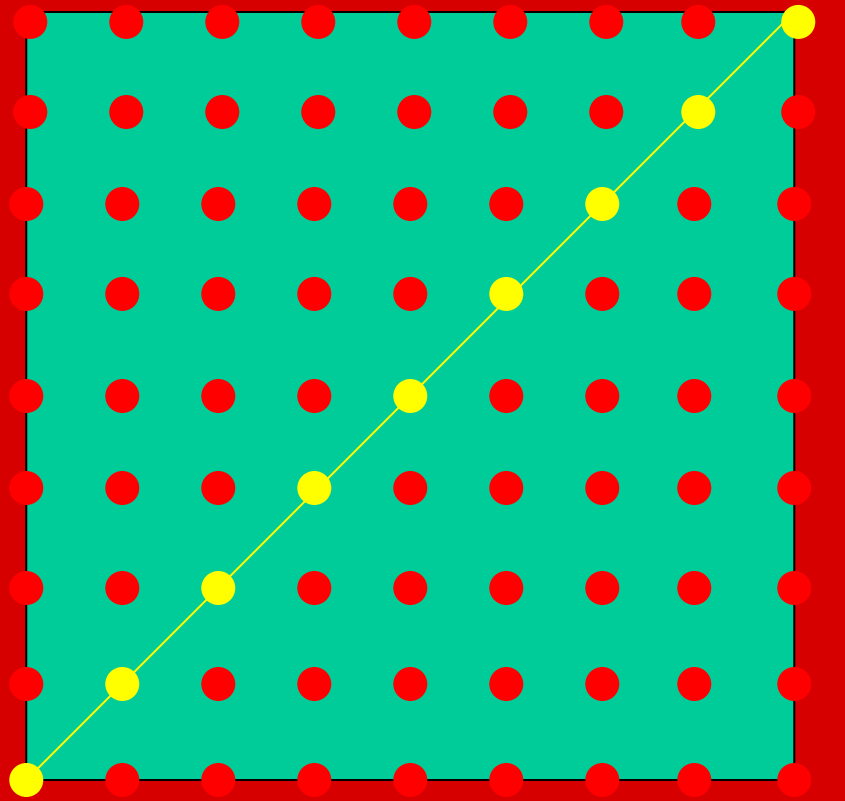
RD NMR Spectroscopy

(Szyperski, Wider, Bushweller, Wuthrich. JACS 115, 1993)



Challenge: keep information upon projection

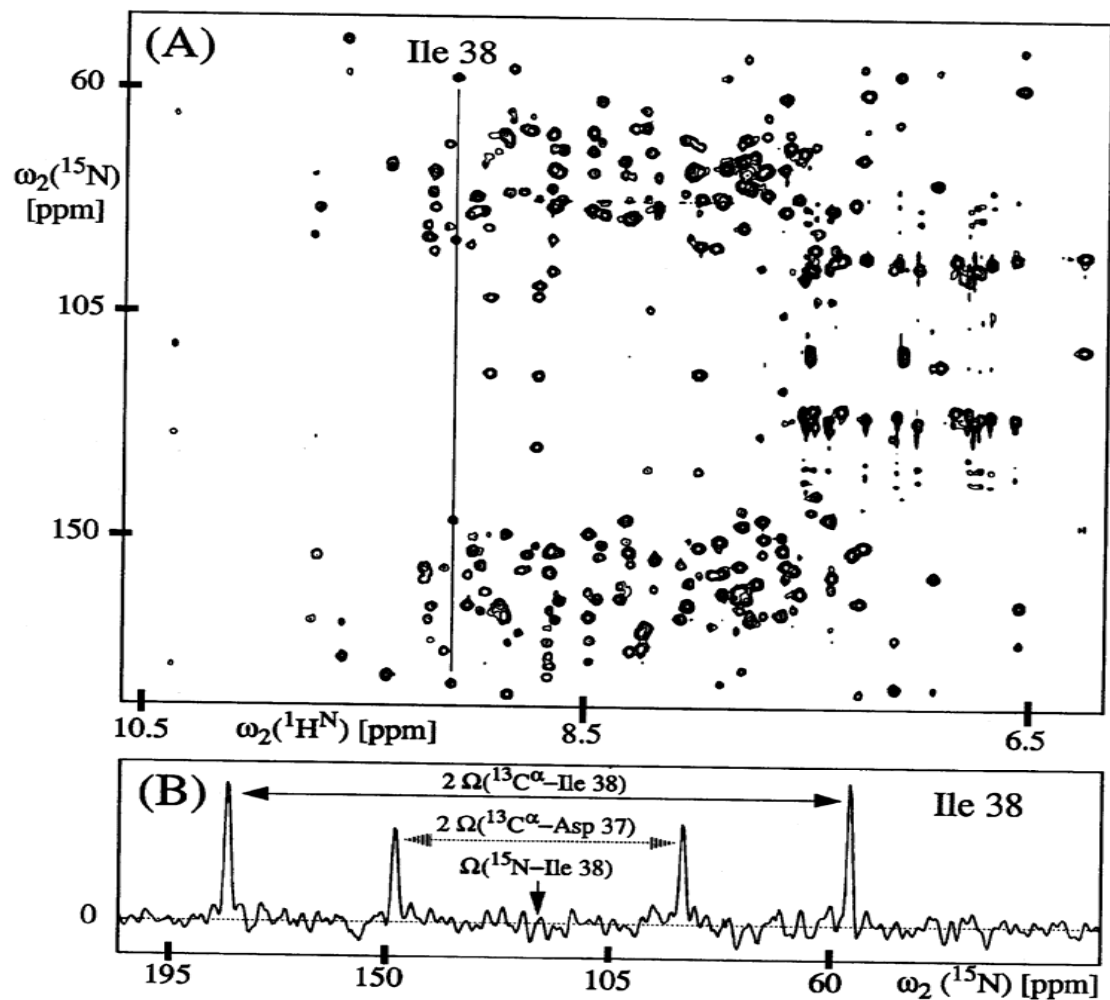
$\tau_1(\text{K})$



$\tau_2(\text{S})$

Transfer amplitude $\sim e^{i\Omega_k t} \cos(\Omega_s t)$

J-9308-ma



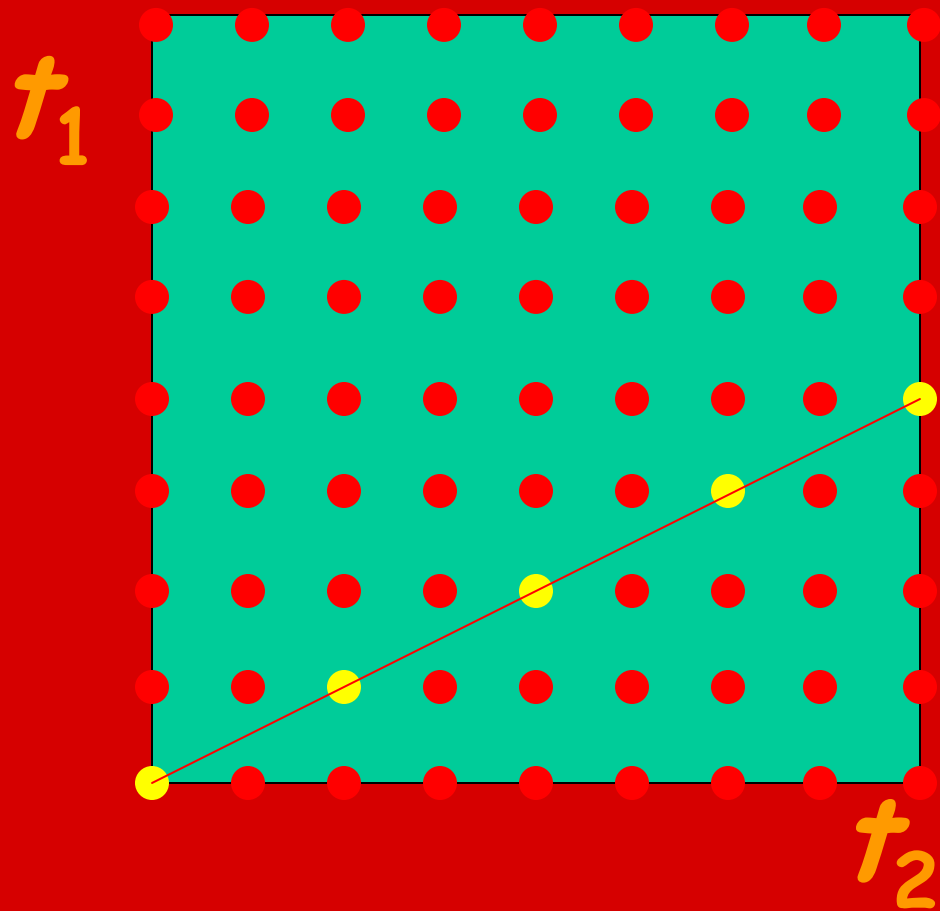
2D RD HNNCA
Szyperski et al.,
JACS 115, 1993
Suppl. Material

Fig. S1

RD NMR variants...

1. Scaling of shift evolution periods

(Szyperski et al., JACS 115,1993)

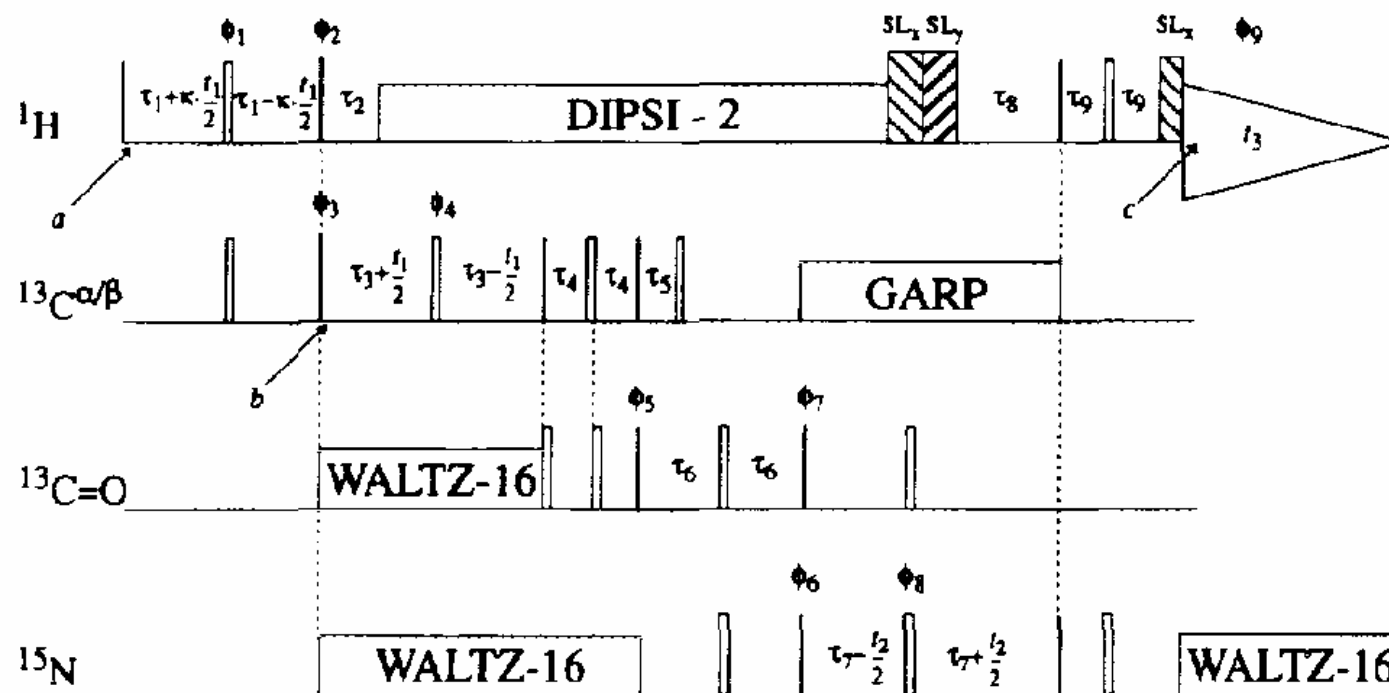


3D $^1\text{H}^{\alpha/\beta}\text{C}^{\alpha/\beta}(\text{CO})\text{NHN}$, a Projected 4D NMR Experiment for Sequential Correlation of Polypeptide $^1\text{H}^{\alpha/\beta}$, $^{13}\text{C}^{\alpha/\beta}$ and Backbone ^{15}N and $^1\text{H}^{\text{N}}$ Chemical Shifts

THOMAS SZYPERSKI, MAURIZIO PELLECCIA, AND KURT WÜTHRICH

Institut für Molekularbiologie und Biophysik, Eidgenössische Technische Hochschule-Hönggerberg, CH-8093 Zurich, Switzerland

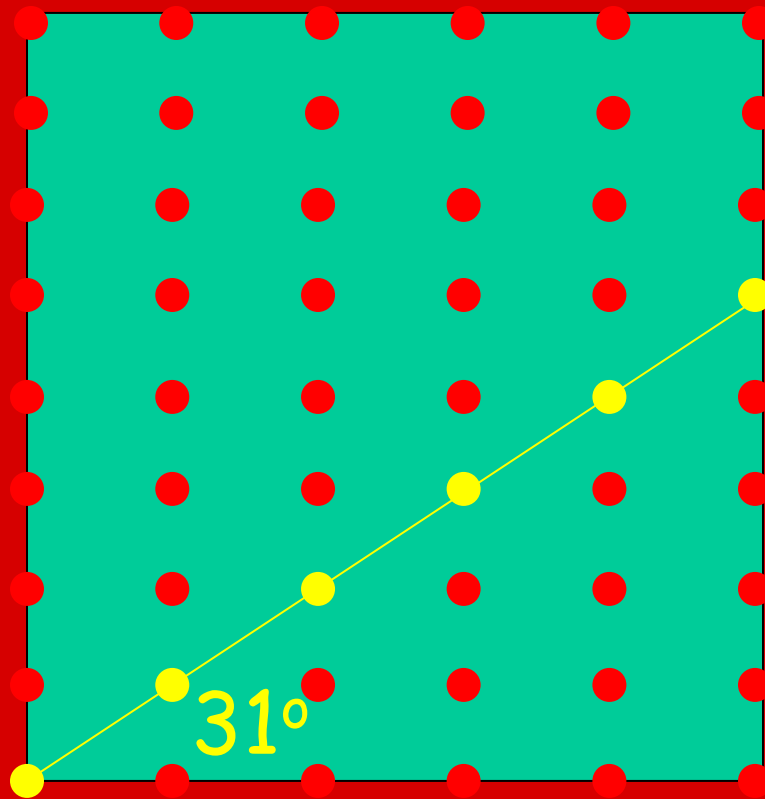
Received June 29, 1994



'tilted projected spectrum'

NMRFam Workshop 06/06/06

$\tau_1(^{13}\text{C}^{\alpha\beta})$

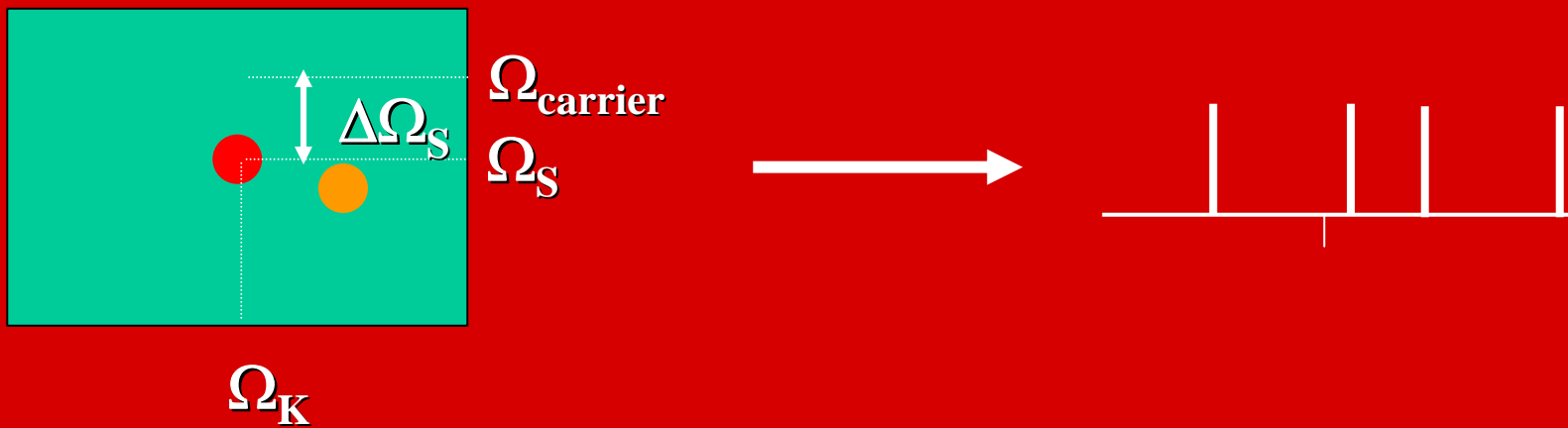


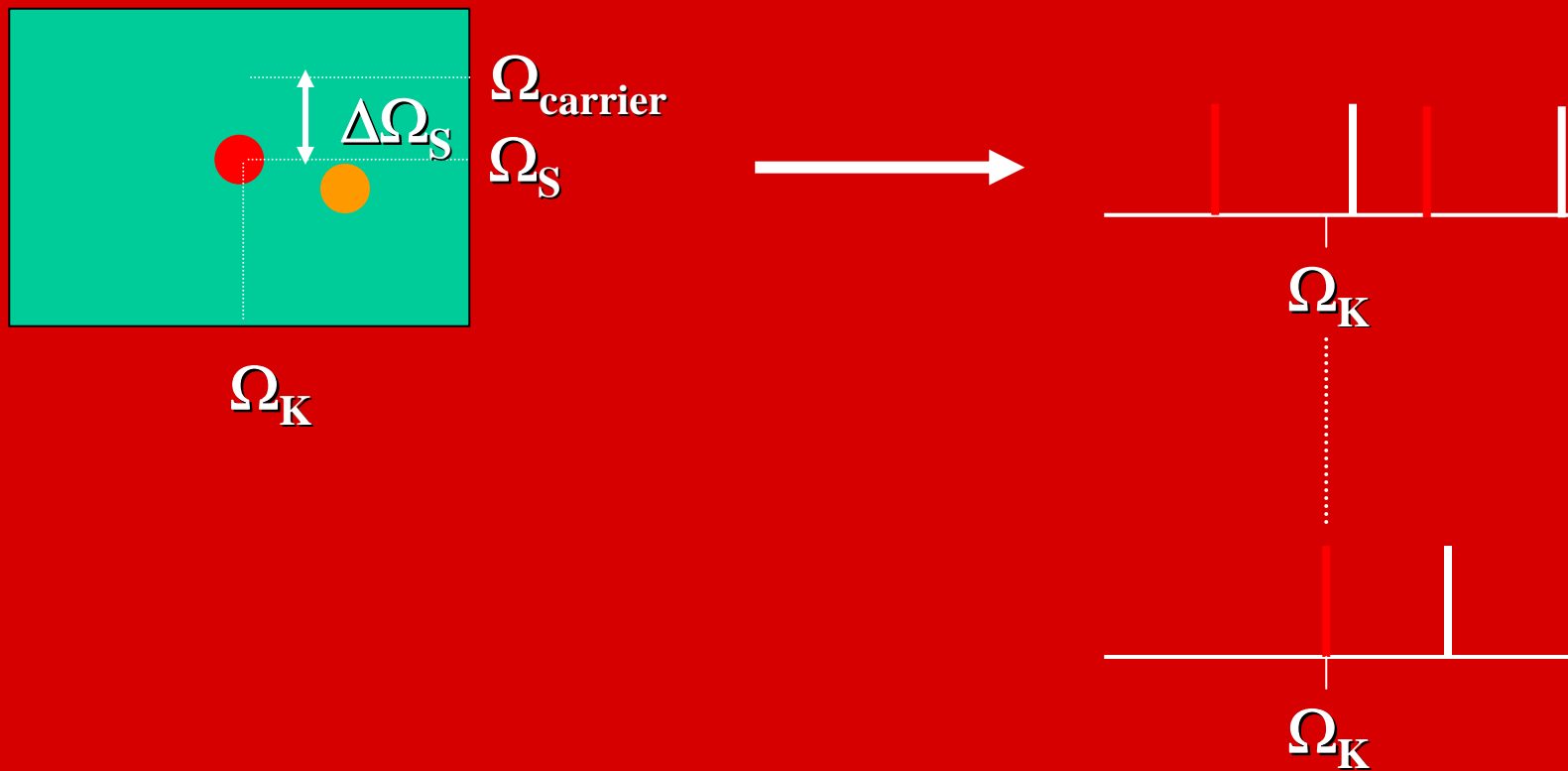
$\kappa = 1.65$

$\tau_2(^1\text{H}^{\alpha\beta})$

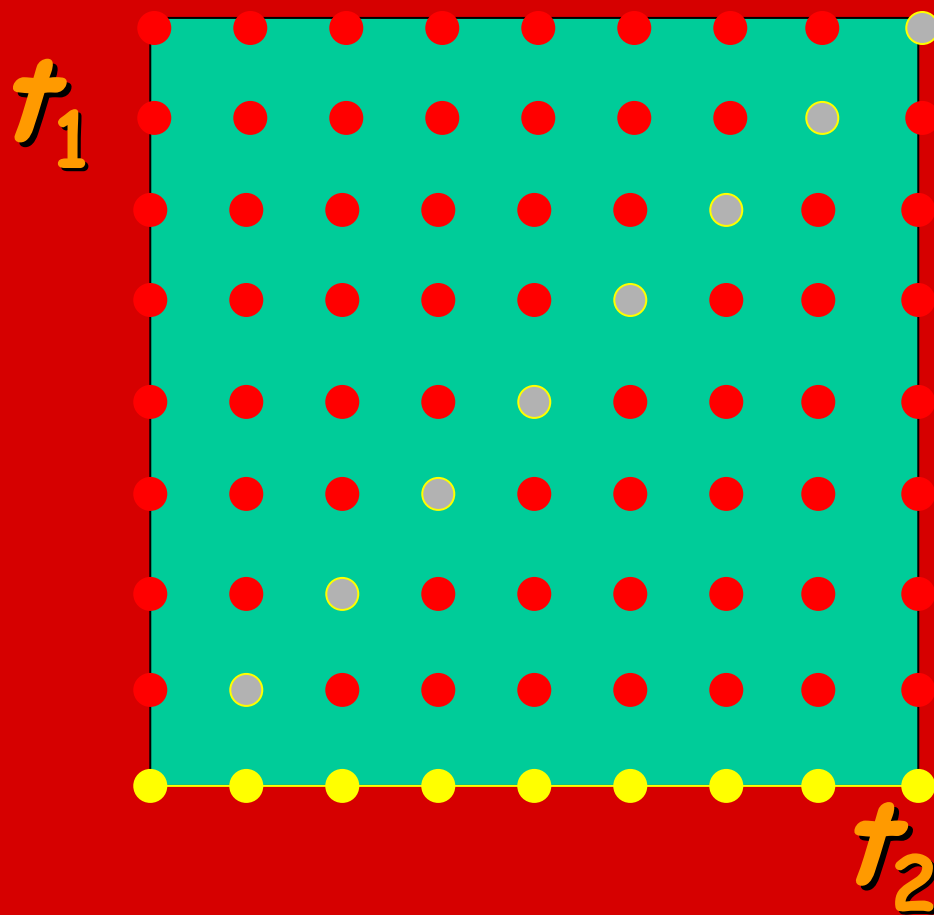
2. Central peak detection

(Szyperski et al., JMR B108, 1995; JACS
118,1996)



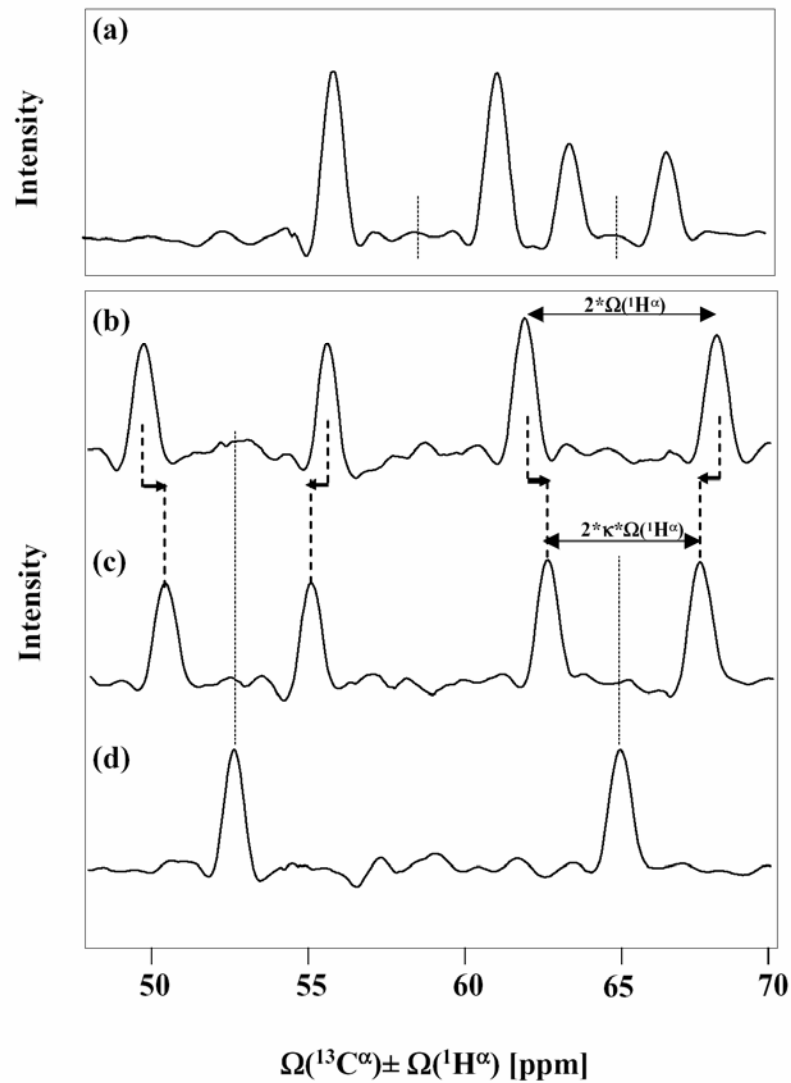


central peak detection



central peak detection \Leftrightarrow
'orthogonal projections'

Identification of shift multiplets

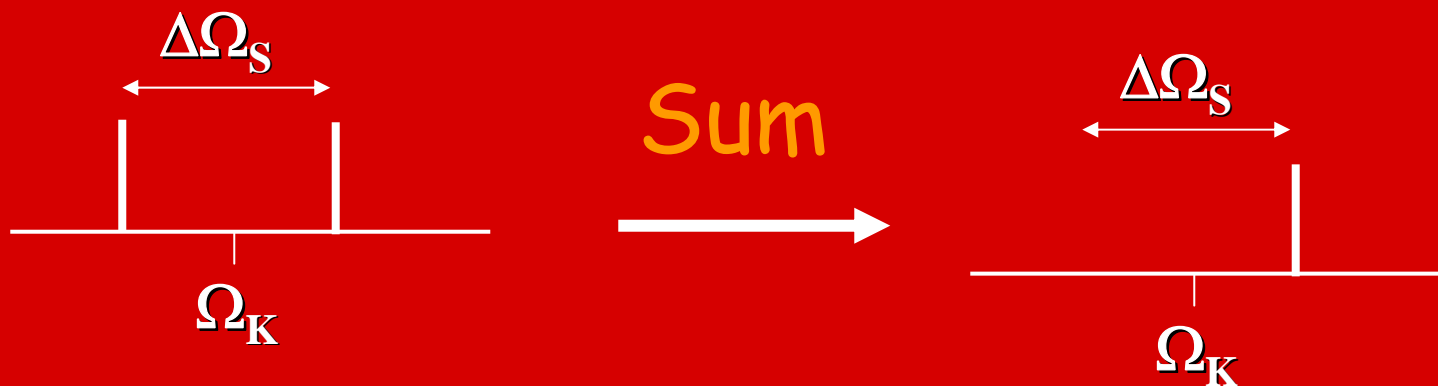


'spin relaxation
time labeling'

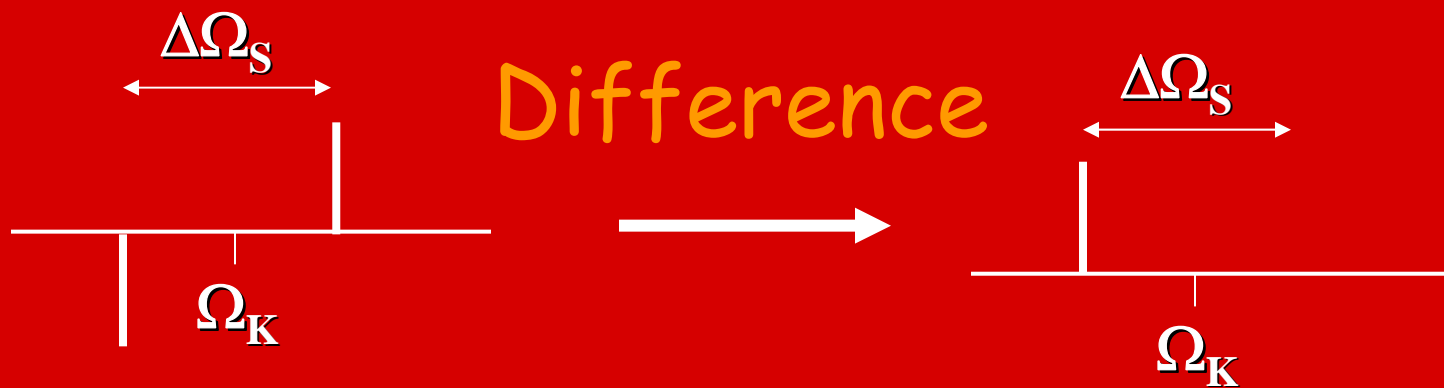
variation of scaling
of evolution periods

central peak detection

3. 'Phase-sensitive' RD NMR (Marion and coworkers, JMR B109, 1995)



Transfer amplitude $\sim e^{i\Omega_K t} \cos(\Omega_S t)$



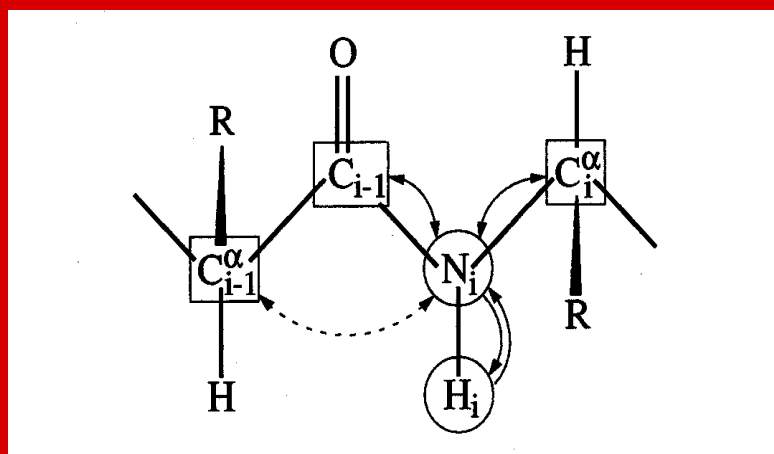
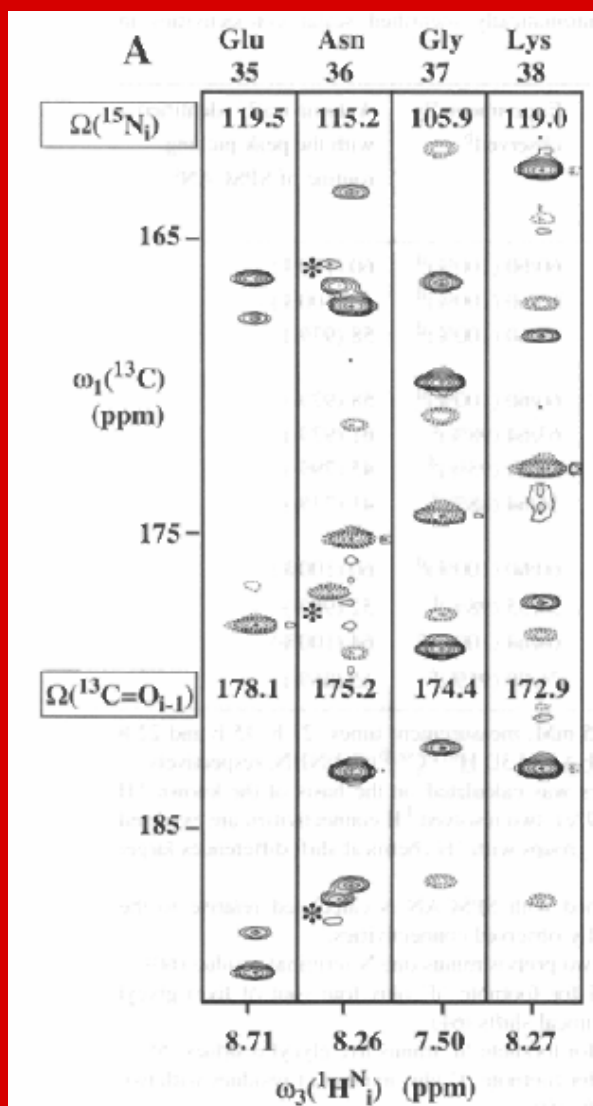
Transfer amplitude $\sim e^{i\Omega_K t} \sin(\Omega_S t)$


The alternative:
TPPI combined with scaling of
shift evolution periods

A Novel Reduced-Dimensionality Triple-Resonance Experiment for Efficient Polypeptide Backbone Assignment, 3D $\text{CO} \text{HN} \text{N} \text{CA}$

THOMAS SZYPERSKI, DANIEL BRAUN, CÉSAR FERNÁNDEZ, CHRISTIAN BARTELS, AND KURT WÜTHRICH
 Institut für Molekularbiologie und Biophysik, Eidgenössische Technische Hochschule-Hönggerberg, CH-8093 Zürich, Switzerland

Received May 26, 1995



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Sequential resonance assignment of medium-sized $^{15}\text{N}/^{13}\text{C}$ -labeled proteins with projected 4D triple resonance NMR experiments

Thomas Szyperski*, Bogdan Banecki**, Daniel Braun & Ralf W. Glaser***
 Institut für Molekularbiologie und Biophysik, Eidgenössische Technische Hochschule-Hönggerberg, CH-8093 Zürich, Switzerland

Received 12 September 1997; Accepted 27 November 1997

4. 'Double RD NMR'

(Lohr and coworkers, JBNMR 1995)

A new triple-resonance experiment for the sequential assignment of backbone resonances in proteins

Frank Löhr and Heinz Rüterjans*

Institut für Biophysikalische Chemie, Johann Wolfgang Goethe Universität Frankfurt am Main, Biozentrum,
Marie Curie Strasse 9, D-60439 Frankfurt am Main, Germany

Received 31 January 1995

Accepted 30 March 1995

Keywords: Triple-resonance NMR spectroscopy; Sequential assignment; Reduced dimensionality; *Desulfovibrio vulgaris* flavodoxin

3D {HACA}, {CON} HN

F3($\Omega_{H_N(i)}$) = 10.05 ppm

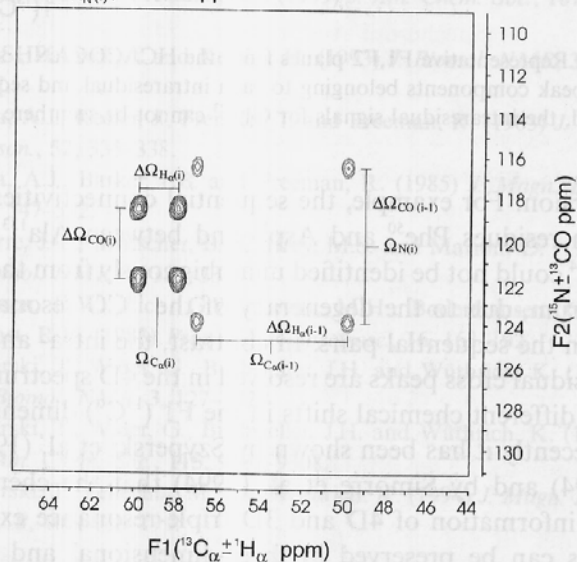


Fig. 5. Expansion of an F1,F2-slice of the HCACOCANH spectrum obtained with the pulse sequence from Fig. 1C. The intraresidual correlation for Cys⁹⁰ (residue i) of *D. vulgaris* flavodoxin and the sequential Ala⁸⁹/Cys⁹⁰ correlation are shown. The midpoints of the rectangles appear at the ¹⁵N chemical shift of Cys⁹⁰ and the ¹³C^α chemical shifts of Cys⁹⁰ and Ala⁸⁹, which can be read directly from the scales at the F1 and F2 axes. ¹H^α and ¹³CO chemical shifts are obtained from the splittings along the two indirectly detected dimensions. The splittings (in Hz) are scaled down using the factors $x=0.625$ and $y=0.2$, such that 1 ppm splitting in F1 corresponds to $\Delta\Omega(H^\alpha)=0.2$ ppm and 1 ppm splitting in F2 corresponds to $\Delta\Omega(CO)=1$ ppm.

2D HNN(CO)CAHA

Novel 2D Triple-Resonance NMR Experiments for Sequential Resonance Assignments of Proteins

Keyang Ding and Angela M. Gronenborn¹

Laboratory of Chemical Physics, National Institute of Diabetes and Digestive and Kidney Diseases, National Institutes of Health, Bethesda, Maryland 20892

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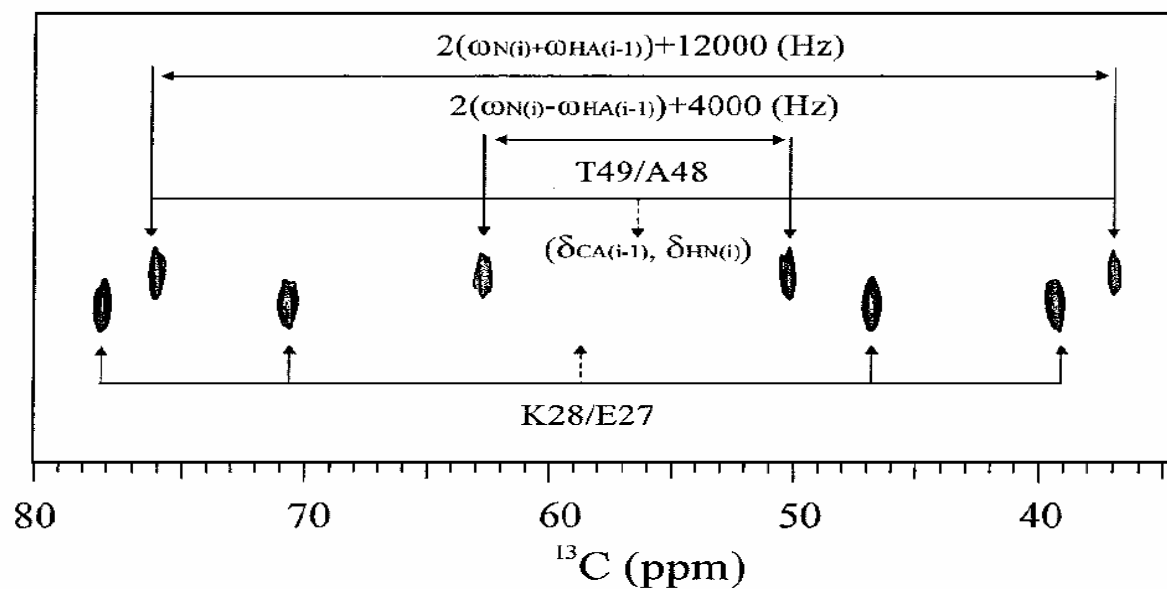


FIG. 6. Expansion of the boxed region in Fig. 5A comprising the cross peaks of K28/E27 and T49/A48 in 2D HN(CO)CAHA. The centers for the cross-peak

Generalization of RD NMR:

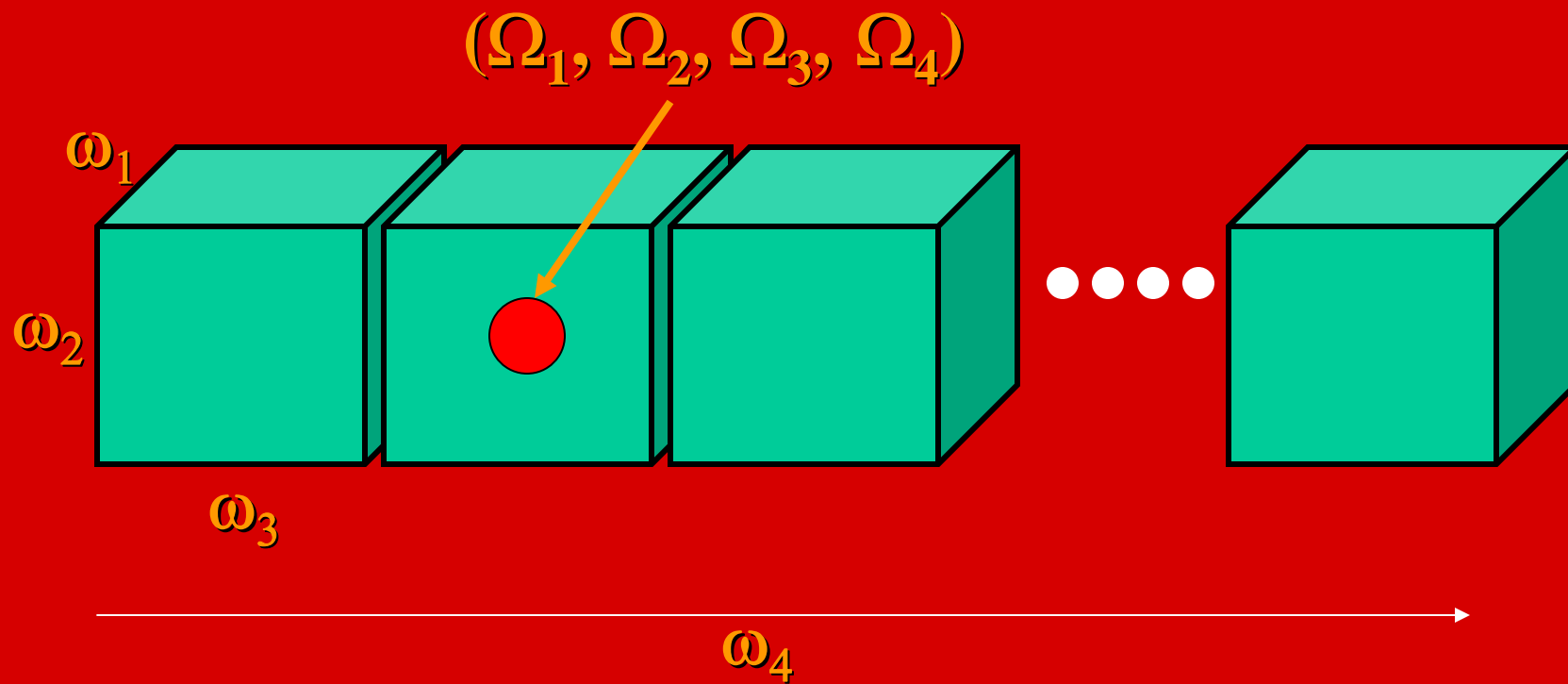
**G-matrix Fourier Transform
NMR Spectroscopy**

(JACS 2003, 125, 1385)

Defining features of GFT NMR

- Repeated joint sampling of an arbitrary number of indirect chemical shift evolution periods so that transfer amplitudes are generated which are proportional to all possible permutations of cosine and sine modulations of the individual shifts
- Linear combination of the sub-spectra resulting from such sampling which yields edited sub-spectra containing signals encoding phase-sensitively detected linear combinations of the jointly sampled shifts

4D FT NMR spectrum



(4, 2)D GFT NMR experiment

$$\Omega_1 + \Omega_2 + \Omega_3$$



$$\Omega_1 + \Omega_2 - \Omega_3$$



$$\Omega_1 - \Omega_2 + \Omega_3$$



$$\Omega_1 - \Omega_2 - \Omega_3$$



$$\Omega_1 + \Omega_2$$



$$\Omega_1 - \Omega_2$$



$$\Omega_1$$

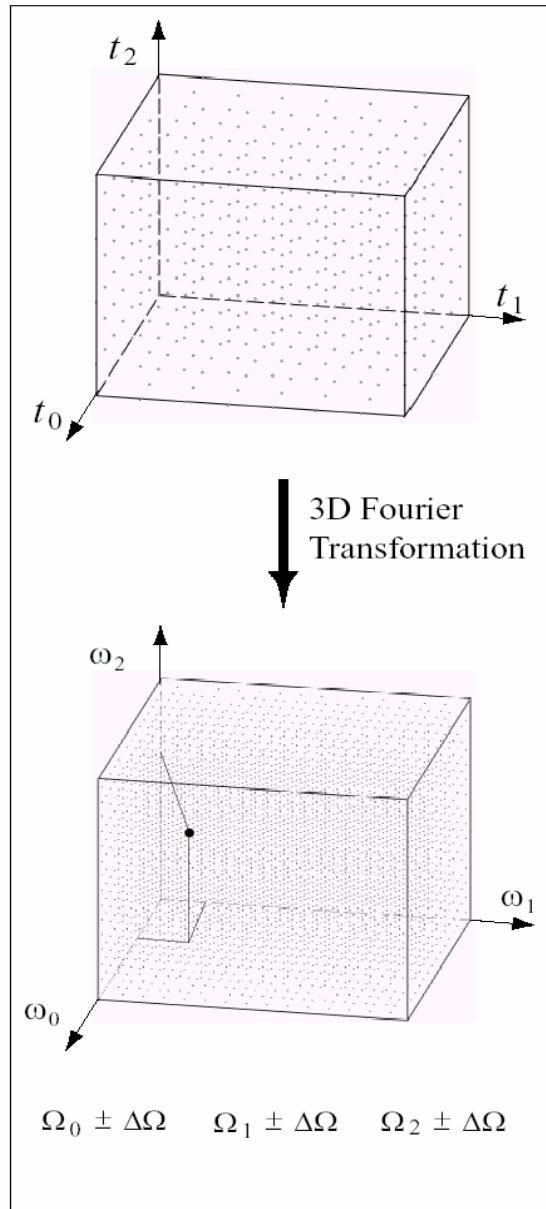


ω_1 (GFT)

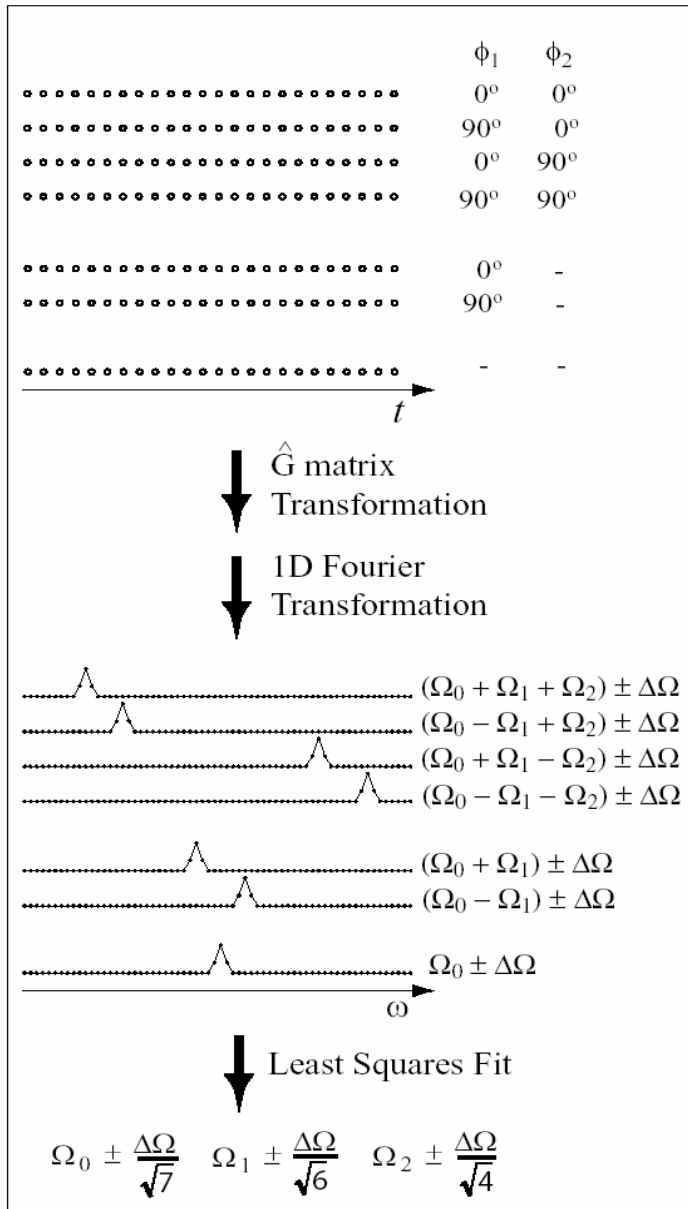
...measurement of linear combinations of shifts in different sub-spectra
...precision arises from over-determination

ω_2

FT NMR

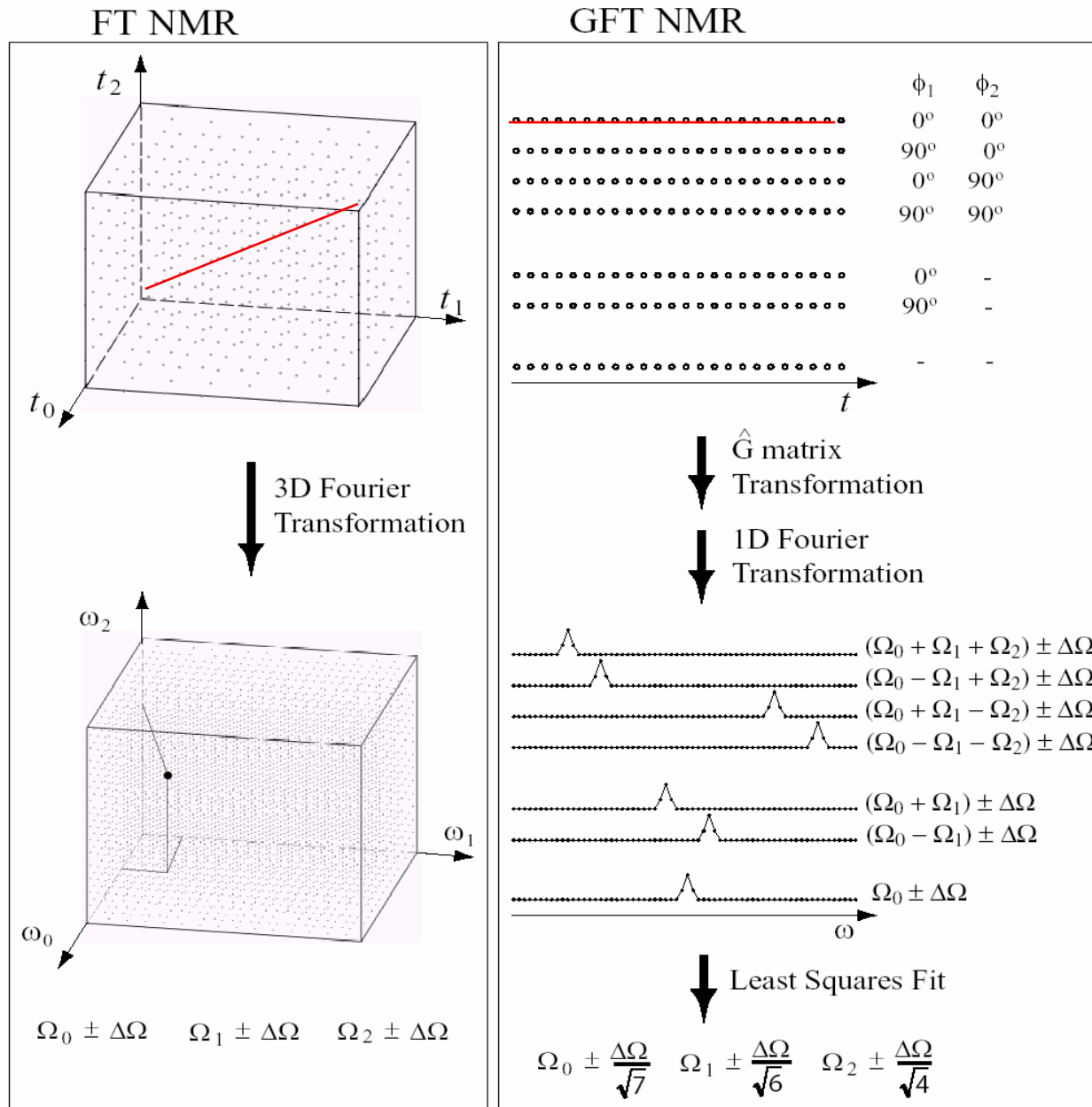


GFT NMR



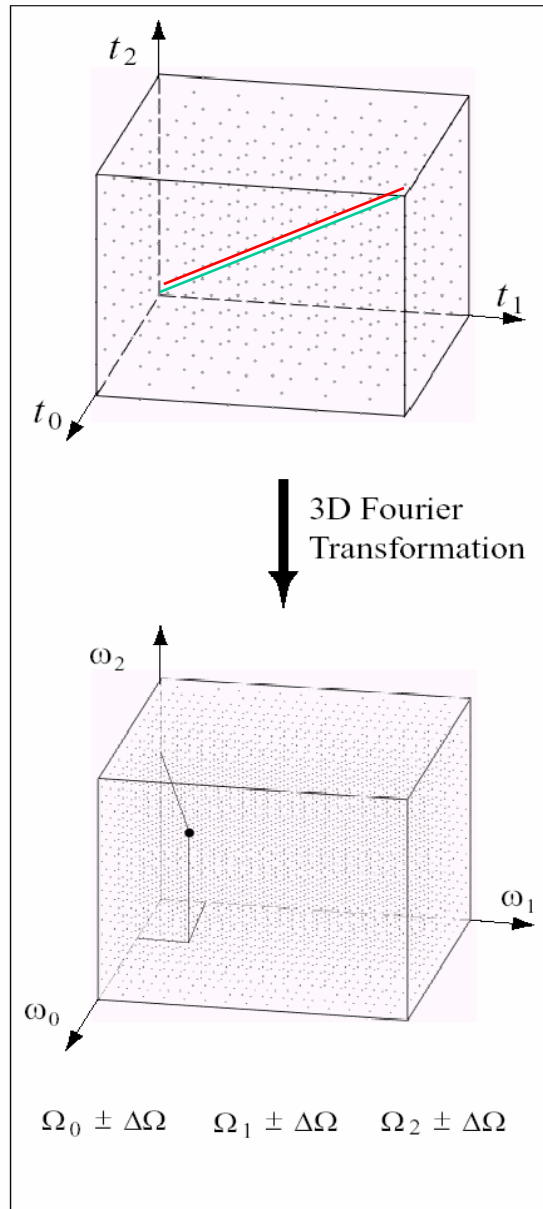
(4,2)D GFT NMR

Joint Sampling of 3D Subspace of an ND FT NMR Experiment

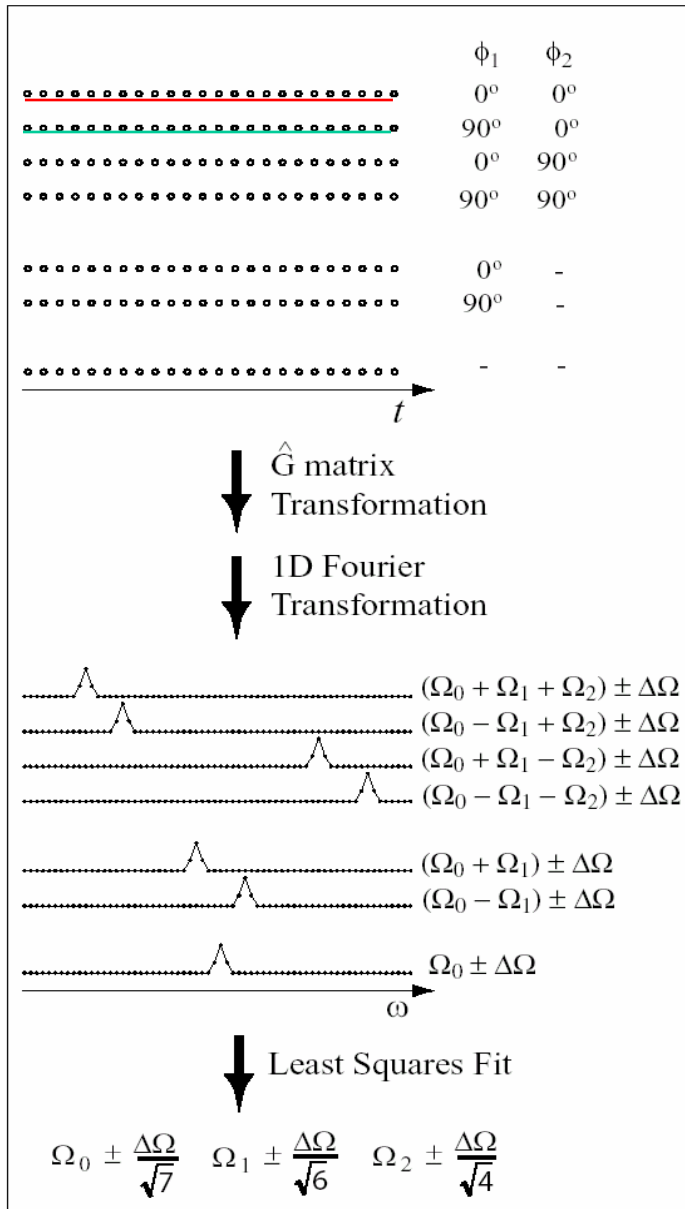


$\cos(\Omega_0 t)$	$\cos(\Omega_1 t)$	$\cos(\Omega_2 t)$
$\cos(\Omega_0 t)$	$\sin(\Omega_1 t)$	$\cos(\Omega_2 t)$
$\cos(\Omega_0 t)$	$\cos(\Omega_1 t)$	$\sin(\Omega_2 t)$
$\cos(\Omega_0 t)$	$\sin(\Omega_1 t)$	$\sin(\Omega_2 t)$

FT NMR



GFT NMR



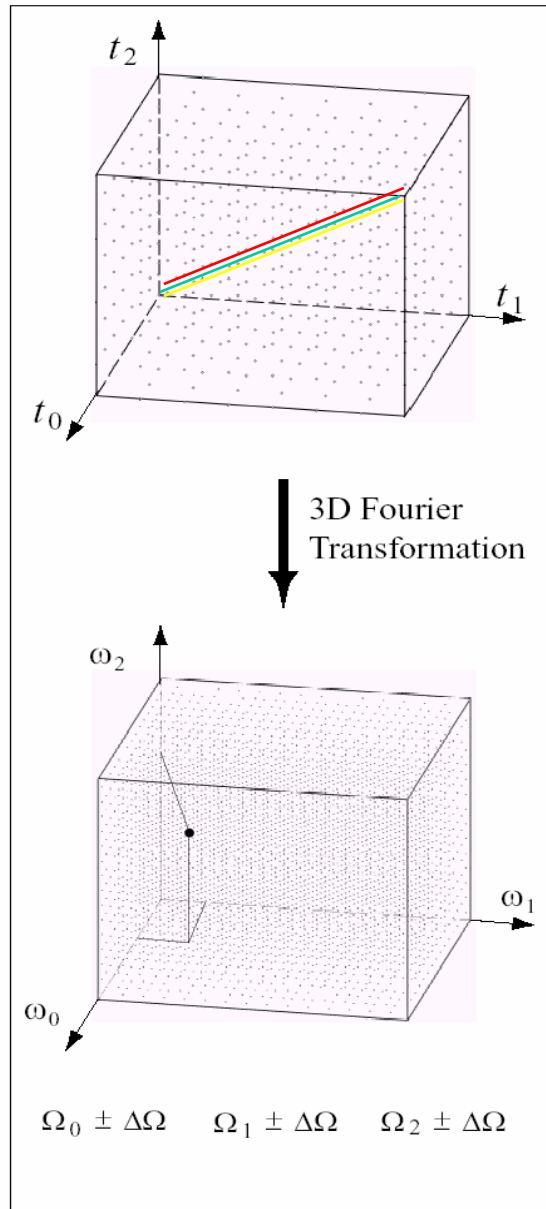
$$\cos(\Omega_0 t) \quad \cos(\Omega_1 t) \quad \cos(\Omega_2 t)$$

$$\cos(\Omega_0 t) \quad \sin(\Omega_1 t) \quad \cos(\Omega_2 t)$$

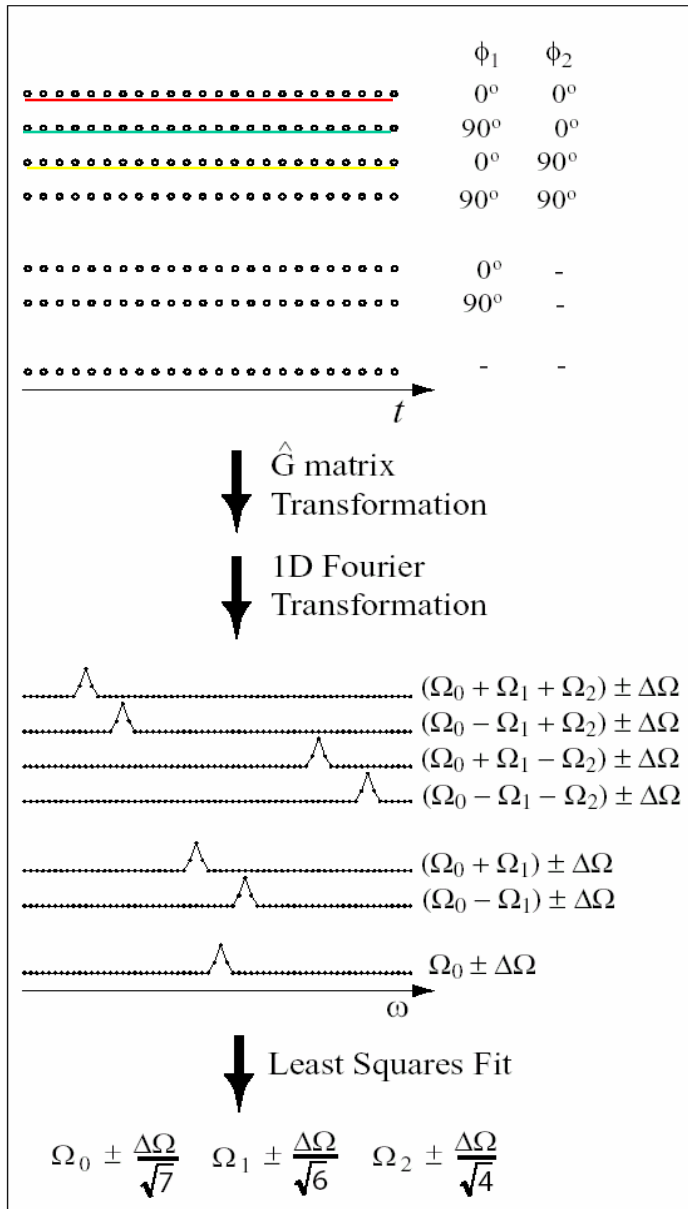
$$\cos(\Omega_0 t) \quad \cos(\Omega_1 t) \quad \sin(\Omega_2 t)$$

$$\cos(\Omega_0 t) \quad \sin(\Omega_1 t) \quad \sin(\Omega_2 t)$$

FT NMR

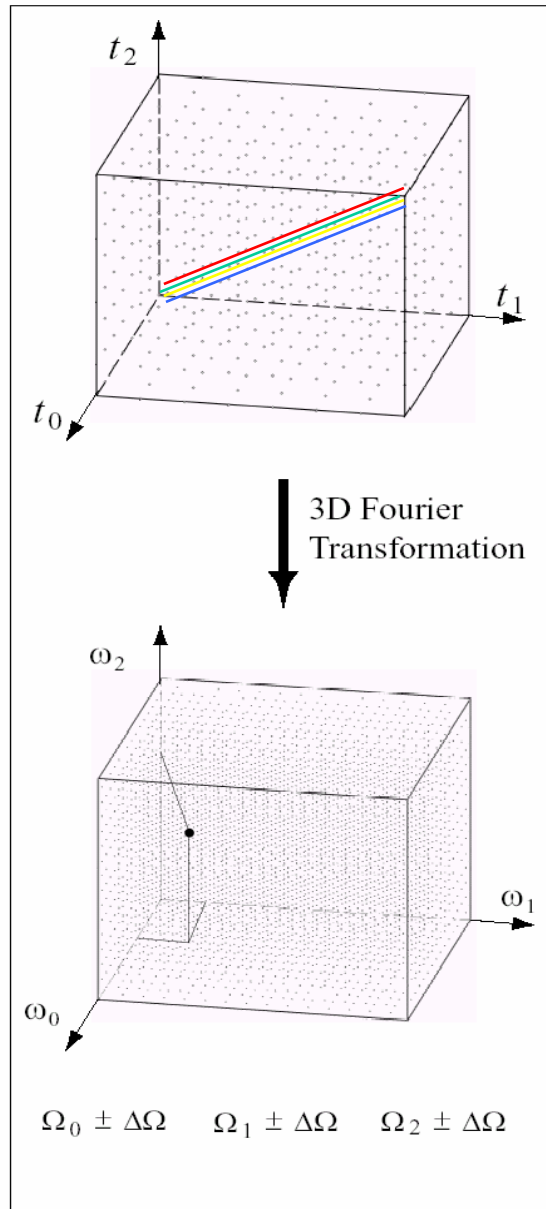


GFT NMR

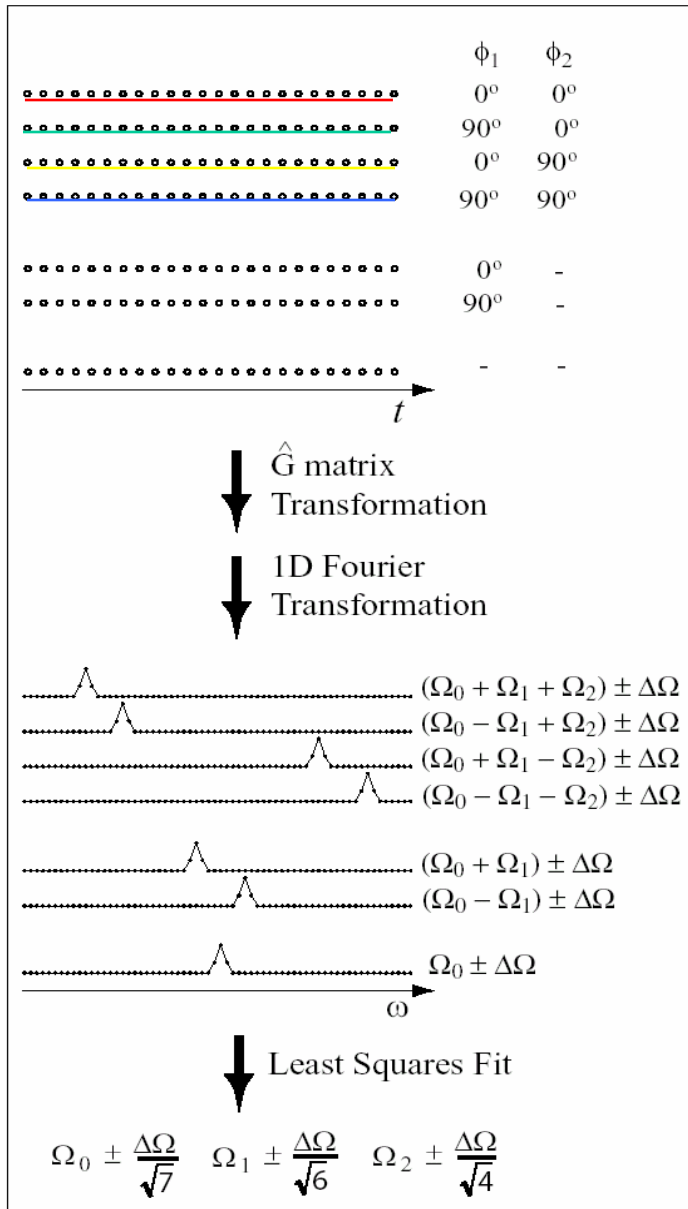


$\cos(\Omega_0 t)$	$\cos(\Omega_1 t)$	$\cos(\Omega_2 t)$
$\cos(\Omega_0 t)$	$\sin(\Omega_1 t)$	$\cos(\Omega_2 t)$
$\cos(\Omega_0 t)$	$\cos(\Omega_1 t)$	$\sin(\Omega_2 t)$
$\cos(\Omega_0 t)$	$\sin(\Omega_1 t)$	$\sin(\Omega_2 t)$

FT NMR



GFT NMR



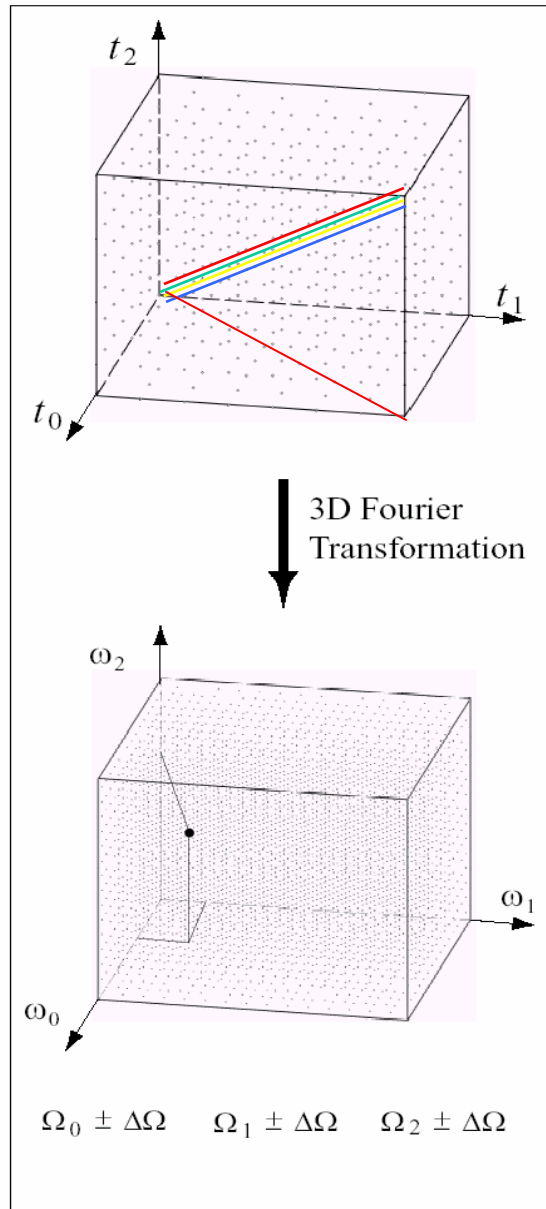
$$\cos(\Omega_0 t) \quad \cos(\Omega_1 t) \quad \cos(\Omega_2 t)$$

$$\cos(\Omega_0 t) \quad \sin(\Omega_1 t) \quad \cos(\Omega_2 t)$$

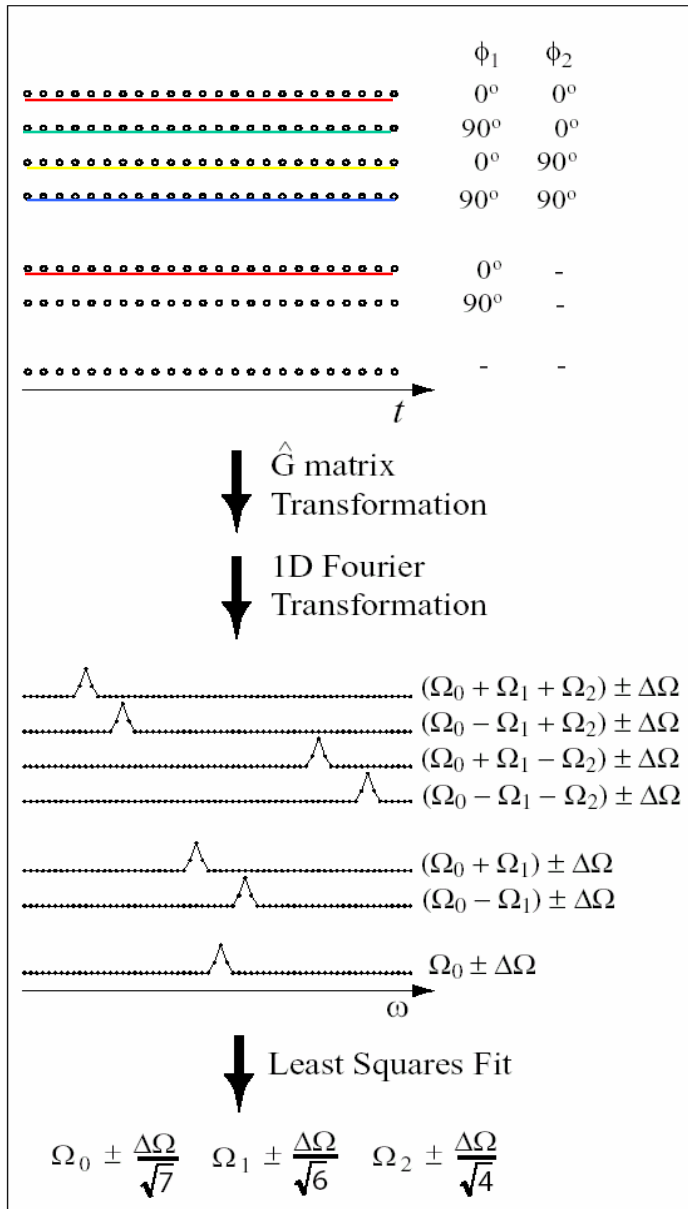
$$\cos(\Omega_0 t) \quad \cos(\Omega_1 t) \quad \sin(\Omega_2 t)$$

$$\cos(\Omega_0 t) \quad \sin(\Omega_1 t) \quad \sin(\Omega_2 t)$$

FT NMR



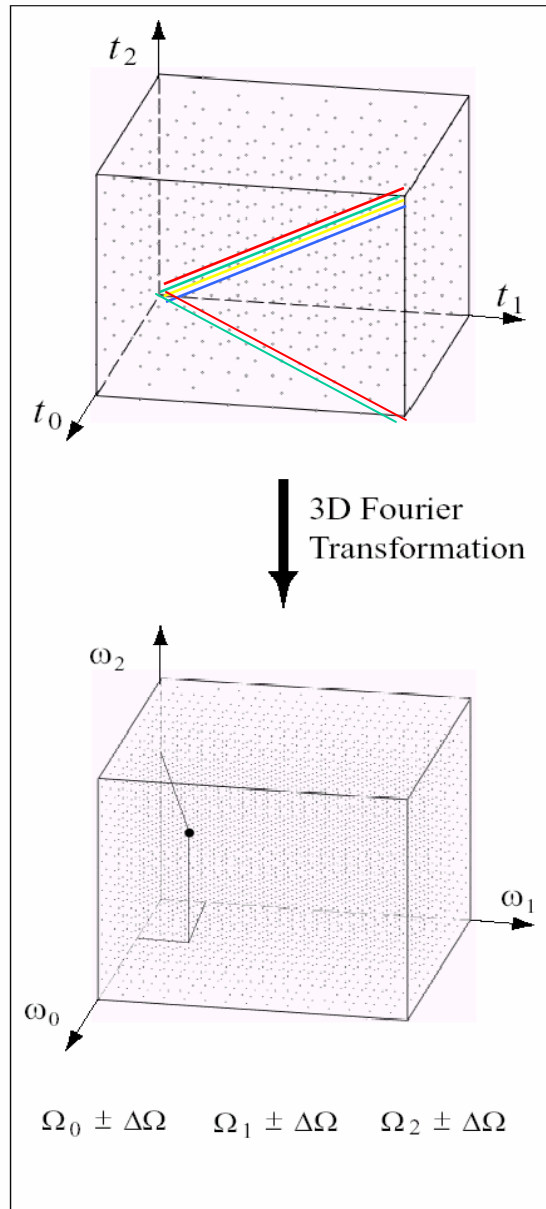
GFT NMR



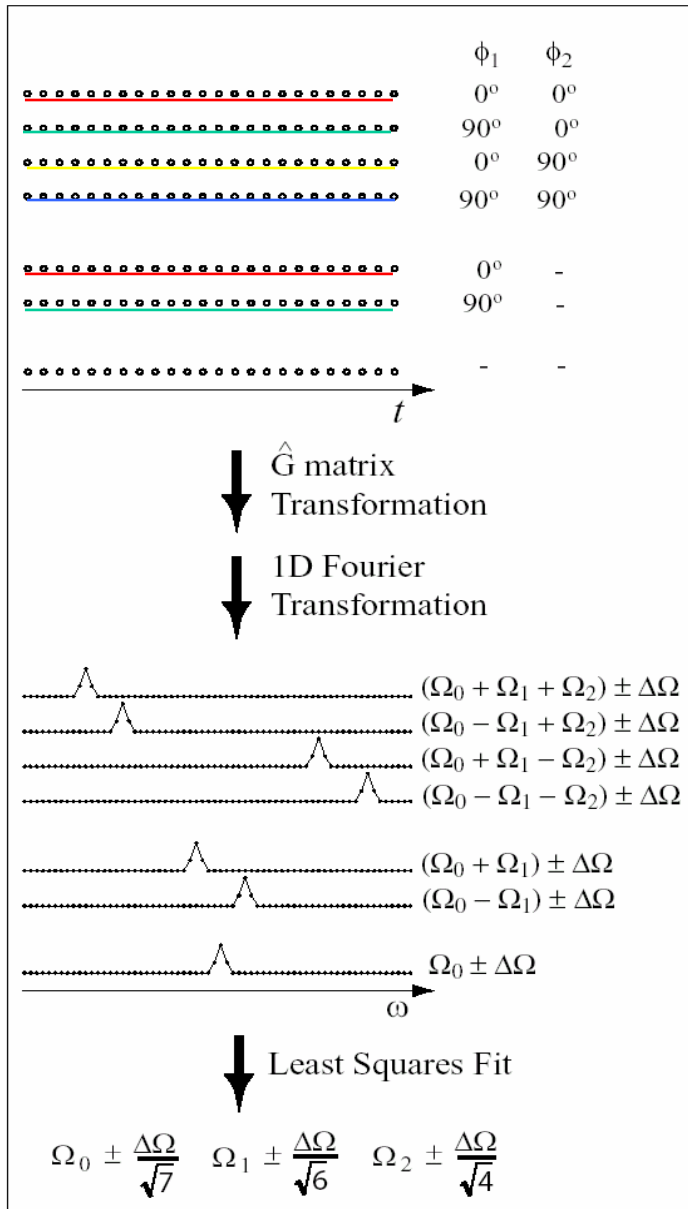
$$\cos(\Omega_0 t)\cos(\Omega_1 t)$$

$$\cos(\Omega_0 t)\sin(\Omega_1 t)$$

FT NMR



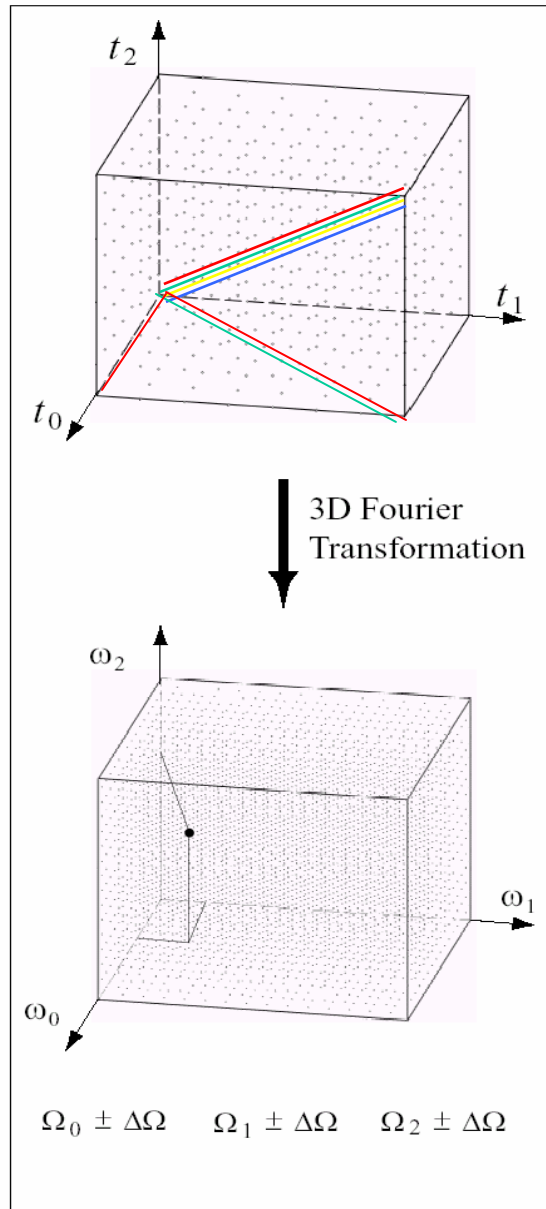
GFT NMR



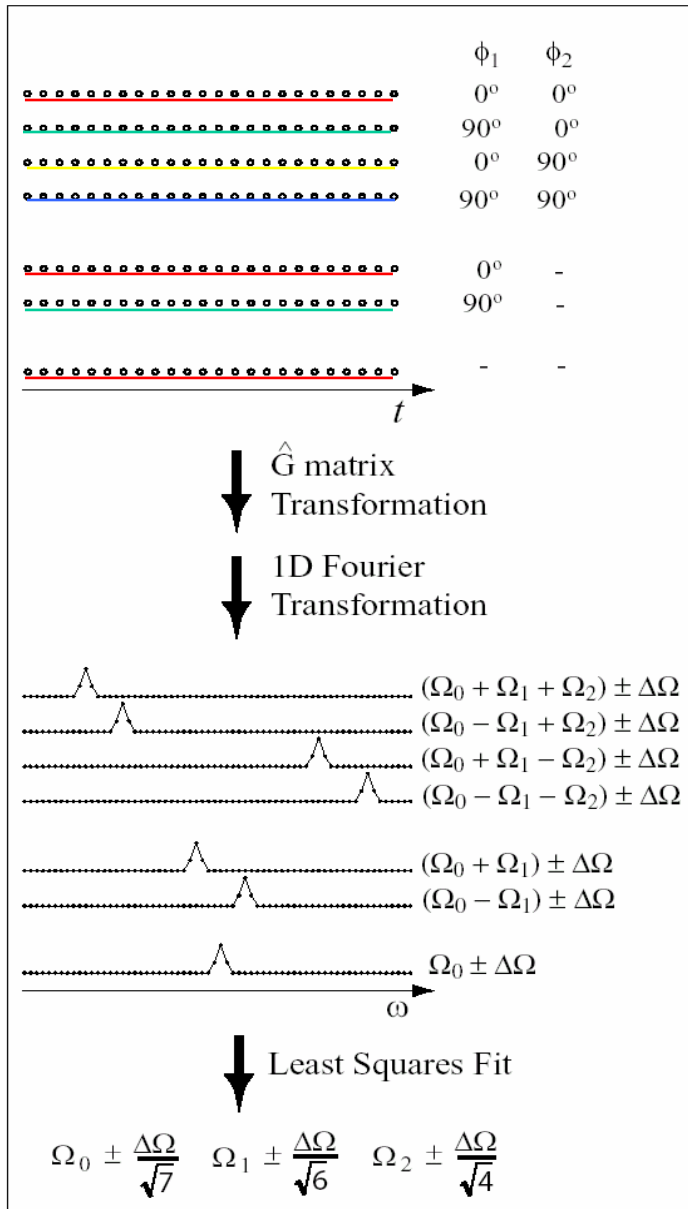
$$\cos(\Omega_0 t)\cos(\Omega_1 t)$$

$$\cos(\Omega_0 t)\sin(\Omega_1 t)$$

FT NMR

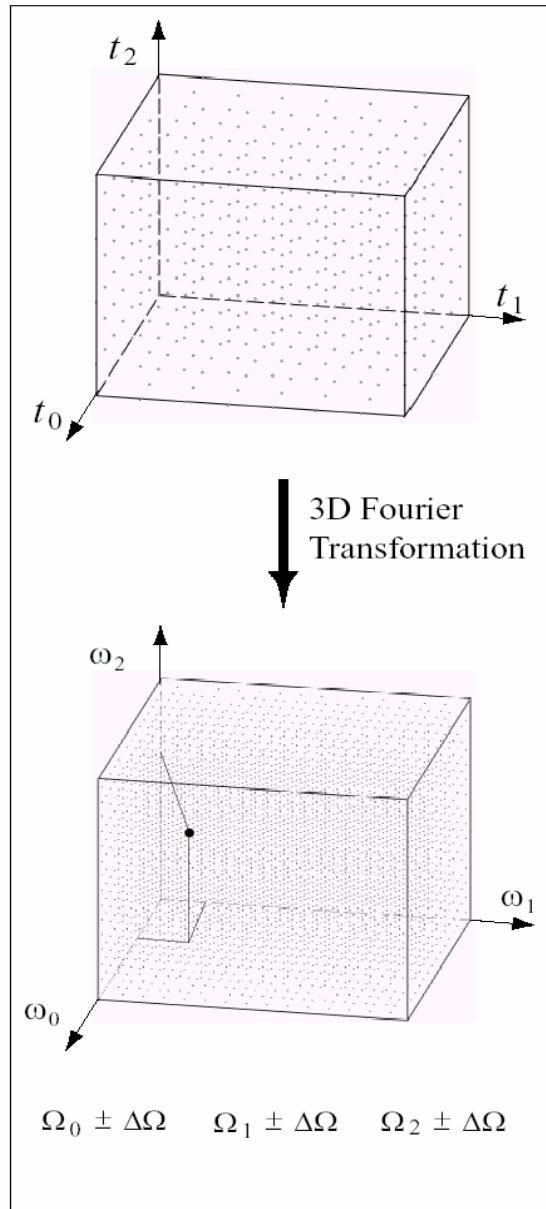


GFT NMR

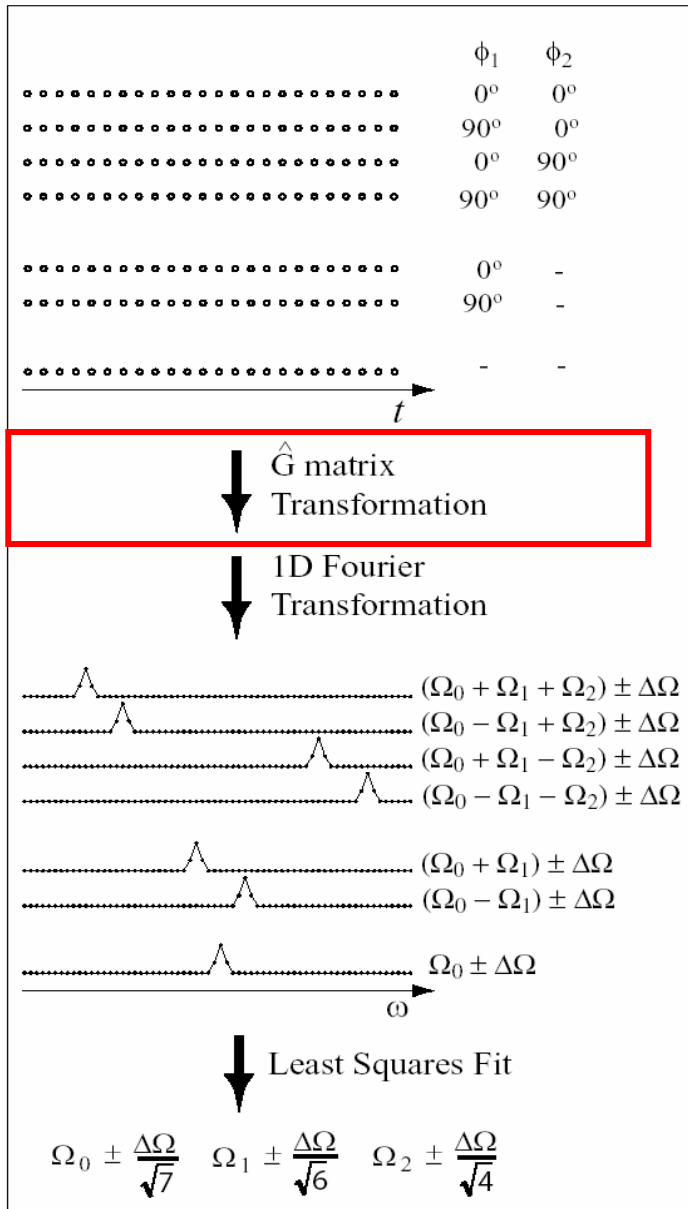


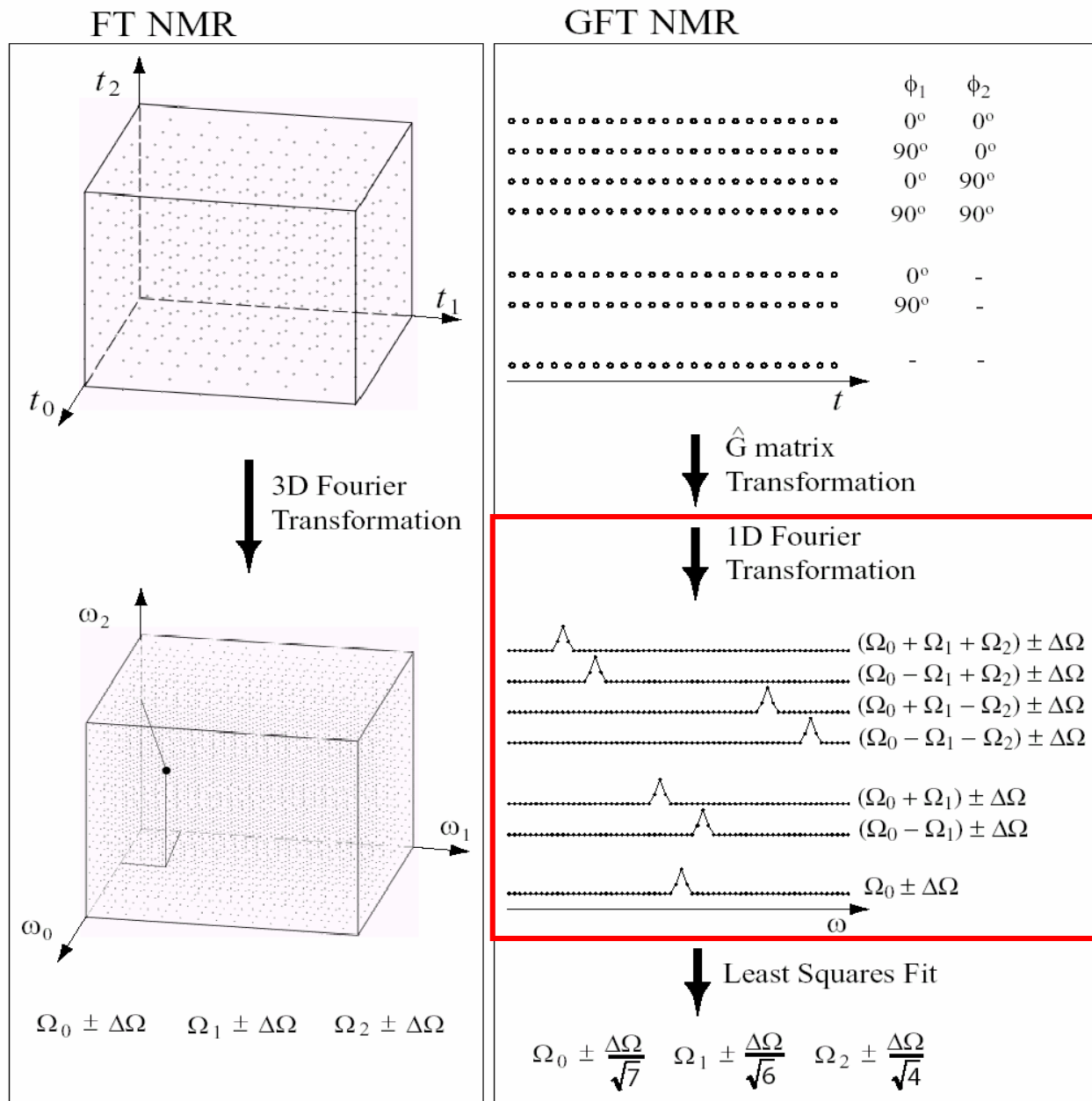
$$\cos(\Omega_0 t)$$

FT NMR



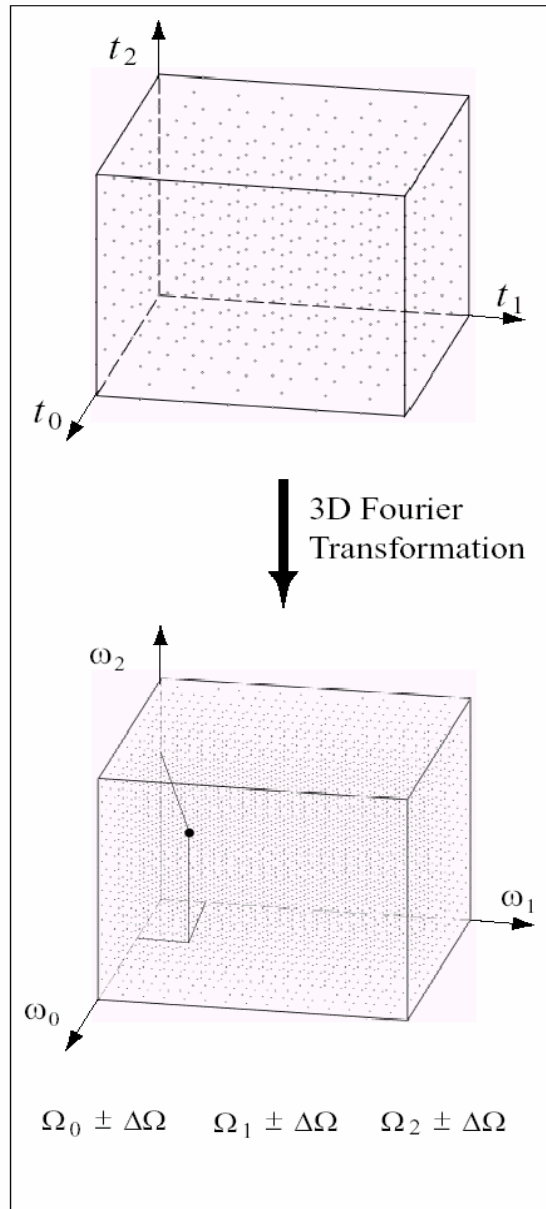
GFT NMR



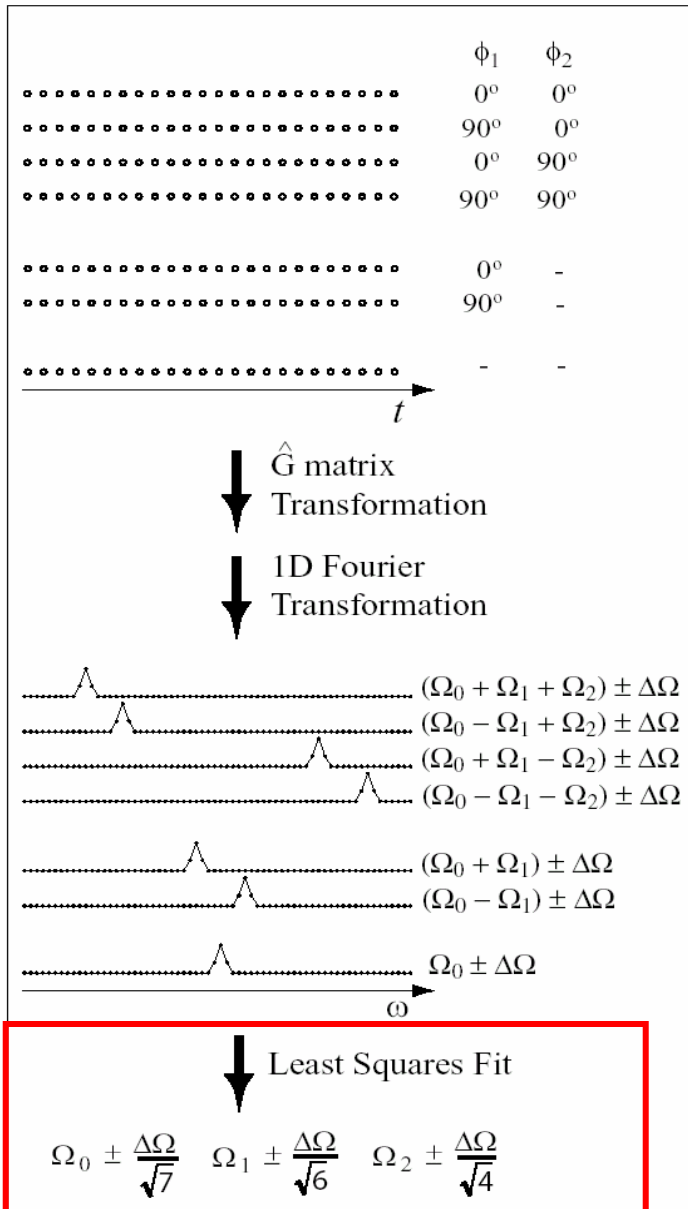


Complete sampling
of linear combinations
of chemical shifts

FT NMR



GFT NMR



The G-matrix:

Phase-sensitive detection of linear combinations of chemical shifts combined with (time domain) editing into different sub-spectra

(4, 2)D GFT NMR

$$S_{1r} \propto \cos(\kappa_0 \Omega_0 t) * \cos(\kappa_1 \Omega_1 t) * \cos(\kappa_2 \Omega_2 t)$$

$$S_{1i} \propto \sin(\kappa_0 \Omega_0 t) * \cos(\kappa_1 \Omega_1 t) * \cos(\kappa_2 \Omega_2 t)$$

$$S_{2r} \propto \cos(\kappa_0 \Omega_0 t) * \sin(\kappa_1 \Omega_1 t) * \cos(\kappa_2 \Omega_2 t)$$

$$S_{2i} \propto \sin(\kappa_0 \Omega_0 t) * \sin(\kappa_1 \Omega_1 t) * \cos(\kappa_2 \Omega_2 t)$$

$$S_{3r} \propto \cos(\kappa_0 \Omega_0 t) * \cos(\kappa_1 \Omega_1 t) * \sin(\kappa_2 \Omega_2 t)$$

$$S_{3i} \propto \sin(\kappa_0 \Omega_0 t) * \cos(\kappa_1 \Omega_1 t) * \sin(\kappa_2 \Omega_2 t)$$

$$S_{4r} \propto \cos(\kappa_0 \Omega_0 t) * \sin(\kappa_1 \Omega_1 t) * \sin(\kappa_2 \Omega_2 t)$$

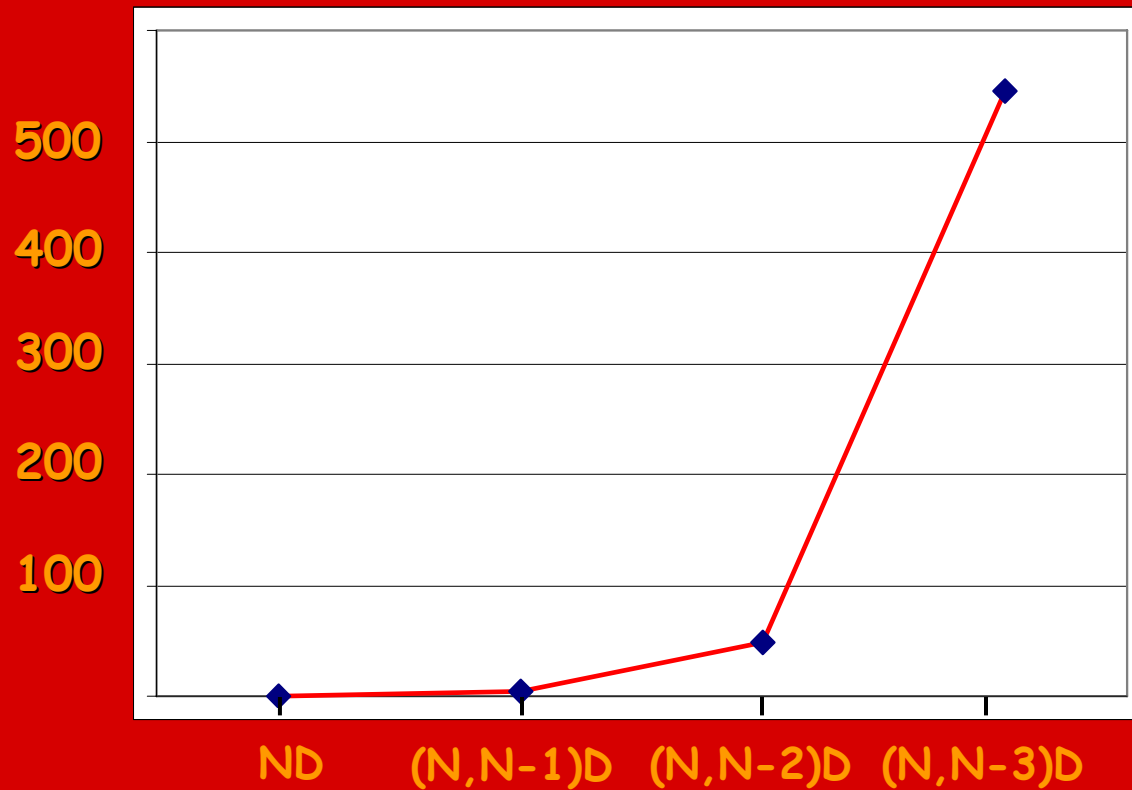
$$S_{4i} \propto \sin(\kappa_0 \Omega_0 t) * \sin(\kappa_1 \Omega_1 t) * \sin(\kappa_2 \Omega_2 t),$$

so that the vector $\mathbf{T}(2) = \mathbf{G}(2) \cdot \mathbf{S}(2)$ is given in complex notation by:

$$\mathbf{T}(2) = \begin{bmatrix} e^{i(\kappa_0 * \Omega_0 + \kappa_1 * \Omega_1 + \kappa_2 * \Omega_2)t} \\ e^{i(\kappa_0 * \Omega_0 - \kappa_1 * \Omega_1 + \kappa_2 * \Omega_2)t} \\ e^{i(\kappa_0 * \Omega_0 + \kappa_1 * \Omega_1 - \kappa_2 * \Omega_2)t} \\ e^{i(\kappa_0 * \Omega_0 - \kappa_1 * \Omega_1 - \kappa_2 * \Omega_2)t} \end{bmatrix} = \begin{bmatrix} 1 & i & i & -1 & i & -1 & -1 & -i \\ 1 & i & -i & 1 & i & -1 & 1 & i \\ 1 & i & i & -1 & -i & 1 & 1 & i \\ 1 & i & -i & 1 & -i & 1 & -1 & -i \end{bmatrix} \cdot \begin{bmatrix} S_{1r} \\ S_{1i} \\ S_{2r} \\ S_{2i} \\ S_{3r} \\ S_{3i} \\ S_{4r} \\ S_{4i} \end{bmatrix} \quad (4).$$

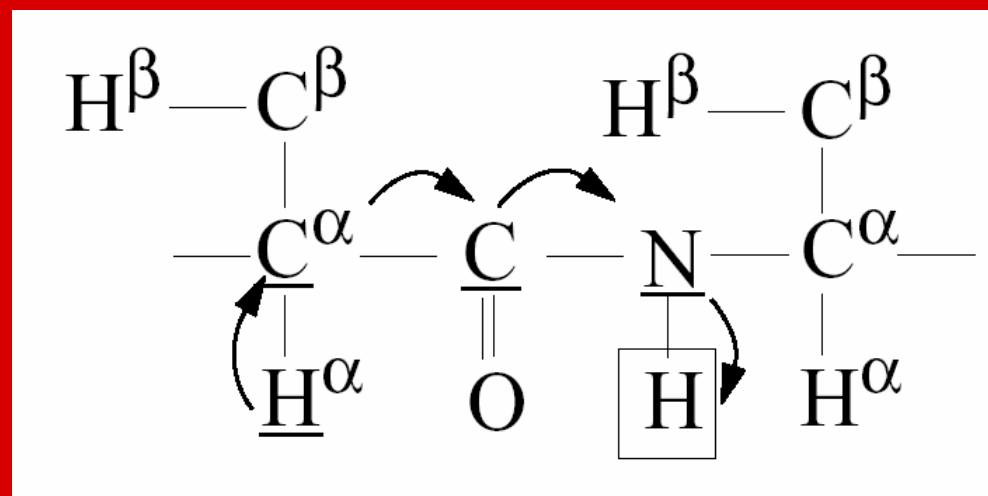
Hence, the four linear combinations of chemical shifts, $\kappa_0 * \Omega_0 \pm \kappa_1 * \Omega_1 \pm \kappa_2 * \Omega_2$, are measured in one of the four sub-spectra each.

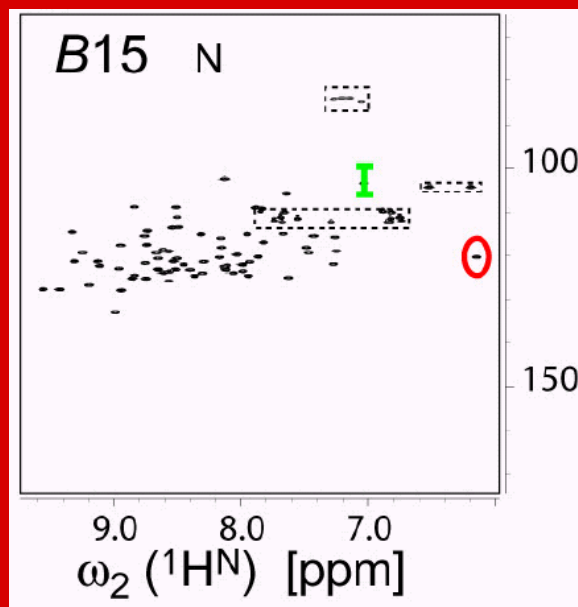
Reduction of minimal measurement time



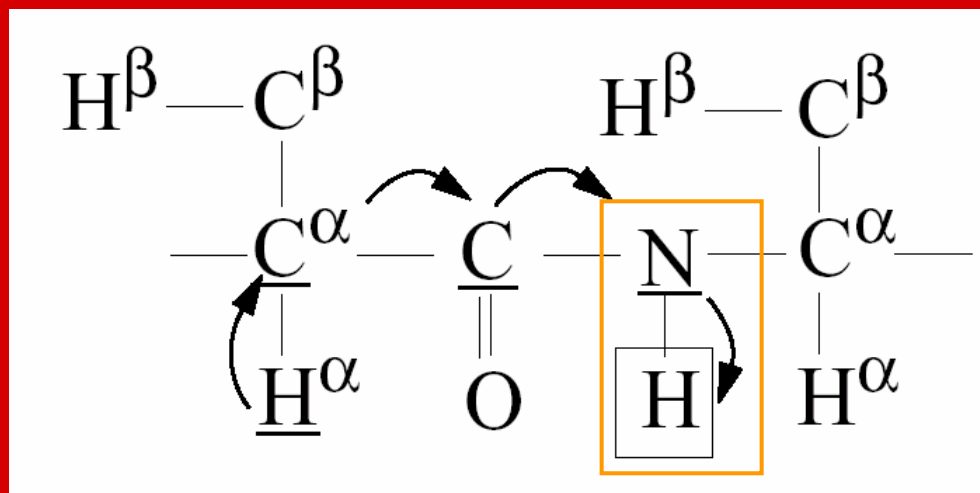
$$\frac{\prod_1^K n_i}{\sum_1^K n_i} * \frac{2^K}{2^{K+1} - 1}$$

(5,2)D HACACONHN

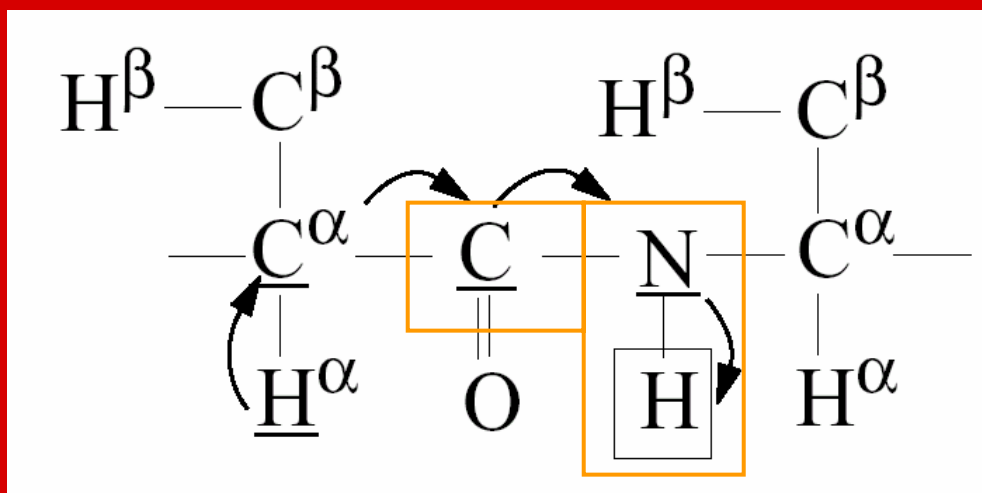
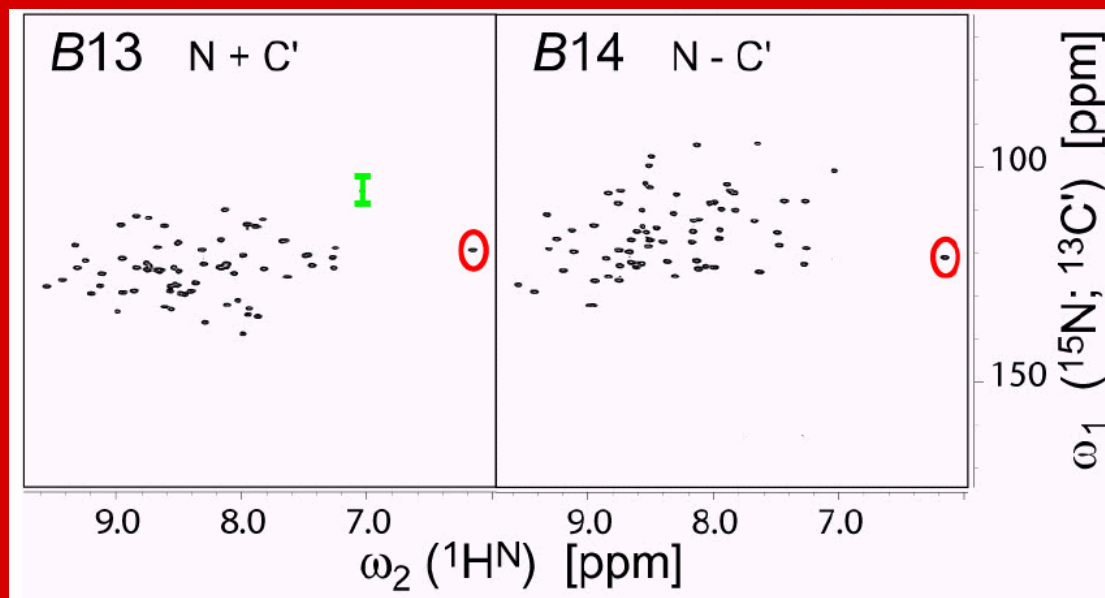




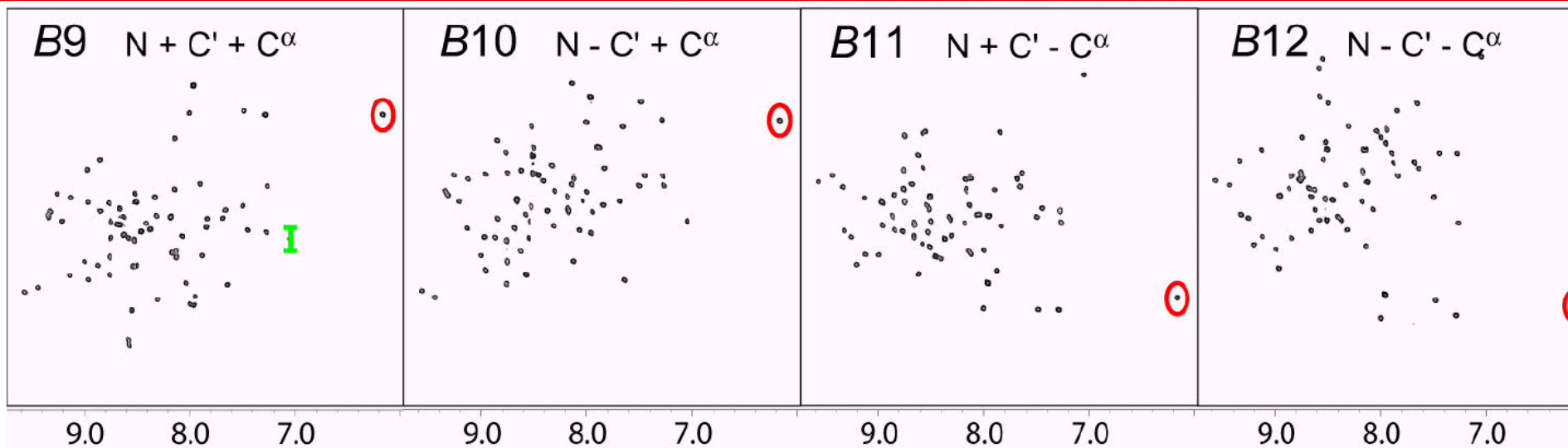
2D
Information
13.8 min



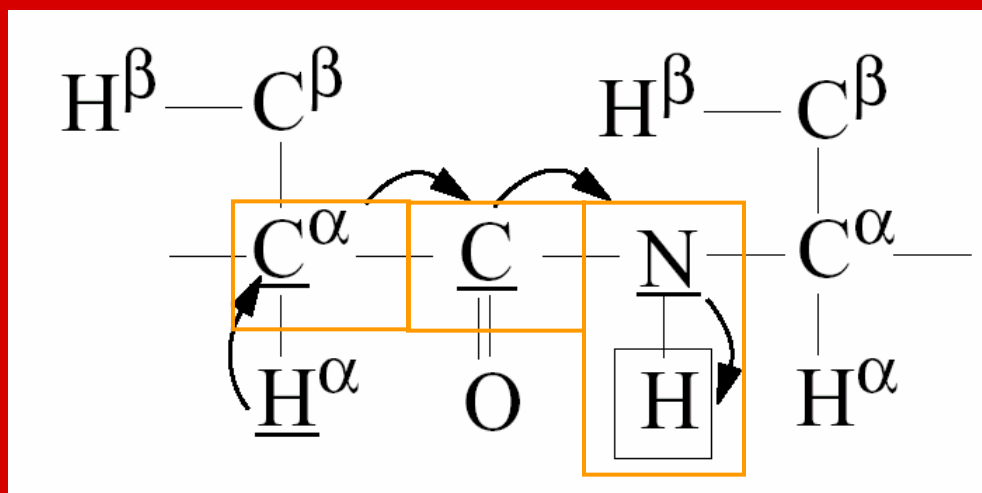
NMRFam Workshop 06/06/06

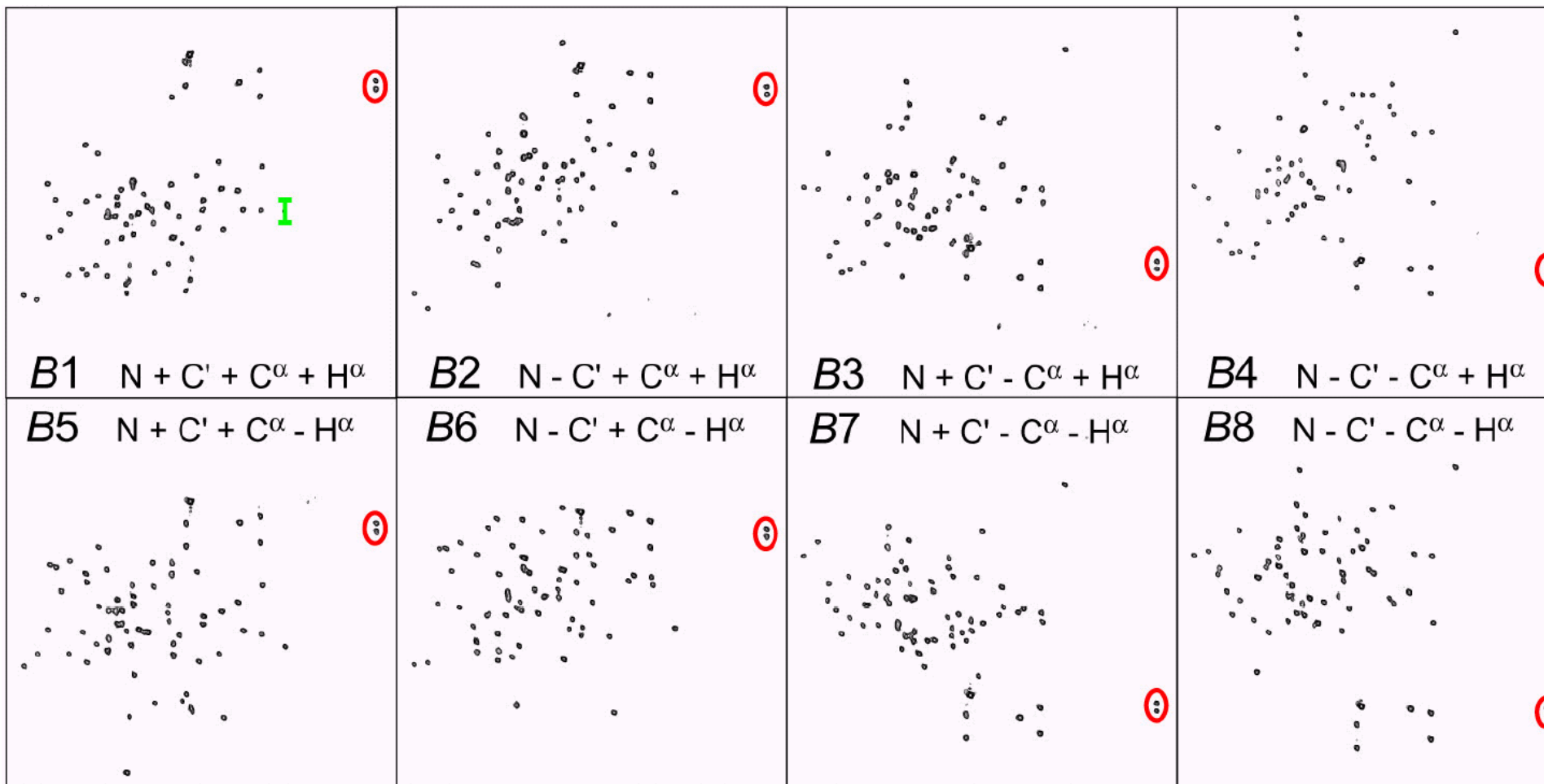


3D
Information
+25.2 min

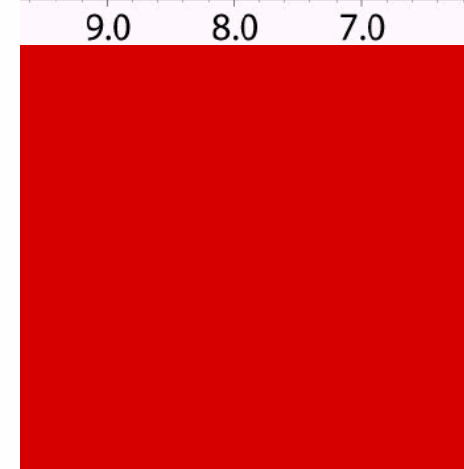
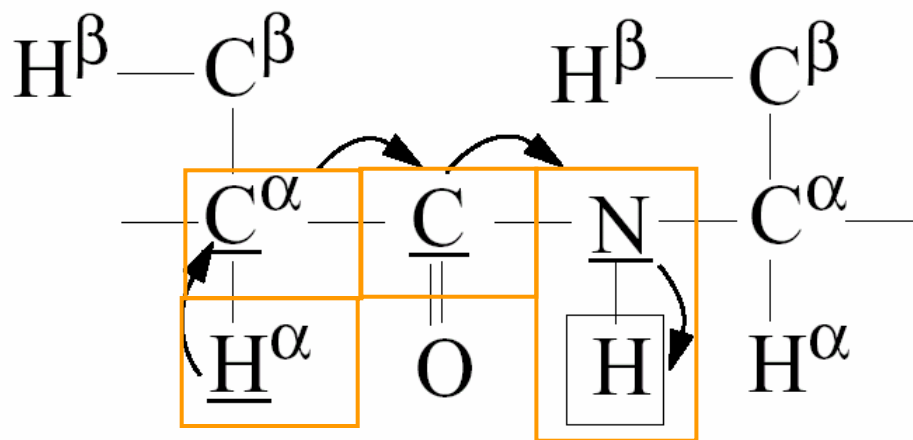


4D
Information
+52.8 min





5D
Information
+108 min



Features of GFT NMR

- Generally applicable acquisition scheme
- Accurate adaptation of measurement times to sensitivity requirement *without* sacrificing digital resolution or high dimensional correlation
- 5D or 6D feasible
- No additional hardware required
- Data size reduction
- Accelerated processing speed
- Robustness of data analysis

Time versus frequency domain editing

- Linear prediction -> time domain editing preferred
- Maximum entropy reconstruction, Filter-diagonalization etc.

GFT NMR - methodological extensions.....

Resonance Assignment of Proteins with High Shift Degeneracy Based on 5D Spectral Information Encoded in G²FT NMR Experiments

Hanudatta S. Atreya, Alexander Eletsy, and Thomas Szyperski*

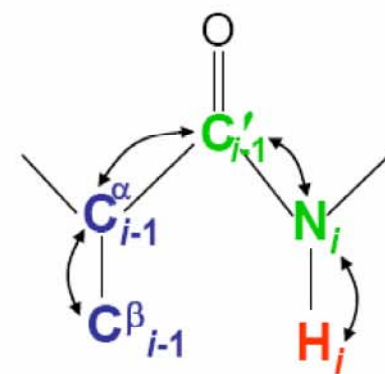
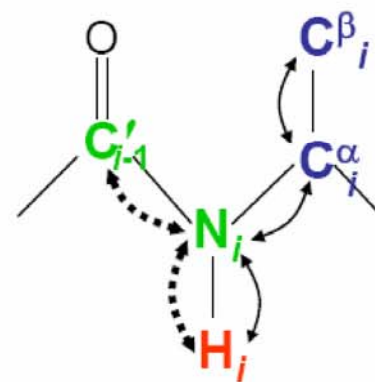
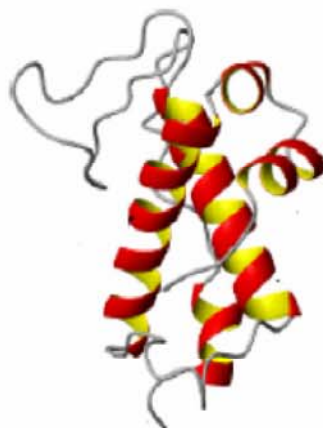
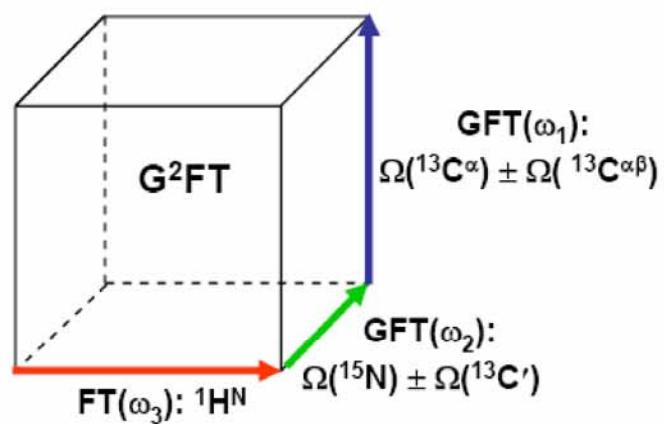
Department of Chemistry, State University of New York at Buffalo, Buffalo, New York 14260

Received December 10, 2004; E-mail: szypersk@chem.buffalo.edu

G²FT NMR

A contribution to establish
NMR-based structural genomics of
membrane proteins

G^2FT (5,3)D $\underline{HN}\{\underline{N}, \underline{CO}\}\{\underline{C}^{\alpha\beta}, \underline{C}^{\alpha}\}$



Longitudinal and transverse
relaxation optimized

GFT NMR:

L-GFT-TROSY

Pervushin, K.; Vogeli, B.; Eletsky, A. *J. Am. Chem. Soc.* **2002**, *124*, 12898–12902.

9642–9647 | PNAS | June 29, 2004 | vol. 101 | no. 26

G-matrix Fourier transform NMR spectroscopy for complete protein resonance assignment

Hanudatta S. Atreya and Thomas Szyperski*

Departments of Chemistry and Structural Biology, State University of New York, Northeast Structural Genomics Consortium, Buffalo, NY 14260

Communicated by Herbert Hauptman, Hauptman–Woodward Medical Research Institute, Buffalo, NY, May 18, 2004 (received for review December 14, 2003)

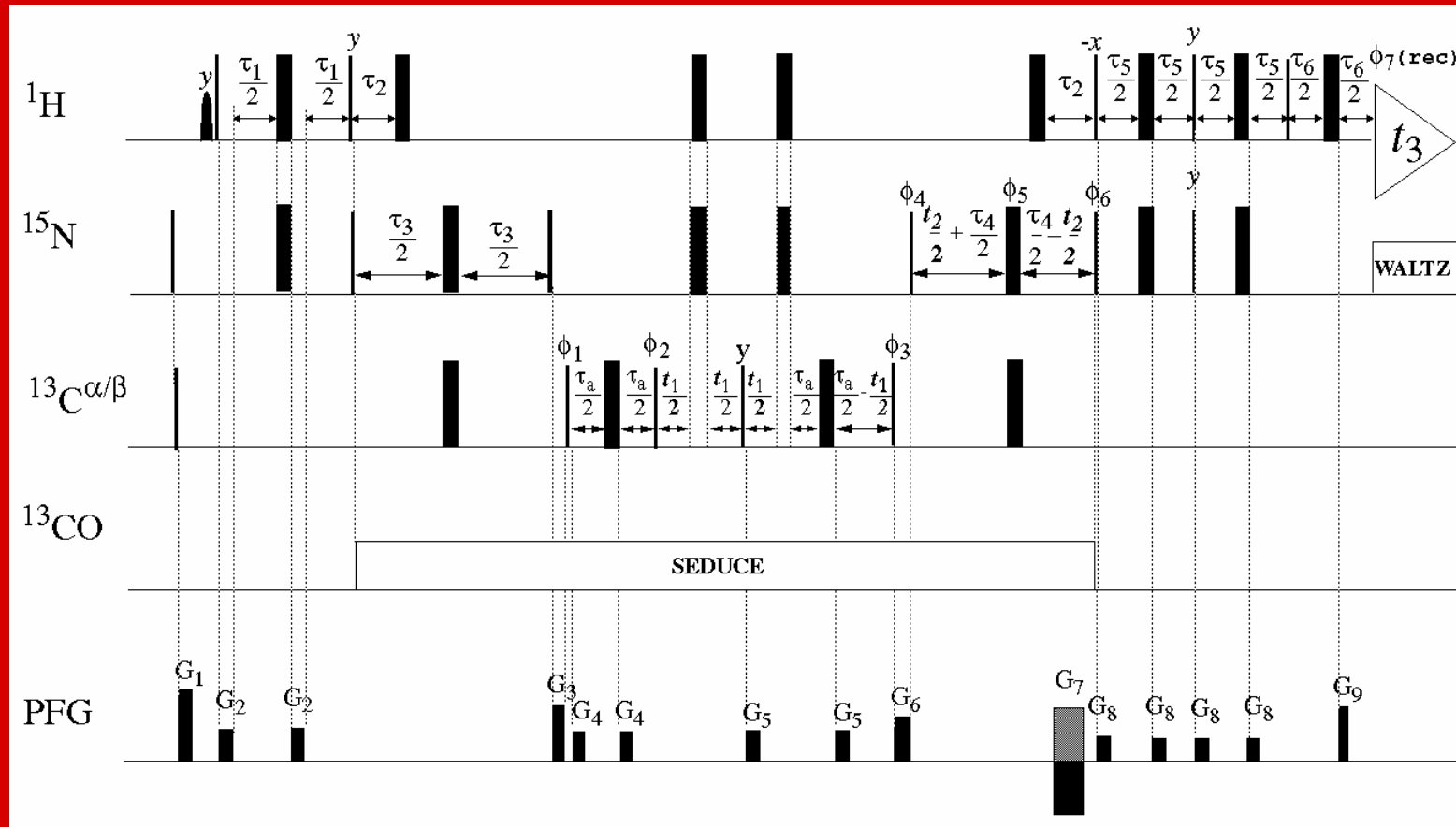
A G-matrix Fourier transform (GFT) NMR spectroscopy-based strategy for resonance assignment of proteins is described. Each of the GFT NMR experiments presented here rapidly affords four-, five-, or six-dimensional spectral information in combination with precise measurements of chemical shifts. The resulting high information content enables one to obtain nearly complete assignments by using only four NMR experiments. For the backbone amide proton detected “out-and-back” experiments, data collection was further accelerated up to ≈ 2.5 -fold by use of longitudinal ^1H relaxation optimization. The GFT NMR experiments were acquired for three proteins with molecular masses ranging from 8.6 to 17 kDa, demonstrating that the proposed strategy is of key interest for automated resonance assignment in structural genomics.

Nearly complete resonance assignments are generally considered a necessity for NMR-based protein structure determination (e.g., refs. 11 and 12). Here we describe a strategy for complete protein resonance assignment based on GFT NMR experiments affording accurate 4D, 5D, and 6D spectral information. Applications are presented for proteins with molecular masses ranging from 8.6 to 17 kDa.

Materials and Methods

NMR Spectrometer and Protein Samples. All measurements were performed at 25°C on Varian INOVA 600 and 750 MHz spectrometers, equipped with conventional $^1\text{H}/^{13}\text{C}/^{15}\text{N}$ triple-resonance probes, by using ≈ 1 mM solutions in 95% $\text{H}_2\text{O}/5\%$

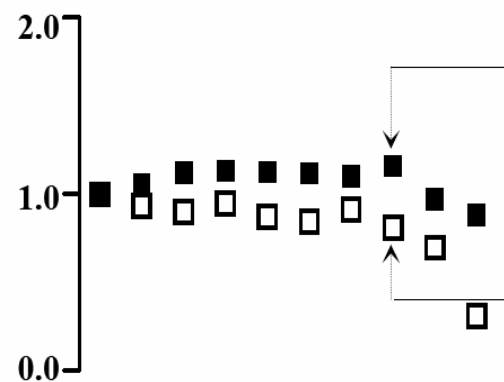
L-(4,3)D HNN(CO)C^{αβ}C^α



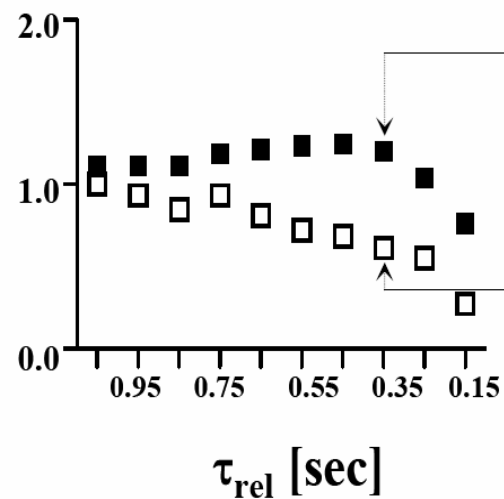
Water and aliphatic ¹H magnetization along +z
at the start of signal detection

(a) $\frac{(S/N)_{\tau_{rel}}}{(S/N)_{\tau_{rel}=1.05s}}$

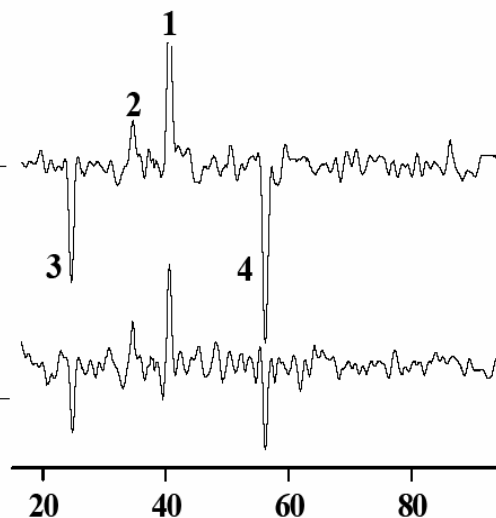
Leu 8



Ala 46

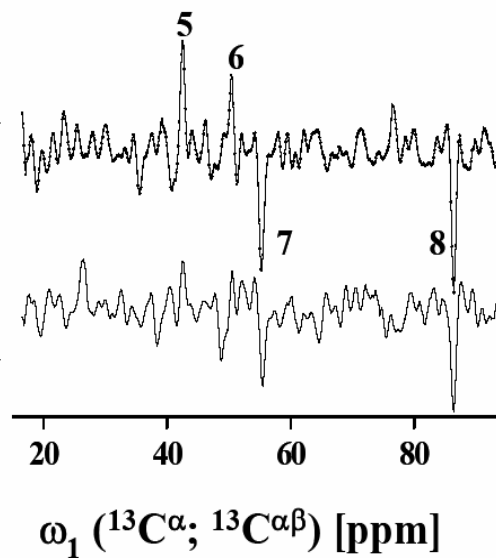


(b) Relaxation delay: 0.35s (d1=0.3s)



L-optimized

Not L-optimized



L-optimized

Not L-optimized

ω_1 ($^{13}\text{C}\alpha$; $^{13}\text{C}\alpha\beta$) [ppm]

....GFT NMR for the
aromatic rings ...

L-optimization of aromatic protons

(nearly) complete resonance assignment of aromatic protons is required for:

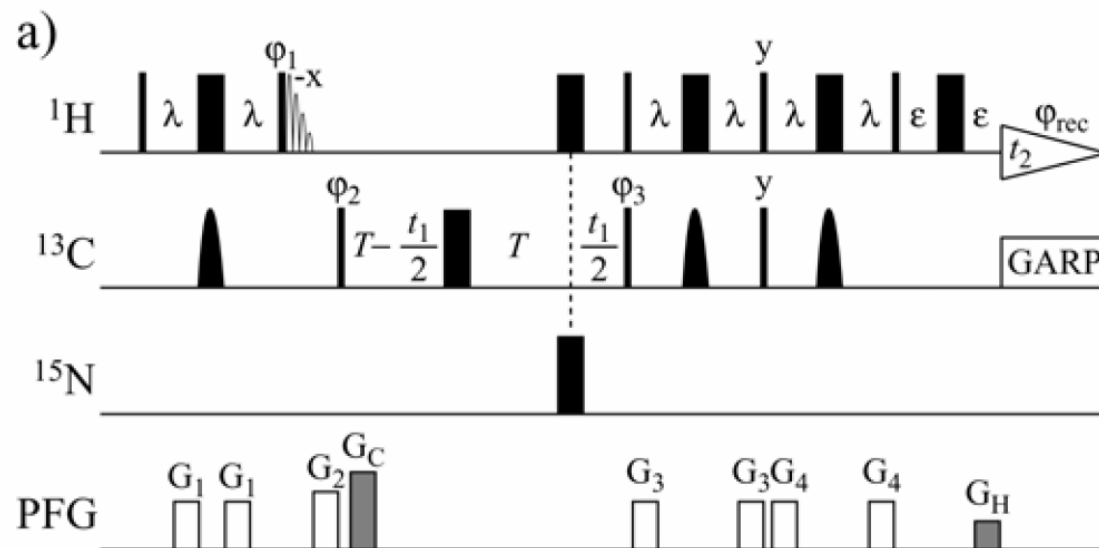
- > high-quality structure determination
- > using aromatic rings to probe protein dynamics

L-GFT-TROSY (4,3)D HCCH

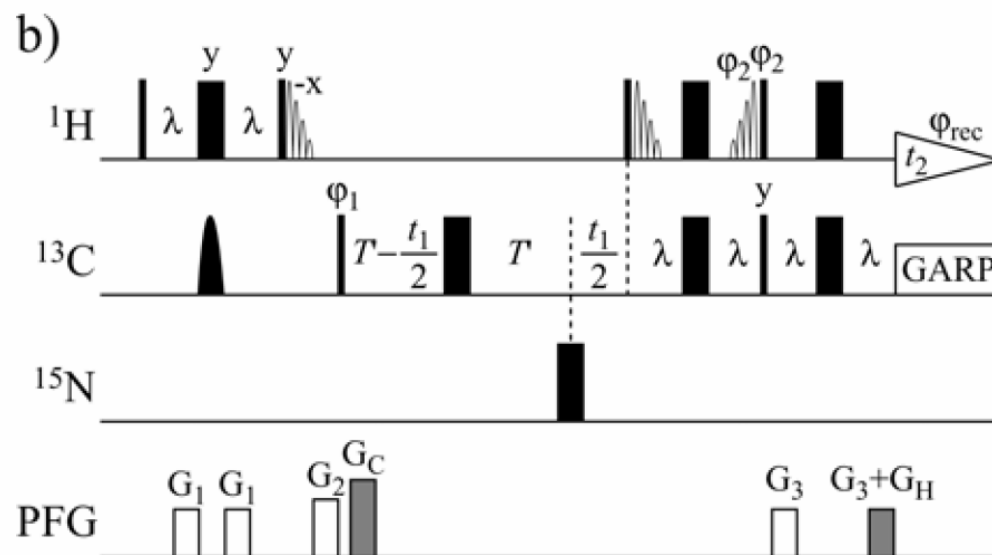
Longitudinal (L-) Relaxation Optimization
for Aromatic Protons:

Water and aliphatic ^1H magnetization along **+z**
at the start of signal detection

Evaluation in 2D NMR



HSQC



TROSY

L-optimization for ^{13}C - ^1H aromatic

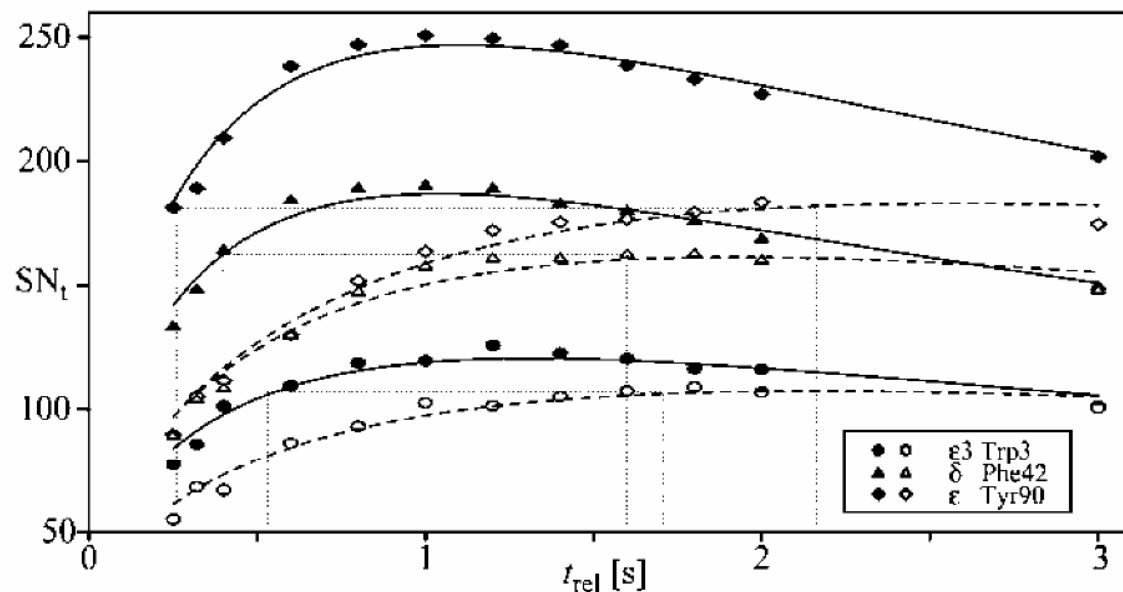
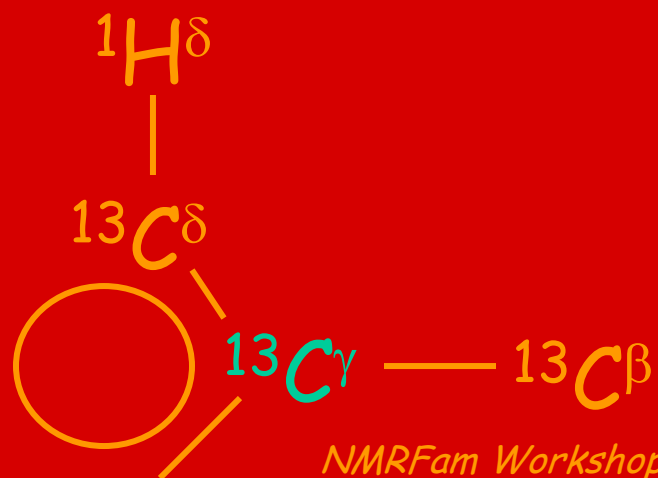
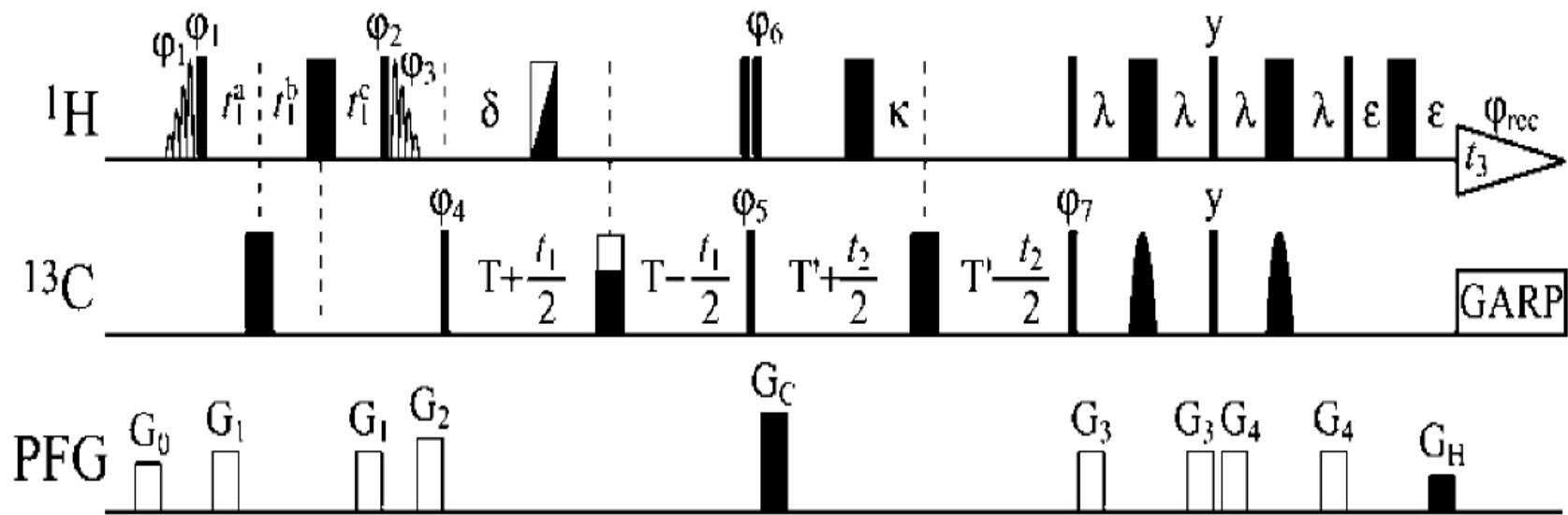


Figure 1. SN_t in *ct* 2D [^{13}C , ^1H]-HSQC versus t_{rel} for three peaks of protein PfR13 (20 °C; 750 MHz). Filled (open) symbols and solid (dashed) lines correspond to spectra acquired *with* (*without*) L-optimization. Vertical lines at ~ 1.6 – 2.2 s indicate $t_{\text{rel}}^{\text{opt}}$ *without* L-optimization, and those at ~ 0.2 – 0.5 s indicate $t_{\text{rel}}^{\text{match}}$ (Table S1) where L-optimized congeners reach the same intrinsic sensitivity.

$$\text{SN}_t = A \frac{1 - \exp(-R_1(t_{\text{rel}} + t_{\text{acq}}))}{\sqrt{t_{\text{rel}} + t_{\text{acq}} + t_{\text{seq}}}}$$

L-GFT-TROSY (4,3)D HCCH



L-GFT-TROSY (4,3)D HCCH
to avoid sampling limited data acquisition:
4D HCCH-information in 25 minutes

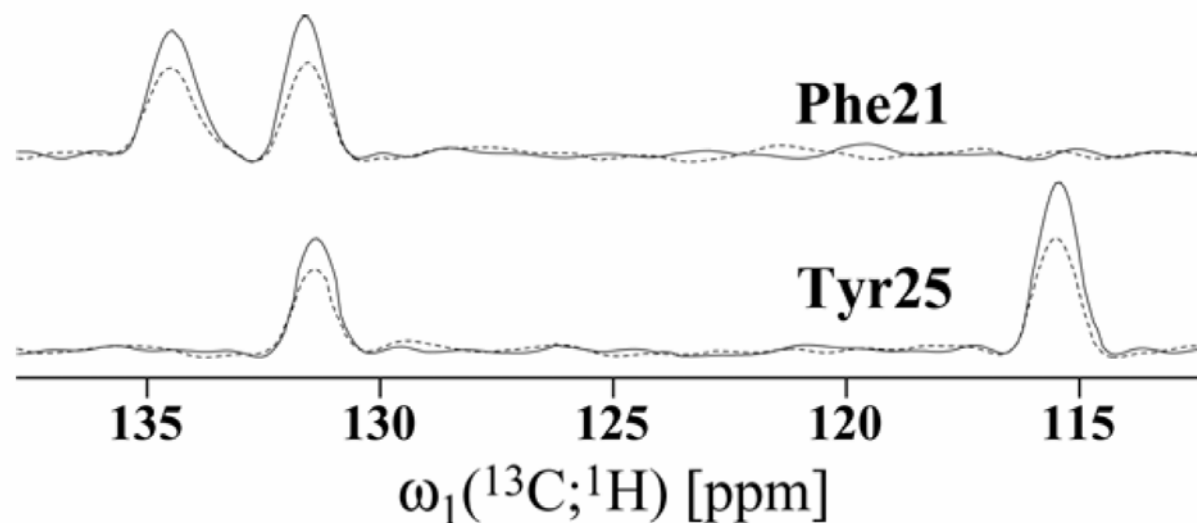


Figure S6. Cross sections taken along the GFT dimension from L-GFT (4,3)D HCCH (solid traces) and GFT (4,3)D HCCH (dotted traces) acquired for 11 kDa protein MaR11 in 25 min each.

L-GFT-TROSY (4,3)D \underline{HCCH} for 21 kDa HR41

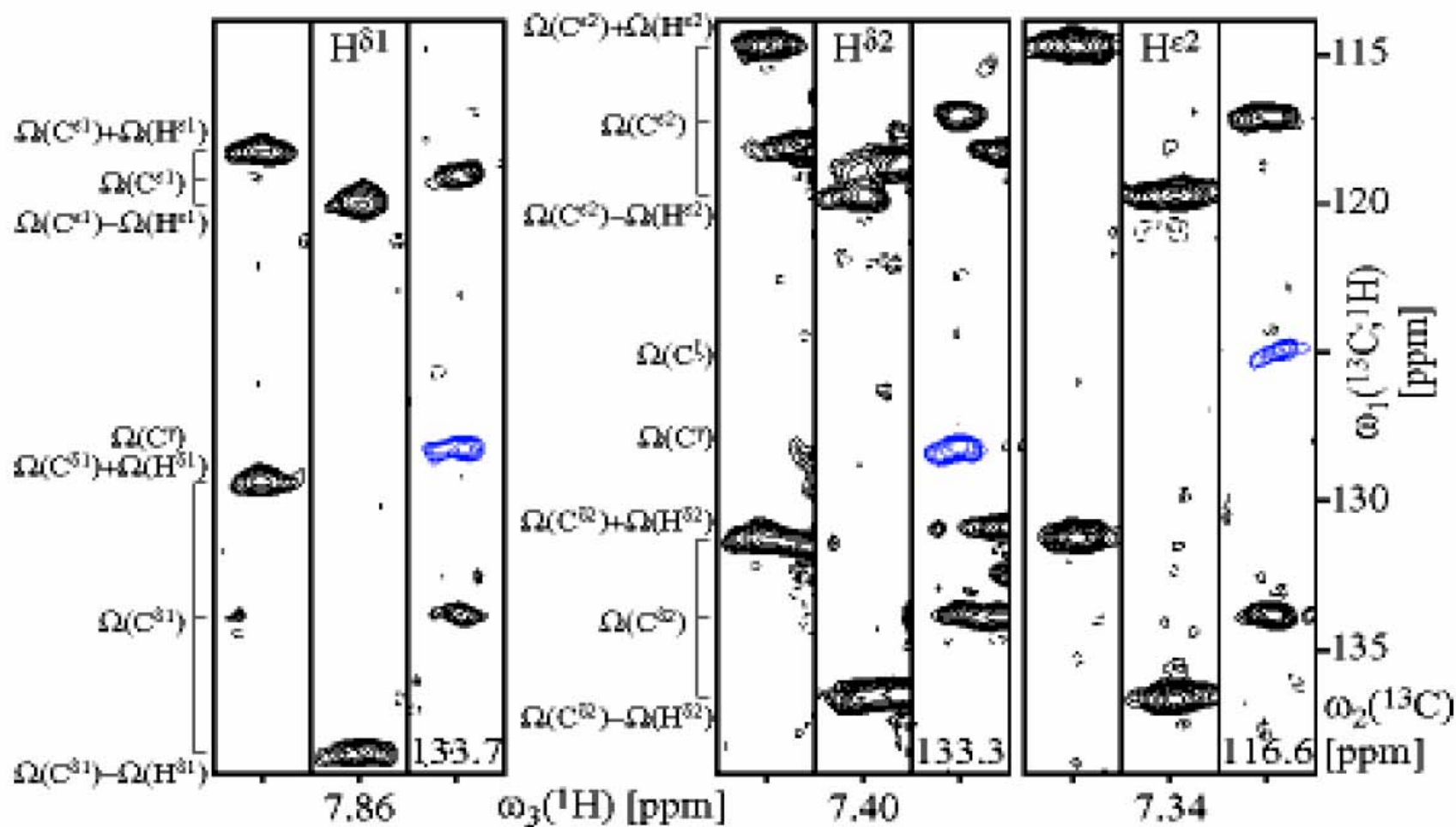


Figure 3. $[\omega_1(^{13}C(1); ^1H(1)), \omega_3(^1H(2))]$ -strips taken along the GFT dimension of L-GFT-TROSY (4,3)D \underline{HCCH} recorded at 750 MHz for 21 kDa HR41 with $t_{rel} = 1$ s. Peaks belong to the slowly flipping ring of Tyr 90. Central peaks arising from $^{13}C/\zeta$ polarization are depicted in blue.

Aromatic ^1H linewidths in HR41

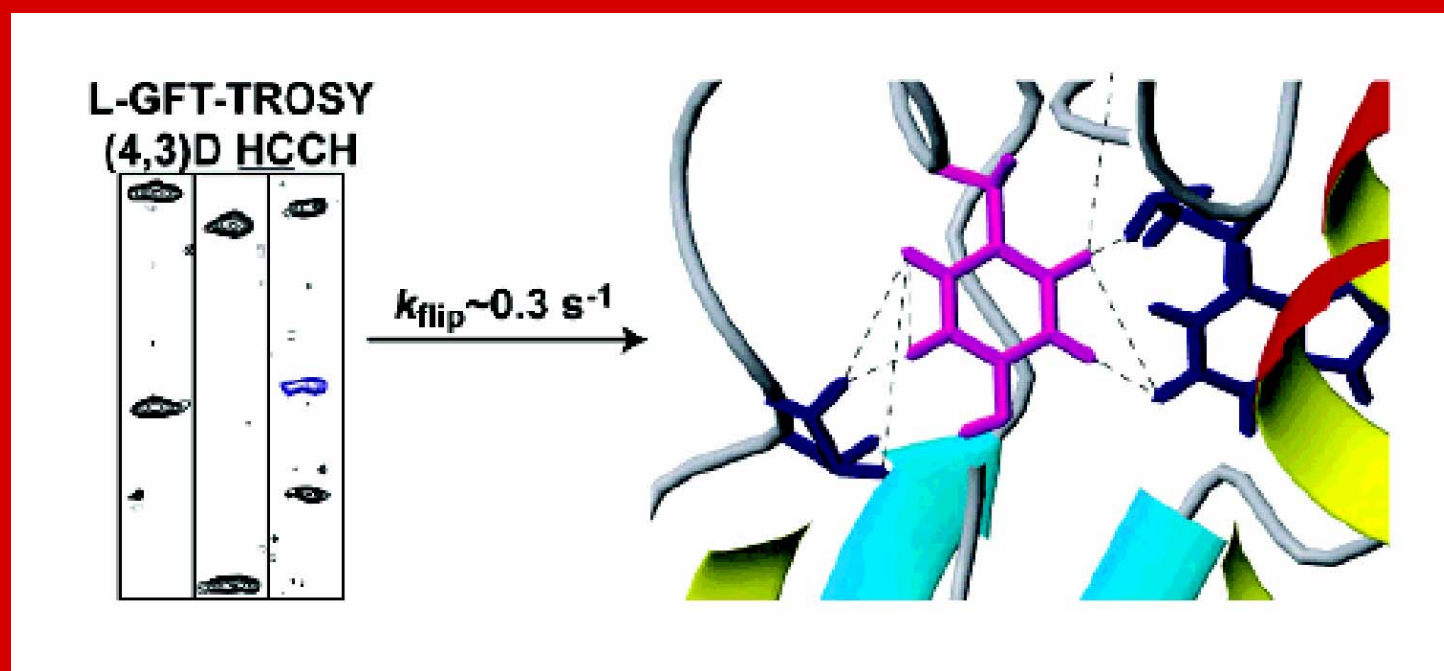
Table S6: $^1\text{H}^{\text{aromatic}}$ line-widths of HR41 at 25 °C from 2D [$^{13}\text{C}, ^1\text{H}$] TROSY and (4,3)D HCCH

Res. No.	Res.	Atom Type	^1H linewidth [Hz]		
			2D [$^{13}\text{C}, ^1\text{H}$] TROSY	L-GFT (4,3)D HCCH	Average
28	Trp	H $^{\delta 1}$	32	-	32
28	Trp	H $^{\epsilon 3}$	42	40	41
28	Trp	H $^{\eta 2}$	40	41	41
28	Trp	H $^{\zeta 2}$	38	-	38
28	Trp	H $^{\zeta 3}$	-	42	42
36	Tyr	H $^{\delta}$	-	21	21
36	Tyr	H $^{\epsilon}$	-	21	21
42	Tyr	H $^{\delta}$	-	35	35
42	Tyr	H $^{\epsilon}$	-	32	32
53	Trp	H $^{\delta 1}$	35	-	35
53	Trp	H $^{\eta 2}$	43	41	42
53	Trp	H $^{\zeta 2}$	-	35	35
53	Trp	H $^{\zeta 3}$	-	39	39
54	Phe	H $^{\epsilon}$	52	-	52
54	Phe	H $^{\zeta}$	44	-	44
65	Trp	H $^{\delta 1}$	-	<37 ^a	<37 ^a
65	Trp	H $^{\eta 2}$	-	39	39
65	Trp	H $^{\zeta 2}$	38	34	36
66	Phe	H $^{\delta}$	-	25	25
66	Phe	H $^{\epsilon}$	27	24	25
66	Phe	H $^{\zeta}$	25	26	26
70	Trp	H $^{\delta 1}$	33	39	36
70	Trp	H $^{\epsilon 3}$	-	34	34
70	Trp	H $^{\eta 2}$	-	42	42
70	Trp	H $^{\zeta 2}$	-	33	33
70	Trp	H $^{\zeta 3}$	-	<36 ^a	<36 ^a

71	Tyr	H $^{\delta}$	-	<29 ^a	<29 ^a
71	Tyr	H $^{\epsilon}$	-	<33 ^a	<33 ^a
78	Tyr	H $^{\epsilon}$	-	<35 ^a	<35 ^a
80	Phe	H $^{\delta}$	-	32	32
80	Phe	H $^{\epsilon}$	41	41	41
80	Phe	H $^{\zeta}$	40	-	40
84	Phe	H $^{\delta}$	39	35	37
84	Phe	H $^{\epsilon}$	44	42	43
84	Phe	H $^{\zeta}$	44	45	45
90	Tyr	H $^{\delta 1}$	45	34	39
90	Tyr	H $^{\delta 2}$	-	36	36
90	Tyr	H $^{\epsilon 1}$	-	32	32
90	Tyr	H $^{\epsilon 2}$	40	38	39
110	Tyr	H $^{\delta}$	31	27	29
110	Tyr	H $^{\epsilon}$	-	27	27
121	Phe	H $^{\delta}$	-	<42 ^a	<42 ^a
121	Phe	H $^{\epsilon}$	-	<42 ^a	<42 ^a
121	Phe	H $^{\zeta}$	39	-	39
125	Trp	H $^{\delta 1}$	34	35	35
125	Trp	H $^{\eta 2}$	-	<41 ^a	<41 ^a
125	Trp	H $^{\zeta 2}$	-	<39 ^a	<39 ^a
132	Phe	H $^{\delta}$	36	35	35
132	Phe	H $^{\epsilon}$	37	38	38
132	Phe	H $^{\zeta}$	39	-	39
145	Trp	H $^{\delta 1}$	37	36	37
145	Trp	H $^{\epsilon 3}$	51	-	51
145	Trp	H $^{\eta 3}$	-	<36 ^a	<36 ^a
145	Trp	H $^{\zeta 2}$	43	44	43
145	Trp	H $^{\zeta 3}$	-	<48 ^a	<48 ^a
Completeness			42%	71%	85%

^a Upper limit only due to spectral overlap.

Ring flipping and functional dynamics in the 21 kDa protein HR41



L-GFT-TROSY (4,3)D HCCH for larger proteins

- L-optimization and PFG-PEP increase intrinsic sensitivity ~2-fold
- L-optimization enables ~3-fold faster data sampling
- TROSY allows use of $^{13}\text{C}_{\text{aro}}$ polarization for central peak detection
- **Nearly complete resonance assignments of aromatic resonances based on 4D spectral information enable**
 - high-quality structure determination
 - use aromatic rings to explore larger amplitude motional modes

**GFT NMR for
high-throughput protein
structure determination**

Approaches for rapid NMR data collection

Approach	Acceleration	Data Processing
Basic		
<i>Reduction of t_{\max}</i>	$< \sim 1.5$ for each dimension	FT
<i>Reduction of t_{rel}</i>	$< \sim 2$	FT
<i>Aliasing</i>	$< \sim 3$	FT
Advanced		
<i>Sparse sampling</i>	$< \sim 2-3$	MER or TWD/FT
<i>L-optimization: Reduction of t_{rel}</i>	$\sim 2-3$	FT
<i>Simultaneous acquisition</i>	$< \sim 2$	FT
<i>Hadamard spectroscopy</i>	$< \sim 2$	HT
<i>Single scan ND NMR</i>	$\sim 10-50$ (each dimension)	FT
<i>RD NMR spectroscopy</i>	~ 10	FT
<i>GFT NMR spectroscopy</i>	$\sim 10^k$ for $(N, N-k)D$	G-matrix FT

From: H. Atreya & T. Szyperski. *Methods Enzymol.* **2005**, *394*, 78–108.

GFT projection NMR based structure determination protocol

sequence specific ^{15}N , ^1H ,
 $^{13}\text{C}_\alpha$ and $^{13}\text{C}_\beta$ assignment

(4,3)D $\text{HNNC}_{\alpha\beta}\text{C}_\alpha$ and
(4,3)D $\text{C}_{\alpha\beta}\text{C}_\alpha(\text{CO})\text{NHN}$

1~2d

$^1\text{H}_\alpha$ / $^1\text{H}_\beta$
assignment

(5,2)D HACACONHN ($^1\text{H}_\alpha$) OR
(4,3)D $\text{H}_{\alpha\beta}\text{C}_{\alpha\beta}(\text{CO})\text{NHN}$ ($^1\text{H}_\alpha$ / $^1\text{H}_\beta$)

1~3d

side-chain assignment
(aliphatic and aromatic)
→ NO C-C TOCSY

(4,3)D HCCH

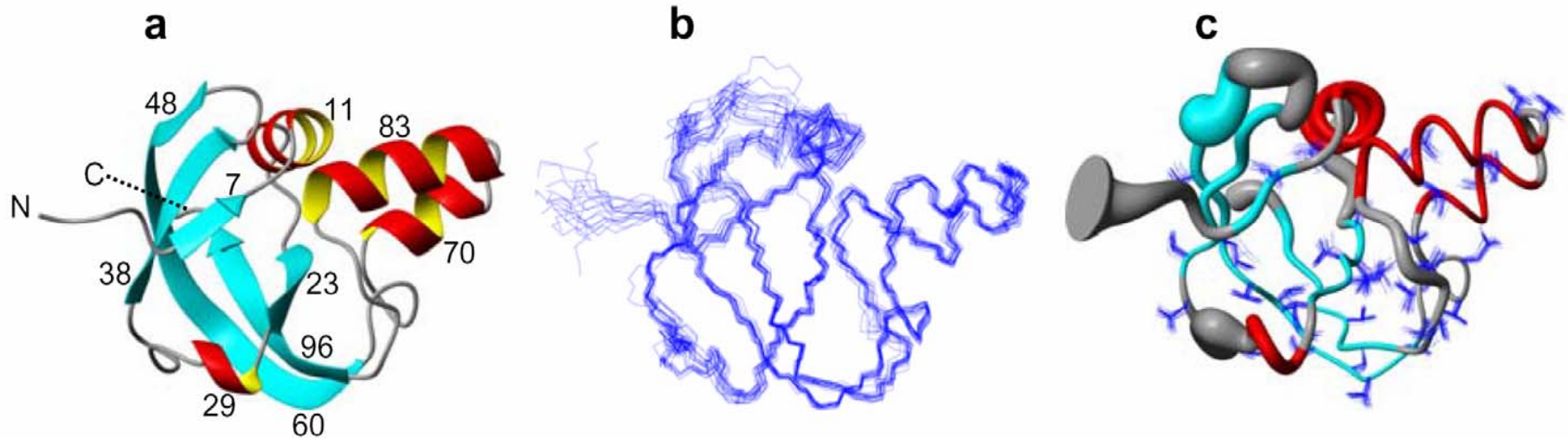
3D $^{15}\text{N}/^{13}\text{C}_{\text{aliph}}/^{13}\text{C}_{\text{arom}}$ -
resolved $^1\text{H}, ^1\text{H}$ -NOESY

5~10d

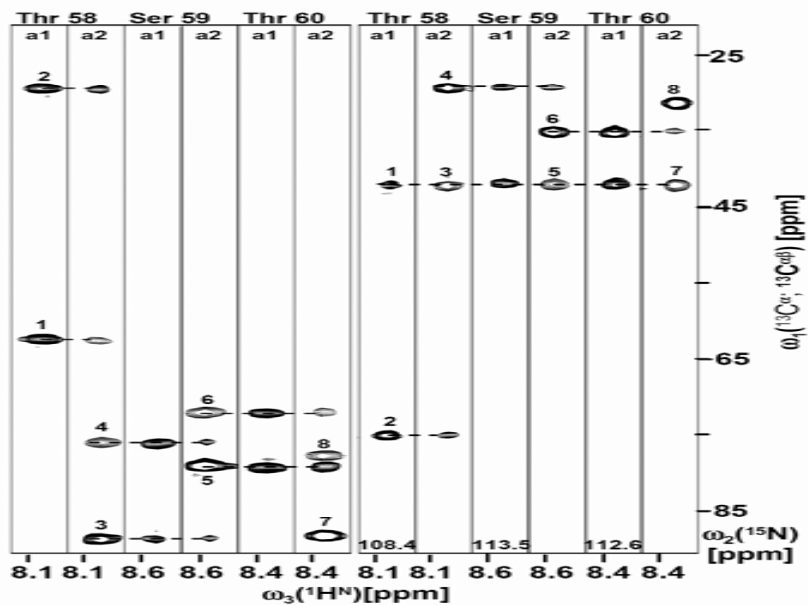
structure
calculation and
refinement

CYANA/AUTOSTRUCTURE

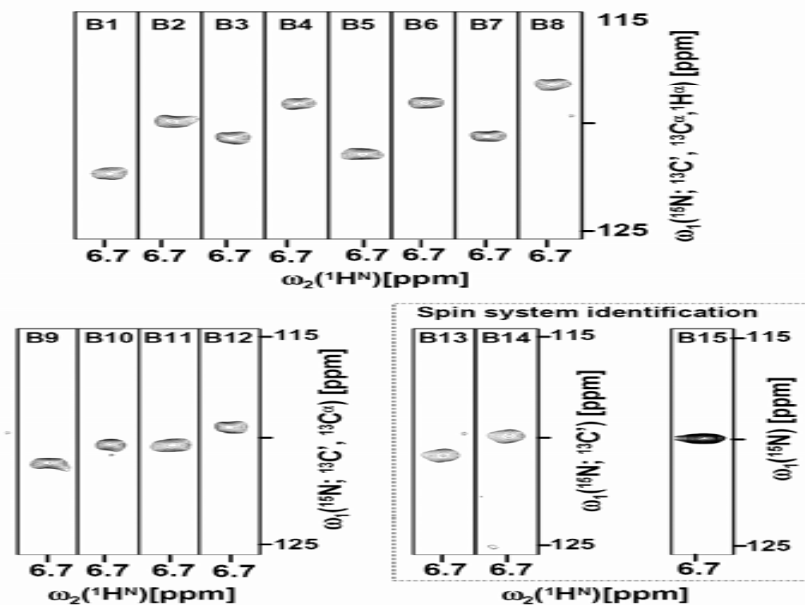
Pilot study (3.2004): structure of 14 kDa YqfB
16.9 hrs GFT spectra for
resonance assignment and
9.1 hrs for simultaneous 3D NOESY
(1 mmol solution at 25 °C
and 600 MHz w/cryogenic probe)



a (4,3)D $\text{HNNC}^{\alpha\beta}\text{C}^{\alpha} / \text{C}^{\alpha\beta}\text{C}^{\alpha}(\text{CO})\text{NHN}$ (10.0 hrs)

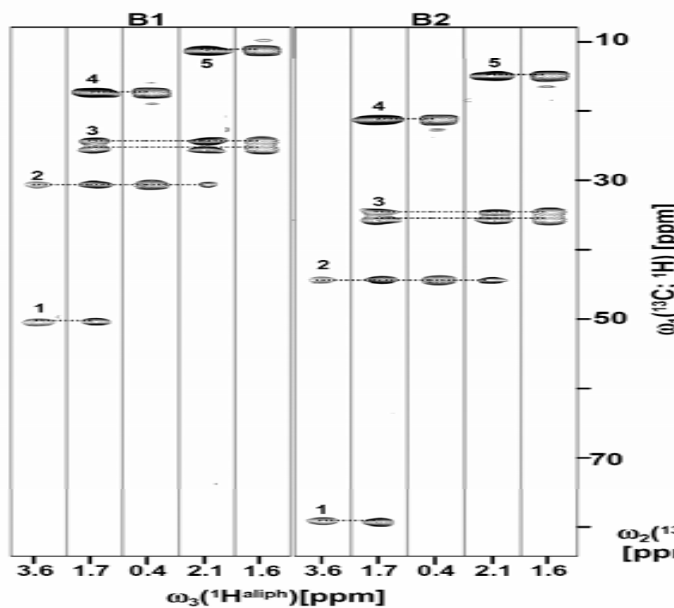


b (5,2)D HACACONHN (1.5 hr); Phe 33

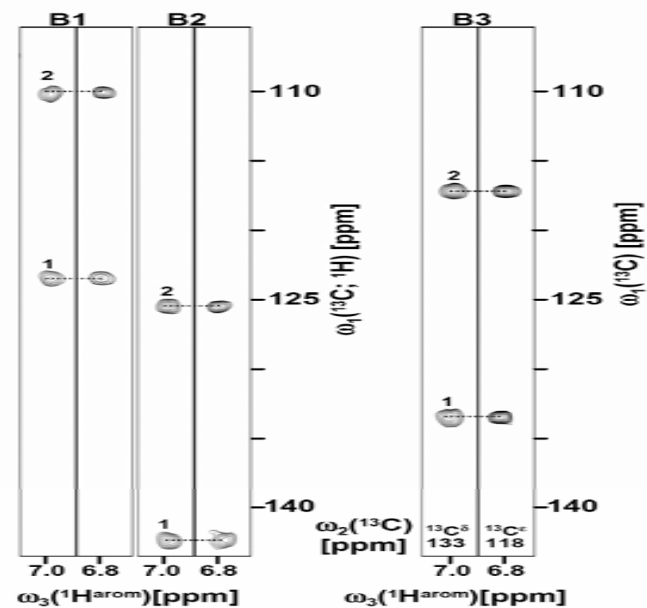


Side chain spin system identification

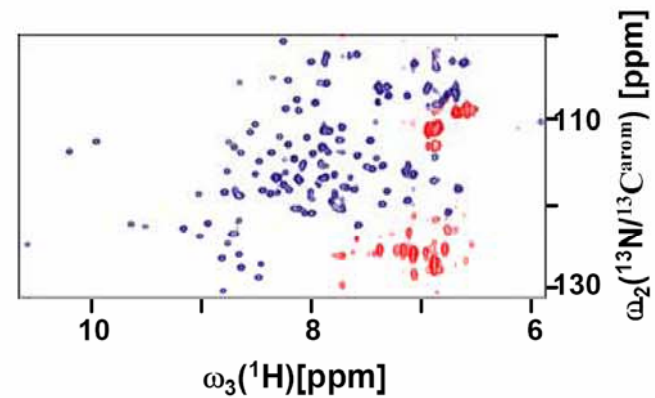
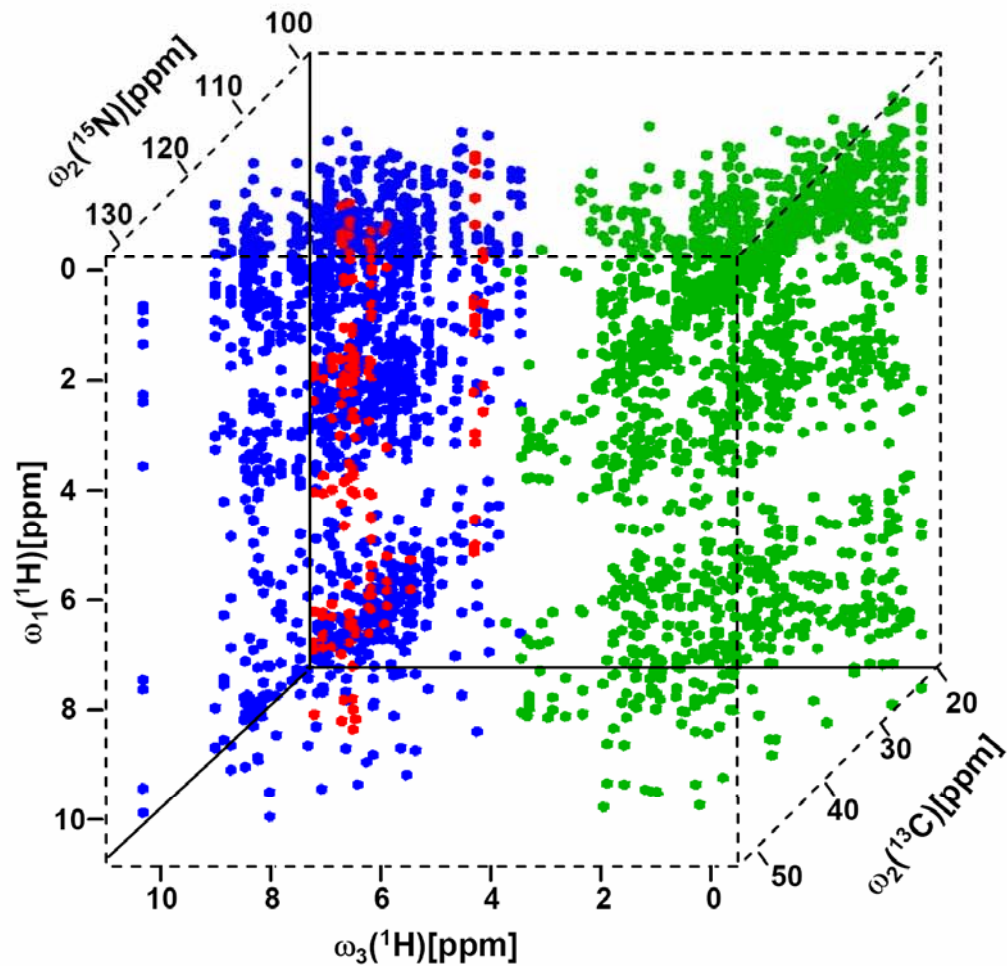
c (4,3)D HCCH (4.0 hrs)
(Aliphatic; Ile 85)



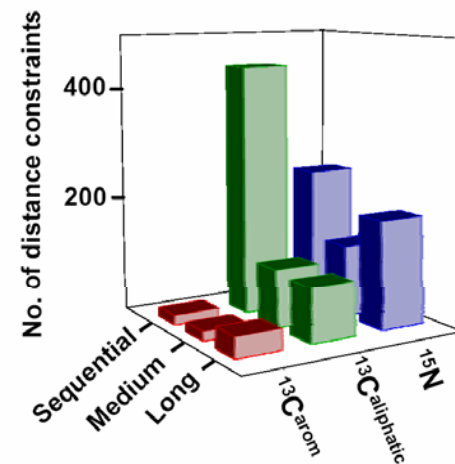
d (4,3)D HCCH (1.4 hrs)
(Aromatic; Tyr 89)



3D [H]-NOESY-[NH/¹³C_{ali}H/¹³C_{aro}H]

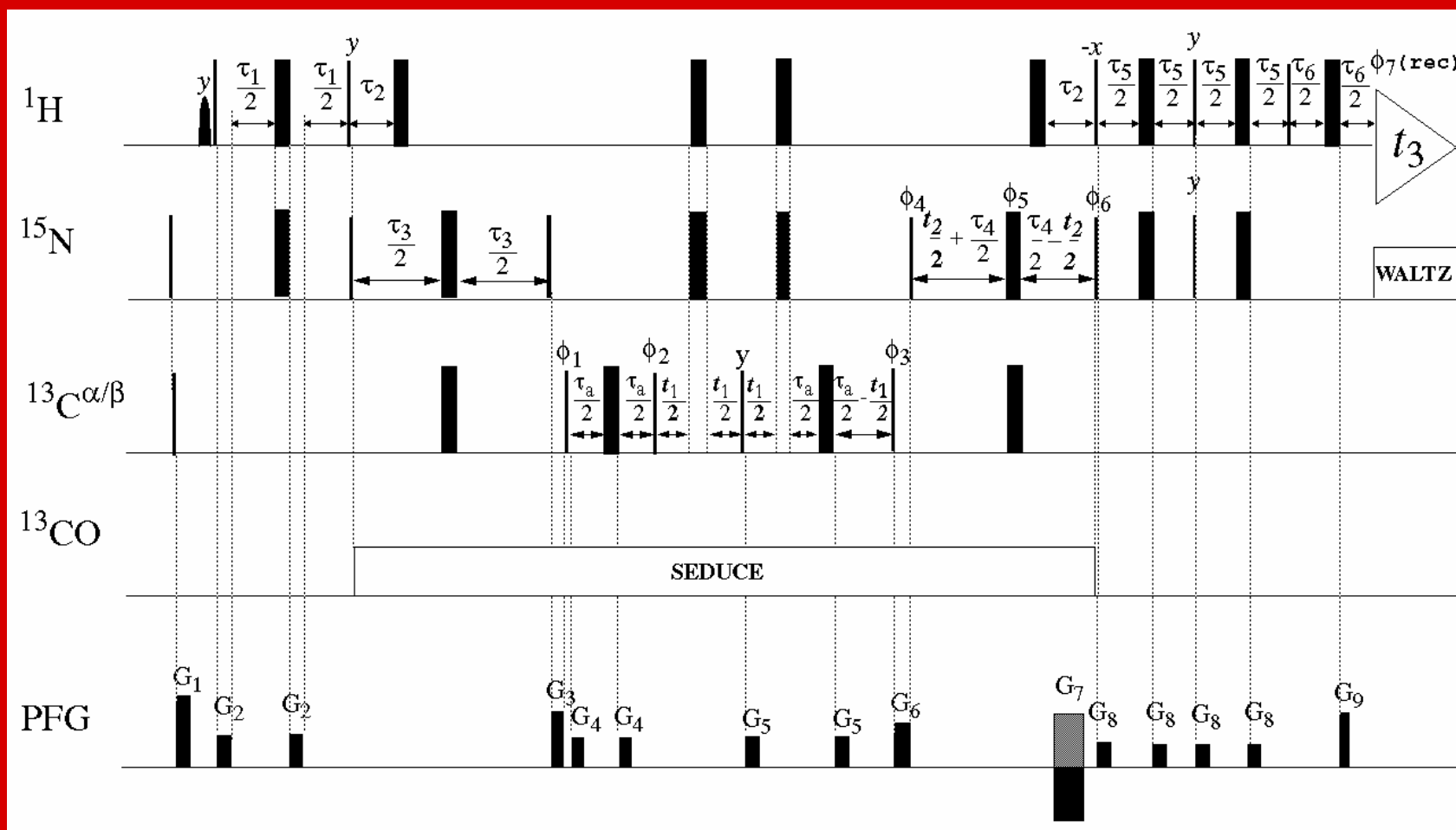


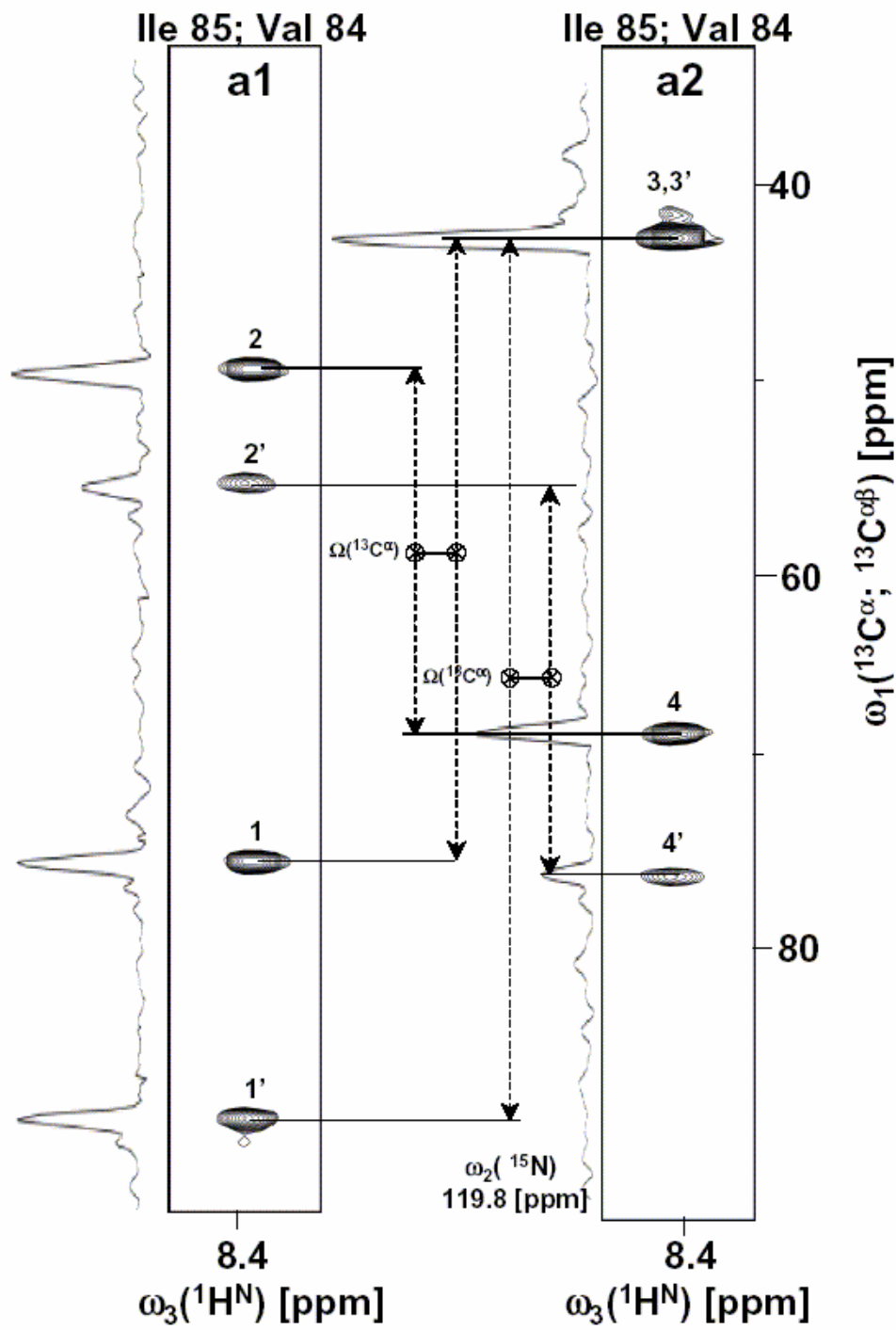
C



L-(4,3)D HNN(CO)C^{αβ}C^α

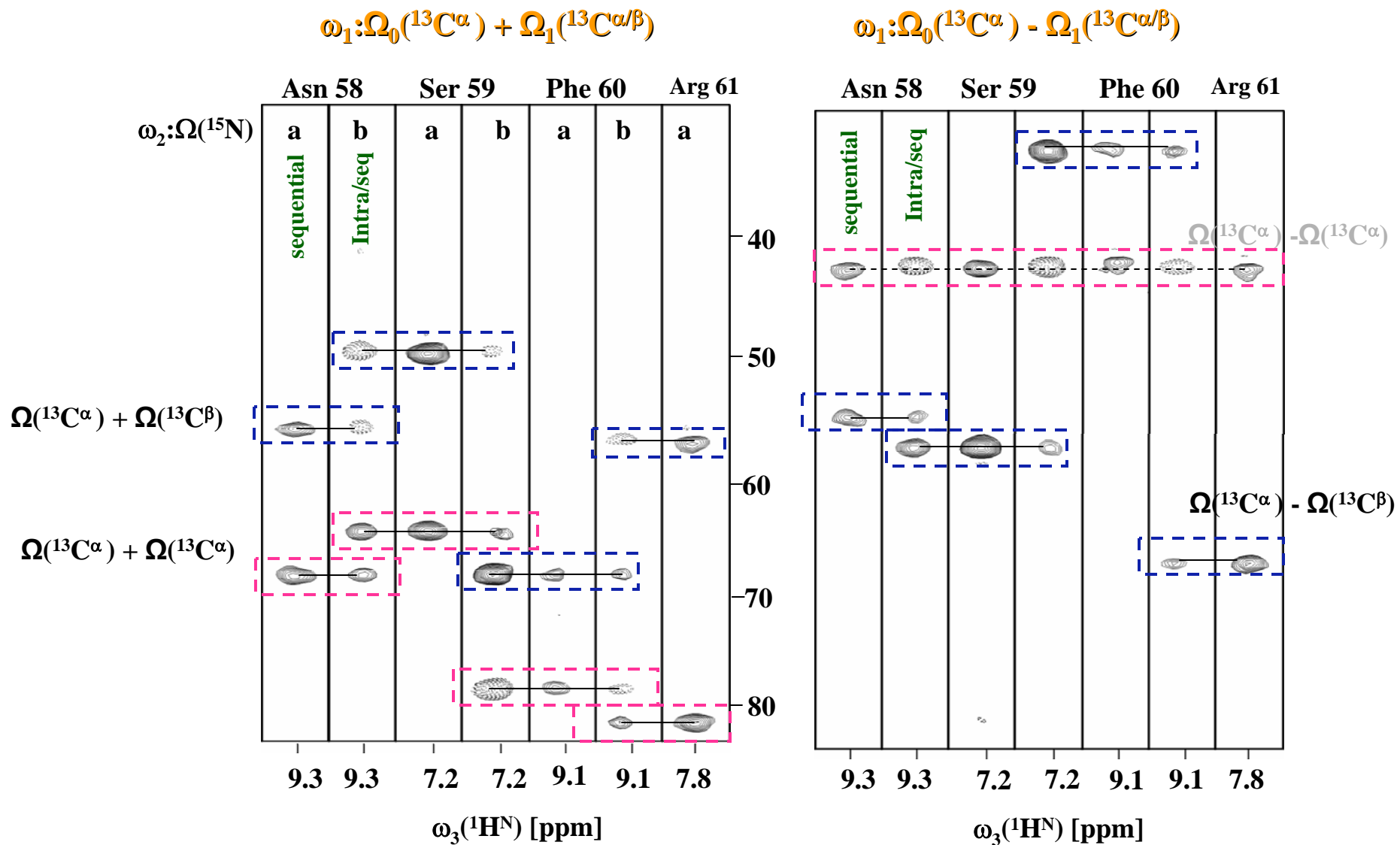
Flip-back of water and aliphatic proton polarization





4D CACB(CO)NHN
 information in
 (4,3)D C_{αβ}C_α(CO)NHN

(4,3)D $\underline{HN} \underline{NC}^{\alpha\beta} \underline{C}^{\alpha} / \underline{C}^{\alpha\beta} \underline{C}^{\alpha} (\underline{CO}) \underline{NHN}$ 'sequential walk'

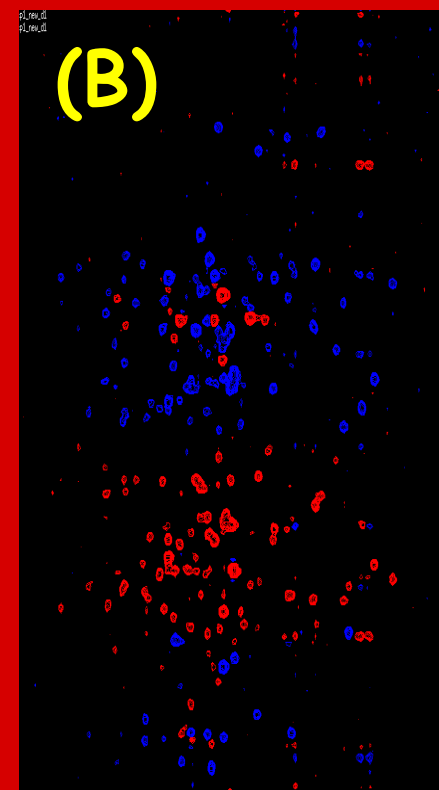
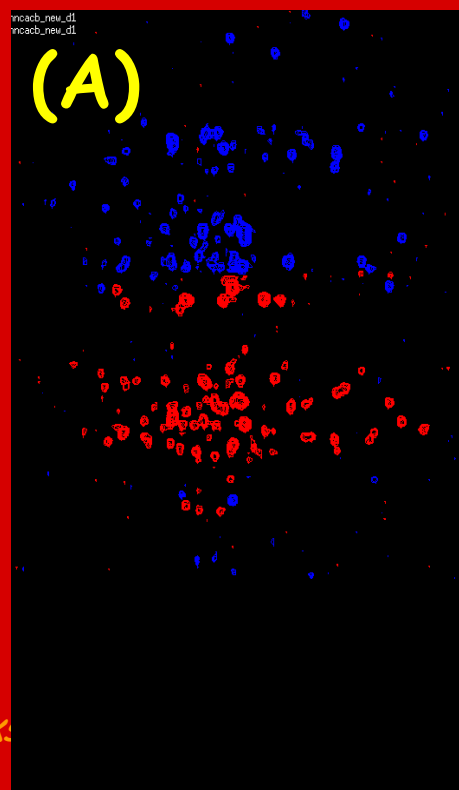
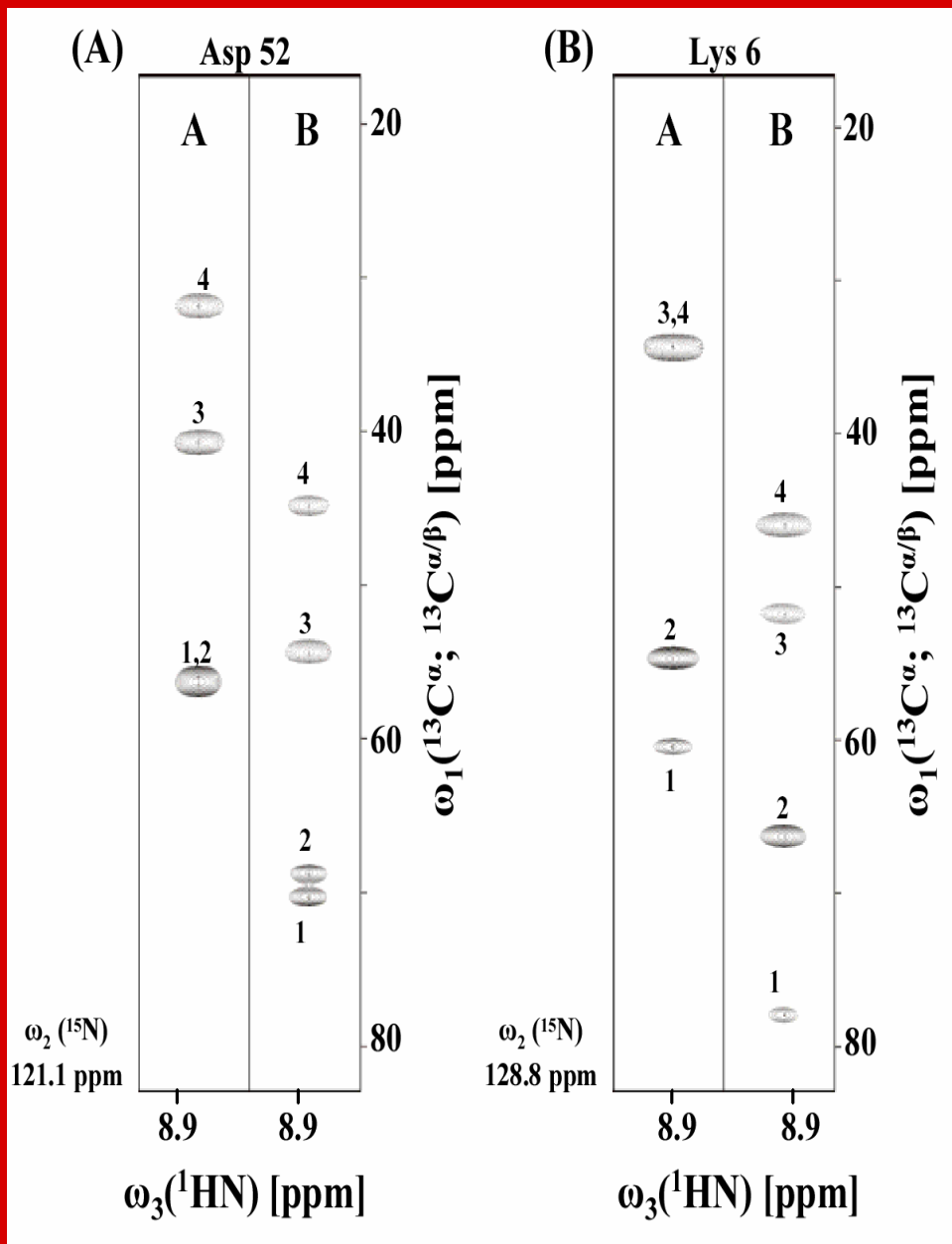


Better signal dispersion

(4,3)D $\text{HNNC}_{\alpha\beta}\text{C}_{\alpha}$ (B)

when compared with

3D HNNCACB (A)



J|A|C|S

A R T I C L E S

Published on Web 06/07/2005

**G-Matrix Fourier Transform NOESY-Based Protocol for
High-Quality Protein Structure Determination**

Yang Shen, Hanudatta S. Atreya, Gaohua Liu, and Thomas Szyperski*

*Contribution from the Departments of Chemistry and Structural Biology, The State University of
New York at Buffalo, Buffalo, New York 14260*

Received January 11, 2005; E-mail: szypersk@chem.buffalo.edu

(4,3)D [HN/H¹³C^{ali}]-NOESY-[NH/¹³C^{ali}H]:

**Rapid acquisition of highly resolved
4D NOESY information**

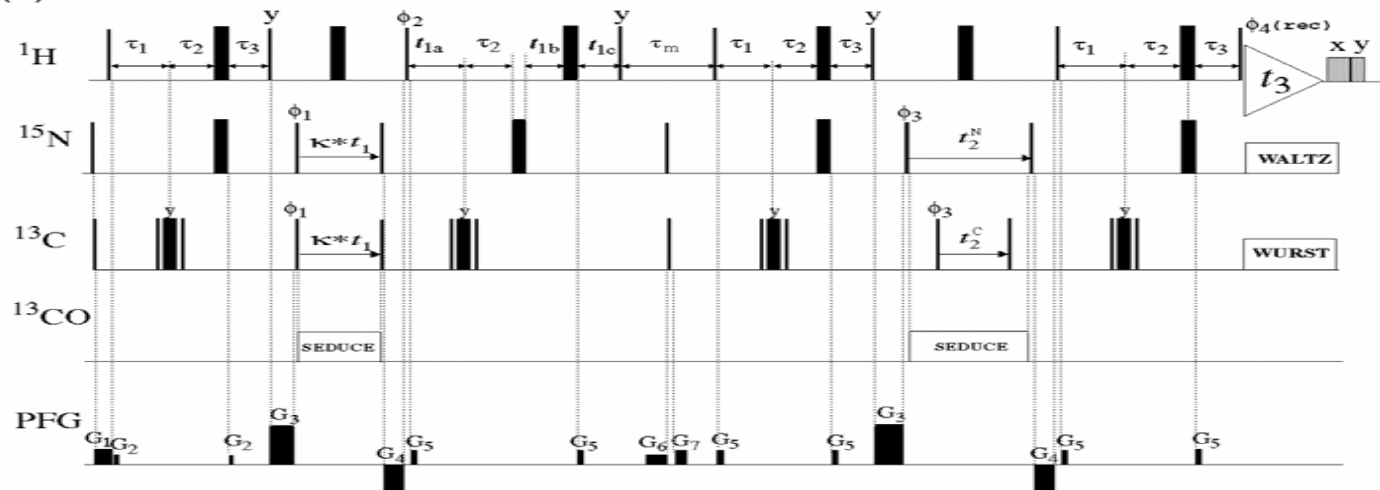
NMRFam Workshop 06/06/06

(a) (4,3)D [HN/¹³C_{ali}H]-NOESY-[NH/¹³C_{ali}H]

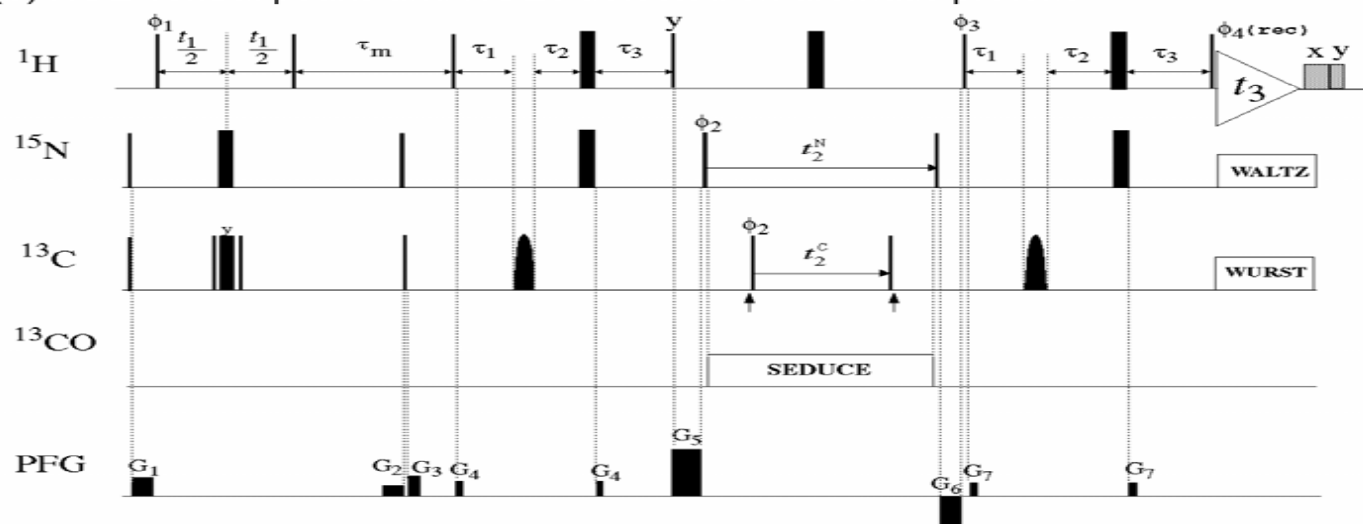
with central peak detection in

(b) 3D [H]-NOESY-[NH/¹³C_{ali}H/¹³C_{aro}H]

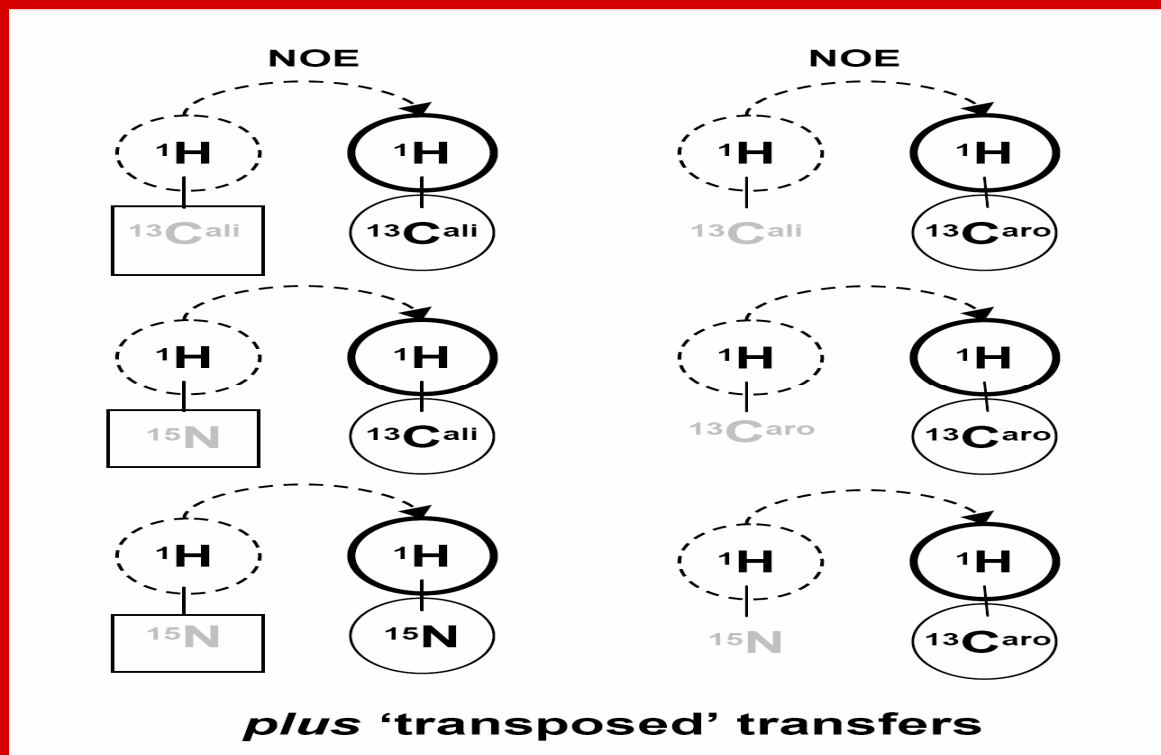
(a) NOE chemical shift doublets



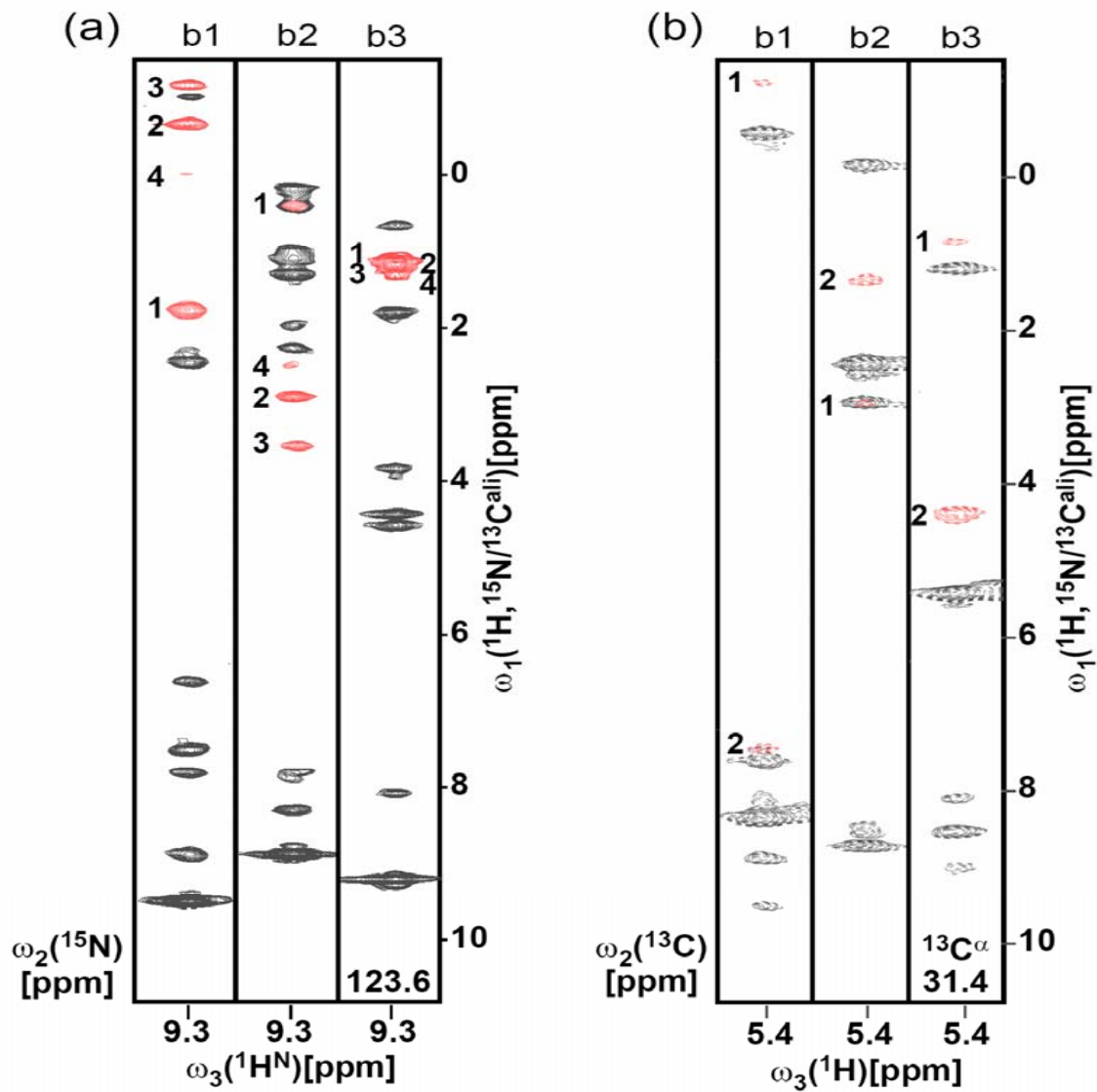
(b) NOE central peaks and NOEs detected on aromatic protons



(4,3)D $[HN/H^{13}C_{ali}]-NOESY-[NH/^{13}C_{ali}H]$
 with central peak detection in
 3D $[H]-NOESY-[NH/^{13}C_{ali}H/^{13}C_{aro}H]$



Information of three 4D and three 3D NOESY spectra



b1: $\Omega(^1\text{H}) + 0.5 \Omega(^{13}\text{C})$

b2: $\Omega(^1\text{H}) - 0.5 \Omega(^{13}\text{C})$

b3: $\Omega(^1\text{H})$

Role of (4,3)D GFT NOESY

- For medium sized proteins ($\tau_r \sim 8-12$ ns), sensitivity of shift doublet detection is ~ 3 times lower than for central peak detection
- For YqfB, 30 hours measurement time resulted in $\sim 70\%$ detection yield for doublets \rightarrow direct assignment of $\sim 70\%$ of *long-range* NOEs

\Rightarrow (4,3)D GFT NOESY is primarily tool for assigning NOEs in 3D NOESY

Northeast Structural Genomics Consortium: A SG Research Network

Bioinformatics / Data Management

Barry Honig, Columbia University
Mark Gerstein, Yale University
Igor Jurisica, Ontario Cancer Inst.
Andrew Laine, Columbia University
Diana Murray, Cornell Medical
Burkhard Rost, Columbia University

X-ray Crystallography

Wayne Hendrickson, Columbia U
Peter Allen, Columbia University
George DeTitta, Hauptman-Woodward
John Hunt, Columbia University
Liang Tong, Columbia University

Protein Production / Biophysics

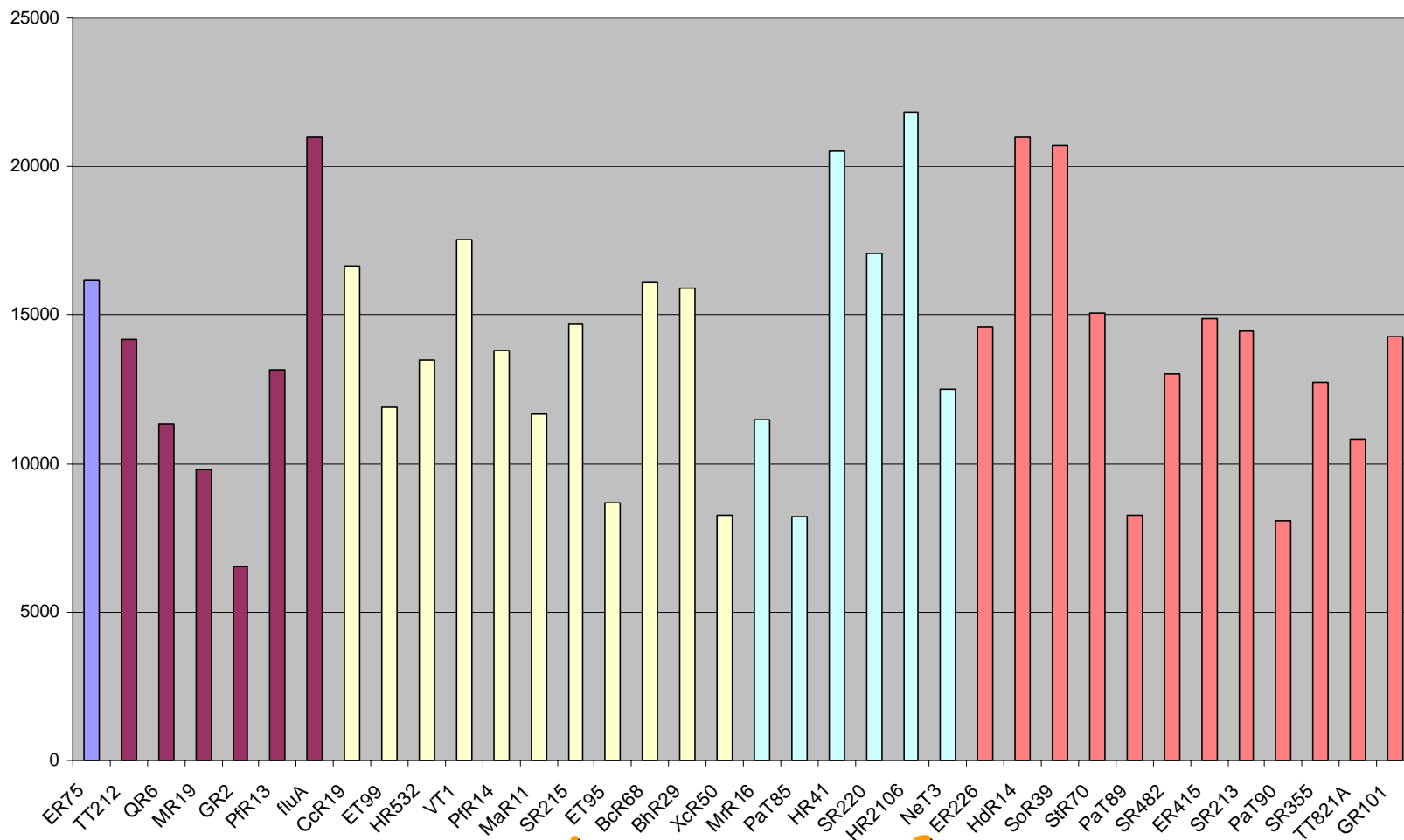
Gaetano Montelione, Rutgers University
Stephen Anderson, Rutgers University
Masayori Inouye, RWJMS - UMDNJ
Cheryl Arrowsmith, Ontario Cancer I.

Protein NMR

Thomas Szyperski, State U of New York
Cheryl Arrowsmith, Ontario Cancer Inst.
Michael Kennedy, Pacific Northwest Natl Labs
Ron Levy, Rutgers University
Jim Prestegard, University of Georgia
Gaetano Montelione, Rutgers University

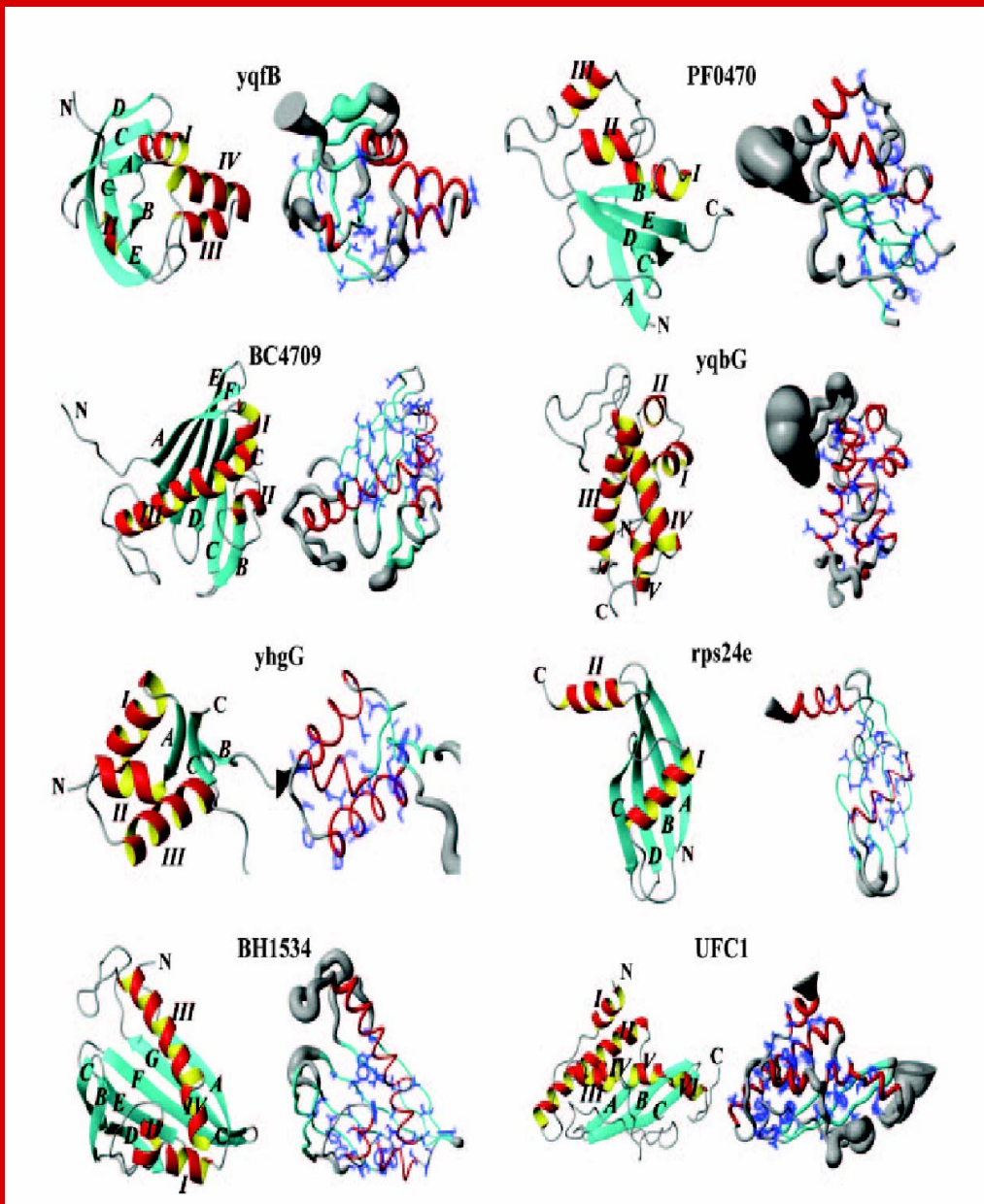
Semi-empiric solution of 'protein folding problem'

36 RD/GFT NMR-based Structures: Molecular weight distribution



....robustness of
semi-automated GFT NMR data analysis

Wealth of structural-biological insight...



SCOP classification

yqfB and PF0470:
'PUA domain'

UFC1:
'Ubiquitin-conjugating
enzyme'

BC4709 and BH1534:
'START domain'

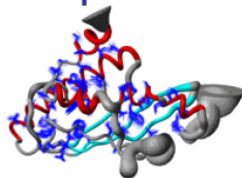
yhgG
'winged-helix DNA-
Binding domain'

rps24e:
'Yggu-like'

yqbG:
no structural homologue
found

<http://www.nsm.buffalo.edu/Research/GFT>

G-matrix Fourier Transform (GFT) Projection NMR Spectroscopy



[Prof. Thomas Szyperski](#)

State University of New York at Buffalo

[On GFT Projection NMR Spectroscopy](#)

Defining features of G-matrix Fourier Transform (GFT) projection NMR spectroscopy ([Kim and Szyperski, 2003](#)):

- (i) joint sampling of $K+1$ chemical shifts $\Omega_0, \Omega_1, \dots, \Omega_K$ encoded in $K+1$ indirect evolution periods of an N D FT NMR experiment,
- (ii) phase-sensitive detection of 2^K linear combinations of chemical shifts $\Omega_0 \pm \Omega_1 \pm \dots \pm \Omega_K$,
- (iii) editing of the 2^K linear combinations of shifts into 2^K ($N-K$)D 'basic' projected sub-spectra, so that each contains one of the linear combinations.

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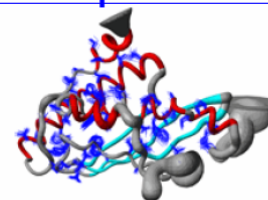
[Talks on GFT NMR](#)

[GFT NMR in the Media](#)

By registering to the UB GFT NMR web site, you will soon receive by email additional parameter sets and pulse programs which have been recently published by Atreya et al. (J. Am. Chem. Soc. 127, 4554 - 4555), Shen et al. (J. Am. Chem. Soc. 127, 9085 - 9099) and Eletsky et al. (J. Am. Chem. Soc. 127, 14578-14579) [[more...](#)]

Support of the National Science Foundation and the National Institutes of Health is acknowledged

[G-matrix Fourier Transform \(GFT\) Projection NMR Spectroscopy](#)



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Please cite "[Kim, S. and Szyperski, T. \(2003\) GFT NMR, a New Approach to Rapidly Obtain Precise High Dimensional NMR Spectral Information. J. Am. Chem. Soc. 125, 1385-1393](#)" and potentially additional publications describing the specific experiments (see '[References](#)') when publishing research resulting from the use of the GFT NMR package

Please cite "[Szyperski, T., Yeh, D. C., Sukumaran, D. K., Moseley, H. N. B. and Montellone, G. T. \(2002\) Reduced-dimensionality NMR spectroscopy for High-Throughput Resonance Assignment. Proc. Natl. Acad. Sci. USA 99, 8009-8014](#)" when publishing research resulting from the use of the RD NMR package

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Relation of GFT NMR Spectroscopy and

'Projection Reconstruction' (PR) NMR
(Kupce & Freeman, JACS 2004, 126, 6429)

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Principles and applications of GFT projection NMR spectroscopy[†]

Thomas Szyperski* and Hanudatta S. Atreya

Departments of Chemistry and Structural Biology, The State University of New York at Buffalo, The Northeast Structural Genomics Consortium, Buffalo, NY 14260, USA

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'Projection' component in 'Projection-reconstruction (PR) NMR' is equivalent to GFT projection NMR

(4, 2)D GFT NMR

$$S_{1r} \propto \cos(\kappa_0 \Omega_0 t) * \cos(\kappa_1 \Omega_1 t) * \cos(\kappa_2 \Omega_2 t)$$

$$S_{1i} \propto \sin(\kappa_0 \Omega_0 t) * \cos(\kappa_1 \Omega_1 t) * \cos(\kappa_2 \Omega_2 t)$$

$$S_{2r} \propto \cos(\kappa_0 \Omega_0 t) * \sin(\kappa_1 \Omega_1 t) * \cos(\kappa_2 \Omega_2 t)$$

$$S_{2i} \propto \sin(\kappa_0 \Omega_0 t) * \sin(\kappa_1 \Omega_1 t) * \cos(\kappa_2 \Omega_2 t)$$

$$S_{3r} \propto \cos(\kappa_0 \Omega_0 t) * \cos(\kappa_1 \Omega_1 t) * \sin(\kappa_2 \Omega_2 t)$$

$$S_{3i} \propto \sin(\kappa_0 \Omega_0 t) * \cos(\kappa_1 \Omega_1 t) * \sin(\kappa_2 \Omega_2 t)$$

$$S_{4r} \propto \cos(\kappa_0 \Omega_0 t) * \sin(\kappa_1 \Omega_1 t) * \sin(\kappa_2 \Omega_2 t)$$

$$S_{4i} \propto \sin(\kappa_0 \Omega_0 t) * \sin(\kappa_1 \Omega_1 t) * \sin(\kappa_2 \Omega_2 t),$$

so that the vector $\mathbf{T}(2) = \mathbf{G}(2) \cdot \mathbf{S}(2)$ is given in complex notation by:

$$\mathbf{T}(2) = \begin{bmatrix} e^{i(\kappa_0 * \Omega_0 + \kappa_1 * \Omega_1 + \kappa_2 * \Omega_2)t} \\ e^{i(\kappa_0 * \Omega_0 - \kappa_1 * \Omega_1 + \kappa_2 * \Omega_2)t} \\ e^{i(\kappa_0 * \Omega_0 + \kappa_1 * \Omega_1 - \kappa_2 * \Omega_2)t} \\ e^{i(\kappa_0 * \Omega_0 - \kappa_1 * \Omega_1 - \kappa_2 * \Omega_2)t} \end{bmatrix} = \begin{bmatrix} 1 & i & i & -1 & i & -1 & -1 & -i \\ 1 & i & -i & 1 & i & -1 & 1 & i \\ 1 & i & i & -1 & -i & 1 & 1 & i \\ 1 & i & -i & 1 & -i & 1 & -1 & -i \end{bmatrix} \cdot \begin{bmatrix} S_{1r} \\ S_{1i} \\ S_{2r} \\ S_{2i} \\ S_{3r} \\ S_{3i} \\ S_{4r} \\ S_{4i} \end{bmatrix} \quad (4).$$

Hence, the four linear combinations of chemical shifts, $\kappa_0 * \Omega_0 \pm \kappa_1 * \Omega_1 \pm \kappa_2 * \Omega_2$, are measured in one of the four sub-spectra each.

G-matrix transformation ⇔ 'generalized hyper-complex FT'

$$S_{+\alpha,+\beta} = 0.25[(S_{rrr}-S_{rjk}-S_{ijr}-S_{irk}) + i(S_{irr}-S_{ijk}+S_{rjr}+S_{rrk})]$$

$$S_{+\alpha,-\beta} = 0.25[(S_{rrr}+S_{rjk}-S_{ijr}+S_{irk}) + i(S_{irr}+S_{ijk}+S_{rjr}-S_{rrk})]$$

$$S_{-\alpha,+\beta} = 0.25[(S_{rrr}+S_{rjk}+S_{ijr}-S_{irk}) + i(S_{irr}+S_{ijk}-S_{rjr}+S_{rrk})]$$

$$S_{-\alpha,-\beta} = 0.25[(S_{rrr}-S_{rjk}+S_{ijr}+S_{irk}) + i(S_{irr}-S_{ijk}-S_{rjr}-S_{rrk})]$$

Kupce E, Freeman R. *J. Am. Chem. Soc.* 2004; **126**: 6429-6440.

The equivalence of G-matrix Eq. (4) with this system of equations becomes readily apparent when considering the correspondence of the following parameters and expressions:

$$S_{+\alpha,+\beta} \leftrightarrow e^{i(\kappa_0^*\Omega_0+\kappa_1^*\Omega_1+\kappa_2^*\Omega_2)t}, \quad S_{+\alpha,-\beta} \leftrightarrow e^{i(\kappa_0^*\Omega_0-\kappa_1^*\Omega_1+\kappa_2^*\Omega_2)t}, \quad S_{-\alpha,+\beta} \leftrightarrow e^{i(\kappa_0^*\Omega_0+\kappa_1^*\Omega_1-\kappa_2^*\Omega_2)t},$$

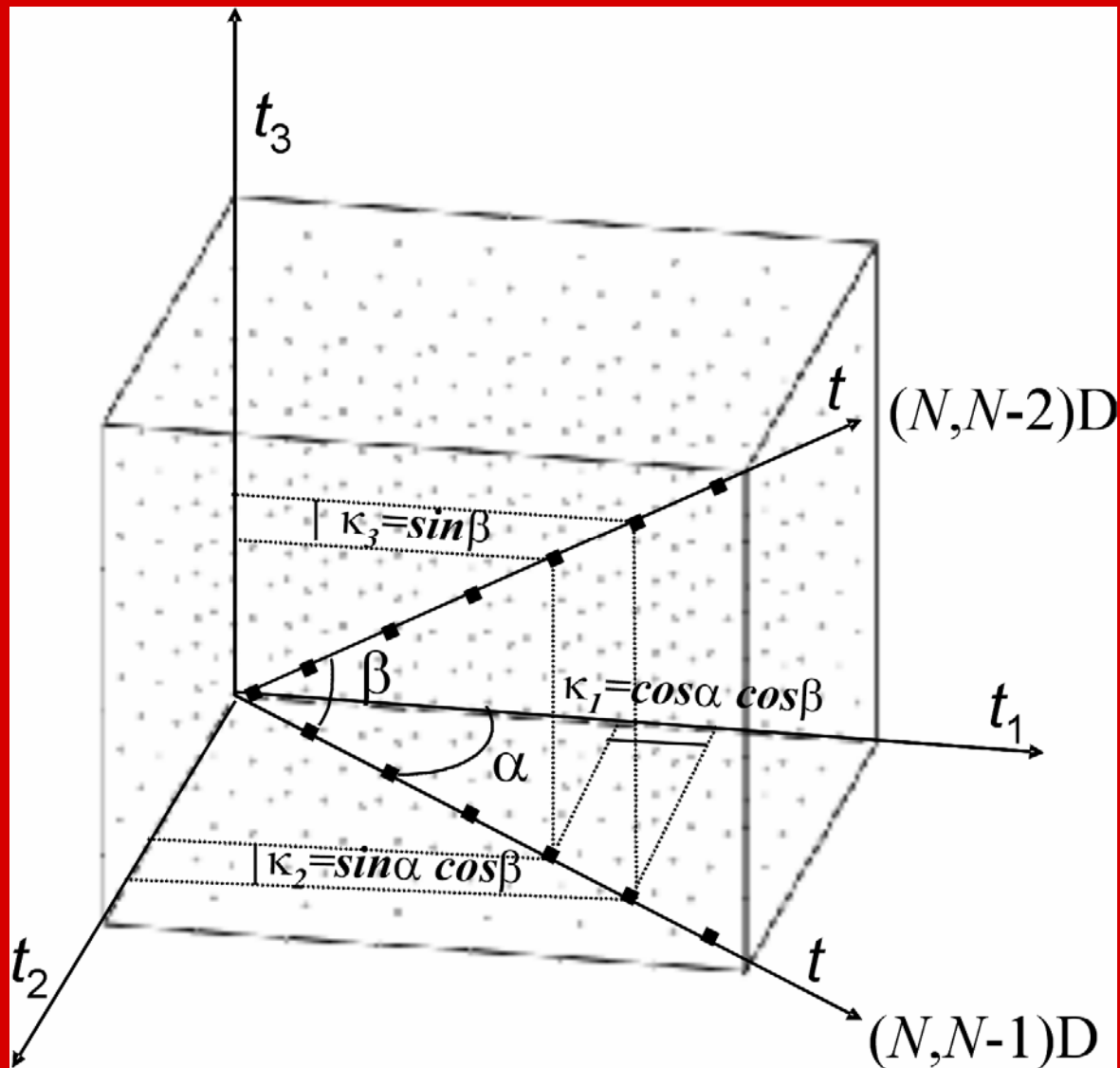
$$S_{-\alpha,-\beta} \leftrightarrow e^{i(\kappa_0^*\Omega_0-\kappa_1^*\Omega_1-\kappa_2^*\Omega_2)t}, \text{ and}$$

$$S_{rrr} \leftrightarrow S_{1r}, S_{rjk} \leftrightarrow S_{4r}, S_{ijr} \leftrightarrow S_{3i}, S_{irk} \leftrightarrow S_{2i}, S_{irr} \leftrightarrow S_{1i}, S_{ijk} \leftrightarrow S_{4i}, S_{rjr} \leftrightarrow S_{3r}, S_{rrk} \leftrightarrow S_{2r}.$$

Moreover, the scaling factors κ_j in Eq (4) are adapted to the use of projection angles α and β (Fig. 1) by setting $\kappa_0 = \cos\alpha \cos\beta$, $\kappa_1 = \sin\alpha \cos\beta$ and $\kappa_2 = \sin\beta$.³⁰

Hence, the projection formalism of PR NMR is equivalent to the GFT NMR formalism.

Scaling of shift evolution periods \Leftrightarrow
'tilt angles of plane projection'



Generalized Reconstruction of n -D NMR Spectra from Multiple Projections: Application to the 5-D HACACONH Spectrum of Protein G B1 Domain

Brian E. Coggins,[†] Ronald A. Venters,[‡] and Pei Zhou^{*†}

*Department of Biochemistry and Duke University NMR Center, Duke University Medical Center,
Durham, North Carolina 27710*

Received November 5, 2003; E-mail: peizhou@biochem.duke.edu

Simultaneously incrementing the evolution parameters has been employed by several groups to speed up multidimensional experiments.^{1,5–8} The resulting intermodulation of chemical shifts can be disentangled, for example, by the G-matrix methodology to produce a set of “base spectra”.⁸ These base spectra, in fact, represent tilted projections at fixed angles. Taking the GFT 5-D HACACONH experiment, for example, base spectra 1–8 are projections at angles ($60^\circ/120^\circ$, $60^\circ/120^\circ$, $60^\circ/120^\circ$, 60°) relative to the orthogonal C^α , H^α , C' , and N axes, respectively. Depending

... an urgent demand for a
unified nomenclature to name
projected NMR experiments
arises...

Table 1. GFT/G²FT NMR experiments

Research group; Experiment name	Magnetization transfer pathway ^a	Linear combination of chemical shifts observed in the GFT dimension(s) (ω_1/ω_2)
<i>Szyperski and co-workers</i>		
1. Backbone and ¹H^{β}/¹³C^{β} resonance assignments		
(5,2)D <u>HACACONHN</u> ⁵	¹ H _{i-1} ^{β} → ¹³ C _{i-1} ^{β} → ¹³ C _{i-1} ^{α} → ¹⁵ N _i → ¹ HN _i	$\Omega(^{15}\text{N}_i) \pm \Omega(^{13}\text{C}_{i-1}^\alpha) \pm \Omega(^{13}\text{C}_{i-1}^\beta) \pm \Omega(^1\text{H}_{i-1}^\beta)$
(5,3)D <u>HACACONHN</u> ¹²	(f ₁) (f ₁) (f ₁) (f ₂) (f ₃)	$\Omega(^{13}\text{C}_{i-1}^\alpha) \pm \Omega(^{13}\text{C}_{i-1}^\beta) \pm \Omega(^1\text{H}_{i-1}^\beta)$
(5,2)D <u>HACA</u> , <u>CONHN</u> ¹²	¹ H _i ^{β} → ¹³ C _i ^{α} → ¹³ C _i ^{β} → ¹³ C _i ^{α} → ¹⁵ N _i → ¹ HN _i	$\Omega(^{15}\text{N}_i) \pm \Omega(^{13}\text{C}_i^\alpha) \pm \Omega(^{13}\text{C}_i^\beta) \pm \Omega(^1\text{H}_i^\beta)$
(5,3)D <u>HACA</u> , <u>CONHN</u> ¹²	(f ₁) (f ₁) (f ₁) (f ₂) (f ₃)	$\Omega(^{13}\text{C}_{i-1}^\alpha) \pm \Omega(^{13}\text{C}_{i-1}^\beta) \pm \Omega(^1\text{H}_{i-1}^\beta)$
(4,3)D <u>CBCACONHN</u> ¹²	¹ H _{i-1} ^{β} → ¹³ C _{i-1} ^{β} → ¹³ C _{i-1} ^{α} → ¹³ C _{i-1} ^{β} → ¹⁵ N _i → ¹ HN _i	$\Omega(^{13}\text{C}_{i-1}^\alpha) \pm \Omega(^{13}\text{C}_{i-1}^\beta); \Omega(^{13}\text{C}_{i-1}^\beta) \pm \Omega(^{13}\text{C}_{i-1}^\alpha)$
(4,3)D <u>CBCA</u> , <u>CONHN</u> ¹²	¹ H _i ^{β} → ¹³ C _i ^{β} → ¹³ C _i ^{α} → ¹³ C _i ^{β} → ¹⁵ N _i → ¹ HN _i	$\Omega(^{13}\text{C}_i^\alpha) \pm \Omega(^{13}\text{C}_i^\beta); \Omega(^{13}\text{C}_i^\beta) \pm \Omega(^{13}\text{C}_i^\alpha)$
(4,3)D <u>HNNC</u> ^{$\alpha\beta$} <u>ulnC</u> ^{α} ¹³	¹ HN _i → ¹⁵ N _i → ¹³ C _{ij-1} ^{β} → ¹³ C _{ij-1} ^{α} → ¹³ C _{ij-1} ^{β} → ¹⁵ N _i → ¹ HN _i	$\Omega(^{13}\text{C}_{ij-1}^\alpha) \pm \Omega(^{13}\text{C}_{ij-1}^\beta); \Omega(^{13}\text{C}_{ij-1}^\beta) \pm \Omega(^{13}\text{C}_{ij-1}^\alpha)$
(4,3)D <u>HNN(CO)C</u> ^{$\alpha\beta$} ¹³	¹ HN _i → ¹⁵ N _i → ¹³ C _{i-1} ^{α} → ¹³ C _{i-1} ^{β} → ¹³ C _{i-1} ^{α} → ¹⁵ N _i → ¹ HN _i	$\Omega(^{13}\text{C}_{i-1}^\alpha) \pm \Omega(^{13}\text{C}_{i-1}^\beta); \Omega(^{13}\text{C}_{i-1}^\beta) \pm \Omega(^{13}\text{C}_{i-1}^\alpha)$
(4,3)D <u>C</u> ^{$\alpha\beta$} ^{α} (<u>CO</u>) <u>NHN</u> ¹³	¹ H _{i-1} ^{β} → ¹³ C _{i-1} ^{β} → ¹³ C _{i-1} ^{α} → ¹³ C _{i-1} ^{β} → ¹⁵ N _i → ¹ HN _i	$\Omega(^{13}\text{C}_{i-1}^\alpha) \pm \Omega(^{13}\text{C}_{i-1}^\beta); \Omega(^{13}\text{C}_{i-1}^\beta) \pm \Omega(^{13}\text{C}_{i-1}^\alpha)$
(5,3)D <u>H</u> ^{$\alpha\beta$} ^{α} (<u>CO</u>) <u>NHN</u> ¹³	(f ₁) (f ₁) (f ₁) (f ₂) (f ₃)	$\Omega(^{13}\text{C}_{i-1}^\alpha) \pm \Omega(^{13}\text{C}_{i-1}^\beta); \Omega(^{13}\text{C}_{i-1}^\beta) \pm \Omega(^{13}\text{C}_{i-1}^\alpha)$
(6,3)D <u>H</u> ^{$\alpha\beta$} ^{α} (<u>CO</u>) <u>NHN</u> ¹³	(f ₁) (f ₁) (f ₁) (f ₂) (f ₃)	$\Omega(^{13}\text{C}_{i-1}^{\beta/\alpha}) \pm \Omega(^{13}\text{C}_{i-1}^{\alpha/\beta}) \pm \Omega(^1\text{H}_{i-1}^{\beta/\alpha}); \Omega(^{13}\text{C}_{i-1}^{\alpha/\beta}) \pm \Omega(^{13}\text{C}_{i-1}^{\beta/\alpha}) \pm \Omega(^1\text{H}_{i-1}^{\alpha/\beta});$
2. Side-chain resonance assignments		
(5,3)D <u>HCC-CH</u> ¹³	¹ H ⁽¹⁾ → ¹³ C ⁽¹⁾ → ¹³ C ⁽²⁾ → ¹³ C ⁽²⁾ → ¹ H ⁽²⁾	$\Omega(^{13}\text{C}^{(2)}) \pm \Omega(^{13}\text{C}^{(1)}) \pm \Omega(^1\text{H}^{(1)})$ 'cross peak'; $\Omega(^{13}\text{C}^{(2)}) \pm \Omega(^{13}\text{C}^{(2)}) \pm \Omega(^1\text{H}^{(2)})$ 'diagonal peak'
(4,2)D <u>HCCH</u> ¹³ (aliphatic/aromatic)	¹ H ⁽¹⁾ → ¹³ C ⁽¹⁾ → ¹³ C ⁽²⁾ → ¹ H ⁽²⁾	$\Omega(^{13}\text{C}^{(2)}) \pm \Omega(^{13}\text{C}^{(1)}) \pm \Omega(^1\text{H}^{(1)})$ 'cross peak'; $\Omega(^{13}\text{C}^{(2)}) \pm \Omega(^{13}\text{C}^{(2)}) \pm \Omega(^1\text{H}^{(2)})$ 'diagonal peak'
(4,3)D <u>HCCH</u> ⁴⁰ (aliphatic/aromatic)	(f ₁) (f ₁) (f ₂) (f ₃)	$\Omega(^{13}\text{C}^{(1)}) \pm \Omega(^1\text{H}^{(1)})$ 'cross peak'; $\Omega(^{13}\text{C}^{(2)}) \pm \Omega(^1\text{H}^{(2)})$ 'diagonal peak'
L-TROSY-(4,3)D <u>HCCH</u> ⁴¹ (aromatic)	¹ H ⁽¹⁾ → ¹³ C ⁽¹⁾ → ¹³ C ⁽²⁾ → ¹ H ⁽²⁾	$\Omega(^{13}\text{C}^{(1)}) \pm \Omega(^1\text{H}^{(1)})$ 'cross peak'; $\Omega(^{13}\text{C}^{(2)}) \pm \Omega(^1\text{H}^{(2)})$ 'diagonal peak'
3. GFT NOESY		
(4,3)D <u>[HC^{ali}/HN]-NOESY-CH^{ali}/NH</u> ⁴²	¹ H ^{ali(1)} → ¹³ C ⁽¹⁾ → ¹ H ^{ali(1)} / ¹ H ^{N(1)} → ¹ H ^{ali(2)} / ¹ H ^{N(2)} → ¹³ C ⁽²⁾ → ¹ H ^{ali(2)} / ¹ H ^{N(2)}	$\Omega(^1\text{H}^{\text{ali}(1)}) \pm \Omega(^{13}\text{C}^{\text{ali}(1)}) \pm \Omega(^1\text{H}^{\text{N}(1)}) \pm \Omega(^{15}\text{N}^{(1)})$ 'cross peak'; $\Omega(^1\text{H}^{\text{ali}(2)}) \pm \Omega(^{13}\text{C}^{\text{ali}(2)}) \pm \Omega(^1\text{H}^{\text{N}(2)}) \pm \Omega(^{15}\text{N}^{(2)})$ 'cross peak';

(continued overleaf)

Table 1. (Continued)

Research group; experiment name	Magnetization transfer pathway ^a	Linear combination of chemical shifts observed in the GFT dimension(s) (ω_1/ω_2)
4. G²FT NMR experiments³⁸		
L-(5,3)D <u>HN(N)CO</u> (<u>C</u> ^{β} ^{α})	¹ HN _i → ¹⁵ N _i → ¹³ C _{i-1} ^{α} → ¹³ C _{i-1} ^{β} → ¹³ C _{i-1} ^{α} → ¹⁵ N _i → ¹ HN _i	$\omega_1: \Omega(^{13}\text{C}_{i-1}^\alpha) \pm \Omega(^{13}\text{C}_{i-1}^\beta); \Omega(^{13}\text{C}_{i-1}^\beta) \pm \Omega(^{13}\text{C}_{i-1}^\alpha)$ $\omega_2: \Omega(^{15}\text{N}_i) \pm \Omega(^{13}\text{C}_{i-1}^\alpha)$
L-(5,3)D <u>HN(NCO)</u> (<u>C</u> ^{β} ^{α})	¹ HN _i → ¹⁵ N _i → ¹³ C _{i-1} ^{α} → ¹³ C _{i-1} ^{β} → ¹³ C _{i-1} ^{α} → ¹⁵ N _i → ¹ HN _i	$\omega_1: \Omega(^{13}\text{C}_{i-1}^\alpha) \pm \Omega(^{13}\text{C}_{i-1}^\beta); \Omega(^{13}\text{C}_{i-1}^\beta) \pm \Omega(^{13}\text{C}_{i-1}^\alpha)$ $\omega_2: \Omega(^{15}\text{N}_i) \pm \Omega(^{13}\text{C}_{i-1}^\alpha)$
(5,3)D <u>[C</u> ^{$\alpha\beta$} ^{α} (<u>CON</u>) <u>HN</u>	¹ H _{i-1} ^{β} → ¹³ C _{i-1} ^{β} → ¹³ C _{i-1} ^{α} → ¹³ C _{i-1} ^{β} → ¹⁵ N _i → ¹ HN _i	$\omega_1: \Omega(^{13}\text{C}_{i-1}^\alpha) \pm \Omega(^{13}\text{C}_{i-1}^\beta); \Omega(^{15}\text{N}_i) \pm \Omega(^{13}\text{C}_{i-1}^\alpha)$
(6,3)D <u>[H</u> ^{$\alpha\beta$} ^{α} (<u>CON</u>) <u>HN</u>	(f ₁) (f ₁) (f ₁) (f ₂) (f ₂) (f ₃)	$\omega_1: \Omega(^{13}\text{C}_{i-1}^\alpha) \pm \Omega(^{13}\text{C}_{i-1}^\beta); \Omega(^{15}\text{N}_i) \pm \Omega(^{13}\text{C}_{i-1}^\alpha)$
(5,3)D <u>HN(N)CO</u> (<u>C</u> ^{β} ^{α})	¹ HN _i → ¹⁵ N _i → ¹³ C _{i-1} ^{α} → ¹³ C _{i-1} ^{β} → ¹³ C _{i-1} ^{α} → ¹⁵ N _i → ¹ HN _i	$\omega_1: \Omega(^{13}\text{C}_{i-1}^\alpha) \pm \Omega(^{13}\text{C}_{i-1}^\beta); \Omega(^{15}\text{N}_i) \pm \Omega(^{13}\text{C}_{i-1}^\alpha)$
(5,3)D <u>[H</u> ^{α} ^{α} (<u>CON</u>) <u>HN</u>	¹ H _{i-1} ^{β} → ¹³ C _{i-1} ^{β} → ¹³ C _{i-1} ^{α} → ¹⁵ N _i → ¹ HN _i	$\omega_1: \Omega(^{13}\text{C}_{i-1}^\alpha) \pm \Omega(^{13}\text{H}_{i-1}^\beta); \Omega(^{15}\text{N}_i) \pm \Omega(^{13}\text{C}_{i-1}^\alpha)$
L-(5,3)D <u>HN(N)CO</u> (<u>C</u> ^{β} ^{α})	¹ HN _i → ¹⁵ N _i → ¹³ C _{ij-1} ^{β} → ¹³ C _{ij-1} ^{α} → ¹³ C _{ij-1} ^{β} → ¹⁵ N _i → ¹ HN _i	$\omega_1: \Omega(^{13}\text{C}_{ij-1}^\alpha) \pm \Omega(^{13}\text{C}_{ij-1}^\beta); \Omega(^{13}\text{C}_{ij-1}^\beta) \pm \Omega(^{13}\text{C}_{ij-1}^\alpha)$ $\omega_2: \Omega(^{15}\text{N}_i) \pm \Omega(^{13}\text{C}_i^\alpha)$
(5,3)D <u>[H</u> ^{α} ^{α} (<u>CON</u>) <u>HN</u>	¹ H _{i-1} ^{β} → ¹³ C _{i-1} ^{β} → ¹³ C _{i-1} ^{α} → ¹⁵ N _i → ¹ HN _i	$\omega_1: \Omega(^{13}\text{C}_{i-1}^\alpha) \pm \Omega(^{13}\text{H}_{i-1}^\beta); \Omega(^{15}\text{N}_i) \pm \Omega(^{13}\text{C}_{i-1}^\alpha)$
L-(5,3)D <u>HN(N)CO</u> (<u>C</u> ^{β} ^{α})	¹ HN _i → ¹⁵ N _i → ¹³ C _{i-1} ^{β} → ¹³ C _{i-1} ^{α} → ¹³ C _{i-1} ^{β} → ¹⁵ N _i → ¹ HN _i	$\omega_1: \Omega(^{13}\text{C}_{i-1}^\alpha) \pm \Omega(^{13}\text{C}_{i-1}^\beta); \Omega(^{13}\text{C}_{i-1}^\beta) \pm \Omega(^{13}\text{C}_{i-1}^\alpha)$ $\omega_2: \Omega(^{15}\text{N}_i) \pm \Omega(^{13}\text{C}_{i-1}^\alpha)$
<i>Gao and co-workers⁴³</i>		
1. Backbone and ¹³C^{β} resonance assignments		
(3,2)D <u>HNNCO</u> ²²	¹ HN _i → ¹⁵ N _i → ¹³ C _{i-1} ^{α} → ¹⁵ N _i → ¹ HN _i	$\Omega(^{15}\text{N}_i) \pm \Omega(^{13}\text{C}_{i-1}^\alpha)$
(3,2)D <u>HNNCA</u>	¹ HN _i → ¹⁵ N _i → ¹³ C _{ij-1} ^{β} → ¹⁵ N _i → ¹ HN _i	$\Omega(^{15}\text{N}_i) \pm \Omega(^{13}\text{C}_{ij-1}^\beta)$
(3,2)D <u>HNNCABC</u>	¹ HN _i → ¹⁵ N _i → ¹³ C _{ij-1} ^{β} → ¹³ C _{ij-1} ^{α} → ¹³ C _{ij-1} ^{β} → ¹⁵ N _i → ¹ HN _i	$\Omega(^{15}\text{N}_i) \pm \Omega(^{13}\text{C}_{ij-1}^\alpha) / \Omega(^{13}\text{C}_{ij-1}^\beta)$
(3,2)D <u>HNN(CO)CA</u>	¹ HN _i → ¹⁵ N _i → ¹³ C _{i-1} ^{α} → ¹³ C _{i-1} ^{β} → ¹³ C _{i-1} ^{α} → ¹⁵ N _i → ¹ HN _i	$\Omega(^{15}\text{N}_i) \pm \Omega(^{13}\text{C}_{i-1}^\alpha)$
(3,2)D <u>HNN(CA)CO</u>	¹ HN _i → ¹⁵ N _i → ¹³ C _i ^{α} → ¹³ C _i ^{β} → ¹³ C _i ^{α} → ¹⁵ N _i → ¹ HN _i	$\Omega(^{15}\text{N}_i) \pm \Omega(^{13}\text{C}_i^\alpha)$
(3,2)D <u>HNN(CO)CABC</u>	¹ HN _i → ¹⁵ N _i → ¹³ C _{i-1} ^{β} → ¹³ C _{i-1} ^{α} → ¹³ C _{i-1} ^{β} → ¹⁵ N _i → ¹ HN _i	$\Omega(^{15}\text{N}_i) \pm \Omega(^{13}\text{C}_{i-1}^\alpha) / \Omega(^{13}\text{C}_{i-1}^\beta)$
(3,2)D <u>CBCANHN</u>	¹ H _{ij-1} ^{β} → ¹³ C _{ij-1} ^{β} → ¹³ C _{ij-1} ^{α} → ¹⁵ N _i → ¹ HN _i	$\Omega(^{15}\text{N}_i) \pm \Omega(^{13}\text{C}_{ij-1}^\alpha) / \Omega(^{13}\text{C}_{ij-1}^\beta)$

(continued overleaf)

Table 2: Translation of Projection (Reconstruction) NMR experiments to GFT-NMR nomenclature

Research Group; Projection NMR experiments (with Tilt angles)	Equivalent GFT NMR experiment(s) ^a (with corresponding scaling factors)
Marion and co-workers 1. 3D ¹³ C/ ¹⁵ N filtered NOESY ¹⁵	(4,3)D [<u>H</u> C ^{alt}]-NOESY-[<u>NH</u>]
Kozminski and co-workers 1. 2D RD-HNCA ⁴¹ 2. 2D RD-HN(CO)CA ⁴¹ 3. 2D RD-HACANH ⁴¹ 4. 2D DQ-HN(CACB) ⁴² 5. 2D DQ-HN(CO)(CACB) ⁴² 6. 2D HNCO ⁴³ 7. 2D HNCA ⁴³ 8. 2D HN(CO)CA ⁴³ 9. 2D H(N)COCA ⁴³	(3,2)D HNNCA (3,2)D HNN(CO)CA (4,2)D HACANH (4,2)D HNNC ^{αβ} C ^α (4,2)D HNN(CO)C ^{αβ} C ^α (3,2)D HNNCO (3,2)D HNNCA (3,2)D HNN(CO)CA (3,2)D HN(N)COCA
Brutscher and co-workers 1. 2D DQ/ZQ HNCA ⁴⁴ 2. 2D DQ/ZQ HN(CO)CA ⁴⁴ 3. 2D DQ/ZQ HNCACB ⁴⁴ 4. 2D DQ/ZQ HN(COCA)CB ⁴⁴ 5. 2D DQ/ZQ HN(CA)HA ⁴⁴ 6. 2D DQ/ZQ HN(COCA)HA ⁴⁴	(3,2)D HNNCA (3,2)D HNN(CO)CA (3,2)D HNNC ^{αβ} C ^α (3,2)D HNN(COCA)CB (3,2)D HNN(CA)HA (3,2)D HNN(COCA)HA
Kupce and Freeman 1. 3D HNCO ²⁷ Tilt angles: α=30 ⁰ Tilt angles: α=0 ⁰ , 90 ⁰ 2. 3D HNCA ²⁸ Tilt angles: α=±30 ⁰ Tilt angles: α=0 ⁰ , 90 ⁰ 3. 3D HN(CO)CA ²⁸ Tilt angles: α=±60 ⁰ Tilt angles: α=0 ⁰ , 90 ⁰ 4. 4D HNCOCA ³⁰ Tilt angles: α=±45 ⁰ ; β=±45 ⁰ Tilt angles: α=0 ⁰ ; β=0 ⁰ α=90 ⁰ ; β=0 ⁰ α=0 ⁰ ; β=90 ⁰ 5. The 'TILT' experiment: 3D ¹⁵ N-NOESY-HSQC and ¹⁵ N-TOCSY-HSQC ⁴⁵ Tilt angle: α=0 ⁰ α=±30 ⁰	1. (3,2)D HNNCO Scaling factors (κ): N=0.5; CO=0.87 2D [¹³ C', ¹ H] Projection of 3D HNNCO, 2D [¹⁵ N, ¹ H] HSQC 2. (3,2)D HNNCA Scaling factors (κ): N=0.5; CA=0.87 2D [¹³ C', ¹ H] Projection of 3D HNNCA, 2D [¹⁵ N, ¹ H] HSQC 3. (3,2)D HNN(CO)CA Scaling factors (κ): N=0.87; CA=0.5 2D [¹³ C', ¹ H] Projection of 3D HNN(CO)CA, 2D [¹⁵ N, ¹ H] HSQC 4. (4,2)D HNNCOCA Scaling factors(κ): N=0.71; CO=0.5; CA=0.5 2D [¹³ C', ¹ H] Projection of 4D HNNCOCA 2D [¹³ C ^α , ¹ H] Projection of 4D HNNCOCA 2D [¹⁵ N, ¹ H] HSQC 5. (3,2)D [<u>H</u>]-NOESY-[<u>NH</u>] / (3,2)D [<u>H</u>]-TOCSY-[<u>NH</u>] Scaling factors(κ): H=1.0, N=0.0 H=0.87, N=0.5

Zhou and co-workers

1. 5-D HACACONH³³

Tilt angles:
N=±60, CO=±60, CA=±60, HA=±60

Tilt angles:
N=0⁰, CO=90⁰, CA=90⁰, HA=90⁰
N=90⁰, CO=0⁰, CA=90⁰, HA=90⁰
N=90⁰, CO=90⁰, CA=0⁰, HA=90⁰
N=90⁰, CO=90⁰, CA=90⁰, HA=0⁰

2. (4,2)D PR-HNCACB³⁴

Tilt angles:
N=86.0⁰, CA=15.5⁰, CB=75.0⁰
N=73.9⁰, CA=33.7⁰, CB=61.3⁰
N=54.7⁰, CA=54.7⁰, CB=54.7⁰
N=33.7⁰, CA=73.9⁰, CB=61.3⁰
N=15.5⁰, CA=86.0⁰, CB=75.0⁰

Tilt angles:
N=0⁰, CA=90⁰, CB=90⁰
N=90⁰, CA=0⁰, CB=90⁰
N=90⁰, CA=90⁰, CB=0⁰

3. (4,2)D PR-HN(CO)CACB³⁴
Tilt angles same as in (2)

4. (4,2)D PR-Intra-HNCACB³⁴
Tilt angles same as in (2)

5. (4,2)D PR-HNCACO³⁴
Tilt angles same as in (2) with
CB shift evolution replaced by CO

6. (4,2)D PR-HNCOCA³⁴
Tilt angles same as in (2) with
CA shift evolution replaced by CO and
CB shift evolution replaced by CA

7. (4,2)D PR-HNCO_{i1}CA_i³⁴
Tilt angles same as in (2) with
CA shift evolution replaced by CO and
CB shift evolution replaced by CA

8. (4,2)D PR-HACANH³⁴
Tilt angles same as in (2) with
CA shift evolution replaced by HA and
CB shift evolution replaced by CA

9. (4,2)D PR-HACA(CO)NH³⁴
Tilt angles same as in (2) with
CA shift evolution replaced by HA and
CB shift evolution replaced by CA

1. (5,2)D HACACONHN

Scaling factor (κ):
N=0.5, CO=0.5, CA=0.5, HA=0.5

2D [¹⁵N, ¹H] HSQC
2D [¹³C', ¹H] Projection of 4D/5D HACACONHN
2D [¹³C^α, ¹H] Projection of 4D/5D HACACONHN
2D [¹H^α, ¹H] Projection of 4D/5D HACACONHN

2. (4,2)D HNNC^{αβ}C^α

Scaling factors(κ):
N=0.07, C^α=0.96, C^β=0.26
N=0.28, C^α=0.83, C^β=0.48
N=0.58, C^α=0.58, C^β=0.58
N=0.83, C^α=0.28, C^β=0.48
N=0.96, C^α=0.07, C^β=0.26

2D [¹⁵N, ¹H] HSQC
2D [¹³C^α, ¹H] Projection of 3D/4D HNNC^{αβ}C^α
2D [¹³C^β, ¹H] Projection of 4D HNNC^{αβ}C^α

3. (4,2)D HNN(CO)C^{αβ}C^α
Scaling Factors same as in (2)

4. (4,2)D Intra-HNNC^{αβ}C^α
Scaling Factors same as in (2)

5. (4,2)D Intra-HNNCACO
Scaling Factors same as in (2) with
C^β shift evolution replaced by CO

6. (4,2)D HNNCOCA
Scaling Factors same as in (2) with
C^α replaced by CO and
C^β replaced by CA

7. (4,2)D HNN<CO,CA>
Scaling Factors same as in (2) with
C^α shift evolution replaced by CO and
C^β shift evolution replaced by CA

8. (4,2)D HACANHN
Scaling Factors same as in (2) with
C^α shift evolution replaced by HA and
C^β shift evolution replaced by CA

9. (4,2)D HACA(CO)NH
Tilt angles same as in (2) with
CA shift evolution replaced by HA and
CB shift evolution replaced by CA

<p>10. (4,2)D PR CH₃-N NOESY⁴⁶</p> <p>Tilt angles: 100 Projection angles distributed evenly in angle space: N=α_i; H= β_i; C=γ_i; i=1..100</p>	<p>10. (4,2)D [<u>HC^{all}]-NOESY-[NH]</u></p> <p>Scaling factors(κ): N = cos(α_i), H = cos(β_i), C^{all} = cos(γ_i); i=1..100</p>
<p>11. (4,3)D HC(CO)NH-TOCSY and (4,3)D HC(C)NH-TOCSY⁴⁷</p> <p>Tilt angles: α=0⁰, ±18⁰, ±36⁰, ±54⁰, ±72⁰, 90⁰</p>	<p>11. (4,3)D HC(CO)NH-TOCSY and (4,3)D HC(C)NH-TOCSY</p> <p>Scaling factors(κ): ¹H=1.0, 0.95, 0.81, 0.58, 0.31, 0.0 ¹³C=0.0, 0.31, 0.58, 0.81, 0.95, 1.0</p>
<p>Wüthrich and co-workers⁴⁸</p>	
<p>1. 4D APSY-HNCOCA</p> <p>Tilt angles: α=±30⁰; β=0⁰ α=±60⁰; β=0⁰</p> <p>Tilt angles: α=0⁰; β=±30⁰ α=0⁰; β=±60⁰</p> <p>Tilt angles: α=90⁰; β=±30⁰ α=90⁰; β=±60⁰</p> <p>Tilt angles: α=±30⁰; β=±30⁰ α=±60⁰; β=±30⁰ α=±45⁰; β=±60⁰</p> <p>Tilt angles: α=0⁰; β=0⁰ α=90⁰; β=0⁰ α=0⁰; β=90⁰</p>	<p>1. Set of (3,2)D and (4,2)D GFT NMR experiments:</p> <p>(3,2)D HN(N)COCA Scaling factors(κ): CO=0.5; CA=0.87; CO=0.87; CA=0.5</p> <p>(3,2)D HNN(CO)CA Scaling factors(κ): N=0.5; CA=0.87 N=0.87; CA=0.5</p> <p>(3,2)D HNNCO Scaling factors(κ): N=0.5; CO=0.87 N=0.87; CO=0.5</p> <p>(4,2)D HNNCOCA Scaling factors(κ): N=0.5; CO=0.44; CA=0.75 N=0.5; CO=0.75; CA=0.44 N=0.87; CO=0.35; CA=0.35</p> <p>2D [¹³C^α, ¹H] Projection of 4D HNNCOCA 2D [¹³C^β, ¹H] Projection of 4D HNNCOCA 2D [¹⁵N, ¹H] HSQC</p>
<p>2. 5D APSY-HACACONH</p> <p>Tilt angles: α=±30⁰; β=0⁰; γ=0⁰ α=±60⁰; β=0⁰; γ=0⁰</p> <p>Tilt angles: α=0⁰; β=±30⁰; γ=0⁰ α=0⁰; β=±60⁰; γ=0⁰</p> <p>Tilt angles: α=0⁰; β=0⁰; γ=±30⁰ α=0⁰; β=0⁰; γ=±60⁰</p> <p>Tilt angles: α=90⁰; β=±30⁰; γ=0⁰ α=90⁰; β=±60⁰; γ=0⁰</p> <p>Tilt angles: α=90⁰; β=0⁰; γ=±30⁰ α=90⁰; β=0⁰; γ=±60⁰</p>	<p>2. A set of (3,2)D GFT NMR experiments</p> <p>(3,2)D (HACA)CONHN Scaling factors(κ): N = 0.87; CO=0.5 Scaling factors(κ): N = 0.5; CO=0.87</p> <p>(3,2)D (HA)CA(CO)NHN Scaling factors(κ): N = 0.87; CA=0.5 N = 0.5; CA=0.87</p> <p>(3,2)D HA(CACO)NHN Scaling factors(κ): N = 0.87; HA=0.5 N = 0.5; HA=0.87</p> <p>(3,2)D (HA)CACO(N)HN Scaling factors(κ): CA = 0.5; CO=0.87 CA = 0.87; CO=0.5</p> <p>(3,2)D HA(CA)CO(N)HN Scaling factors(κ): CO = 0.87; HA=0.5 CO = 0.5; HA=0.87</p>

<p>Tilt angles: α=0⁰; β=90⁰; γ=±30⁰ α=0⁰; β=90⁰; γ=±60⁰</p> <p>Tilt angles: α=0⁰; β=0⁰; γ=0⁰ α=90⁰; β=0⁰; γ=0⁰ α=0⁰; β=90⁰; γ=0⁰ α=0⁰; β=0⁰; γ=90⁰</p>	<p>(3,2)D HACA(CON)HN Scaling factors(κ): CA = 0.87; HA = 0.5 CA = 0.5; HA = 0.87</p> <p>2D [¹⁵N, ¹H] HSQC 2D [¹³C^α, ¹H] Projection of 4D HNNCOCA 2D [¹³C^β, ¹H] Projection of 4D HNNCOCA 2D [¹H^α, ¹H] Projection of 4D HNNCOCA</p>
<p>Wagner and co-workers⁴⁹</p>	
<p>3D RD-HCcoNH-TOCSY</p>	<p>(4,3)D HC(CO)NHN-TOCSY</p>
<p>Markely and co-workers³⁷</p>	
<p>1. 3D HNCO^b</p> <p>Tilt angles: α=50⁰, 35⁰, 10⁰, 70⁰, 20⁰, 25⁰, 45⁰</p> <p>2. 3D HNCACB^b</p> <p>Tilt angles: α=20⁰, 10⁰, 30⁰, 40⁰, 50⁰, 60⁰, 70⁰</p> <p>3. 3D CBCA(CO)NHN^b</p> <p>Tilt angles: α=50⁰, 55⁰, 40⁰, 70⁰, 30⁰, 65⁰, 20⁰</p>	<p>1. (3,2)D HNNCO</p> <p>Scaling factors(κ): N=0.76, 0.57, 0.17, 0.94, 0.34, 0.42, 0.71 CO = 0.64, 0.82, 0.98, 0.34, 0.94, 0.90, 0.71</p> <p>2. (3,2)D HNNCACB</p> <p>Scaling factors(κ): N=0.34, 0.17, 0.50, 0.64, 0.76, 0.87, 0.94 CA/CB=0.94, 0.98, 0.87, 0.76, 0.64, 0.50, 0.34</p> <p>3. (3,2)D CBCA(CO)NHN</p> <p>Scaling factors(κ): N=0.76, 0.82, 0.65, 0.94, 0.87, 0.90, 0.34 CA/CB=0.64, 0.57, 0.76, 0.34, 0.50, 0.42, 0.94</p>

^a Only basic spectra are considered, unless otherwise indicated.

^b The tilt angles for mouse protein Mm202773 are considered.³⁷

Classification of 'Projected NMR spectra'

- Which chemical shifts are jointly sampled?
- Which orthogonal projections are acquired?
- What is the 'dimensionality' of the spectral information?
- Are conventional ND spectra reconstructed?
- How many 'GFT dimensions'?

Seho Kim, Hanudatta Atreya, Gaohua Liu, Yang Shen,
Alexander Eletski, Jeffrey Mills, David Parish, Duanxiang Xu,
Catherine du Penhoat, Qi Zhang, Kiran Singarapu

Dinesh Sukumaran

Gaetano Montelione
Cheryl Arrowsmith

National Science Foundation (MCB)

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