



**PULSE PROGRAM
CATALOGUE:
II. BIOMOLECULAR
NMR EXPERIMENTS**

Teodor Parella

Servei RMN, Universitat Autònoma de Barcelona

E-mail: teodor.parella@uab.cat



TOPSPIN v3.0
NMRGuide



UAB

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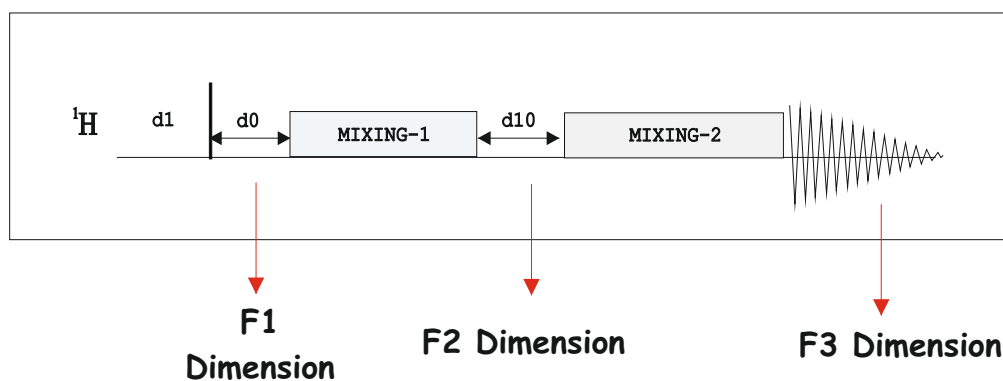
2D HSQC
3D HCCH-TOCSY experiments
HCP Quantitative
P-FIDS

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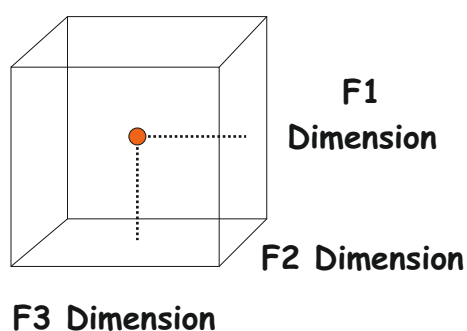
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BASIC 3D HOMONUCLEAR EXPERIMENTS

General Scheme for 3D Homonuclear Experiments



The delays $d0$ and $d10$ represent two independent variable periods that provide two independent frequency dimensions (F2 and F3). The third dimension is directly generated from the FID period (F1 Dimension), as in 1D or 2D experiments.



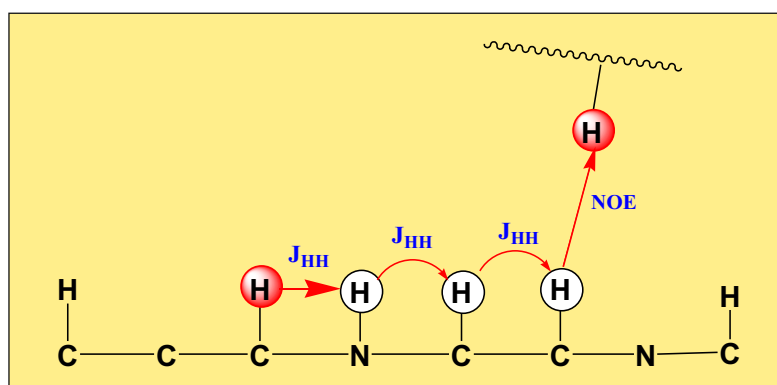
3D Homonuclear Experiments

- 3D TOCSY-NOESY experiment (**mlevnoesy3d**)
- 3D TOCSY-ROESY experiment (**mlevroesy3d**)
- 3D NOESY-TOCSY experiment (**noesymlv3d**)
- 3D NOESY-TOCSY experiment using presaturation (**noesymlevpr3d**)
- 3D NOESY-NOESY experiment using presaturation (**noesynoesypr3d**)

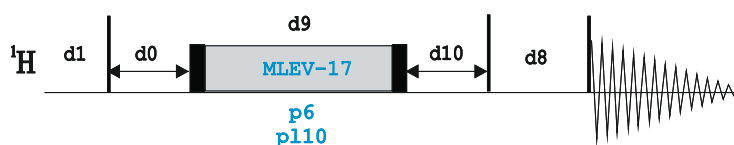
Also see related 2D NOESY, 2D ROESY and 2D TOCSY experiments

References:

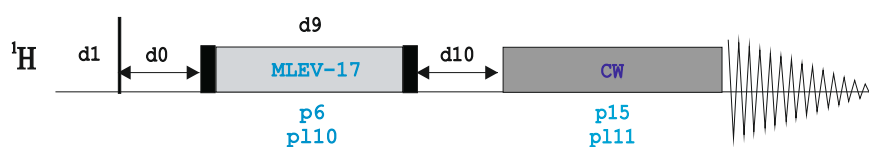
- A. Bax & D.G. Davis, J. Magn. Reson. 65, 355-360 (1985)
A. Bax & D.G. Davis, J. Magn. Reson. 63, 207-213 (1985)

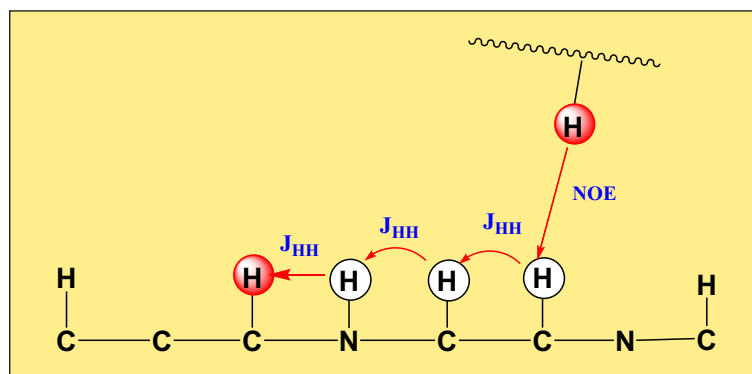


mlevnoesy3d

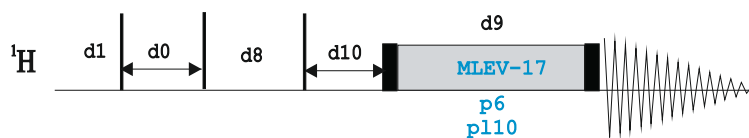


mlevroesy3d

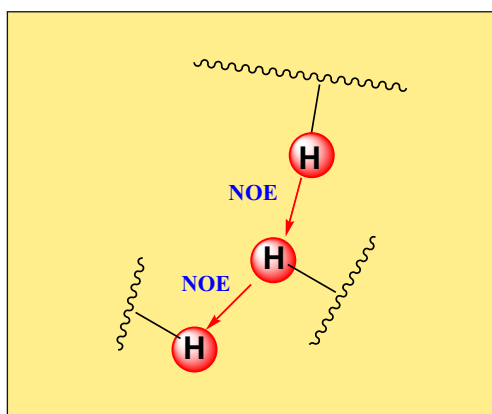
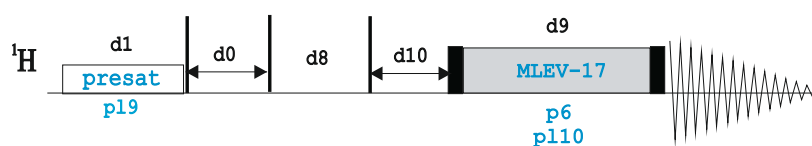




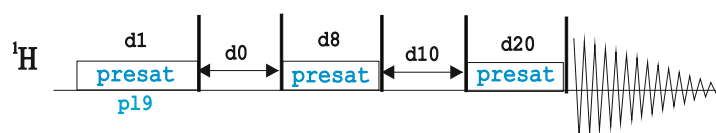
noesymlv3d



noesymlvpr3d



noesypr3d



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BASIC 3D X-EDITED TOCSY EXPERIMENTS

3D Basic X-edited TOCSY

- 3D ^1H - ^{13}C TOCSY-HMQC experiment using presaturation (**mlevhmqcpr3d**)
- 3D ^1H - ^{13}C HMQC-TOCSY experiment using BIRD (**hmqcmlevbi3d**)
- 3D ^1H - ^{13}C HSQC-TOCSY experiment using echo/antiecho, adiabatic pulses and MLEV-17 (**hsqcetgpm13d.2**)
- 3D ^1H - ^{13}C HSQC-TOCSY experiment using PEP, adiabatic pulses and DIPSI-2 (**hsqcdietgpsisp3d.2**)

Also see:

2D TOCSY experiment

2D HSQC-TOCSY experiments and Measurement of long-range proton-carbon coupling constants

3D TOCSY-HSQC experiments

2D X-filtered/edited TOCSY experiments

Other Protein NMR experiments involving TOCSY:

HCCH-TOCSY Experiment

HCC(CO)NH Experiment

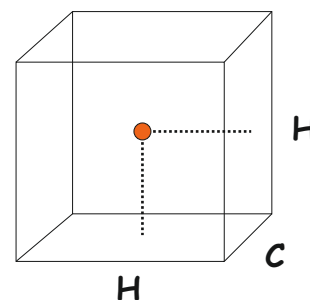
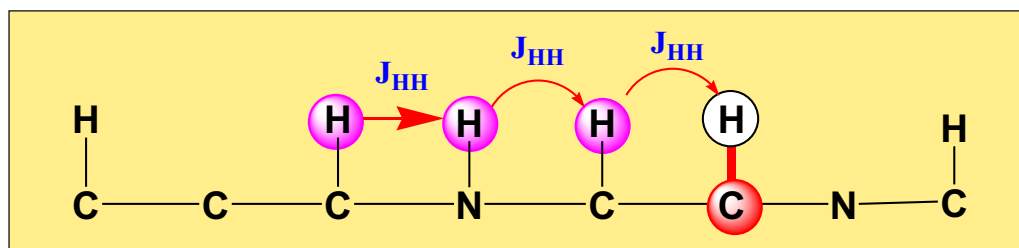
^{13}C - ^{13}C TOCSY

References:

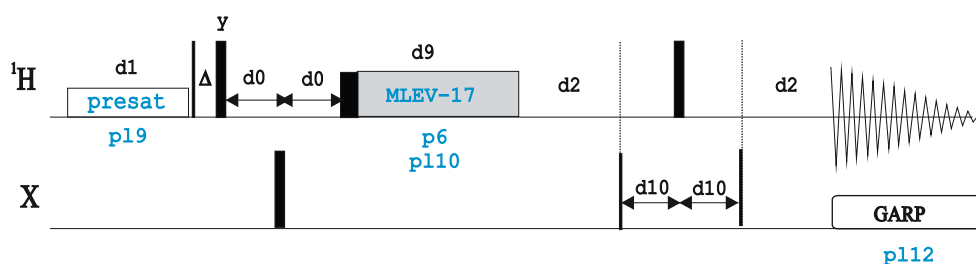
A. Bax and S. Subramanian, J. Magn. Reson. 67, 565-569 (1986)

A. Bax & D.G. Davis, J. Magn. Reson. 65, 355-360 (1985)

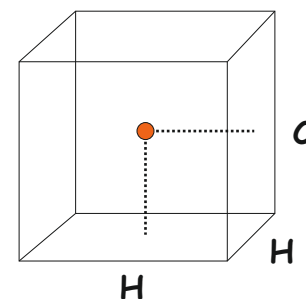
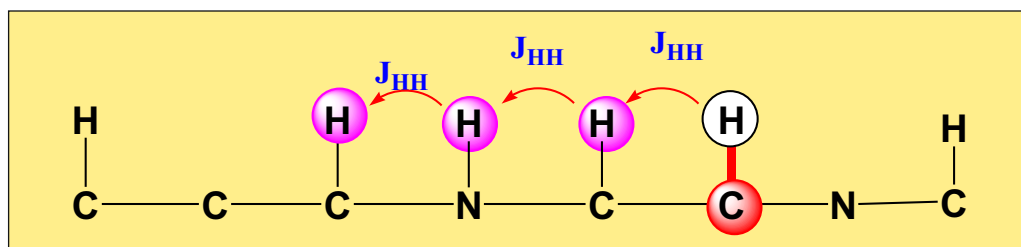
TOCSY-HMQC



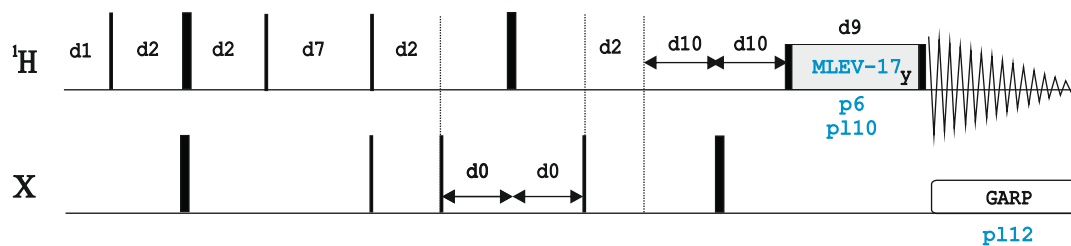
mlevhmqcpr3d



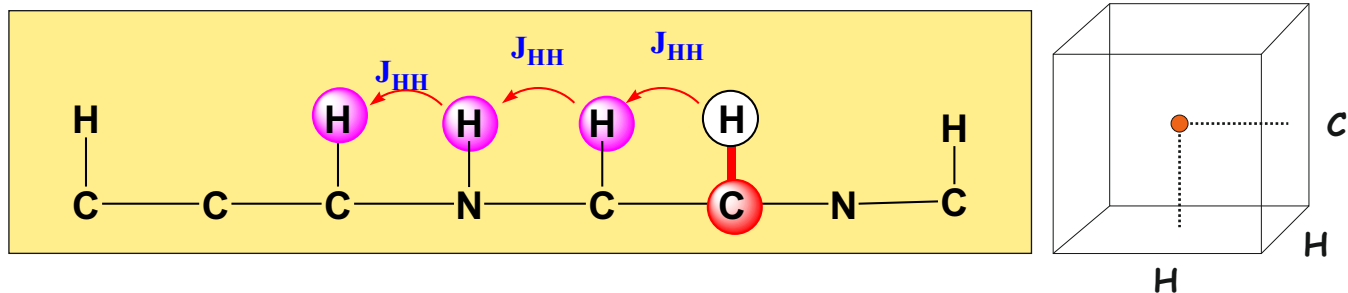
HMQC-TOCSY



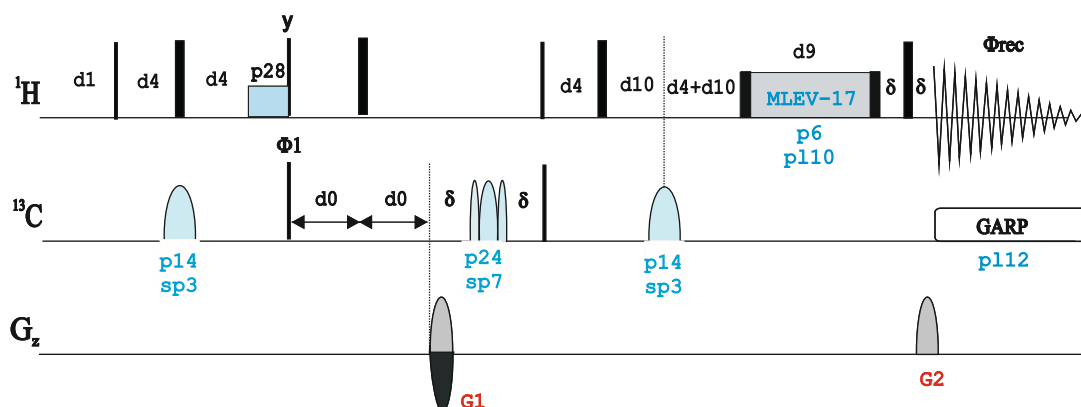
hmqcmlevbi3d



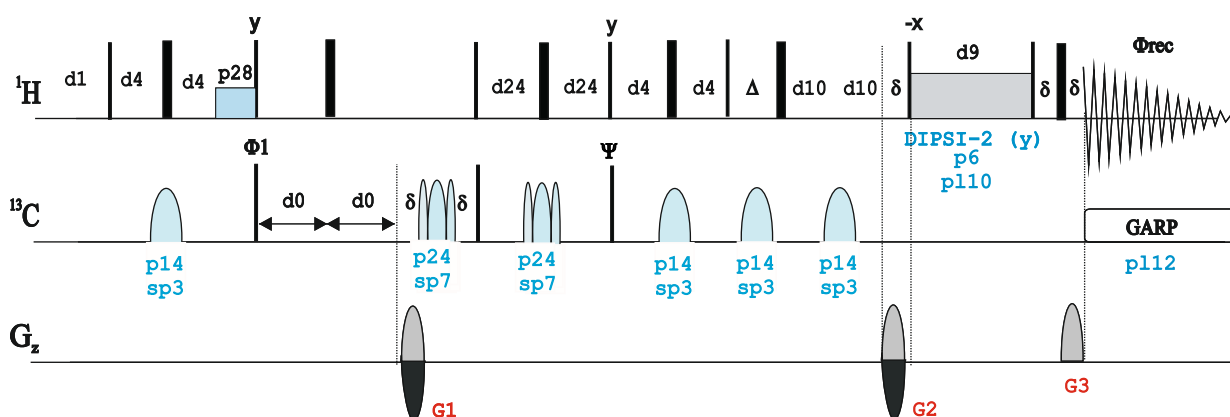
HSQC-TOCSY



hsqcetgpm13d.2



hsqcdietgpsisp3d.2



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3D TOCSY-HSQC EXPERIMENTS

3D TOCSY-HSQC

Gradient-enhanced from f2 channel:

- ge-3D ^1H - ^{13}C TOCSY-HSQC experiment using echo-antiecho (**mlevhsqcetgp3d** | MLEVHSQCETGP3D)

Gradient-enhanced from f3 channel:

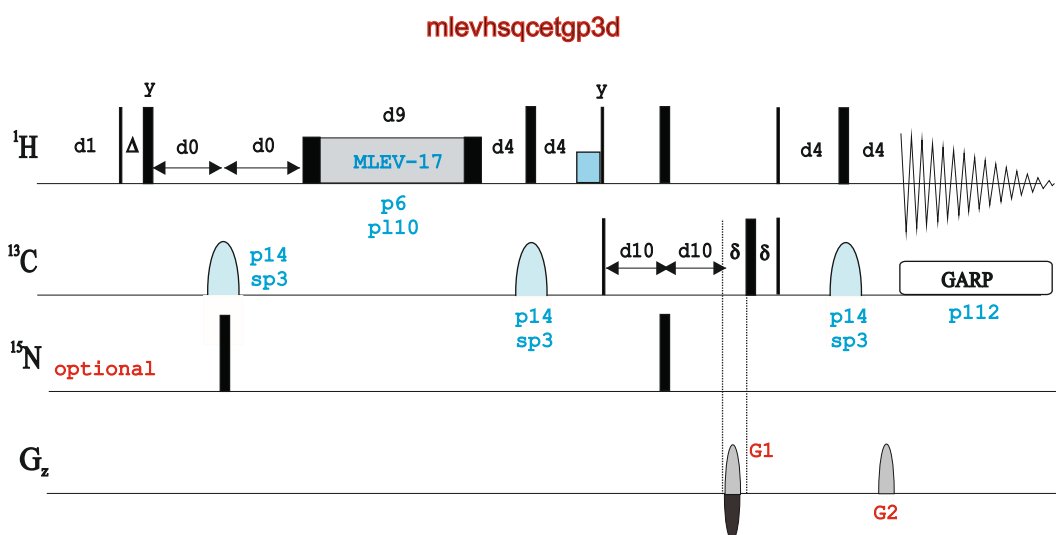
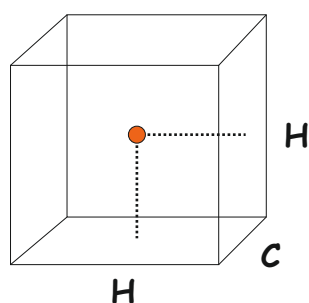
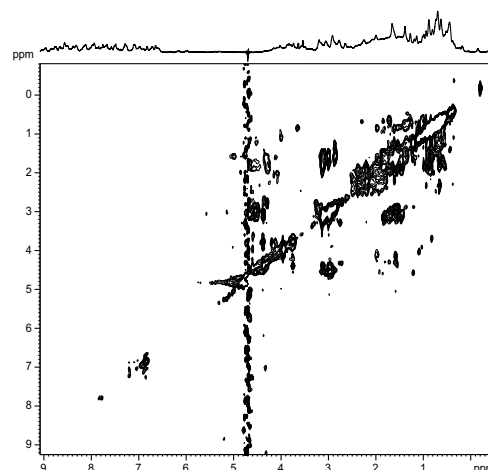
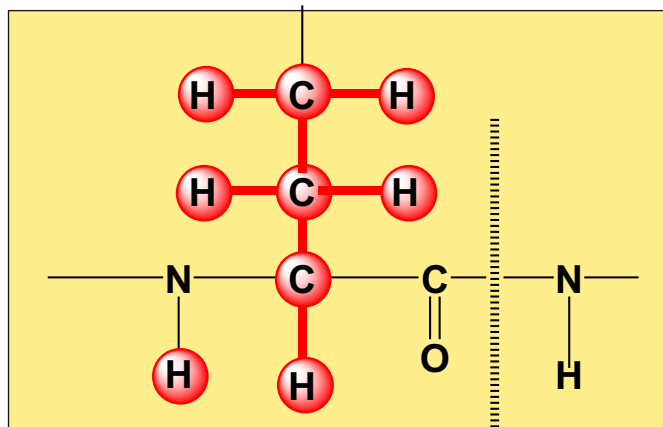
- ge-3D ^1H - ^{15}N TOCSY-HSQC with MLEV using echo-antiecho (**mlevhsqcetf3gp3d** | MLEVHSQCETF3GP3D)
- ge-3D ^1H - ^{15}N TOCSY-HSQC with DIPSI-2 and PEP (**dipsihsqcf3gpsi3d** | DIPSIHSQCF3GPSI3D)
- ge-3D ^1H - ^{15}N TOCSY-HSQC with DIPSI-2 using TROSY (**dipsitretf3gp3d** | DIPSITRETF3GP3D)

Also see:

2D TOCSY experiment

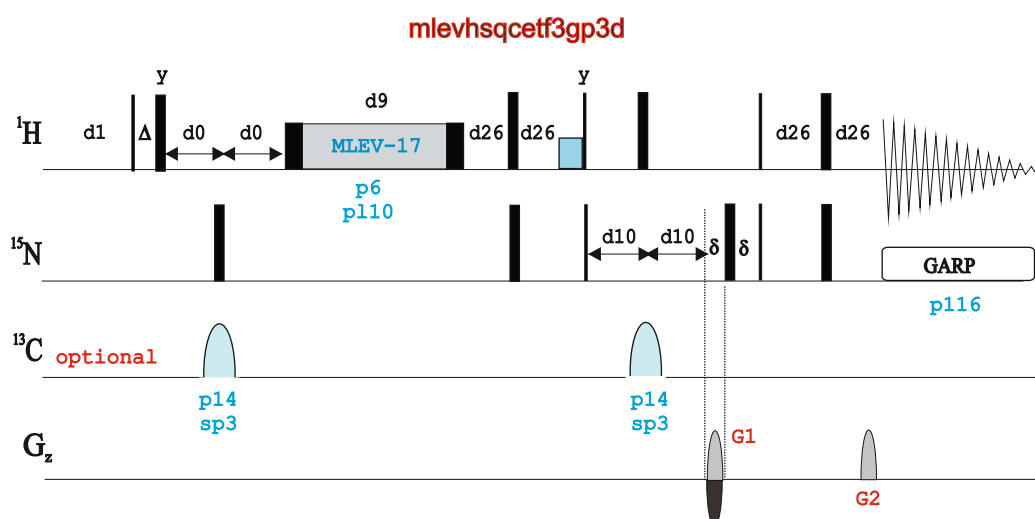
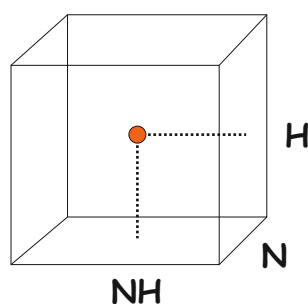
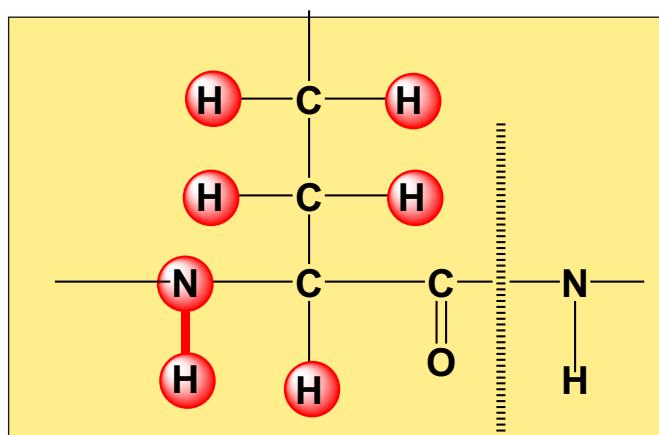
2D & 3D HSQC-TOCSY experiments

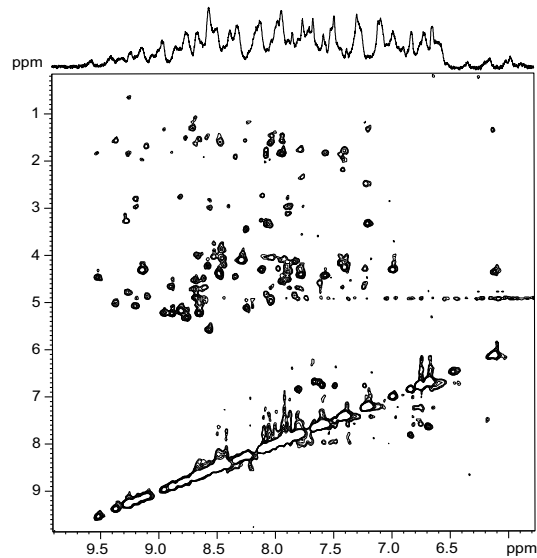
2D X-filtered/edited TOCSY experiments



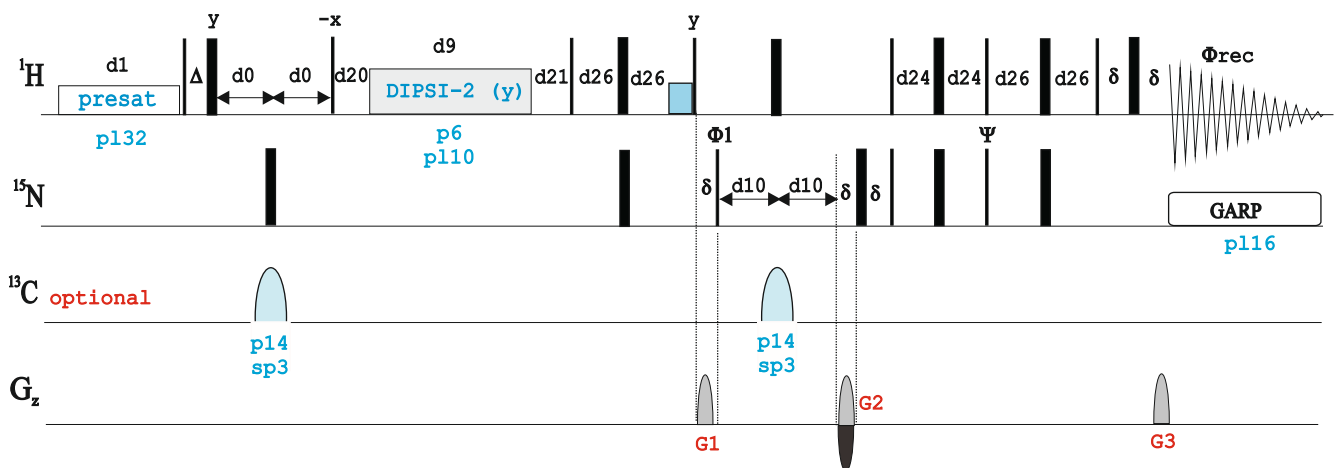
References:

1. A. Bax & D.G. Davis, J. Magn. Reson. 65, 355-360 (1985)
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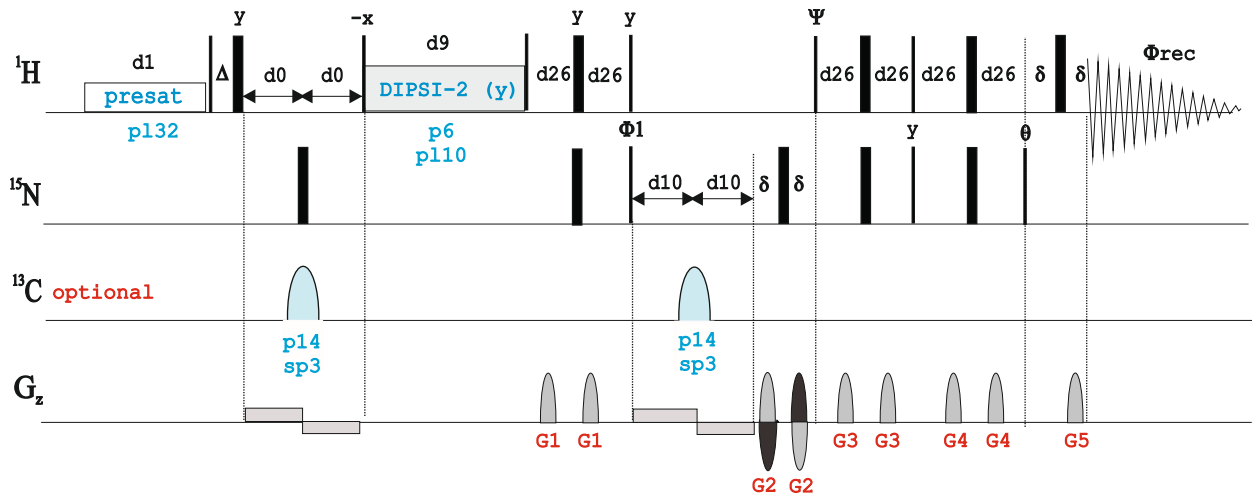




dipsihsqcf3gpsi3d



dipsitretf3gp3d



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2D $^{13}\text{C}/^{15}\text{N}$ -FILTERED TOCSY EXPERIMENTS

2D $^{13}\text{C}/^{15}\text{N}$ -filtered TOCSY

ge-2D w_1 - ^{13}C , ^{15}N -filtered TOCSY experiment

- ge-2D w_1 - ^{13}C , ^{15}N -filtered TOCSY using DIPSI2 and WATERGATE (dipsi2gp phwgx1)

ge-2D w_2 - ^{13}C , ^{15}N -filtered TOCSY experiment

- ge-2D w_2 - ^{13}C , ^{15}N -filtered TOCSY using DIPSI2 and WATERGATE (dipsi2gp phwgx2)

ge-2D w_1, w_2 - ^{13}C , ^{15}N -filtered TOCSY experiment

- Phase-sensitive ge-2D w_1, w_2 ^{13}C , ^{15}N -filtered TOCSY using DIPSI2 and WATERGATE (selective pulses) (dipsi2gp phwgxf)

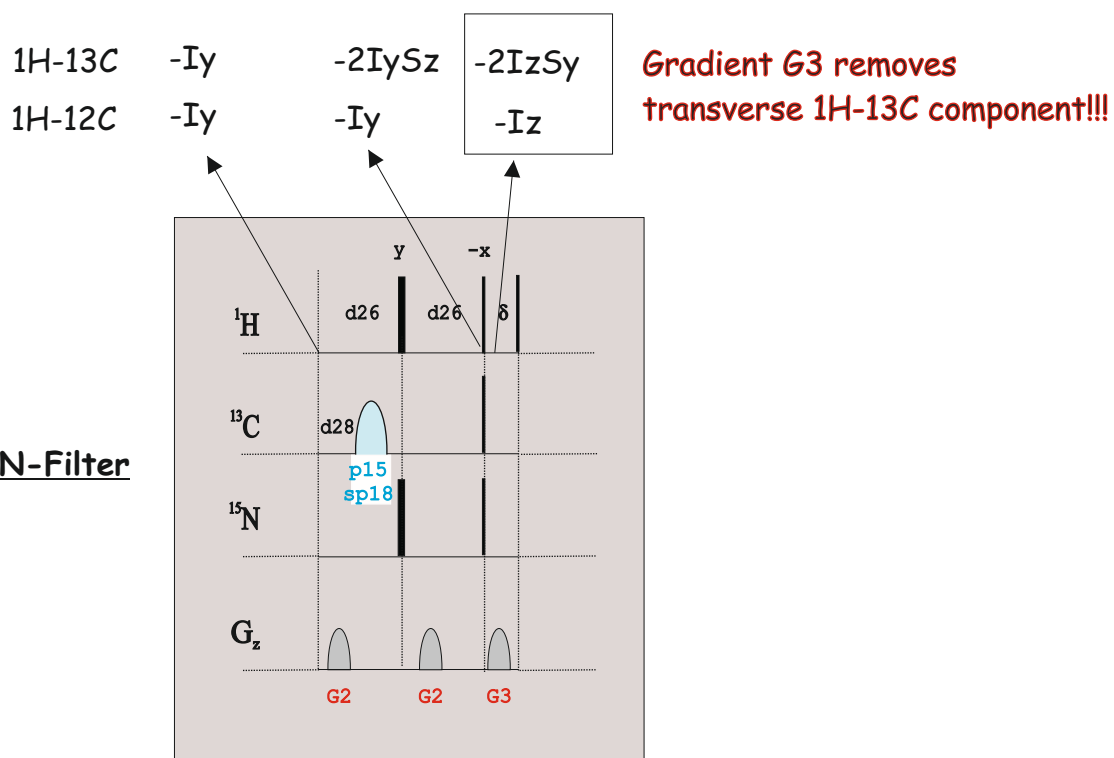
Also see:

2D TOCSY experiment

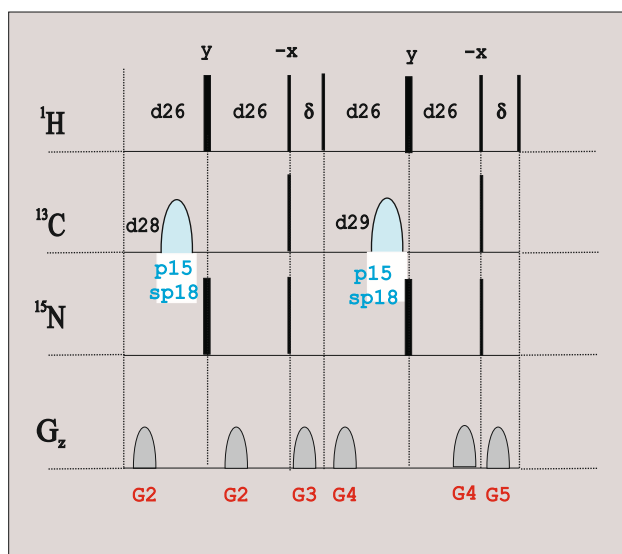
3D TOCSY-HSQC and 3D HSQC-TOCSY experiments

1. A.L. Breeze, Prog. NMR Spectrosc. 36, 323-372 (2000).
2. C. Zwahlen, P. Legault, S.J.F. Vincent, J. Greenblatt, R. Konrat & L.E. Kay, J. Am. Chem. Soc. 119 6711-6721 (1997).
3. K. Ogura, H. Terasawa & F. Inagaki, J. Biomol. NMR 8, 492-498 (1996).
4. J. Iwahara, J.M. Wojciak & R.T. Clubb, J. Biomol. NMR 19, 231-241 (2001).

Single ^{13}C , ^{15}N -Filter



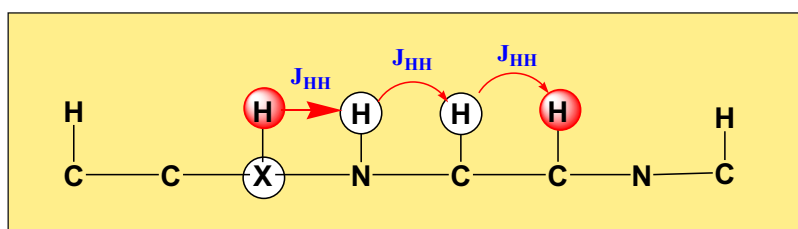
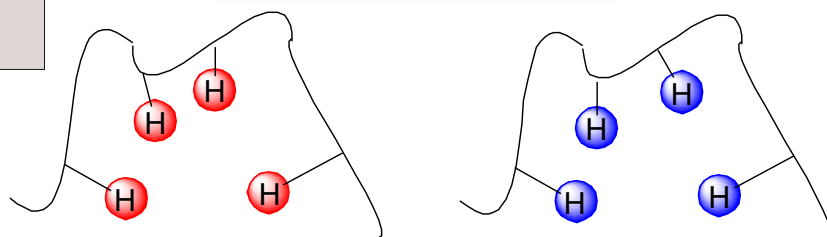
Double ^{13}C , ^{15}N -Filter



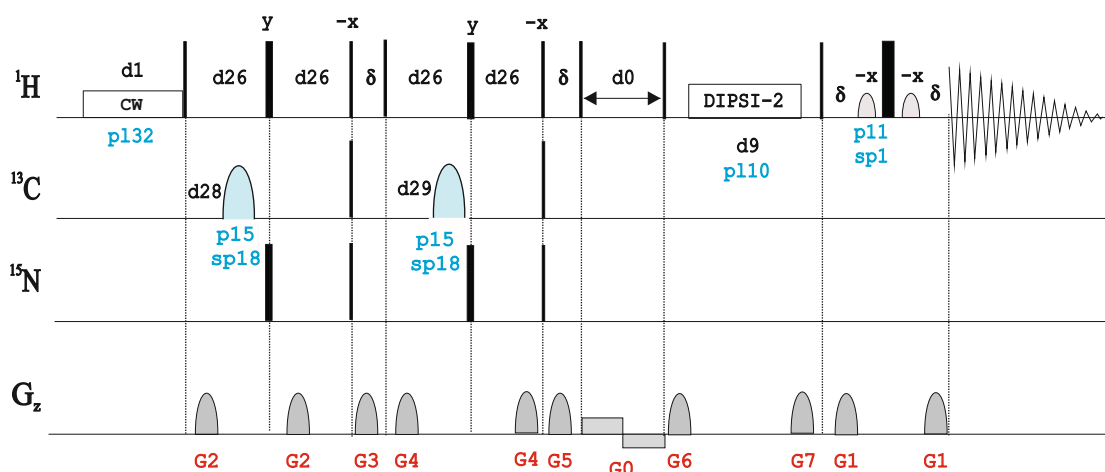
$d26: 1/(4 \cdot J(\text{NH}))$
 $d28: 1/(4 \cdot J(\text{CH})_{\text{min}})$
 $d29: 1/(4 \cdot J(\text{CH})_{\text{max}})$

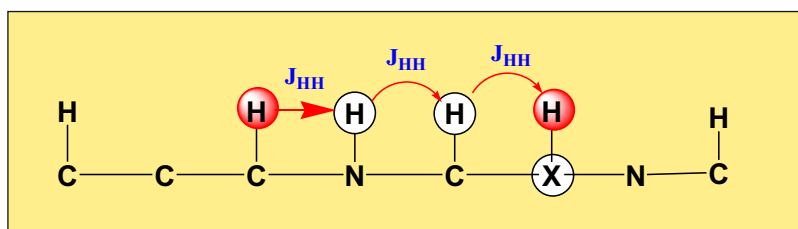
Differentiation between TOCSY in labeled/unlabeled Compounds

● Unlabeled
 ● Labeled

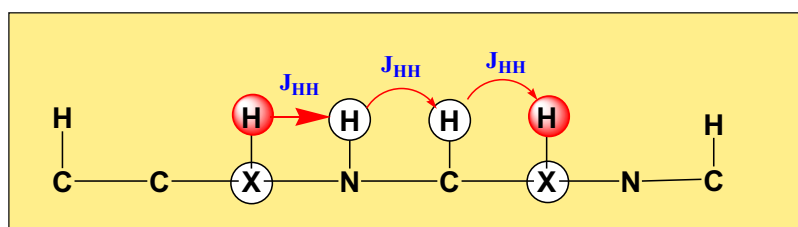
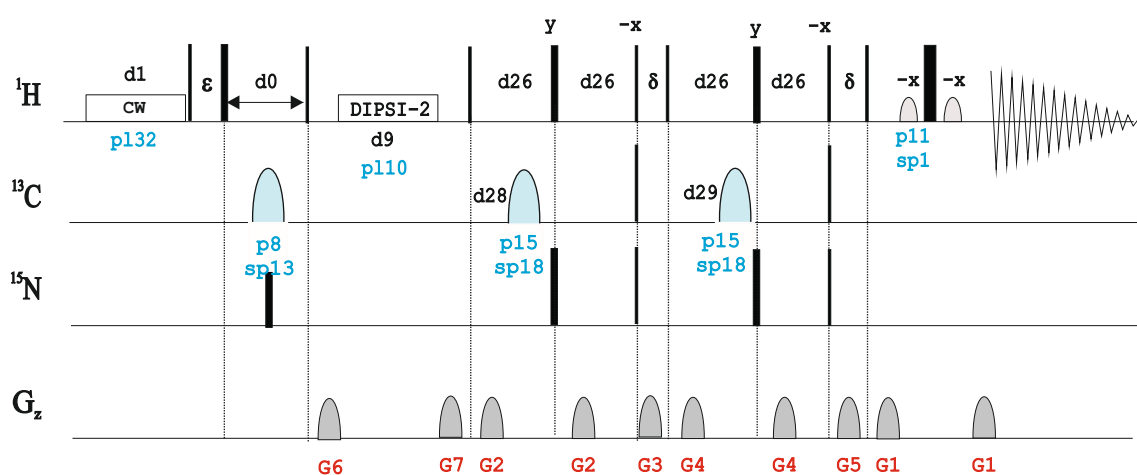


dipsi2gp phwgx1

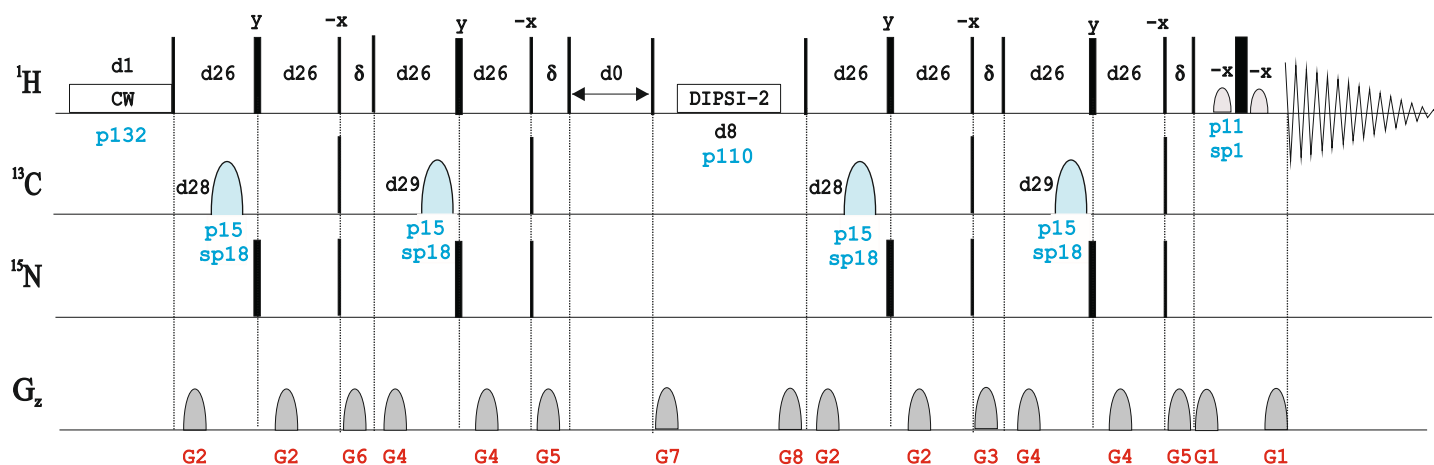




dpsi2gp phwgx2



dpsi2gp phwgxf



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NMRGuide

3D HCCH-COSY
3D HCCH-TOCSY

HCCH-COSY / HCCH-TOCSY

○ HCCH-COSY

- 3D HC(C)H-COSY experiment (**hcchcogp3d** | HCCHCOGP3D)
- 3D (H)CCH-COSY experiment (**hcchcogp3d2**)
- 3D (H)CCH-COSY experiment using TROSY for aromatic residues (**trhcchcogp3d**)

4D HCCH-COSY experiment (**hcchcogp4d**)

○ HCCH-TOCSY

- 3D HC(C)H-TOCSY experiment (**hcchdigp3d** | HCCHDIGP3D)
- 3D (H)CCH-TOCSY experiment (**hcchdigp3d2** | HCCHDIGP3D2)
- 3D HC(C)H-TOCSY using adiabatic TOCSY experiment (**hcchatgp3d** | HCCHATGP3D)
- 3D (H)CCH-TOCSY using adiabatic TOCSY experiment (**hcchatgp3d2**)

4D HCCH-TOCSY experiment (**hcchdigp4d**)

○ ge-2D Long-range HCCH correlation

Phase-sensitive ge-2D Long-range (H)C(C)H using echo-antiecho (**hcchetgplr**)

Also see 3D HCCH-E.COSY experiments for J measurement

- 3D HC(C)H[HA]-E.COSY (**hcchecosgp3d** | HCCHECOSGP3D) - $3J[\text{HA-HB}]$ via E.COSY
- 3D HC(C)H[CO]-E.COSY (**hcchcosygp3d** | HCCHCOSYGP3D) - $3J[\text{CO-HB}]$ via E.COSY
- 3D (H)C(C)CH[CO]-E.COSY (**hccccosygp3d** | HCCCCOSYGP3D) - $3J[\text{CG-CO}]$ via E.COSY

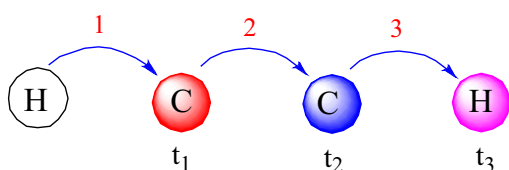
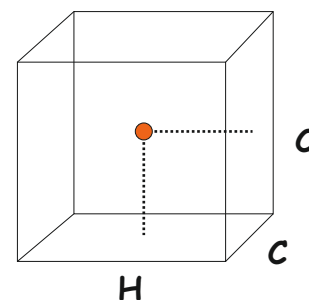
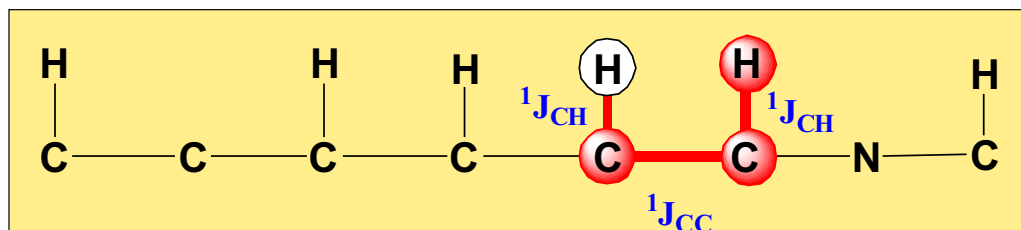
Also see HCCH-type experiments in "Nucleic Acids Experiments"

- 3D TROSY-(H)CCH-COSY for intra-base correlation (**na_trhcchco3d**)
- 3D H(C)CH-E.COSY experiment (**na_hcchecgp3d** | NA_HCCHECGP3D)
- 3D HCC-TOCSY-CCH-COSY experiment (**na_hcchfwdigp3d** | NA_HCCHFWDIGP3D)
- 3D HCC-TOCSY-CCH-E.COSY experiment (**na_hcchfwdiecg3d** | NA_HCCHFWDIECGP3D)
- 3D HCC-TOCSY-CCH-E.COSY experiment using jump-and-return (11) (**na_hcchfwdiecgpr3d**)
- 3D forward directed quantitative gamma HCCH-TOCSY (**na_ghcchfwdigp3d** | NA_GHCCHFWDIGP3D)

Related Experiments:
HCC(CO)NH Experiment
13C-13C TOCSY

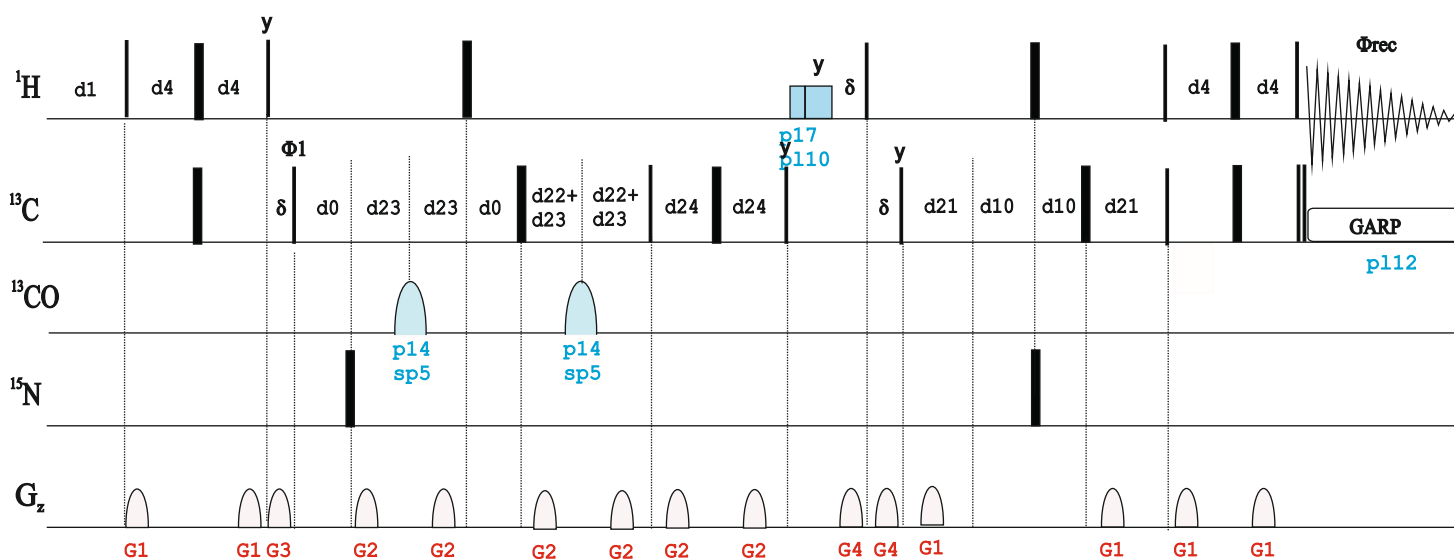
References:

1. L.E. Kay, G.Y. Xu, A.U. Singer, D.R. Muhandiram & J. D. Forman-Kay J. Magn. Reson. B 101, 333 - 337 (1993))
2. W.Peti, C. Griesinger & W. Bermel, J. Biomol. NMR 18, 199 - 205 (2000)

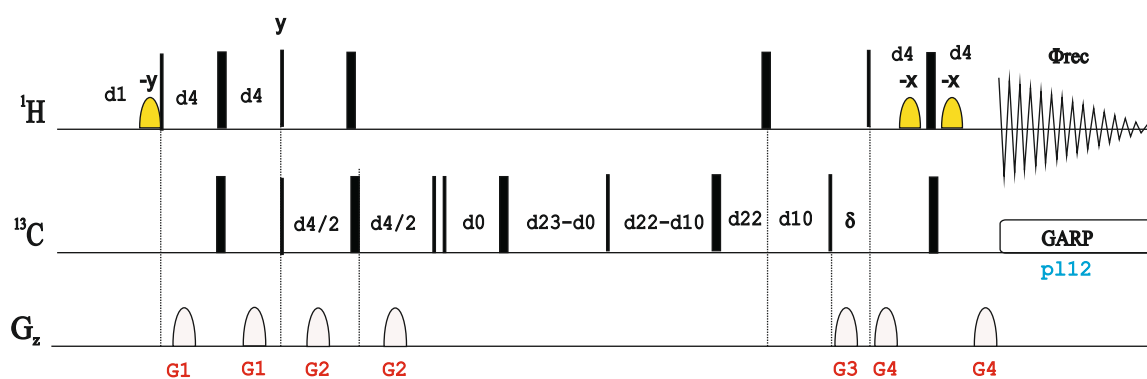


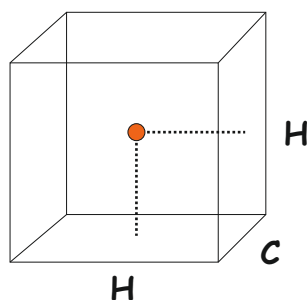
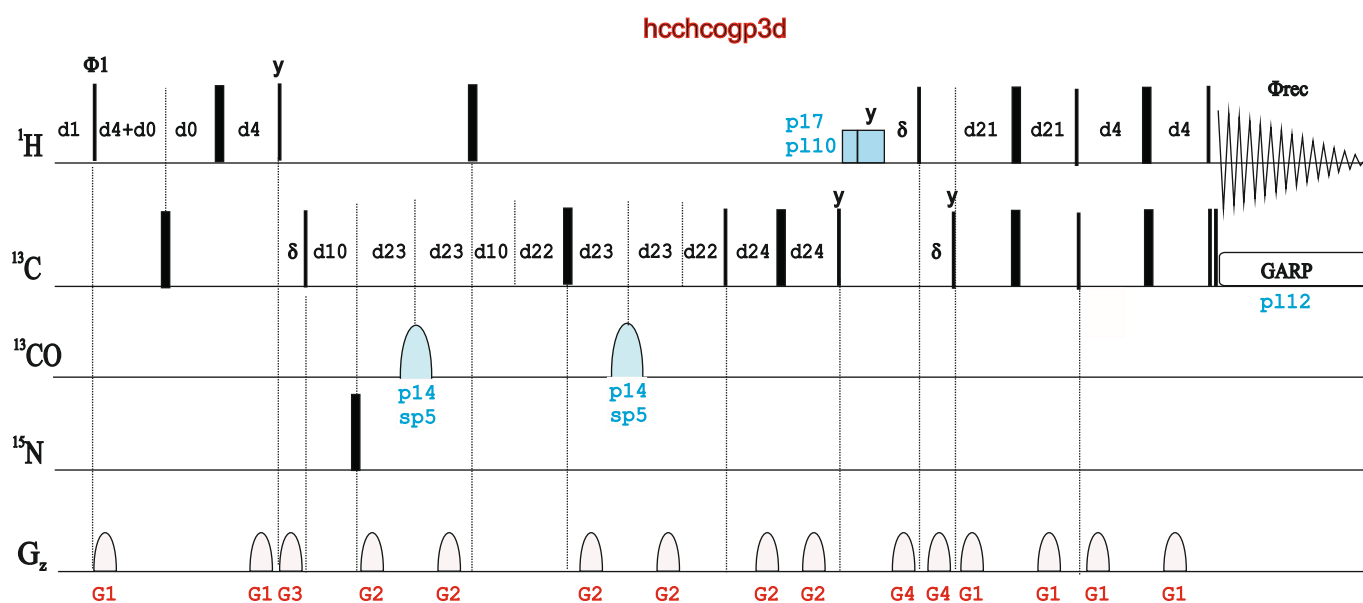
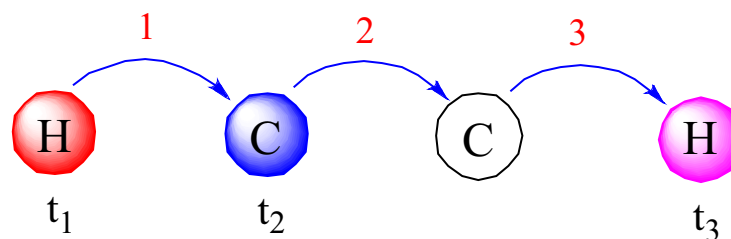
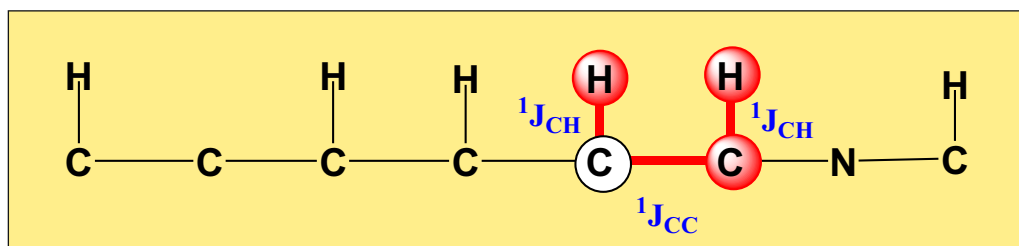
$d4 : 1/(4J(CH)) - \tau a$ [1.6 msec]
 $d21: 1/(6J'(CH)) - \tau c$ [1.1 msec]
 $d22: d22+d23^2+\tau_{max}^2 \cdot 0.5 = 1/(4J(CC)) : 3.6m-d23^2-(\tau_0^2+d1/4)$
 $d23: \tau b$ [475 usec]
 $d24: 1/(4J(CC))$ [3.6 msec]

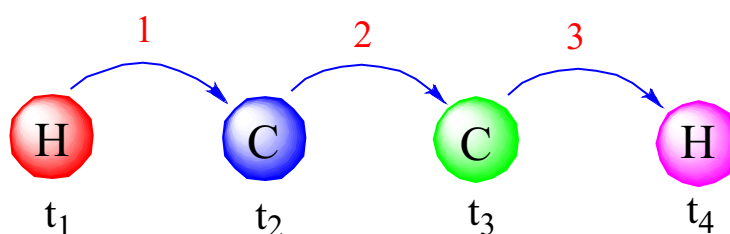
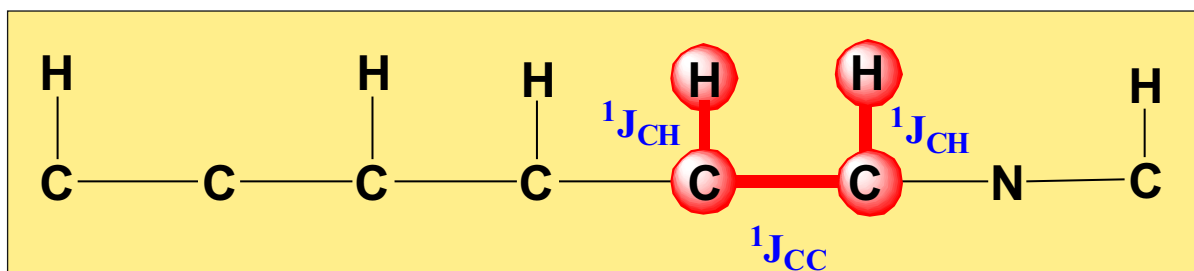
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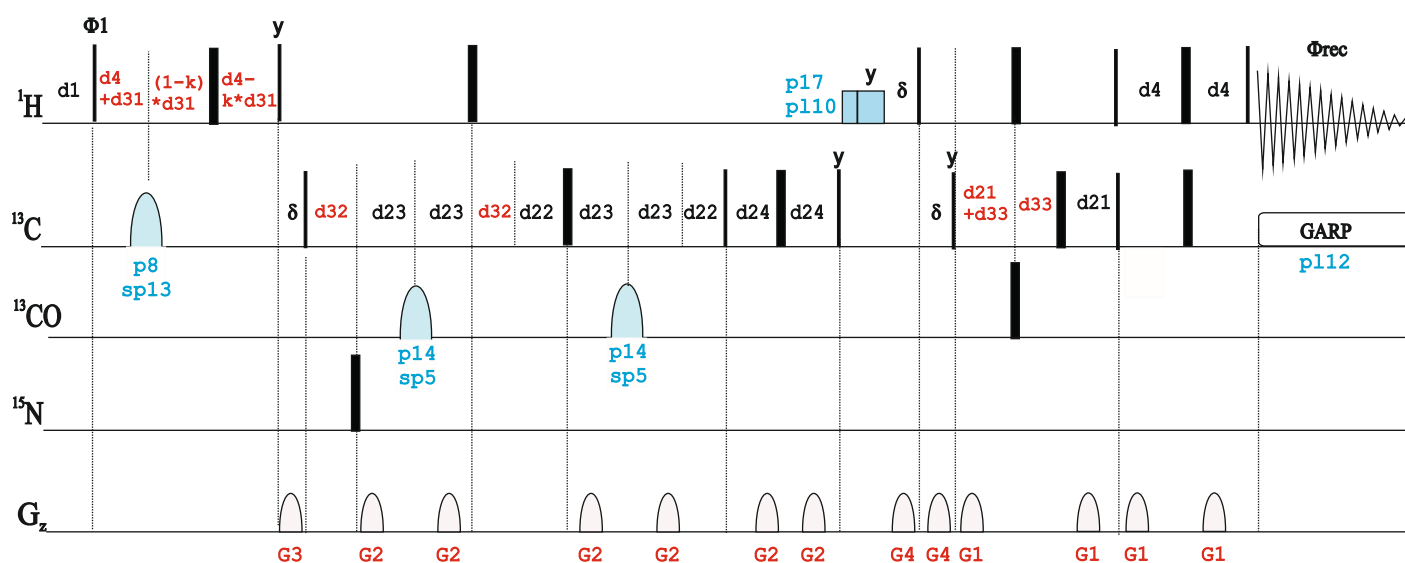
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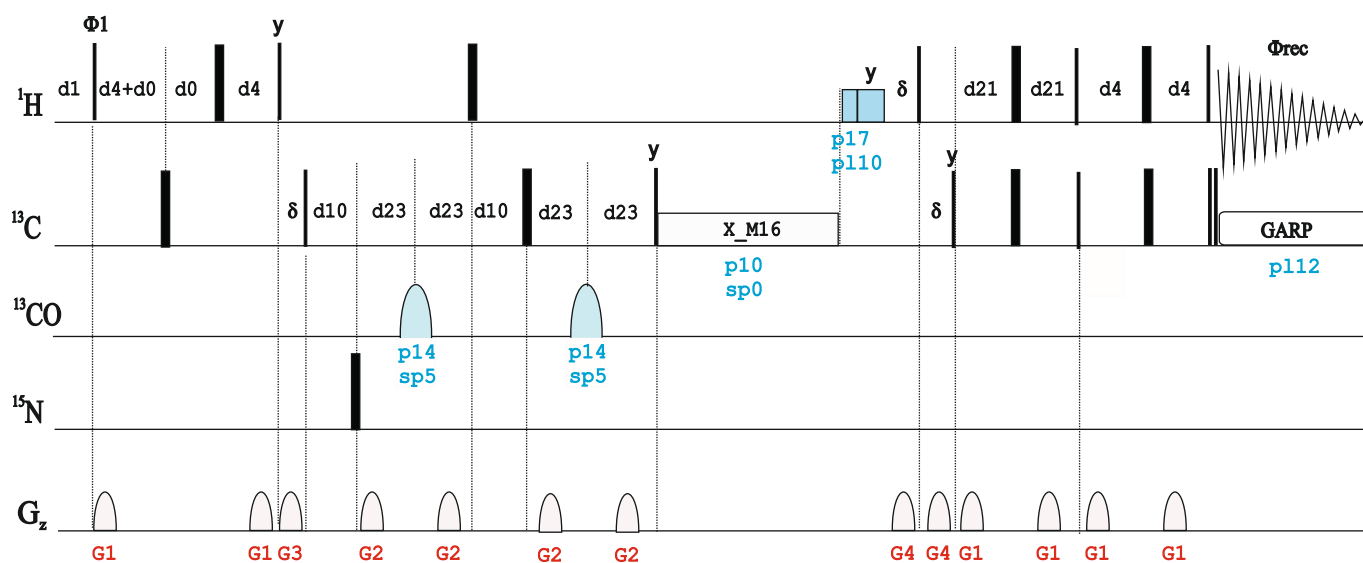
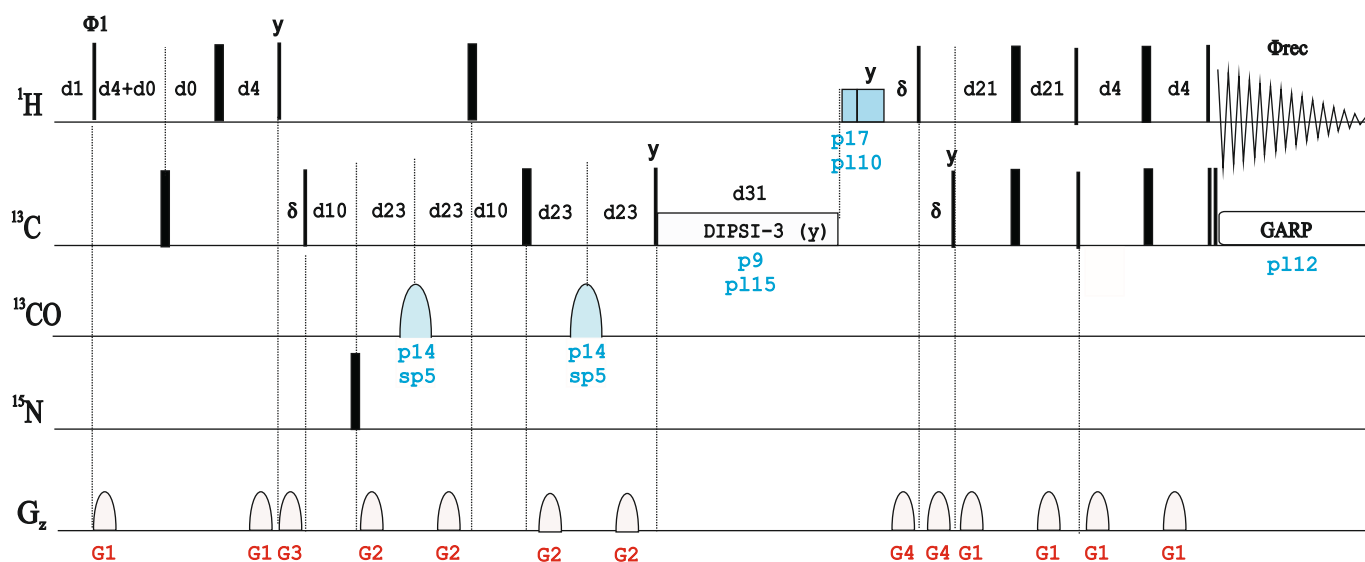
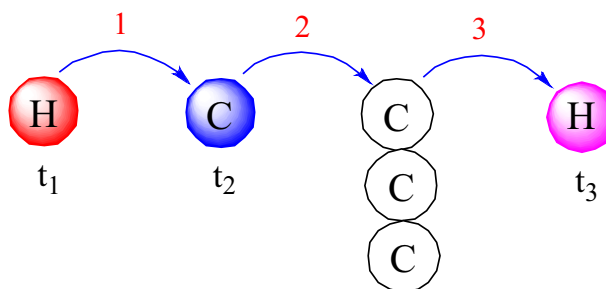
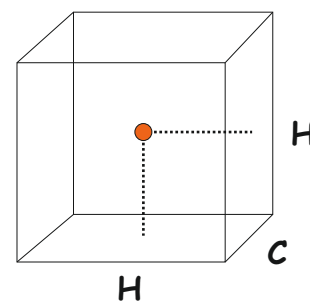


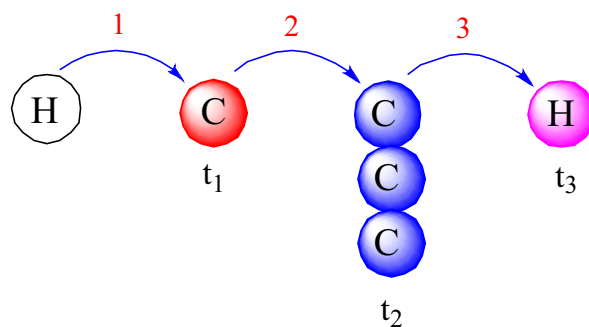
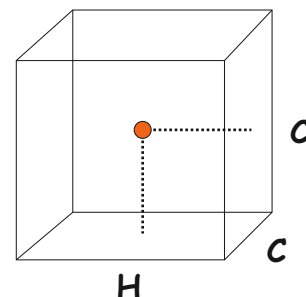
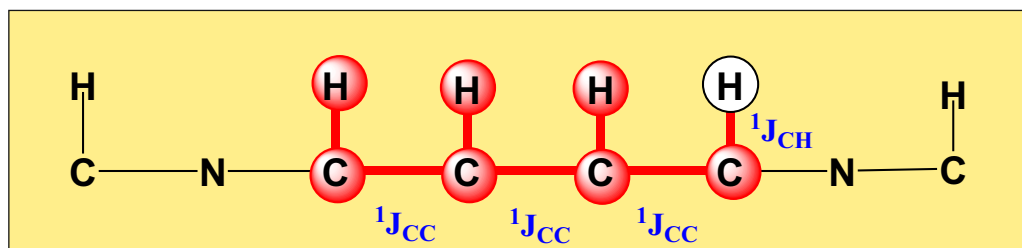




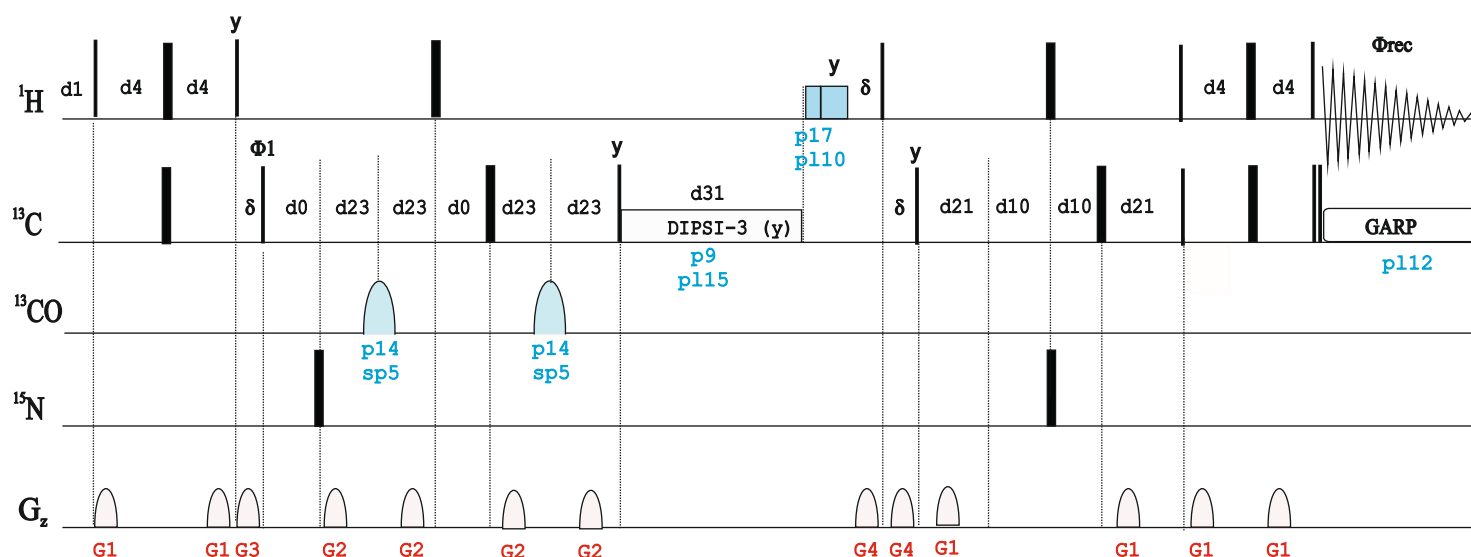
hcchcogp4d



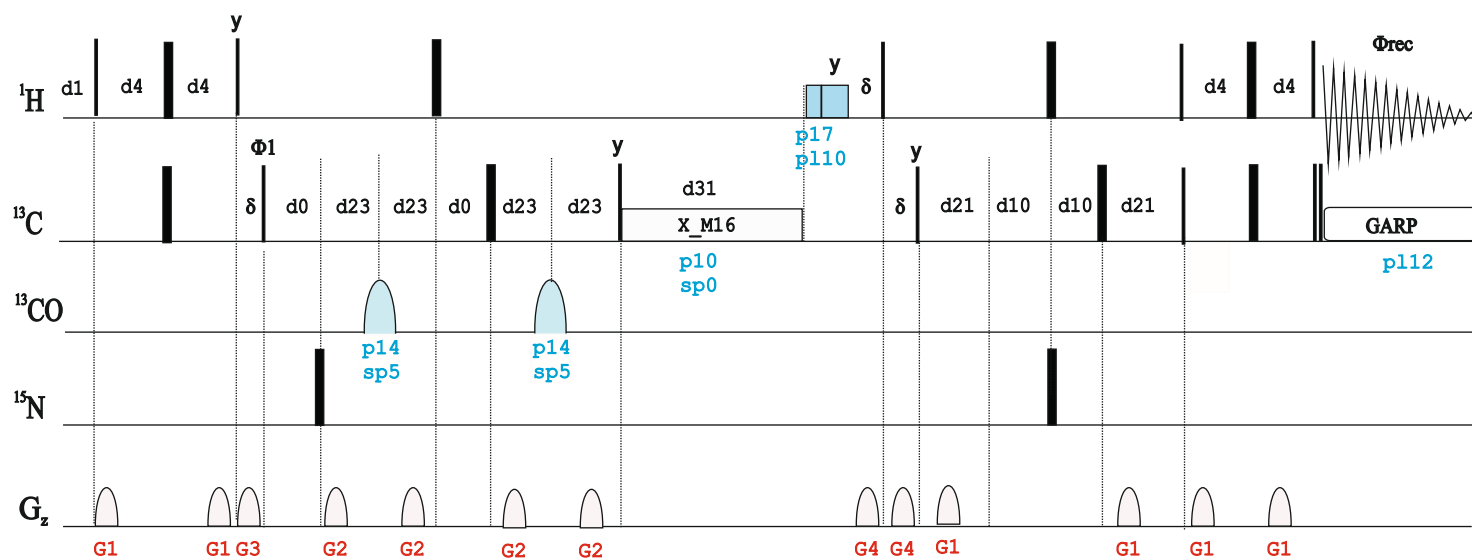


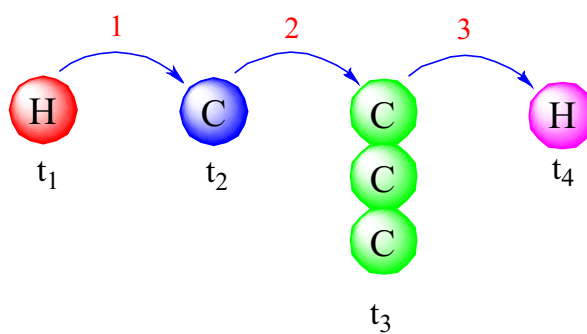
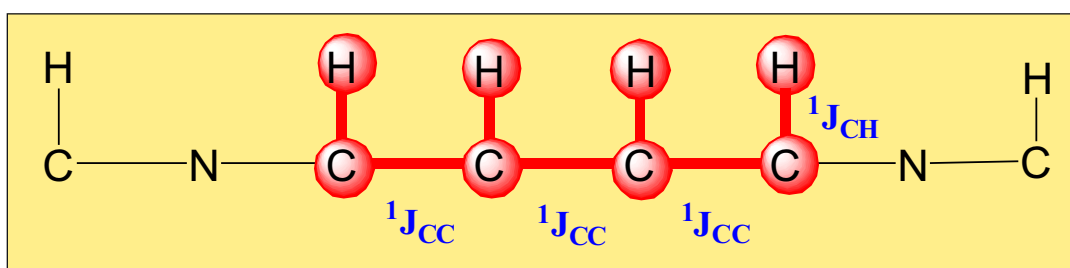
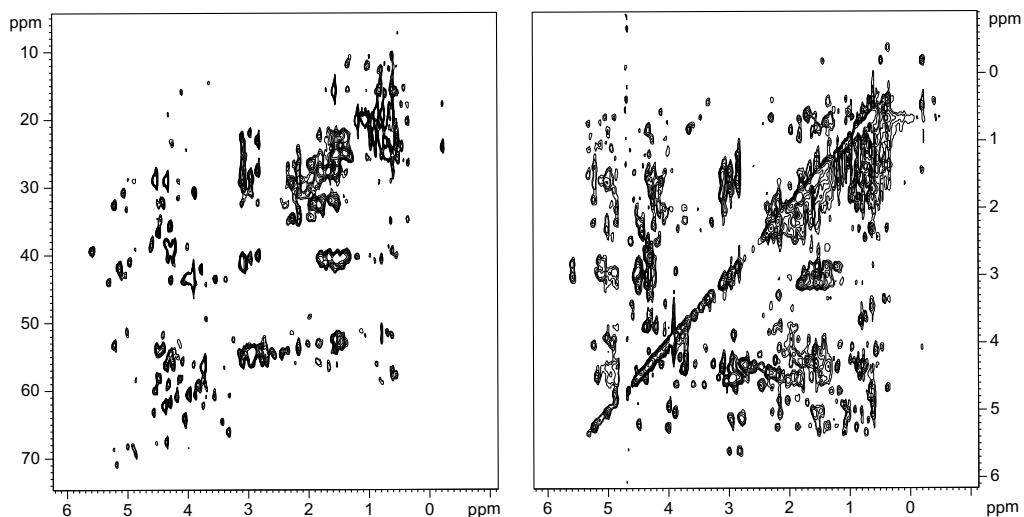


hcchdip3d2

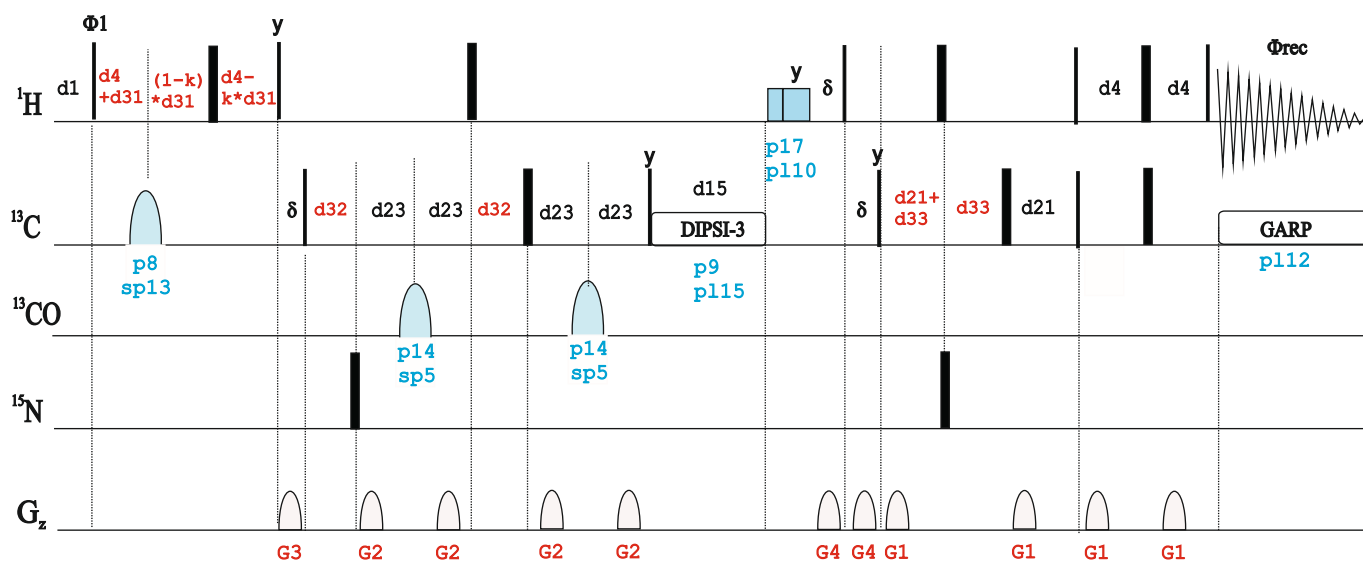


hcchatg3d2



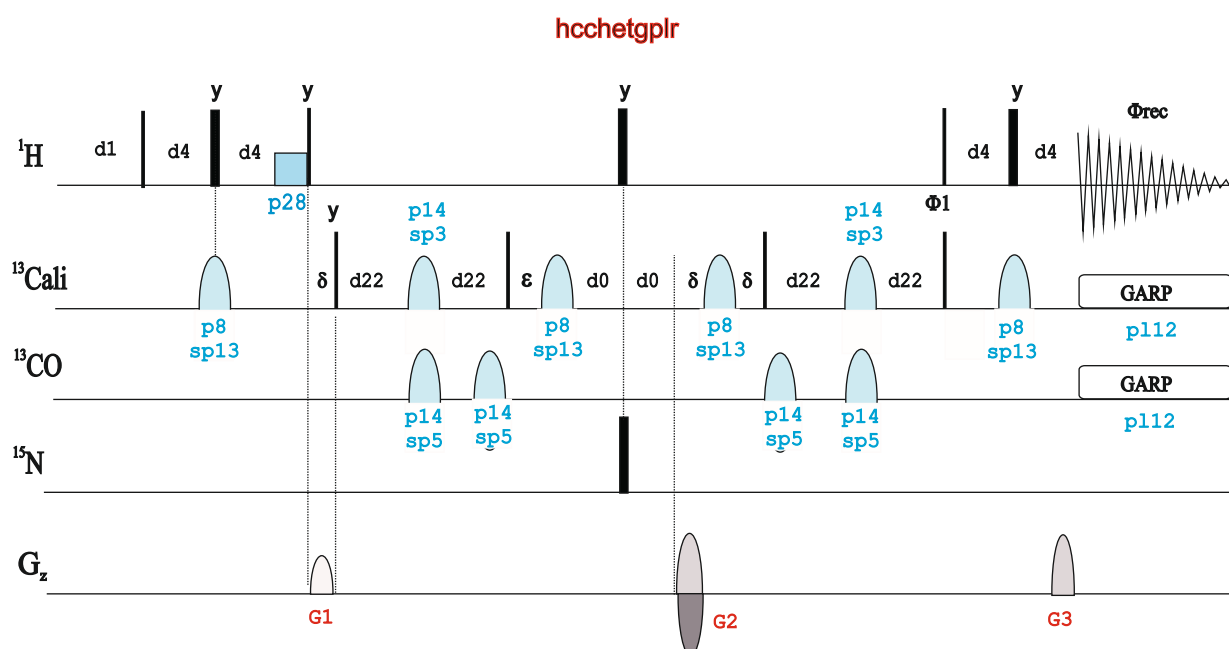
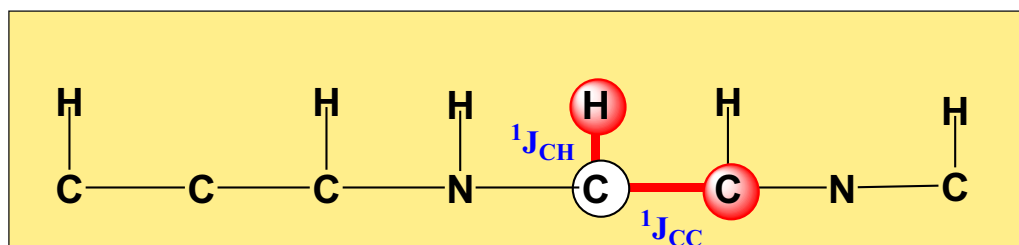


hcchdigp4d



2D (H)C(C)H:

A. Bax, D. Max & D. Zax, J. Am. Chem. Soc. 114, 6923-6925 (1992)



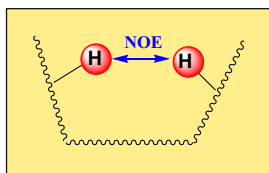
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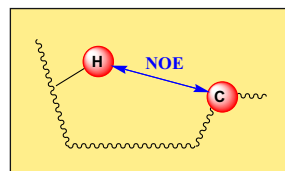
3D NOESY-HSQC EXPERIMENTS

Edited NOESY experiments for labeled proteins:

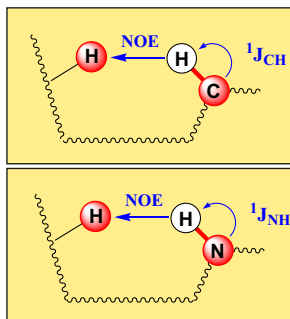
2D NOESY
2D ROESY



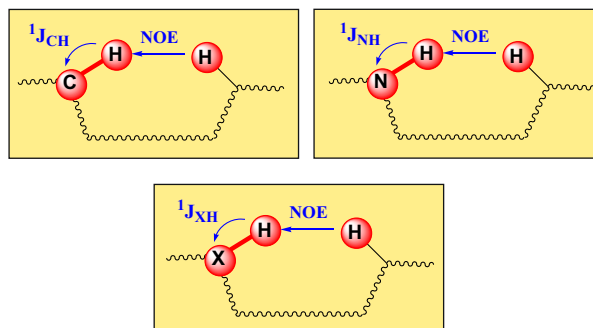
2D HOESY



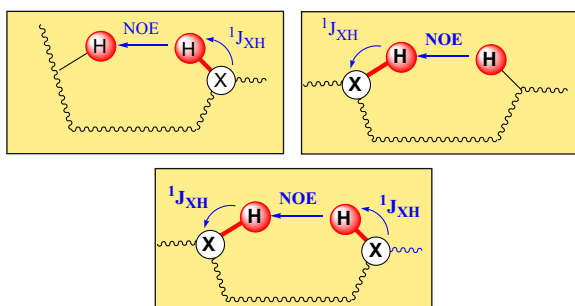
2D/3D HSQC-NOESY



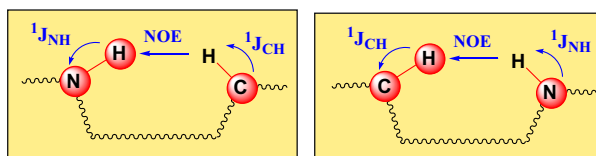
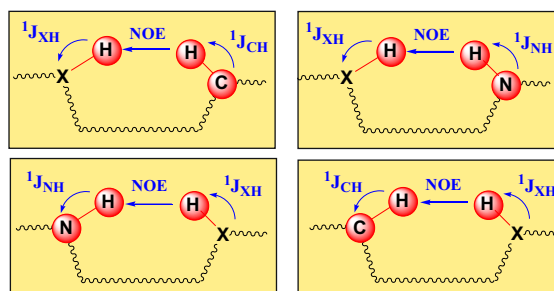
2D/3D NOESY-HSQC



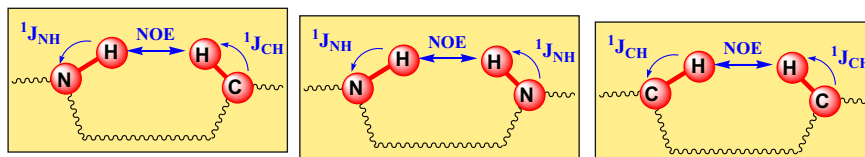
2D/3D w1/w2 12C,14N-Edited NOESY



3D w3 12C,14N-Edited HSQC-NOESY
3D w1 12C,14N-Edited NOESY-HSQC



3D HSQC-NOESY-HSQC



4D HSQC-NOESY-HSQC

3D Basic X-edited NOESY

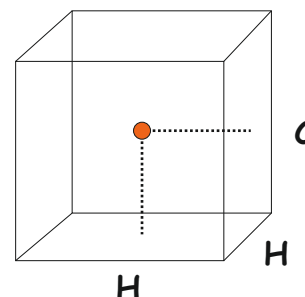
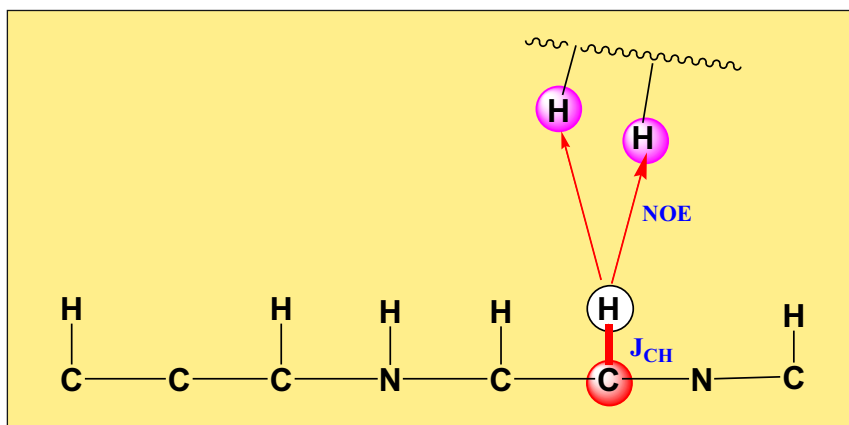
- 3D ^1H - ^{13}C NOESY-HMQC experiment using presaturation (**noesyhmqcpr3d**)
- 3D ^1H - ^{13}C HMQC-NOESY experiment using BIRD (**hmqcnoesybi3d**)

Also see:

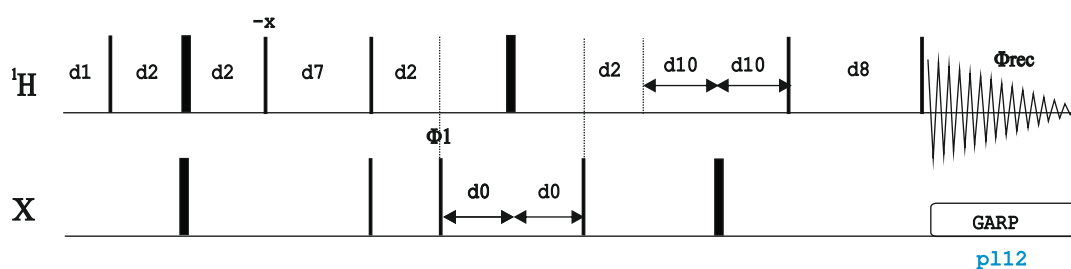
2D HMQC and 2D NOESY experiments
2D & 3D HSQC-NOESY Experiments
3D NOESY-HSQC Experiments

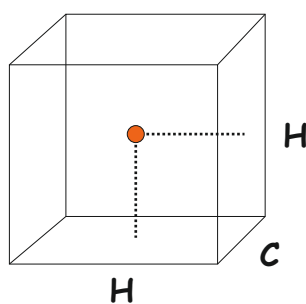
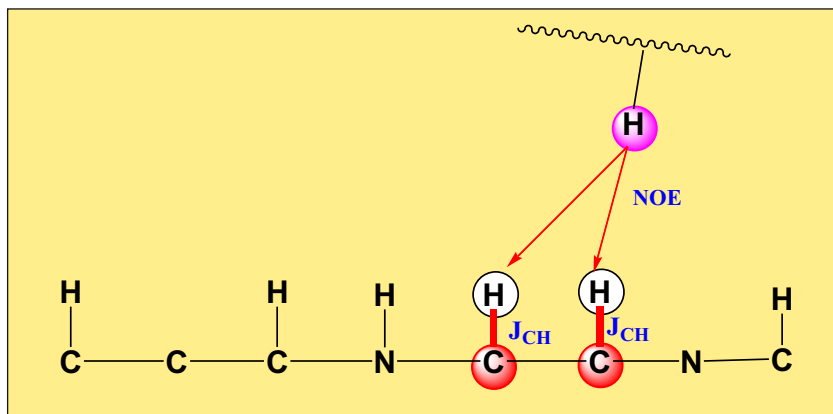
References:

A. Bax and S. Subramanian, J. Magn. Reson. 67, 565-569 (1986)
A. Bax & D.G. Davis, J. Magn. Reson. 65, 355-360 (1985)

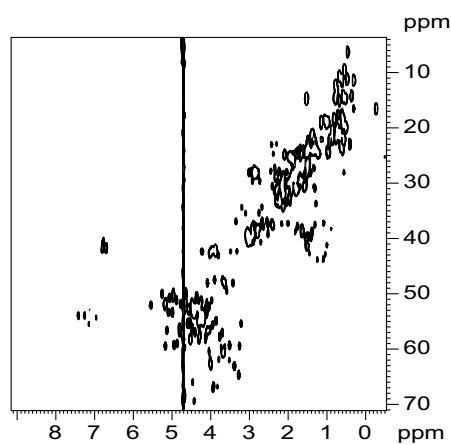
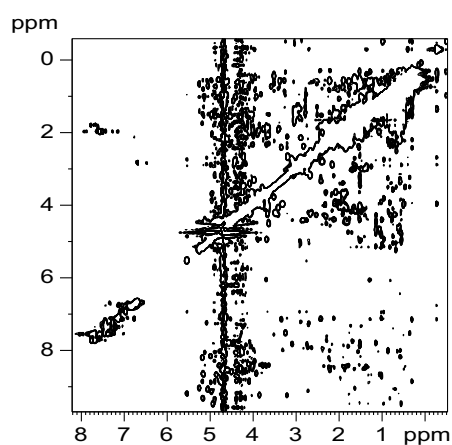
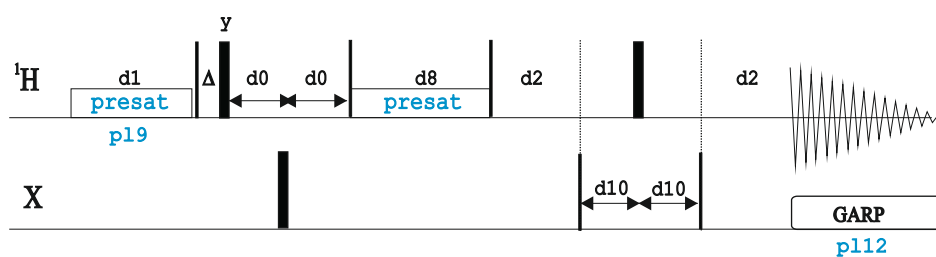


hmqcnoesybi3d





noesyhmqcpr3d



3D NOESY-HSQC / 3D NOESY-HMQC

- Gradient-enhanced from f2 channel:

3D ^1H - ^{13}C NOESY-HSQC experiment

- using echo-antiecho (**noesyhsqcetgp3d** | NOESYHSQCETGP3D)
- using PEP (**noesyhsqcetgps3d** | NOESYHSQCETGPSI3D)

- Gradient-enhanced from f3 channel:

3D ^1H - ^{15}N NOESY-HSQC experiment

- using echo-antiecho (**noesyhsqcetf3gp3d** | NOESYHSQCETF3GP3D)
- using PEP (**noesyhsqc3gps3d** | NOESYHSQC3GPSI3D)
- using PEP and water flip-back (**noesyhsqc3gps3d** | NOESYHSQC3GPSI3D)
- using WATERGATE with 3919 (**noesyhsqc3gp193d** | NOESYHSQC3GP193D)
- using WATERGATE with shaped pulses (**noesyhsqc3gpwg3d**)
- using TROSY (**noesytre3gp3d** | NOESYTRTF3GP3D)
- using ZQ-TROSY and WATERGATE (**noesy3gp3d** | NOESY3GP3D)
- using TROSY for aromatic residues and WATERGATE (**noesy3gp3d** | NOESY3GP3D)

3D ^1H - ^{15}N NOESY-HMQC experiment

- using WATERGATE (**noesyhm3gp3d**)

- Gradient-enhanced from f2 and f3 channel:

3D NOESY- ^{13}C , ^{15}N -HSQC experiment

- with simultaneous evolution (**noesyhsqc3gp3d.2** | NOESYHSQC3GPSI3D.2)
- with simultaneous evolution, sensitivity improvement and adiabatic ^{13}C pulses (**noesyhsqc3gpsism3d** | NOESYHSQC3GPSISM3D)

Also see NOESY-HSQC experiments in Nucleic Acid Experiments:

3D ^1H - ^{13}C NOESY-CT-HSQC using echo-antiecho (**na_noesyhsqcct3gp3d**)

3D ^1H - ^{13}C NOESY-HSQC using WATERGATE and refocusing of $J(\text{C}5\text{C}6)$ during t_1 (**na_c6noesyhsqc3gp3d**)

3D ^1H - ^{15}N NOESY-HSQC using WATERGATE (**na_noesyhsqc3gpwg3d**)

Related Experiments:

2D NOESY

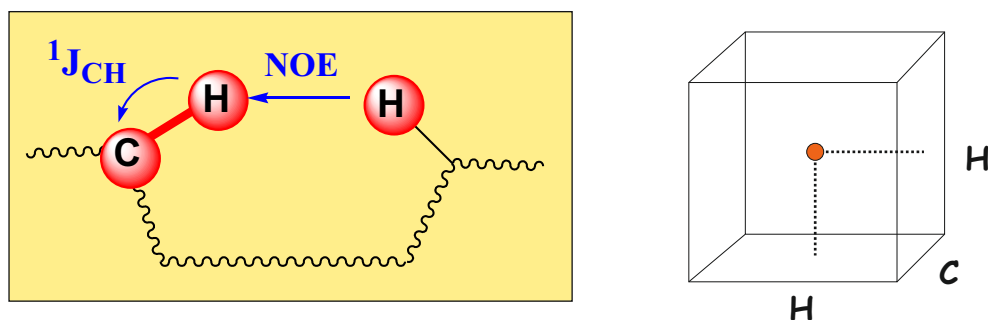
3D NOESY-HSQC

3D HSQC-NOESY-HSQC

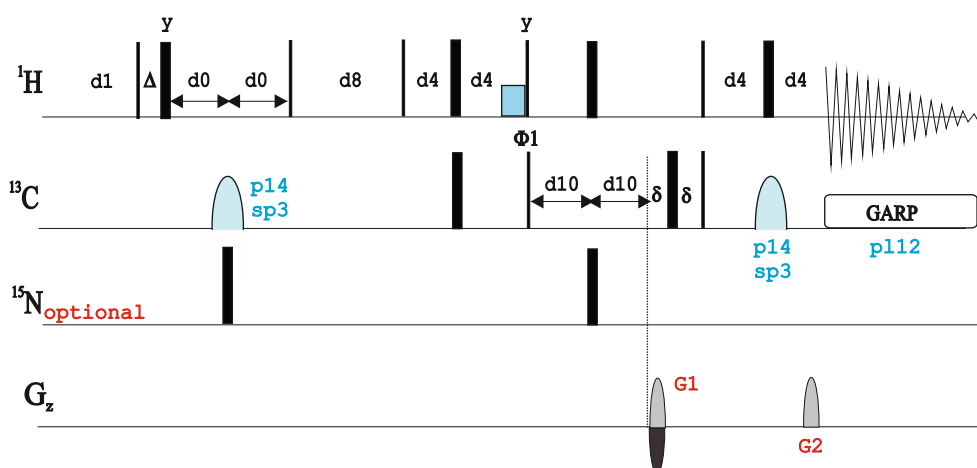
2D & 3D X-filtered/edited NOESY

NOESY-HSQC:

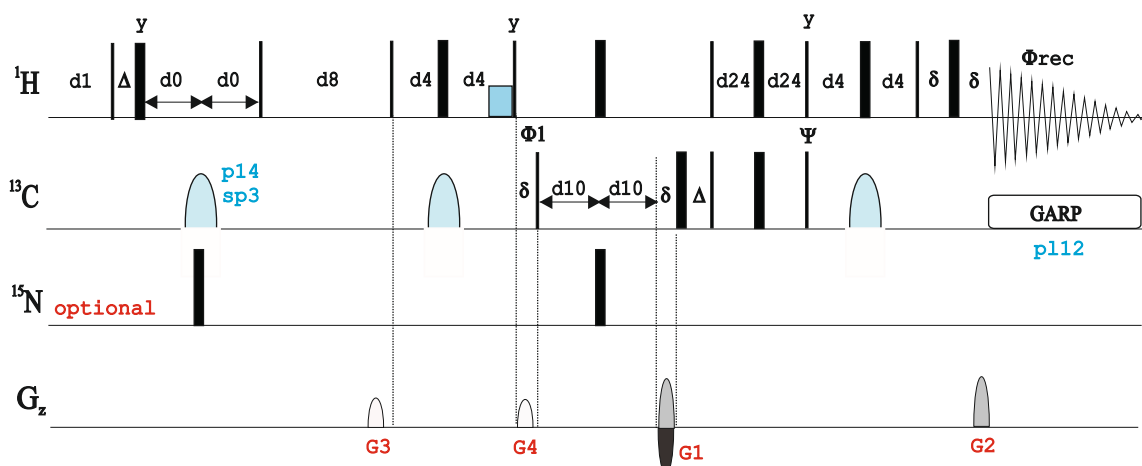
1. A.L. Davis, J. Keeler, E.D. Laue & D. Moskau, J. Magn. Reson. 98, 207-216 (1992)
2. O. Zhang, L.E. Kay, J.P. Olivier & J.D. Forman-Kay, J. Biomol. NMR 4, 845 - 858 (1994)
3. G. Zhu, X.M. Kong & K.H. Sze, J. Biomol. NMR 13, 77-81 (1999)
4. K.V. Pervushin, G. Wider, R. Riek & K. Wuethrich, PNAS, 96, 9607-9612 (1999)

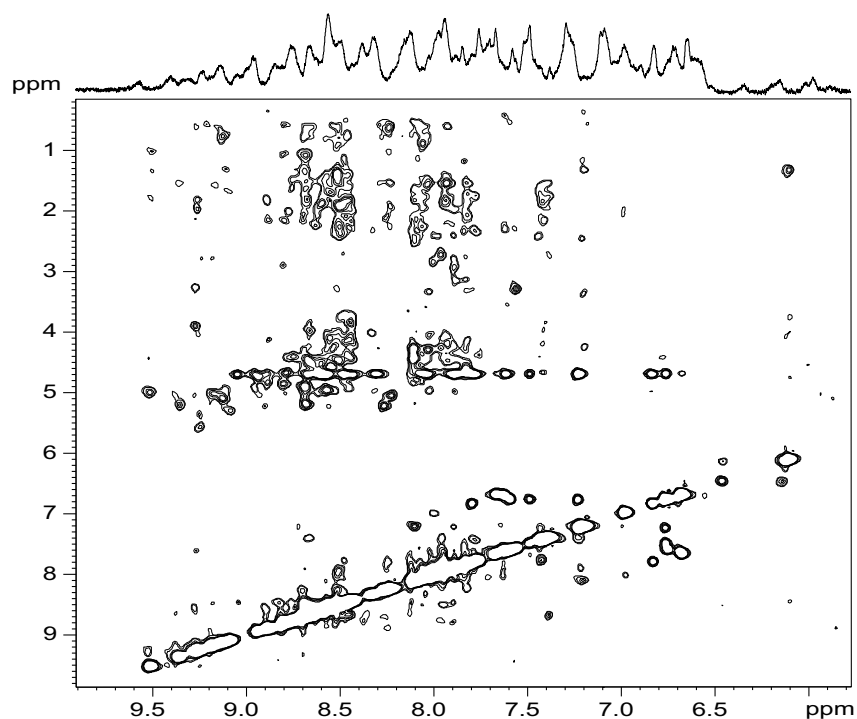
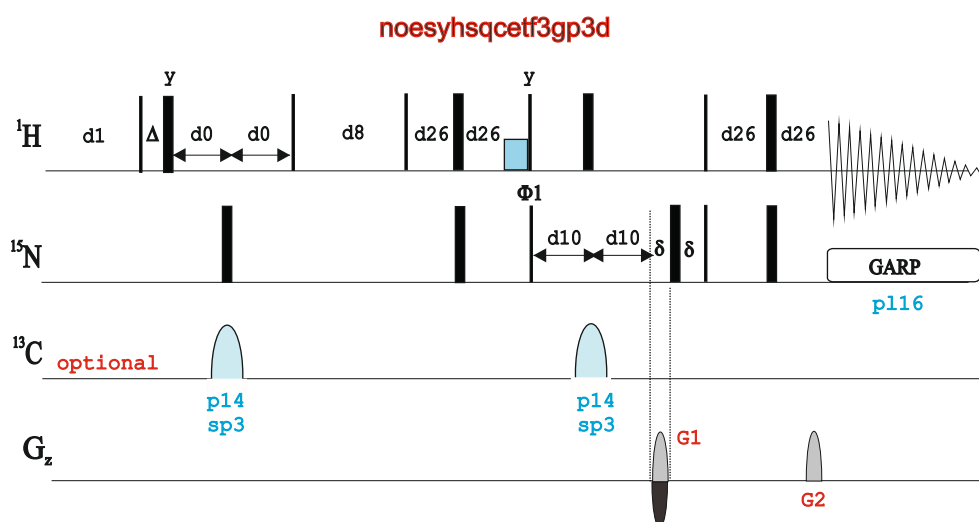
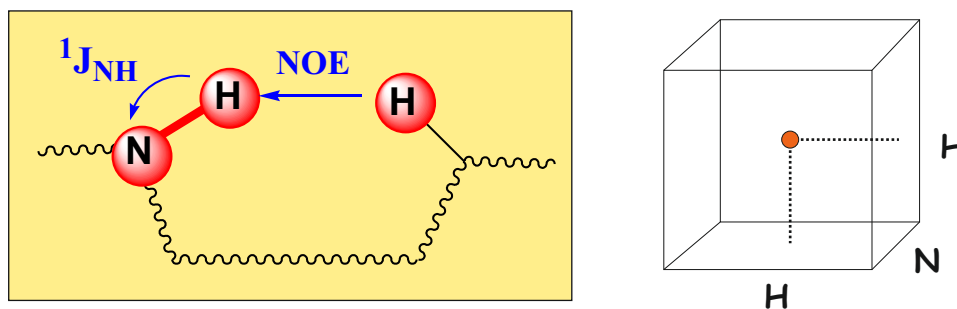


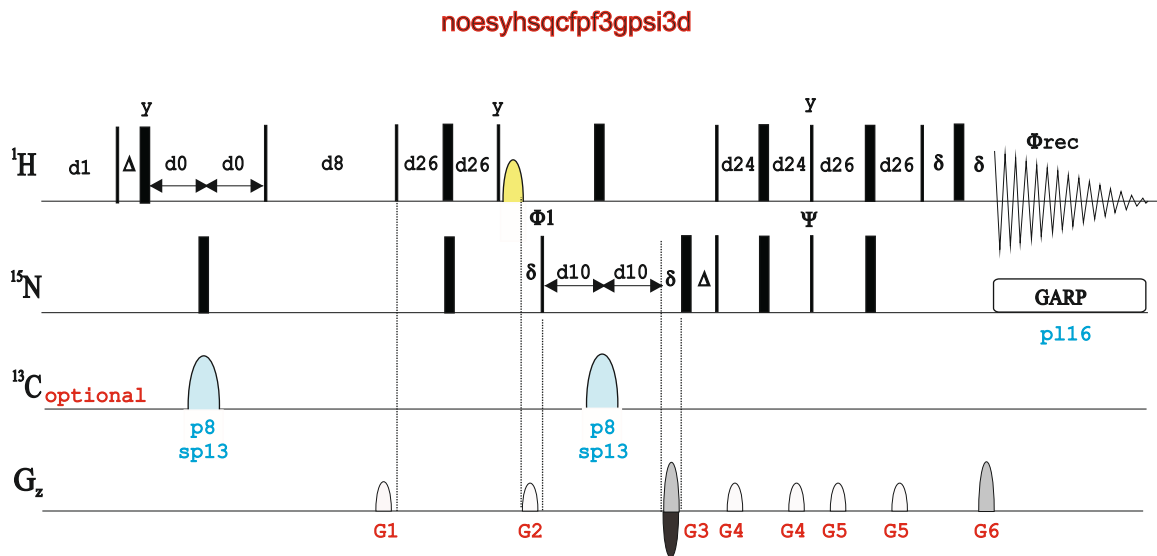
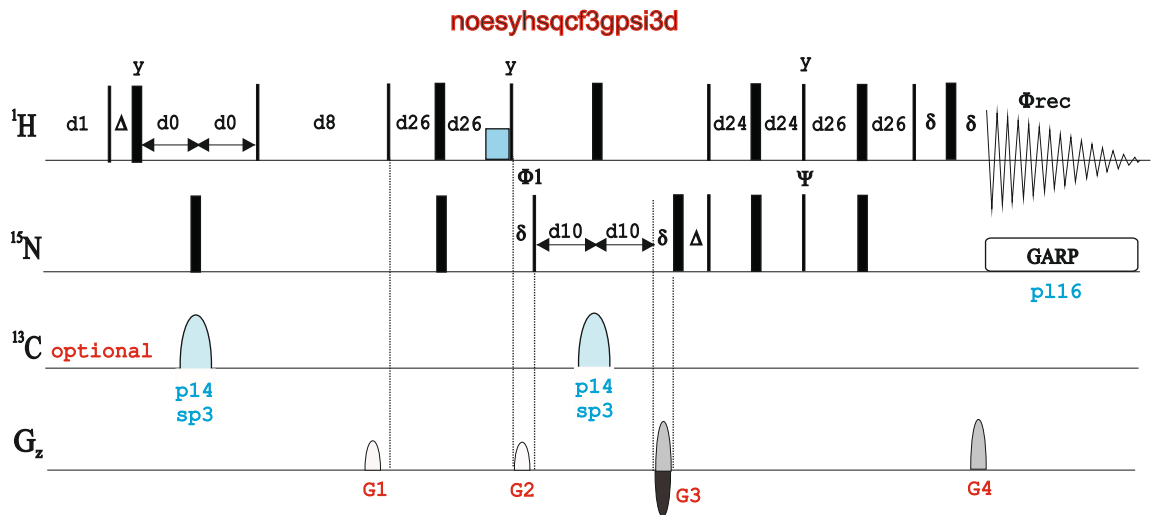
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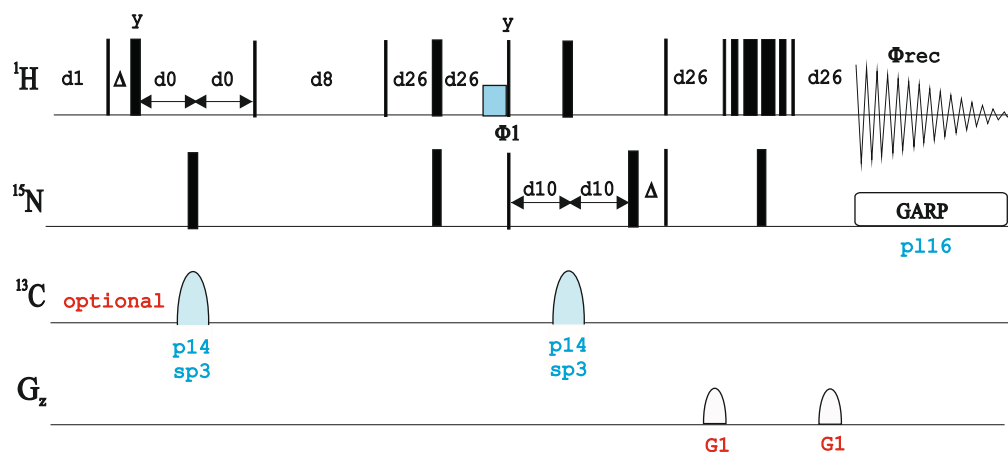
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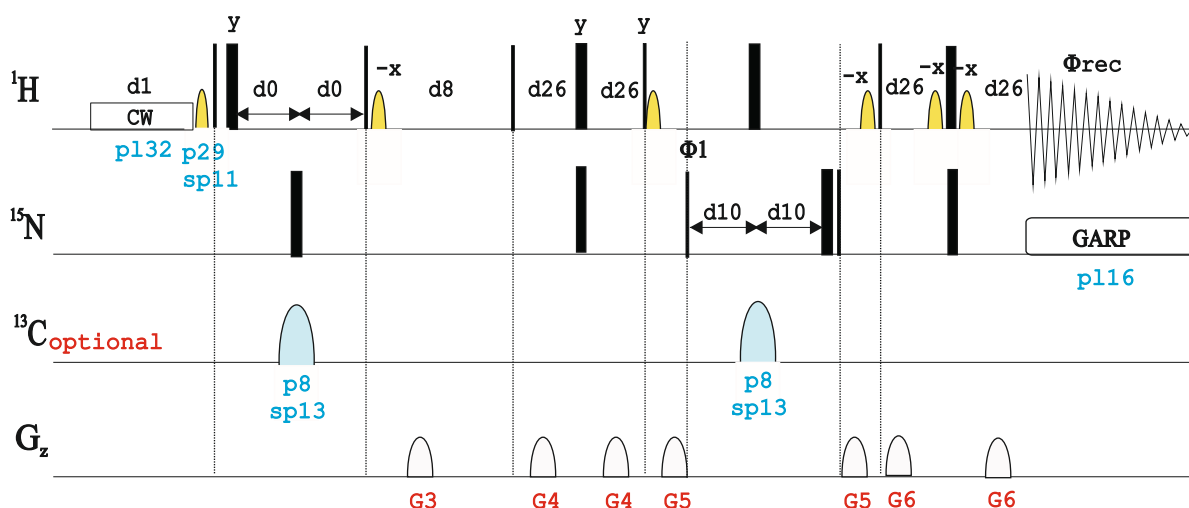




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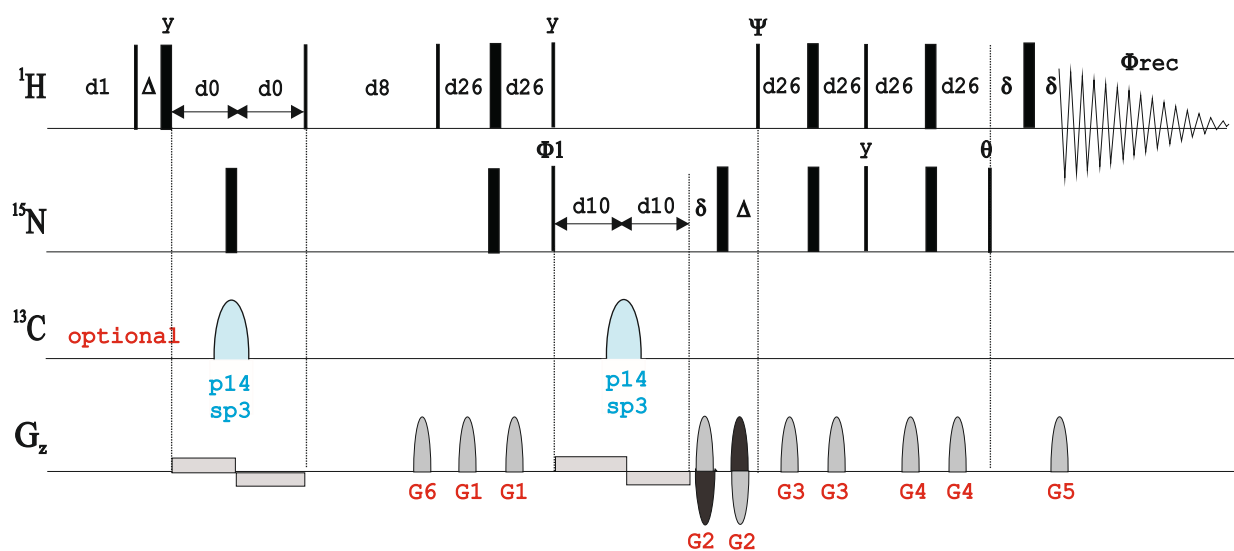


noesyhsqcf3gpwg3d



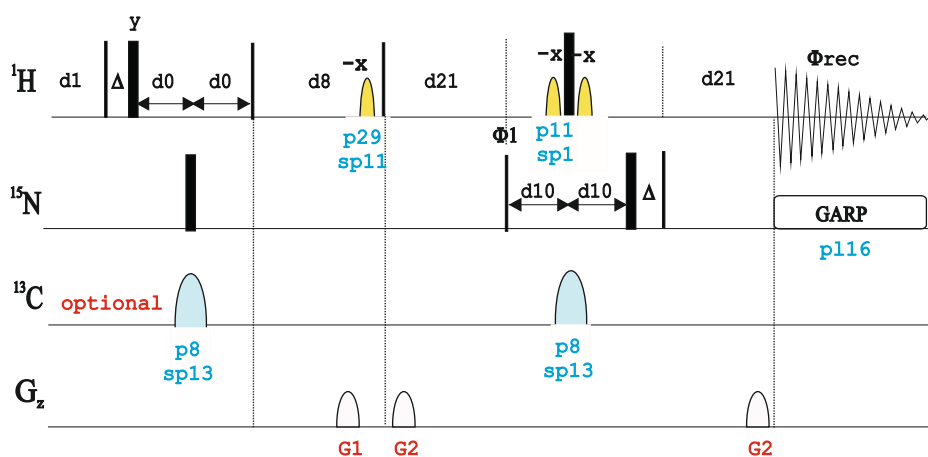
NOESY-TROSY

noesytreff3gp3d



NOESY-HMQC

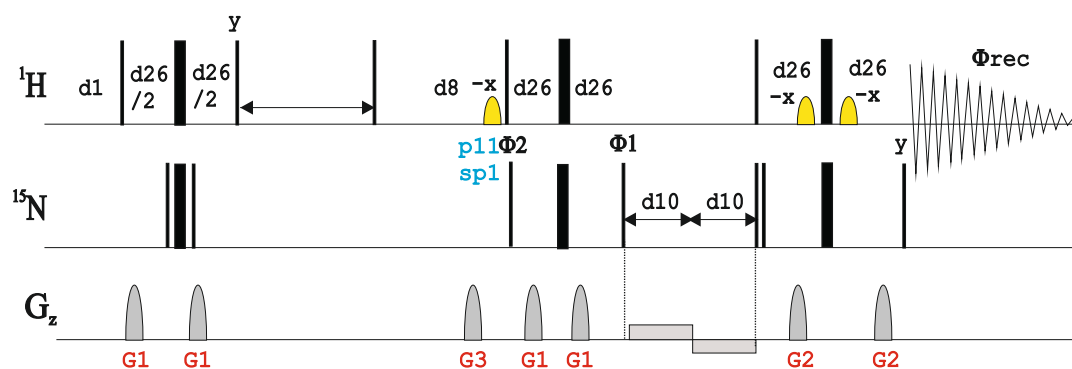
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NOESY-ZQ-TROSY

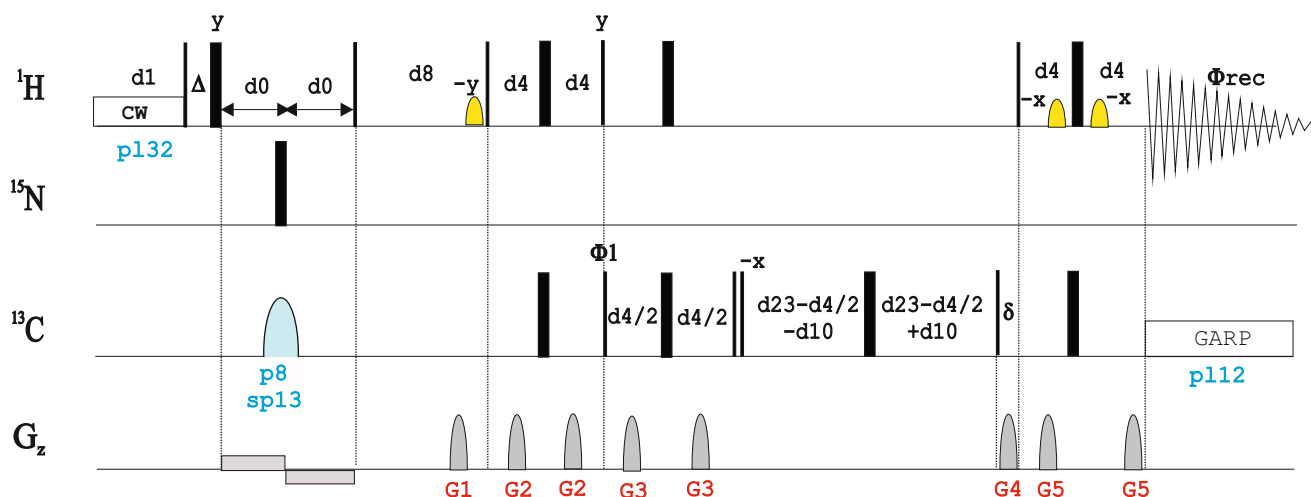
K.V. Pervushin, G. Wider, R. Riek & K. Wuethrich, Proc. Natl. Acad. Sci USA 96, 9607-9612 (1999)

noesyztgp3d

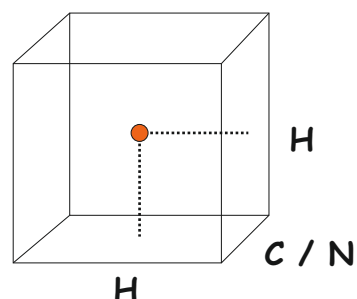
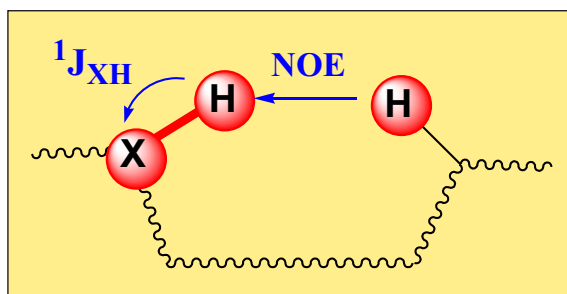


NOESY-TROSY for Aromatic Residues

noesytrosyargpphgw



S.M. Pascal, D.R. Muhandiram, T. Yamazaki, J.D. Forman-Kay & L.E. Kay, *J. Magn. Reson.* B103, 197 - 201 (1994)



The timing diagram illustrates the sequence of events for the ^1H , ^{15}N , and ^{13}C channels, along with the G_z magnetization. The ^1H channel (top) shows a series of pulses with delays $d1$, Δ , $d0$, $d8$, $d26$, $d26$, δ , $d24$, $d26$, $d26-d4/2$, $d26$, $d26$, δ , and δ . The ^{15}N channel (middle) shows pulses with delays ϵ , $d20$, $d20$, $d10$, $d10$, δ , Δ , and Φ_1 . The ^{13}C channel (bottom) shows pulses with delays $d4$, $d4/2$, and $d4$. The G_z channel (bottom) shows four pulses labeled $G1$, $G2$, $G3$, and $G4$. The ^1H channel also shows a Φ_{rec} pulse. The ^{15}N channel shows a GARP pulse with a $p116$ delay. The ^{13}C channel shows a GARP pulse with a $p112$ delay. The ^{13}C channel also shows a $p8$ delay and a $sp13$ pulse. The ^{15}N channel shows a GARP pulse with a $p116$ delay. The ^{13}C channel shows a GARP pulse with a $p112$ delay. The G_z channel shows four pulses labeled $G1$, $G2$, $G3$, and $G4$.

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3D and 4D HSQC-NOESY-HSQC EXPERIMENTS

3D HSQC-NOESY-HSQC

- 3D ^1H - ^{13}C HSQC-NOESY- ^1H - ^{15}N HSQC (**noesyngp3d** | NOESYNGP3D)
- 3D ^1H - ^{15}N HSQC-NOESY- ^1H - ^{13}C HSQC (**noesyngp3d** | NOESYNGP3D)

4D HSQC-NOESY-HSQC

4D HSQC-NOESY-HMQC

4D HMQC-NOESY-HMQC

- ^{13}C - ^{13}C
 - 4D ^1H - ^{13}C HSQC-NOESY- ^1H - ^{13}C HSQC (**hsqcnoesyhsqcccgp4d** | Hsqcnoesyhsqcccgp4d)
- ^{13}C - ^{15}N
 - 4D ^1H - ^{13}C HSQC-NOESY- ^1H - ^{15}N HSQC (**hsqcnoesyhsqccngp4d** | Hsqcnoesyhsqccngp4d)
 - 4D ^1H - ^{13}C HSQC-NOESY- ^1H - ^{15}N HMQC (**hsqcnoesyhmqqccngp4d**)
 - 4D ^1H - ^{13}C HMQC-NOESY- ^1H - ^{15}N HSQC (**hmqcnoesyhmqqcngp4d**)
- ^{15}N - ^{13}C
 - 4D ^1H - ^{15}N HSQC-NOESY- ^1H - ^{13}C HSQC (**hsqcnoesyhsqccngp4d** | Hsqcnoesyhsqccngp4d)
- ^{15}N - ^{15}N
 - 4D ^1H - ^{13}C HSQC-NOESY- ^1H - ^{15}N HSQC (**hsqcnoesyhsqccngp4d** | Hsqcnoesyhsqccngp4d)
 - 4D ^1H - ^{13}C HMQC-NOESY- ^1H - ^{15}N HMQC (**hmqcnoesyhmqqcngp4d**)

Related Experiments:

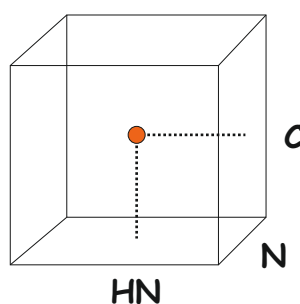
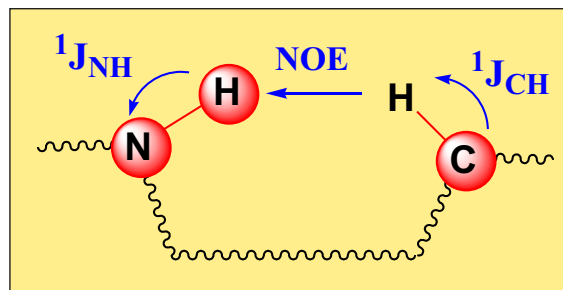
2D NOESY

3D NOESY-HSQC

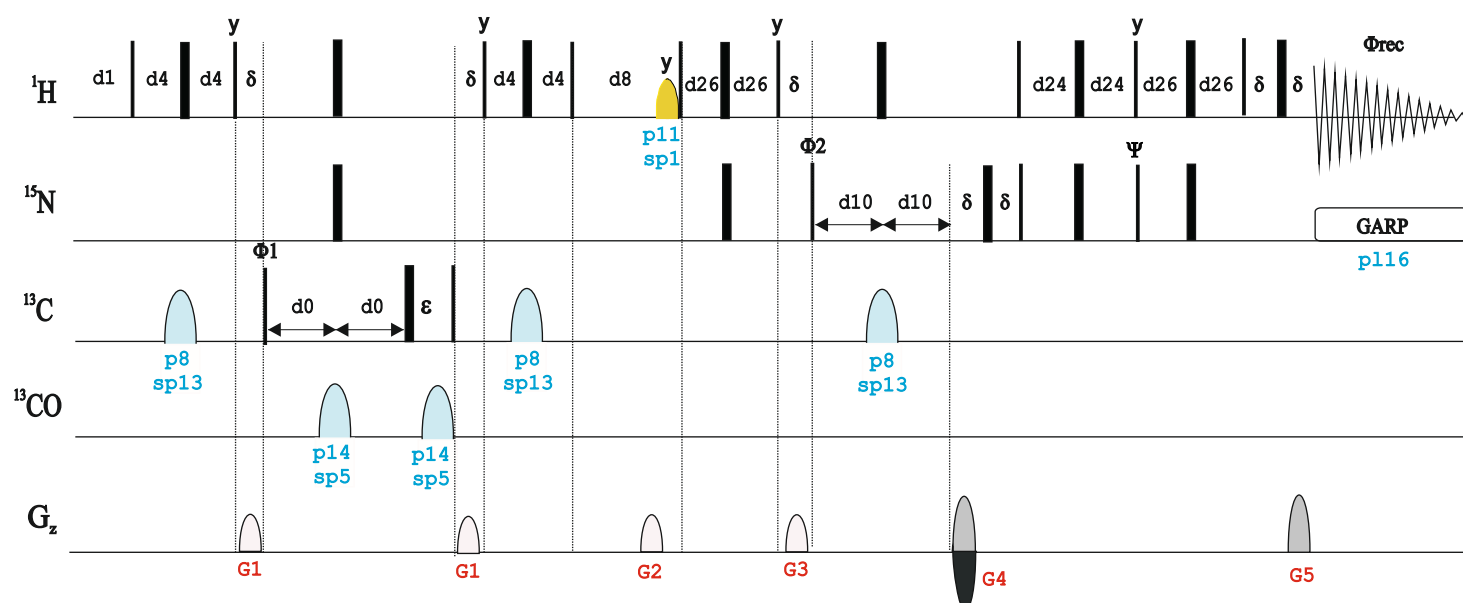
2D & 3D X-filtered/edited NOESY

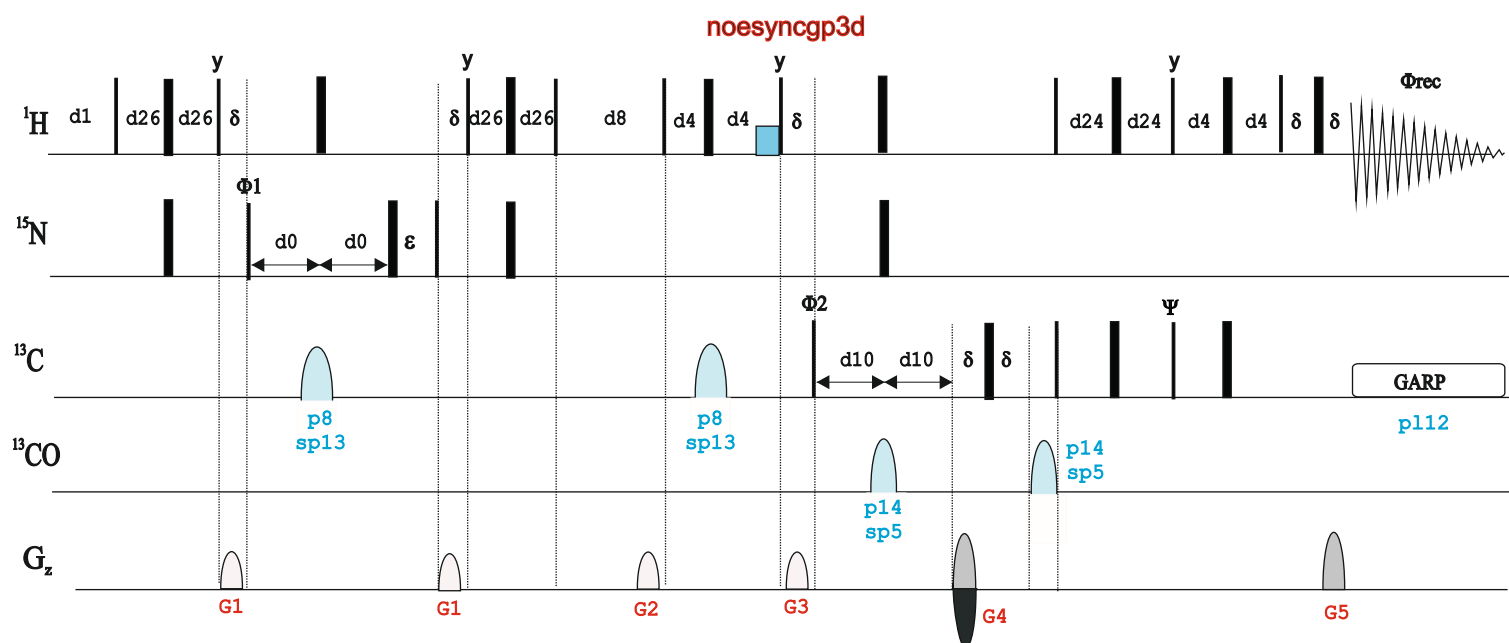
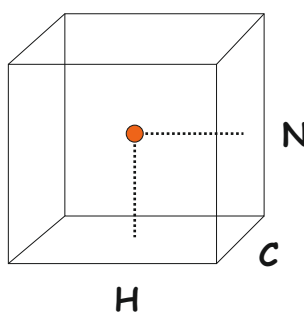
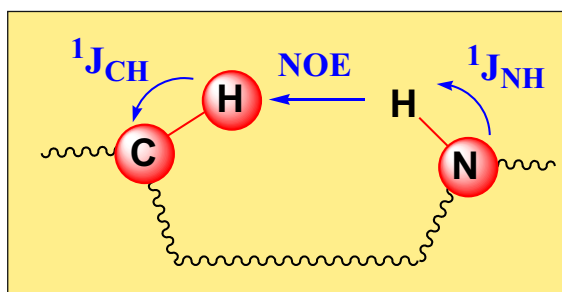
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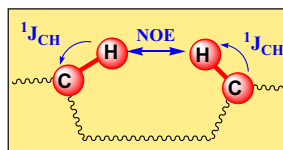
T. Diercks, M. Coles & H. Kessler, J. Biomol. NMR, 15, 177-180 (1999)



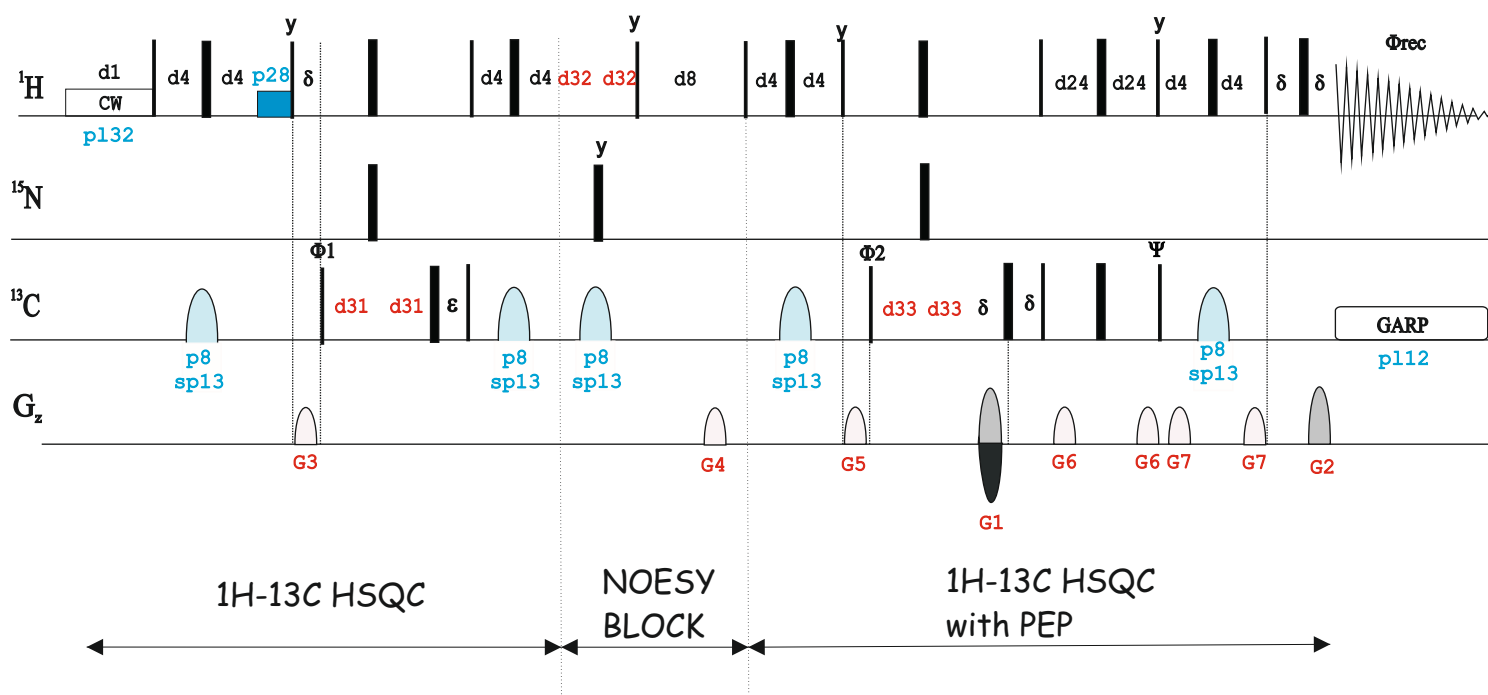
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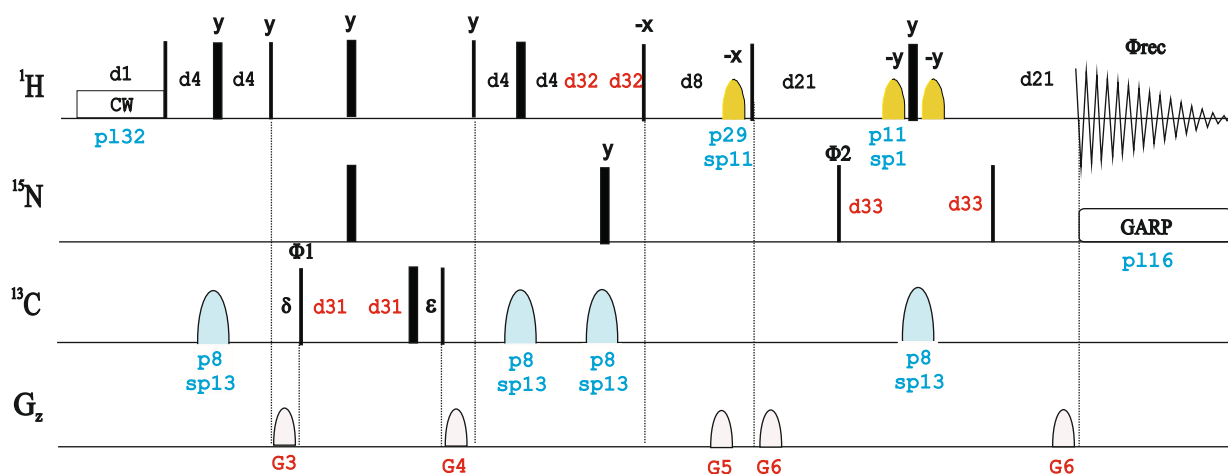


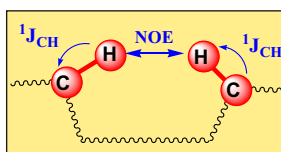




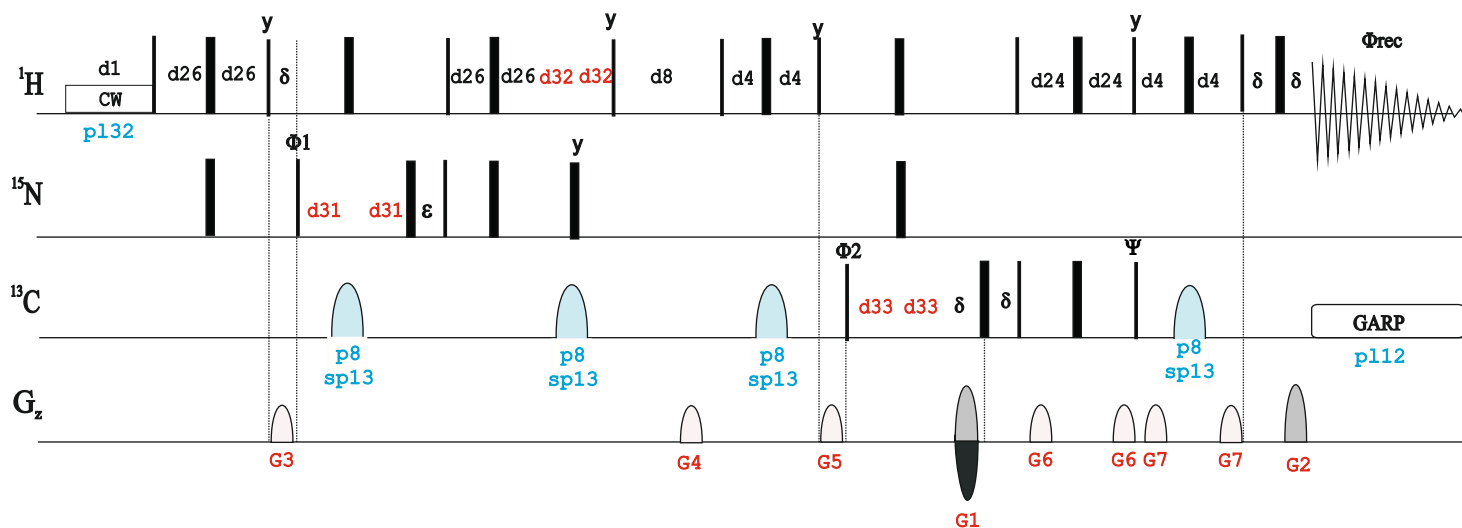
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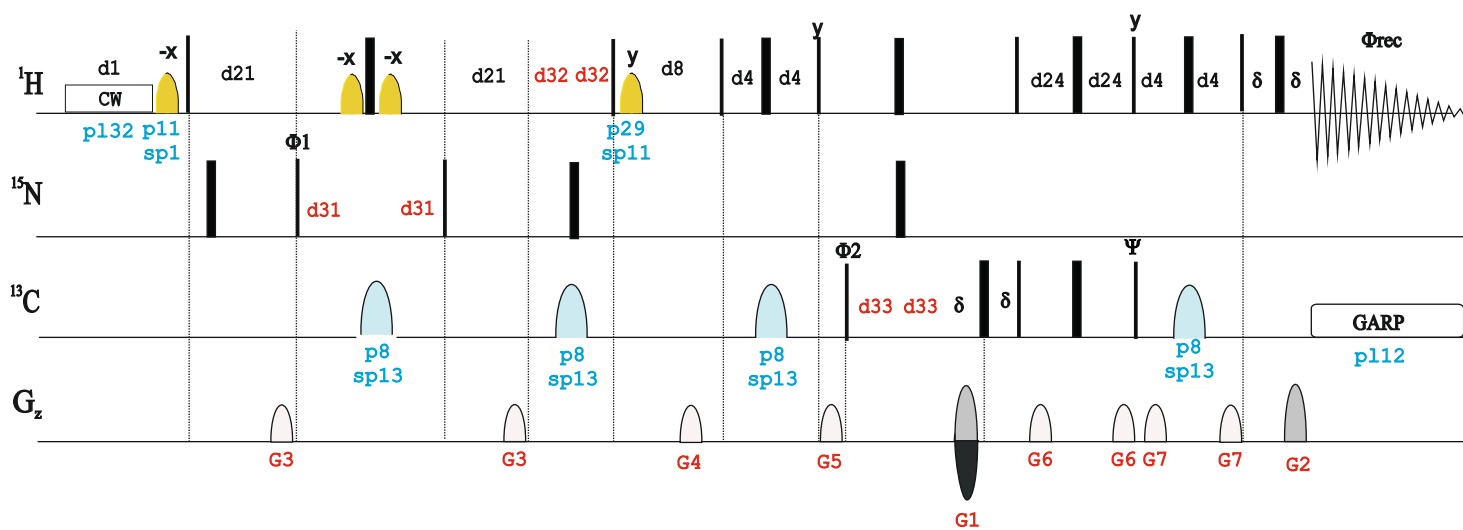


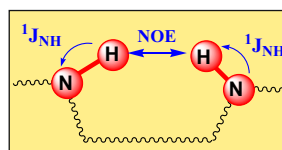


hsqcnoesyhsqcncgp4d

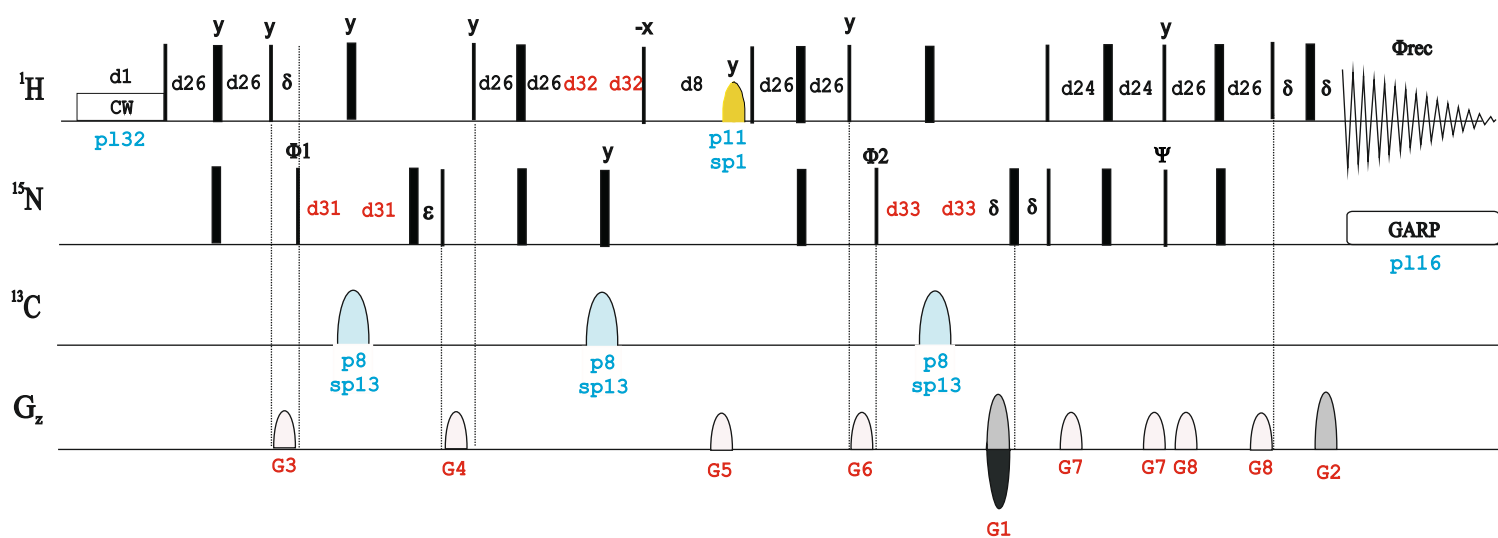


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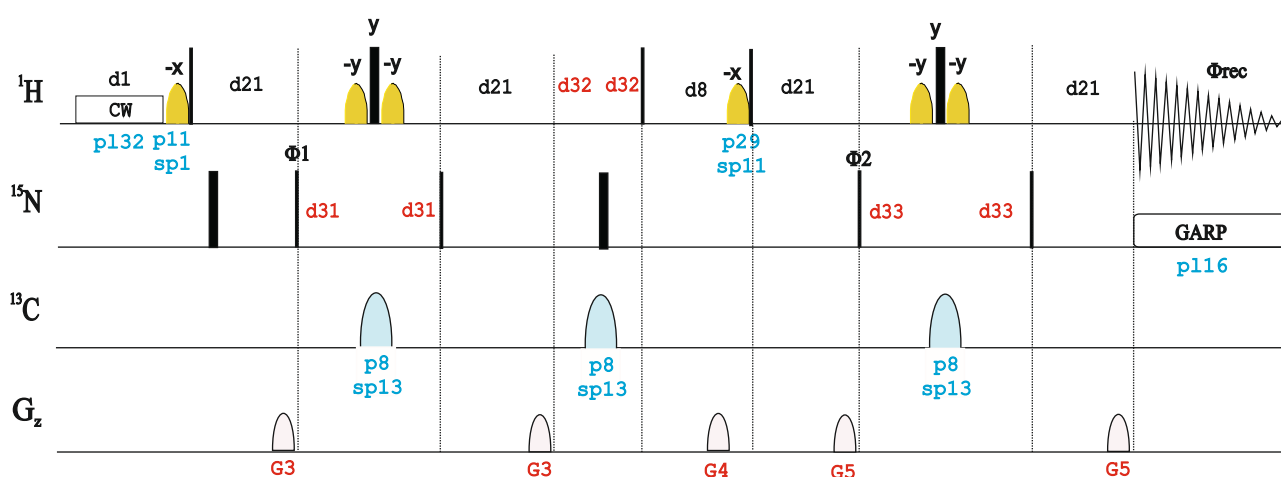




hsqcnoesyhsqcngp4d



hmqcnoesyhmqcngp4d



BRUKER PULSE PROGRAM CATALOGUE

NMRGuide

2D X-FILTERED/EDITED NOESY EXPERIMENTS

2D X-Filtered/edited NOESY

ge-2D w_1, w_2 ^{13}C -filtered/edited NOESY experiment

- Phase-sensitive ge-2D w_1, w_2 ^{13}C -filtered/edited NOESY with presaturation (**noesygp-phprxf** | **NA_NOESYGP-PPHPRXF**)
- Phase-sensitive ge-2D w_1, w_2 ^{13}C -filtered/edited NOESY with WATERGATE (3-9-19) (**noesygp-phxf19** | **NA_NOESYGP-PHXF19**)

ge-2D w_1, w_2 ^{15}N -filtered/edited NOESY experiment

- Phase-sensitive ge-2D w_1, w_2 ^{15}N -filtered/edited NOESY using WATERGATE (3-9-19) (**noesyf3gp-phxf19** | **NOESYF3GP-PHXF19**)

ge-2D w_1 ^{13}C , ^{15}N -Doubly Filtered NOESY experiment

- ge-2D w_1 ^{13}C , ^{15}N -Doubly Filtered NOESY using WATERGATE (**noesygp-phwgx1** | **NOESYGP-PH-WGX1**)

ge-2D w_2 ^{13}C , ^{15}N -Doubly Filtered NOESY experiment

- ge-2D w_2 ^{13}C , ^{15}N -Doubly Filtered NOESY using WATERGATE (**noesygp-phwgx2** | **NOESYGP-PH-WGX2**)

ge-2D w_1, w_2 ^{13}C , ^{15}N -Doubly Filtered NOESY experiment

- Phase-sensitive ge-2D w_1, w_2 ^{13}C , ^{15}N -Doubly Filtered NOESY with WATERGATE (selective pulses) (**noesygp-phwgxf** | **NOESYGP-PH-WGXf**)
- Phase-sensitive ge-2D w_1, w_2 ^{13}C , ^{15}N -Doubly Filtered NOESY with WATERGATE (selective pulses) (**noesygp-phwgxf.2** | **NOESYGP-PH-WGXf.2**)

Related Experiments:

2D NOESY

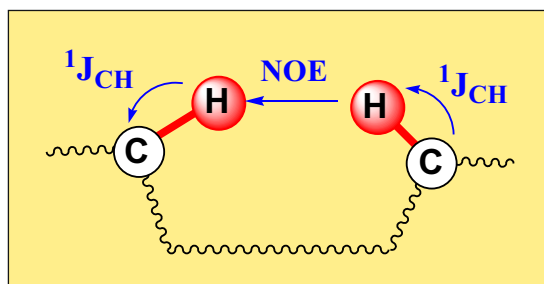
3D NOESY-HSQC

3D X-filtered/edited NOESY

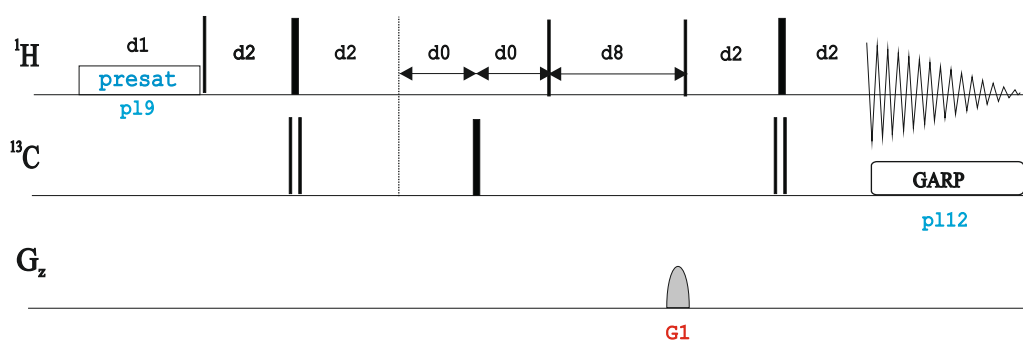
3D and 4D HSQC-NOESY-HSQC

References:

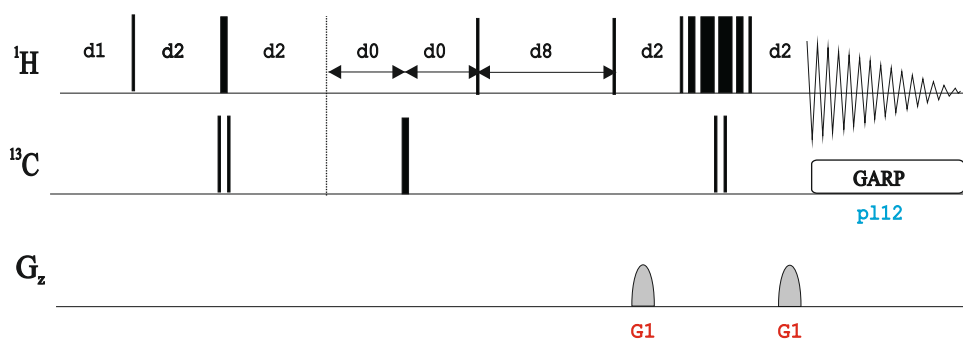
1. A.L. Breeze, Prog. NMR Spectrosc. 36, 323-372 (2000)
2. C. Zwahlen, P. Legault, S.J.F. Vincent, J. Greenblatt, R. Konrat & L.E. Kay, J. Am. Chem. Soc. 119 6711-6721 (1997)
3. K. Ogura, H. Terasawa & F. Inagaki, J. Biomol. NMR 8, 492-498 (1996)
4. J. Iwahara, J.M. Wojciak & R.T. Clubb, J. Biomol. NMR 19, 231-241 (2001)



noesygpphprxf

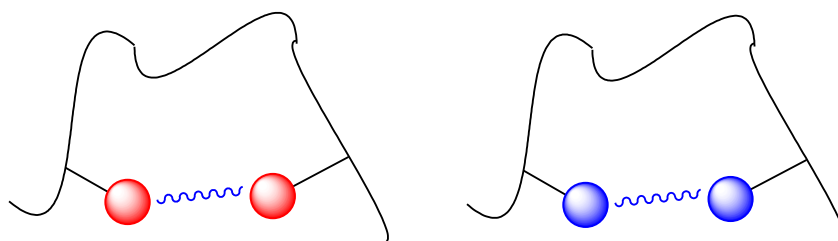


noesygpphxf19

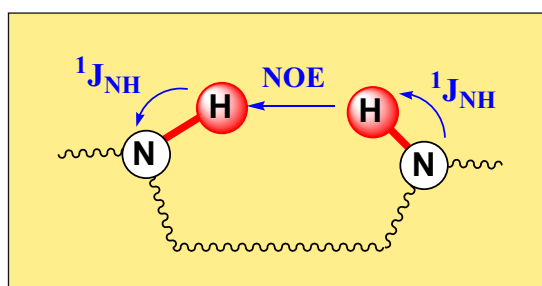
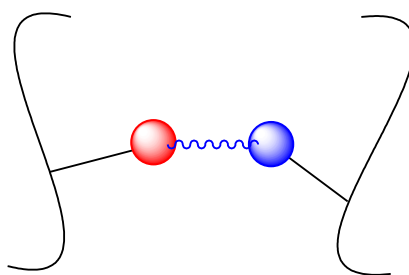


● Unlabeled
● Labeled

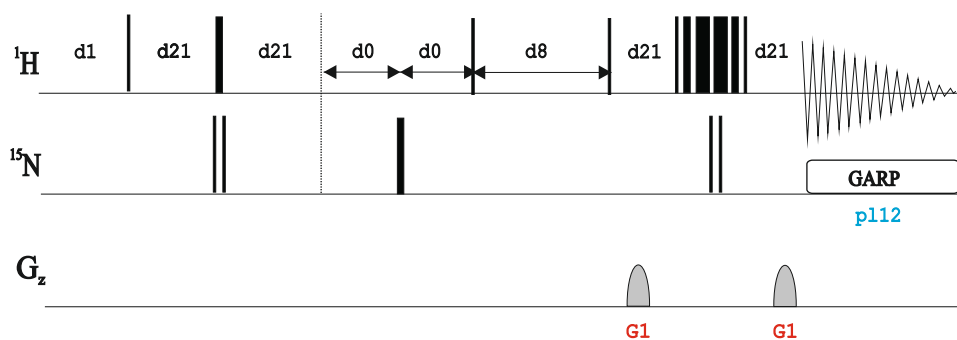
Intramolecular NOEs



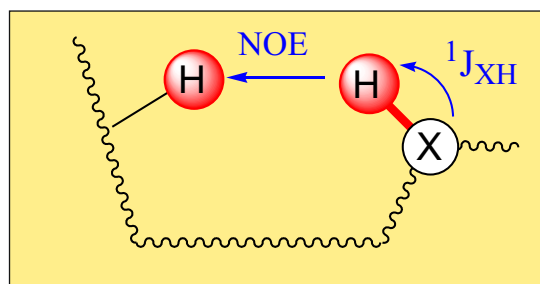
Intermolecular NOEs



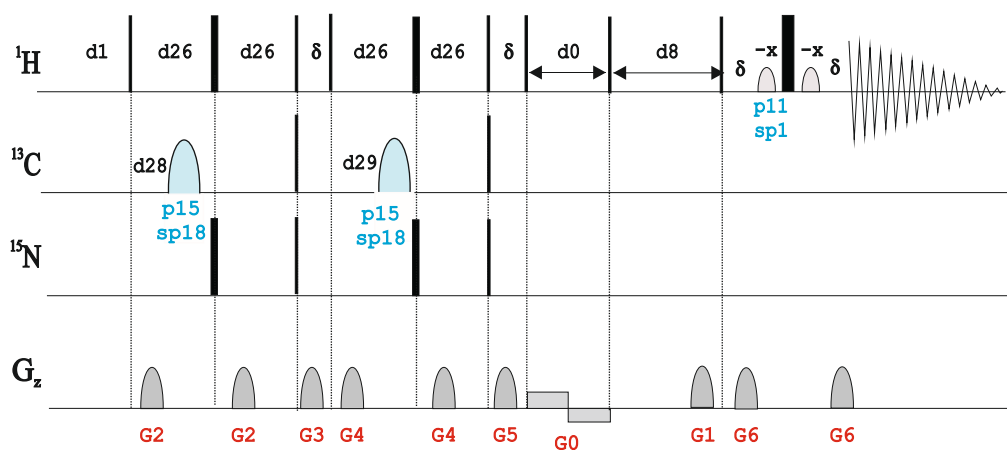
noesyf3gpphxf19



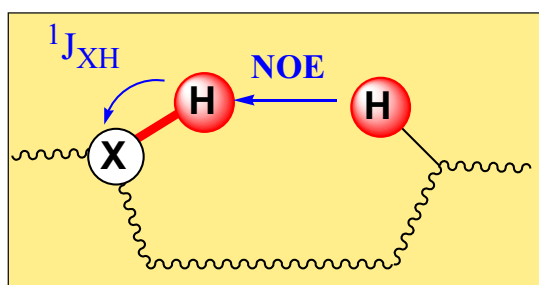
w1-¹³C,¹⁵N-Doubly Filtered NOESY
H[C12,N14] (t1) → H (t2)



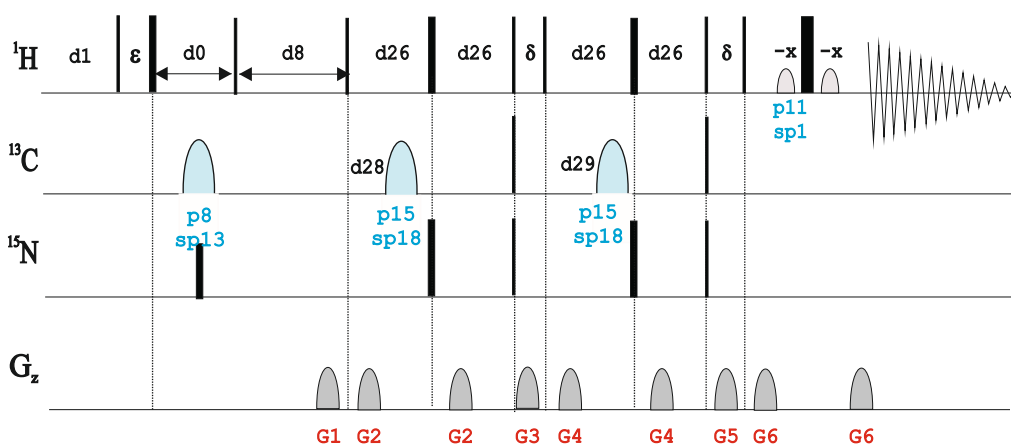
noesygp phwgx1



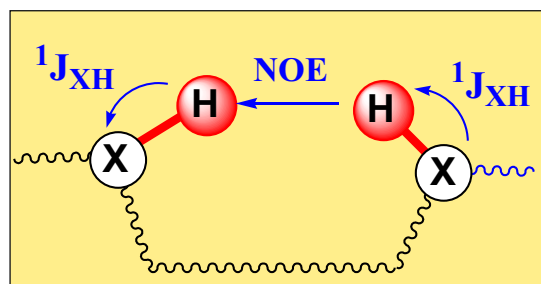
w2-¹³C,¹⁵N-Doubly Filtered NOESY
H (t1) → H[C12,N14] (t2)



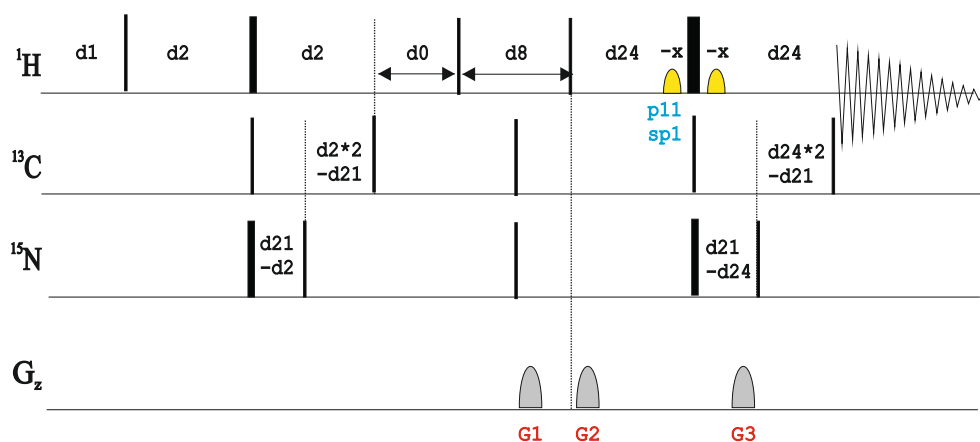
noesygp phwgx2



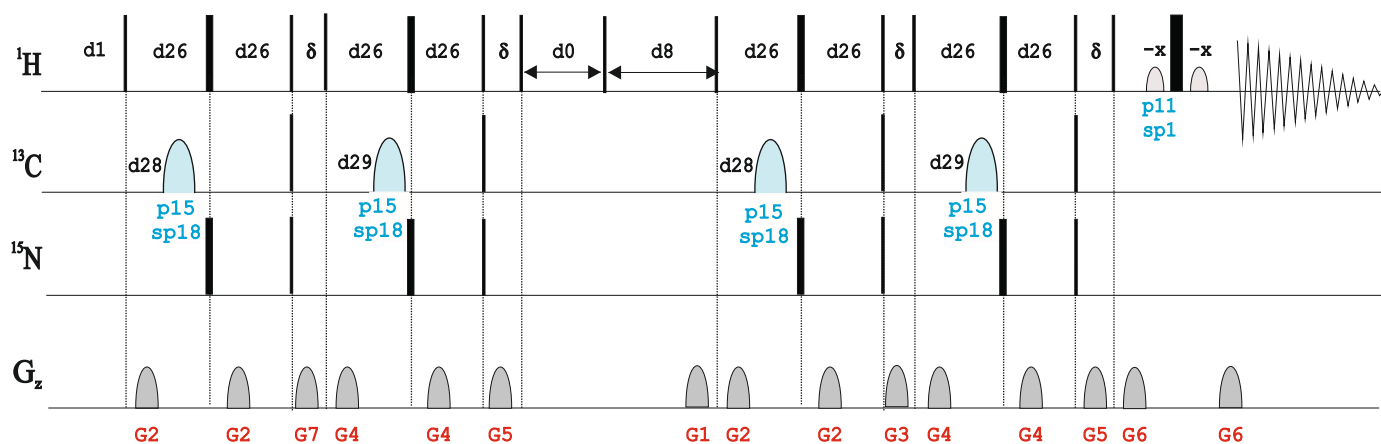
w1,w2-13C,15N-Doubly Filtered NOESY
H[C12,N14] (t1) -> H[C12,N14] (t2)



noesygp phw gxf



noesygp phw gxf.2



BRUKER PULSE PROGRAM CATALOGUE

NMRGuide

3D DOUBLY-¹³C,¹⁵N-FILTERED
HSQC-NOESY & NOESY-HSQC
EXPERIMENTS

3D X-Filtered HSQC-NOESY 3D X-Filtered NOESY-HSQC

ge-3D ^{13}C , ^{15}N -Doubly Filtered HSQC-NOESY experiment

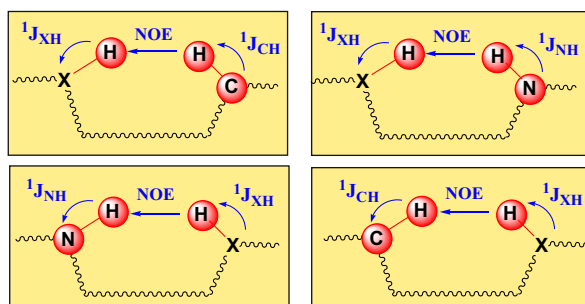
- W_3 - ^{13}C , ^{15}N -Doubly Filtered 3D ^1H - ^{13}C -HSQC-NOESY using WATERGATE (hsqcgpnwngx33d | HSQC6PNO W6X33D)
- W_3 - ^{13}C , ^{15}N -Doubly Filtered 3D ^1H - ^{15}N -HSQC-NOESY using WATERGATE (hsqcf3gpnwngx33d | HSQC6PNO W6X33D)

ge-3D ^{13}C , ^{15}N -filtered/edited NOESY-HSQC experiment

- w_1 - ^{13}C , ^{15}N - Filtered 3D NOESY- ^1H - ^{13}C -HSQC using WATERGATE (noesyhsqcgpwgx13d | NOESYHSQC6PW6X13D)
- w_1 - ^{13}C , ^{15}N - Filtered 3D NOESY- ^1H - ^{15}N -HSQC using WATERGATE (noesyhsqcf3gpwngx13d | NOESYHSQC6PW6X13D)
- w_1 - ^{13}C , ^{15}N - Filtered 3D NOESY- ^1H - ^{15}N -HSQC using PEP and echo-antiecho (noesyhsqcfpf3gpsix13d)
- 3D w_1 - $^{12}\text{C}/^{14}\text{N}$ - Filtered NOESY- ^{13}C , ^{15}N -HSQC experiment with simultaneous evolution and editing between labeled-unlabeled part (noesyhsqcdgpsm3d | NOESYHSQC6PSM3D)
- 3D w_1 - $^{12}\text{C}/^{14}\text{N}$ - Filtered NOESY- ^{13}C , ^{15}N -HSQC experiment with simultaneous evolution, sensitivity improvement and editing between labeled-unlabeled part (noesyhsqcdgpsism3d | NOESYHSQC6PSISM3D)

Also see:

NOESY, NOESY-HSQC, HSQC-NOESY, and HSQC-NOESY-HSQC experiments



w3-Filtered 3D HSQC-NOESY

w1-Filtered 3D NOESY-HSQC

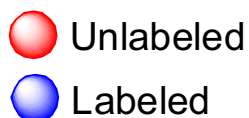
References:

1. A.L. Breeze, Prog. NMR Spectrosc. 36, 323-372 (2000)
2. C. Zwaalen, P. Legault, S.J.F. Vincent, J. Greenblatt, R. Konrat & L.E. Kay, J. Am. Chem. Soc. 119 6711-6721 (1997)
3. K. Ogura, H. Terasawa & F. Inagaki, J. Biomol. NMR 8, 492-498 (1996)
4. J. Iwahara, J.M. Wojciak & R.T. Clubb, J. Biomol. NMR 19, 231-241 (2001)

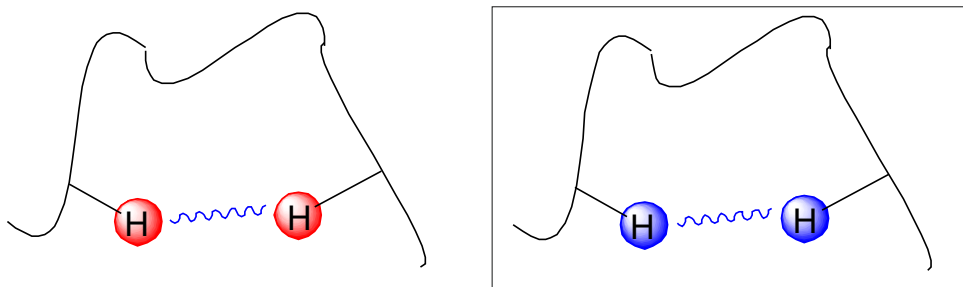
In a mixture of a $^{13}\text{C},^{15}\text{N}$ -compound and a natural-abundance $^{12}\text{C},^{14}\text{N}$ compound there is some different NOE pathways:

- i) Intramolecular Unlabeled-Unlabeled NOEs
- ii) Intramolecular Labeled-Labeled NOEs
- iii) Intermolecular Labeled-Unlabeled NOEs

X-Filtered/Edited NOESY experiments can distinguish between them:



Intramolecular NOEs



Intermolecular NOEs

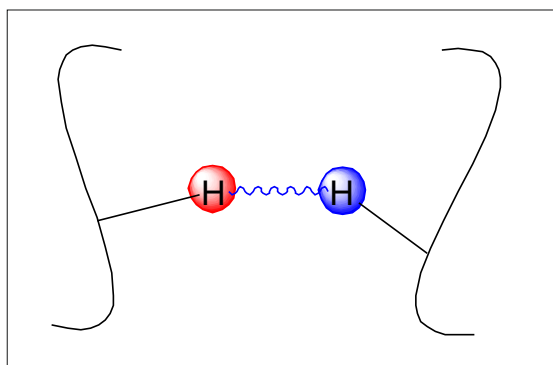


Diagram illustrating the setup for a 3D NMR experiment involving ^1H , ^{13}C , and ^{15}N nuclei, showing the G_z axis and the resulting peaks.

The G_z axis is labeled with values: G2, G2, G3, G4, G4, G5.

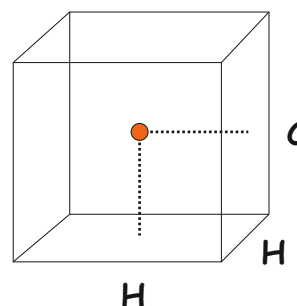
The peaks are labeled as follows:

- ^1H : d26, δ , d26, δ
- ^{13}C : d28, d29
- ^{15}N : p15, sp18, p15, sp18

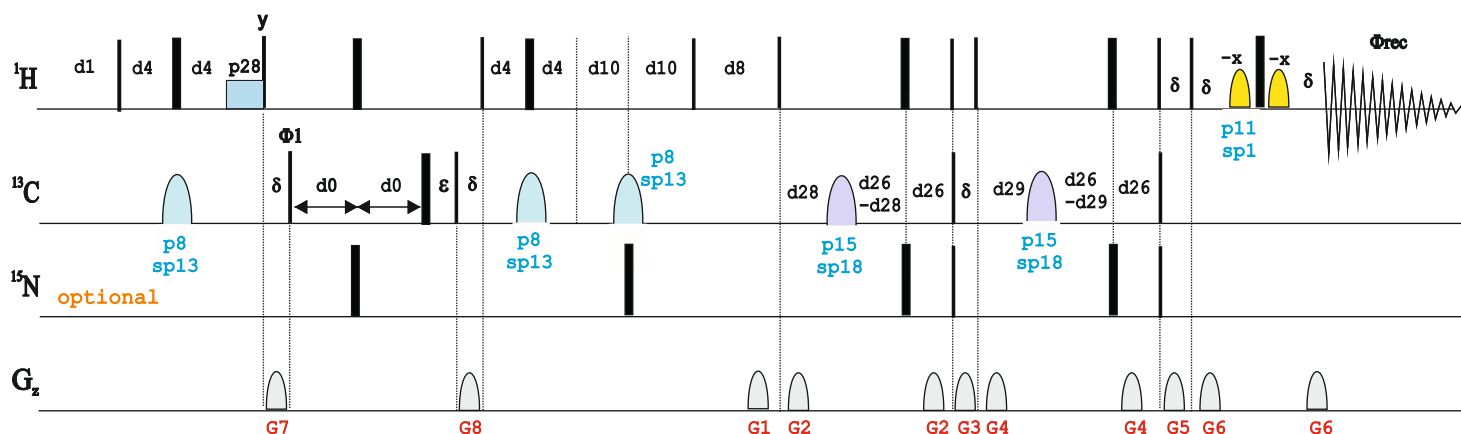
The diagram also indicates the axes for the ^1H and ^{13}C nuclei: y and -x.

d26: $1/(4 \cdot J(\text{NH}))$
d28: $1/(4 \cdot J(\text{CH})_{\text{min}})$
d29: $1/(4 \cdot J(\text{CH})_{\text{max}})$

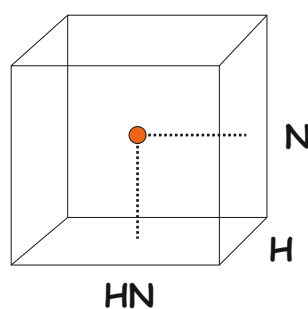
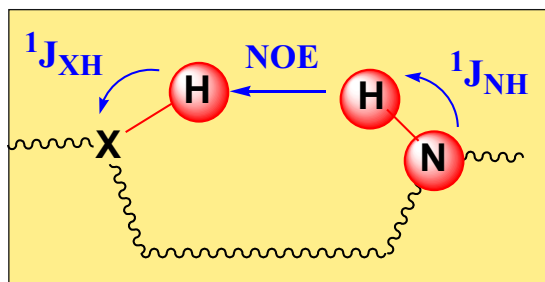
The diagram shows two chemical environments. On the left, a nucleus **X** is coupled to a proton **H** via scalar coupling, labeled $^1J_{XH}$. On the right, a proton **H** is coupled to a carbon **C** via scalar coupling, labeled $^1J_{CH}$. A double-headed arrow labeled **NOE** connects the two protons, indicating a Nuclear Overhauser Effect between them.



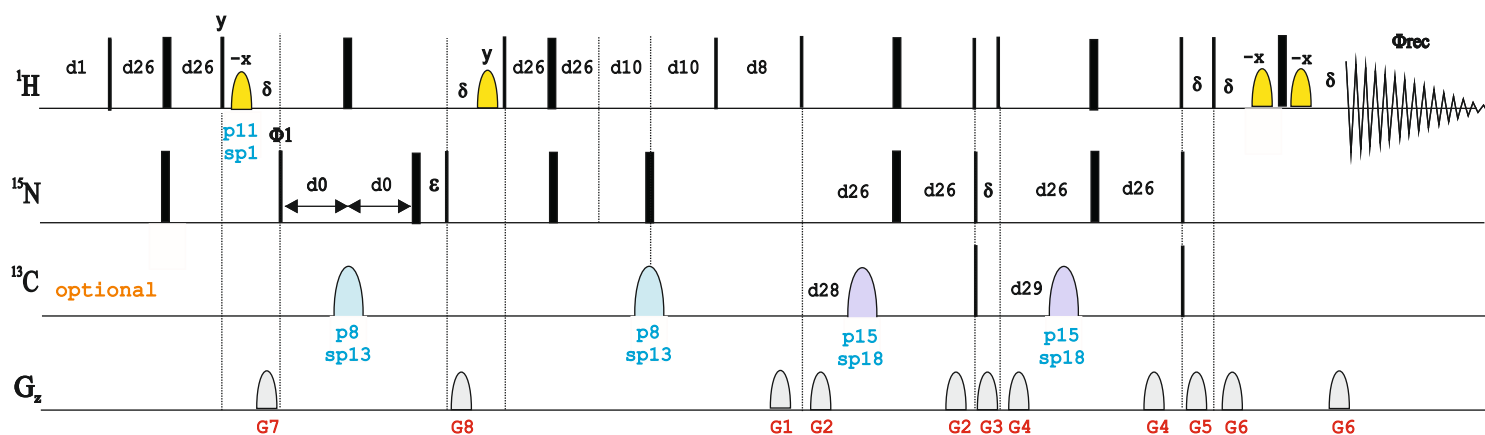
hsqcgpnwngx33d



N15 (t1) → H[N15] (t2) → H[(C12),N14] (t3)

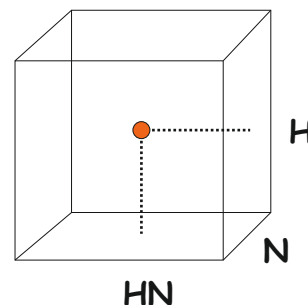
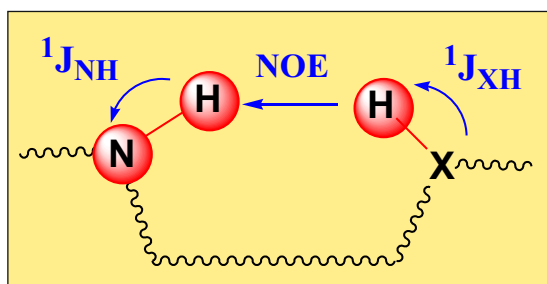


hsqcf3gpnowgx33d

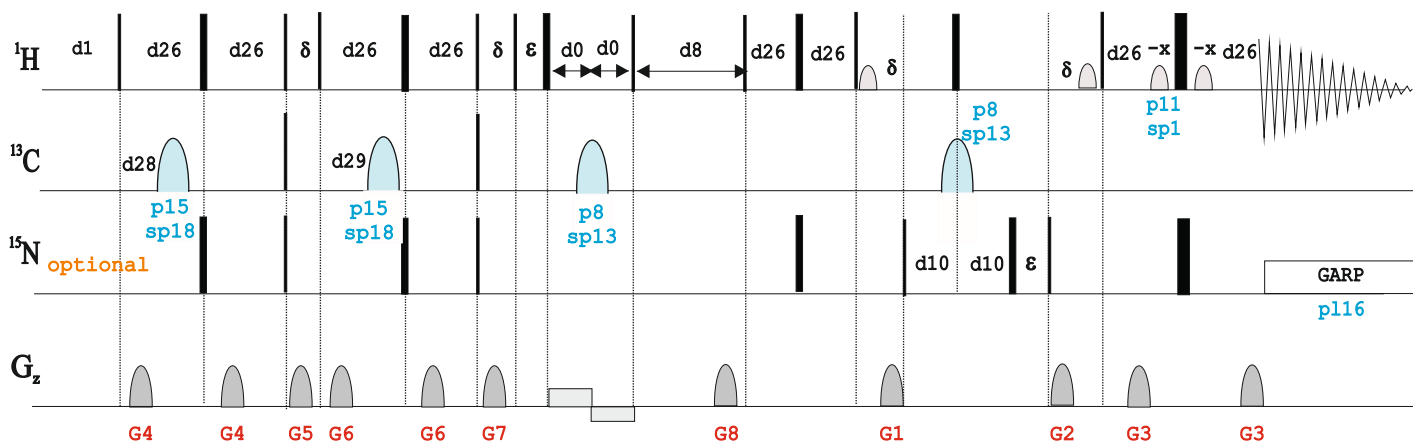


w1-13C,15N-Doubly Filtered NOESY-HSQC experiment

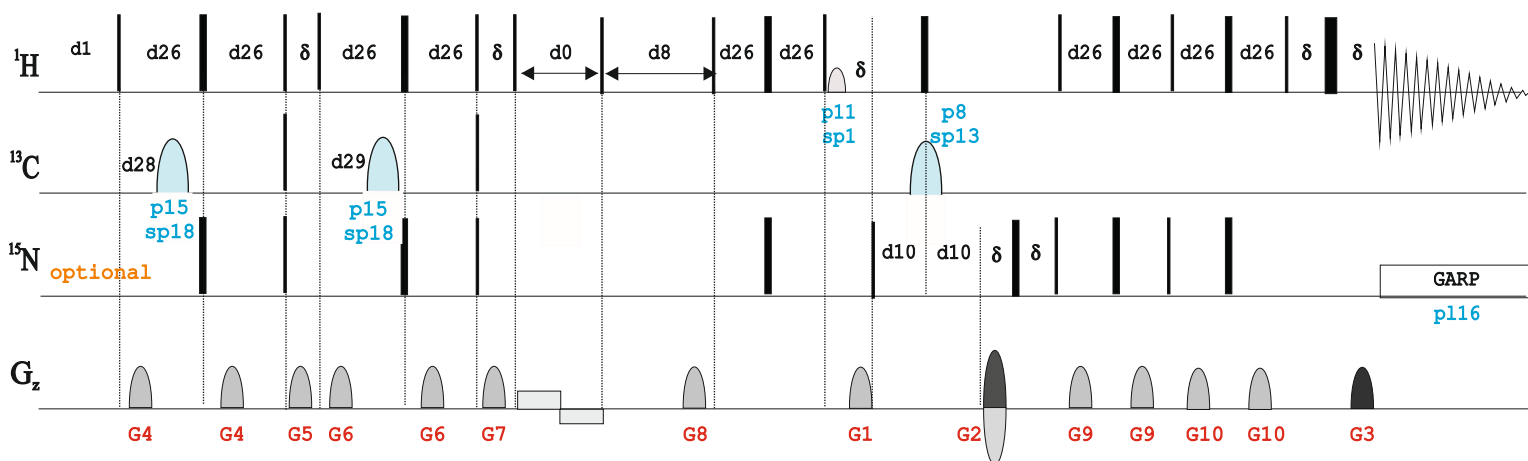
$H[(C12),N14] (+1) \rightarrow N15 (+2) \rightarrow H[N15] (+3)$



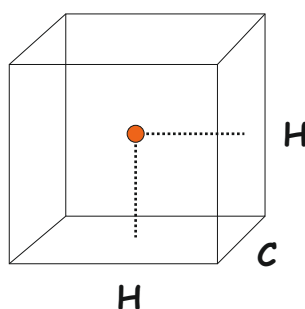
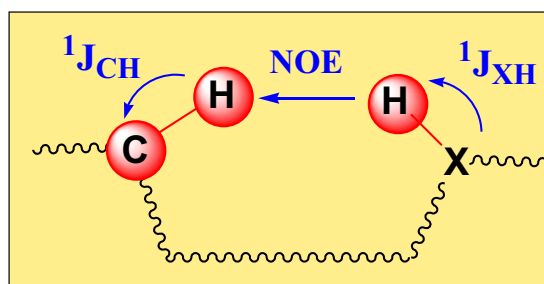
noesyhsqc3gpwgx13d



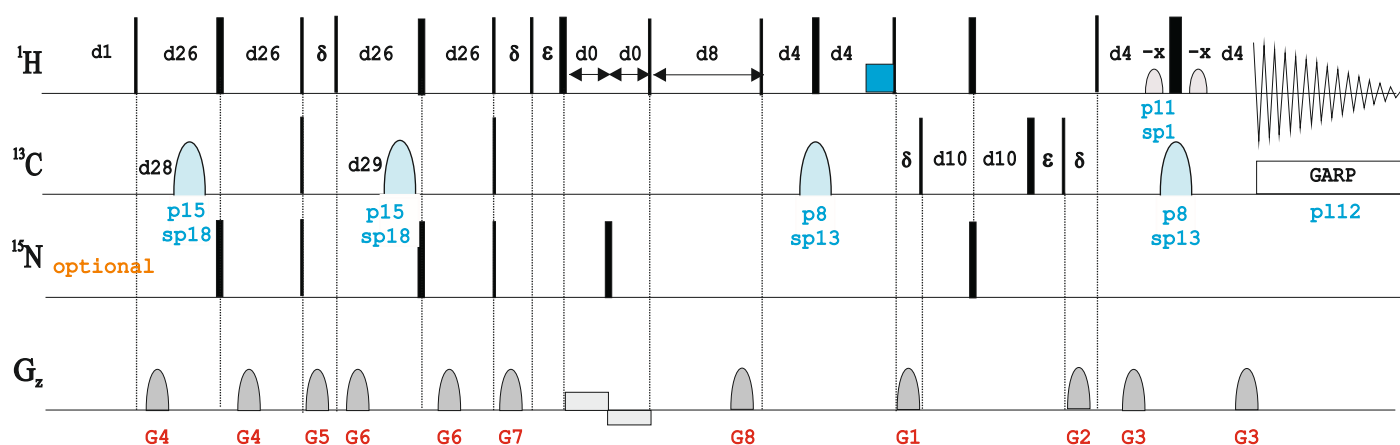
noesyhsqc3gpsix13d



w1-13C,15N-Doubly Filtered NOESY-HSQC experiment

$$H[(C12),N14] (t1) \rightarrow C13 (t2) \rightarrow H[C13] (t3)$$


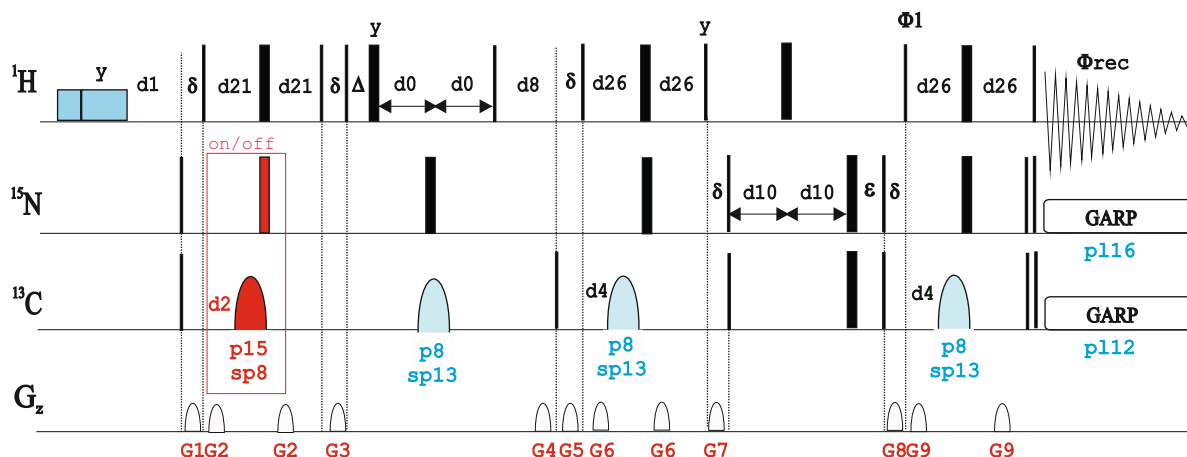
noesyhsqcpwgx13d



12C,14N vs 13C,15N-edited NOESY-HSQC:

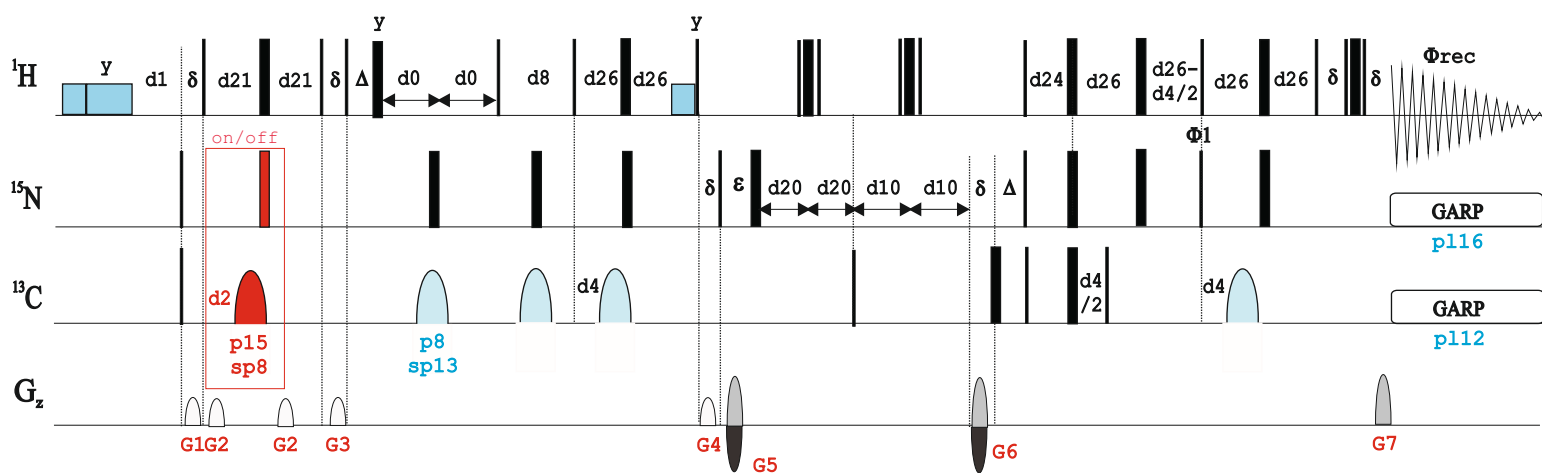
C. Eichmueller, W. Schueler, R. Konrat & B. Kraeutler, J. Biomol. NMR 21, 107-116 (2001)

noesyhsqcedgpsm3d



use AU-program split [2 F2] to create separate datasets

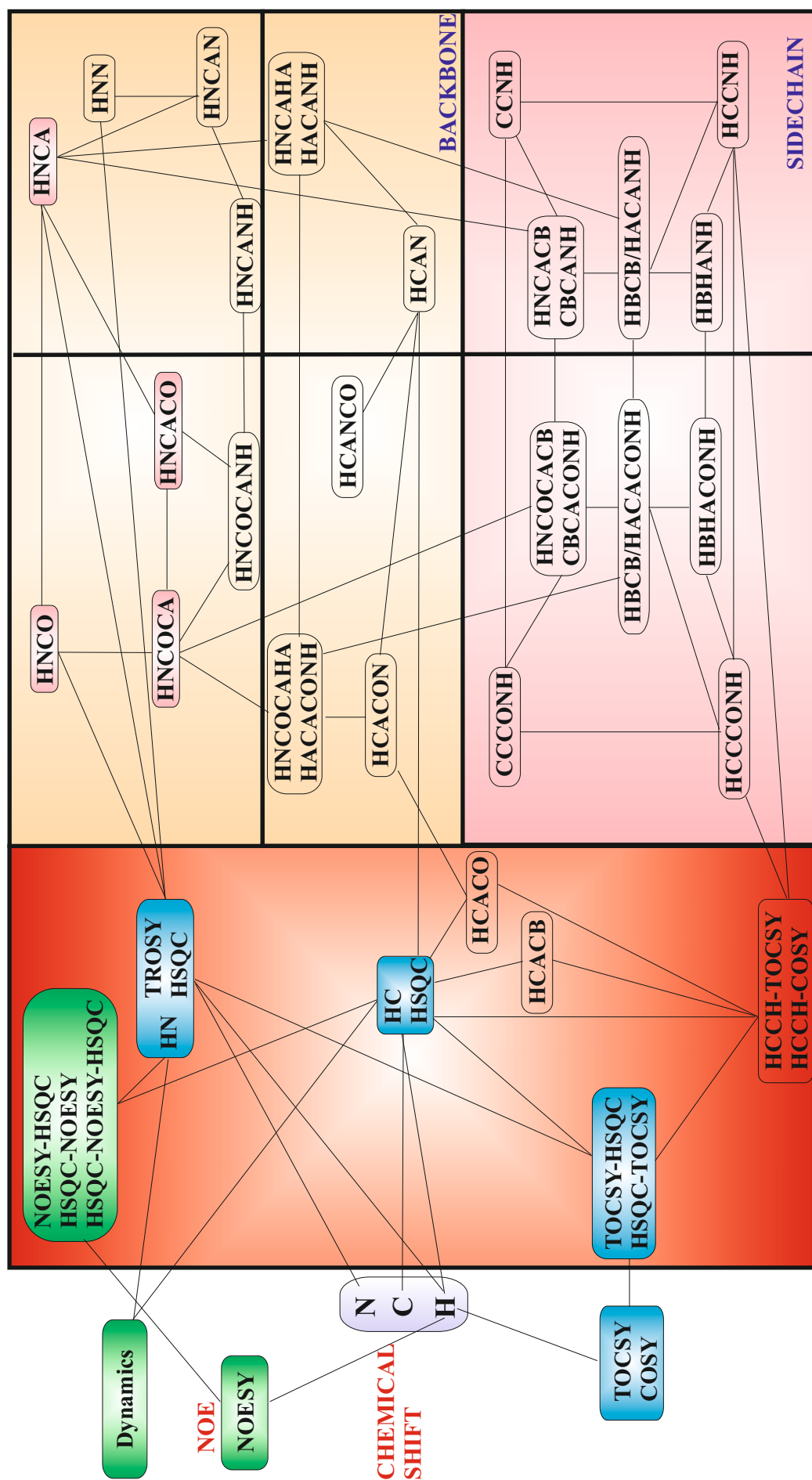
noesyhsqcedgpsism3d



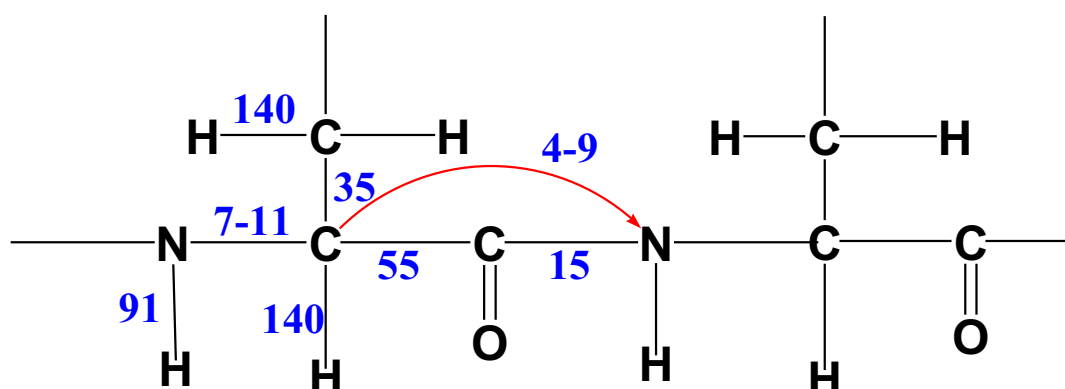
BRUKER PULSE PROGRAM CATALOGUE

NMRGuide

PROTEIN NMR BACKBONE EXPERIMENTS



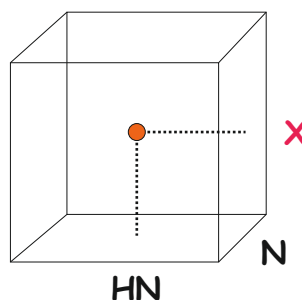
Interpulse delays are optimized as a function of the following heteronuclear coupling constants:



Identifier	Power	Duration	sparam	cpdprg	Description	Remarks
PROTON PULSES & POWER LEVELS						
p1,p2	pl1				High Power Pulse	
p6	pl10	25u			TOCSY	
p15	pl11				ROESY	Power as 125u pulse
p26,pcpd1	pl19	55-65u		dipsi2	Decoupling pulse	
p11	sp1	1.5-2m	SINC1.1000		Water flipback pulse	
CARBON PULSES & POWER LEVELS						
p3,p4	pl2				High Power Pulse	
p9	pl15	25u		dipsi3	CC-TOCSY or HC-Cross polarization	
p13	sp2	320u	Q5.1000		on-resonance 90° (Cali or CO)	
p13	sp8	320u	Q5tr.1000		on-resonance time-reversed 90° (Cali or CO)	
p14	sp3	256u	Q3.1000		on-resonance 180° (Cali or CO)	
p14	sp5/sp7	256u	Q3.1000		off-resonance 180° (Cali or CO)	
		1500u	Q5.1000		on-resonance 90° (CA)	
		1500u	Q5tr.1000		on-resonance time-reversed 90° (CA)	
p24	sp9	1000u	Q3.1000		on-resonance 180° (CA)	
p24	sp7	2000u	Crp60comp.4		Adiabatic 180° refocusing	Power as 25u pulse
p8	sp13	500u	Crp60,0.5,20.1		Adiabatic 180° inversion	Power as 25u pulse
pcpd2	pl12	60u-80u		garp	Low Power Pulse for broadband decoupling	
pcpd2, p31	sp15,pl13	1500u	Crp42,1.5,20.2	p5m4sp180,p31	Adiabatic Decoupling	Power as GARP + 2dB
		750u	Crp42,1.5,20.3		Adiabatic Bilev	
pcpd2, p31	sp15,pl28	768u	Q3.1000	mlevsp180,p31	CA or CO selective decoupling	
pcpd2, p31	sp15,pl28	100u	Gauss5.256	mlevsp180,p31	Selective CO Decoupling	Power as 25u pulse
NITROGEN PULSES & POWER LEVELS						
p21,p22	pl3				High Power Pulse	
pcpd3	pl16	200-300u		garp	Low Power Pulse for broadband decoupling	
DEUTERIUM PULSES & POWER LEVELS						
pcpd4	pl17	250u		garp	Low Power Pulse for broadband decoupling	

Delay	Coupling Constant	length (ms)	Remarks	Experiment
d3	1/(3JCH)	2.2		
d4	1/(4JCH)	1.6-1.8		
d21	1/(6JCH)	1.1		
d21	1/(2JNH)	5.5		
d22	1/(4JCOCA)	4.0		
d22	1/(2JCOCA)	3.6	Two-bond	
d22	1/(2JCOCA)	4.4	One-bond	
d23	1/(2JNCO)	12.0		
d24	1/(4JCC)	3.6		
d26	1/(4JNH)	2.3		
d21	T(N)	12.4		
d23	T(C)	12.0	2T=24ms<1/4JCH	

H(N)-Detection



HN,N,CO

HNCO
HN(CA)CO
(HACA)CONH

HN,N,CA

HNCA
HN(CO)CA
SeqHNCA
IntraHNCA

HN,N,N

(H)N(CA)NNH
(H)N(COCA)NNH

NH,N,HN

H(NCA)NNH
H(NCOCA)NNH

HN,N,HA

HN(CA)HA
HA(CA)NH
HA(CACO)NH

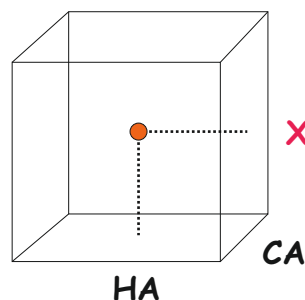
HN,N,Cali

CBCA(CO)NH
HN(CO)CBCA
CBCANH
SeqCBCANH
IntraCBCANH
HNCBCA
CCANH
CCA(CO)NH
CC(CO)NH
(H)CC(CO)NH

HN,N,Hali

HBHA(CO)NH
HBHANH
H(CC)(CO)NH

HA-Detection



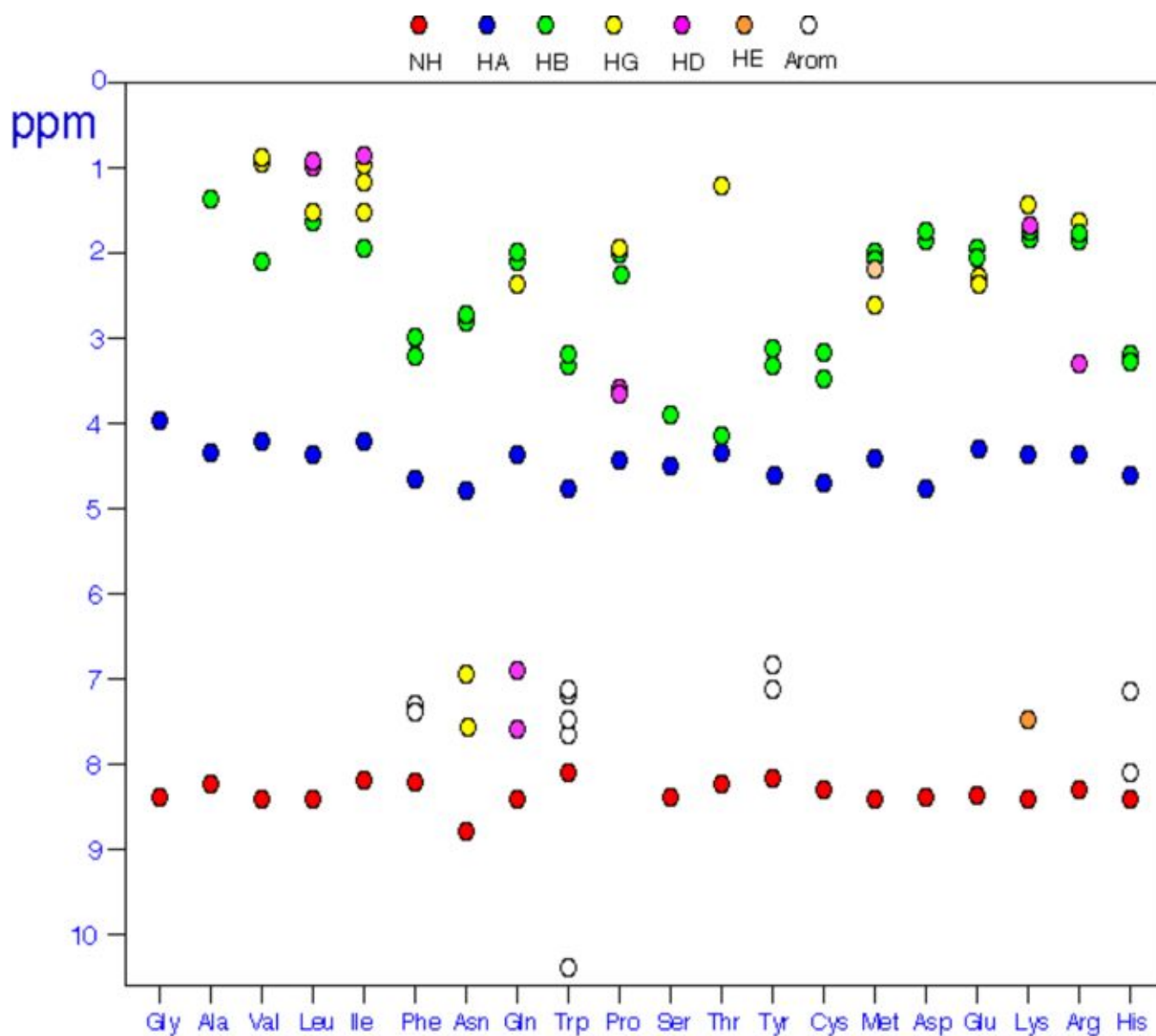
HA,CA,CO

HACACO

HA,CA,N

HACAN
HACA(CO)N
HCBCA(CO)N

^1H Chemical Shifts of random-coil 20 aa



BRUKER PULSE PROGRAM CATALOGUE

NMRGuide

3D HNCO

Experiment Description

The HNCO experiment correlates the NH group ($d(NH)$ and $d(N)$) with the carbonyl carbon ($d(CO)$) of the preceding residue. It is the basis for more complicated triple-resonance 3D, 4D ... NMR pulse sequences

Sample Requirements

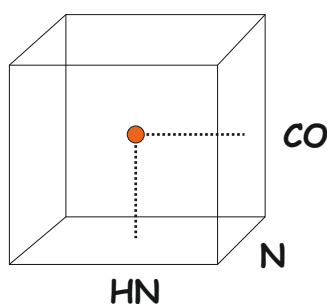
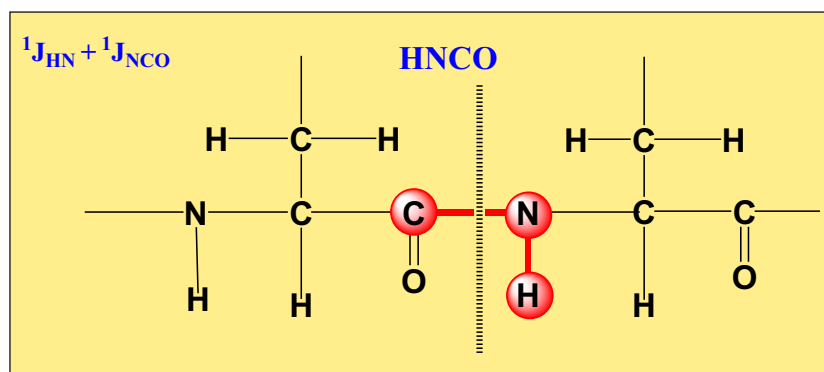
$^{13}C,^{15}N$ -doubly labeled protein

Hardware Requirements

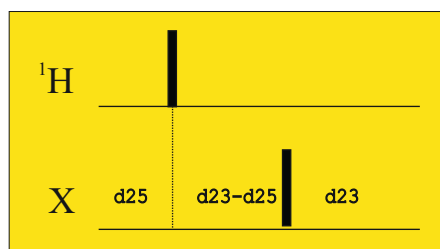
Triple Channel Configuration

References

1. S. Grzesiek & A. Bax, J. Magn. Reson. 96, 432 - 440 (1992)
2. J. Schleucher, M. Sattler & C. Griesinger, Angew. Chem. Int. Ed. 32, 1489-1491 (1993)
3. L.E. Kay, G.Y. Xu & T. Yamazaki, J. Magn. Reson. A109, 129-133 (1994)
4. T. Schulte-Herbrueggen & O.W. Sorensen, J. Magn. Reson. 144, 123 - 128 (2000)



Concatenated Periods in 3D Triple-Resonance NMR Experiments



Fixed period
Overall Duration: $2d23$

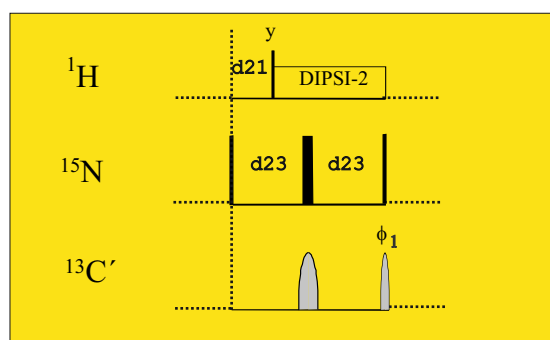
^1H Chemical shift: $d25 - (d23-d25) - d23 = 2d25-2d23$

X Chemical shift: $d25 + (d23-d25) - d23 = 0$

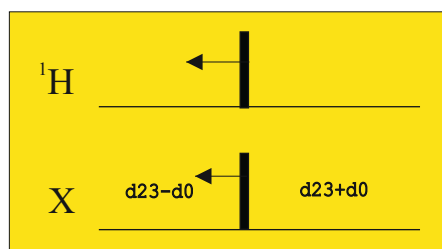
J(XH) Coupling Constant: $d25 - (d23-d25) + d23 = 2d25$

J(HH) and J(XX) Coupling Constant: $d25 + (d23-d25) + d23 = 2d23$

A related building block is largely used in 3D experiments in which J(XY) evolves during d23 whereas J(HH) is refocused during d25 and decoupled



Constant-time ^{15}N -evolution periods



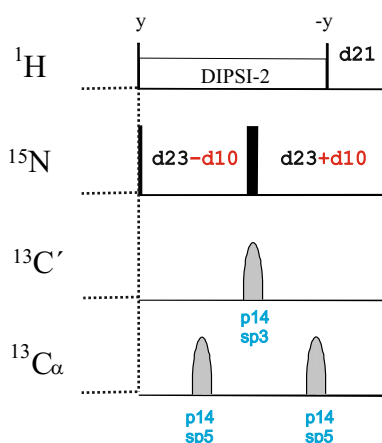
Variable Constant-time period
Overall Duration: $2d_{23}$

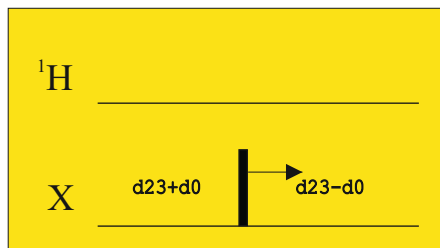
^1H Chemical shift: $(d_{23} - d_0) - (d_{23} + d_0) = -2d_0$

X Chemical shift: $(d_{23} - d_0) - (d_{23} + d_0) = -2d_0$

$J(\text{XH})$ Coupling Constant: $(d_{23} - d_0) + (d_{23} + d_0) = 2d_{23}$

$J(\text{HH})$ and $J(\text{XX})$ Coupling Constant: $(d_{23} - d_0) + (d_{23} + d_0) = 2d_{23}$





Variable Constant-time period
Overall Duration: $2d_{23}$

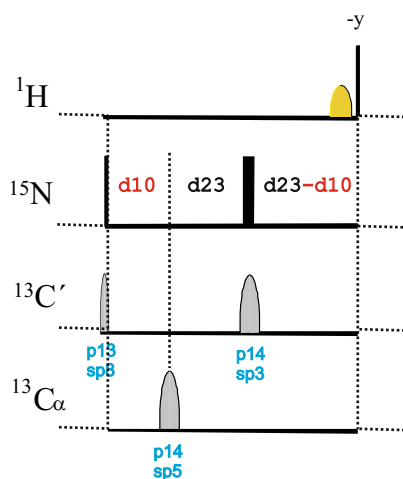
^1H Chemical shift: $(d_{23} + d_0) + (d_{23} - d_0) = 2d_{23}$

X Chemical shift: $(d_{23}+d_0) - (d_{23}-d_0) = 2d_0$

$J(\text{XH})$ Coupling Constant: $(d_{23}+d_0) - (d_{23}-d_0) = 2d_0$

$J(\text{HH})$ and $J(\text{XX})$ Coupling Constant: $(d_{23}+d_0) + (d_{23}-d_0) = 2d_{23}$

trhncogp3d

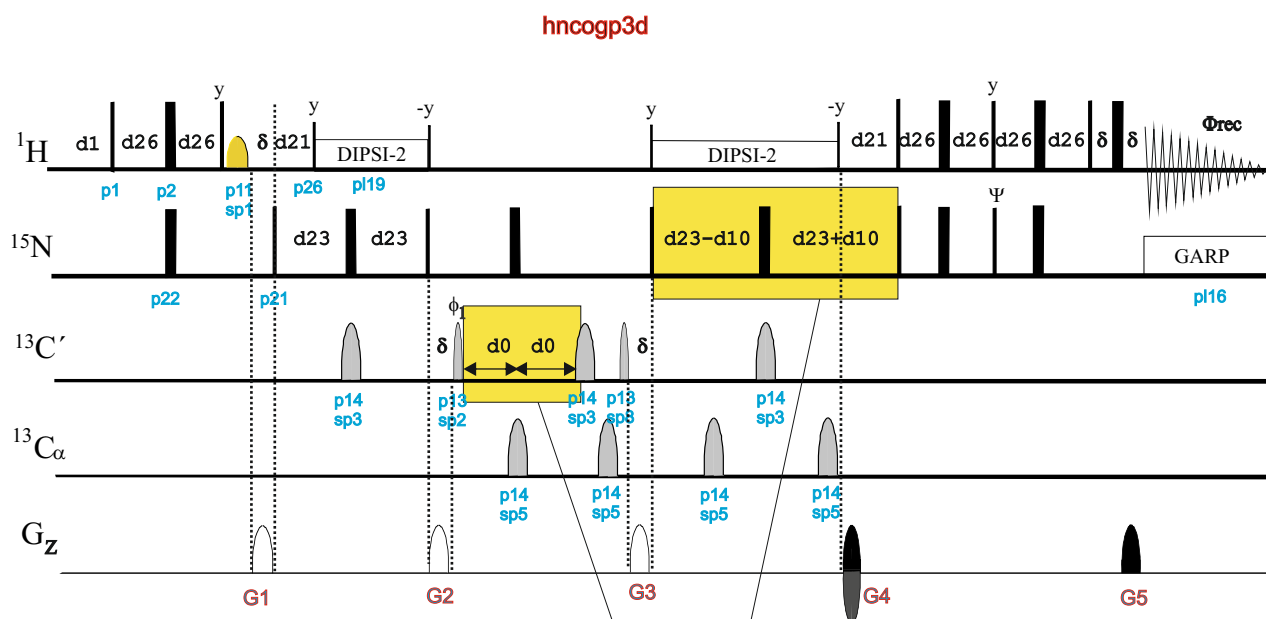


Practical fine adjustment of pulse lengths and power levels.

1. Load the basic parameter set for the HNCO experiment: **rpar HNCOGP3D all**
2. Load the basic pulses and power levels according to your available probehead: **getprosol**
3. Change the parmcode in eda from 3D to 1D (see mc command) and then set td in the indirect F1 and F2 dimensions to 1. Also increases td in the detected dimension up to 8K, for instance.

	F3	F2	F1	Frequency axis
Experiment				
PULPROG =	hncogp3d			Current pulse program
AQ_mod =	DQD			Acquisition mode
FnMODE =	Echo-Antiecho			Acquisition mode for 2D/3D
TD =	8192	1	1	Size of fid
NS =	16			# of scans
DS =	32			# of dummy scans
TD0 =	1			Loop count for 'td0'
Width				
SW [ppm] =	14.0019	72.0079	22.0844	Spectral width
SWH [Hz] =	7002.801	3649.635	2777.778	Spectral width
IN_010 [s] =		0.00013700	0.00018000	Increment for delay D10 (F2), t
ND_010 =		2	2	# of delays in pulse program fo

4. Set **ns** and start acquisition with **rga** and **zg**.
5. When the data is transformed with **ef**, the program asks for the procno number.
If you type 2, for instance, the corresponding 1D H(NCO) spectrum is displayed in the "filename 1 2" file

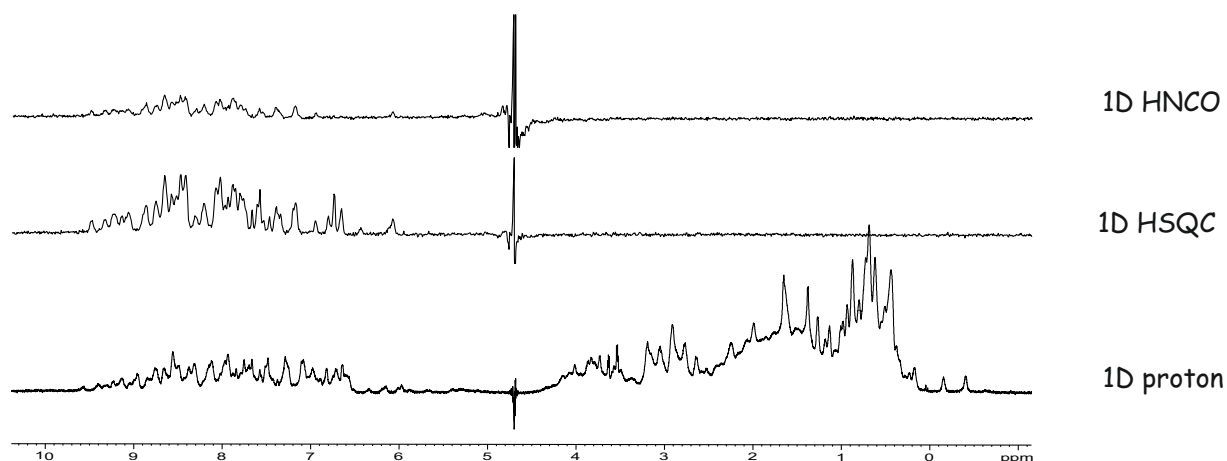


In the 1D H(NCO) experiment, d0 and d10 are fixed to a minimum fixed value of 3us.

6. Once the 1D data shows signals in the NH region, the overall signal must be maximized by individual optimization of the different parameters of the sequence. This process is performed from the "1 2" file and executing the **popt** program. In the case of **hncogp3d** the most important pulses are:

Hard 1H pulse (p1) at pl1
Water 90 selective 1H pulse (p11) at sp1
Hard 15N 90 pulse (p21) at pl3
Selective 13CO 180° pulse (p14) at sp3
Selective 13CO 90° pulse (p13) at sp2 and sp8
Selective 13CA 180° pulse (p14) at sp5

Usually, pulse length are fixed and the power level is varied over an specific range up to a maximum value is obtained.

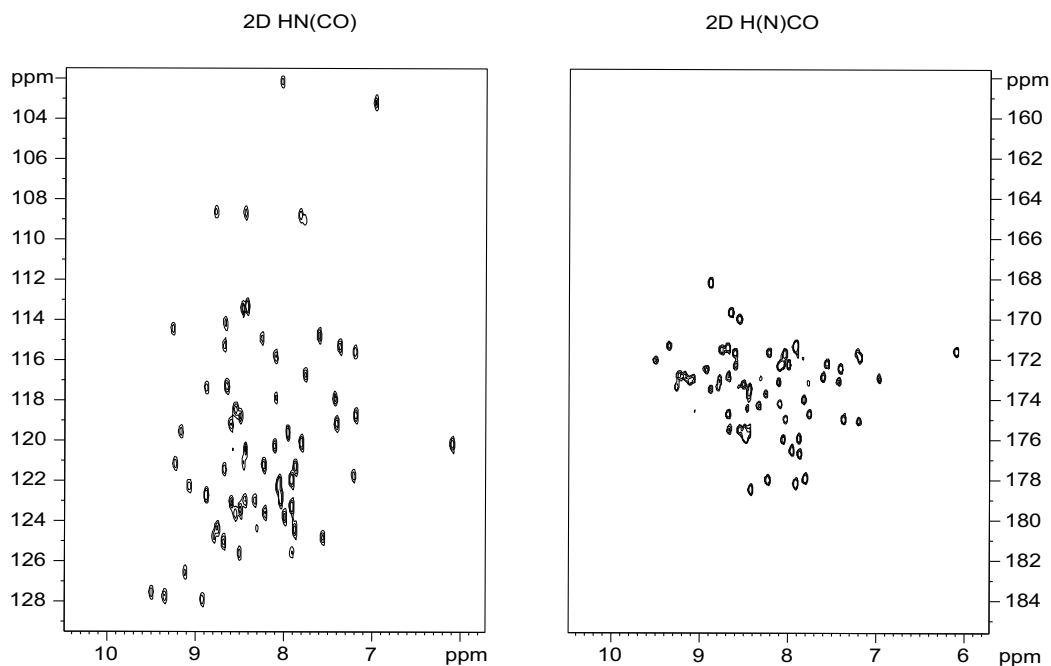


Although sequences included into the pp directory are highly robust, this same 1D calibration protocol based on the use of **zg/popt** can be used to optimize other parameters and to design better alternatives or modify the existing ones according to the used sample conditions:

Required number of scans
Setting of delay durations
Check for proper gradient strengths
Use of alternative purge gradients
Use of additional water flip-back pulses
Check for proper and minimum phase cycling
.....

Recording 2D Planes:

Once the acquisition parameters have been finely adjusted, it is recommended to record the first 2D planes of the 3D spectrum. This is automatically set from the original dataset and setting the corresponding *td* values according to the required resolution in each dimension. Thus, an 2D HN(CO) spectrum is acquired by setting *td* to 2k(1H), 64(N) and 1(CO) in *eda*. Otherwise, a 2D H(N)CO spectrum is acquired by setting *td* to 2k(1H), 1(N) and 64(CO), for instance. These preliminary spectra could be also used to check for useful offsets and spectral windows in each dimension.



Experiment Version vs Labeling Strategy and Protein Size:

Basically, all 3D experiments can be designed with different pulse timings as a function of sample requirements and performance. The most typical approaches are:

- i) **PEP Block** in step 5: Maximum Theoretical sensitivity for IS spin systems
- ii) **WATERGATE Block** in step 5: Better solvent suppression
- iii) **TROSY Block** in step 5: TROSY editing for large proteins. heteronuclear decoupling is removed during N evolution and during acquisition.
 - 1. Conventional
 - 2. Echo/Antiecho
- iv) **^2H -decoupling** during CA evolution: For ^2H -labeled Proteins

3D HNCO experiment

- 3D HNCO using PEP (**hncogp3d** | HNCOGP3D)
- 3D HNCO using WATERGATE (**hncogpwg3d** | HNCOGPWG3D)
- 3D HNCO using TROSY (**trhncogp3d** | TRHNCOGP3D):
 - using echo-antiecho gradient (**trhncoetgp3d** | TRHNCOETGP3D)
 - with ^2H -decoupling (**trhncogp2h3d** | TRHNCOGP2H3D)

Also see:

3D APSY-HNCO experiment:

Reduced-Dimensionality (3,2)-HNCO (**rd_hnco_32** | APSY_HNCO_32)

3D SOFAST/BEST-HNCO experiment:

3D BEST-HNCO (**b_hncogp3d** | B_HNCOGP3D)
3D BEST-HNCO using TROSY (**b_trhncogp3d**)
3D BEST-intraHNCO (**b_hncoigp3d** | B_HNCOIGP3D)
3D BEST-intraHNCO using TROSY (**b_trhncoigp3d**)

3D HNCO-type experiments for T1, T2 and T1(rho) relaxation measurements

3D HNCO-type experiments for J measurements

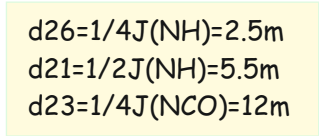
3D HNCO-type experiments for RDC measurements

3D HNCO-type experiments for Hydrogen-Bonds J measurements

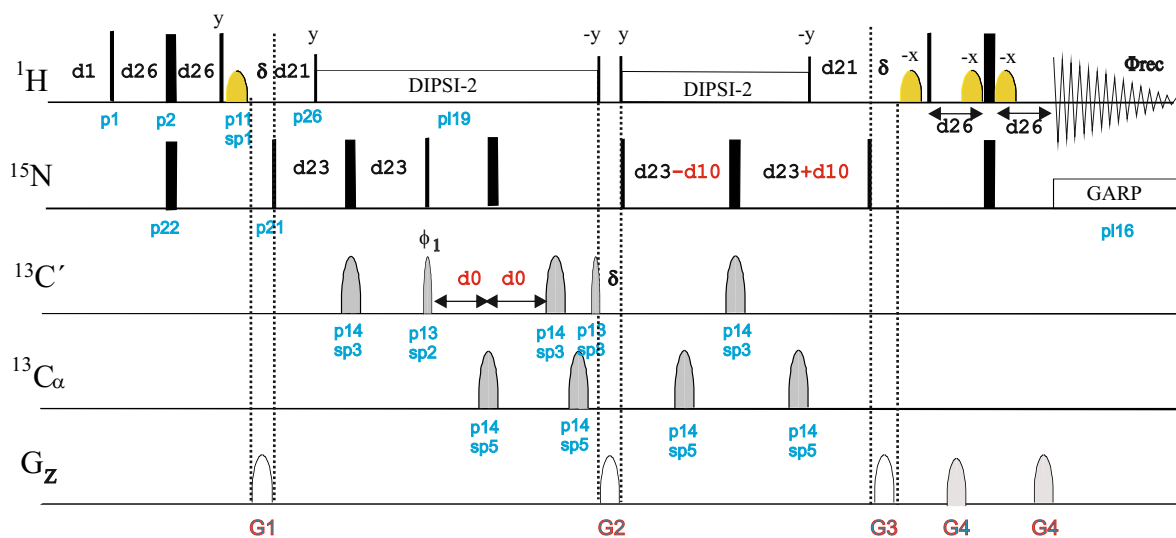
3D Carbon-Detected HNCO experiments

Related Experiments:

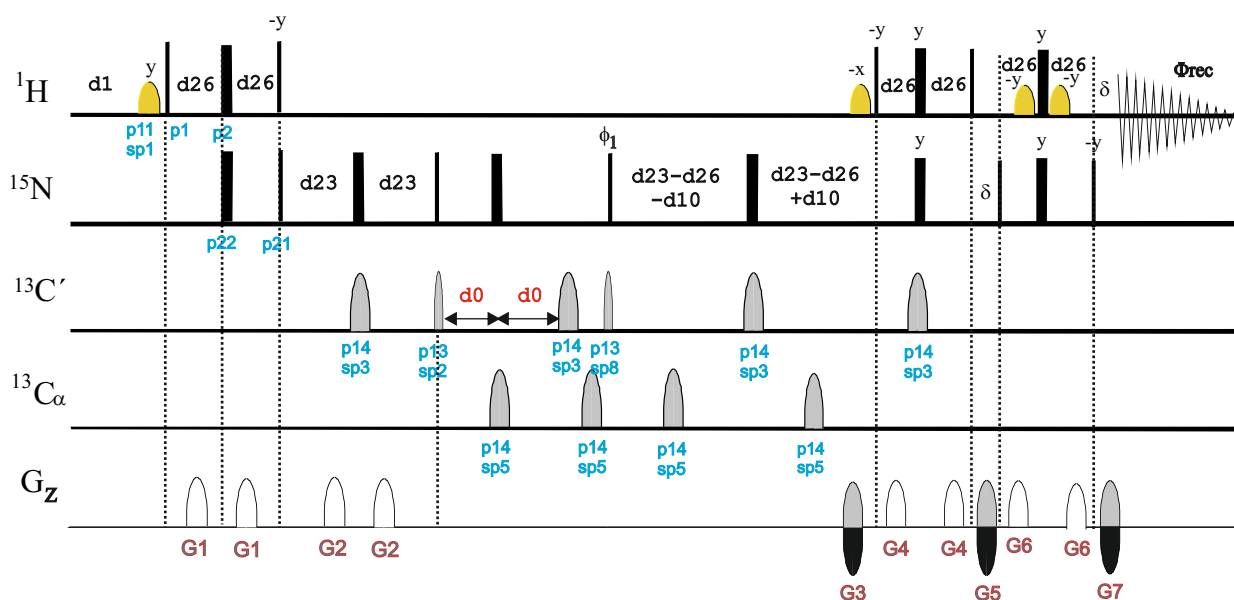
intra-HNCO, HN(CA)CO experiments

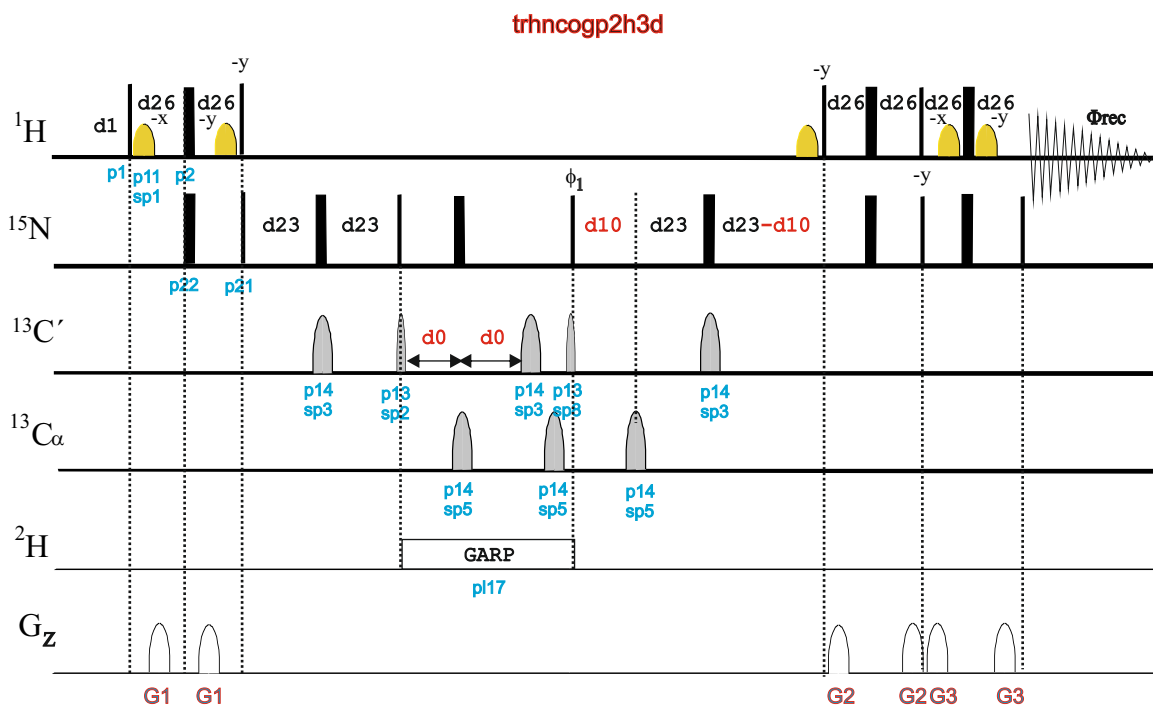
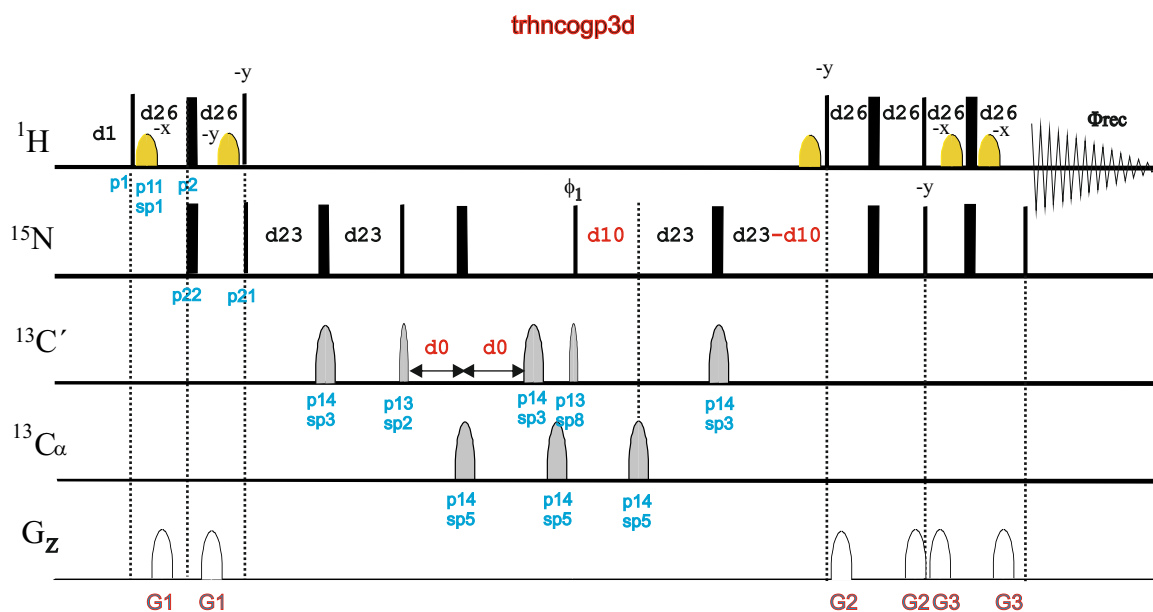


hncogpwg3d



trhncoetgp3d





BRUKER PULSE PROGRAM CATALOGUE

NMRGuide

3D HNCA

Experiment Description

The HNCA experiment correlates the NH group ($d(NH)$ and $d(N)$) with the alpha carbon ($d(CA)$) of the same and of the preceding residue.

Sample Requirements

$^{13}C,^{15}N$ -doubly labeled protein

Hardware Requirements

Triple Channel Configuration

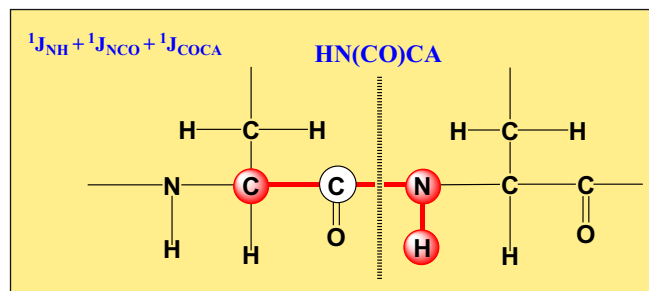
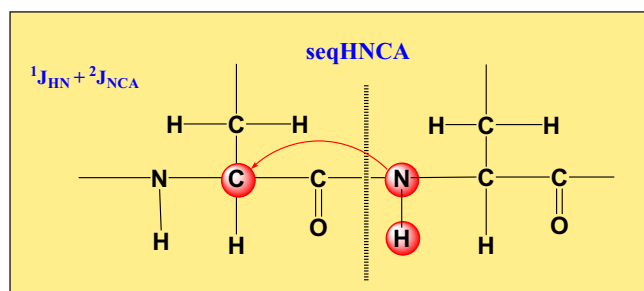
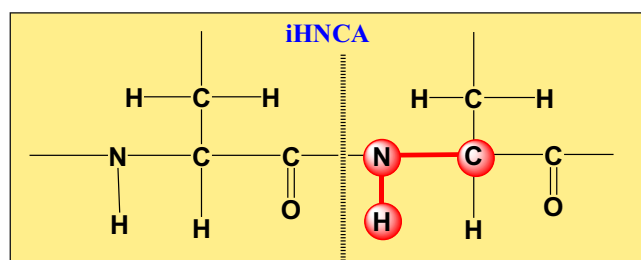
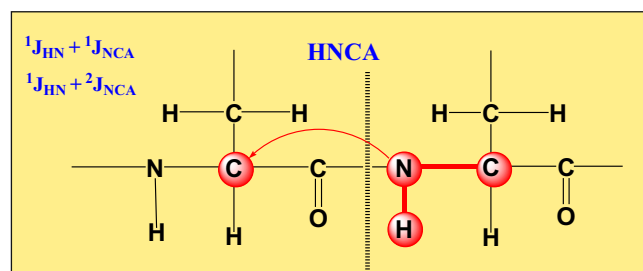
References

1. S. Grzesiek & A. Bax, J. Magn. Reson. 96, 432 - 440 (1992)
2. J. Schleucher, M. Sattler & C. Griesinger, Angew. Chem. Int. Ed. 32, 1489-1491 (1993).
3. L.E. Kay, G.Y. Xu & T. Yamazaki, J. Magn. Reson. A109, 129-133 (1994))

Main Features:

1. HNCA provides one inter-residue and one intra-residue cross peak.
2. The intensity of the HNCA peaks are less intense than in the HNCO experiment.
3. The inter-residue cross peak is generally less intense than the intra-residue cross peak

Comparison of different 3D experiments detecting HN, N and CA



3D HNCA experiment

- 3D HNCA using PEP (**hncagp3d** | HNCAGP3D)
 - with ^2H -decoupling (**hncagp2h3d** | HNCAGP2H3D)
- 3D HNCA using WATERGATE (**hncagpwg3d** | HNCAGPWG3D)
 - with ^2H -decoupling (**hncagpwg2h3d** | HNCAGPWG2H3D)
- 3D HNCA with selective C β /C=O decoupling (**hncadhgp3d**)
- 3D HNCA using TROSY(**trhncagp3d2.2** | TRHNCAGP3D2.2) :
 - using echo-antiecho gradient (**trhncaetgp3d** | TRHNCAETGP3D)
 - using echo-antiecho gradient and with ^2H -decoupling (**trhncaetgp2h3d** | TRHNCAETGP2H3D)
 - with HMQC steps (**trhncagp3d.2** | TRHNCAGP3D.2)
 - with ^1H -decoupling (**trhncagp3d2** | TRHNCAGP3D2)
 - with ^1H -decoupling and HMQC steps (**trhncagp3d** | TRHNCAGP3D)
 - with ^2H -decoupling and HMQC steps (**trhncagp2h3d** | TRHNCAGP2H3D)
 - with ^2H -decoupling (**trhncagp2h3d2** | TRHNCAGP2H3D2)

Also see:

3D APSY-HNCA experiment:

Reduced-Dimensionality (3,2)-HNCA (**rd_hnca_32** | APSY_HNCA_32)

3D SOFAST/BEST-HNCO experiments:

3D BEST-HNCA (**b_hncagp3d** | B_HNCAGP3D)

3D BEST-HNCA using TROSY (**b_trhncagp3d**)

3D HNCA-type experiments for J measurements

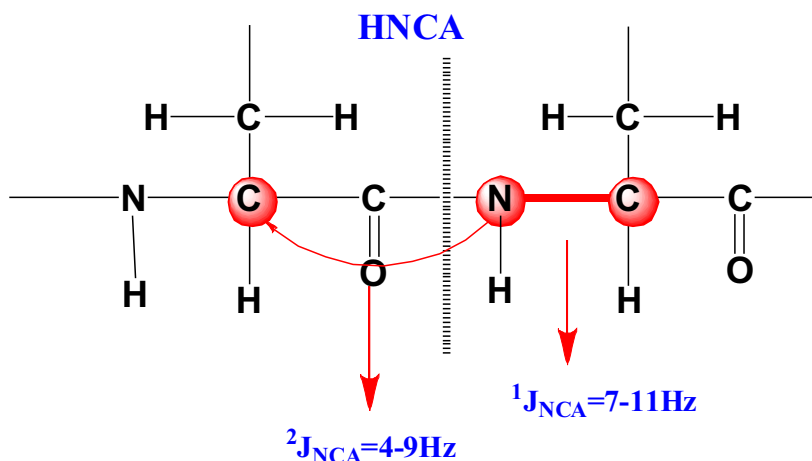
3D HNCA-type experiments for RDC measurements

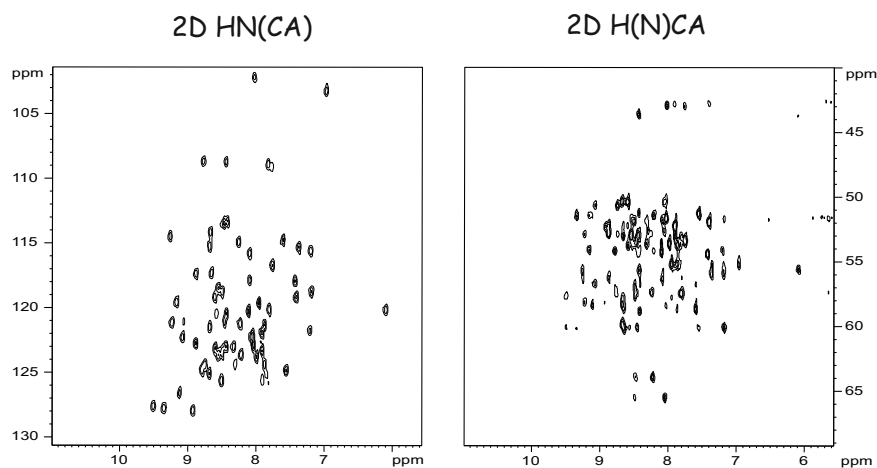
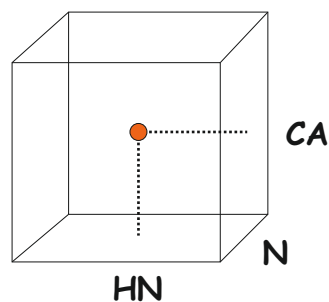
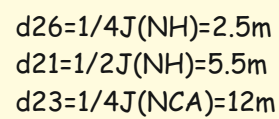
3D Carbon-Detected HNCA experiments

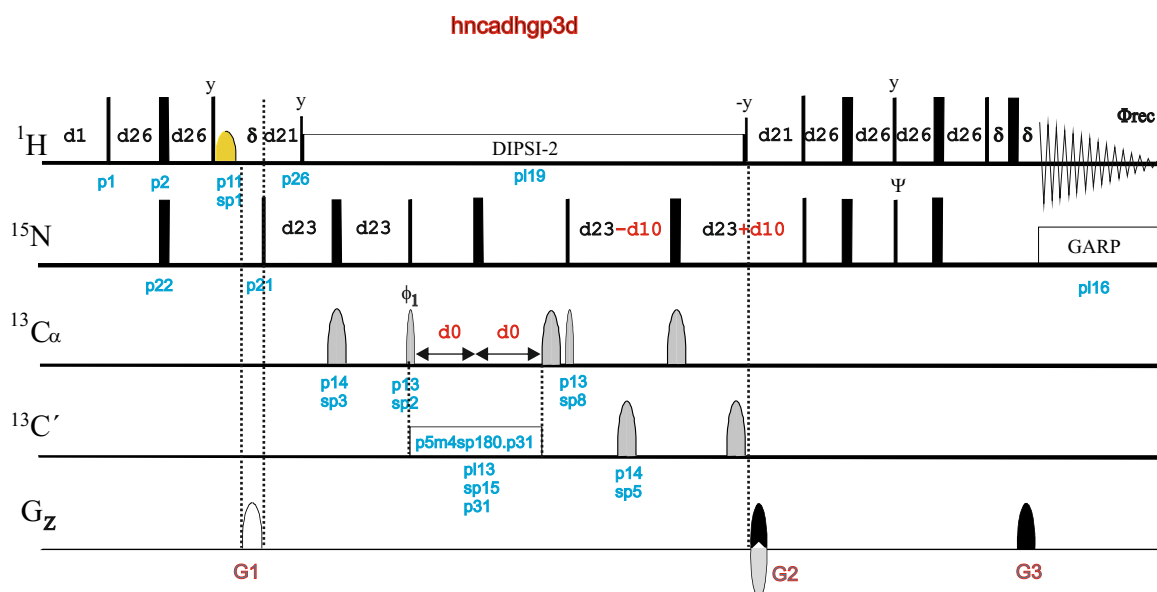
Related Experiments:

intra-HNCA, sequential-HNCA, HN(CO)CA

In all experiments involving a N-CA transfer, two complementary pathways are involved:

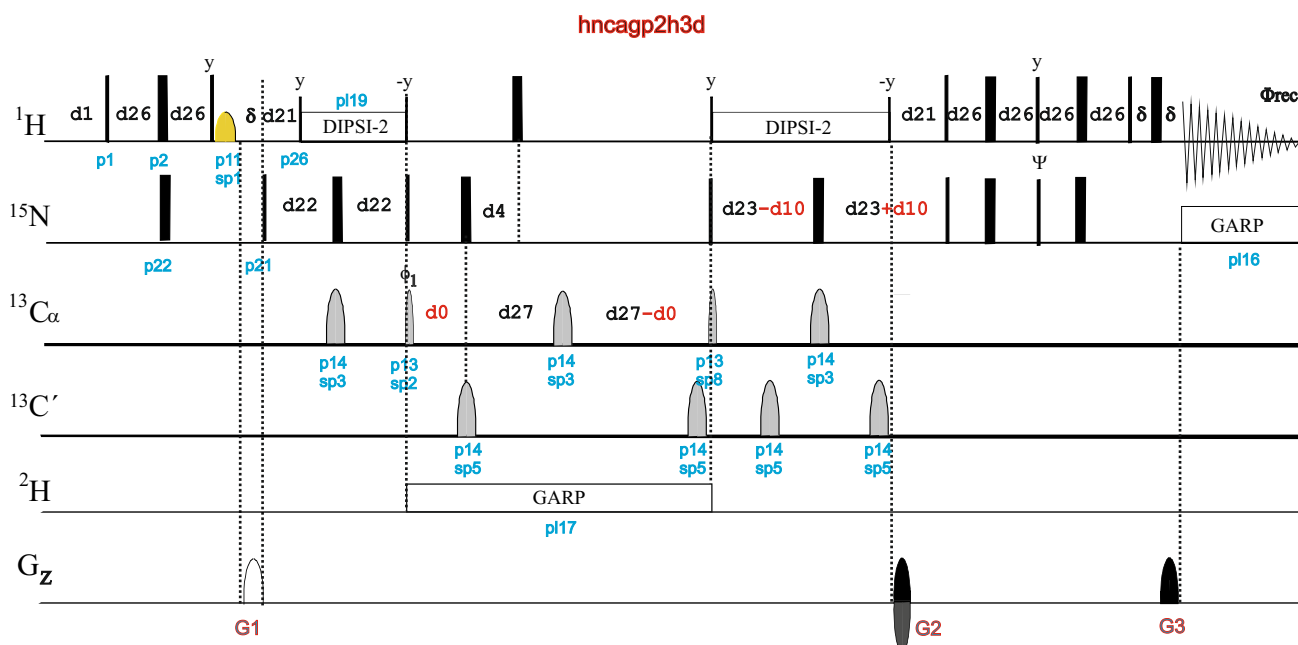


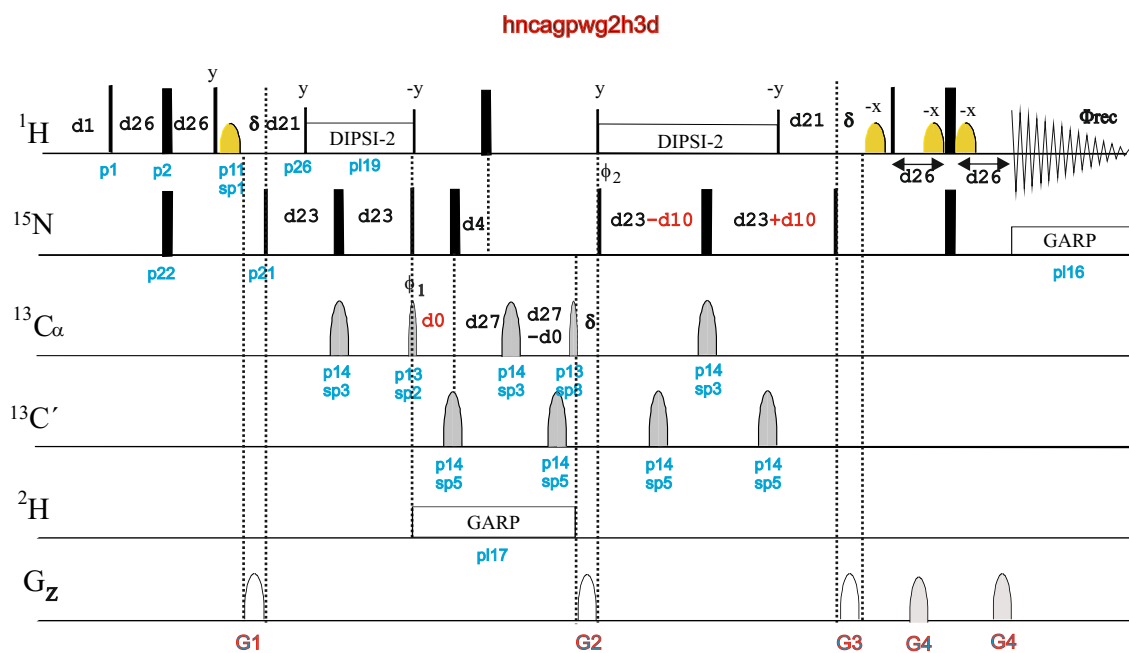
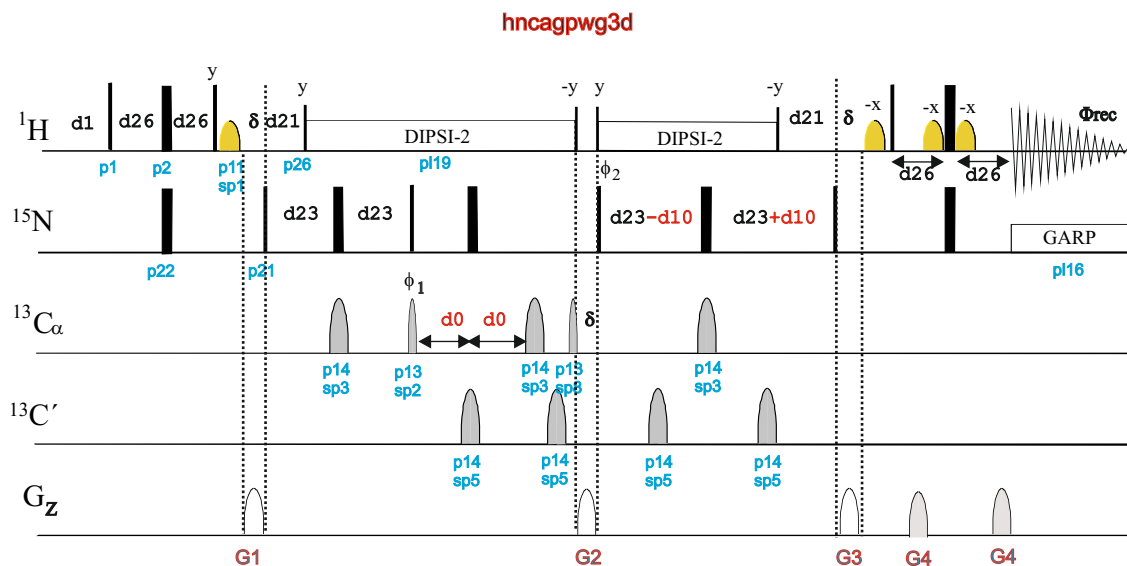




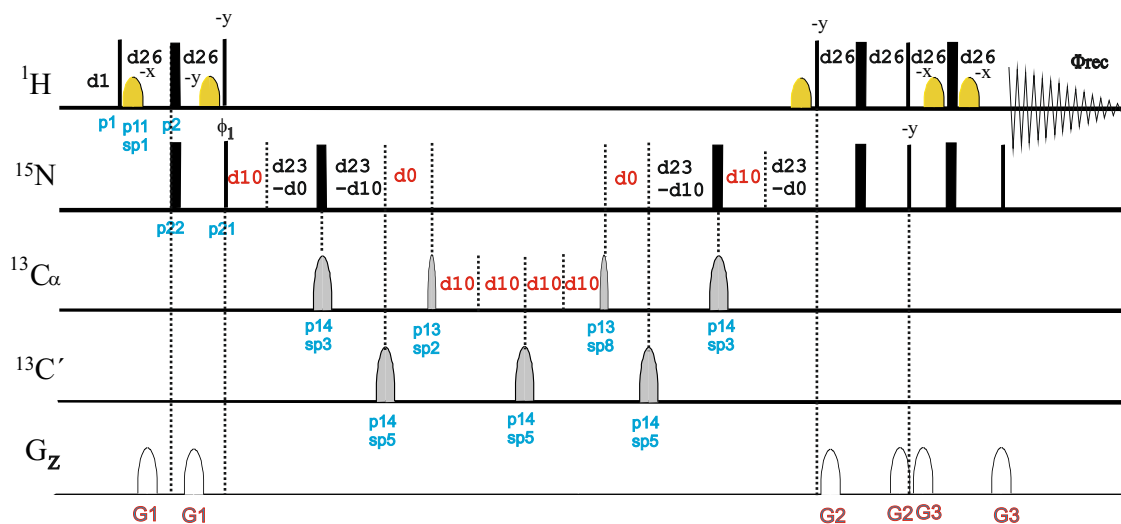
Selective CB/CO Decoupling:

H. Matsuo, E. Kupce, H. Li & G. Wagner, J. Magn. Reson. B 113, 91-96 (1996)

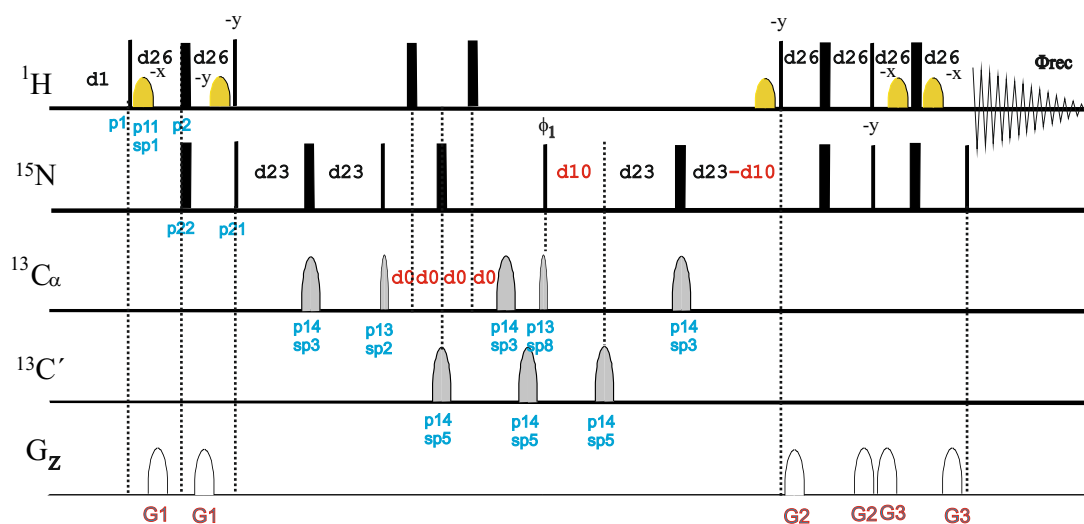


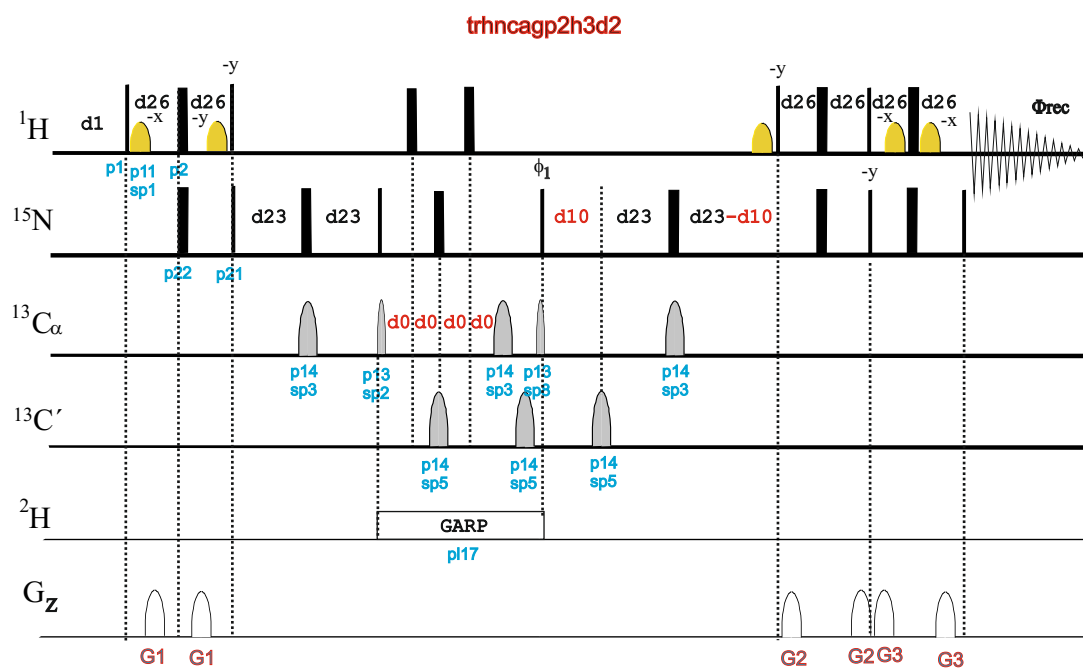
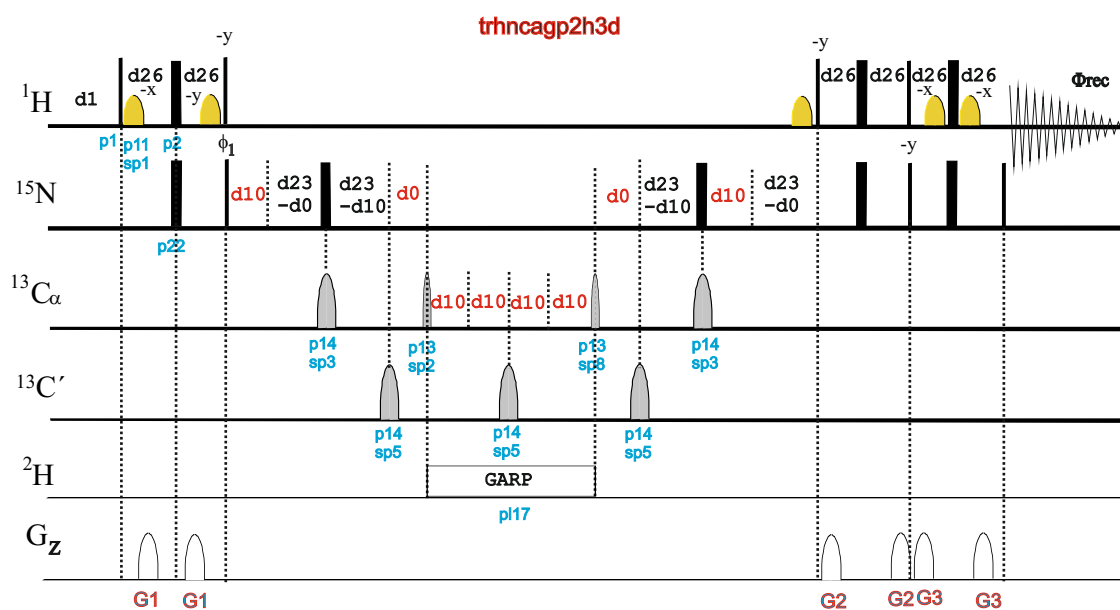


trhncagp3d

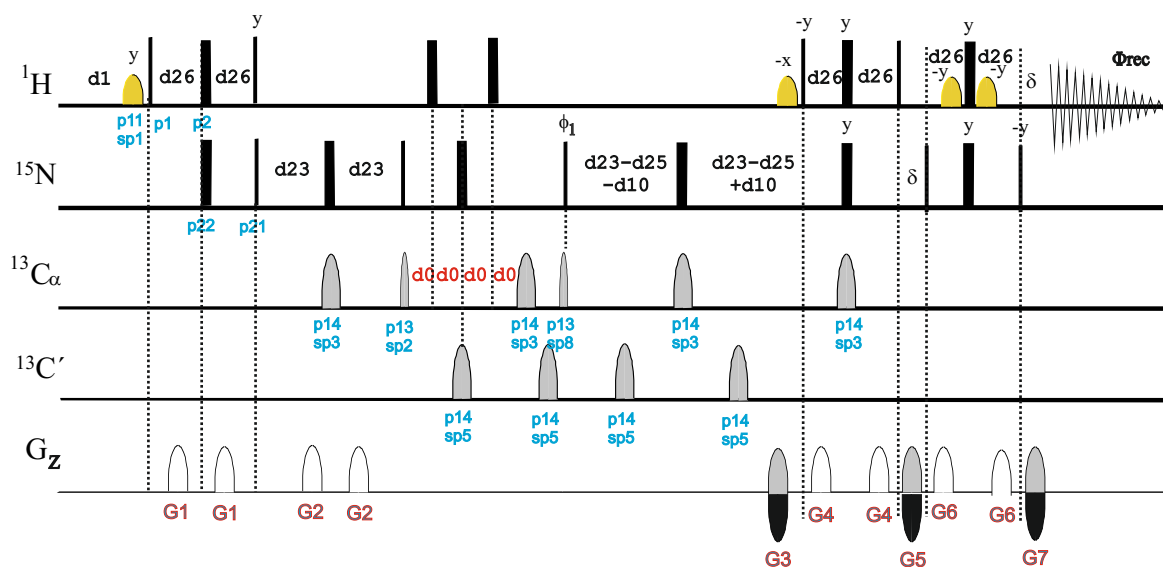


trhncagp3d2

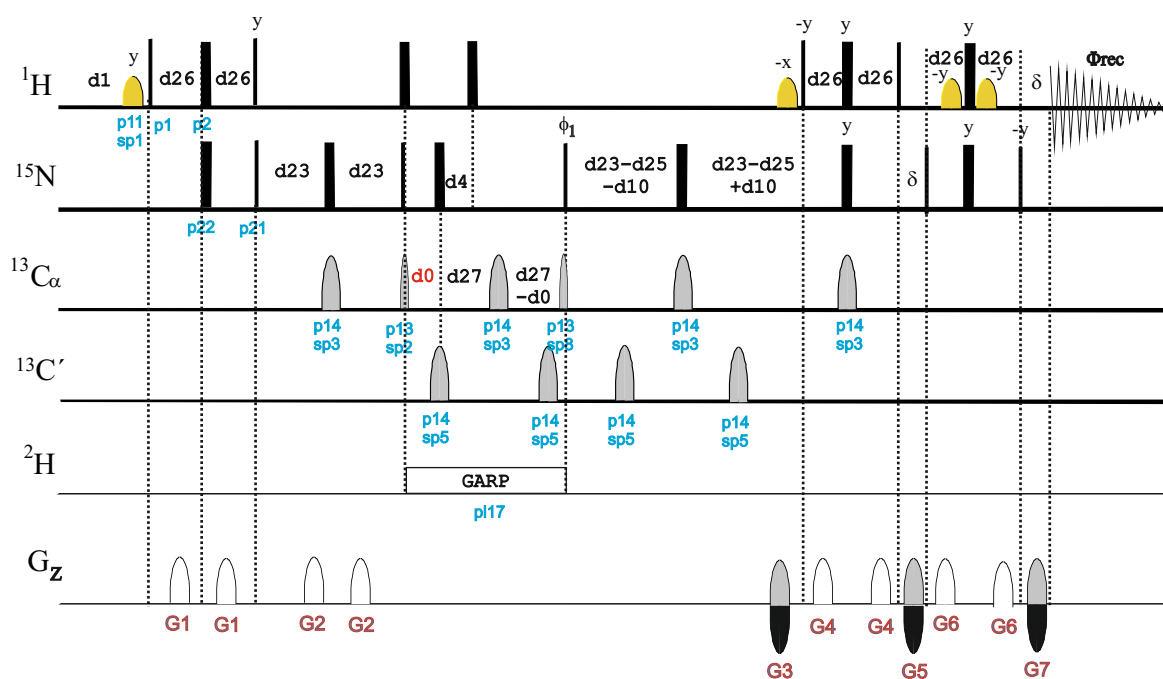




trhncaetgp3d



trhncaetgp2h3d



BRUKER PULSE PROGRAM CATALOGUE

NMRGuide

3D HN(CA)CO

HNCACO Experiment

3D HN(CA)CO experiment

- 3D HN(CA)CO using PEP (**hncacogp3d** | HNCACOGP3D)
 - with ^2H -decoupling and suppression of protonated carbons (**hncacogp2h3d** | HNCACOGP2H3D)
 - with ^2H -decoupling (**hncacogp2h3d.2** | HNCACOGP2H3D.2)
- 3D HN(CA)CO using WATERGATE (**hncacogpwg3d** | HNCACOGPWG3D)
 - with ^2H -decoupling and suppression of protonated carbons (**hncacogpwg2h3d** | HNCACOGPWG2H3D)
- 3D HN(CA)CO using TROSY (**trhncacogp3d** | TRHNCACOGP3D)
 - with ^2H -decoupling (**trhncacogp2h3d** | TRHNCACOGP2H3D)
 - using echo-antiecho gradient (**trhncacoetgp3d** | TRHNCACOETGP3D)
 - using echo-antiecho gradient and with ^2H -decoupling (**trhncacoetgp2h3d** | TRHNCACOETGP2H3D)

4D HNCACO experiment

- 4D HNCACO using PEP (**hncacogp4d**)
 - with ^2H -decoupling (**hncacogp2h4d**)
- 4D HNCACO using WATERGATE (**hncacogpwg4d**)
 - with ^2H -decoupling (**hncacogpwg2h4d**)
- 4D HNCACO using TROSY (**trhncacogp4d**)
 - with ^2H -decoupling (**trhncacogp2h4d**)
 - using echo-antiecho gradient (**trhncacoetgp4d**)
 - using echo-antiecho gradient and with ^2H -decoupling (**trhncacoetgp2h4d**)

Also see:

3D SOFAST/BEST-HN(CA)CO experiment

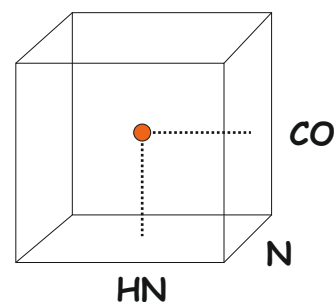
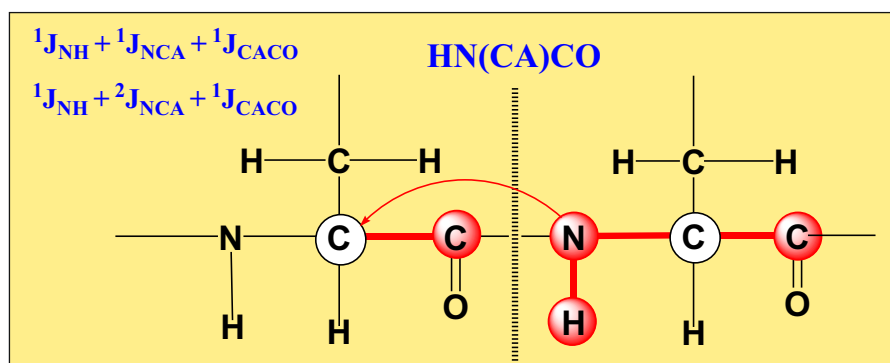
3D BEST-HN(CA)CO (**b_hncacogp3d** | B_HNCACOGP3D)

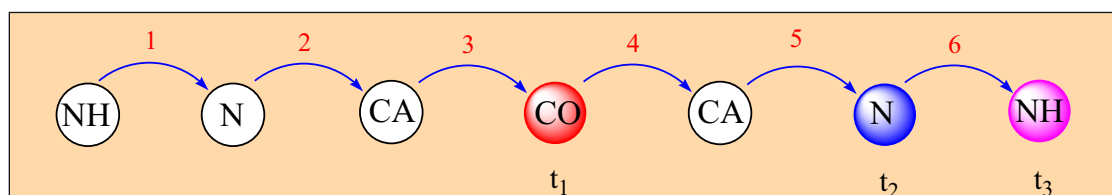
3D BEST-HN(CA)CO using TROSY (**b_trhncacogp3d**)

4D BEST-HNCACO (**b_hncacogp4d**)

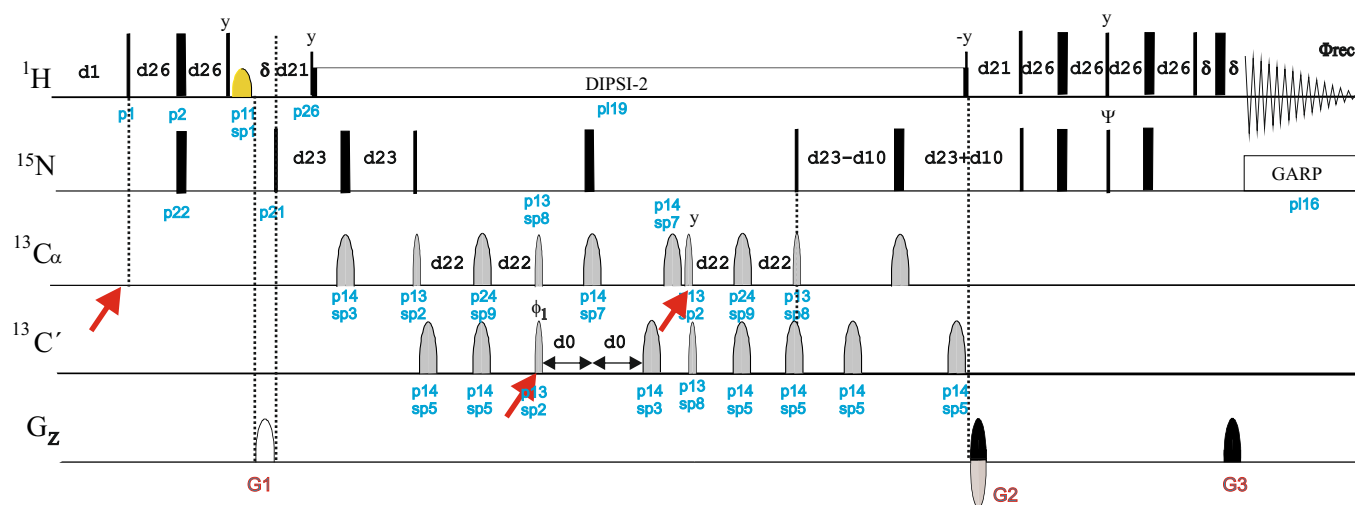
3D CO-Detected (H)NCAACO experiments

Related Experiments:
HNCO Experiment

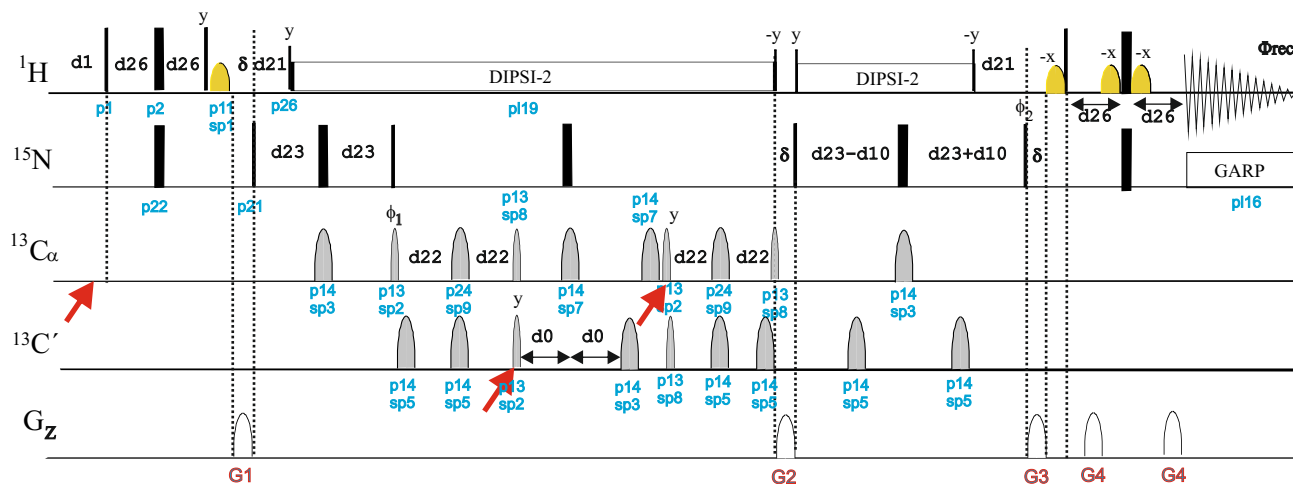




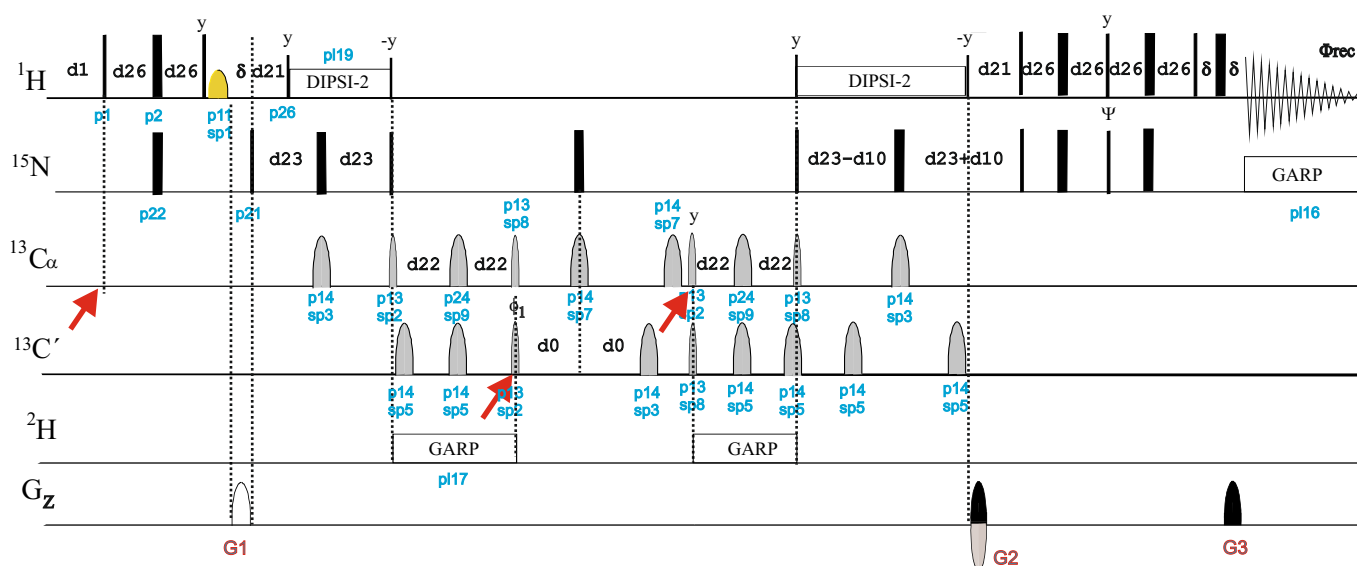
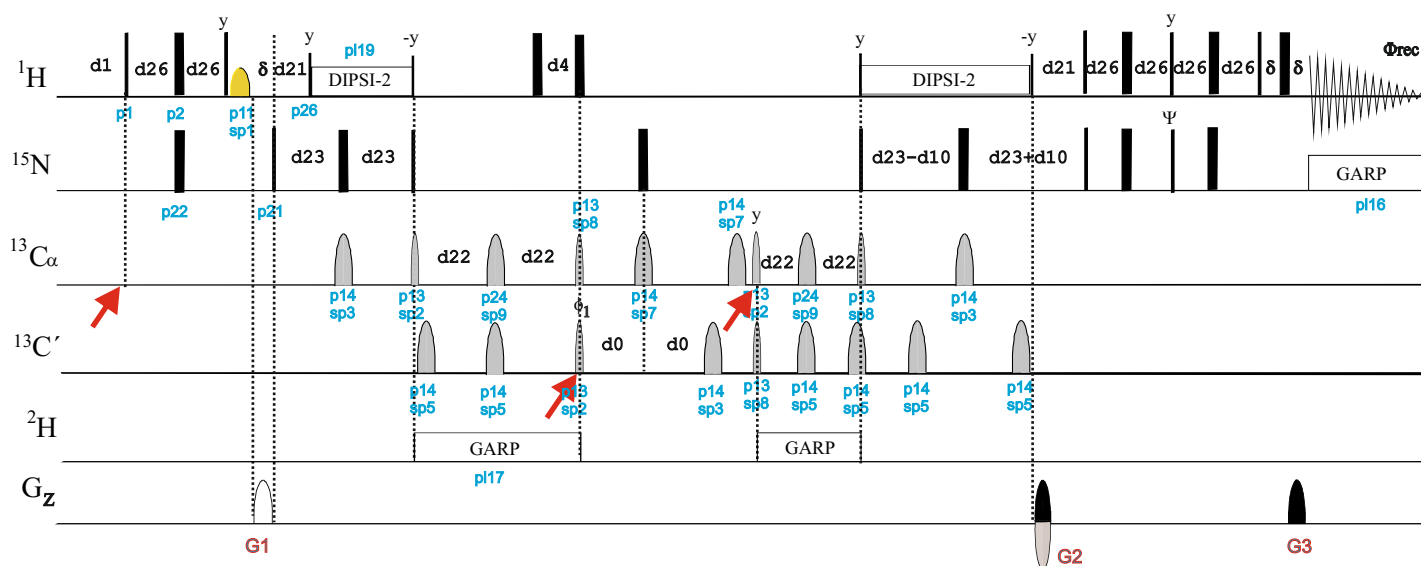
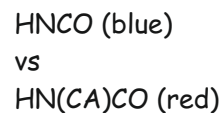
hncacogp3d



hncacogpwp3d



$d26=1/4J(\text{NH})=2.3\text{m}$
 $d21=1/2J(\text{NH})=5.5\text{m}$
 $d23=1/4J(\text{NCO})=12\text{m}$
 $d22=1/4J(\text{COCA})=4\text{m}$
 $d4=1/4J(\text{CH})=1.7\text{m}$



[illegible][illegible]





[illegible]



[illegible]

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NMRGuide

3D HN(CO)CA

HNCOCA Experiment

3D HN(CO)CA experiment

- 3D HN(CO)CA using PEP (**hncocagp3d** | HNCOCAGP3D)
 - with ^2H -decoupling (**hncocagp2h3d** | HNCOCAGP2H3D)
- 3D HN(CO)CA using WATERGATE (**hncocagpwg3d** | HNCOCAGPWG3D)
 - with ^2H -decoupling (**hncocagpwg2h3d** | HNCOCAGPWG2H3D)
- 3D HN(CO)CA using TROSY (**trhncocagp3d** | TRHNCOCAGP3D):
 - with ^2H -decoupling (**trhncocagp2h3d** | TRHNCOCAGP2H3D)
 - using echo-antiecho gradient (**trhncocaetgp3d** | TRHNCOCAETGP3D)
 - using echo-antiecho gradient and with ^2H -decoupling (**trhncocaetgp2h3d** | TRHNCOCAETGP2H3D)

4D HNCOCA experiment

- 4D HNCOCA using PEP (**hncocagp4d**)
 - with ^2H -decoupling (**hncocagp2h4d**)
- 4D HNCOCA using WATERGATE (**hncocagpwg4d**)
 - with ^2H -decoupling (**hncocagpwg2h4d**)
- 4D HNCOCA using TROSY (**trhncocagp4d**)
 - with ^2H -decoupling (**trhncocagp2h4d**)
 - using echo-antiecho gradient (**trhncocaetgp4d**)
 - using echo-antiecho gradient and with ^2H -decoupling (**trhncocaetgp2h4d**)

Also see:

SOFAST/BEST-HN(CO)CA experiment

3D BEST-HN(CO)CA (**b_hncocagp3d** | B_HNCOCAGP3D)

3D BEST-HN(CO)CA using TROSY (**b_trhncocagp3d**)

4D BEST-HNCOCA (**b_hncocagp4d**)

3D APSY-HNCOCA experiment

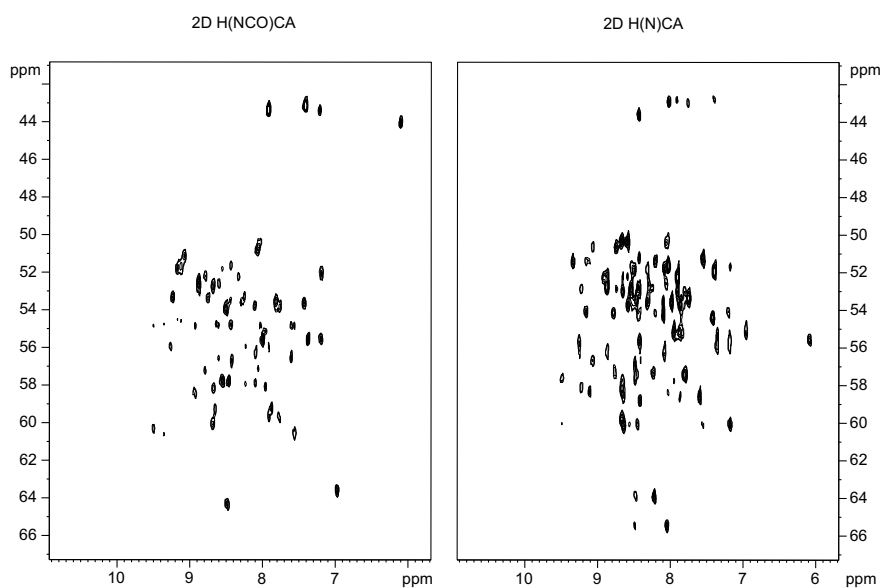
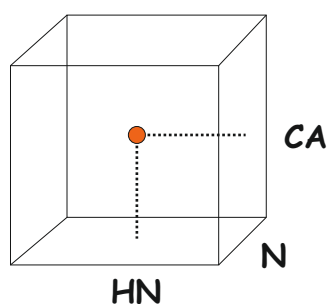
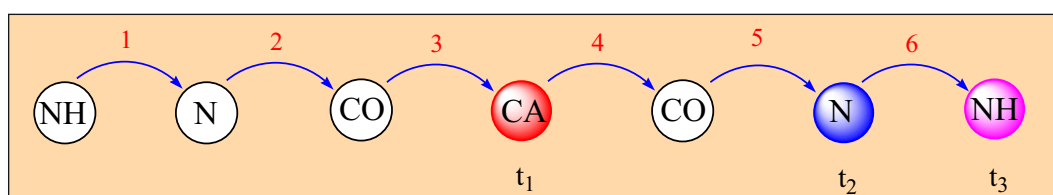
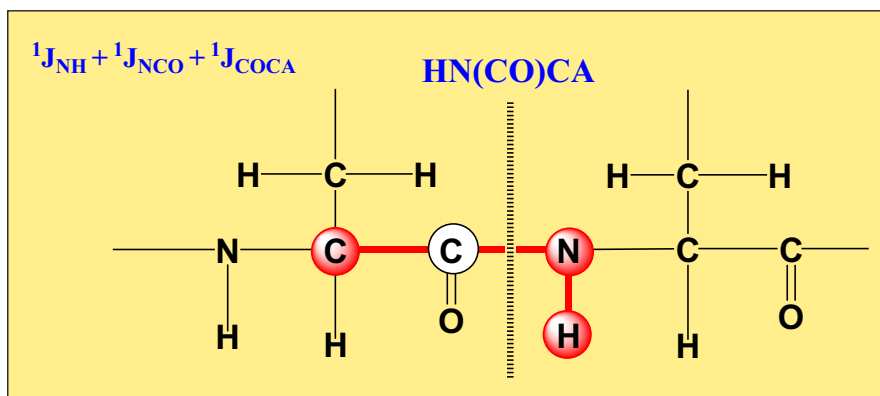
Reduced-Dimensionality (4,2)-HNCOCA (**rd_hncoca_42** | APSY_HNCOCA_42)

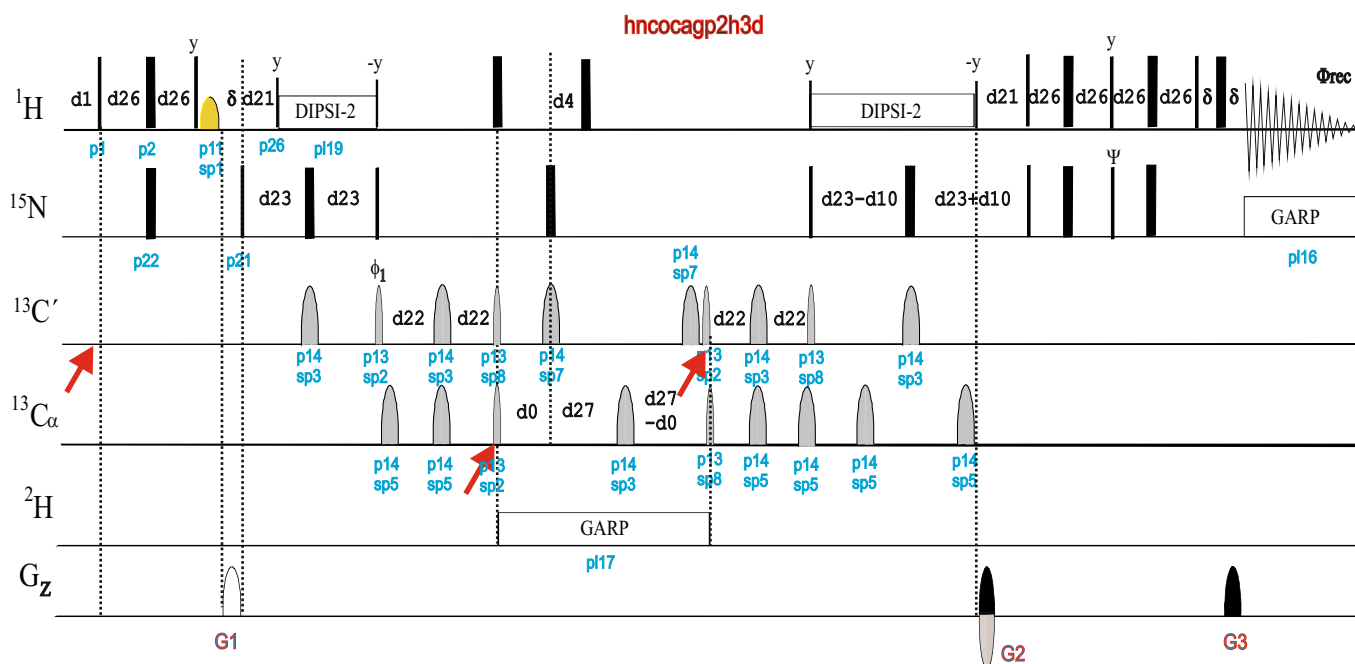
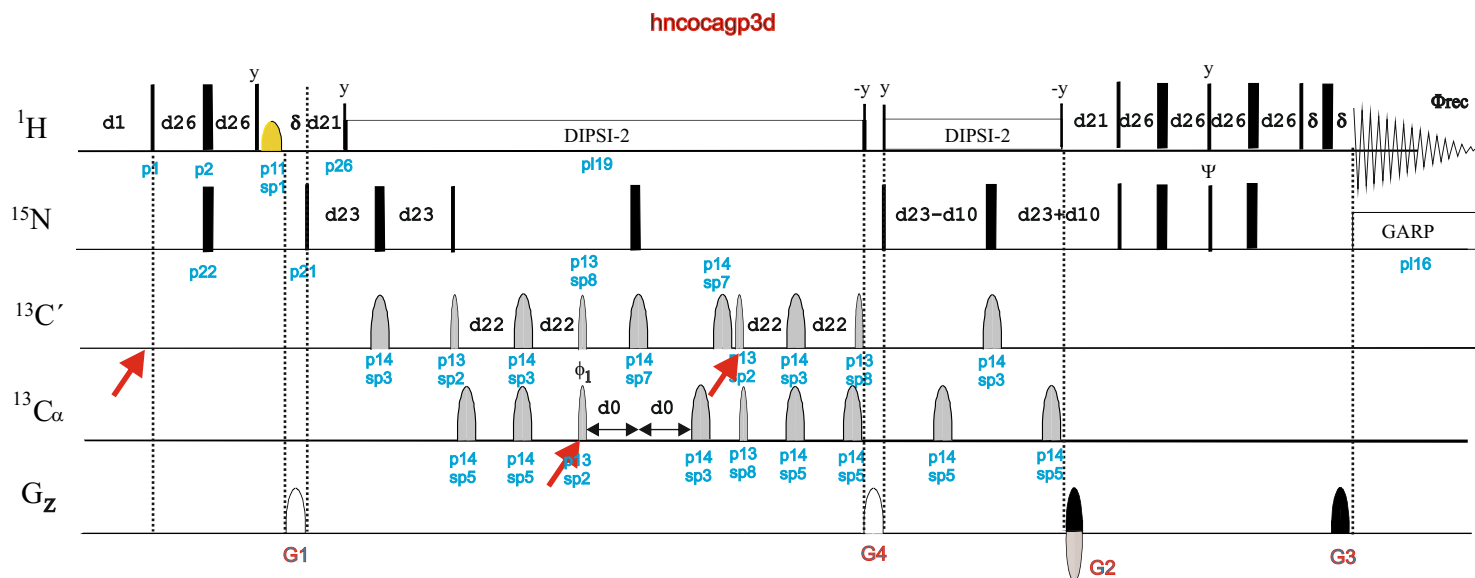
3D (H)NCOCA in "Carbon-Detected Experiments"

3D HNCO-type experiments for J measuring

Related Experiments:

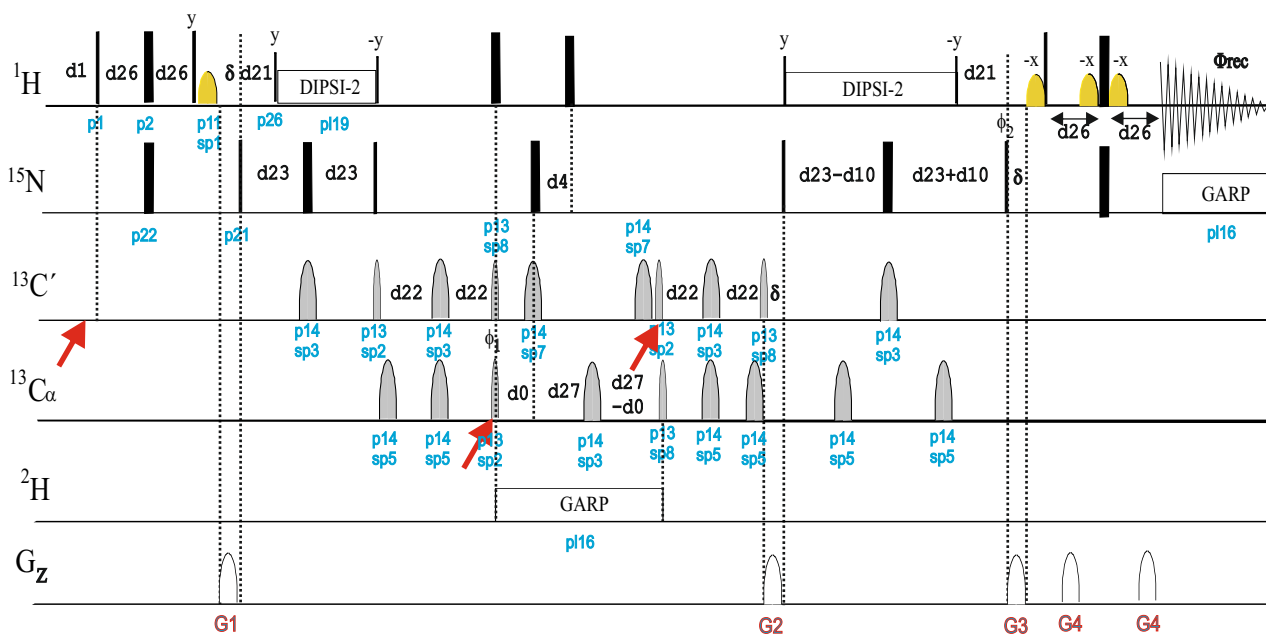
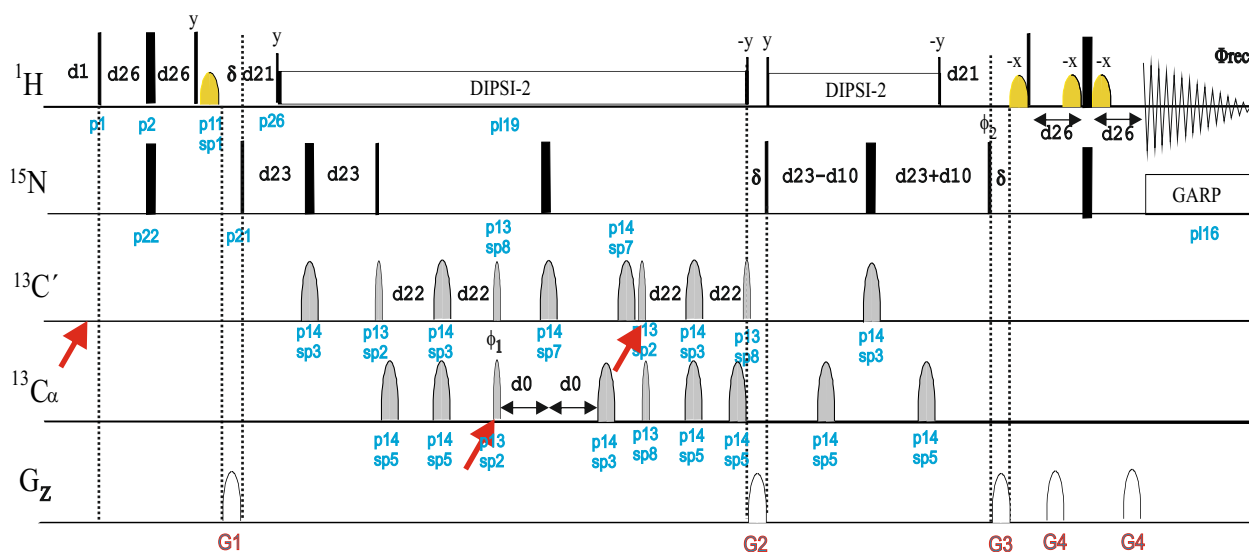
intra-HNCA, HNCA





$d26 = 1/4J(NH) = 2.3m$
 $d21 = 1/2J(NH) = 5.5m$
 $d23 = 1/4J(NCO) = 12m$
 $d22 = 1/4J(COCA) = 4m$

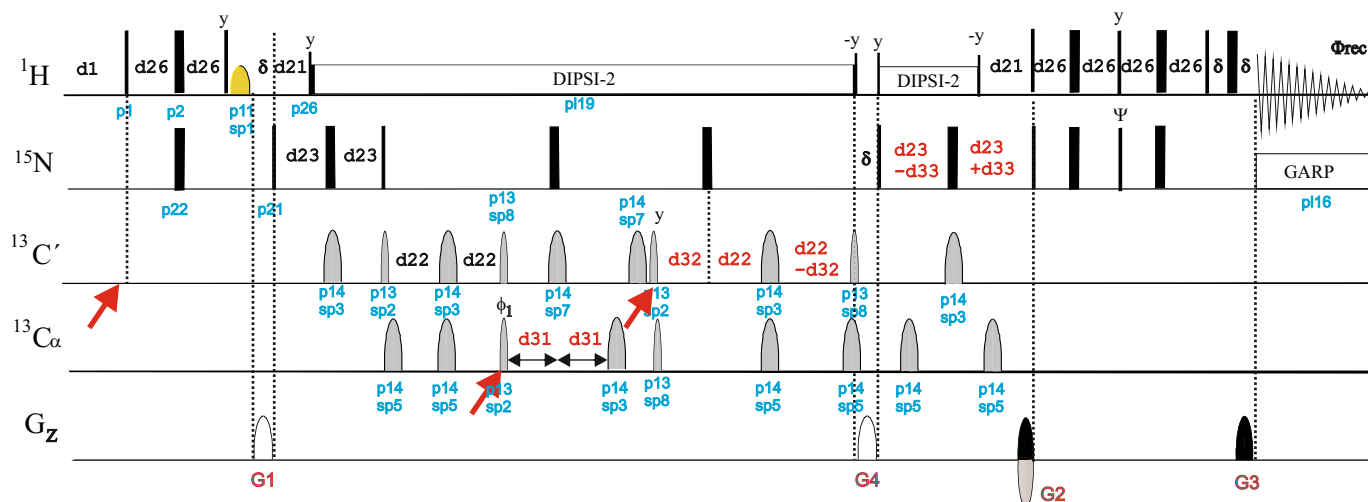
$d27 = CT(CA) = 13.8m$
 $d4 = 1/4J(CH) = 1.7m$



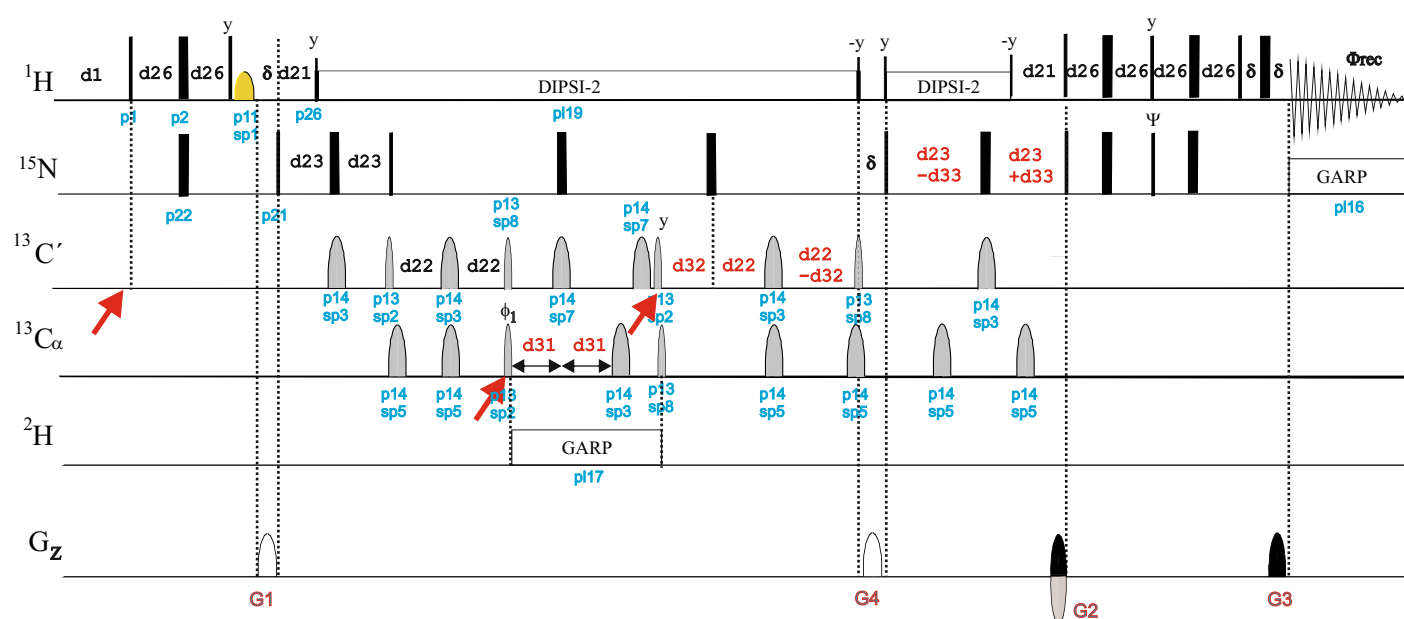


[illegible]

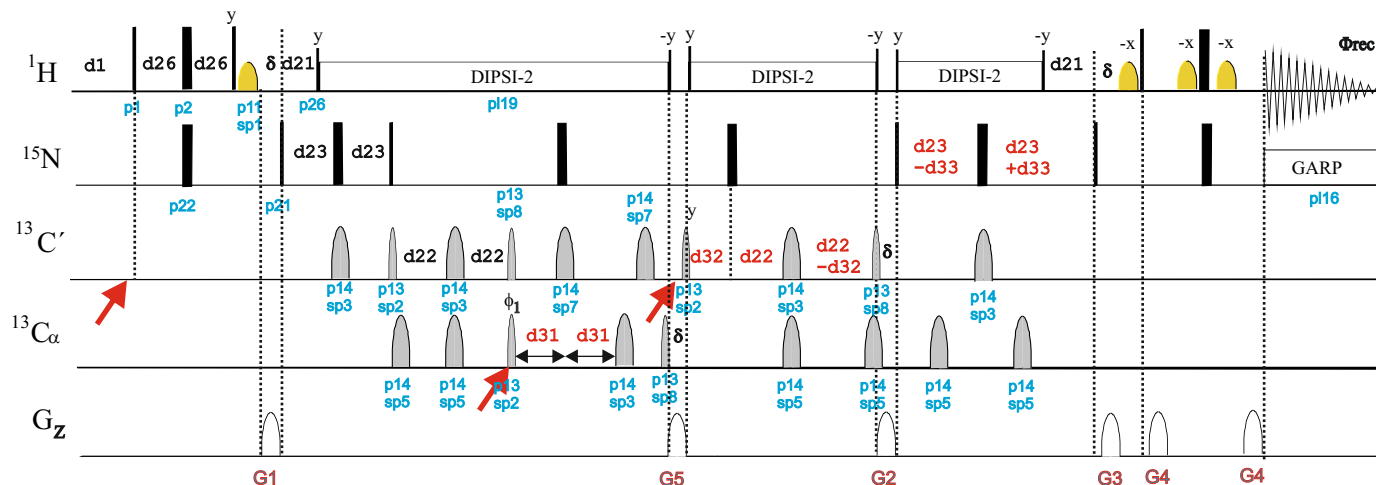
hncocagp4d



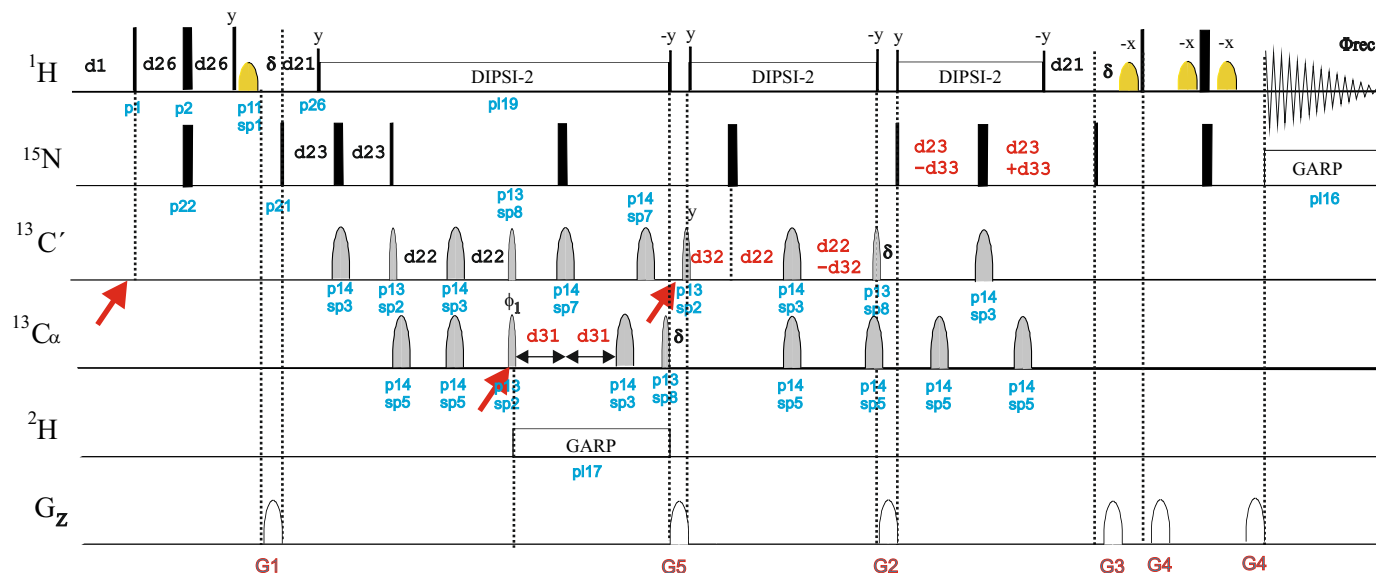
hncocagp2h4d



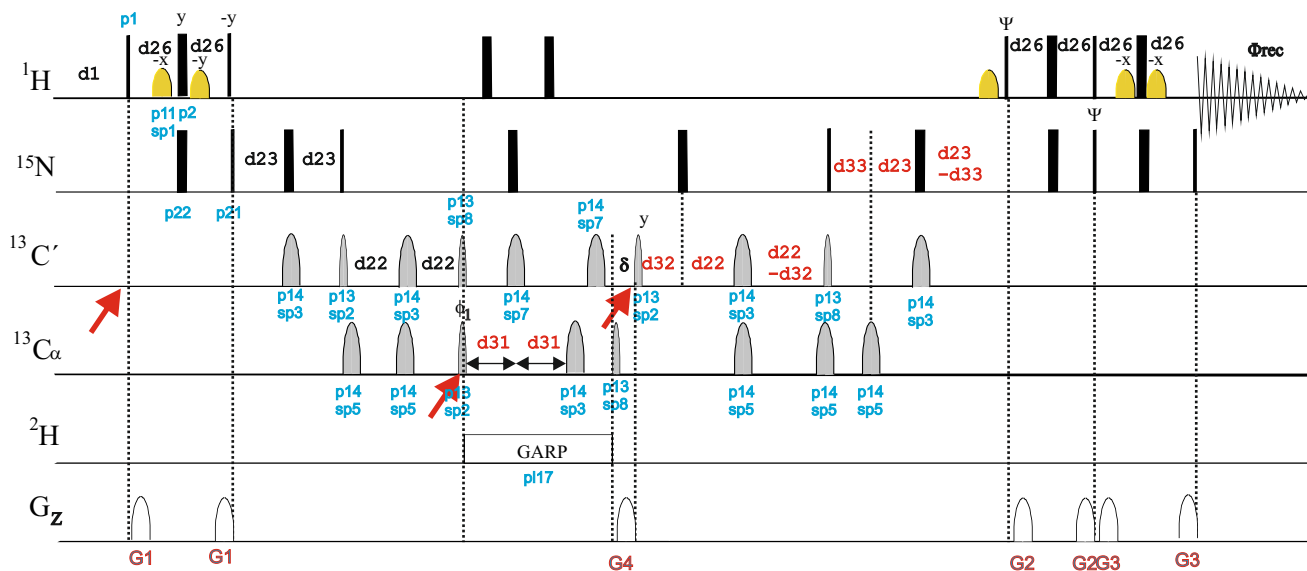
hncocagpwg4d



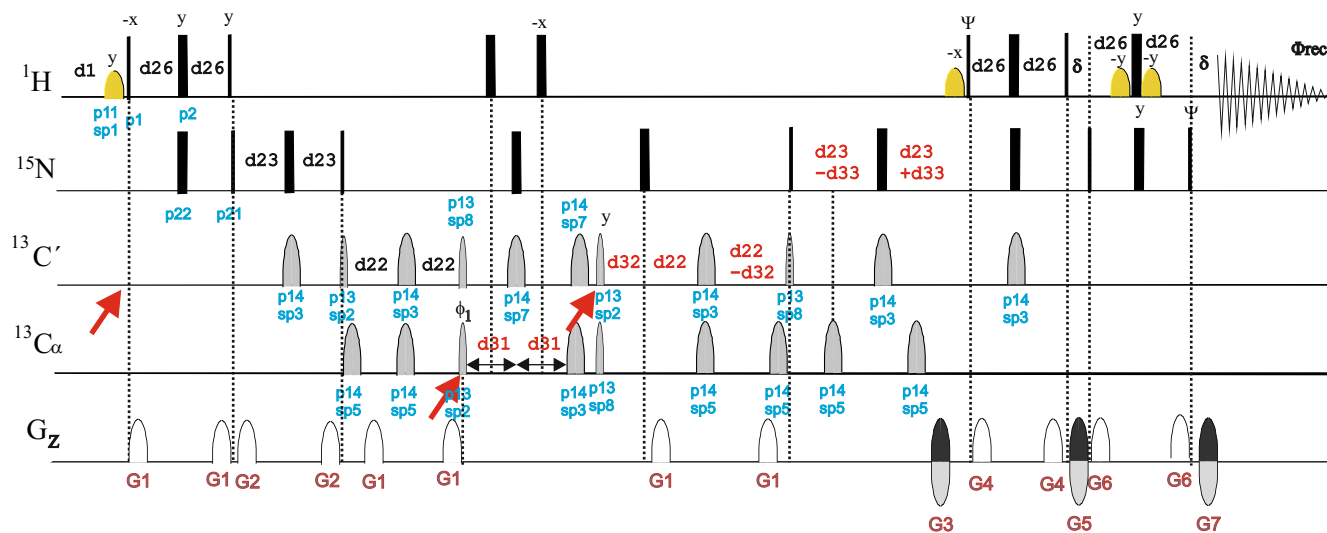
hncocagpwg2h4d



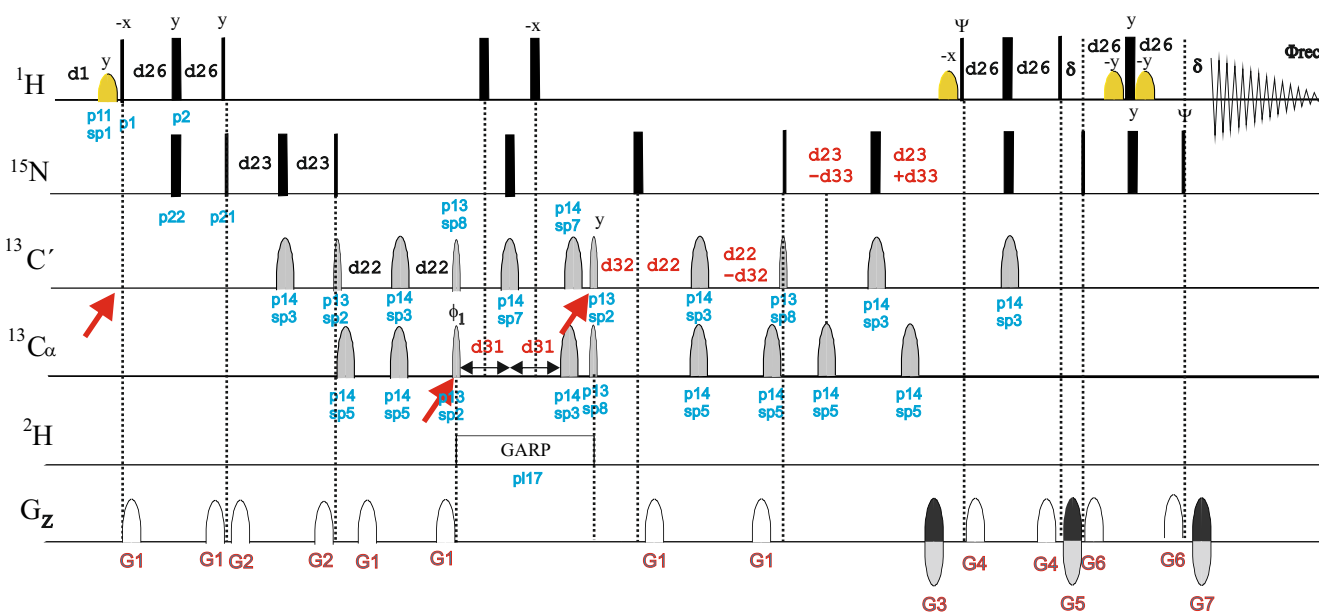
trhncocagp2h4d



trhncocaetgp4d



trhncocaetgp2h4d



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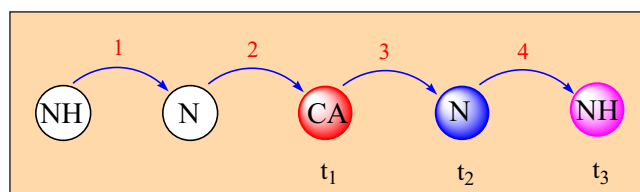
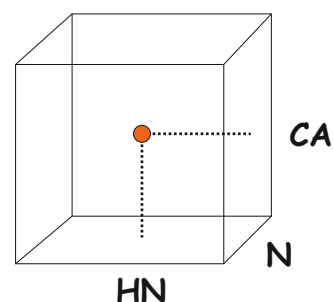
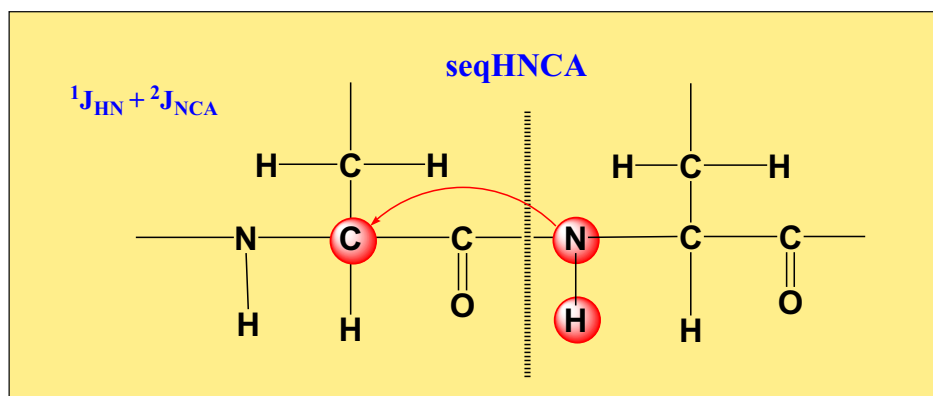
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3D SEQUENTIAL HNCA

3D sequential-HNCA experiment

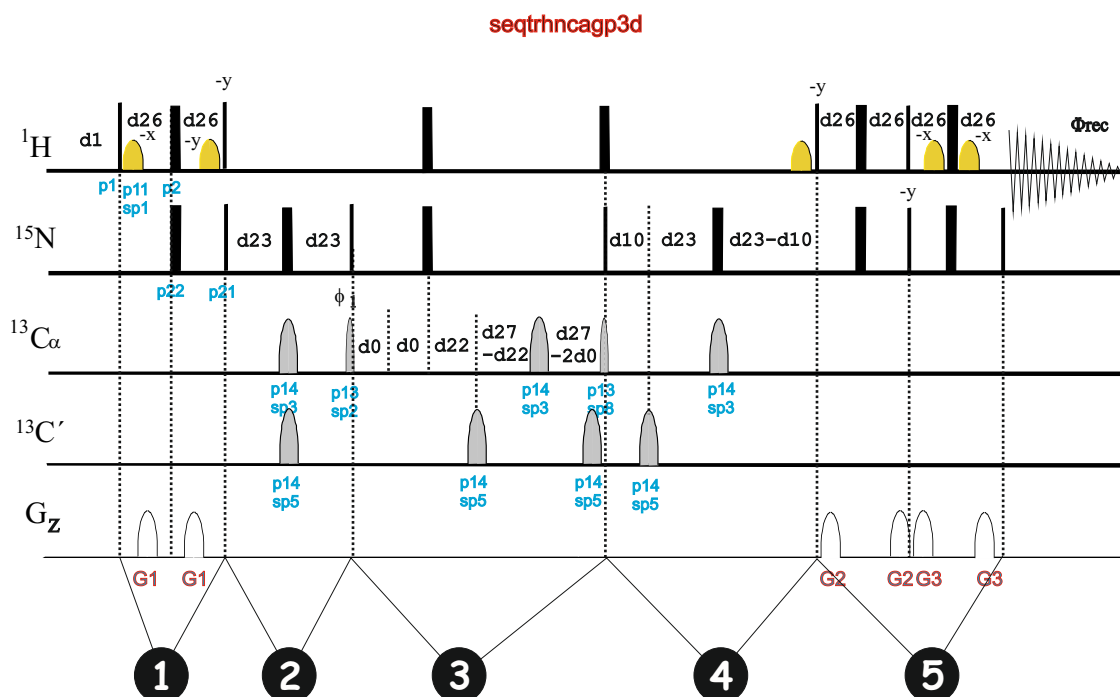
- 3D Sequential HNCA using TROSY (`seqtrhncagp3d` | `SEQTRHNCAGP3D`)
 - with ^2H -decoupling (`seqtrhncagp2h3d` | `SEQTRHNCAGP2H3D`)
 - with gradient echo-antiecho (`seqtrhncagtp3d` | `SEQTRHNCAGTGP3D`)
 - with gradient echo-antiecho and with ^2H -decoupling (`seqtrhncagtp2h3d` | `SEQTRHNCAGTGP2H3D`)

Also see: HNCA, intra-HNCA, HN(CO)CA



$$\begin{aligned} d26 &= 1/4J(\text{NH}) = 2.3\text{m} \\ d23 &= 1/4J(\text{NCA}) = 12\text{m} \\ d22 &= 1/4J(\text{CACO}) = 4.5\text{m} \\ d27 &= 1/4J(\text{CACB}) = 13.3\text{m} \\ d25 &= 1/4J(\text{NH}) = 2.3\text{m} \end{aligned}$$

Identification of evolution elements



1

^1H - ^{15}N INEPT transfer

Concatenated Fixed period consisting of:

2

J(NH) evolution

INEPT ^{15}N -CA

INEPT ^{15}N -CO

Concatenated Constant-time CA evolution period consisting of:

3

$\delta(\text{CA})$ evolution and J(CA-N) decoupling

$\delta(\text{CA})$ evolution and J(CA-H) decoupling

$\delta(\text{CA})$ evolution and J(CA-CO) refocusing

Concatenated Constant-time ^{15}N evolution period consisting of:

4

$\delta(\text{N})$ evolution and J(N-H) evolution

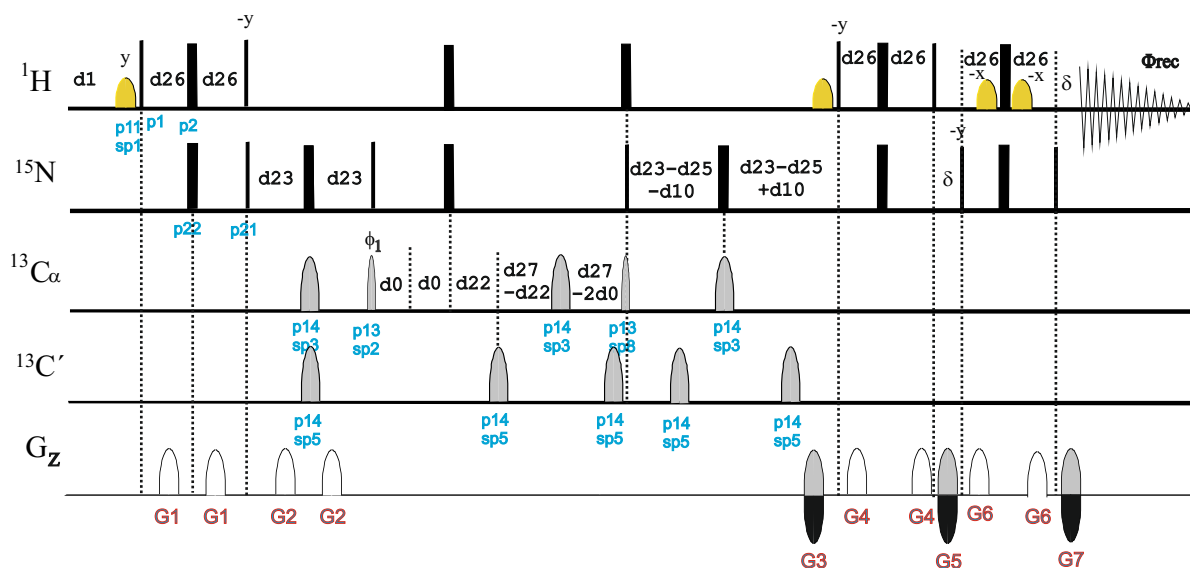
$\delta(\text{N})$ evolution and J(N-CA) refocusing

$\delta(\text{N})$ evolution and J(N-CO) decoupling

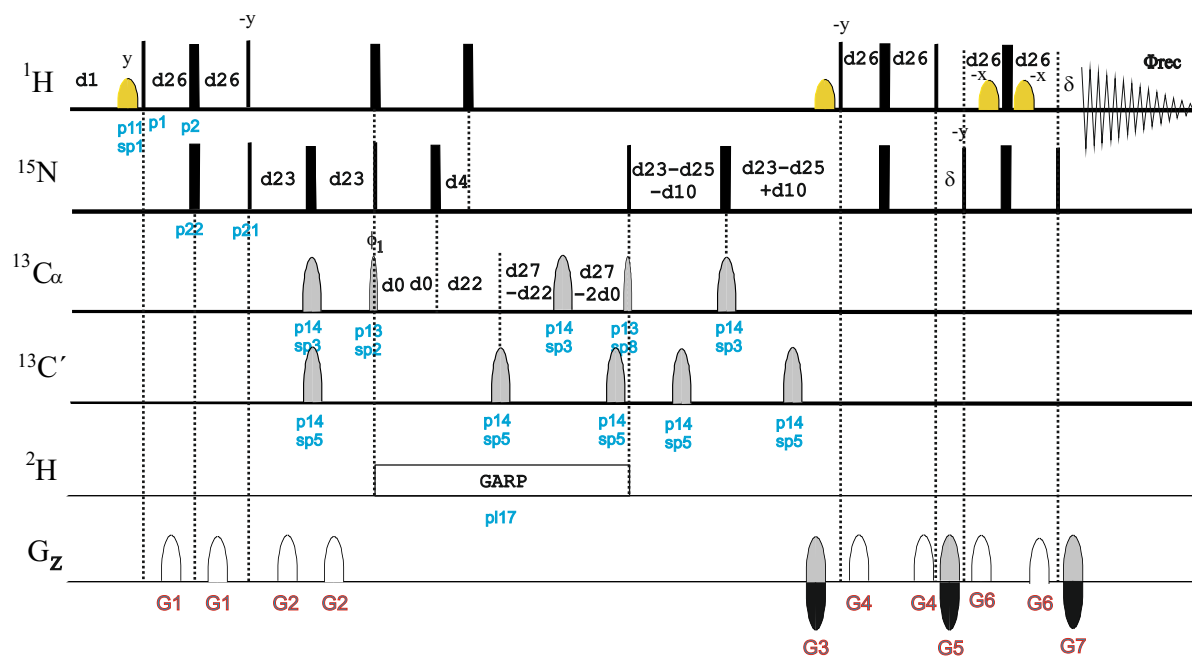
5

^1H - ^{15}N TROSY transfer consisting of two retro-INEPT like blocks

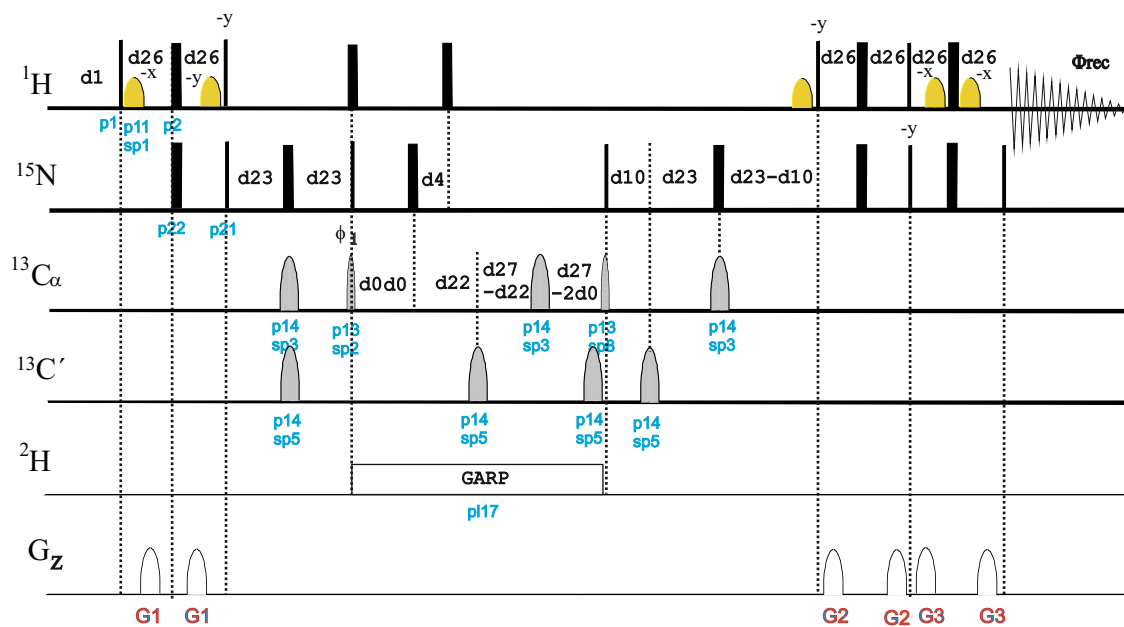
seqtrhncaetgp3d



seqtrhncaetgp2h3d



seqtrhncagp2h3d



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3D INTRA-HNCA

3D intra-HNCA experiment

- 3D Intra-HNCA using PEP (**hncaigp3d** | HNCAIGP3D)
 - with ^2H -decoupling (**hncaigp2h3d** | HNCAIGP2H3D)
- 3D Intra-HNCA using WATERGATE (**hncaigpwg3d** | HNCAIGPWG3D)
 - with ^2H -decoupling (**hncaigpwg2h3d** | HNCAIGPWG2H3D)
- 3D Intra-HNCA using TROSY (**trhncaigp3d** | TRHNCAIGP3D)
 - with ^2H -decoupling (**trhncaigp2h3d** | TRHNCAIGP2H3D)
 - with gradient echo-antiecho (**trhncaietgp3d** | TRHNCAIETGP3D)
 - with gradient echo-antiecho and with ^2H -decoupling (**trhncaietgp2h3d** | TRHNCAIETGP2H3D)

Also see:

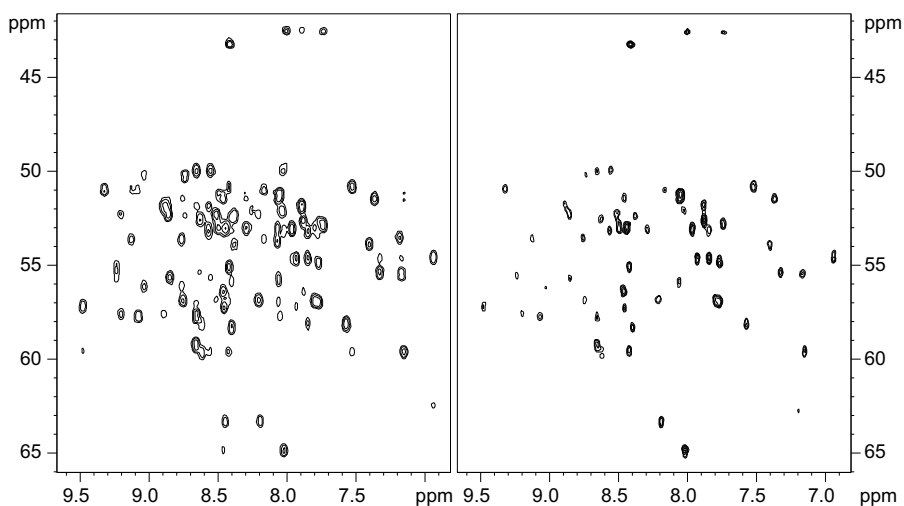
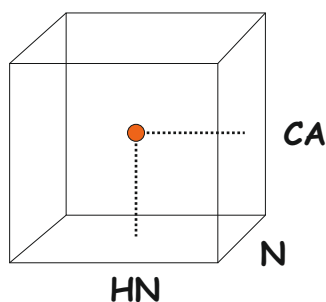
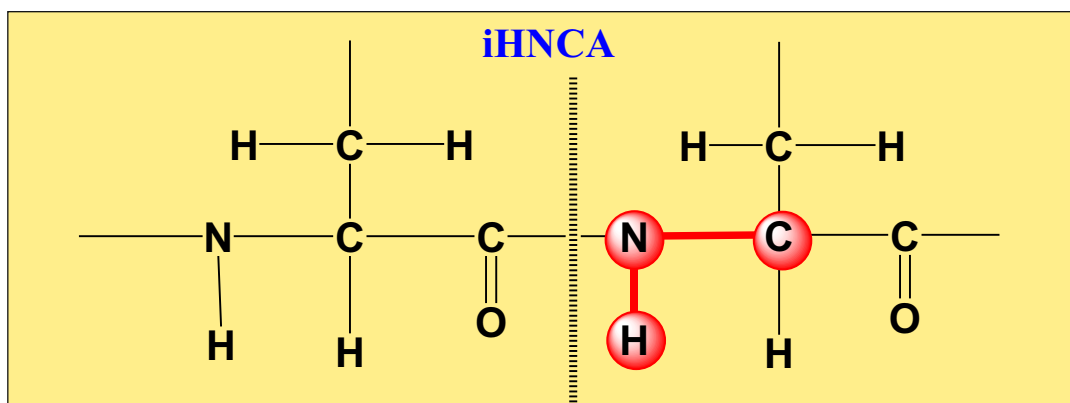
3D SOFAST/BEST-intraHNCA experiment

3D BEST-intraHNCA (**b_hncaigp3d** | B_HNCAIGP3D)

3D BEST-intraHNCA using TROSY (**b_trhncaigp3d**)

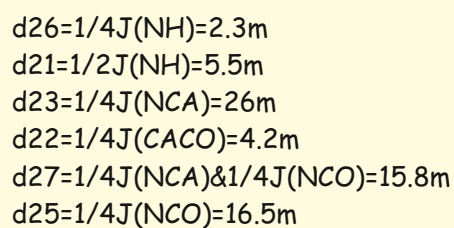
Related Experiments:

seq-HNCA, HNCA, HN(CO)CA

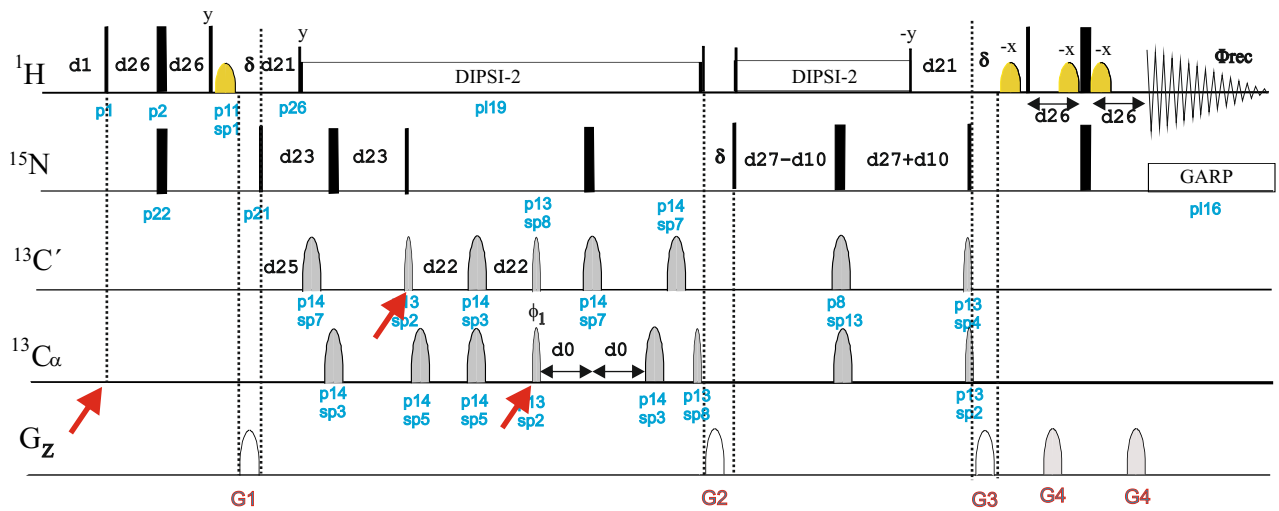


2D H(N)CA

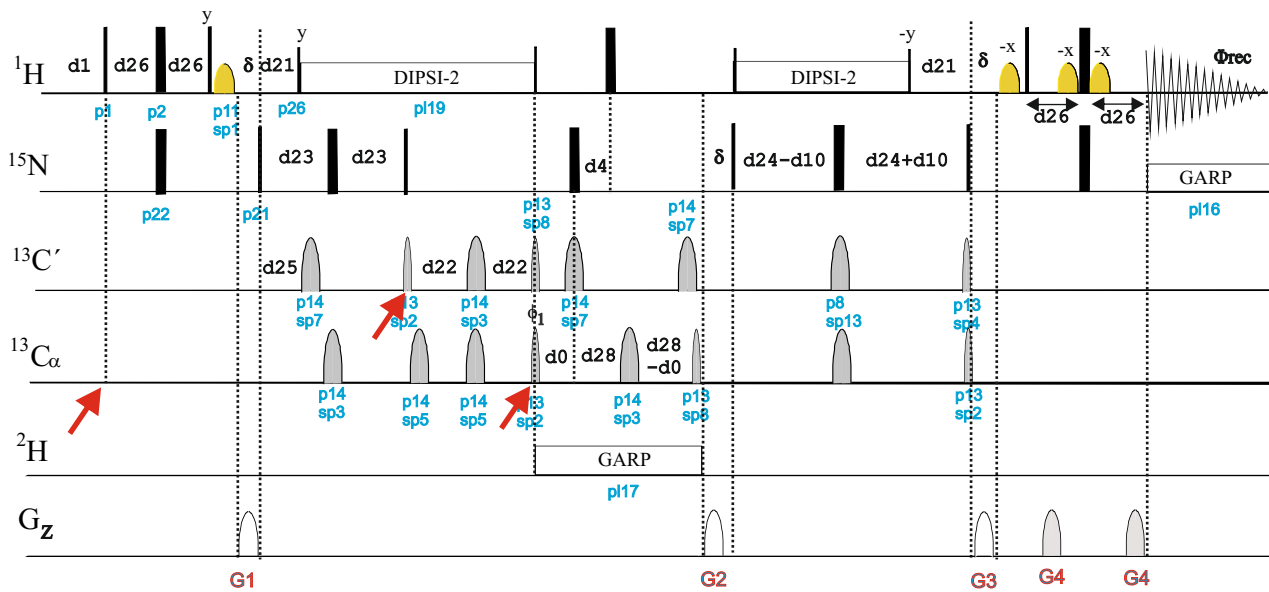
2D intra-H(N)CA



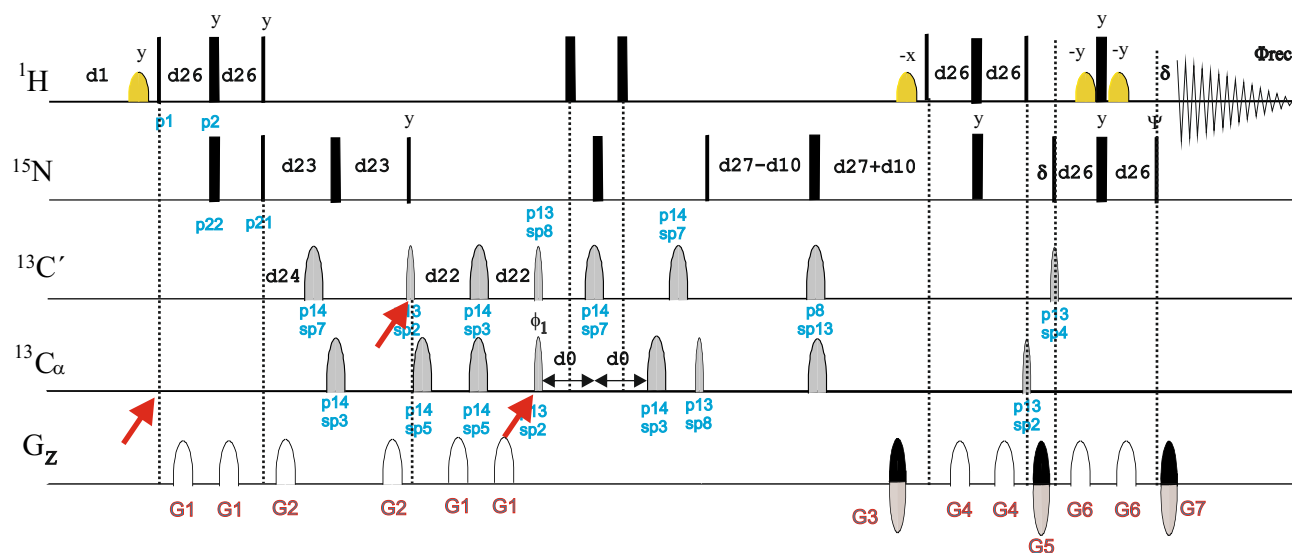
hncaigpwg3d



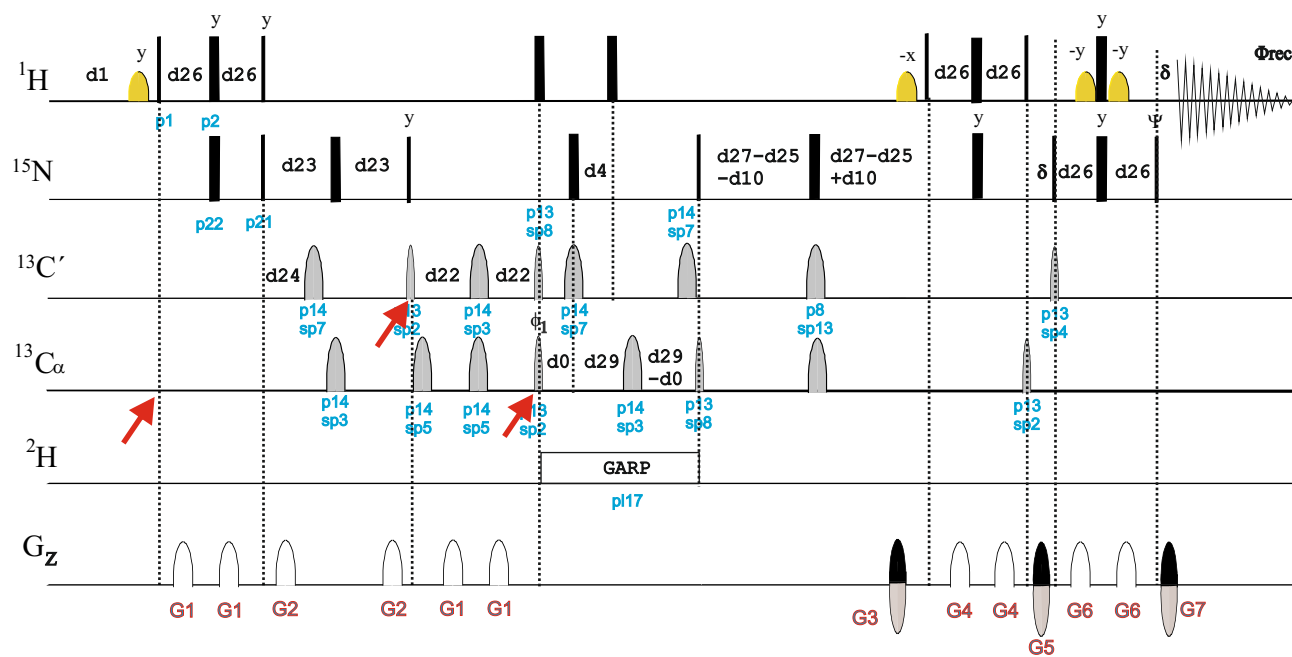
hncaigpwg2h3d

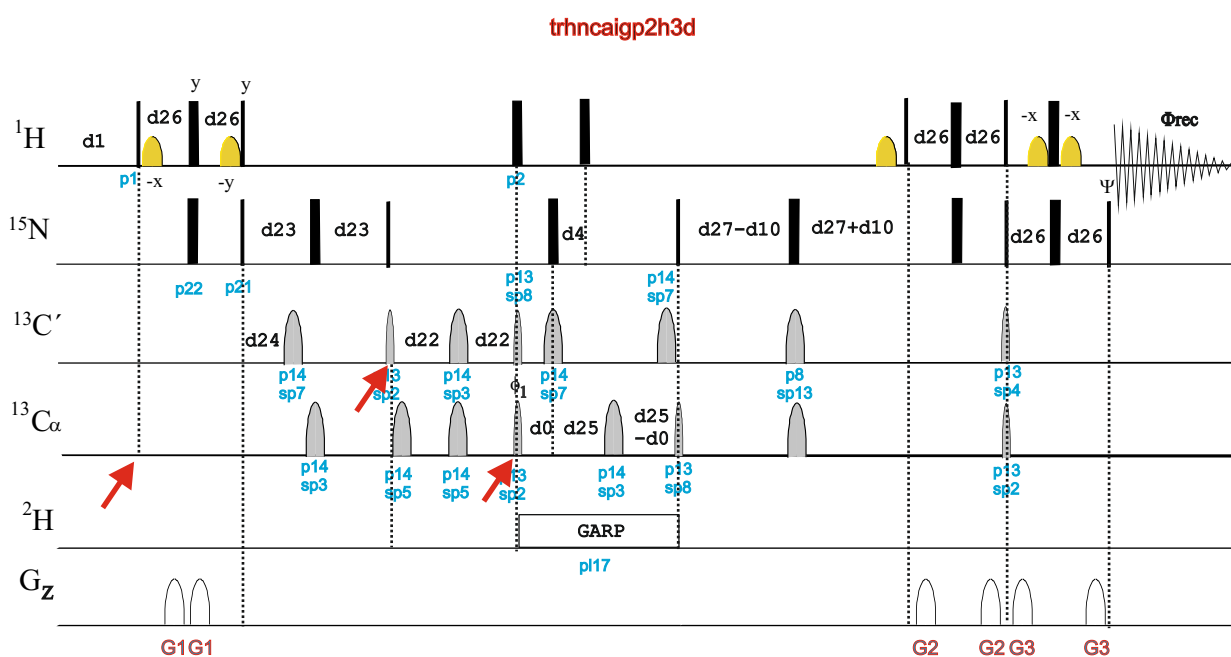
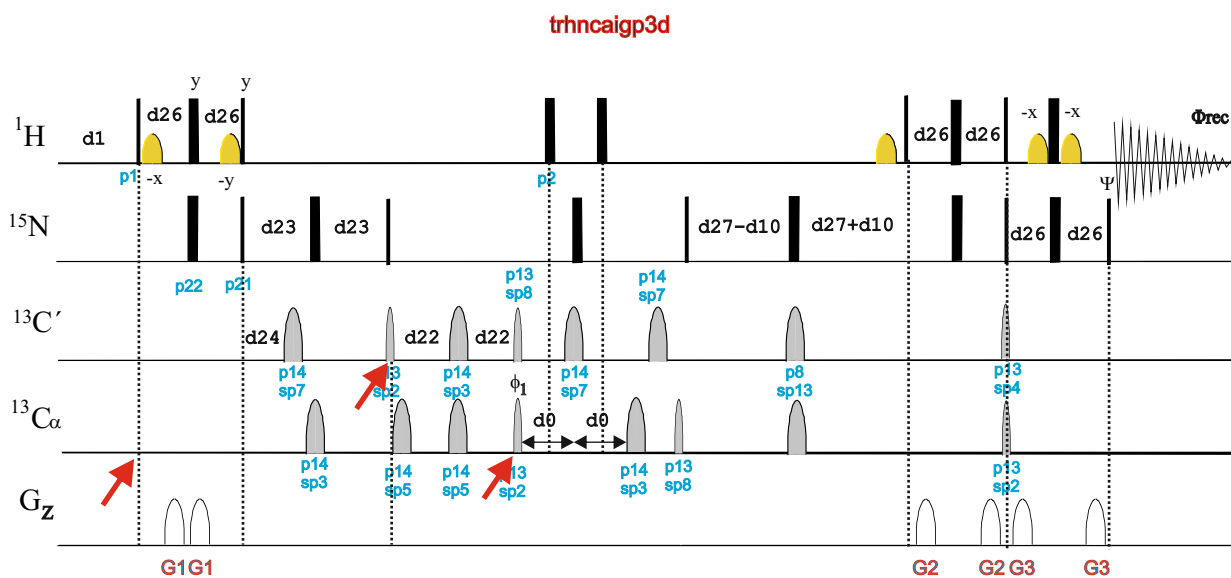


trhncaietgp3d



trhncaietgp2h3d





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3D HNCANNH

HNCANNH Experiment

3D (H)N(CA)NNH experiment

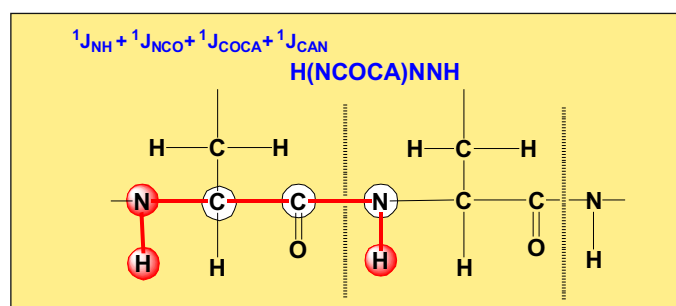
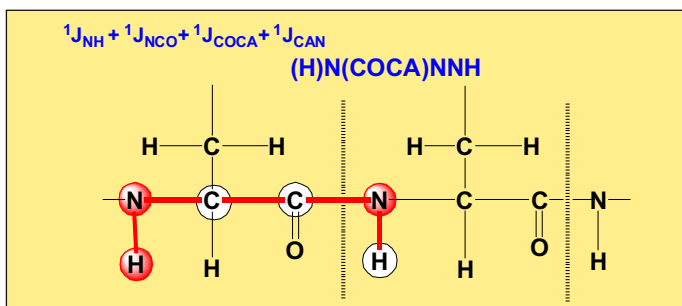
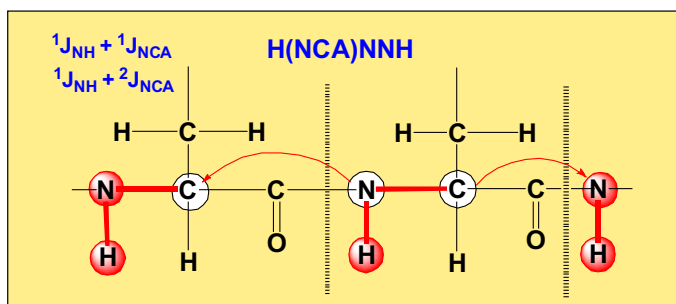
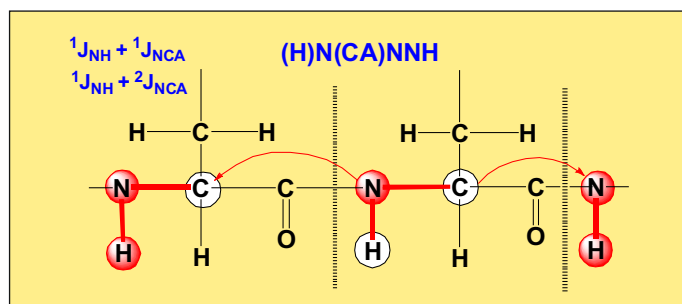
- 3D (H)N(CA)NNH (**hncannhgp3d** | HNCANNHGP3D)
- 3D (H)N(CA)NNH with ^2H -decoupling (**hncannhgp2h3d** | HNCANNHGP2H3D)
- 3D (H)N(CA)NNH using WATERGATE (**hncannhgpwg3d**)
- 3D (H)N(CA)NNH using WATERGATE and ^2H -decoupling (**hncannhgpwg2h3d**)
- 3D (H)N(CA)NNH using TROSY (**trhncannhgp3d**)
- 3D (H)N(CA)NNH using TROSY and ^2H -decoupling (**trhncannhgp2h3d**)
- 3D (H)N(CA)NNH using TROSY and echo-antiecho (**trhncannhetgp3d**)
- 3D (H)N(CA)NNH using TROSY, echo-antiecho and ^2H -decoupling (**trhncannhetgp2h3d**)

3D H(NCA)NNH experiment

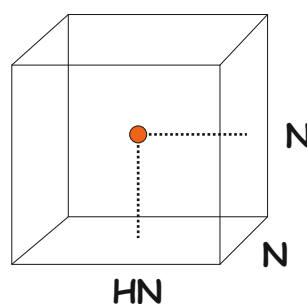
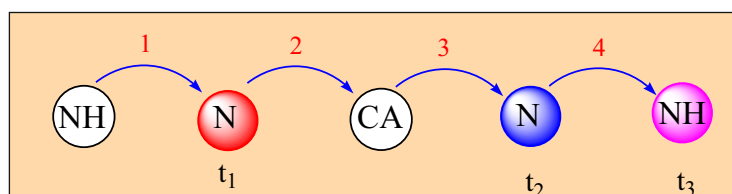
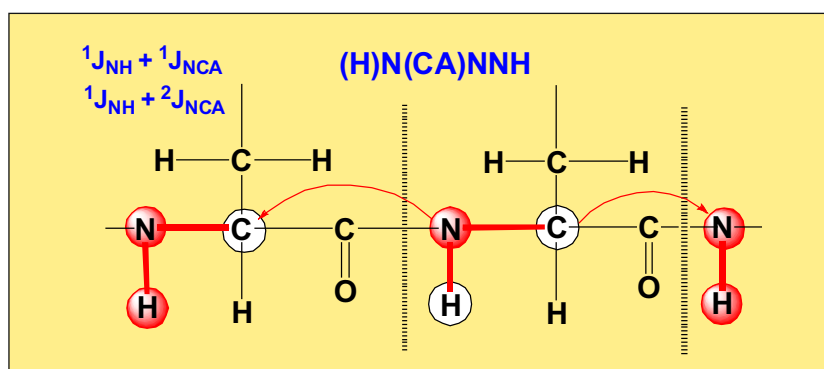
- 3D H(NCA)NNH (**hncannhgp3d.2**)
- 3D H(NCA)NNH with ^2H -decoupling (**hncannhgp2h3d.2**)
- 3D H(NCA)NNH using WATERGATE (**hncannhgpwg3d.2**)
- 3D H(NCA)NNH using WATERGATE and ^2H -decoupling (**hncannhgpwg2h3d.2**)
- 3D H(NCA)NNH using TROSY (**trhncannhgp3d.2**)
- 3D H(NCA)NNH using TROSY and ^2H -decoupling (**trhncannhgp2h3d.2**)
- 3D H(NCA)NNH using TROSY and echo-antiecho (**trhncannhetgp3d.2**)
- 3D H(NCA)NNH using TROSY, echo-antiecho and ^2H -decoupling (**trhncannhetgp2h3d.2**)

Also see:

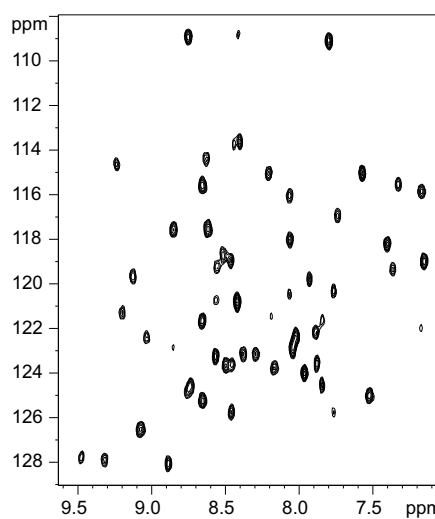
HNCOCANNH Experiment



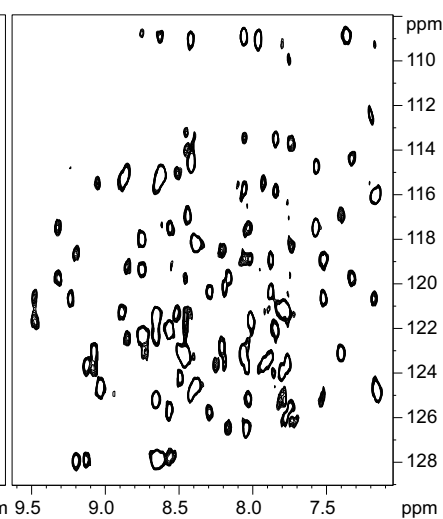
R. Weisemann, H. Rueterjans & W. Bermel, J. Biomol. NMR 3, 113-120 (1993)



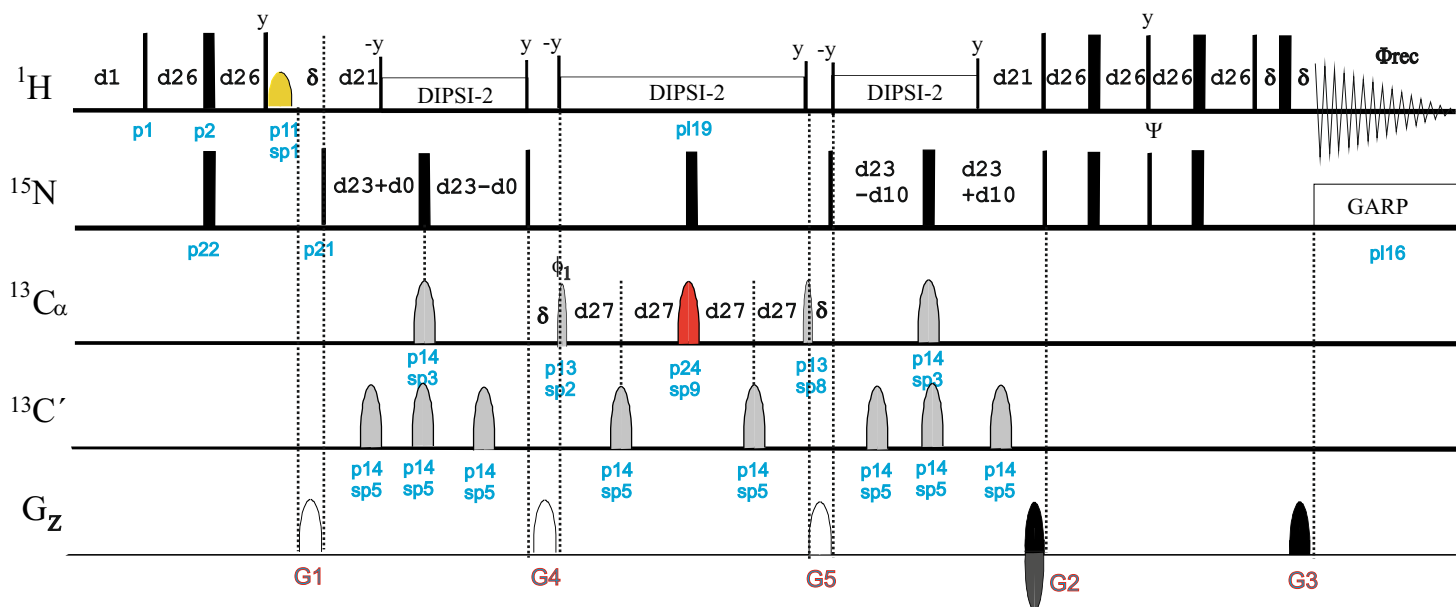
2D (HNCA)NH



2D (H)N(CAN)H

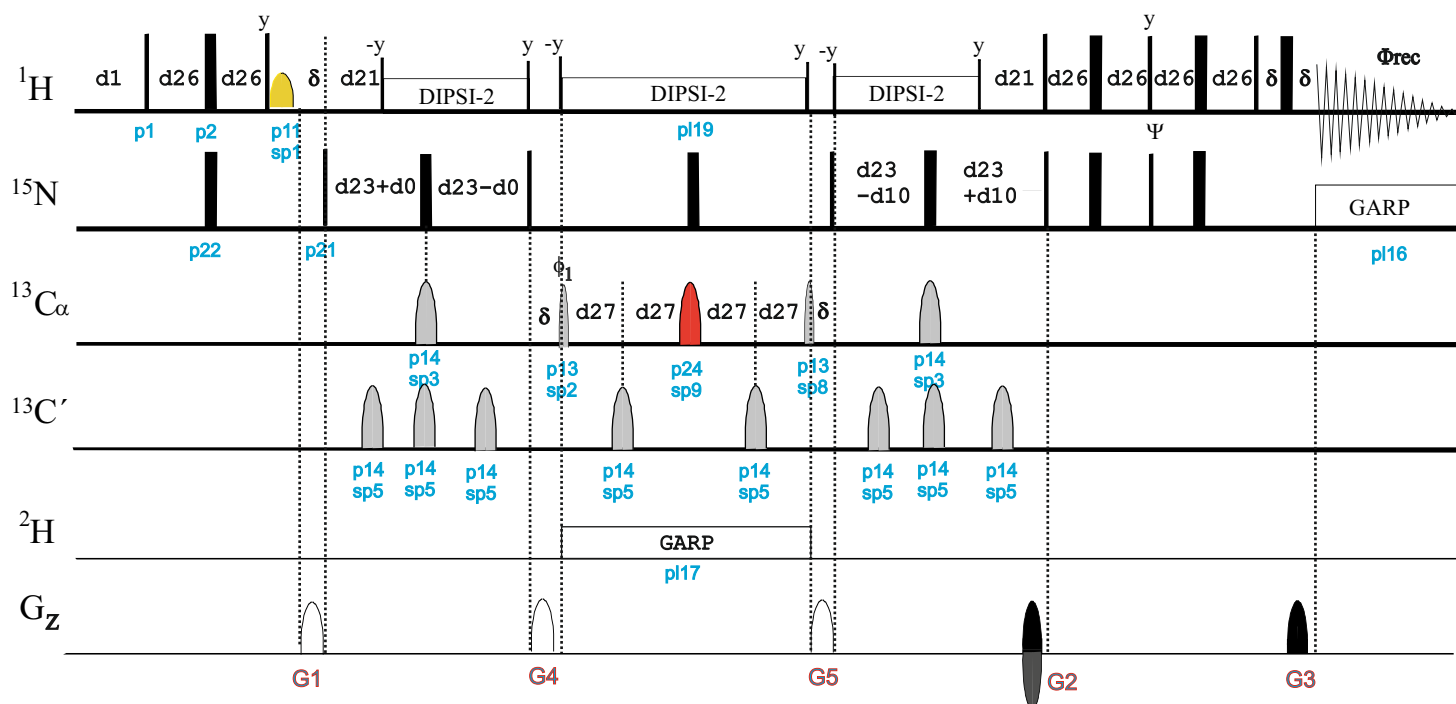


hncannhgp3d



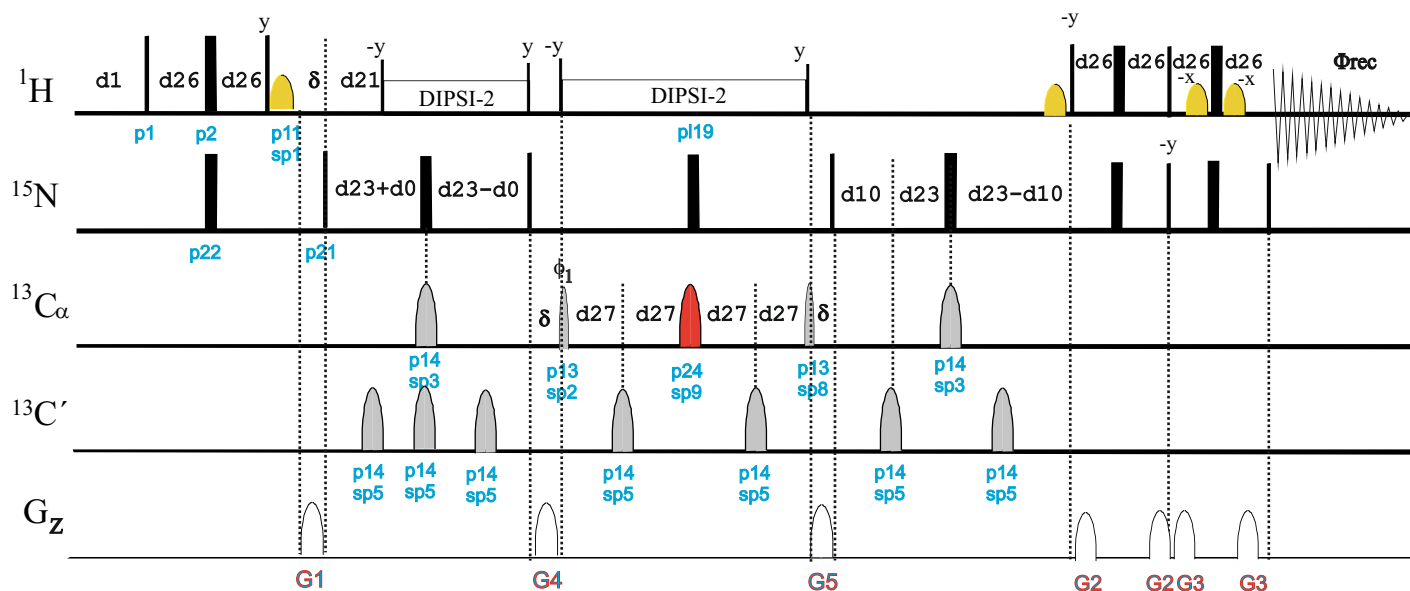
d21: $1/(2J(\text{NH}))$	[5.5 msec]
d23: $1/(4J(\text{NCa}))$	[12.4 msec]
d26: $1/(4J'(\text{NH}))$	[2.3 msec]
d27: $1/(4J'(\text{NCa}))$	[12.5 msec]

hncannhgp2h3d

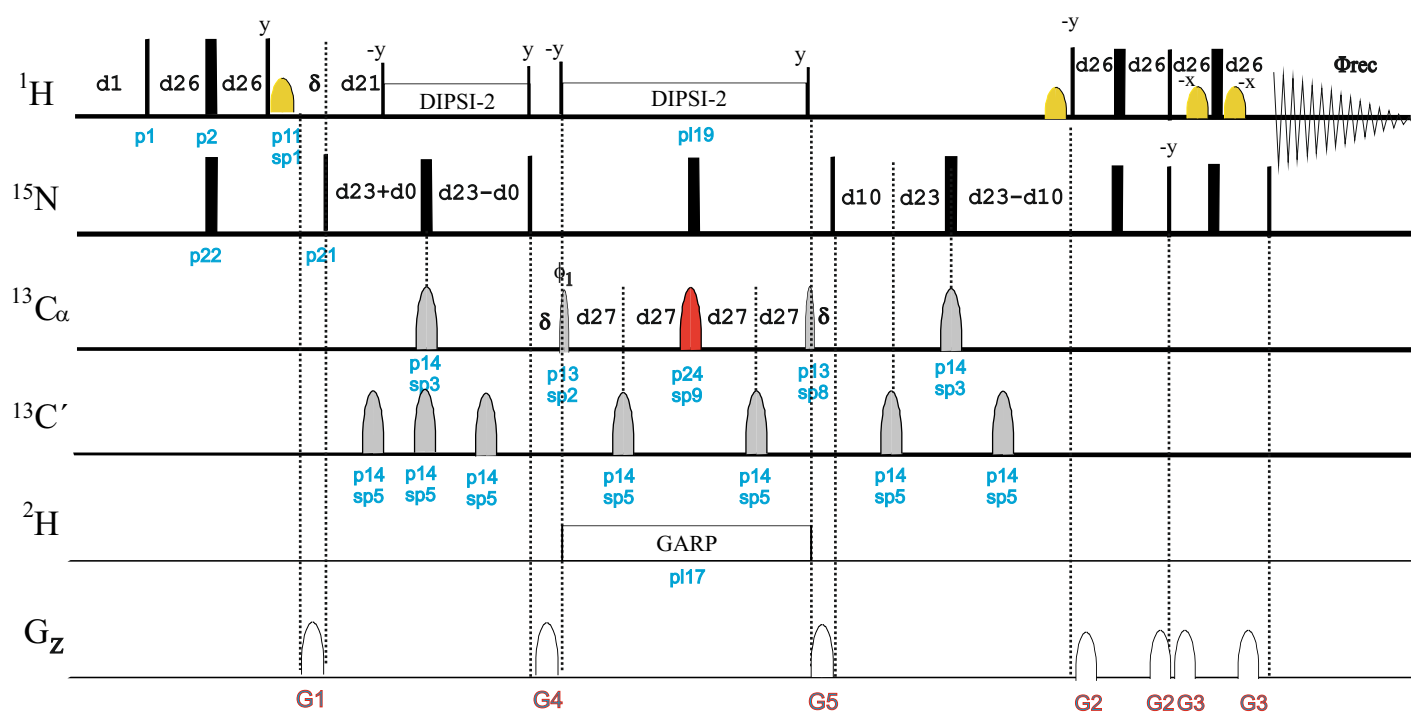


[illegible]

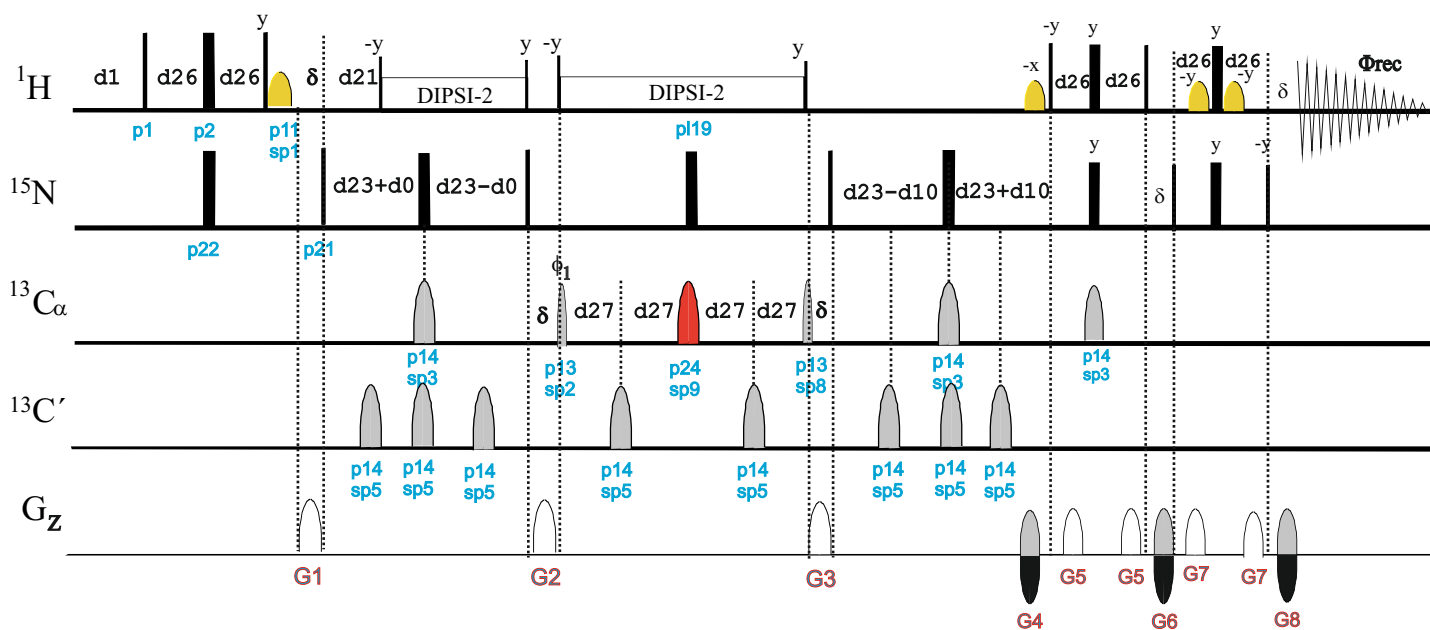
trhncannhgp3d



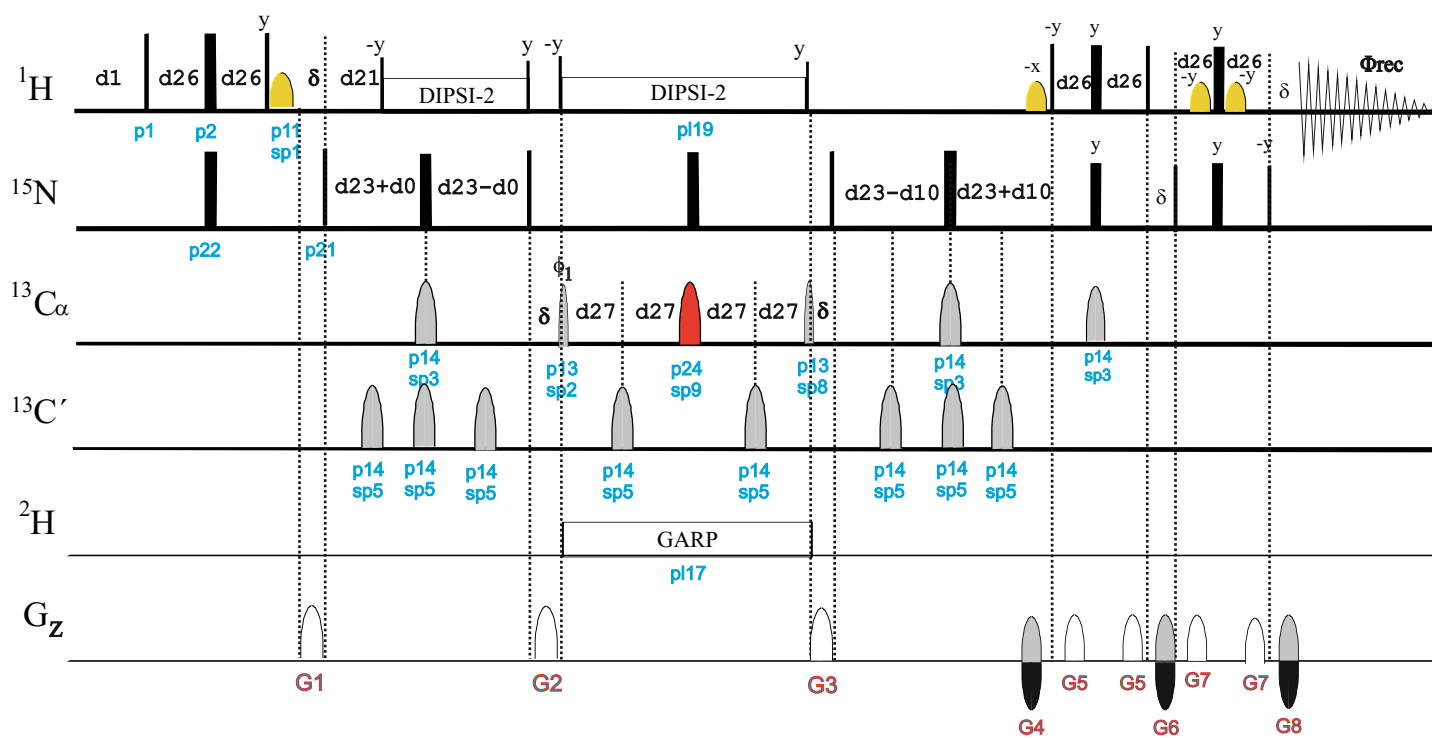
trhncannhgp2h3d

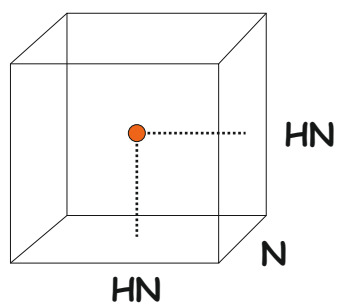
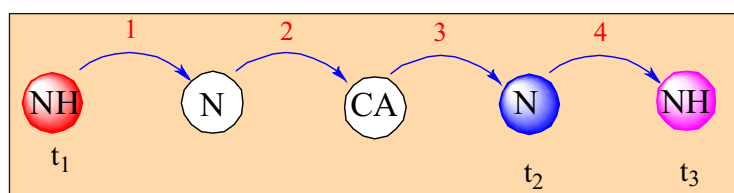
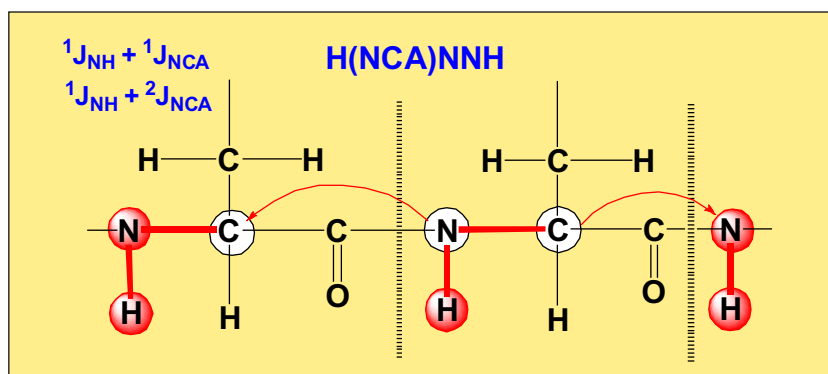


trhncannhetgp3d

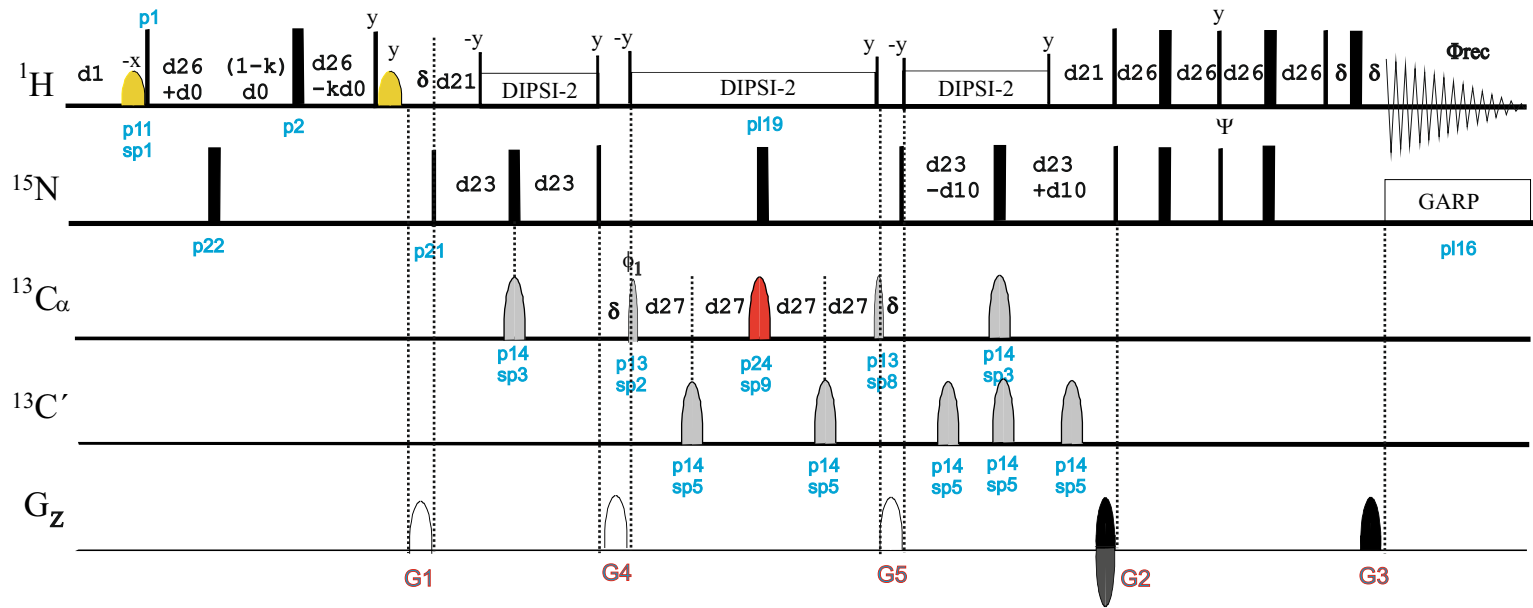


trhncannhetgp2h3d

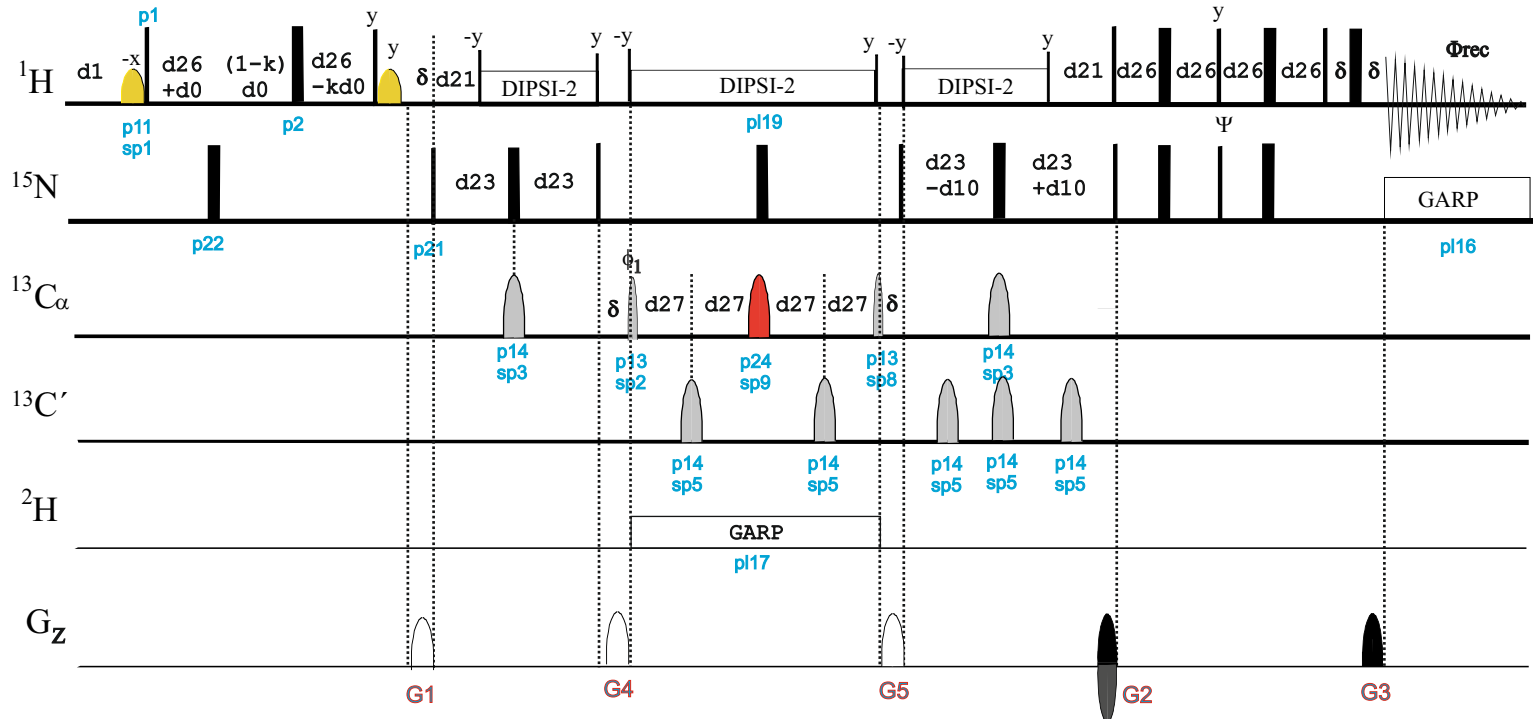




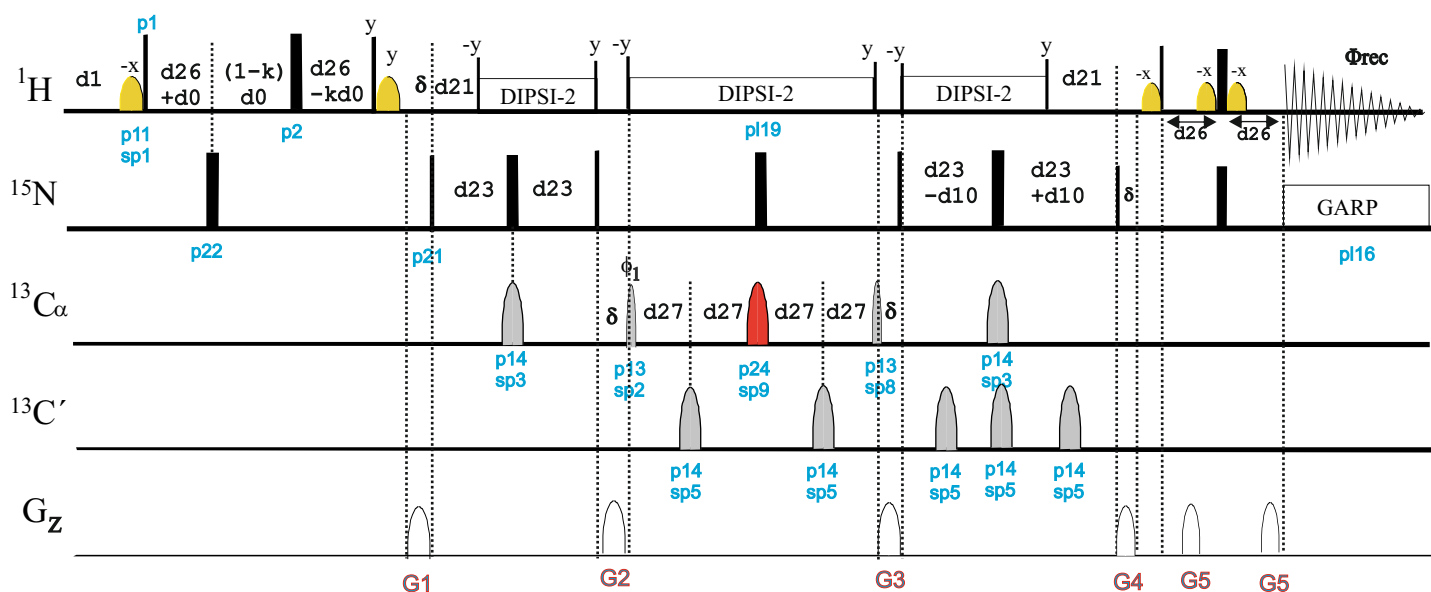
hncannhgp3d.2



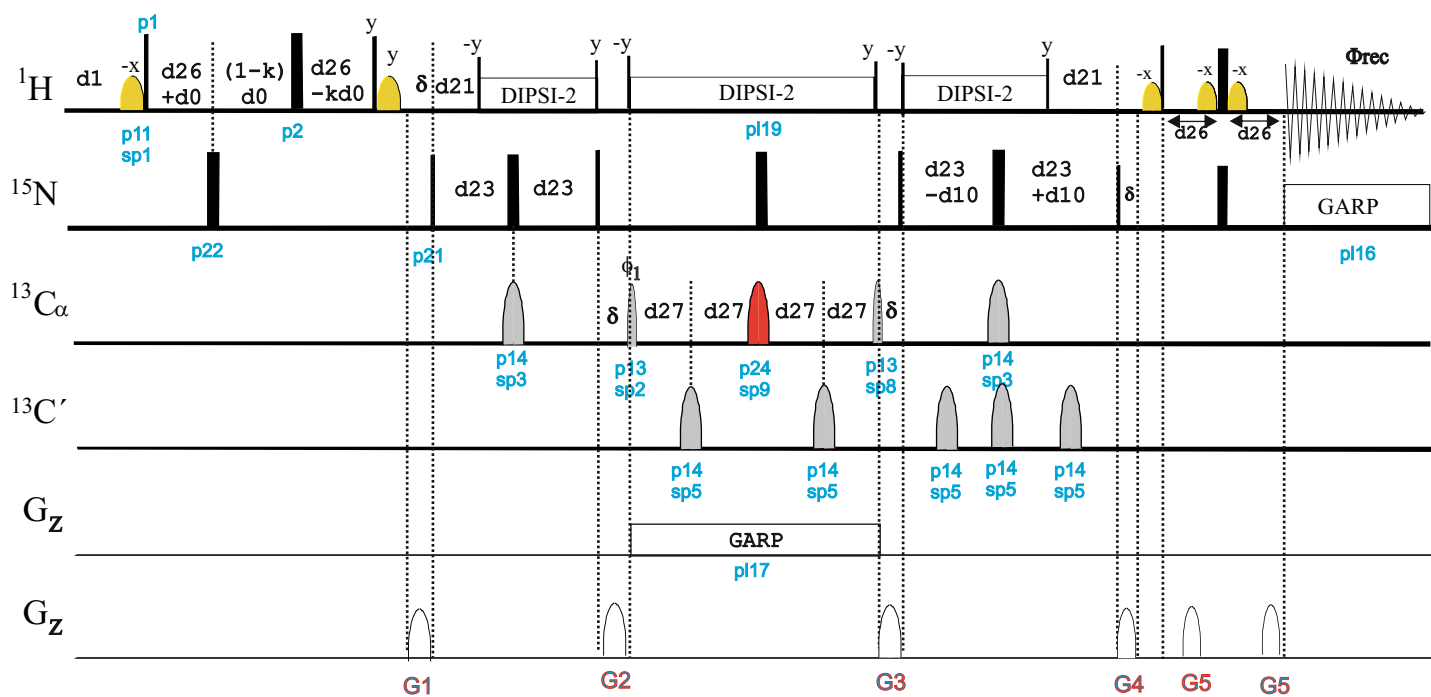
hncannhgp2h3d.2



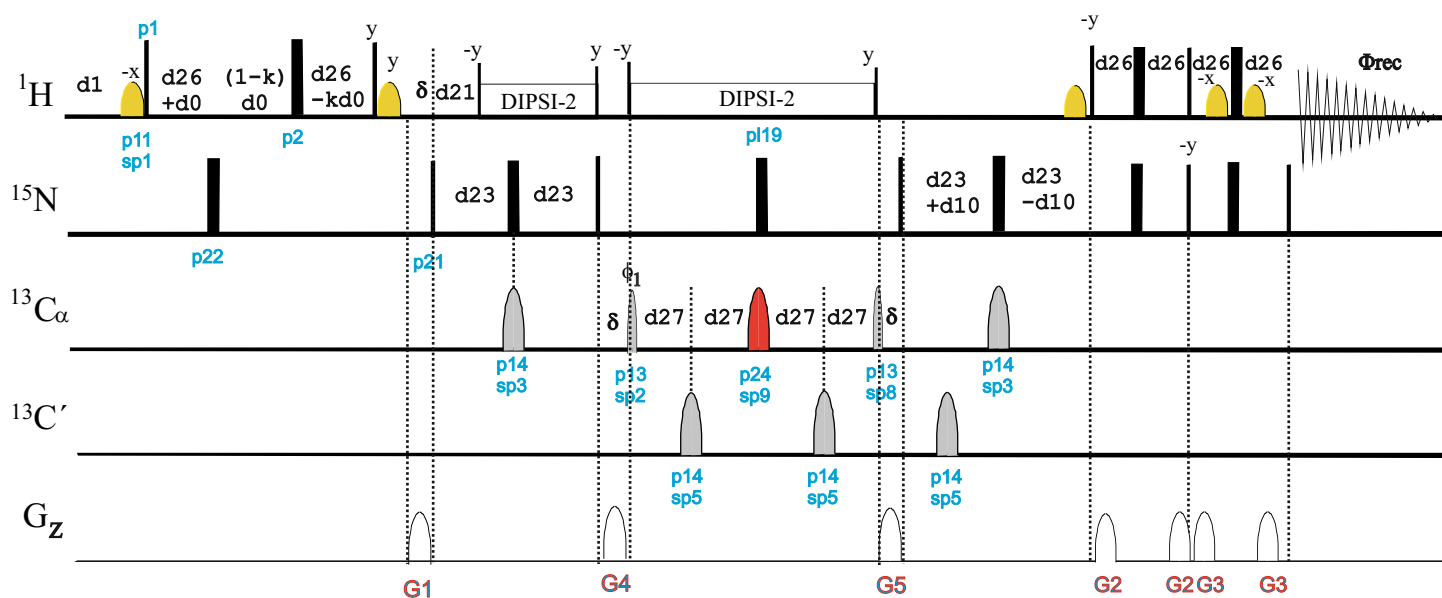
hncannhgpwg3d.2



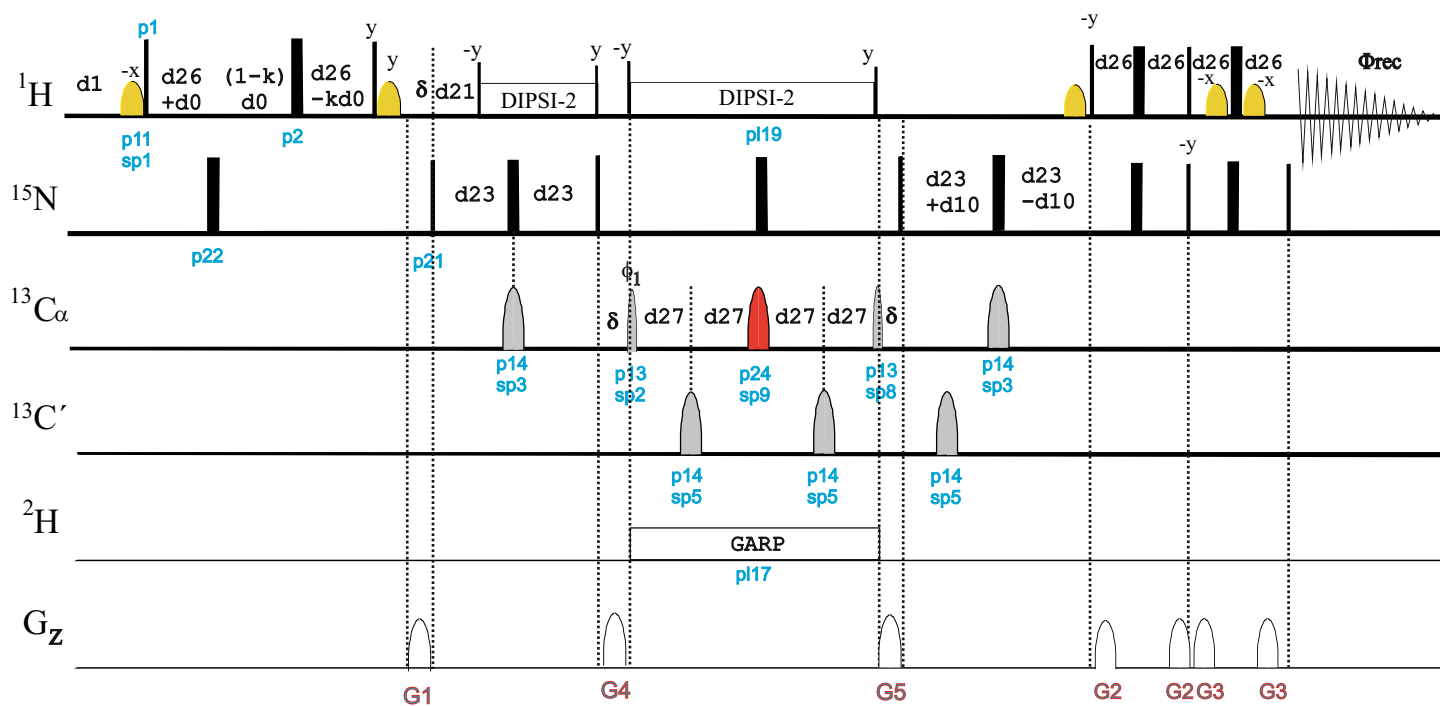
hncannhgpwg2h3d.2



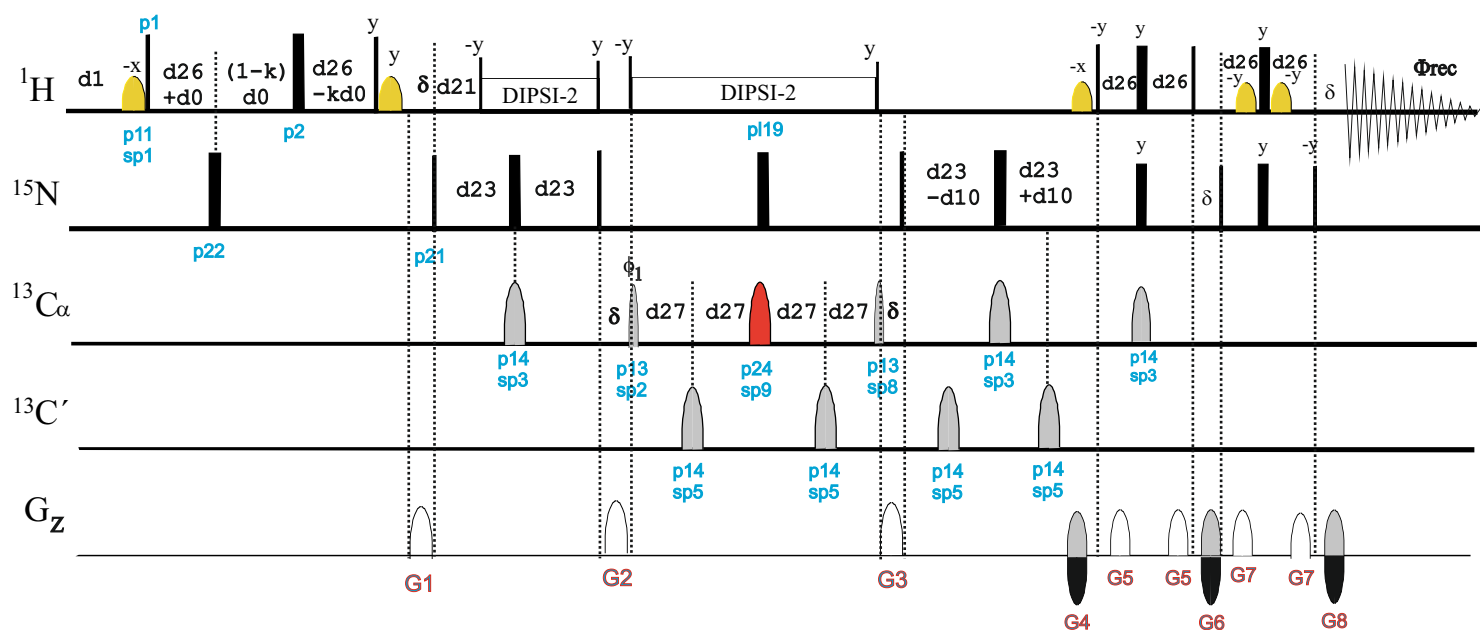
trhncannhgp3d.2



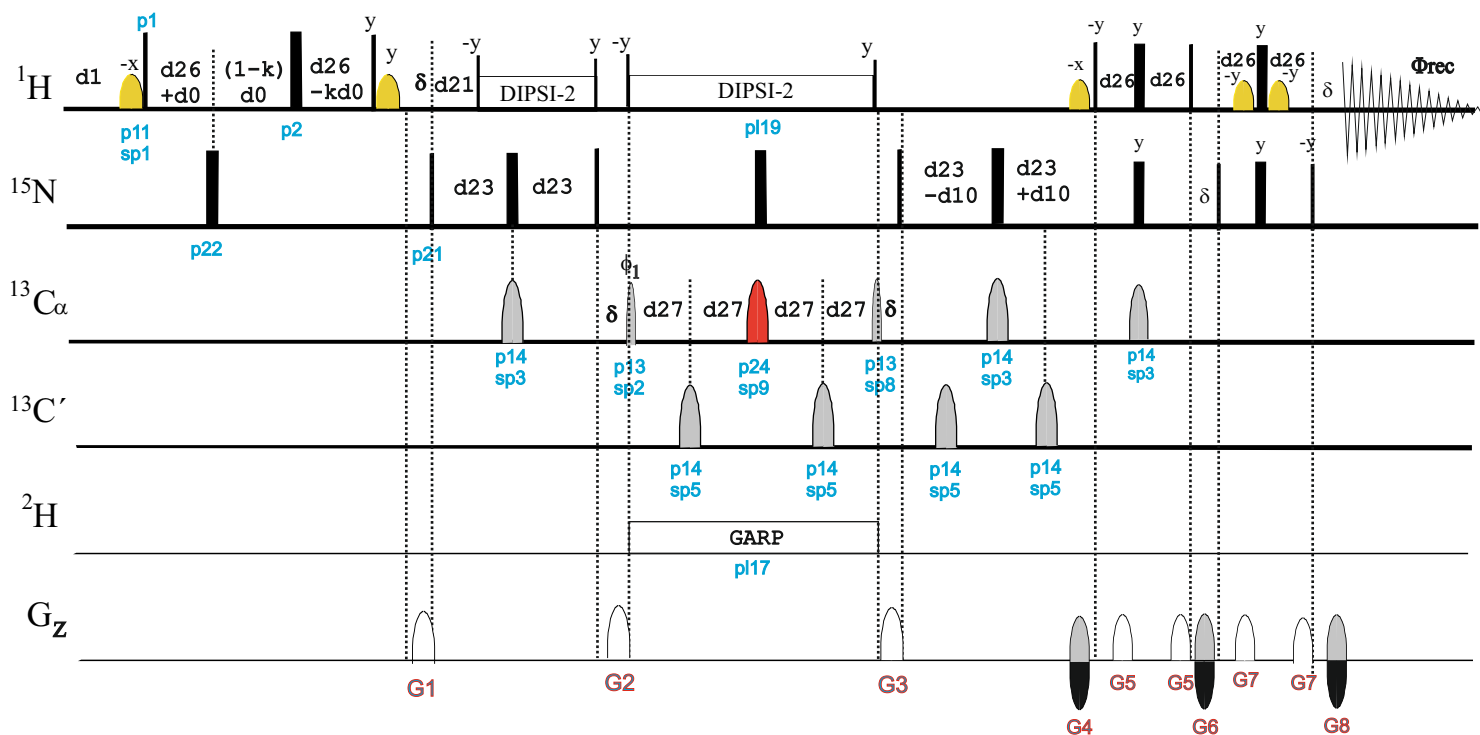
trhncannhgp2h3d.2



trhncannhetgp3d.2



trhncannhetgp2h3d.2



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3D HNCOCANNH

HNCOCANNH Experiment

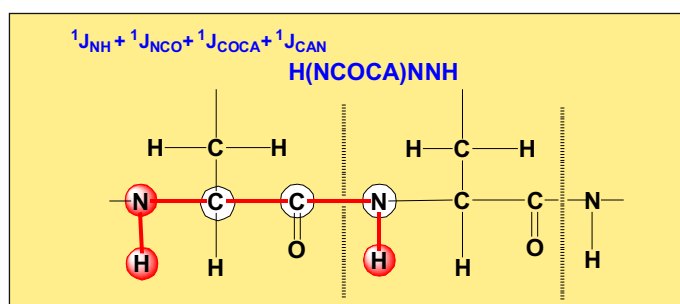
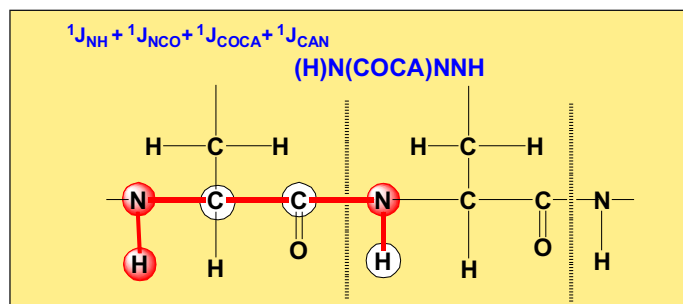
3D (H)N(COCA)NNH experiment

- 3D (H)N(COCA)NNH (**hncocannhgp3d**)
- 3D (H)N(COCA)NNH with ^2H -decoupling (**hncocannhgp2h3d**)
- 3D (H)N(COCA)NNH using WATERGATE (**hncocannhgpwg3d**)
- 3D (H)N(COCA)NNH using WATERGATE and ^2H -decoupling (**hncocannhgpwg2h3d**)
- 3D (H)N(COCA)NNH using TROSY (**trhncocannhgp3d**)
- 3D (H)N(COCA)NNH using TROSY and ^2H -decoupling (**trhncocannhgp2h3d**)
- 3D (H)N(COCA)NNH using TROSY and echo-antiecho (**trhncocannhetgp3d**)
- 3D (H)N(COCA)NNH using TROSY, echo-antiecho and ^2H -decoupling (**trhncocannhetgp2h3d**)

3D H(NCOCA)NNH experiment

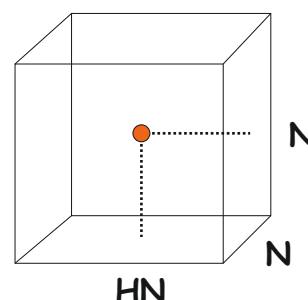
- 3D H(NCOCA)NNH (**hncocannhgp3d.2**)
- 3D H(NCOCA)NNH with ^2H -decoupling (**hncocannhgp2h3d.2**)
- 3D H(NCOCA)NNH using WATERGATE (**hncocannhgpwg3d.2**)
- 3D H(NCOCA)NNH using WATERGATE and ^2H -decoupling (**hncocannhgpwg2h3d.2**)
- 3D H(NCOCA)NNH using TROSY (**trhncocannhgp3d.2**)
- 3D H(NCOCA)NNH using TROSY and ^2H -decoupling (**trhncocannhgp2h3d.2**)
- 3D H(NCOCA)NNH using TROSY and echo-antiecho (**trhncocannhetgp3d.2**)
- 3D H(NCOCA)NNH using TROSY, echo-antiecho and ^2H -decoupling (**trhncocannhetgp2h3d.2**)

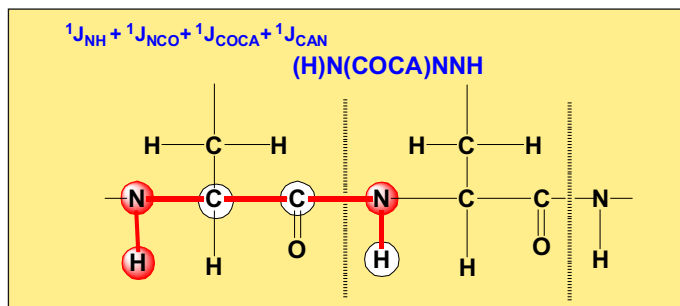
Also see:
HNCANNH Experiment



References:

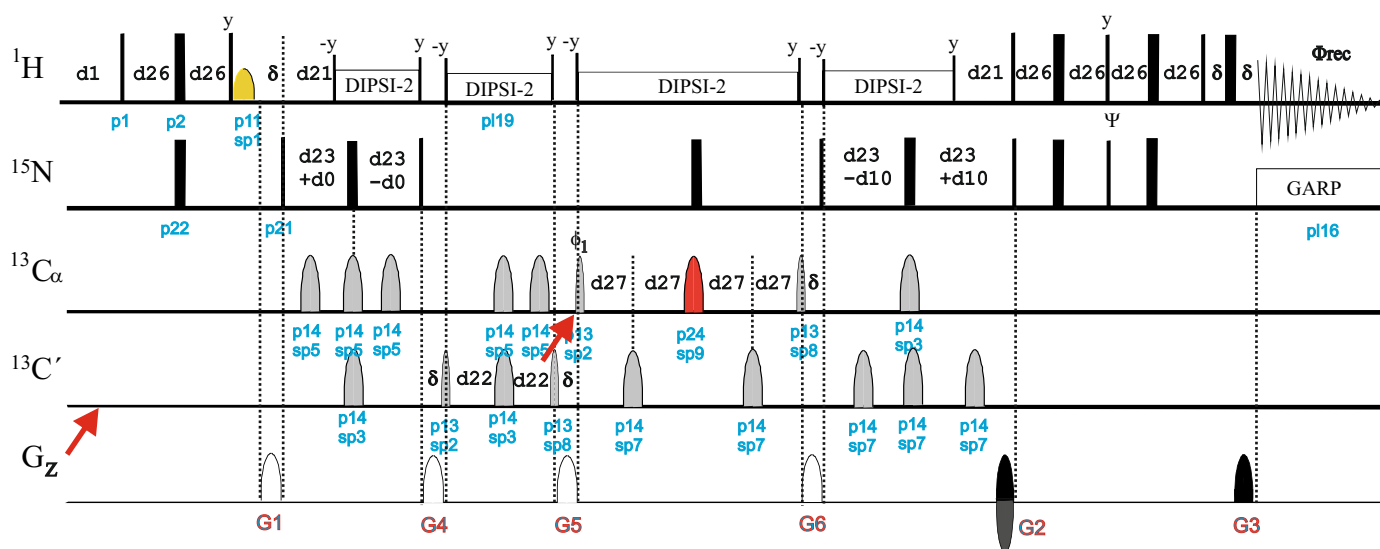
1. C. Bracken, A.G. Palmer & J. Cavanagh, J. Biomol. NMR 9, 94-100 (1997)
2. S.C. Panchal, N.S. Bhavesh & R.V. Hosur, J. Biomol. NMR 20, 135-147 (2001)
3. Z.-Y. J. Sun, D.P. Frueh, P. Selenko, J.C. Hoch & G. Wagner, J. Biomol. NMR 33, 43-50 (2005)



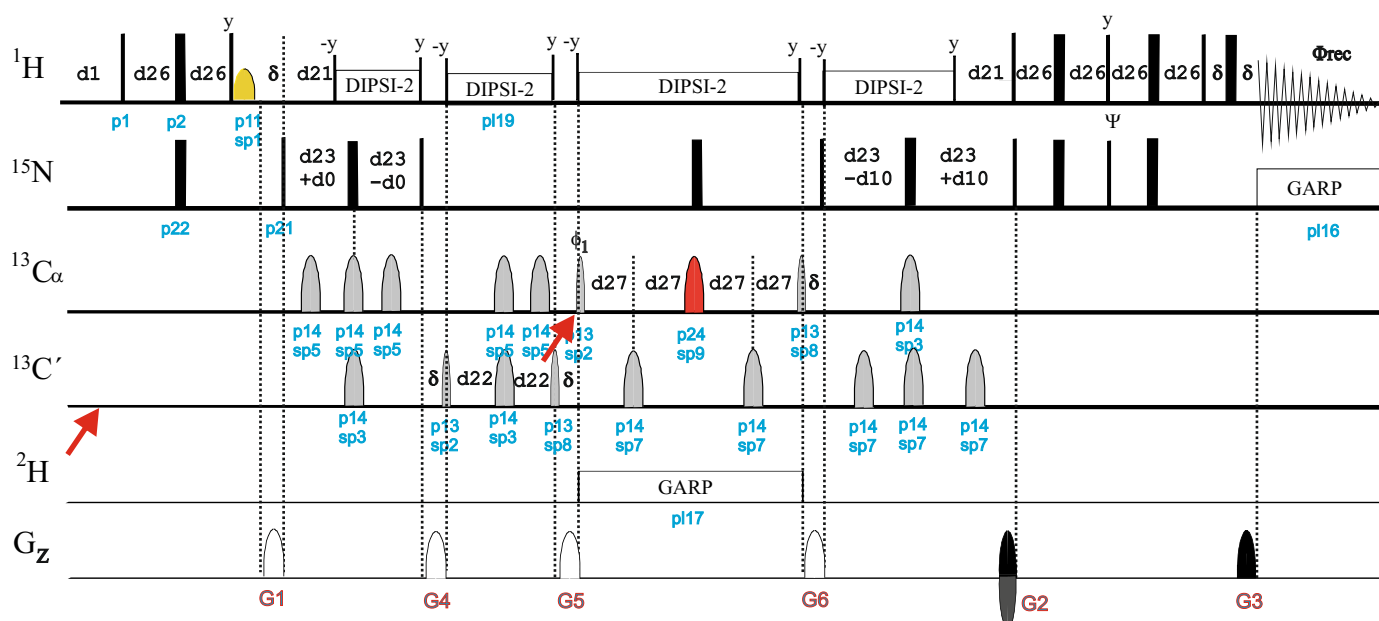


d21: $1/(2J(NH))$	[5.5 msec]
d22: $1/(4J(CO\alpha))$	[4.5 msec]
d23: $1/(4J(N\alpha))$	[12.4 msec]
d26: $1/(4J'(NH))$	[2.3 msec]
d27: $1/(4J'(N\alpha))$	[12.5 msec]

hncocannhgp3d



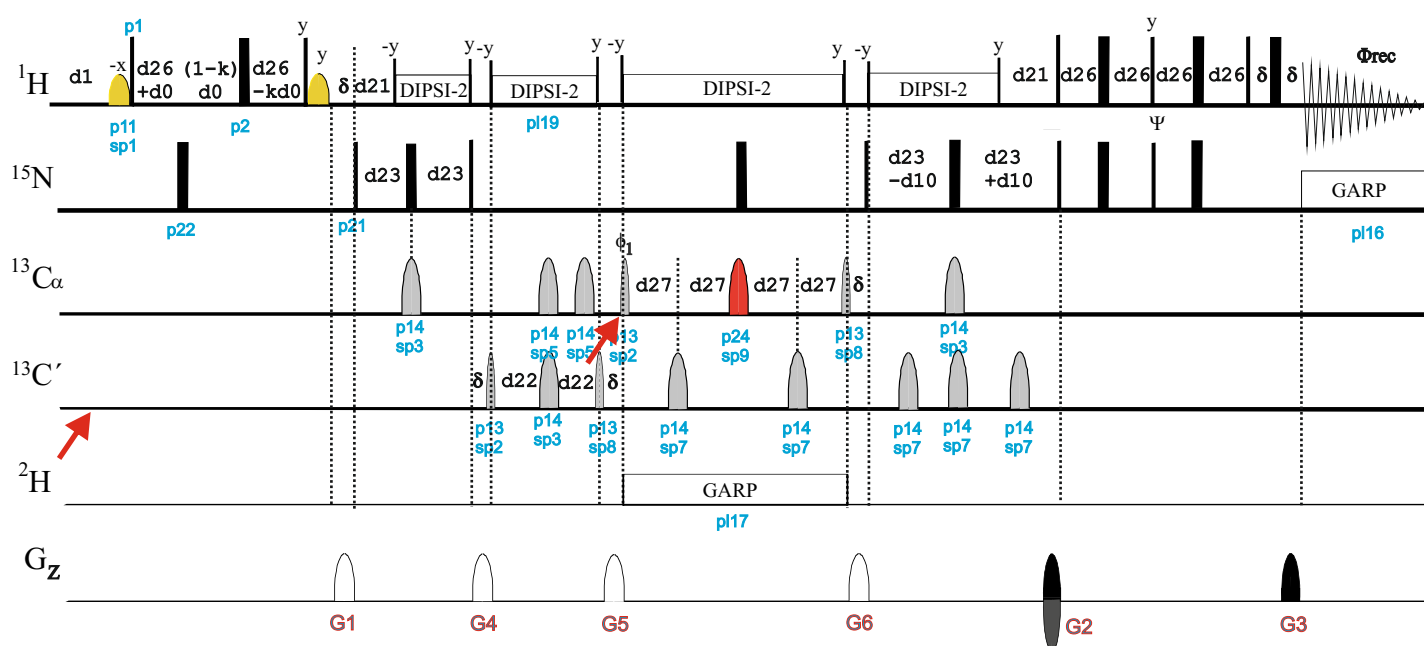
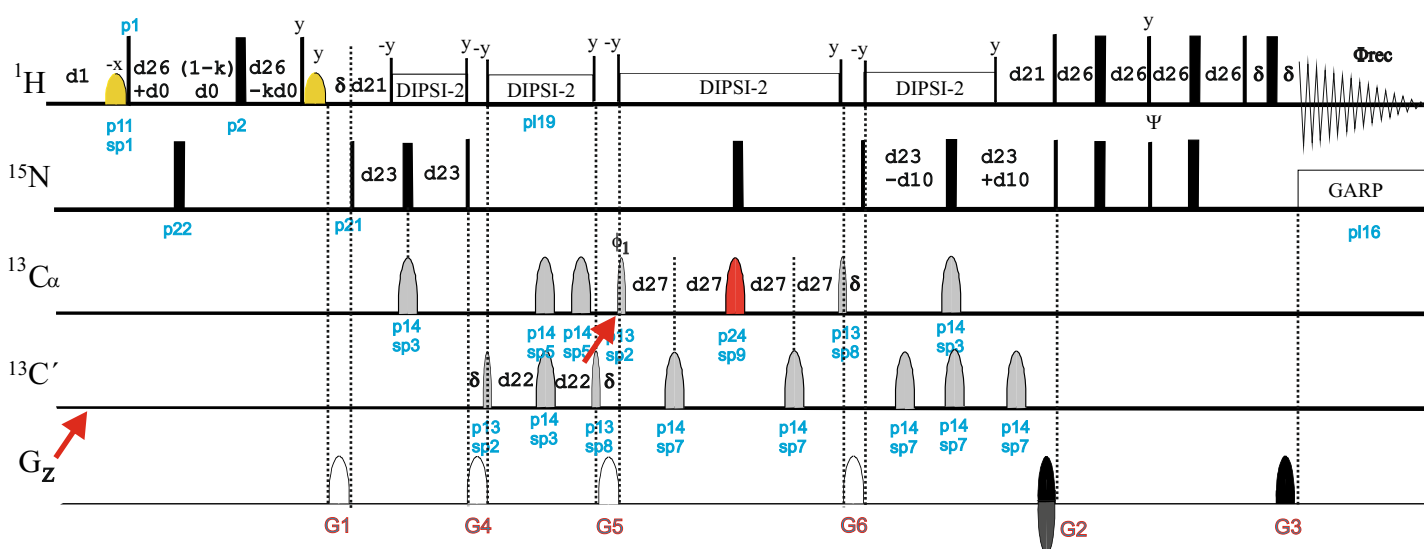
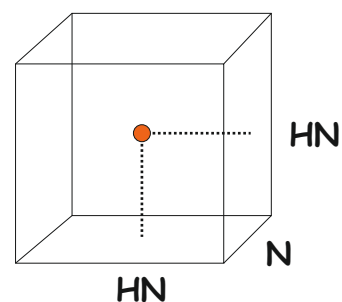
hncocannhgp2h3d



[illegible]

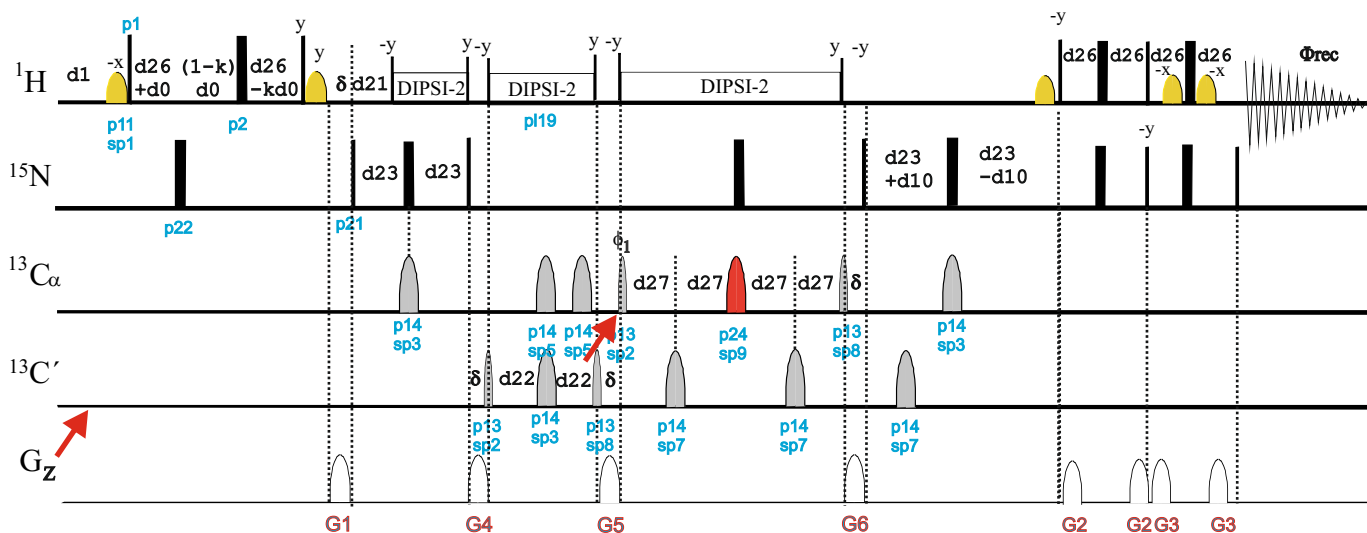
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[illegible][illegible]

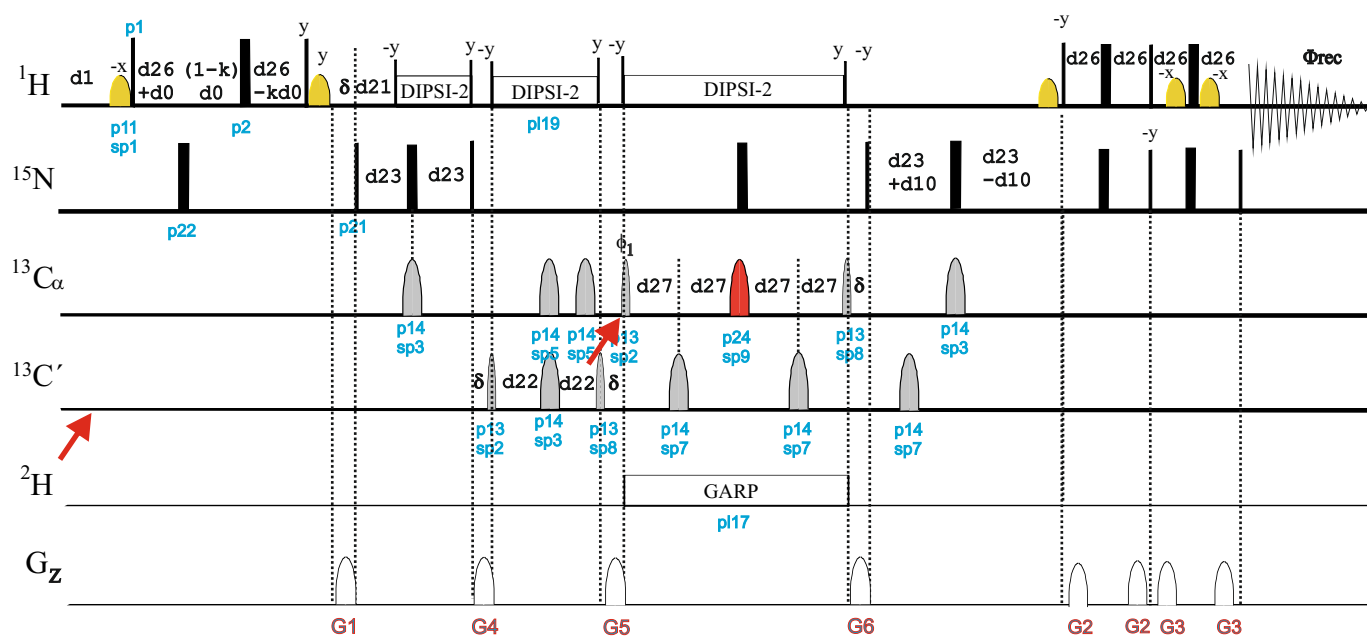


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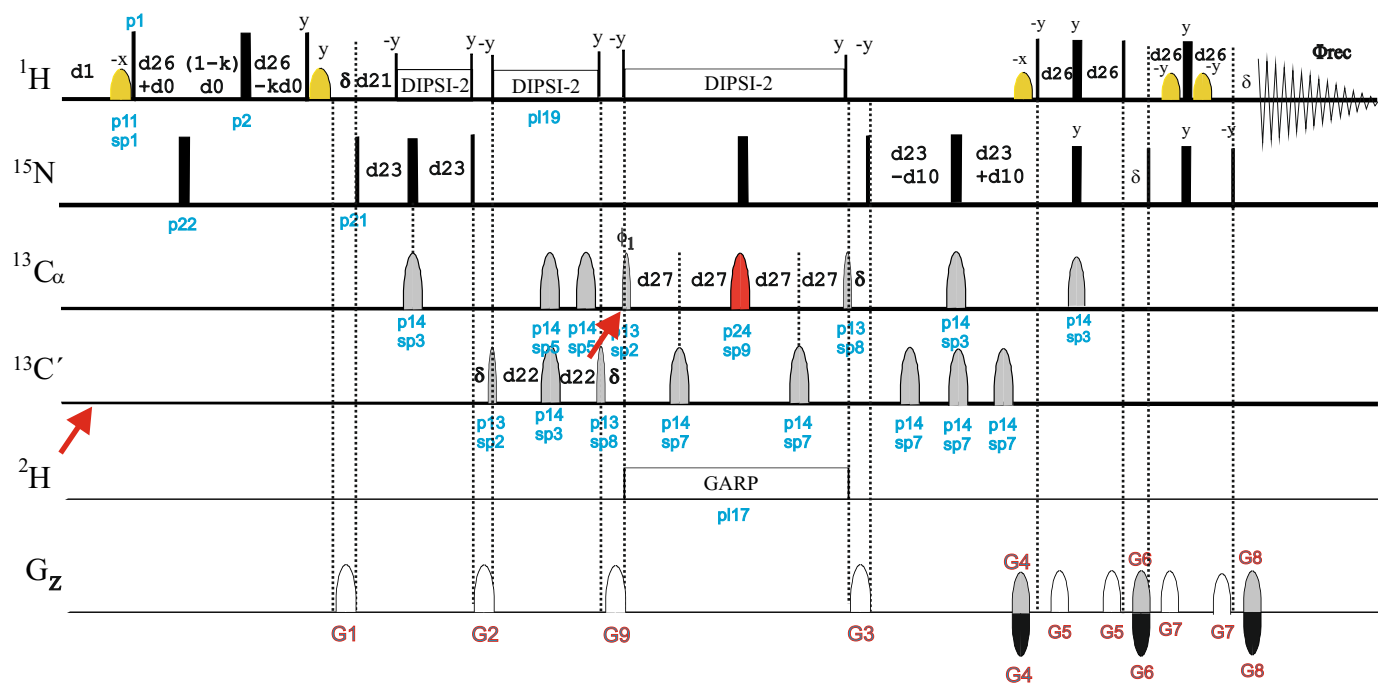
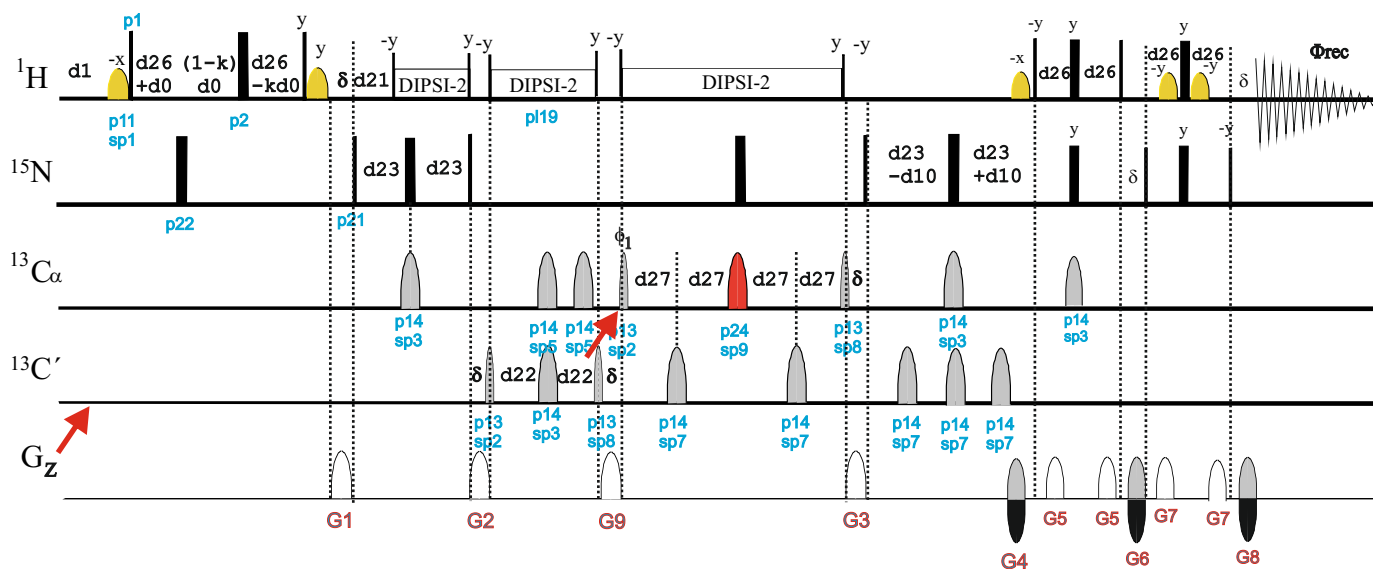
trhncocannhgp3d.2



trhncocannhgp2h3d.2



trhncocannhetgp2h3d.2



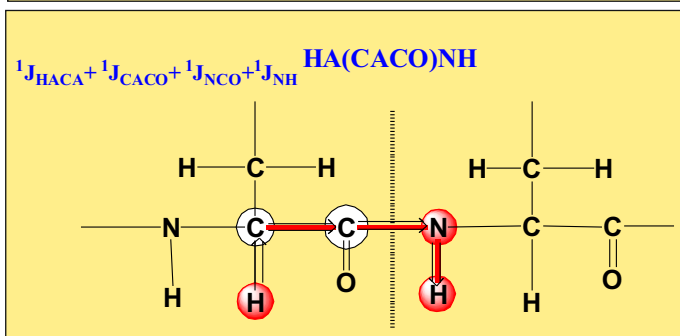
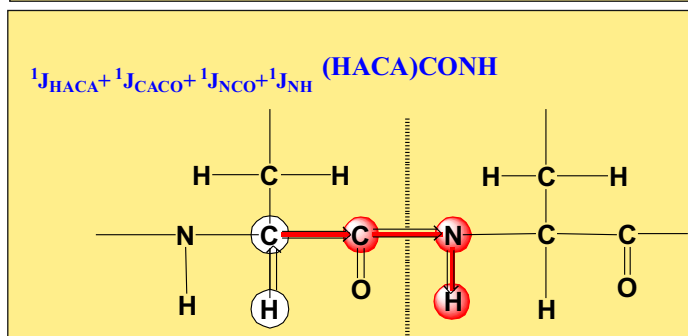
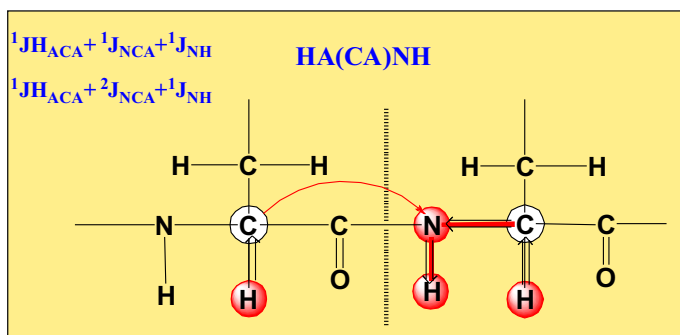
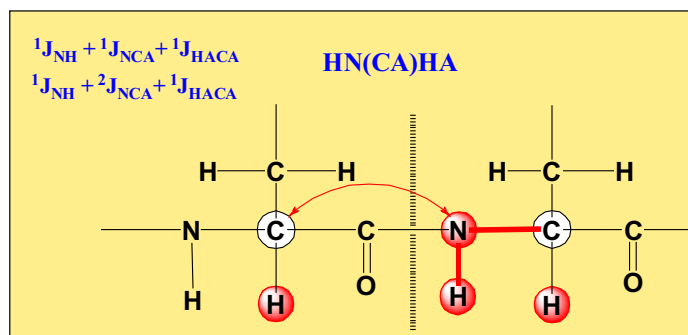
BRUKER PULSE PROGRAM CATALOGUE

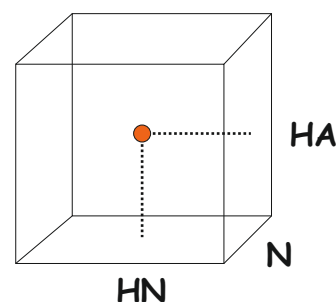
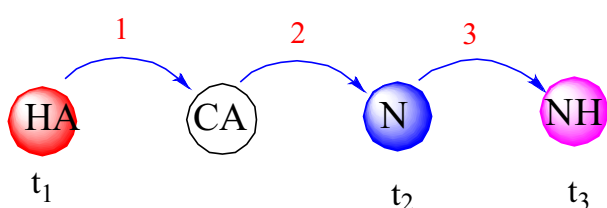
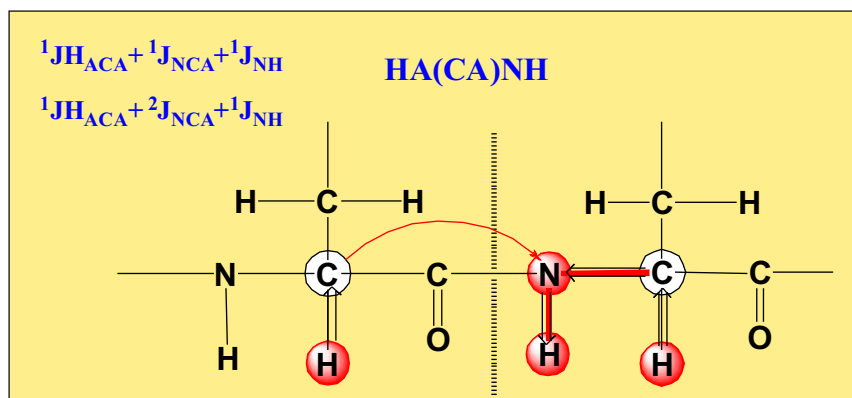
NMRGuide

3D HN(CA)HA
3D HA(CA)NH
3D HA(CACO)NH

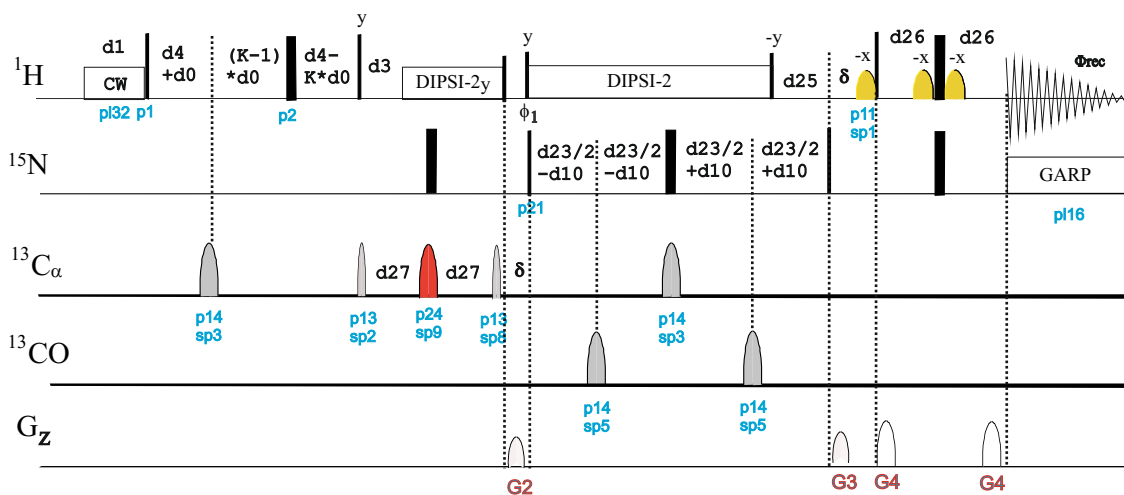
Miscellaneous NH-Detected Backbone Experiments

- 3D HA(CA)NH using WATERGATE (hanhgpgw3d)
- 3D HA(CACO)NH using WATERGATE (haconhgpgw3d)
- 3D (HACA)CONH using PEP (hcaconhgpgw3d)
- 3D (HACA)CONH using WATERGATE (hcaconhgpgw3d)
- 3D HN(CA)HA (hncah3d)

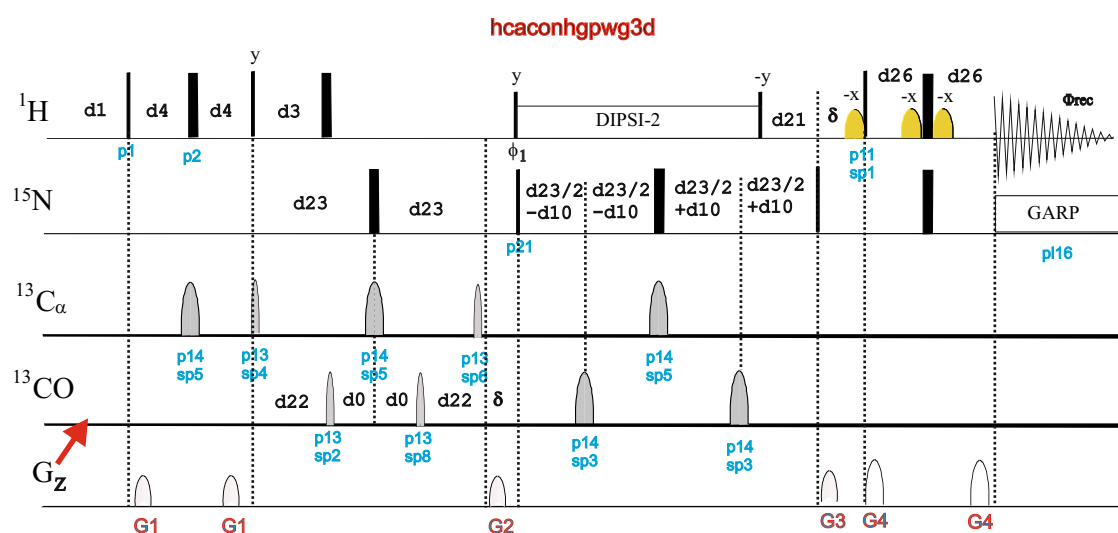
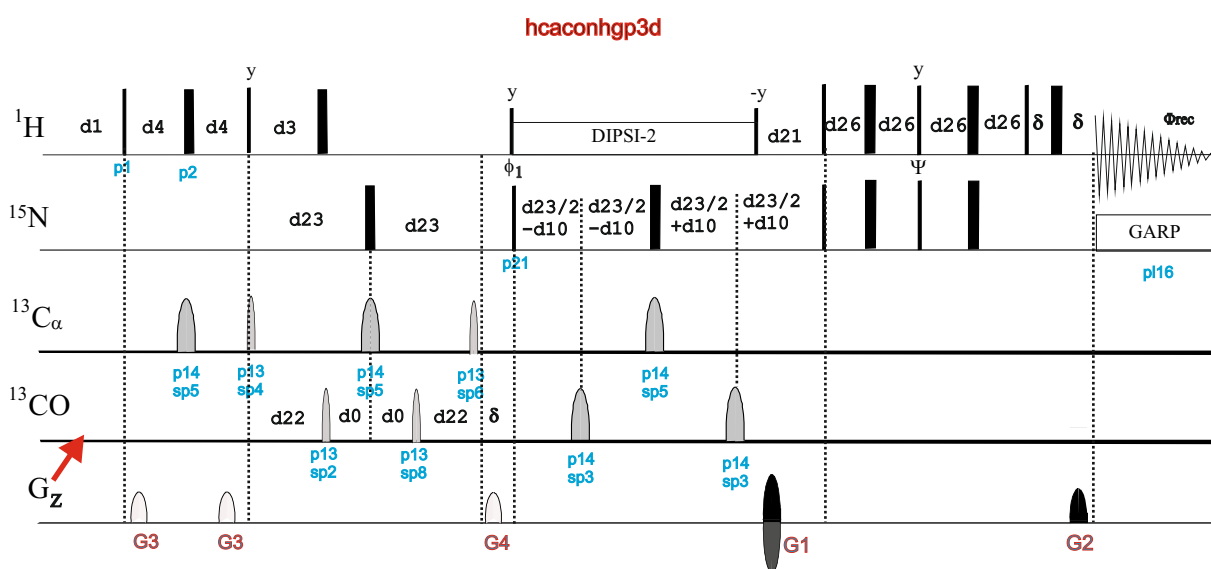
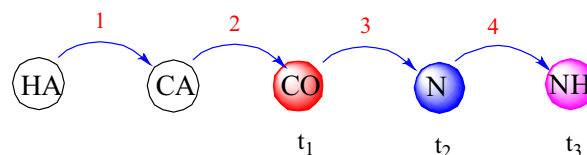
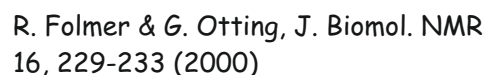




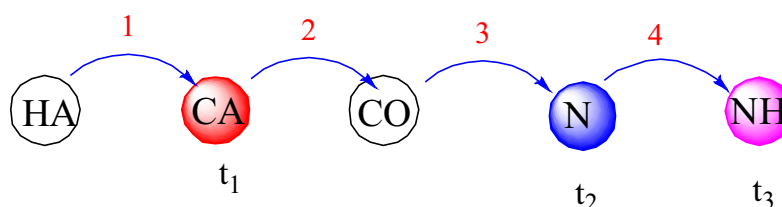
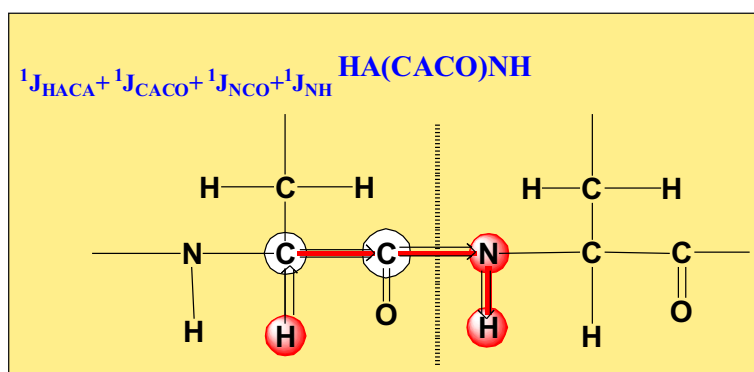
hanhgpgwg3d



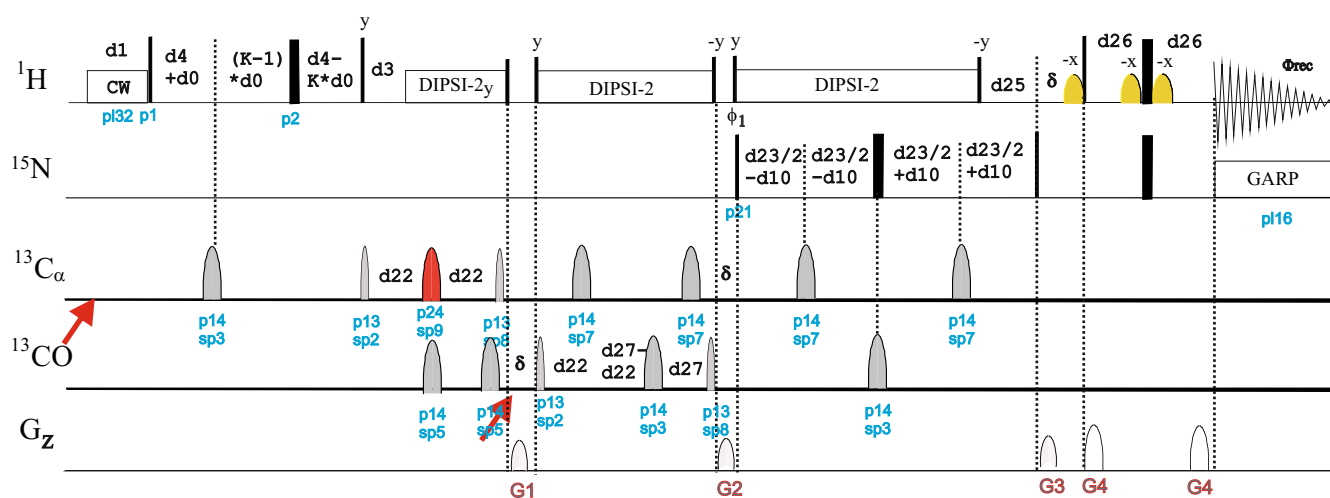
d3 : $1/(3J(\text{CH}))$	[2.2 msec]
d4 : $1/(4J(\text{CH}))$	[1.8 msec]
d21: $1/(4J(\text{NCa})), \text{T(N)}$	[12.4 msec]
d25: $1/(2J(\text{NH}))$	[5.5 msec]
d26: $1/(4J(\text{NH}))$	[2.3 msec]
d27: $1/(4J'(\text{NCa}))$	[11 msec]



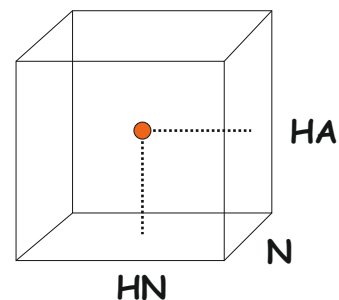
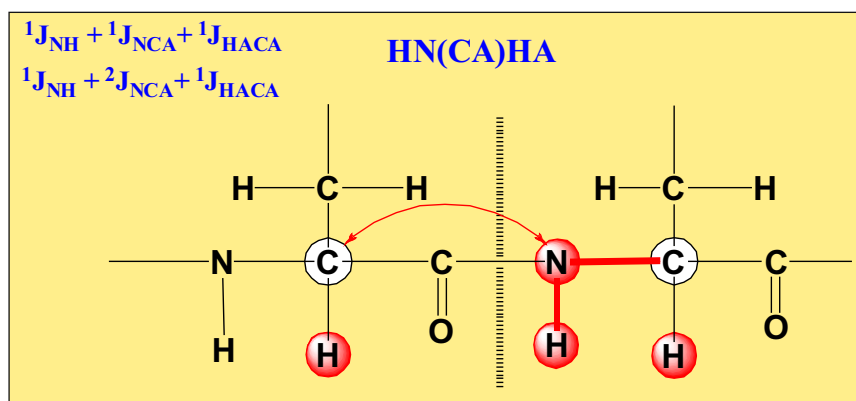
d3 : 1/(6J(HCa))	[1.16 msec]
d4 : 1/(4J(HCa))	[1.5 msec]
d21: 1/(2J(NH))	[5.5 msec]
d22: 1/(4J(CaCO))	[4.5 msec]
d23: 1/(4J(NCa))	[12.4 msec]
d26: 1/(4J'(NH))	[2.3 msec]



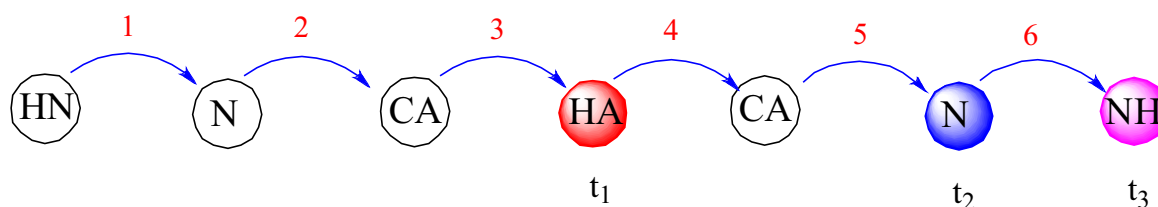
haconhgpwg3d



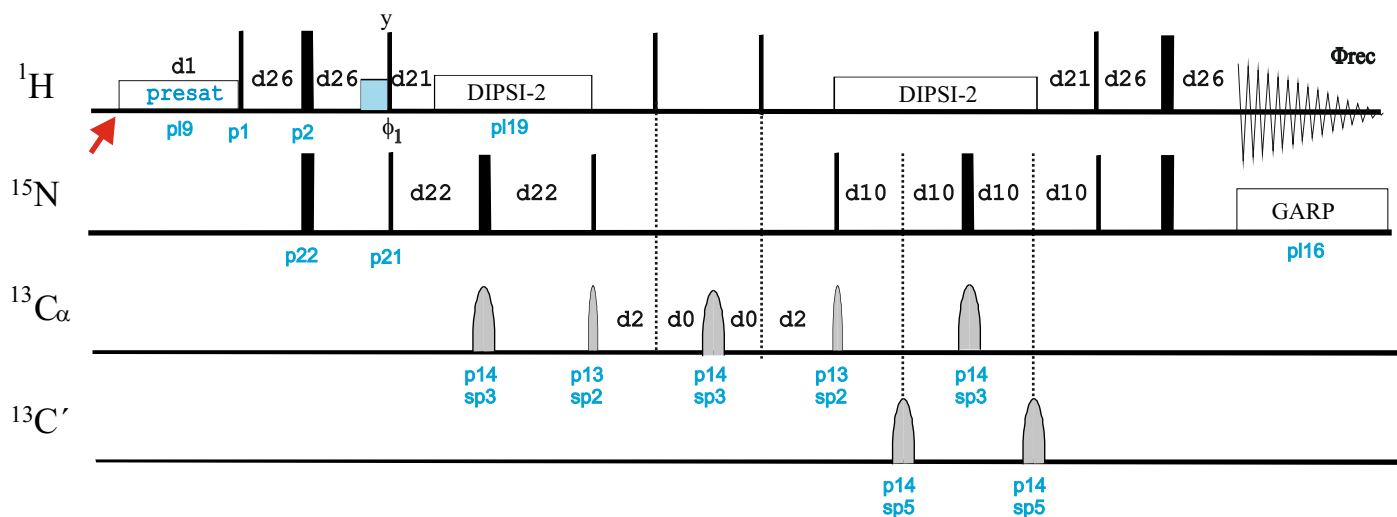
d3 : $1/(3J(\text{CH}))$	[2.2 msec]
d4 : $1/(4J(\text{CH}))$	[1.8 msec]
d22: $1/(4J'(\text{CaCO}))$	[4.4 msec]
d23: $1/(4J(\text{NCO})), T(\text{N})$	[12.4 msec]
d25: $1/(2J(\text{NH}))$	[5.5 msec]
d26: $1/(4J(\text{NH}))$	[2.3 msec]
d27: $1/(4J'(\text{NCO}))$	[12.4 msec]



; S. Seip, J. Balbach & H. Kessler, J. Magn. Reson. 100,
; 406-410 (1992)



hncah3d



d2 : $1/(2J(CH))$	[3 msec]
d21: $1/(2J'(NH))$	[4.5 msec]
d22: $1/(4J(N-C\alpha))$	[11 msec]
d26: $1/(4J(NH))$	[2.75m]

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HA-DETECTED BACKBONE EXPERIMENTS

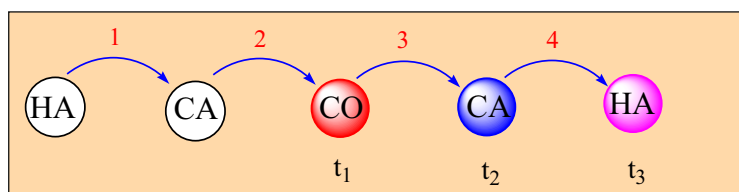
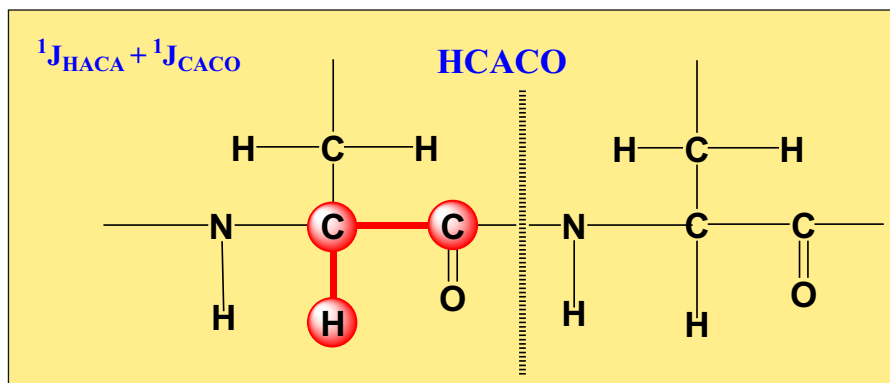
HA-Detected Backbone Experiments

- 3D HCACO experiment (**hcacogp3d** | HCACOGP3D)

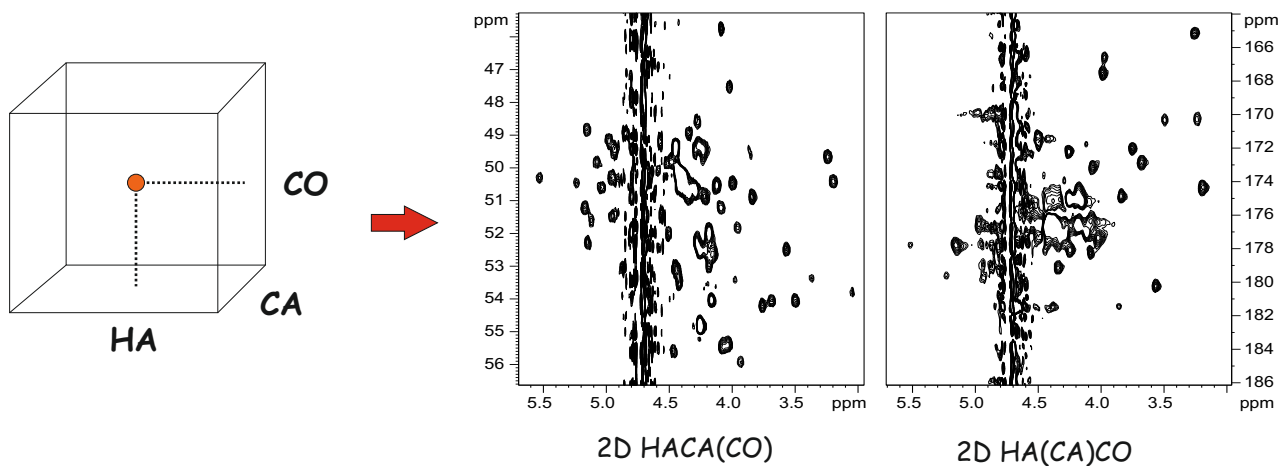
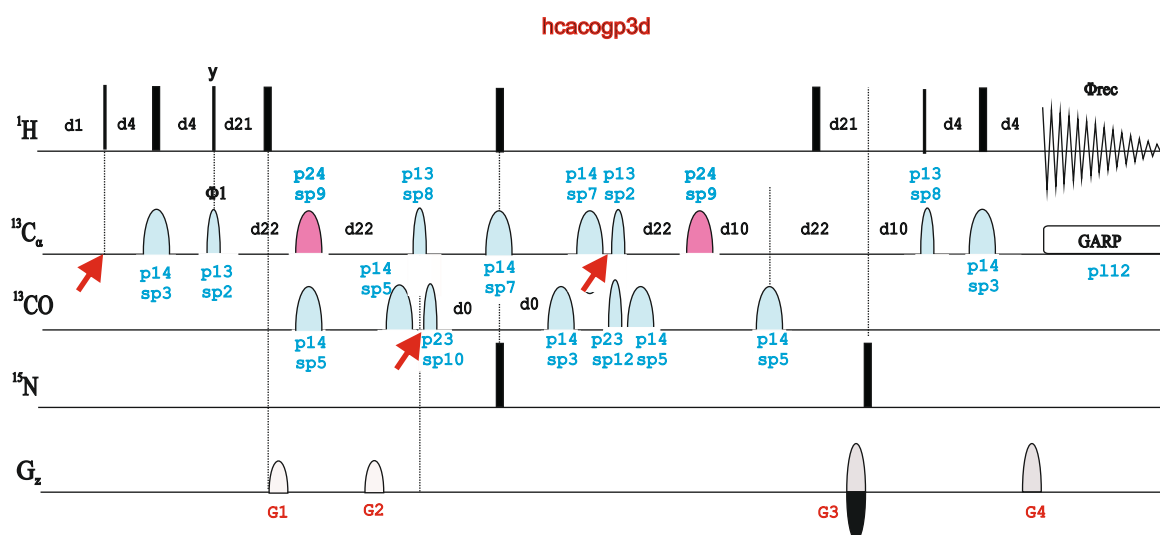
Also see:

3D HCACO-type experiments for J measuring
¹³C-detected CACO-type experiments

- 2D H(CA)N with ²H-decoupling (**hcanp2h**)
- 3D HCAN using PEP (**hcanp3d**)
- 2D H(CACO)N with ²H-decoupling (**hcaconp2h**)
- 3D HCA(CO)N using PEP (**hcaconp3d**)
- 3D HCBCA(CO)N (**hcbcaconp3d**)

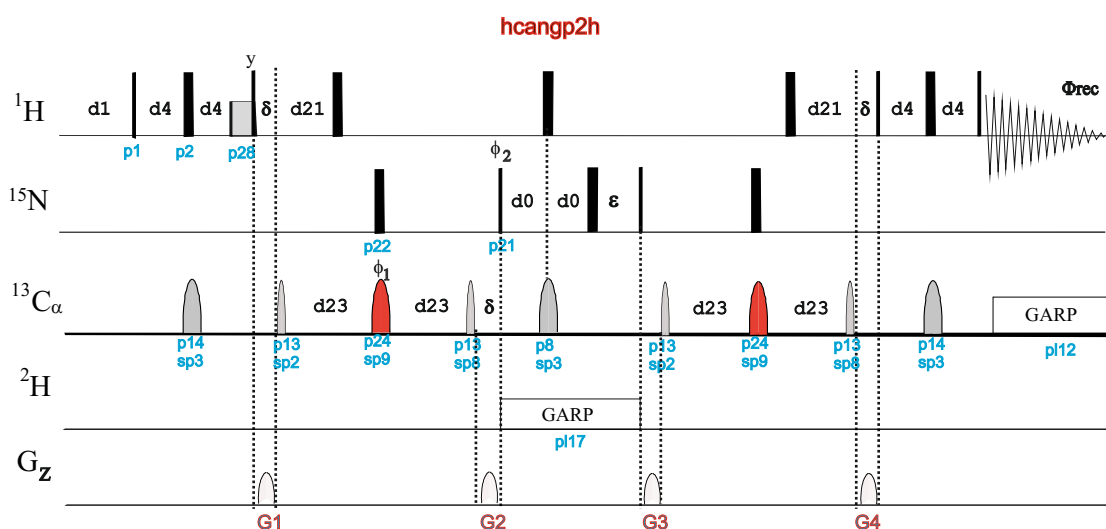
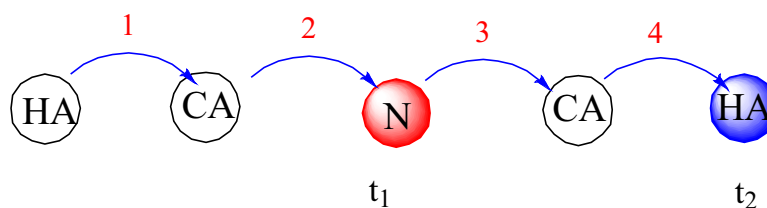
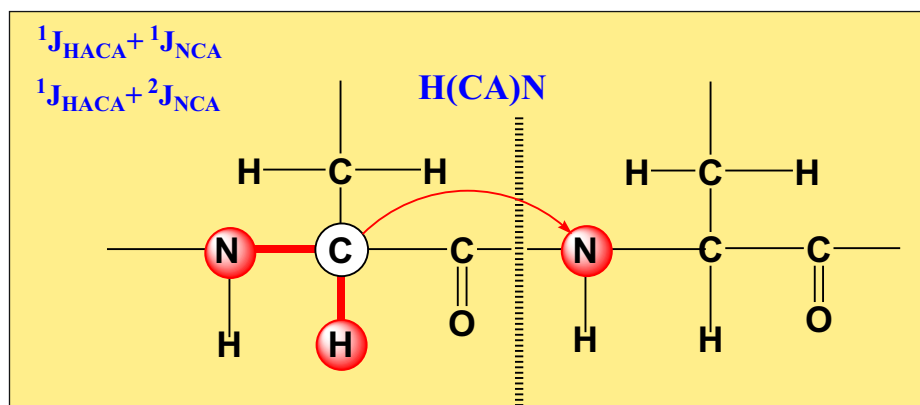


$d4 = 1/4J(\text{CAHA}) = 1.7\text{m}$
 $d21 = 1/4J(\text{CH})$ or $1/6J(\text{CH}) = 1.7\text{m}$ or 1.2m
 $d22 = 1/4J(\text{CACO}) = 4.5\text{m}$

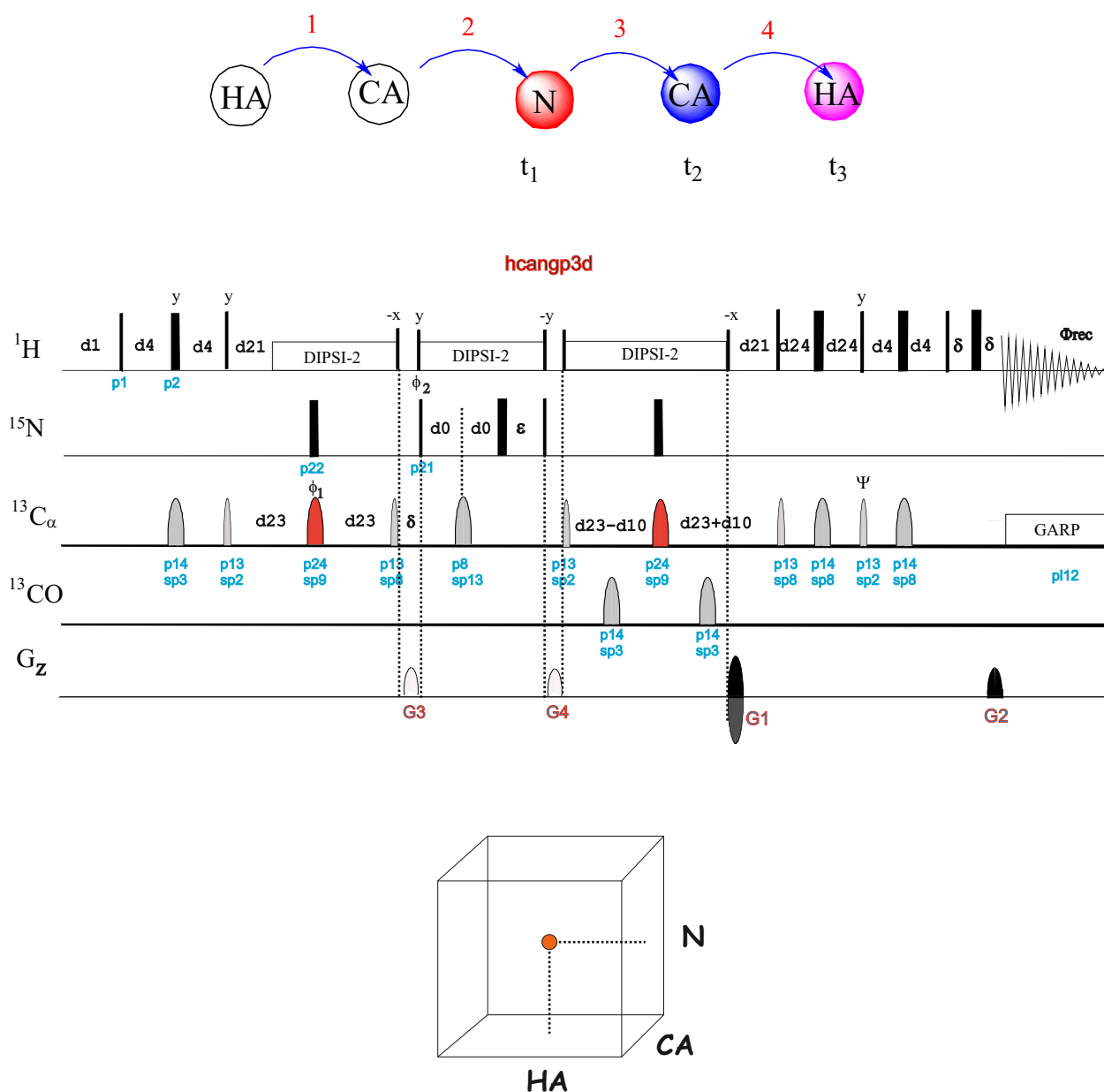


2D H(CA)N Experiment

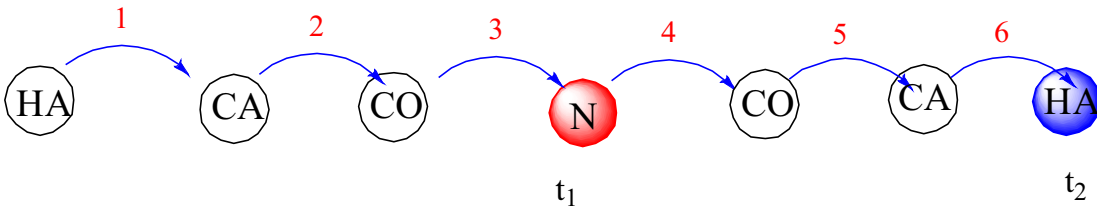
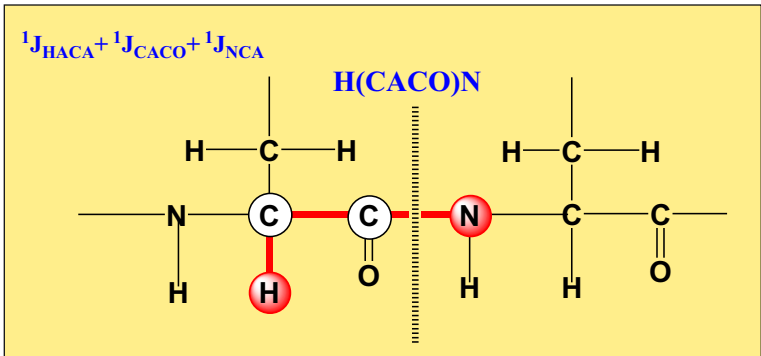
A.C. Wang, S. Grzesiek, R. Tschudin, P.J. Lodi & A. Bax, J. Biomol. NMR 5, 376-382 (1995)



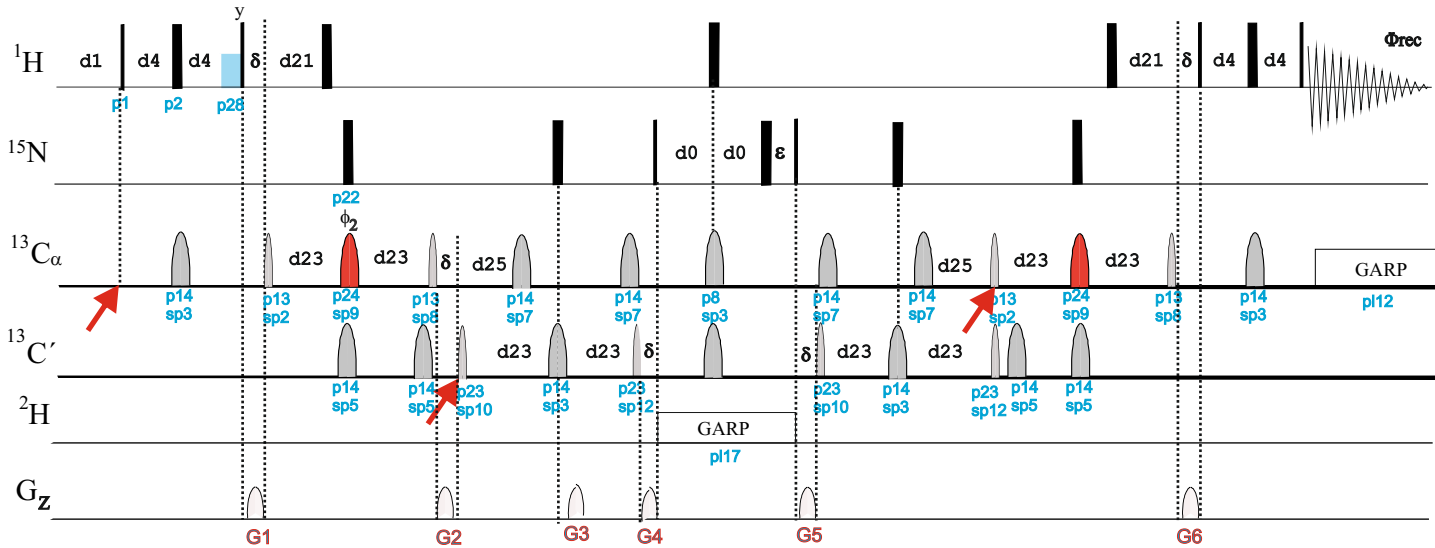
3D HCAN Experiment



2D H(CACO)N Experiment

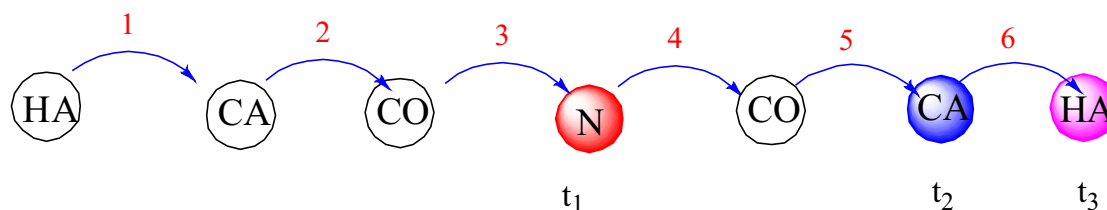
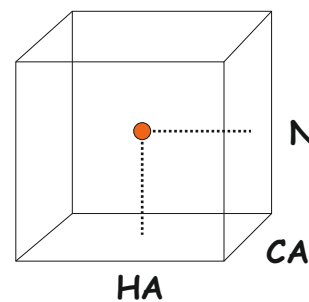
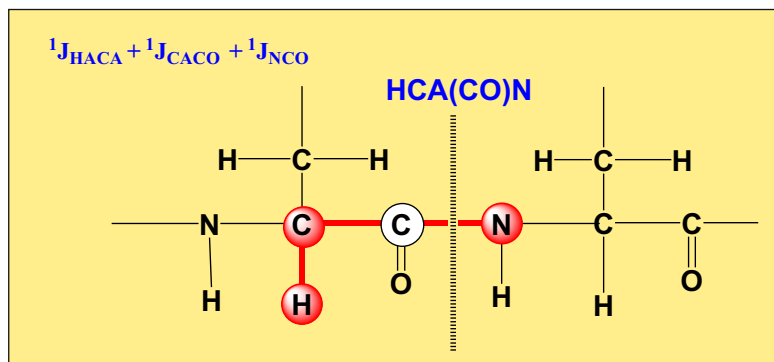


hcacong2h

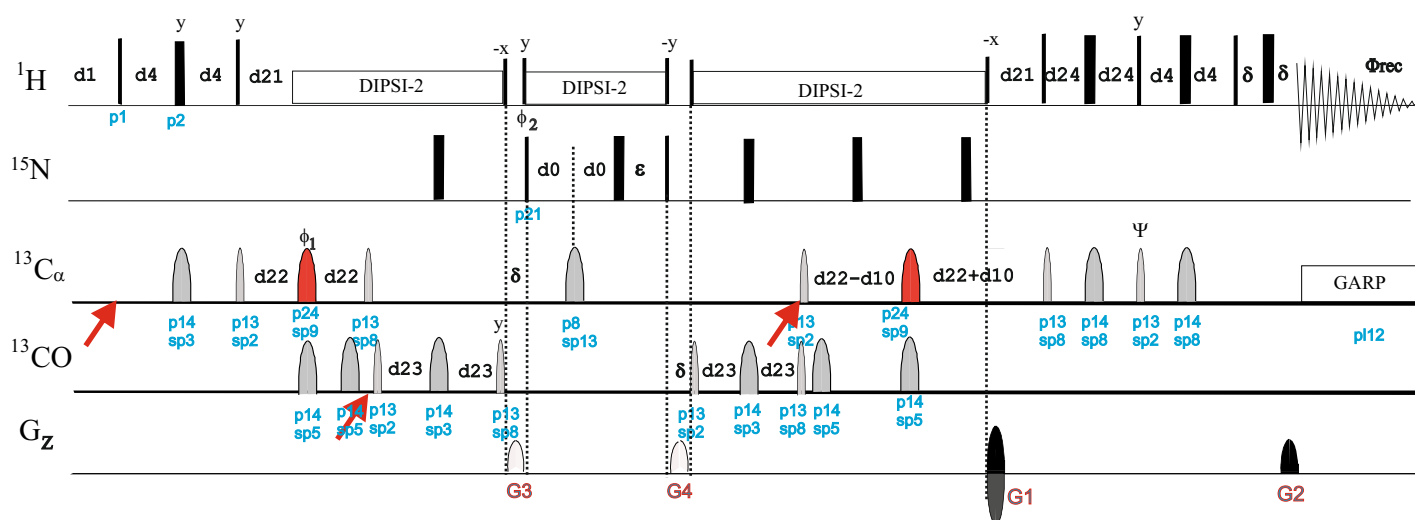


d4 : $1/(4J(\text{H}\text{C}\alpha))$	[1.5 msec]
d21: $1/(4J^-(\text{H}\text{C}\alpha))$	[1.55 msec]
d22: $1/(4J(\text{C}\alpha\text{CO}))$	[4.5 msec]
d23: $1/(4J(\text{NCO}))$	[13.1 msec]
d25: $1/(4J^-(\text{C}\alpha\text{CO}))$	[4.5 msec]

2D HCA(CO)N Experiment



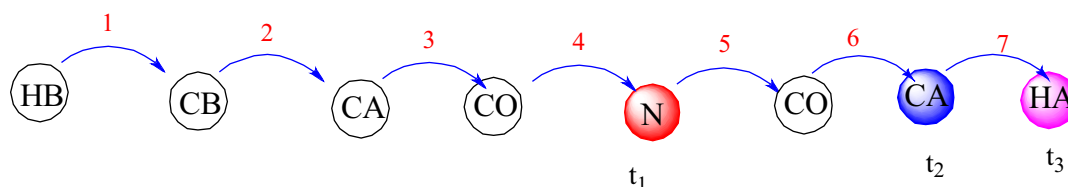
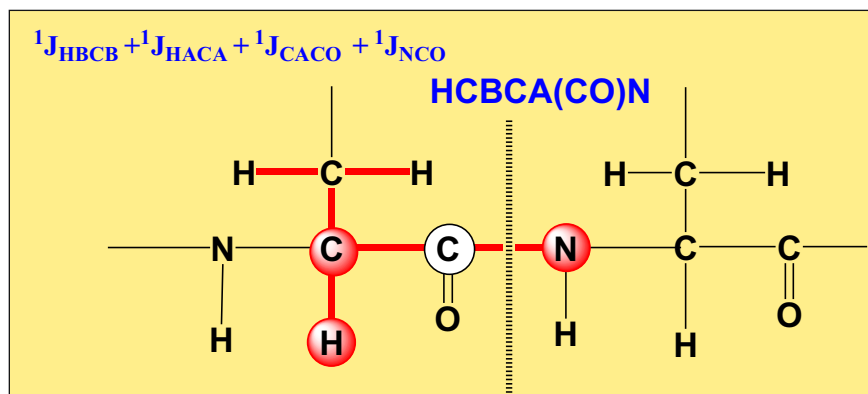
hcacong3d



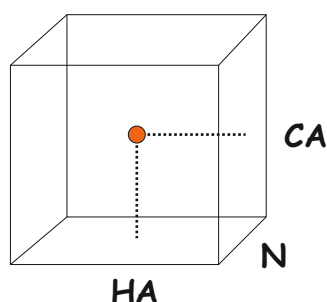
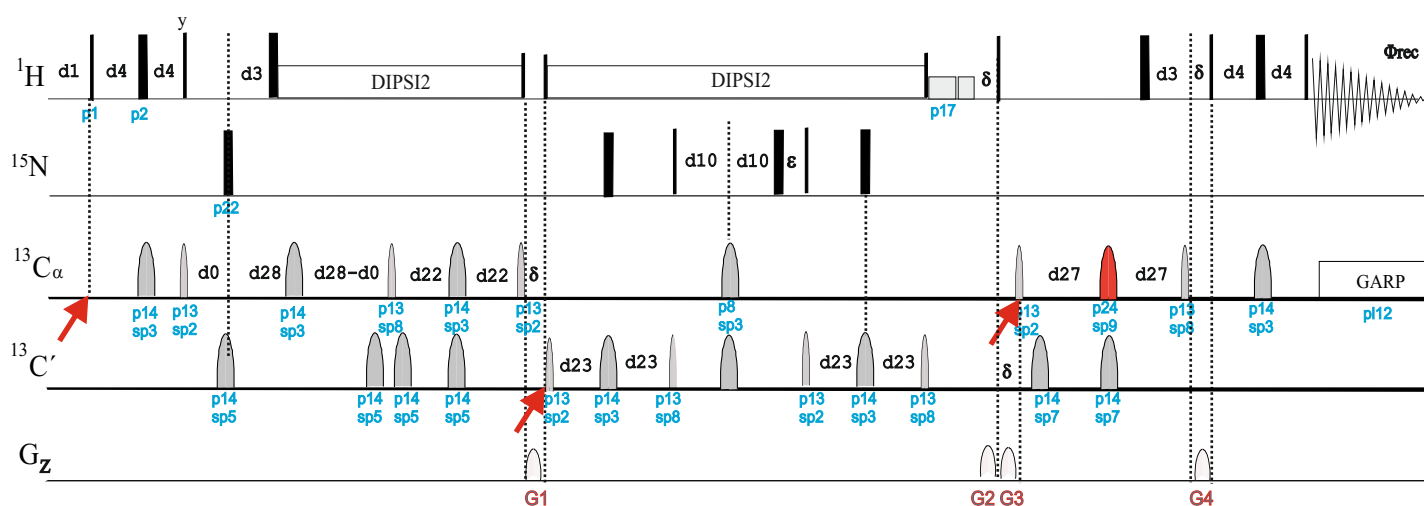
d4 : $1/(4J(\text{HCA}))$	[1.6 msec]
d21: $1/(3J(\text{HCA}))$	[2.2 msec]
d22: $1/(4J(\text{CACO}))$	[4.5 msec]
d23: $1/(4J(\text{NCA}))$	[12 msec]
d24: $1/(8J(\text{HCA}))$ for all multiplicities $1/(4J(\text{HCA}))$ for CH	

2D HCBCA(CO)N Experiment

1. V. Kanelis, L. Donaldson, D.R. Muhandiram, D. Rotin, J.D. Foreman-Kay & L.E. Kay, J. Biomol. NMR 16, 253-259 (2000))
2. A.C. Wang, S. Grzesiek, R. Tschudin, P.J. Lodi & A. Bax, J. Biomol. NMR 5, 376-382 (1995))



hcbcacong3d



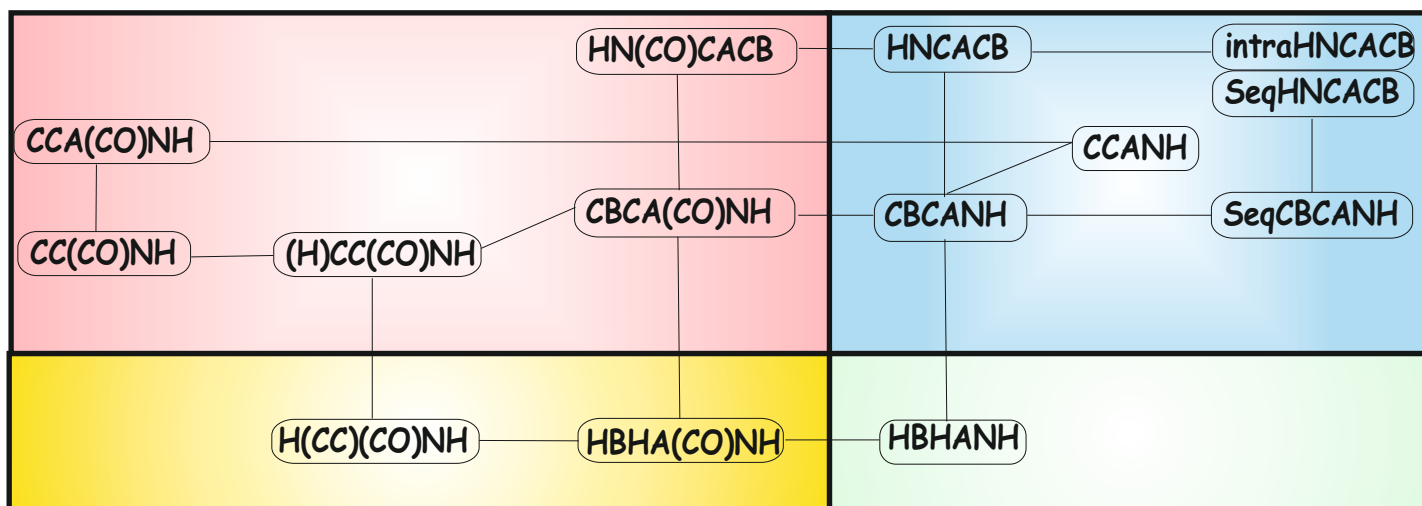
d3 : 1/(6J(HCa))	[1.1 msec]
d4 : 1/(4J(HCa))	[1.6 msec]
d22: 1/(4J'(COCa))	[3.6 msec]
d23: 1/(4J(NCO))	[12 msec]
d27: 1/(4J(COCa))	[4.2 msec]
d28: 1/(8J(CaCb))	[3.6 msec]

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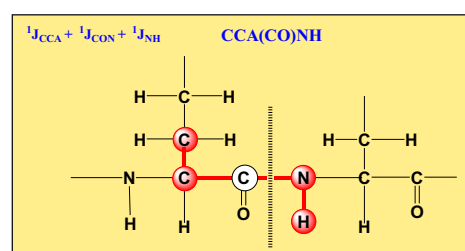
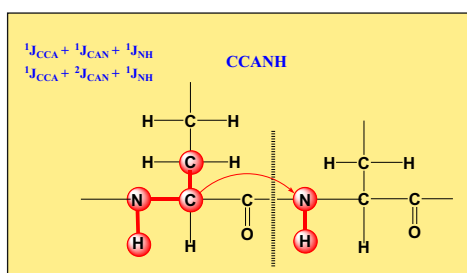
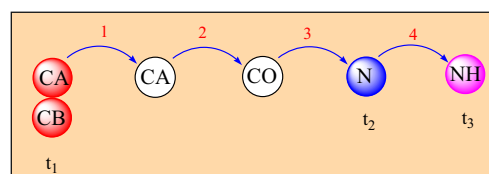
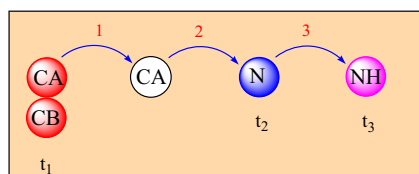
PROTEIN NMR.
BACKBONE-SIDECHAIN
3D EXPERIMENTS

3D BACKBONE-SIDECHAIN



A. Experiments Involving CO into the Magnetization Transfer Mechanism

Example: CCANH vs CCA(CO)NH:

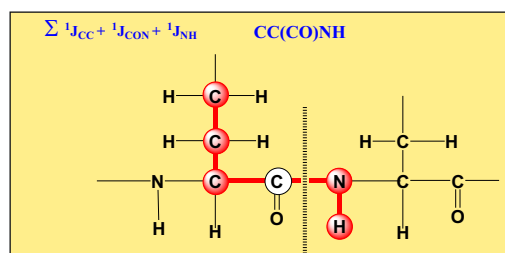
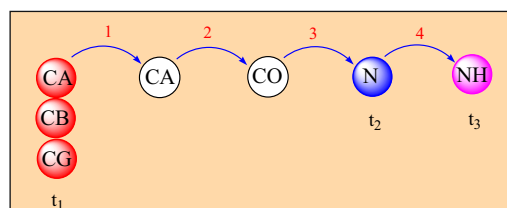
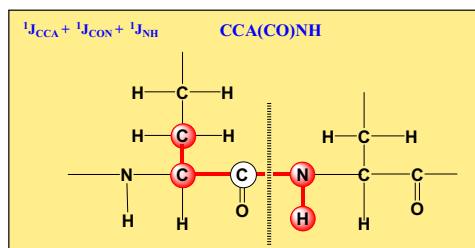
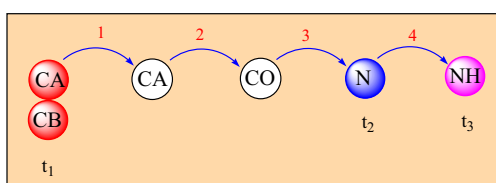


Other examples:

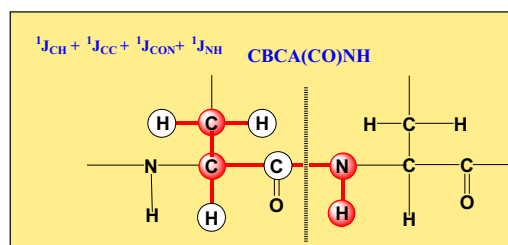
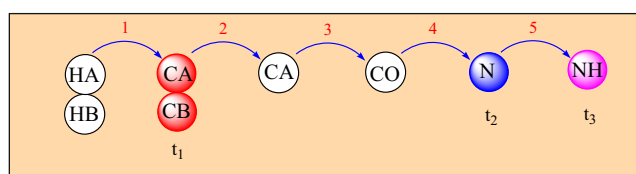
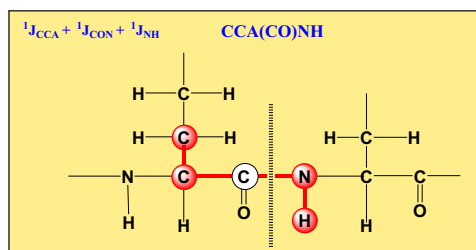
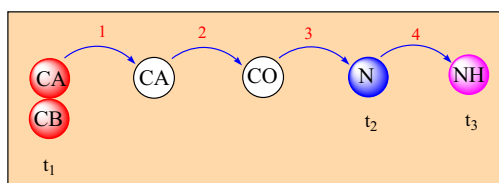
$CBCA(CO)NH$ vs $CBCANH$

$HN(CO)CACB$ vs $HNCACB$

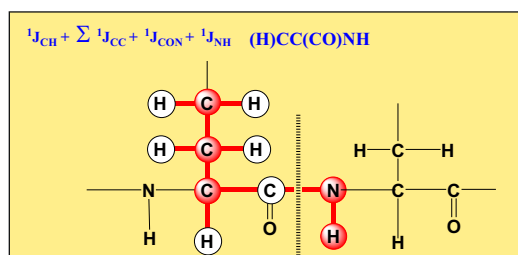
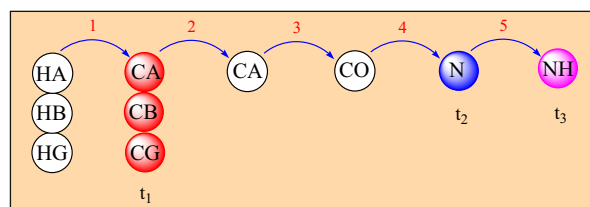
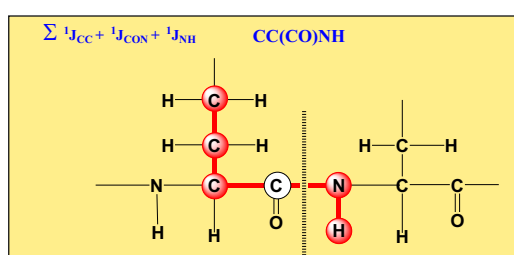
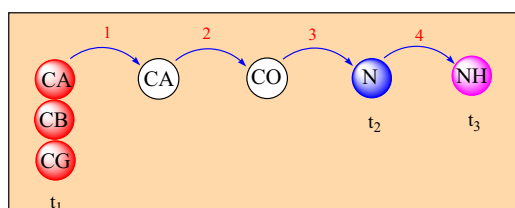
B. COSY vs TOCSY CC Transfer. Example: CCA(CO)NH vs CC(CO)NH



C. Starting from ^{13}C or from 1H . Example1: CCA(CO)NH vs CBCA(CO)NH

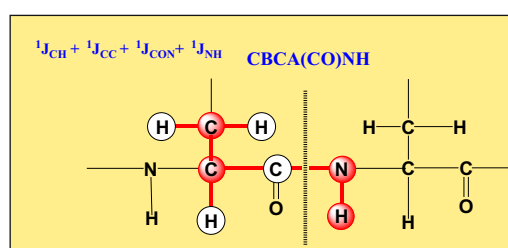
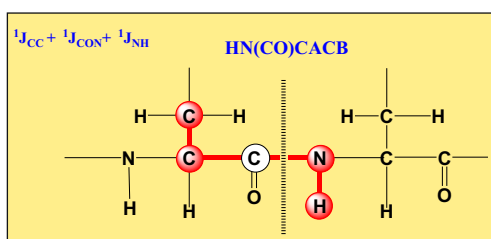
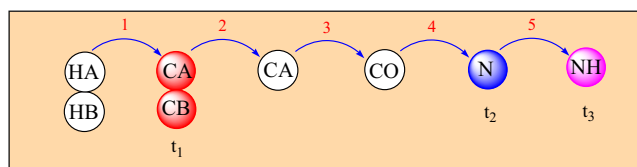
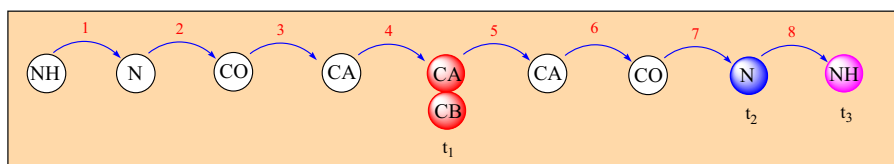


Example 2: CC(CO)NH vs (H)CC(CO)NH:



D. Out-and-back vs Out-and-Stay. Examples: HN(CO)CACB vs CBCA(CO)NH

Other examples: HNCACB vs CBCANH



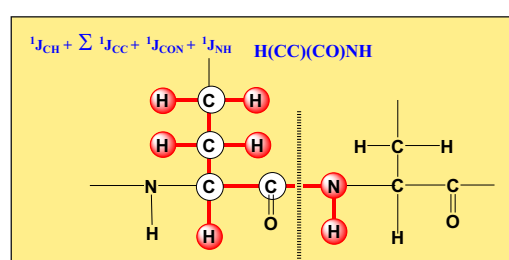
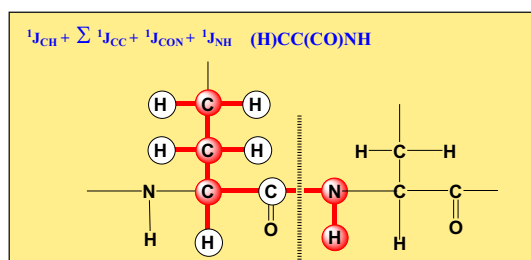
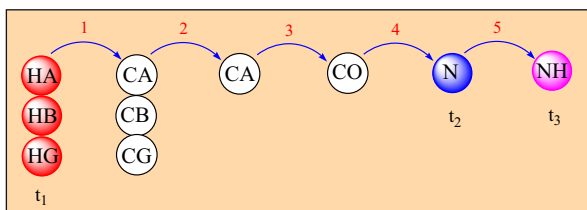
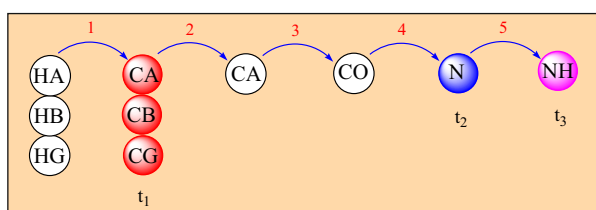
E. Evolving Aliphatic Carbons or Aliphatic protons.

Example (H)CC(CO)NH vs H(CC)(CO)NH:

Other examples:

CBCA(CO)NH vs HBHA(CO)NH

CBCANH vs HBHANH



BRUKER PULSE PROGRAM CATALOGUE

NMRGuide

3D CBCACONH

CBCACONH experiment

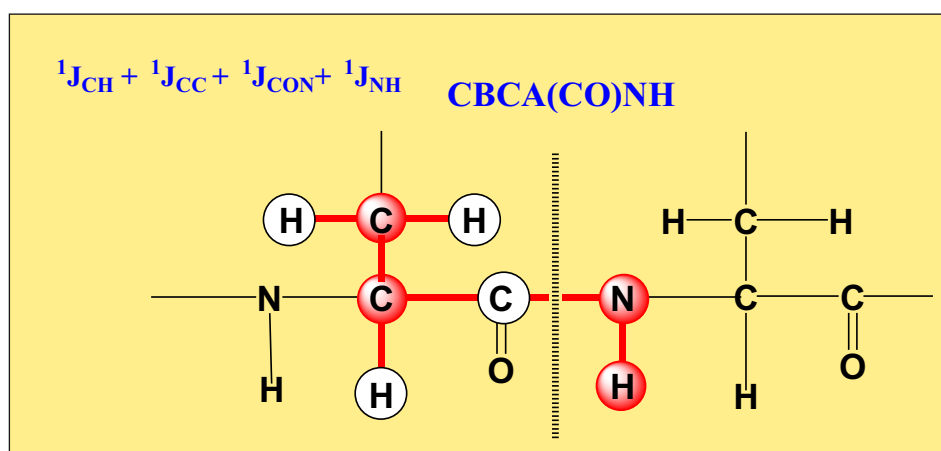
- 3D CBCA(CO)NH using PEP (`cbcaconhgp3d` | `CBCACONHGP3D`)
- 3D CBCA(CO)NH using WATERGATE (`cbcaconhgpgw3d` | `CBCACONHGPGW3D`)
- 3D CBCA(CO)NH using WATERGATE and filter for CG (`cbcaconhgpgw3d.2`)
- 3D CBCA(CO)NH using TROSY (`trcbcaconhgp3d` | `TRCBCACONHGP3D`)
- 3D CBCA(CO)NH using TROSY and gradient echo-antiecho (`trcbcaconhetgp3d` | `TRCBCACONHETGP3D`)
- 4D CBCACONH using WATERGATE (`cbcaconhgpgw4d`)
- 5D HBHACBCACONH using WATERGATE (`hbhacbcconhgpgw5d`)

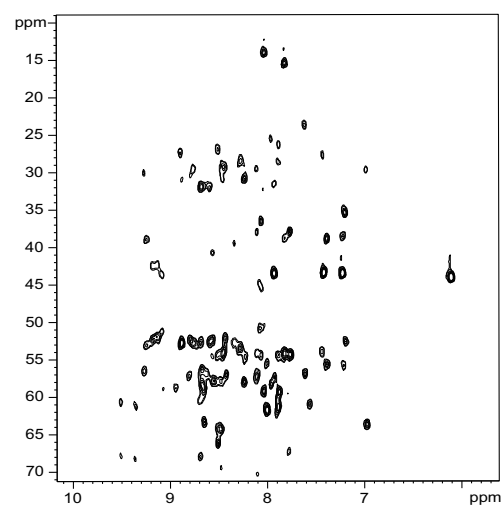
Also see:

CBCANH experiments

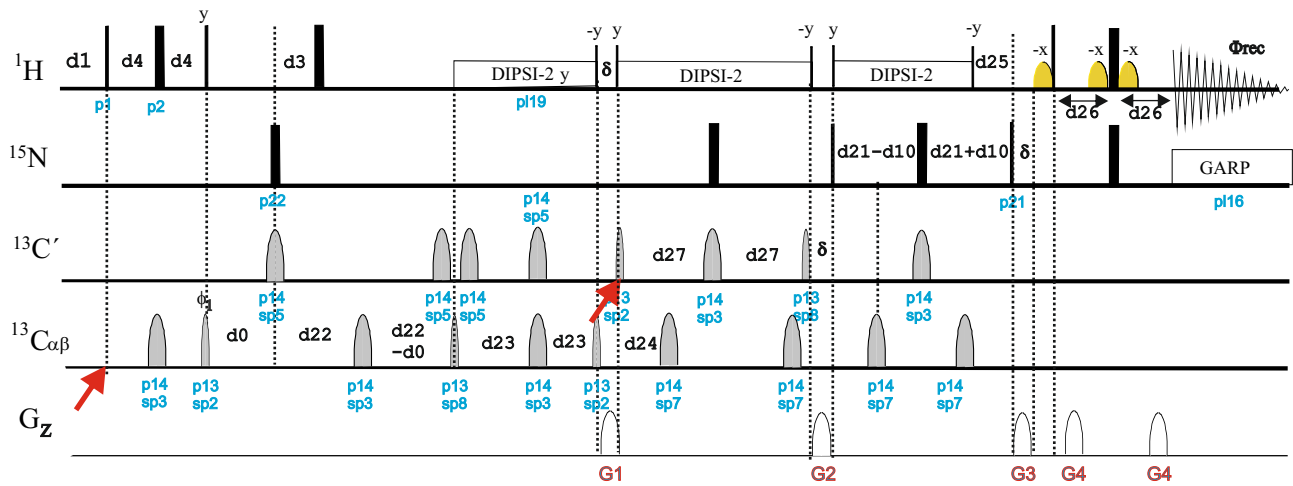
HN(CO)CACB experiments

HCCCONH experiments

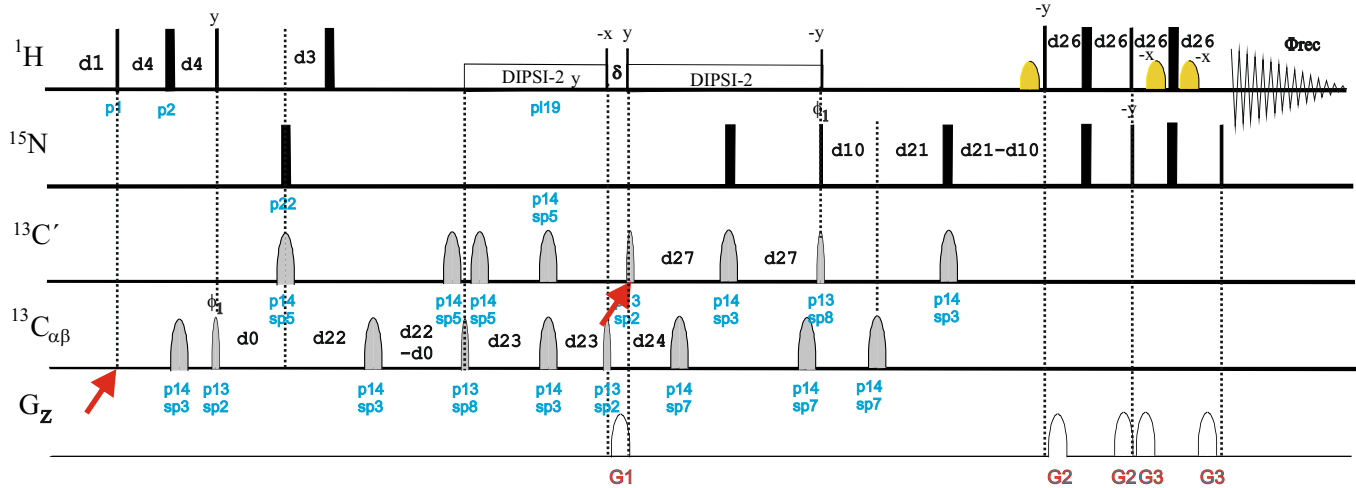




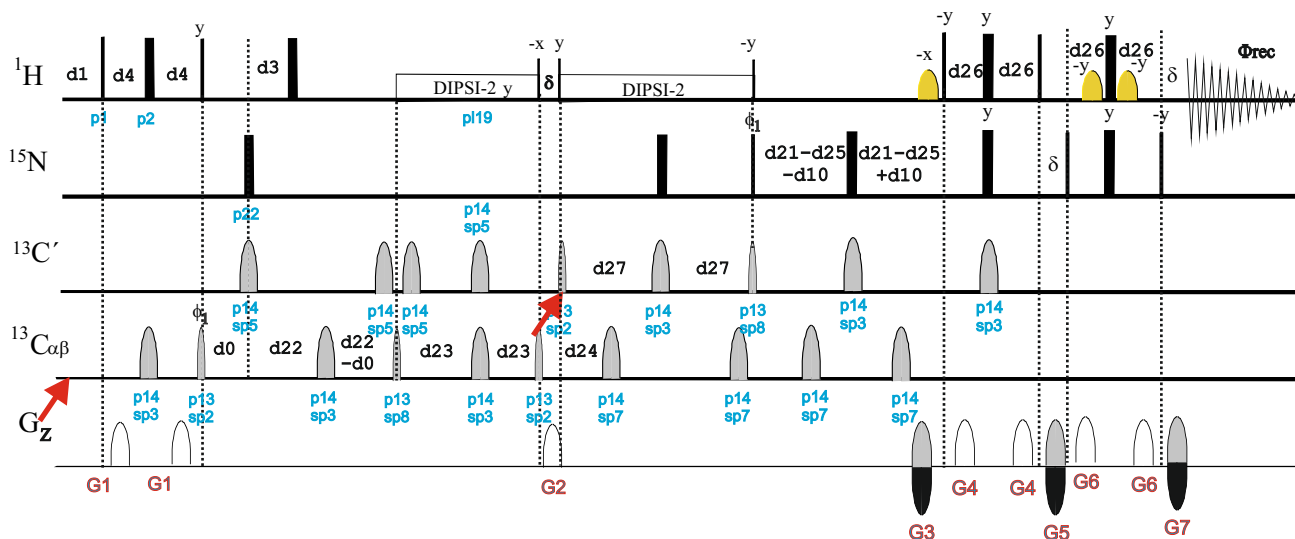
cbcaconhpgwg3d



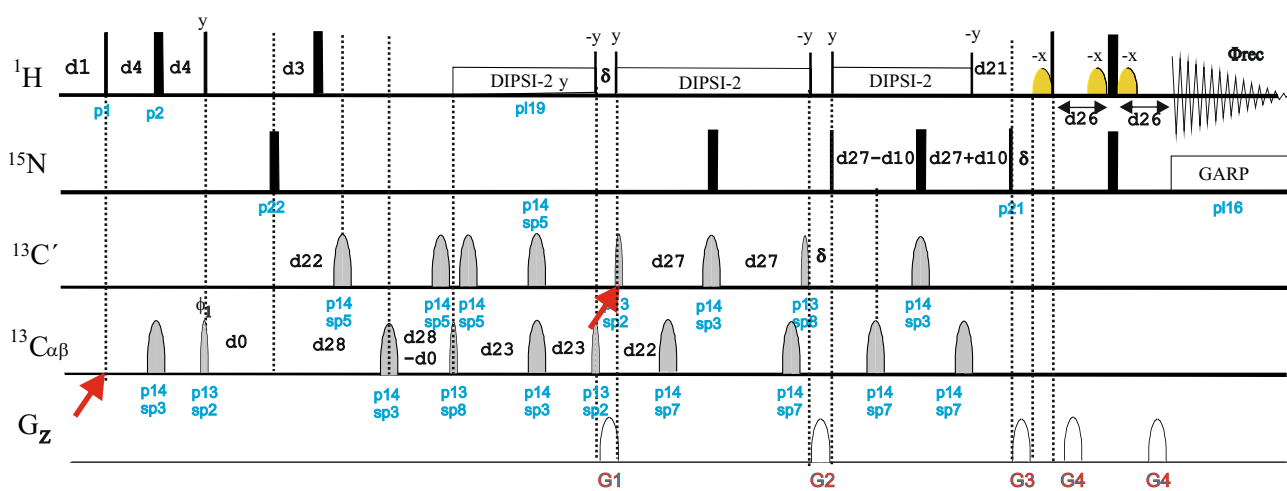
trcbcaconhpg3d



trcbcaconhetgp3d



cbcaconhgpwg3d.2



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BRUKER PULSE PROGRAM CATALOGUE

NMRGuide

3D HN(CO)CACB

3D HN(CO)CACB experiment

- 3D HN(CO)CACB using PEP (**hncocacbgp3d** | HNCOCACBP3D):
 - with ^2H -decoupling (**hncocacbgp2h3d** | HNCOCACBP2H3D)
- 3D HN(CO)CACB using WATERGATE (**hncocacbgpwg3d** | HNCOCACBPWG3D)
 - with ^2H -decoupling (**hncocacbgpwg2h3d** | HNCOCACBPWG2H3D)
- 3D HN(CO)CACB using TROSY (**trhncocacbgp3d** | TRHNCOCACBP3D):
 - with ^2H -decoupling (**trhncocacbgp2h3d** | TRHNCOCACBP2H3D)
 - using gradient echo-antiecho (**trhncocacbetgp3d** | TRHNCOCACBETGP3D)
 - using gradient echo-antiecho and with ^2H -decoupling (**trhncocacbetgp2h3d** | TRHNCOCACBETGP2H3D)

Also see:

APSY-HNCOCACB experiment

Reduced-Dimensionality (3,2)-HNCOCACB (**rd_hncocacb_32** | APSY_HNCOCACB_32)

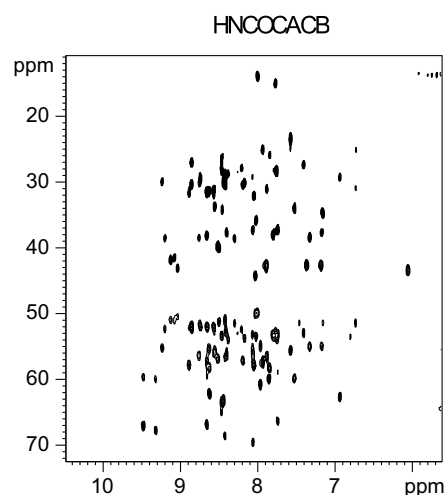
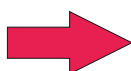
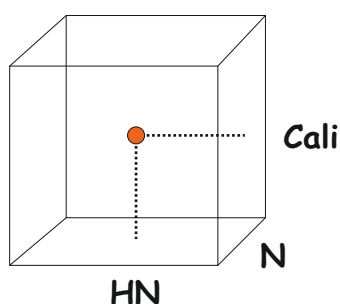
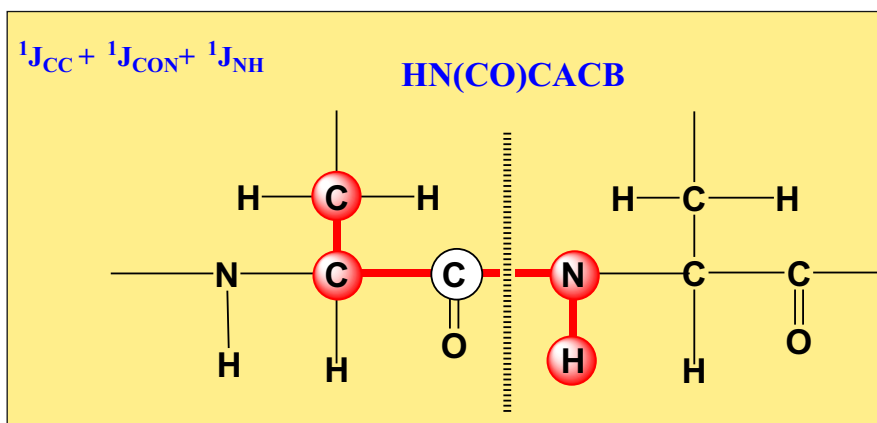
SOFAST/BEST-HNCOCACB experiment

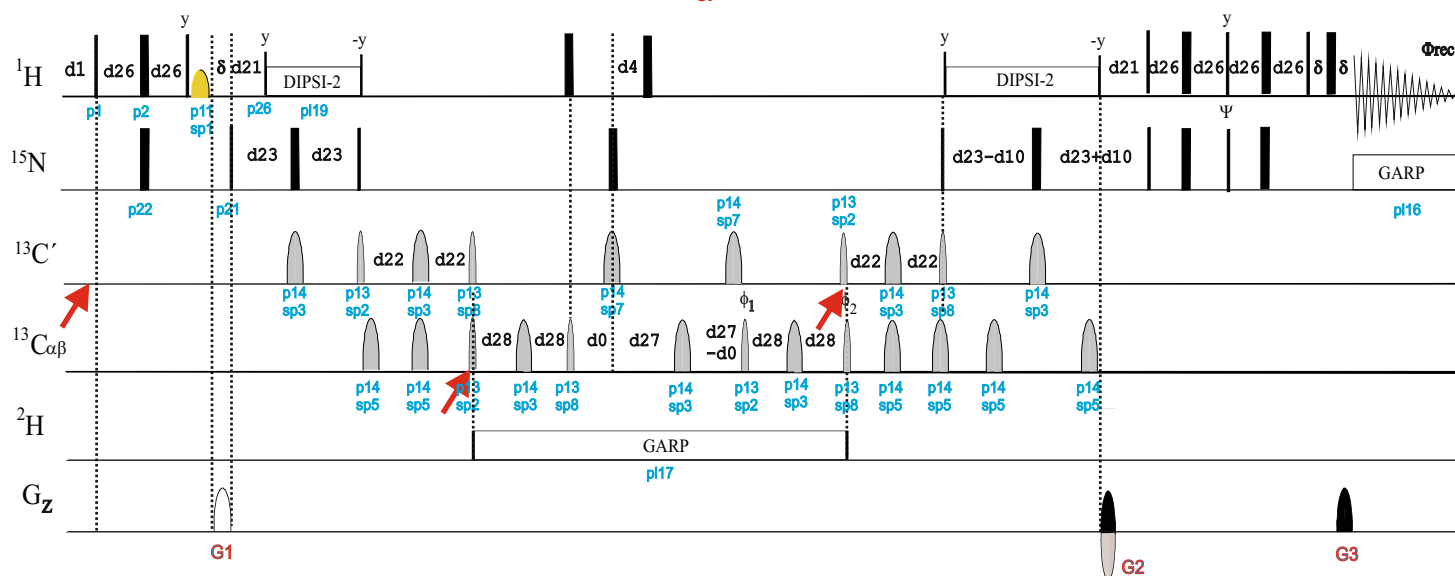
3D BEST-HN(CO)CACB (**b_hncocacbgp3d** | B_HNCOCACBP3D)

3D BEST-HN(CO)CACB using TROSY (**b_trhncocacbgp3d**)

4D BEST-HNCOCACB (**b_hncocacbgp4d**)

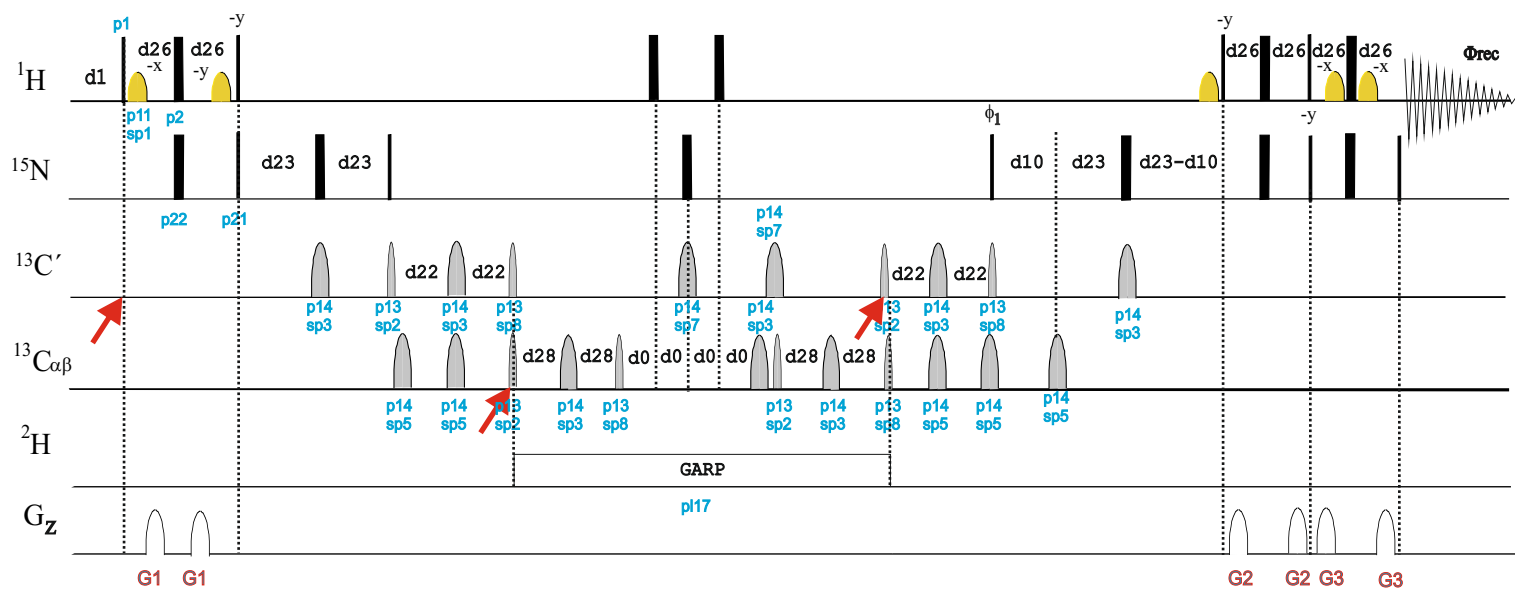
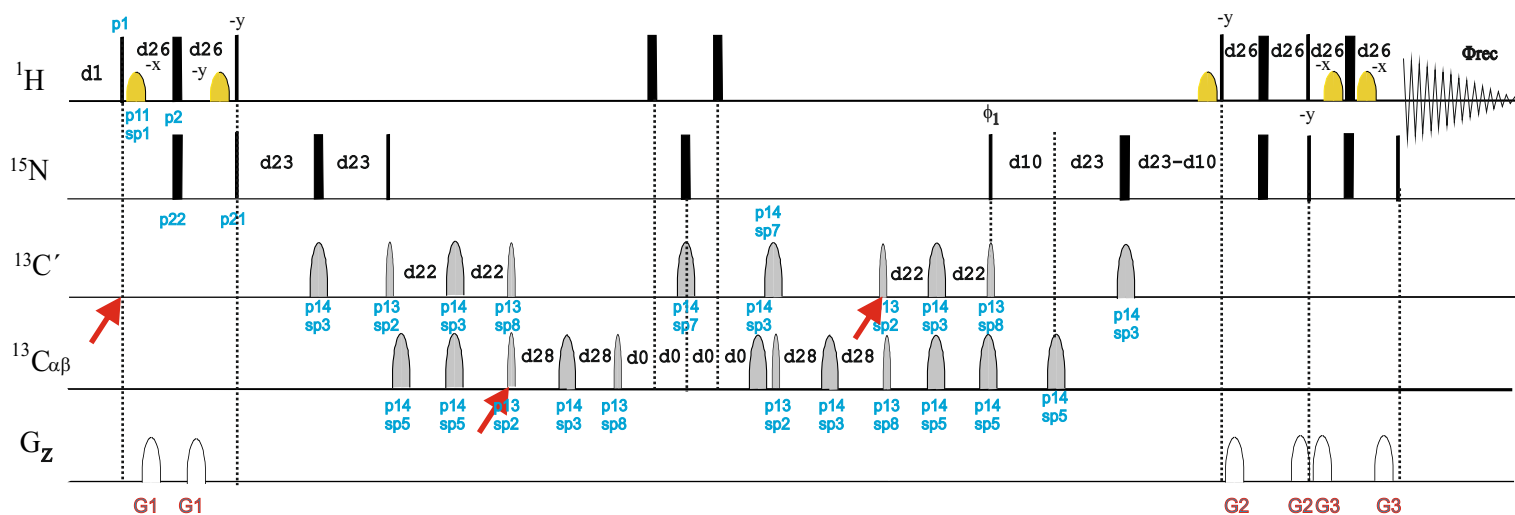
3D HNCACB and CBCA(CO)NH experiments





d26=1/4J(NH)=2.3m
d21=1/2J(NH)=5.5m
d23=1/4J(NCO)=12m
d22=1/4J(CACO)=4m
d28=1/4J(CACB)=3.6m

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3D CBCANH

CBCANH experiment

- 3D CBCANH using PEP (**cbcanhgp3d** | CBCANHGP3D)
- 3D CBCANH using WATERGATE (**cbcanhgpwg3d** | CBCANHGPWG3D)
- 3D CBCANH using TROSY (**trcbcanhgp3d** | TRCBCANHGP3D)
- 3D CBCANH using TROSY and gradient echo-antiecho (**trcbcanhetgp3d** | TRCBCANHETGP3D)
- 4D HBHACBCANH using WATERGATE (**hbhacbcanhgpwg4d**)

Also see:

HNCACB experiments

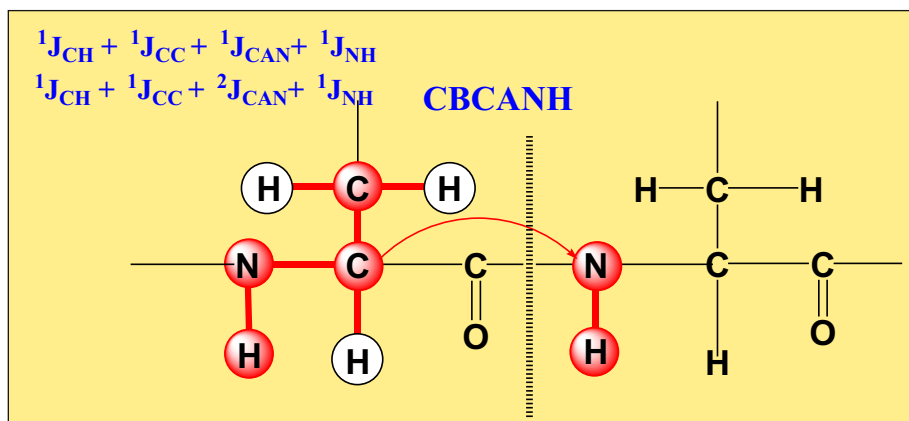
Sequential CBCANH experiments

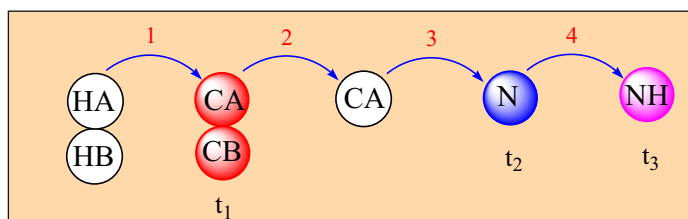
CBCA(CO)NH experiments

CCANH experiments

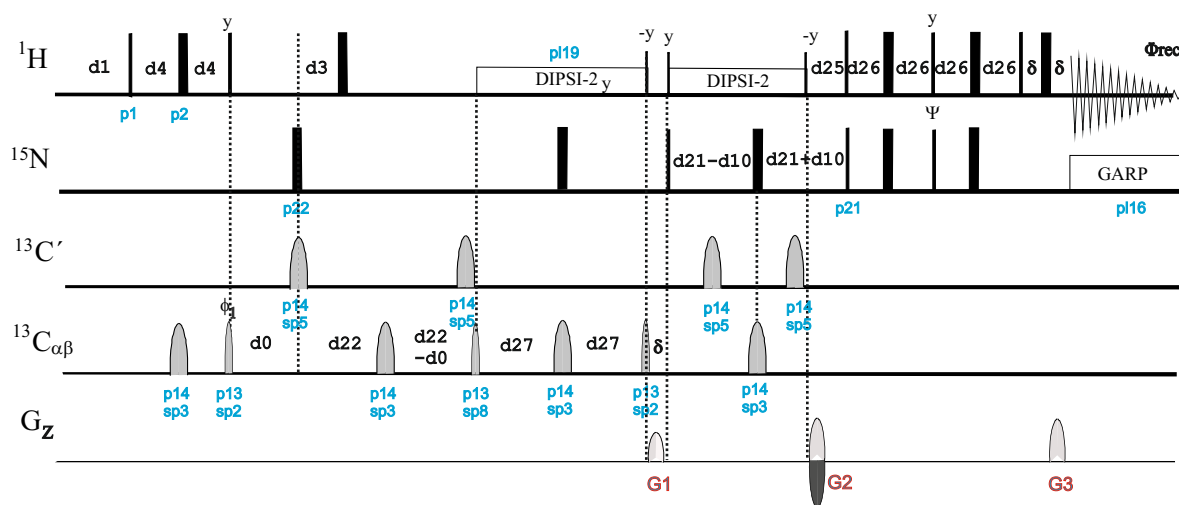
References:

S. Grzesiek & A. Bax, J. Magn. Reson. 99, 201-207 (1992)

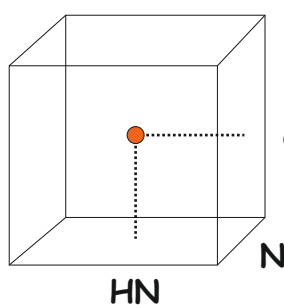




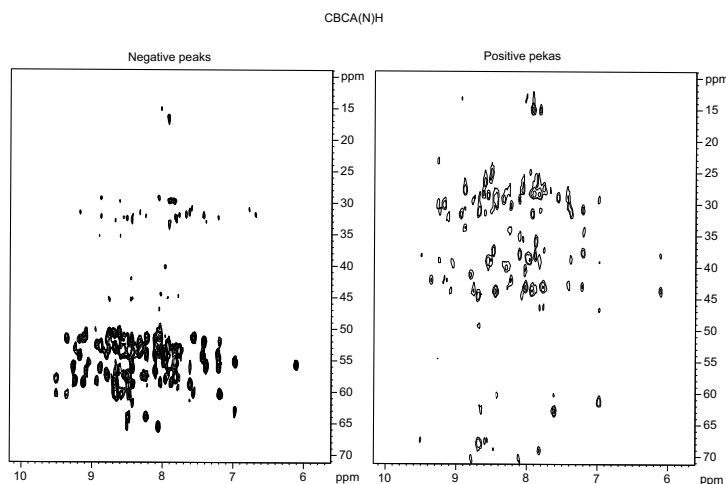
cbcanhgp3d

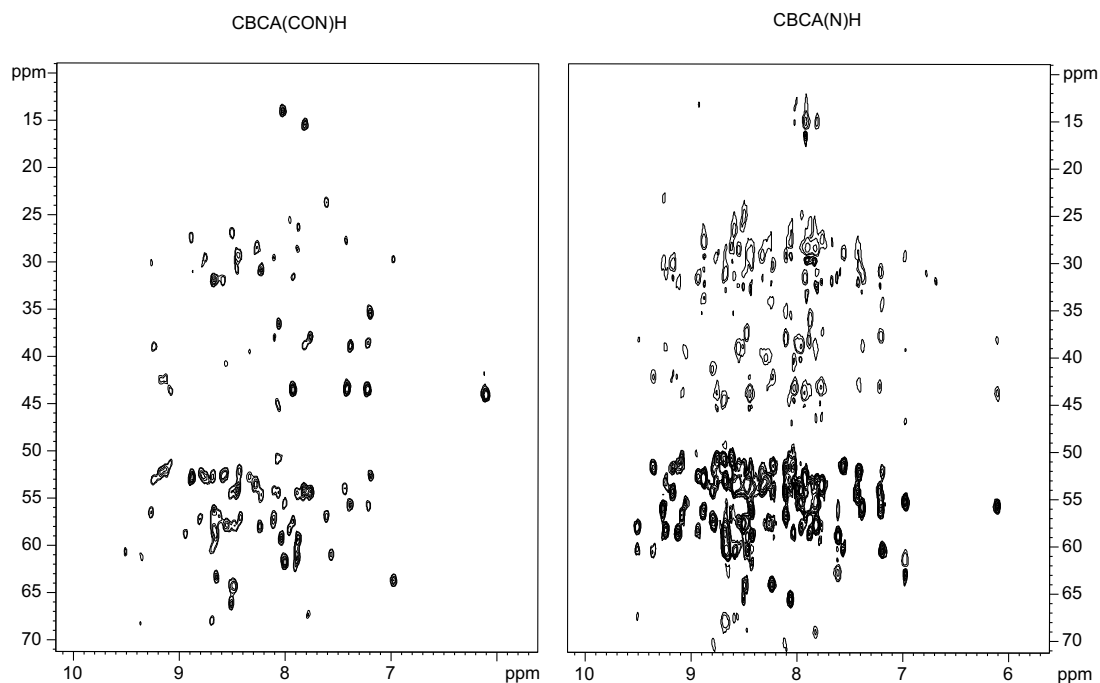
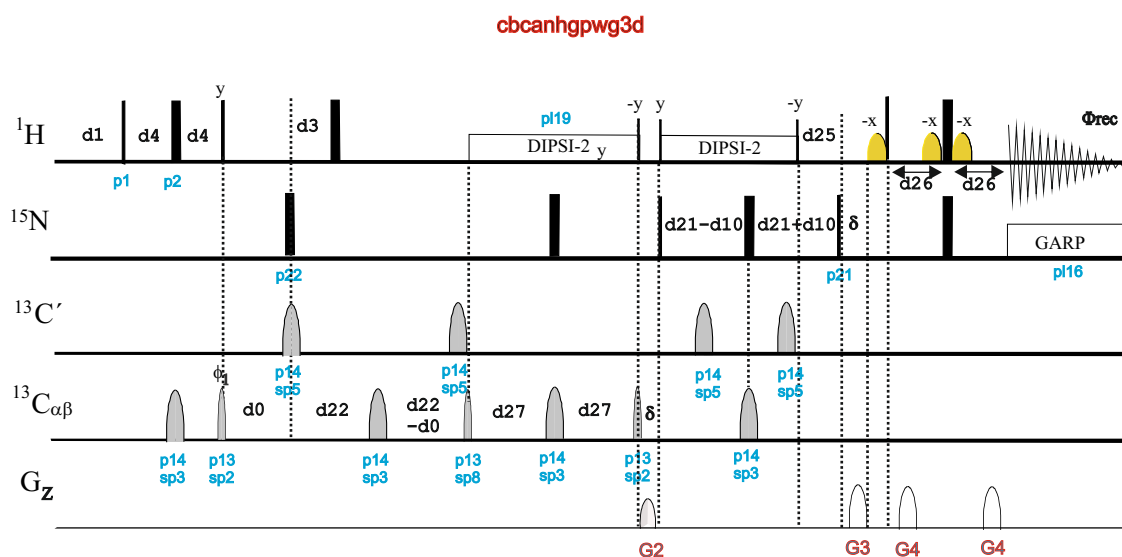


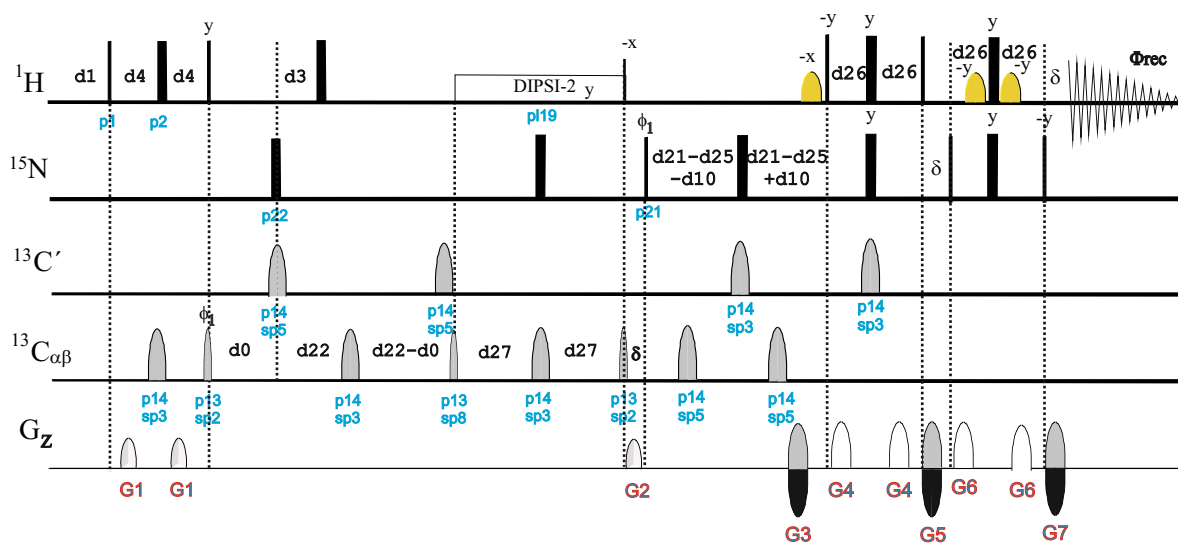
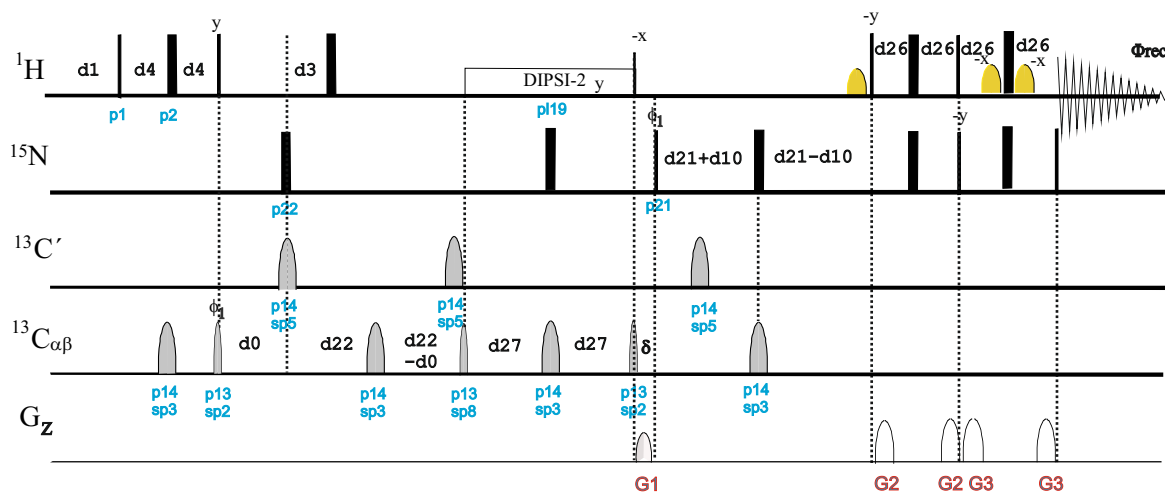
$$\begin{aligned} d4 &= 1/4J(\text{CH}) = 1.7\text{m} \\ d3 &= 1/6J(\text{CH}) = 1.1\text{m} \\ d22 &= 1/4J(\text{CBCA}) = 3.6\text{m} \\ d27 &= 1/4J(\text{NCO}) = 11\text{m} \\ d21 &= 1/4J(\text{NCO}) = 12.4\text{m} \\ d25 &= 1/2J(\text{NH}) = 5.5\text{m} \\ d26 &= 1/4J(\text{NH}) = 2.3\text{m} \end{aligned}$$



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3D SEQUENTIAL CBCANH

3D Sequential CBCANH experiment

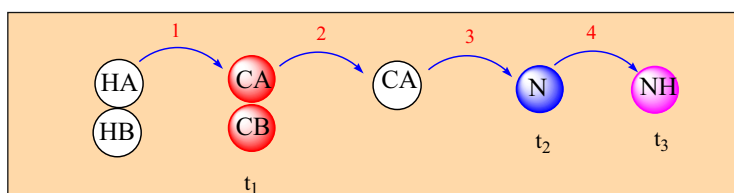
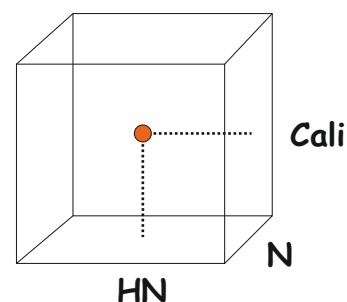
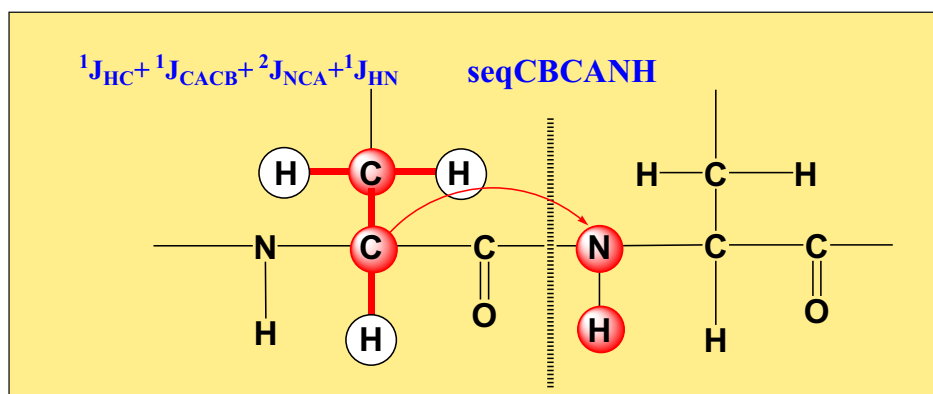
- 3D Sequential CBCANH using TROSY (`seqtrcbcanhgp3d` | `SEQTRCBCANHGP3D`)

Also see:

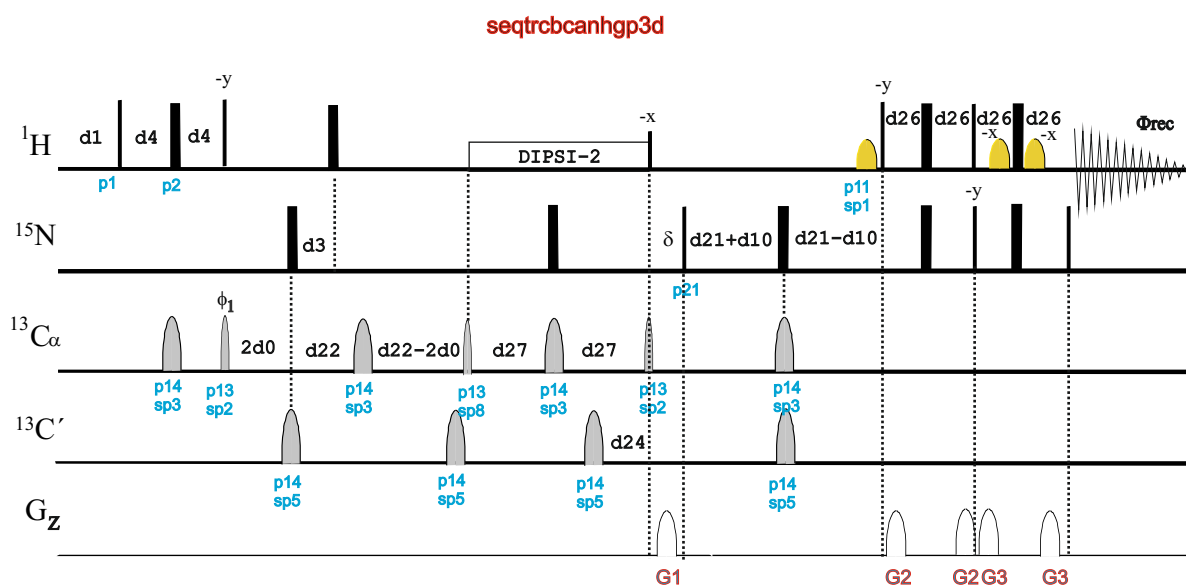
CBCANH experiments

Sequential HNCACB experiment

Ref: A. Meissner & O.W. Sorensen, J. Magn. Reson. 151, J. Biomol. NMR 20, 188-180 (2001))



$d26 = 1/4J(NH) = 2.3m$
 $d21 = 1/4J(NCA) = 12.4m$
 $d22 = 1/8J(CACB) = 3.6m$
 $d27 = 1/4J(NCA) = 11m$
 $d24 = 1/4J(CACO) = 4.5m$
 $d4 = 1/4J(CH) = 1.7m$
 $d3 = 1/6J(CH) = 1.1m$



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3D HNCACB

3D HNCACB experiment

- 3D HNCACB using PEP (**hncacb3d** | **HNCACB3D**):
 - with ^2H -decoupling (**hncacbgp2h3d** | **HNCACBGP2H3D**)
- 3D HNCACB using WATERGATE (**hncacbgpwg3d** | **HNCACBGPW2H3D**)
 - with ^2H -decoupling (**hncacbgpwg2h3d** | **HNCACBGPW62H3D**)
- 3D HNCACB using TROSY (**trhncacb3d** | **TRHNCACB3D**):
 - with ^2H -decoupling (**trhncacbgp2h3d** | **TRHNCACBGP2H3D**)
 - with gradient echo-antiecho (**trhncacbetgp3d** | **TRHNCACBETGP3D**)
 - with gradient echo-antiecho and with ^2H -decoupling (**trhncacbetgp2h3d** | **TRHNCACBETGP2H3D**)

Also see:

3D APSY-HNCACB experiment

Reduced-Dimensionality (3,2)-HNCACB (**rd_hncacb_32** | **APSY_HNCACB_32**)

3D SOFAST/BEST-HNCACB experiment

3D BEST-HNCACB (**b_hncacb3d** | **B_HNCACB3D**)

3D BEST-HNCACB using TROSY (**b_trhncacb3d**)

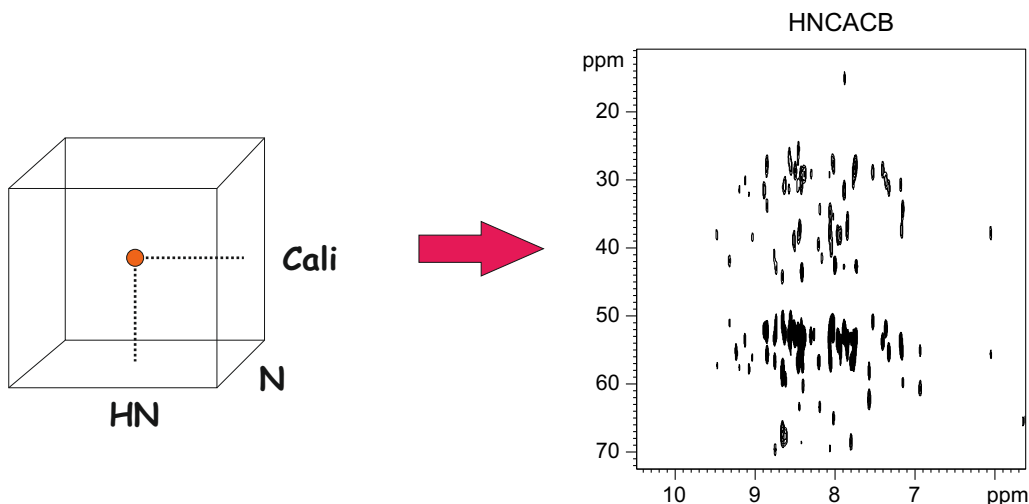
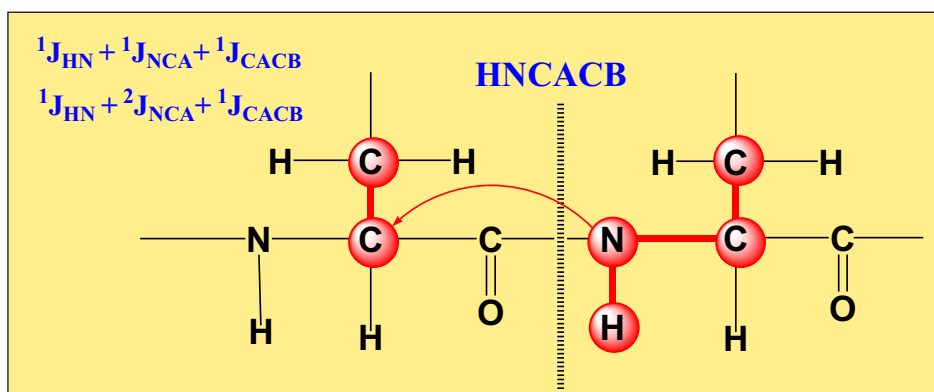
3D HNCACB for J Measurements

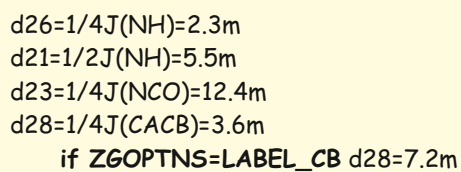
3D HNCACB[CO]-E.COSY (**hncacbgpjc3d** | **HNCACBGPJC3D**) - $3J[\text{CO-CB}]$ via E.COSY

3D HNCA(CO)CB and CBCANH experiments

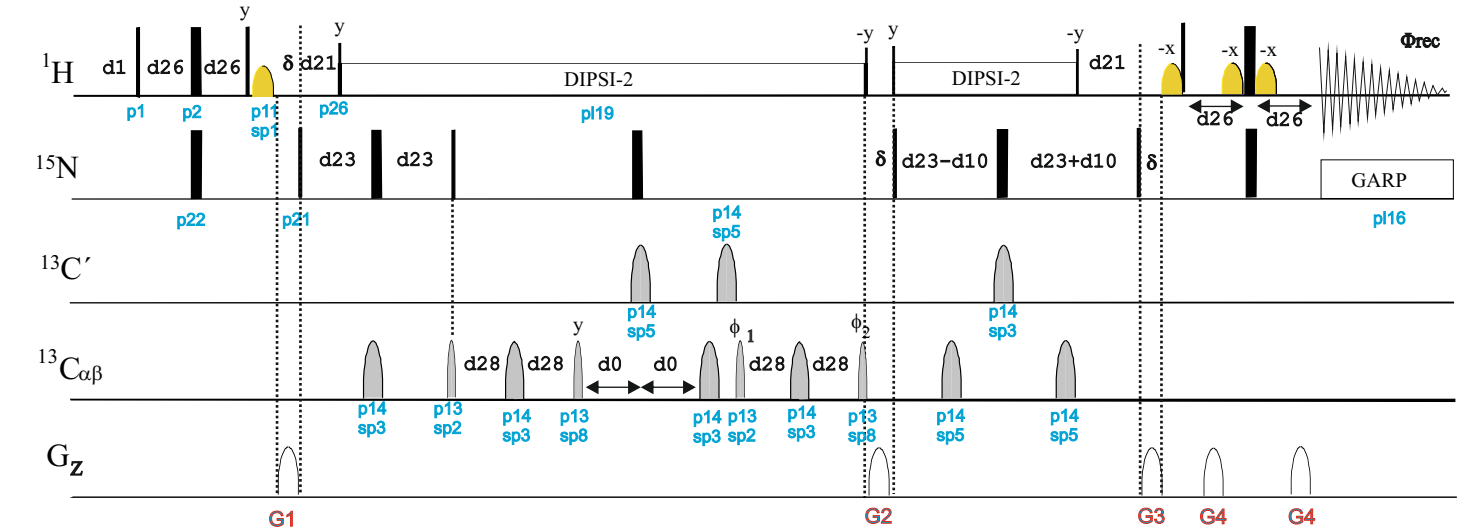
3D intra-HNCACB & 3D sequential-HNCACB experiments

1. M. Wittekind & L. Mueller, J. Magn. Reson. B 101, 201-205 (1993)
2. D.R. Muhandiram & L.E. Kay, J. Magn. Reson. B 103, 203-216 (1994)

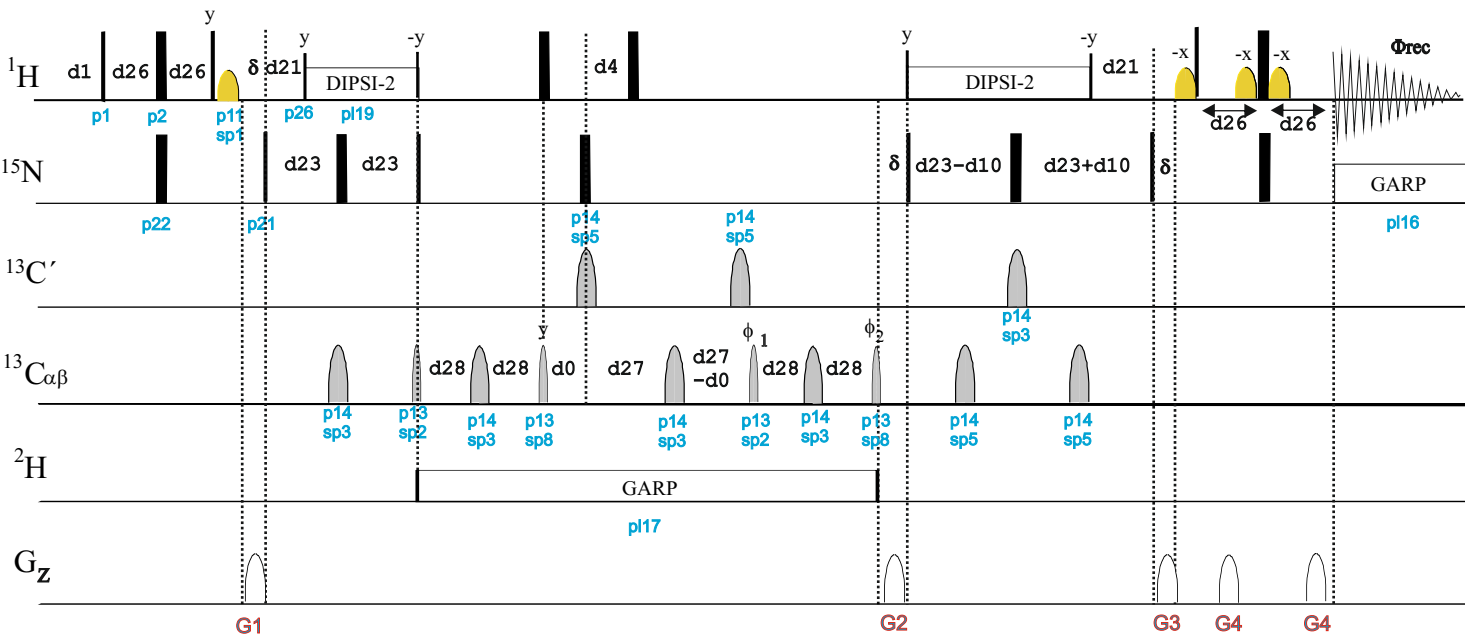


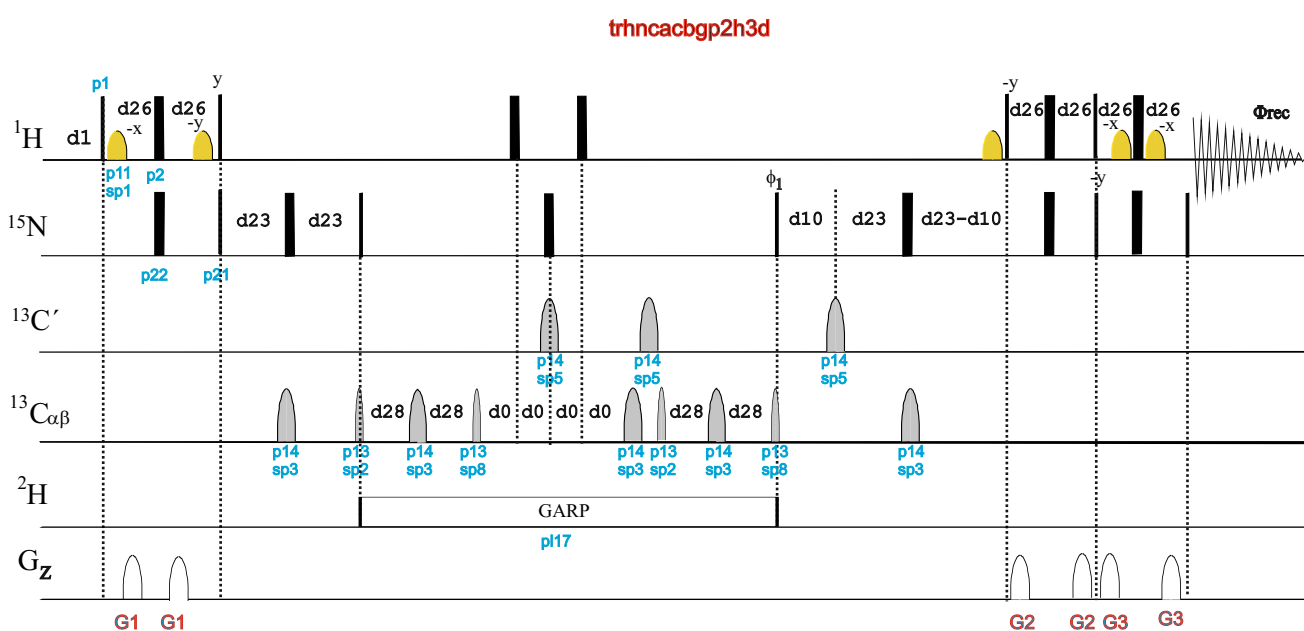
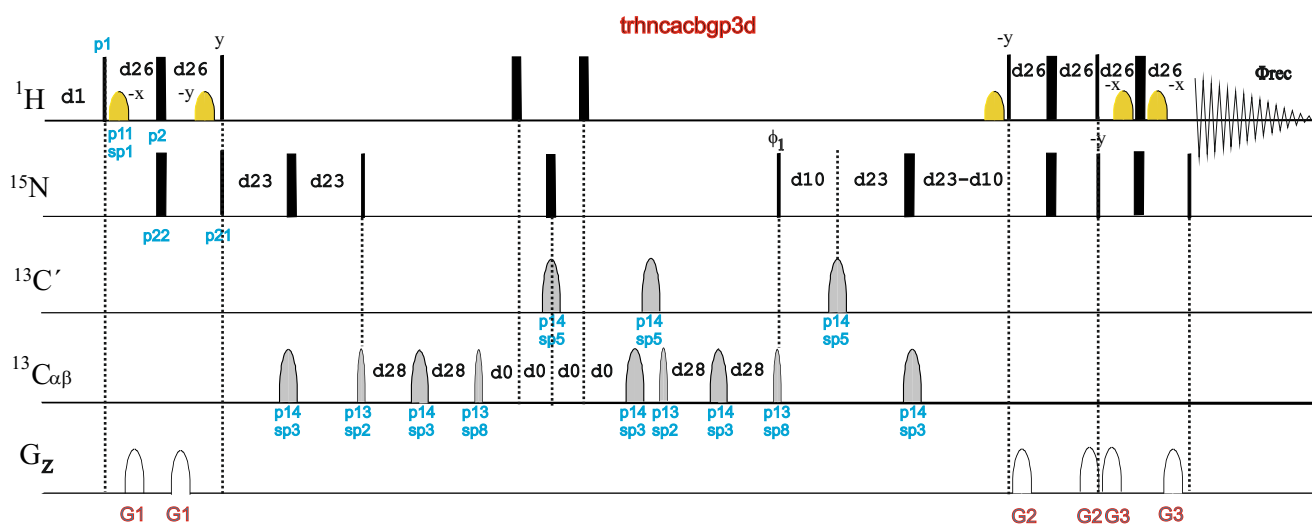


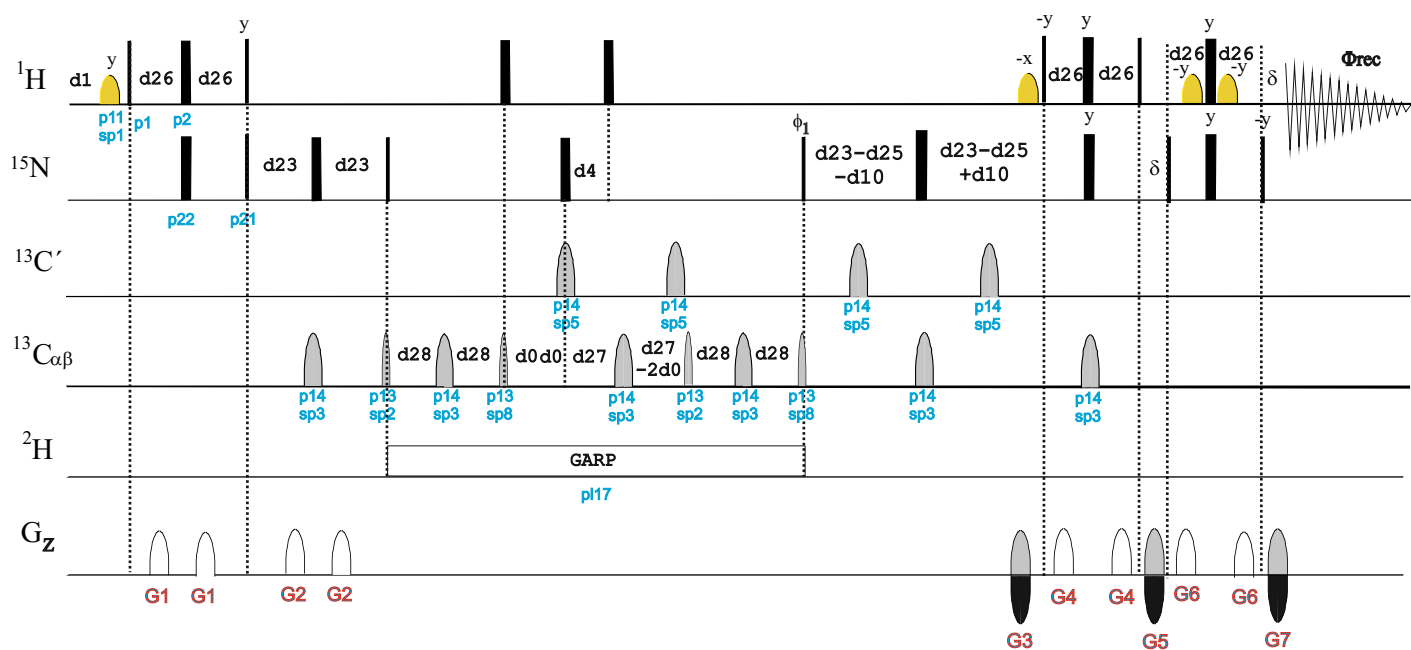
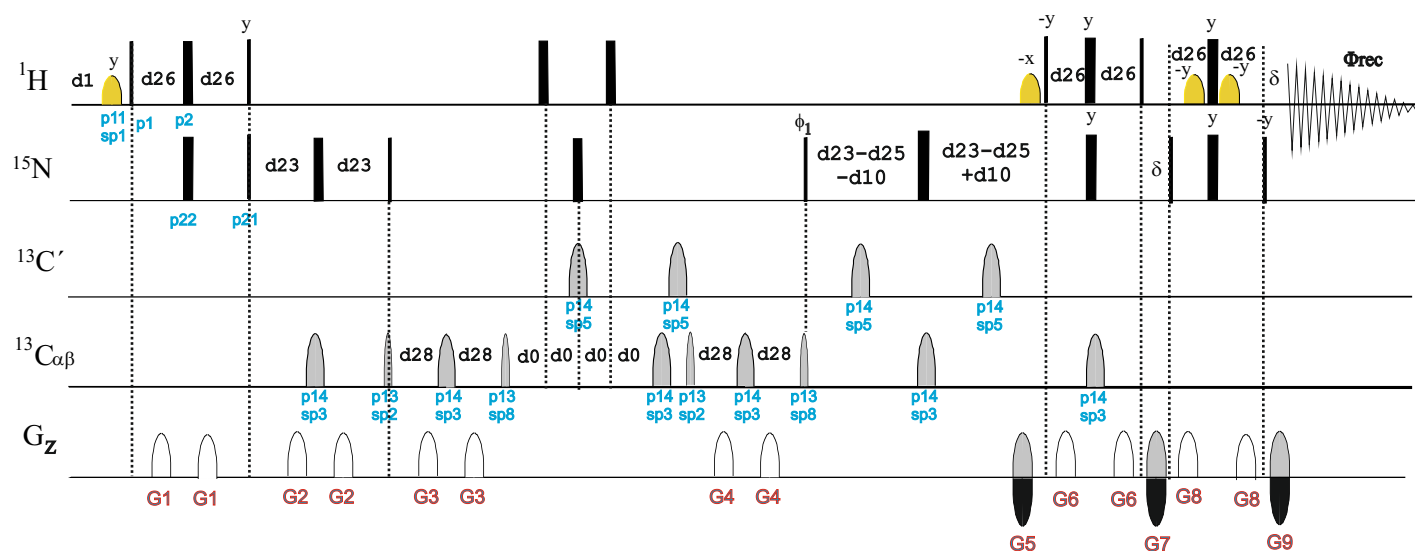
hncacbgpwg3d



hncacbgpwg2h3d







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3D SEQUENTIAL HNCACB

3D Sequential-HNCACB experiment

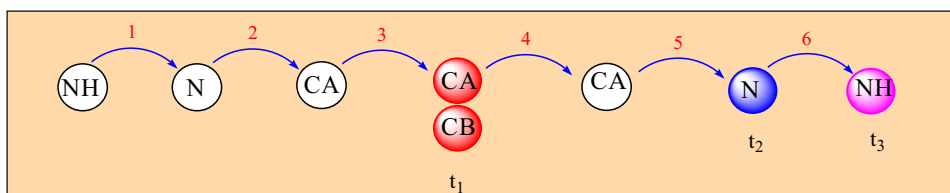
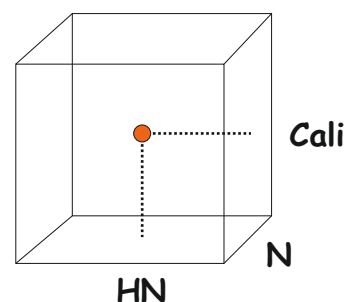
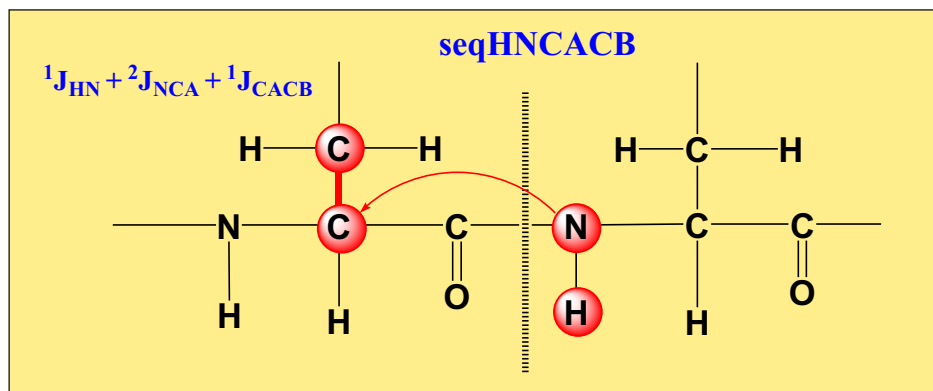
- 3D Sequential HNCACB using TROSY (`seqtrhncacbgp3d` | `SEQTRHNCACBGP3D`)
 - with ^2H -decoupling (`seqtrhncacbgp2h3d` | `SEQTRHNCACBGP2H3D`)
 - Using gradient echo-antiecho (`seqtrhncacbetgp3d` | `SEQTRHNCACBETGP3D`)
 - Using gradient echo-antiecho and with ^2H -decoupling (`seqtrhncacbetgp2h3d` | `SEQTRHNCACBETGP2H3D`)

Also see:

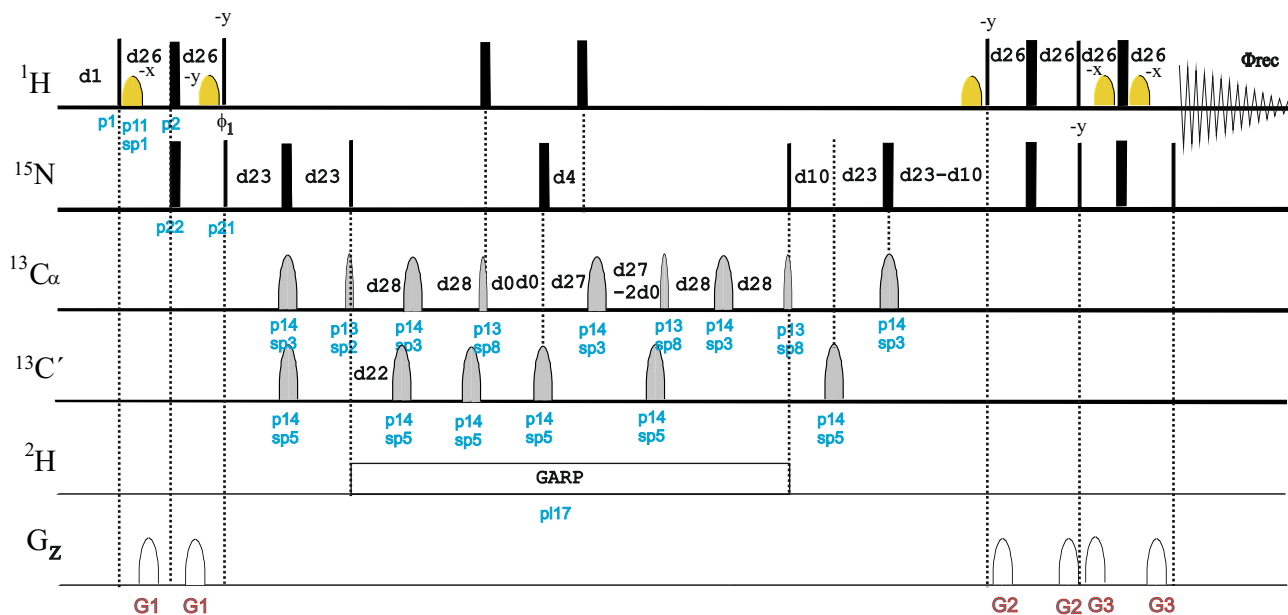
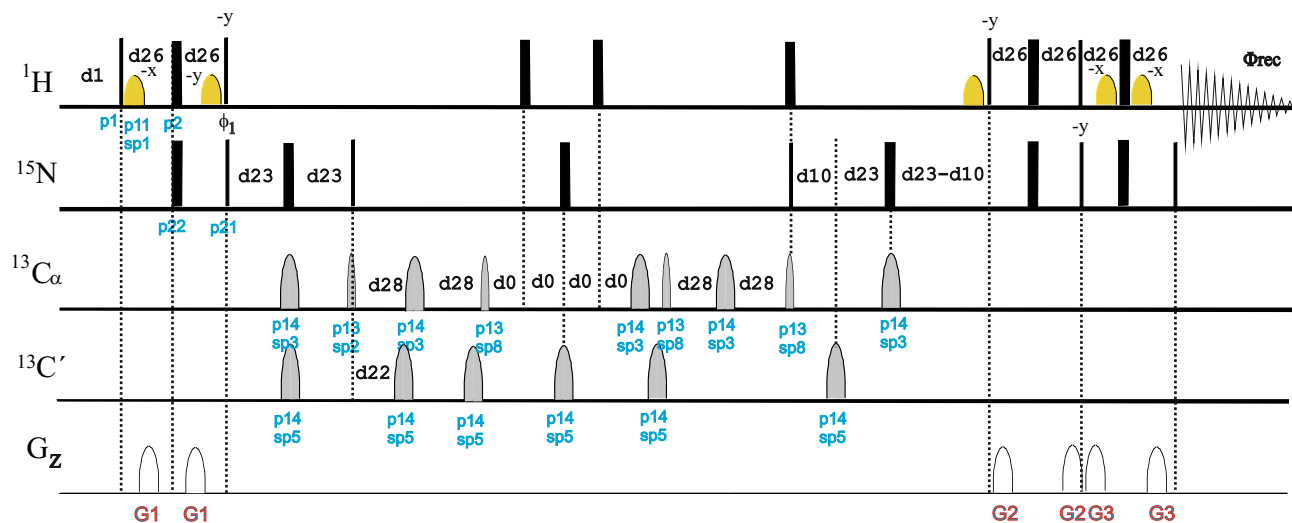
3D HNCACB and intra-HNCACB experiments
3D sequential CBCANH experiments

References:

A. Eletsky, A. Kienhoefer & K. Pervushin, J. Biomol. NMR 20, 188-180 (2001)



$d26 = 1/4J(\text{NH}) = 2.3\text{m}$
 $d23 = 1/4J(\text{NCA}) = 12\text{m}$
 $d22 = 1/4J(\text{CACO}) = 4.5\text{m}$
 $d28 = 1/8J(\text{CACB}) = 5\text{m}$
 $d25 = 1/4J(\text{NH}) = 2.3\text{m}$



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3D Intra-HNCACB

3D intra-HNCACB experiment

- 3D Intra-HNCACB using PEP (**hncacbigp3d** | HNCACBIGP3D)
 - with ^2H -decoupling (**hncacbigp2h3d** | HNCACBIGP2H3D)
- 3D Intra-HNCACB using WATERGATE (**hncacbigpwg3d** | HNCACBIGPWG3D)
 - with ^2H -decoupling (**hncacbigpwg2h3d** | HNCACBIGPWG2H3D)
- 3D Intra-HNCACB using TROSY (**trhncacbigp3d** | TRHNCACBIGP3D)
 - with ^2H -decoupling (**trhncacbigp2h3d** | TRHNCACBIGP2H3D)
 - With gradient echo-antiecho (**trhncacbietgp3d** | TRHNCACBIETGP3D)
 - With gradient echo-antiecho and with ^2H -decoupling (**trhncacbietgp2h3d** | TRHNCACBIETGP2H3D)

Also see:

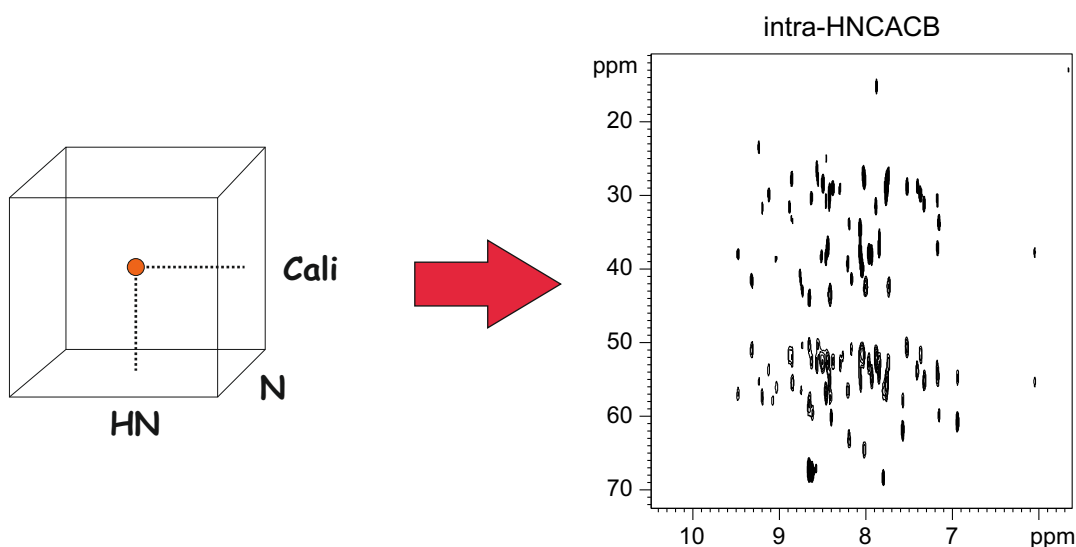
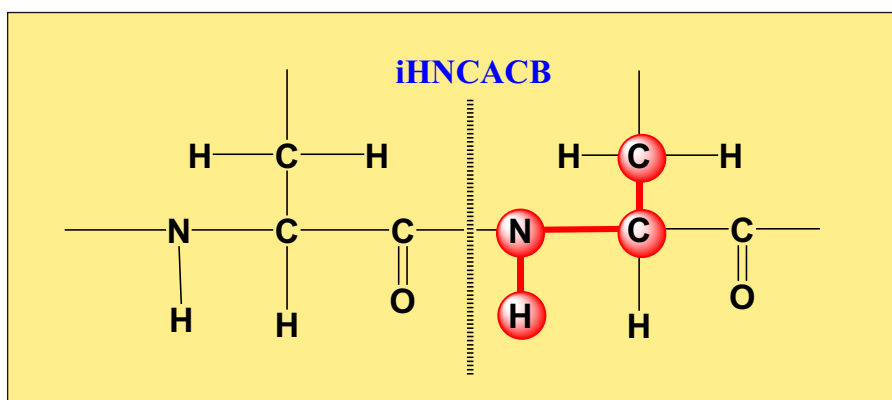
3D SOFAST/BEST intra-HNCACB experiment

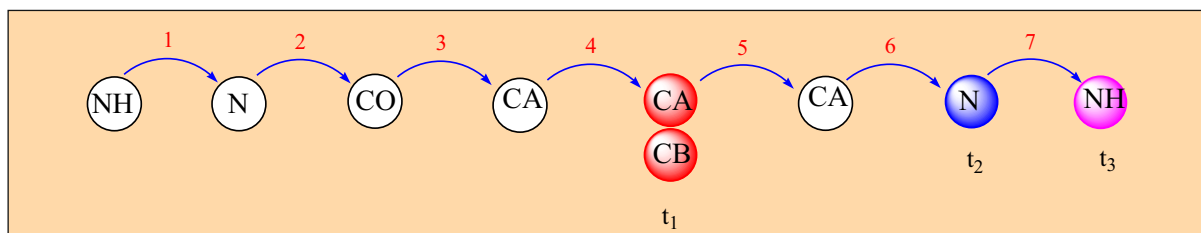
3D BEST-intraHNCACB (**b_hncacbigp3d** | B_HNCACBIGP3D)

3D BEST-intraHNCACB using TROSY (**b_trhncacbigp3d**)

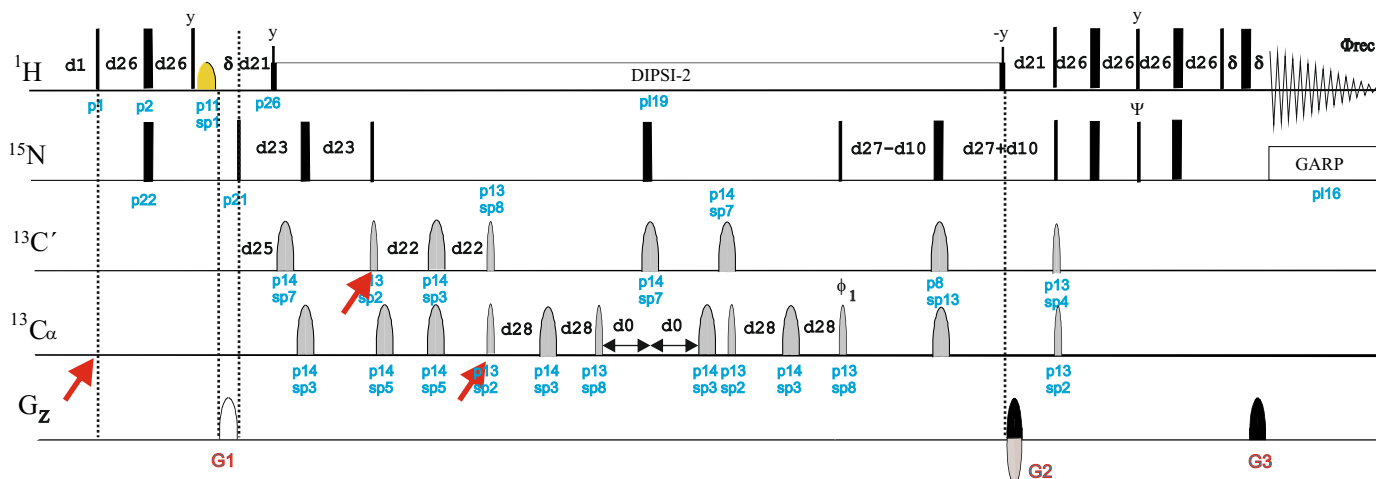
3D HNCACB and sequential-HNCACB experiments

D.Nietlispach, Y. Ito & E.D. Laue, J. Am. Chem. Soc. 124, 11199-11207 (2002)



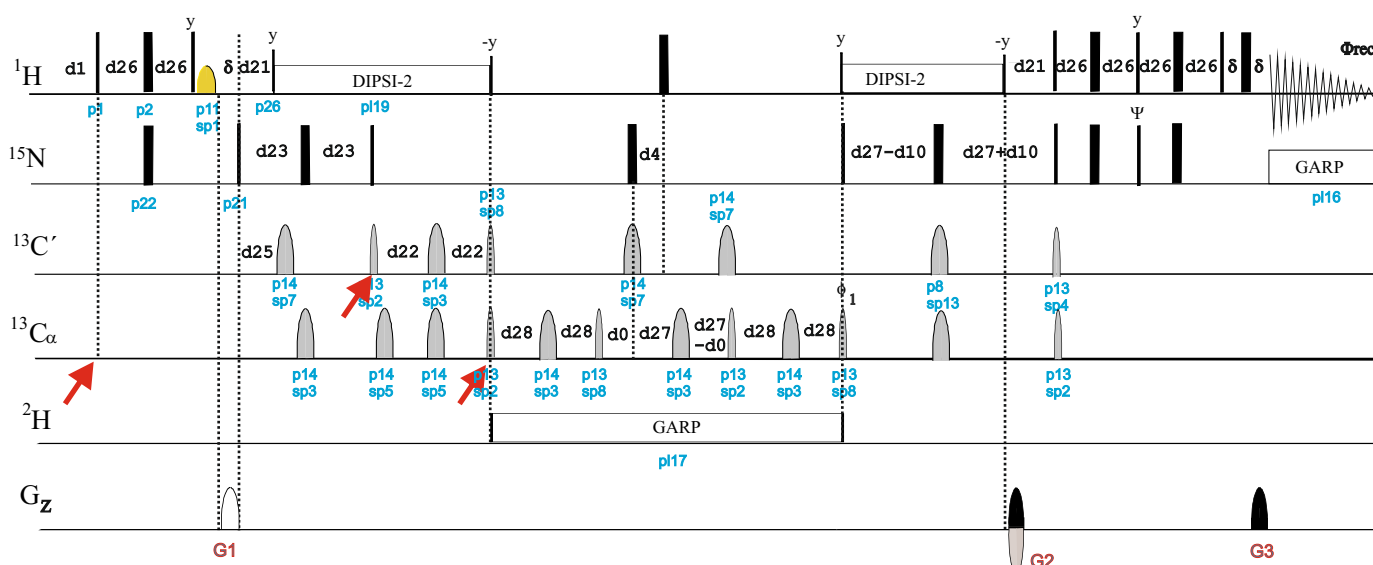


hncacbigp3d

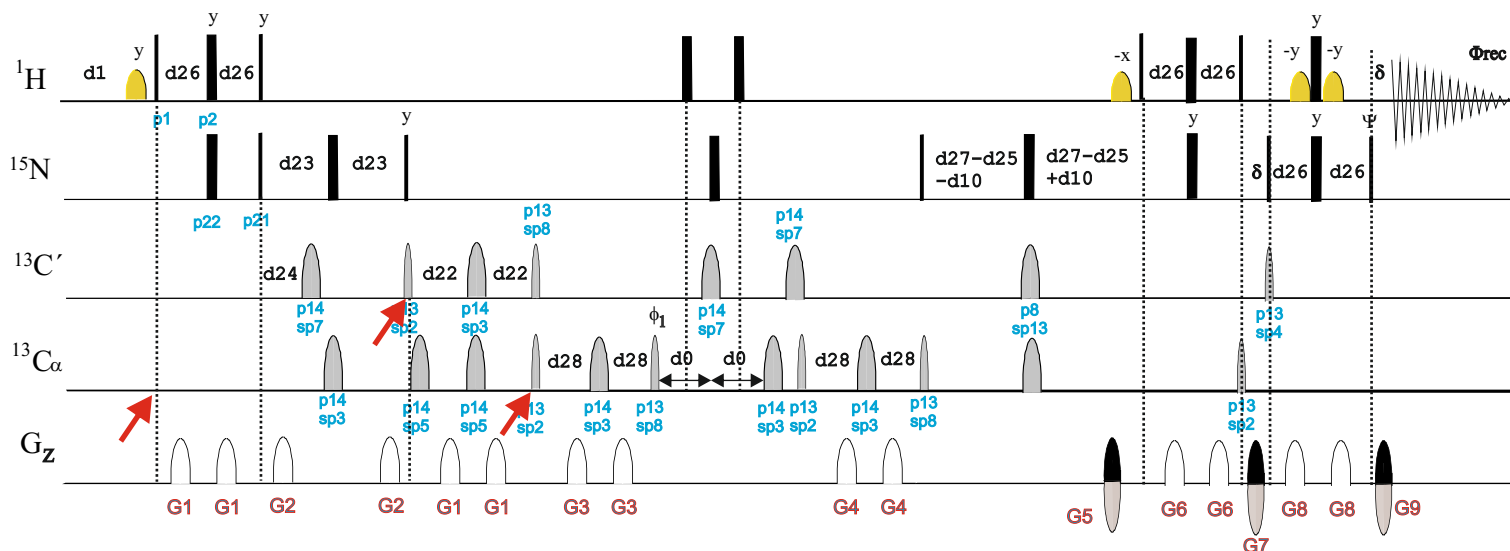


$d26 = 1/4J(\text{NH}) = 2.3\text{m}$
 $d21 = 1/2J(\text{NH}) = 5.5\text{m}$
 $d23 = 1/4J(\text{NCA}) = 26\text{m}$
 $d22 = 1/4J(\text{CACO}) = 4.2\text{m}$
 $d27 = 1/4J(\text{NCA}) \& 1/4J(\text{NCO}) = 15.8\text{m}$
 $d25 = 1/4J(\text{NCO}) = 16.5\text{m}$
 $d28 = 1/(8J(\text{CaCb})) = 3.6\text{m}$ (7.2m if **ZGPTNS = -DLABEL_CB**)

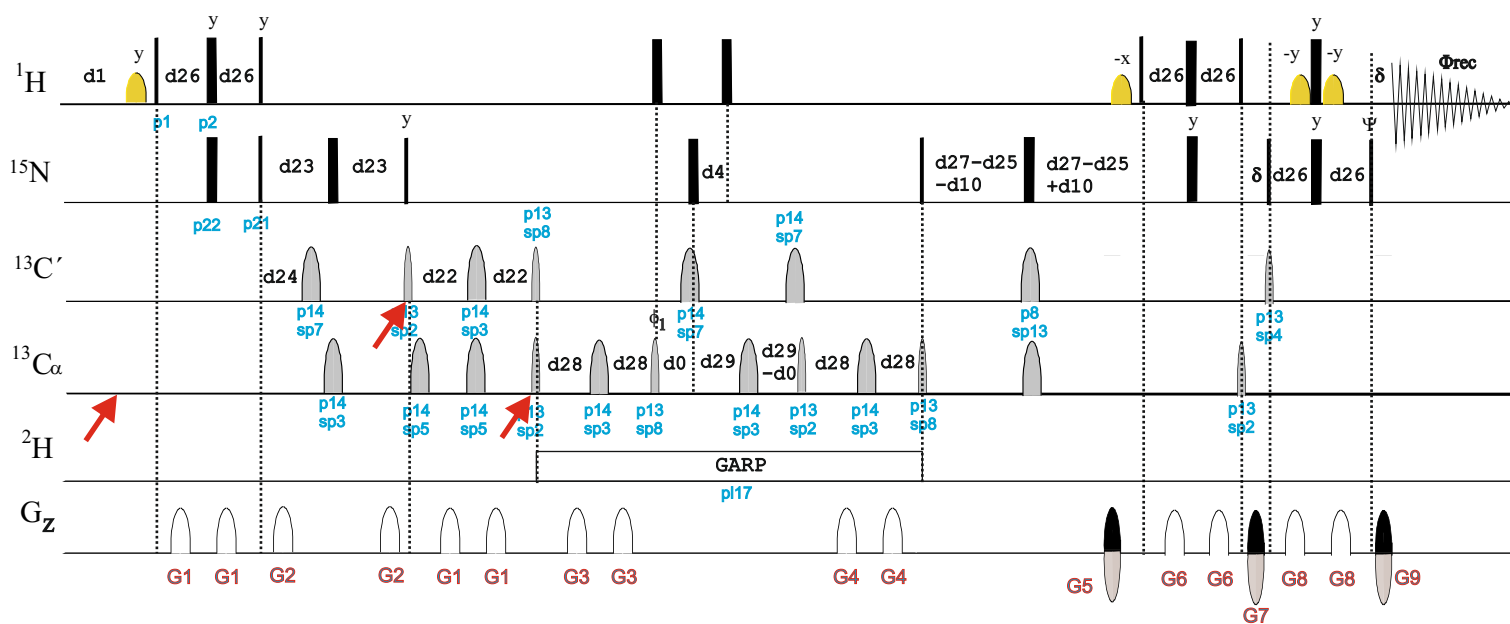
hncacbigp2h3d

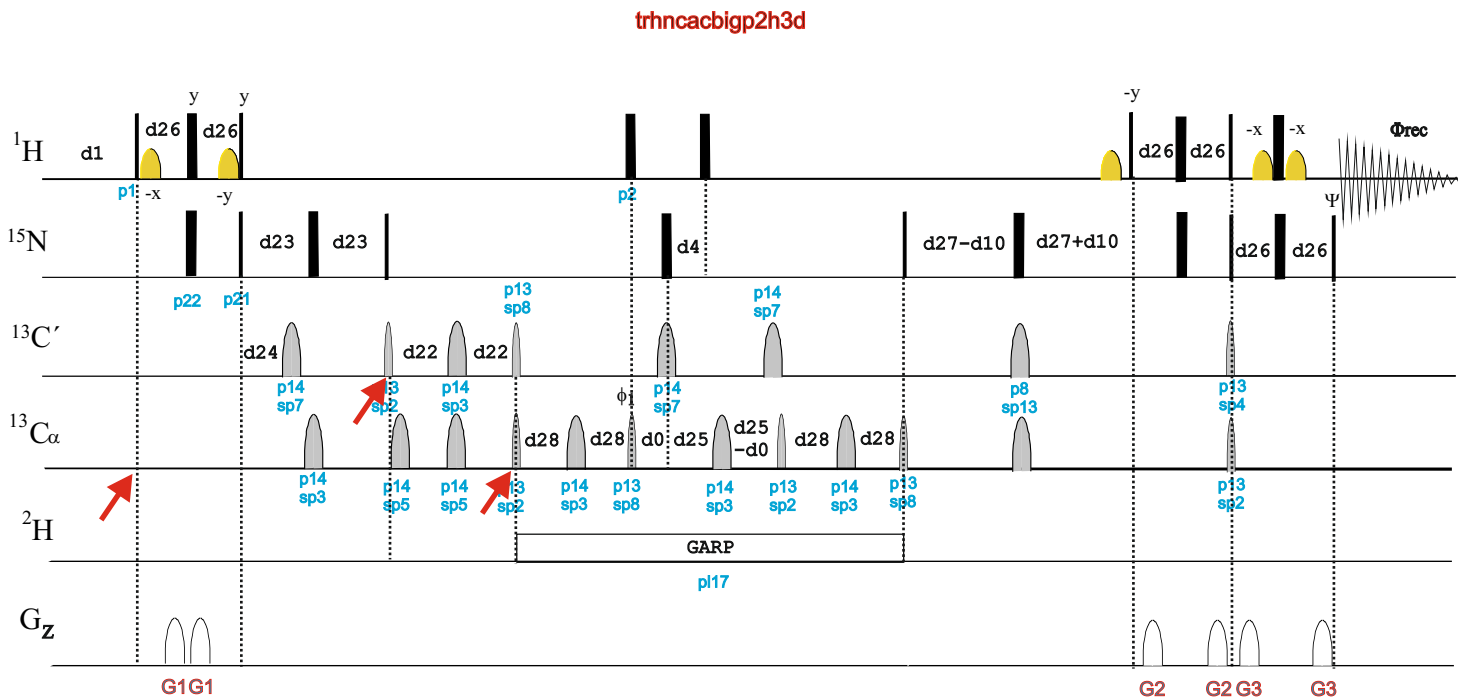
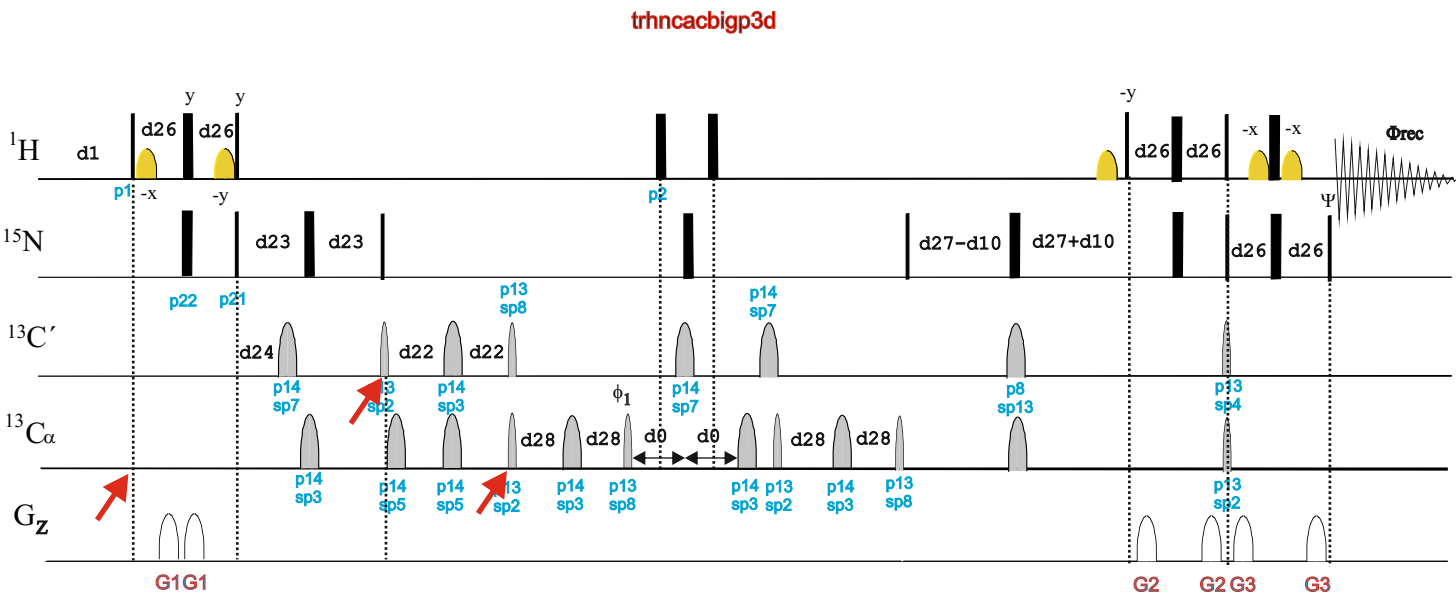


trhncacbietgp3d



trhncacbietgp2h3d





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NMRGuide

3D CCANH

3D CCANH experiment

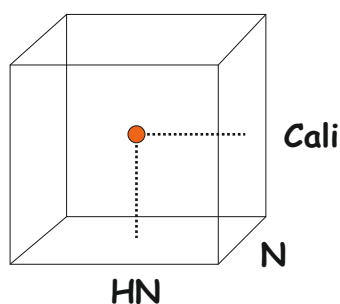
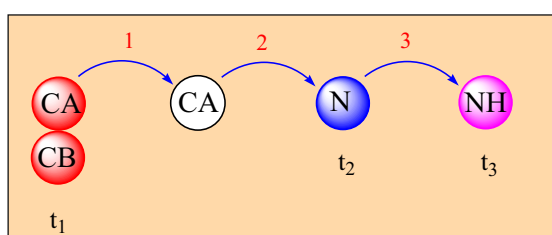
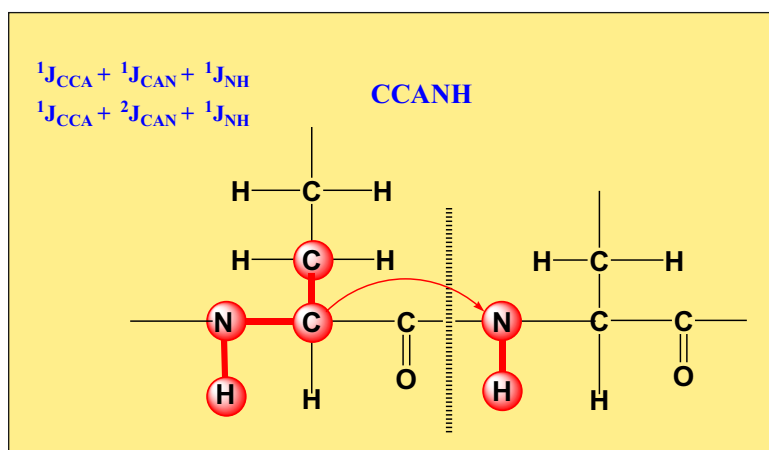
- 3D CCANH using PEP (**ccanhgp3d** | *ccanhgp3d*)
- 3D CCANH using PEP with ^2H -decoupling (**ccanhgp2h3d** | *ccanhgp2h3d*)
- 3D CCANH using PEP and ^1H -NOE (**ccanhgp3d.2** | *ccanhgp3d.2*)

Also see:

CCA(CO)NH and 3D CC(CO)NH experiments

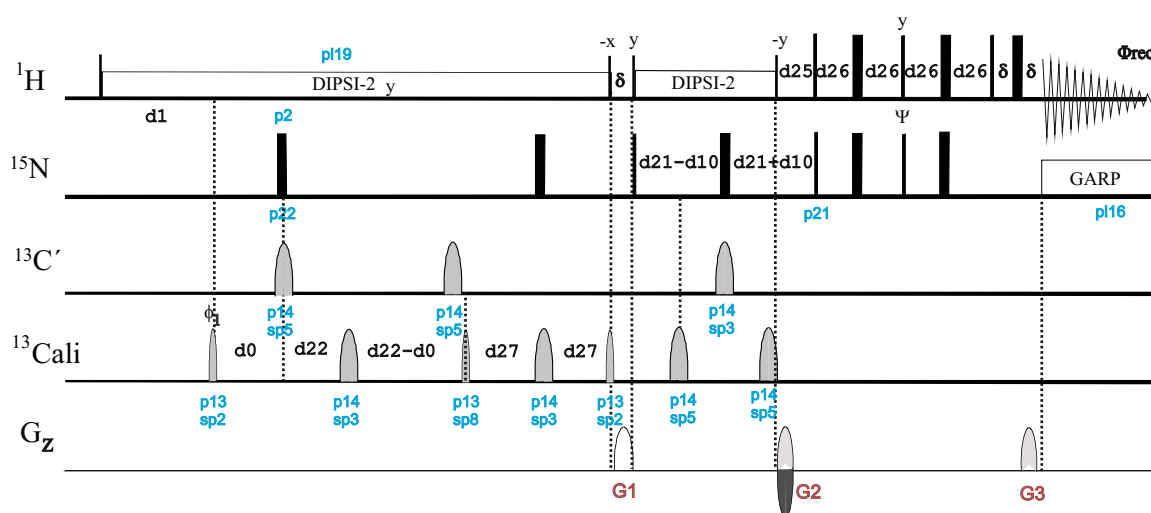
3D & 4D HCCCONH Experiments

S. Grzesiek & A. Bax, J. Biomol. NMR 3, 185-204 (1993)



[illegible]

d21=1/4J(NCO)=12.4m
d22=1/4J(CC)=3.6m
d25=1/2J(NH)=5.5m
d26=1/4J(NH)=2.3m
d27=1/4J(CACO)=11m



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NMRGuide

3D CCA(CO)NH
3D CC(CO)NH

CCA(CO)NH and CC(CO)NH Experiments

3D CCA(CO)NH experiment

- 3D CCA(CO)NH using PEP (`ccaconhgp3d` | `CCA CONHGP3D`)
- 3D CCA(CO)NH using PEP with ^2H -decoupling (`ccaconhgp2h3d` | `CCA CONHGP2H3D`)
- 3D CCA(CO)NH using PEP and ^1H -NOE (`ccaconhgp3d.2` | `CCA CONHGP3D.2`)

3D CC(CO)NH experiment

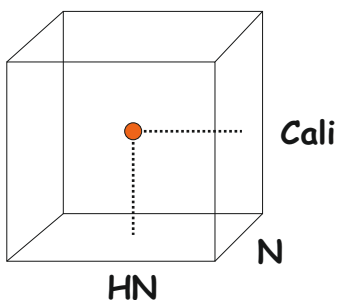
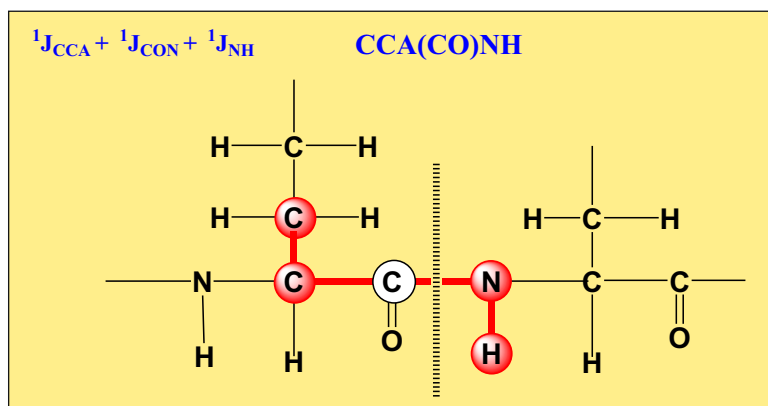
- 3D CC(CO)NH using PEP (`ccconhgp3d` | `CC CONHGP3D`)
- 3D CC(CO)NH using PEP with ^2H -decoupling (`ccconhgp2h3d` | `CC CONHGP2H3D`)

Also see:

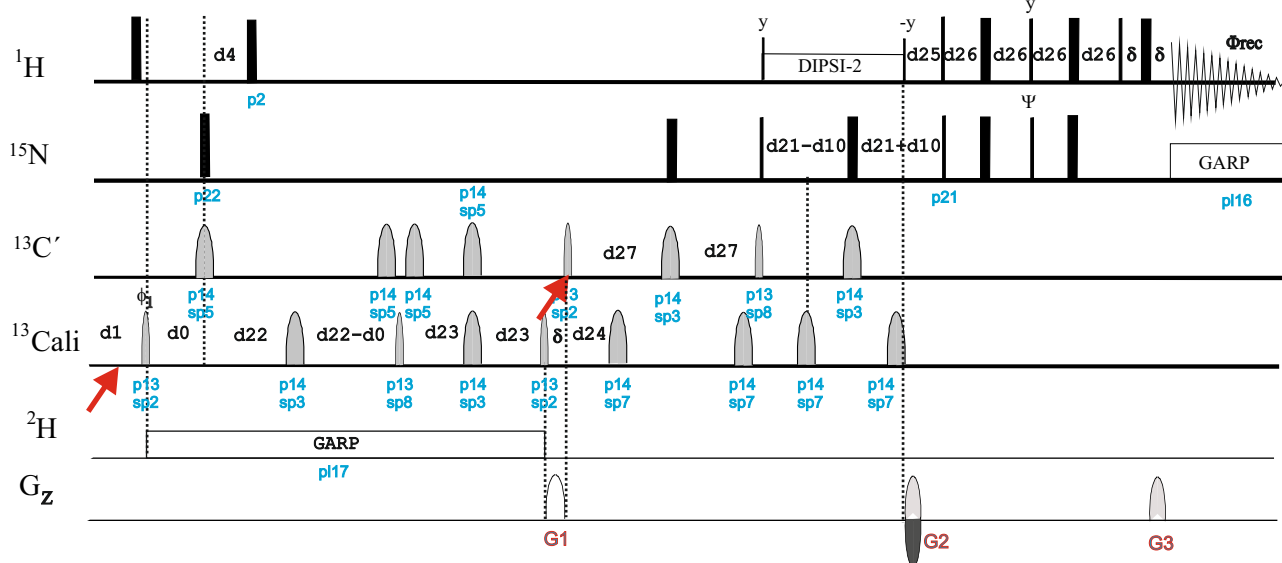
3D CBCACONH, 3D CCANH, 3D (H)CC(CO)NH and H(CCCO)NH experiments

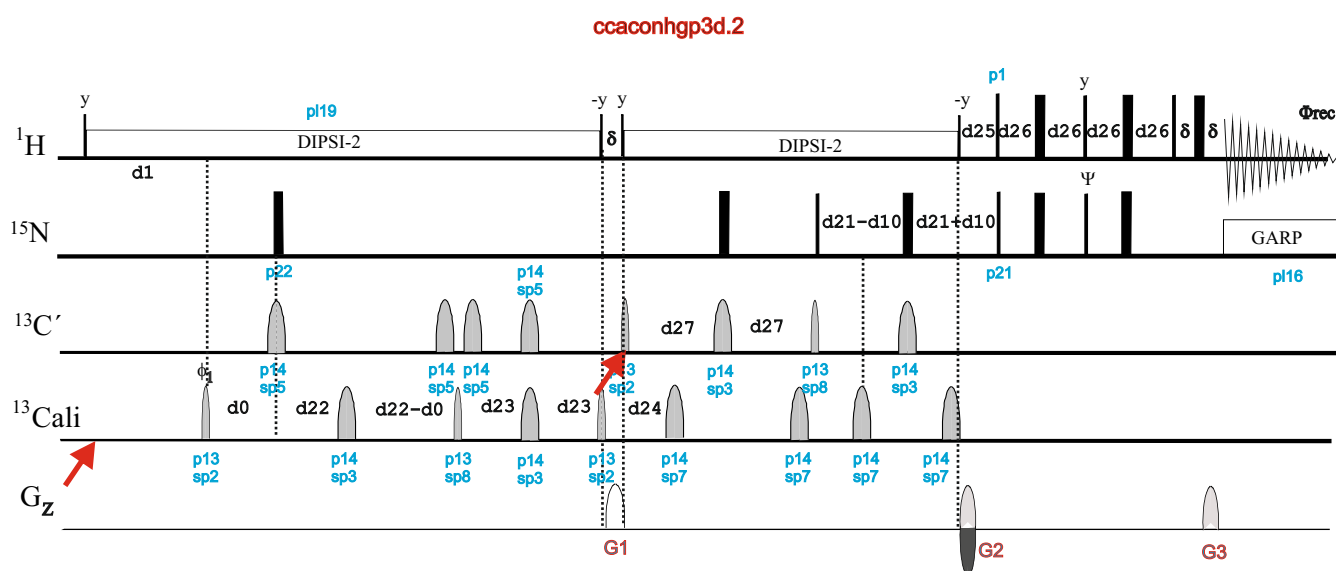
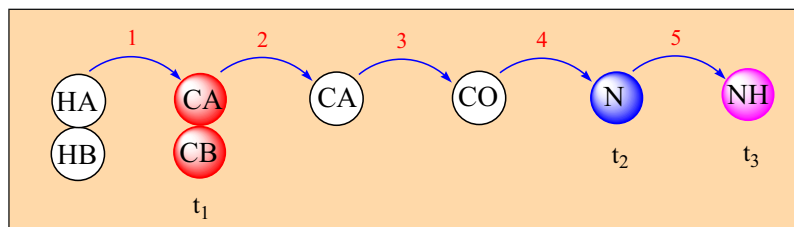
References:

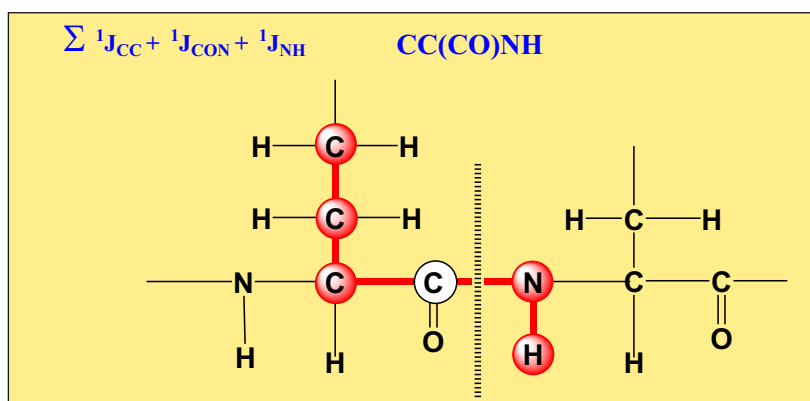
S. Grzesiek & A. Bax, J. Biomol. NMR 3, 185-204 (1993)



$d_{21} = 1/4J(\text{NCO}) = 12.4\text{m}$
 $d_{22} = 1/4J(\text{CC}) = 3.6\text{m}$
 $d_{23} = 1/4J(\text{CBCA}) = 3.6\text{m}$
 $d_{24} = 1/2J(\text{CBCA}) = 4.4\text{m}$
 $d_{25} = 1/2J(\text{NH}) = 5.5\text{m}$
 $d_{26} = 1/4J(\text{NH}) = 2.3\text{m}$
 $d_{27} = 1/4J(\text{CACO}) = 12.4\text{m}$

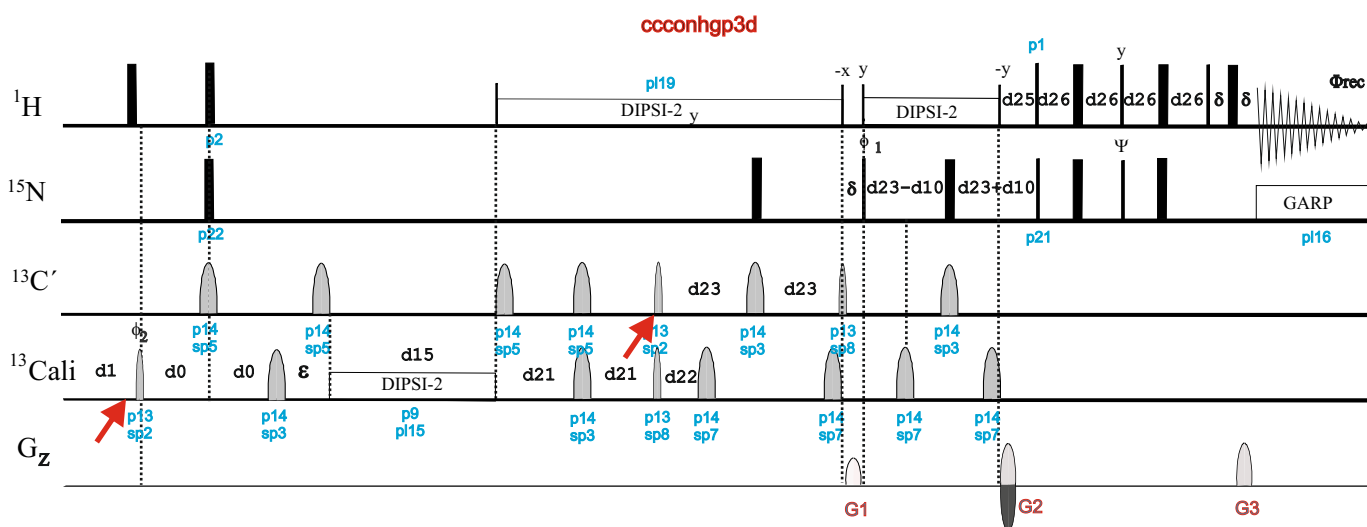
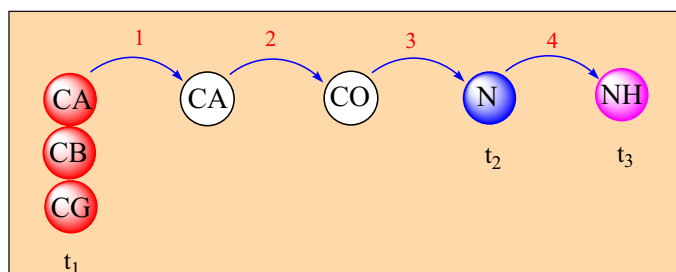




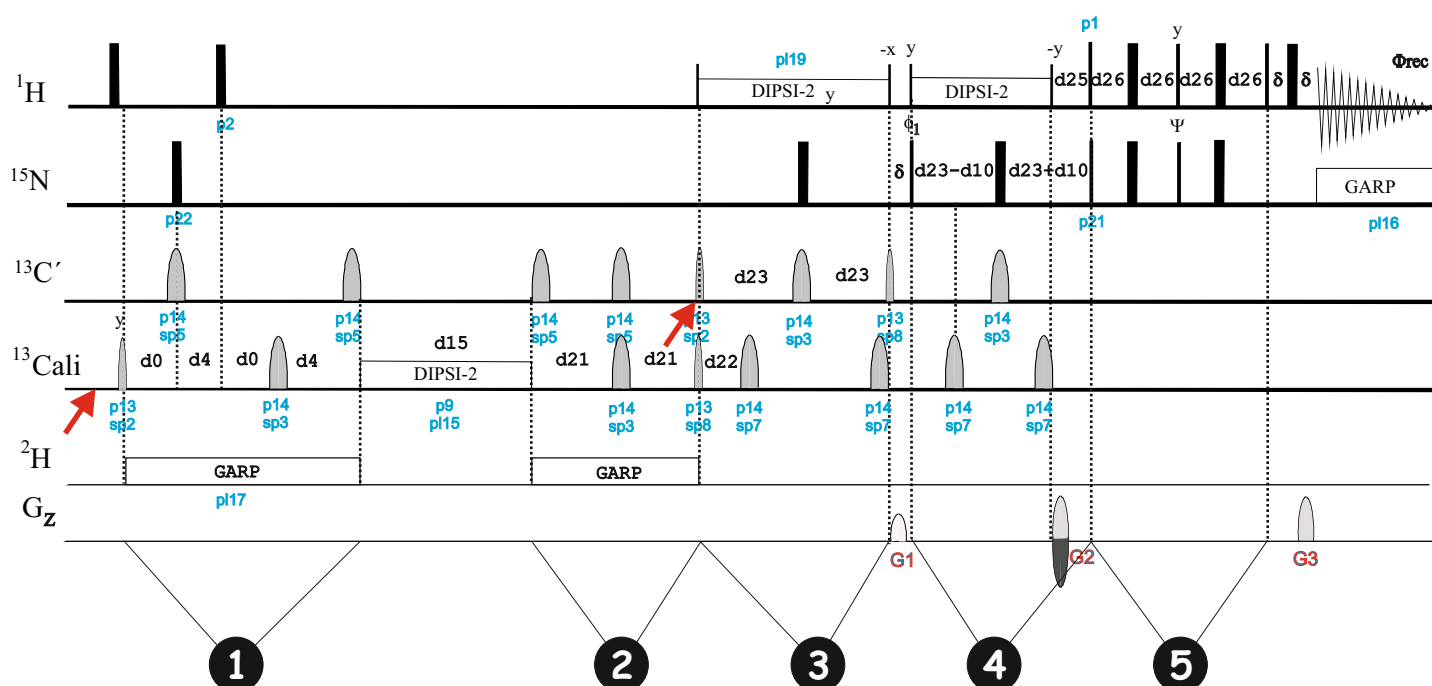


References:

1. G.T. Montelione, B.A. Lyons, S.D. Emerson & M. Tashiro, J. Am. Chem. Soc. 114, 10974-75 (1992)
2. S. Grzesiek, J. Anglister & A. Bax, J. Magn. Reson. 101 B, 114-9 (1993)
3. B.A. Lyons & G.T. Montelione, J. Magn. Reson. 101 B, 206-9 (1993)
4. T.M. Logan, E.T. Olejniczak, R.X. Xu & S.W. Fesik, J. Biomol. NMR 3, 225-31 (1993)
5. R.T. Clowes, W. Boucher, C.H. Hardman, P.J. Domaille & E.D. Laue, J. Biomol. NMR 3, 349-354 (1993)
6. T. Carlomagno, M. Maurer, M. Sattler, M.G. Schwendinger, S.J. Glaser & C. Griesinger, J. Biomol. NMR 8, 161-170 (1996)



ccconhgp2h3d



Variable Cali evolution period consisting of:
 $\delta(\text{Cali})$ evolution and $J(\text{Cali-CO})$ decoupling
 $\delta(\text{Cali})$ evolution and $J(\text{Cali-N})$ decoupling
 $\delta(\text{Cali})$ evolution and $J(\text{Cali-2H})$ decoupling
 $\delta(\text{Cali})$ evolution and $J(\text{Cali-H})$ defocusing
 $\delta(\text{Cali})$ evolution and $J(\text{Cali-Cali})$ evolution

Cali-CO INEPT transfer

CO-N INEPT transfer

$J(\text{CO-H})$ decoupling

$J(\text{CO-H})$ refocusing

Concatenated Constant-time ^{15}N evolution period consisting of:

$\delta(\text{N})$ evolution and $J(\text{N-H})$ evolution

$\delta(\text{N})$ evolution and $J(\text{N-CO})$ refocusing

$\delta(\text{N})$ evolution and $J(\text{N-Cali})$ decoupling

^1H - ^{15}N TROSY transfer consisting of two retro-INEPT like blocks

d15: TOCSY mixing time [12 msec]
 $d21 = 1/4J(\text{CACO}) = 3.6\text{m}$
 $d22 = 1/2J(\text{CACO}) = 4.4\text{m}$
 $d23 = 1/4J(\text{NCO}) = 12.4\text{m}$
 $d25 = 1/2J(\text{NH}) = 5.5\text{m}$
 $d26 = 1/4J(\text{NH}) = 2.3\text{m}$
 $d4 = 1/4J(\text{CH}) = 1.7\text{m}$

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NMRGuide

HCC(CO)NH EXPERIMENTS

HCC(CO)NH experiments

3D (H)CC(CO)NH Experiment

- 3D (H)CC(CO)NH using PEP (**hccconhgp3d3** | HCCCONHGP3D3)
- 3D (H)CC(CO)NH using WATERGATE (**hccconhgpwg3d3** | HCCCONHGPWG3D3)
- 3D (H)CC(CO)NH using TROSY (**trhccconhgp3d3** | TRHCCCONHGP3D3)
 - With gradient echo-antiecho (**trhccconhetgp3d3** | TRHCCCONHETGP3D3)
 - With additional gradient (**trhccconhgp3d3.2** | TRHCCCONHGP3D3.2)
 - With additional gradient and with gradient echo-antiecho (**trhccconhetgp3d3.2** | TRHCCCONHETGP3D3.2)

3D H(CC)(CO)NH Experiment

- 3D H(CC)(CO)NH using PEP (**hccconhgp3d2** | HCCCONHGP3D2)
 - with ^1H - ^{13}C CP transfer (**hccconhgp3d1** | HCCCONHGP3D1)
- 3D H(CC)(CO)NH using WATERGATE (**hccconhgpwg3d2** | HCCCONHGPWG3D2)
- 3D H(CC)(CO)NH using TROSY (**trhccconhgp3d2** | TRHCCCONHGP3D2)
 - With gradient echo-antiecho (**trhccconhetgp3d2** | TRHCCCONHETGP3D2)

4D HCC(CO)NH Experiment

- 4D HCC(CO)NH using WATERGATE (**hccconhgpwg4d**)

Also see:

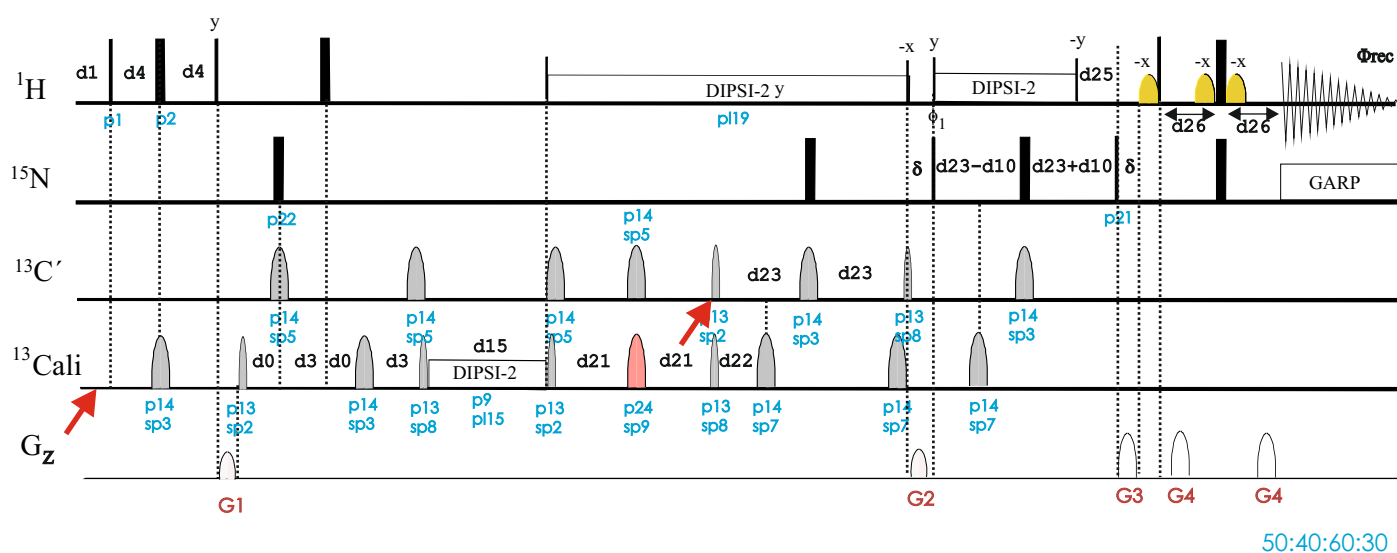
3D HBHA(CO)NH experiment

3D CC(CO)NH & CCA(CO)NH experiments

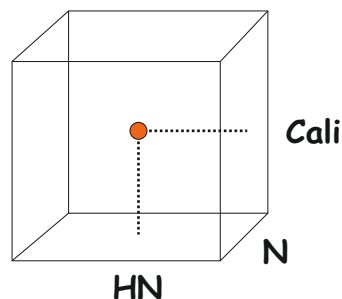
3D CBCA(CO)NH experiment

References:

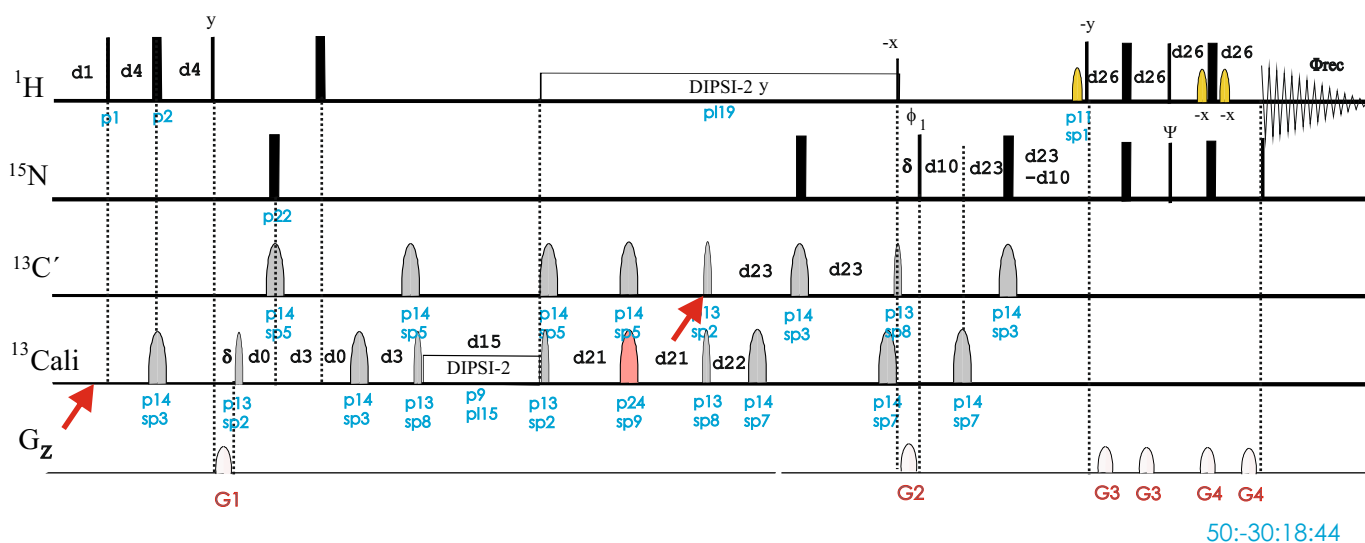
1. G.T. Montelione, B.A. Lyons, S.D. Emerson & M. Tashiro, J. Am. Chem. Soc. 114, 10974-75 (1992)
2. S. Grzesiek, J. Anglister & A. Bax, J. Magn. Reson. 101 B, 114-9 (1993)
3. B.A. Lyons & G.T. Montelione, J. Magn. Reson. 101 B, 206-9 (1993)
4. T.M. Logan, E.T. Olejniczak, R.X. Xu & S.W. Fesik, J. Biomol. NMR 3, 225-31 (1993)
5. R.T. Clowes, W. Boucher, C.H. Hardman, P.J. Domaille & E.D. Laue, J. Biomol. NMR 3, 349-354 (1993)
6. T. Carlomagno, M. Maurer, M. Sattler, M.G. Schwendinger, S.J. Glaser & C. Griesinger, J. Biomol. NMR 8, 161-170 (1996)



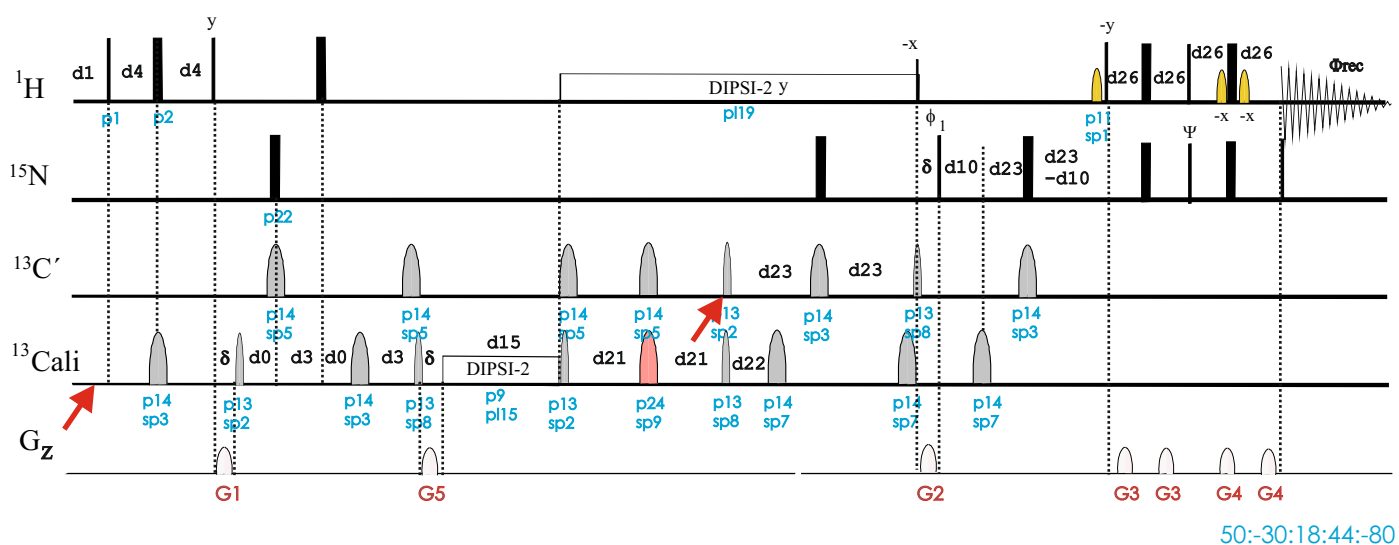
$d3=1/6J(CH)=1.1m$
 $d4=1/4J(CH)=1.7m$
 $d21=1/2J(CACO)=3.6m$
 $d22=1/2J(CACO)=4.4m$
 $d23=1/4J(NCO)=12.4m$
 $d25=1/2J(NH)=5.5m$
 $d26=1/4J(NH)=2.3m$

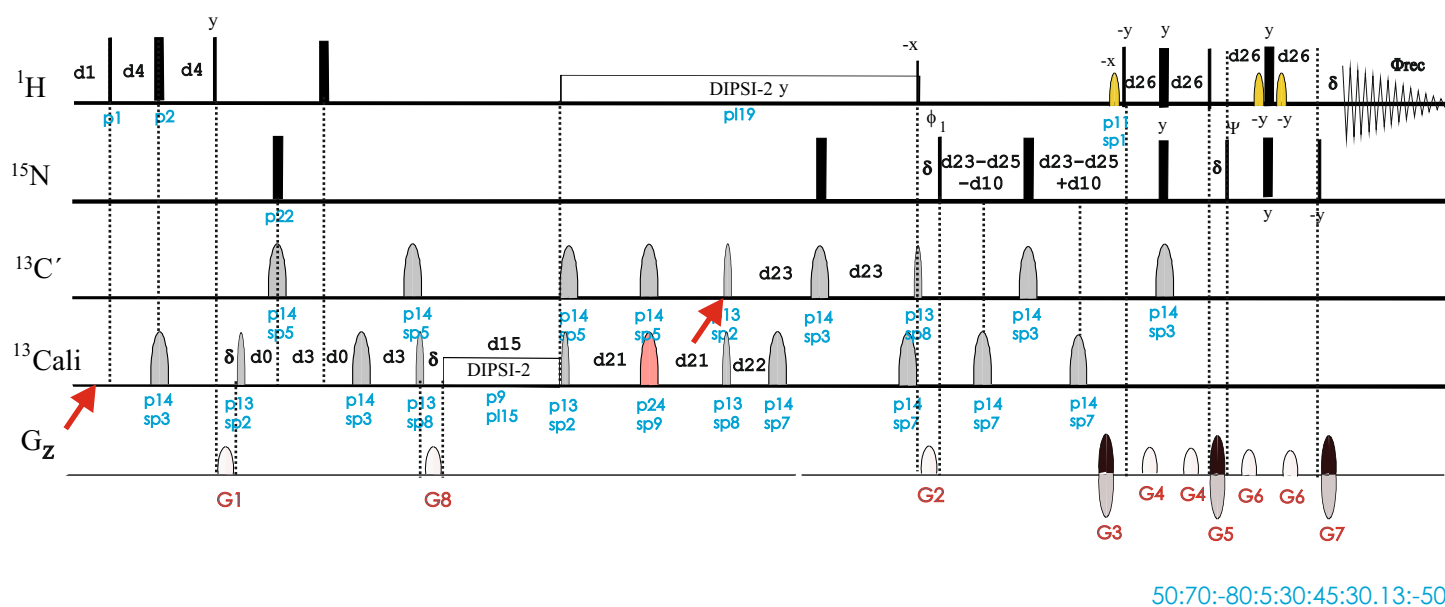
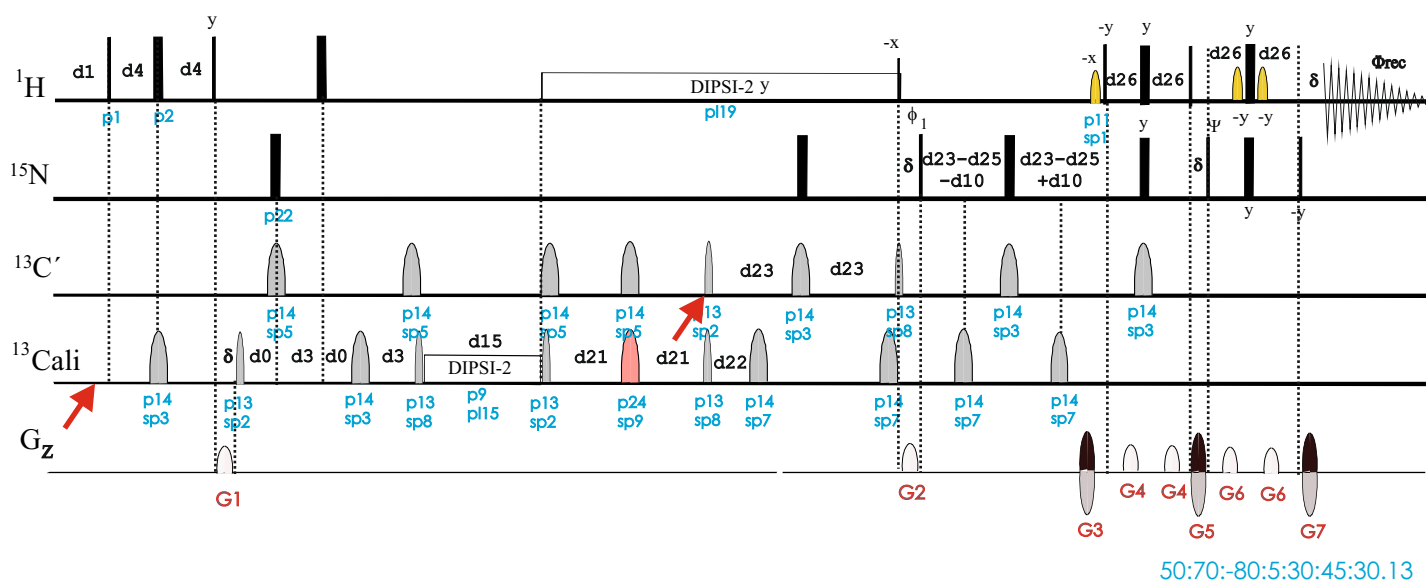


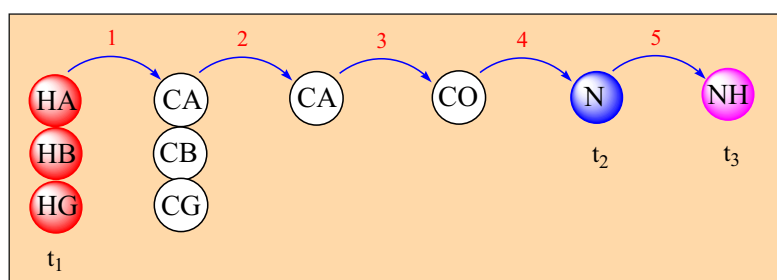
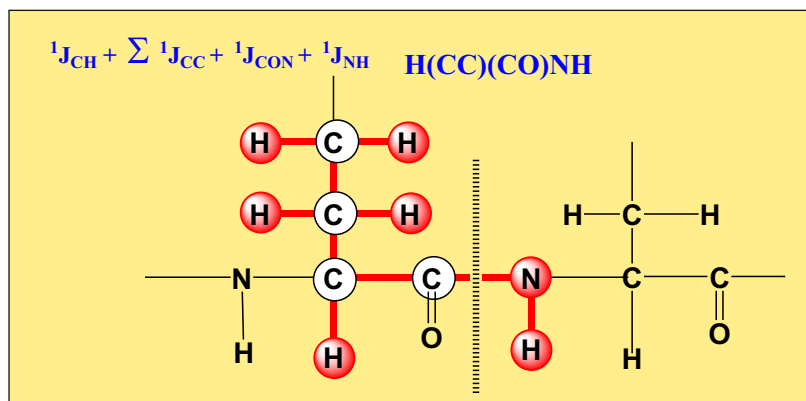
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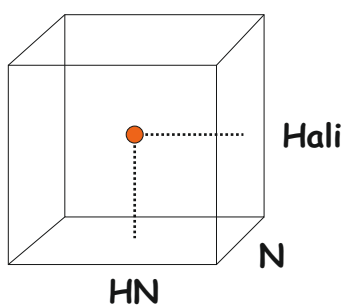
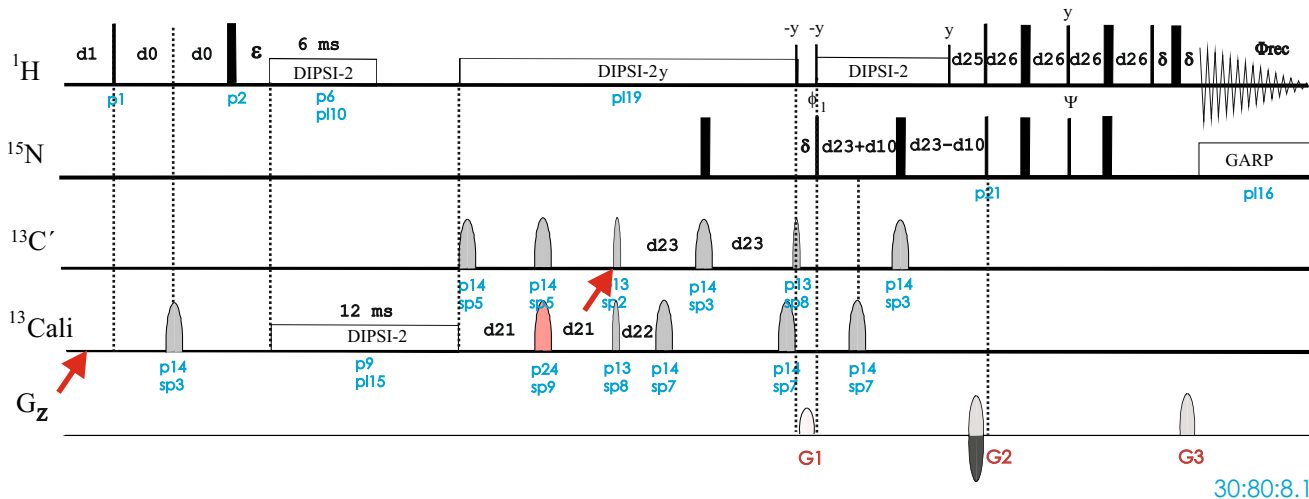
trhccconhgp3d3.2





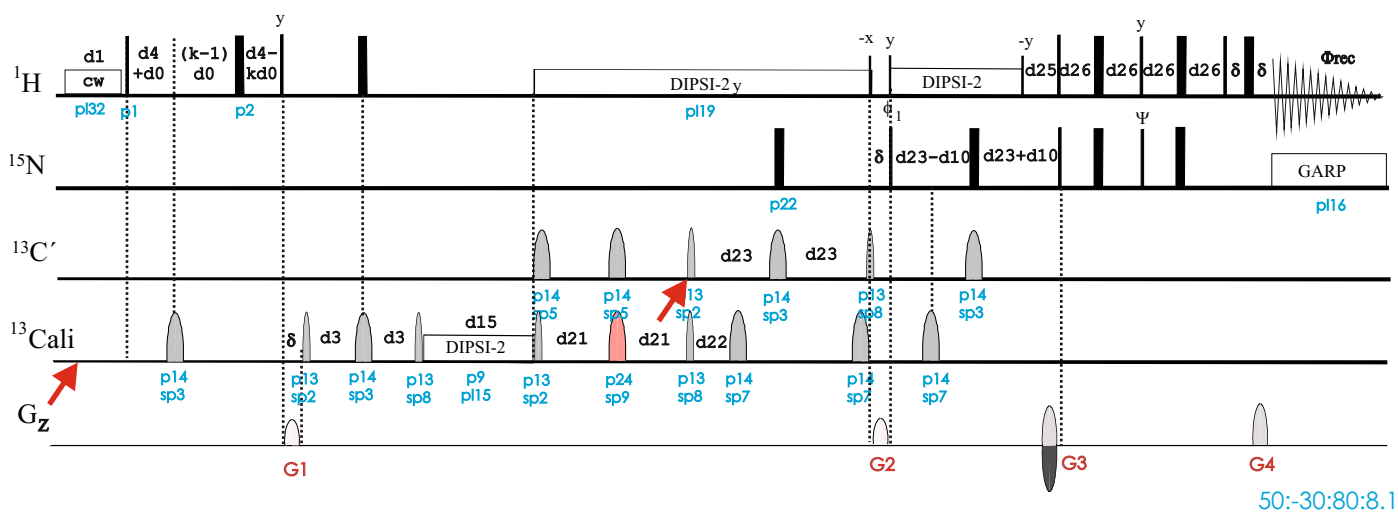


hccconhgp3d1

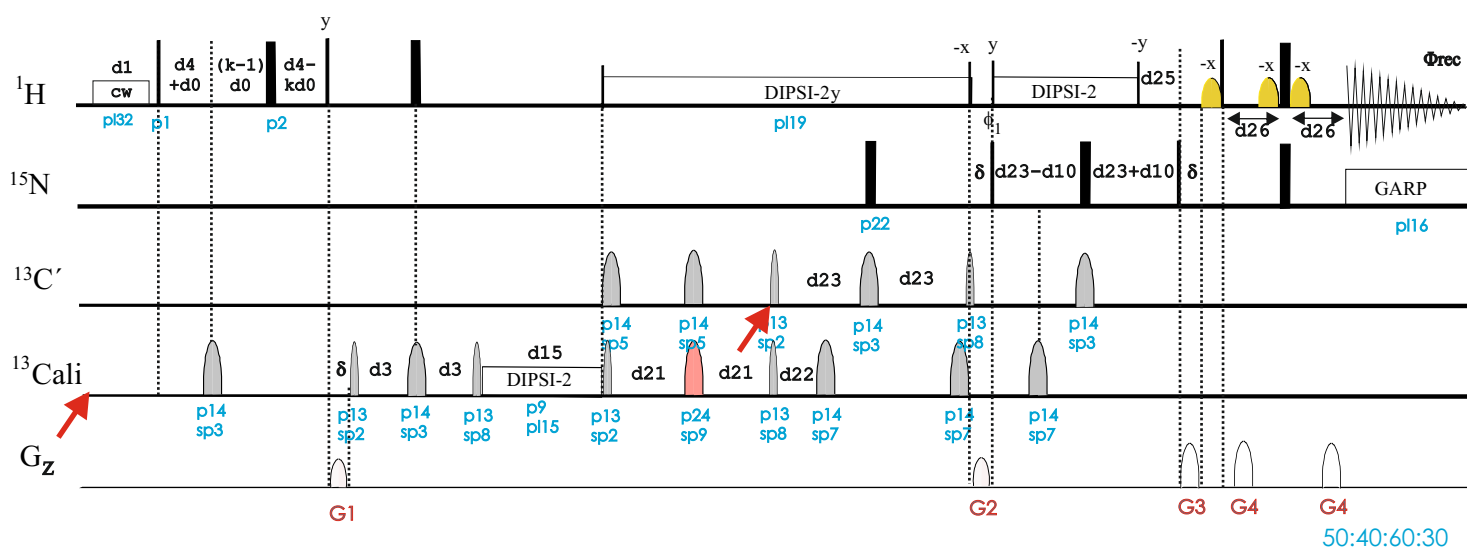


$$\begin{aligned} d3 &= 1/6J(CH) = 1.1m \\ d4 &= 1/4J(CH) = 1.7m \\ d21 &= 1/2J(CACO) = 3.6m \\ d22 &= 1/2J(CACO) = 4.4m \\ d23 &= 1/4J(NCO) = 12.4m \\ d25 &= 1/2J(NH) = 5.5m \\ d26 &= 1/4J(NH) = 2.3m \end{aligned}$$

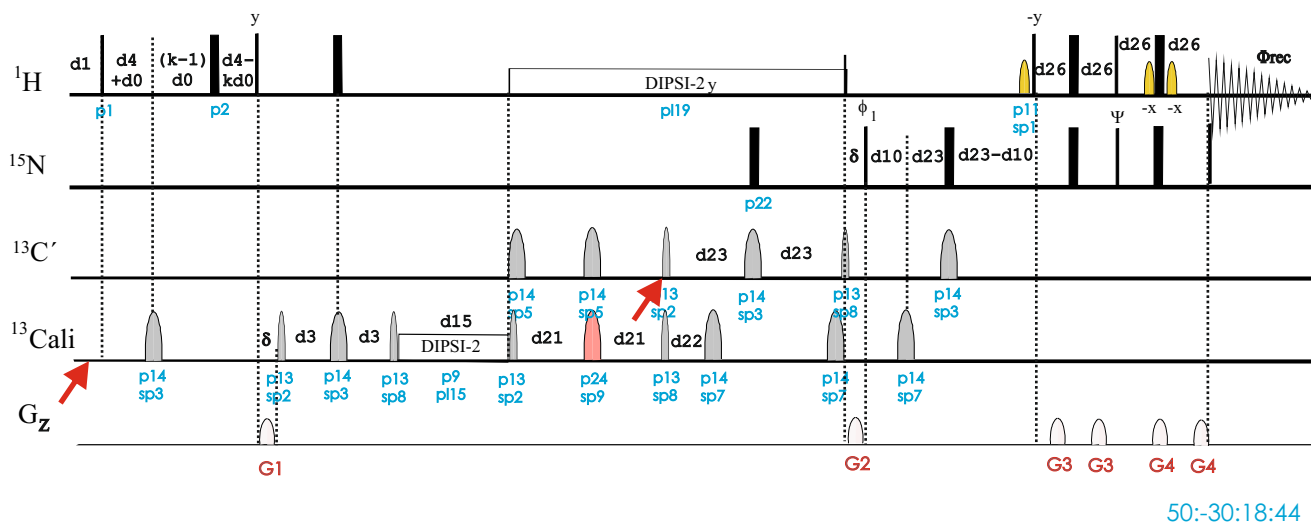
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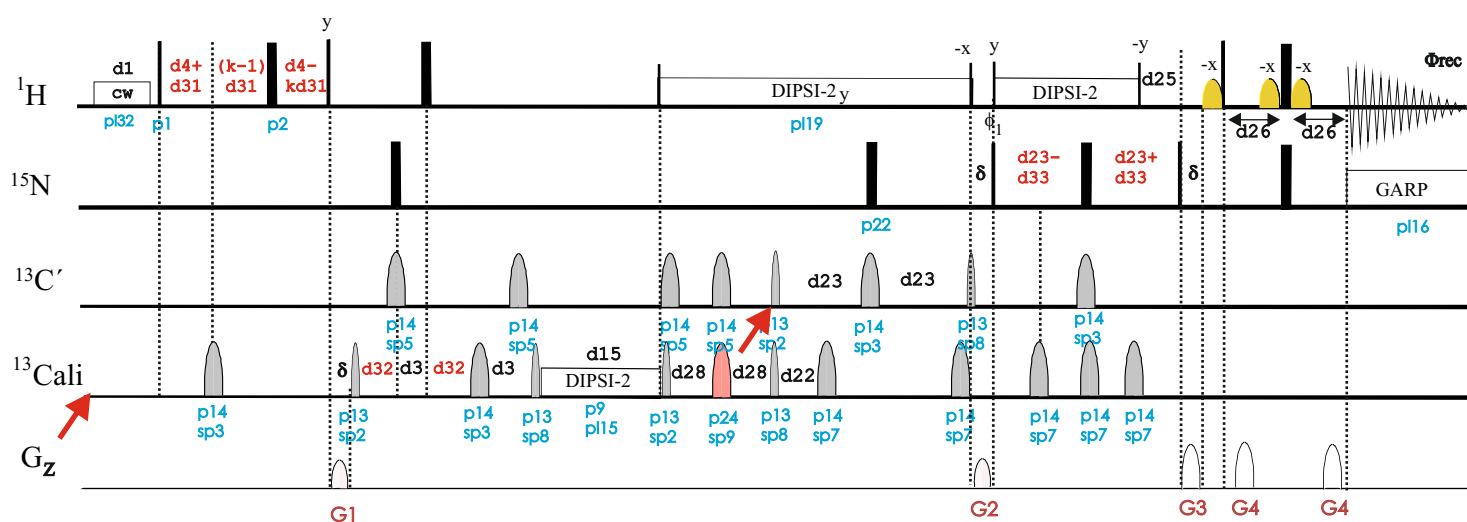
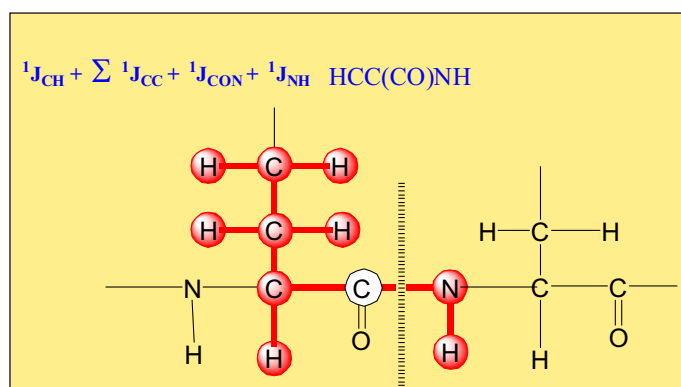
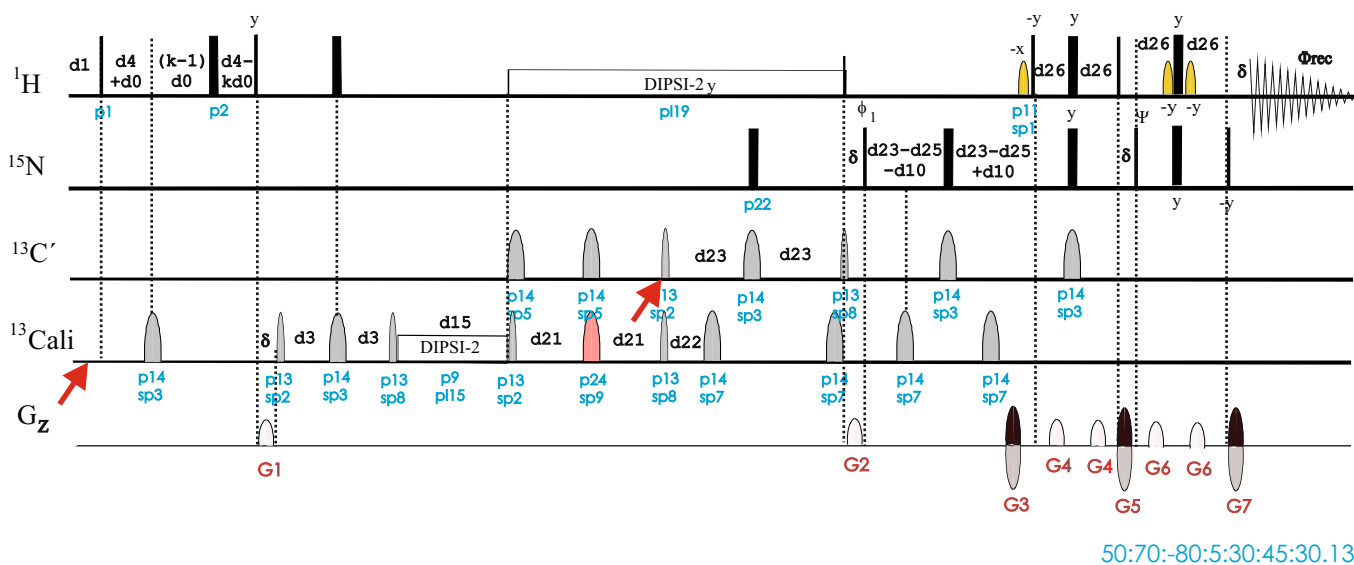


hccconhgpwg3d2



trhccconhgp3d2





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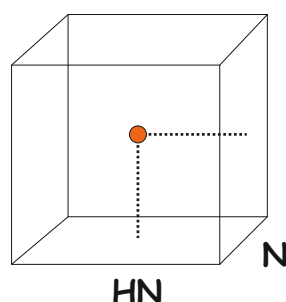
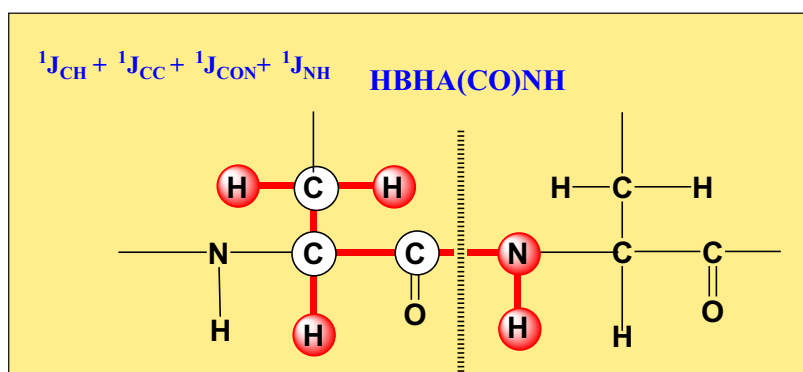
3D HBHA(CO)NH

HBHACONH experiment

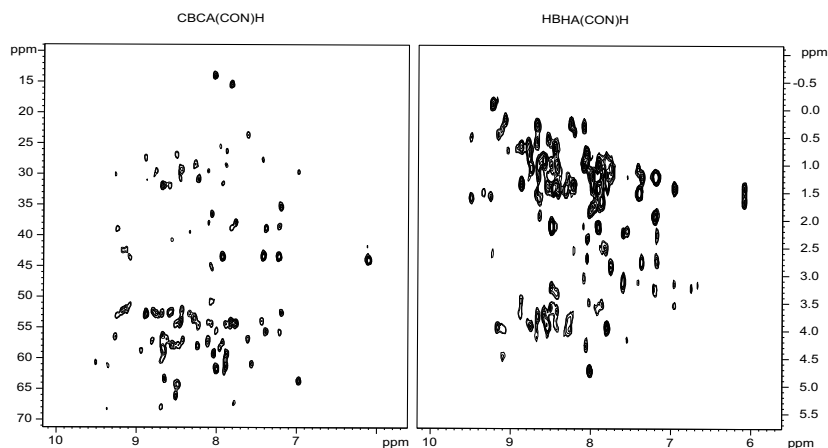
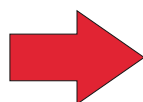
- 3D HBHA(CO)NH with PEP (**hbhaconhgp3d** | HBHACONHGP3D)
- 3D HBHA(CO)NH using WATERGATE (**hbhaconhgpwg3d** | HBHACONHGPWG3D)
- 3D HBHA(CO)NH using TROSY (**trhbhaconhgp3d** | TRHBHACONHGP3D)
- 3D HBHA(CO)NH using TROSY and gradient echo-antiecho (**trhbhaconhetgp3d** | TRHBHACONHETGP3D)
- 4D HBHACONH using WATERGATE (**hbhaconhgpwg4d**)

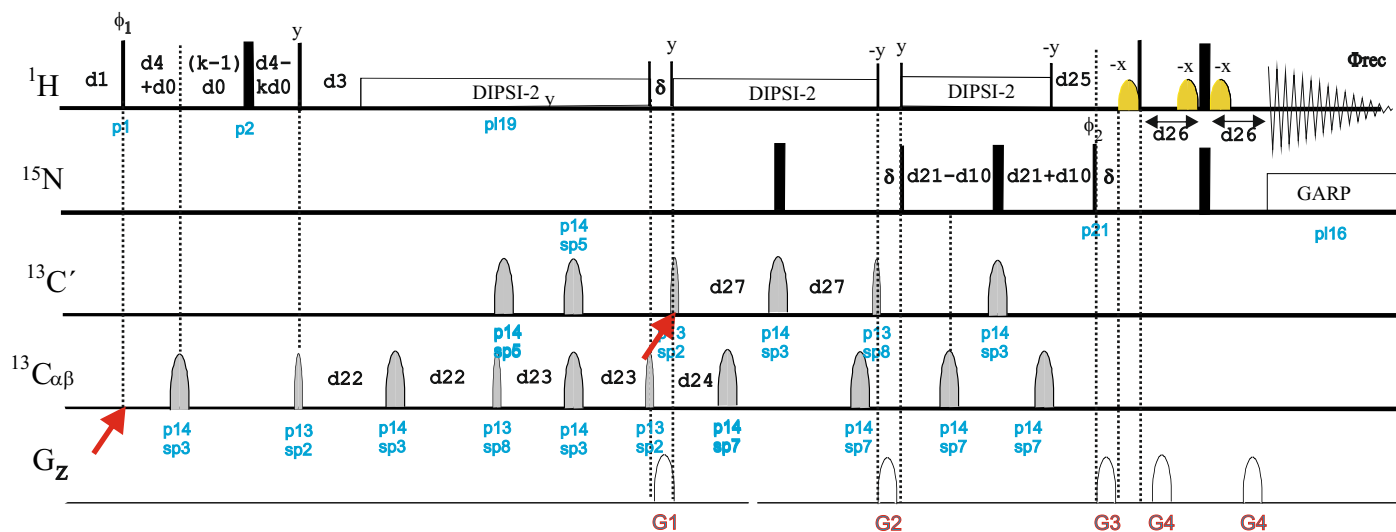
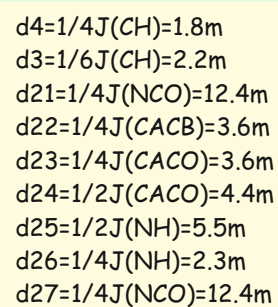
Also see:

3D HBHANH experiment
3D CBCA(CO)NH experiment
3D H(CC)(CO)NH experiment

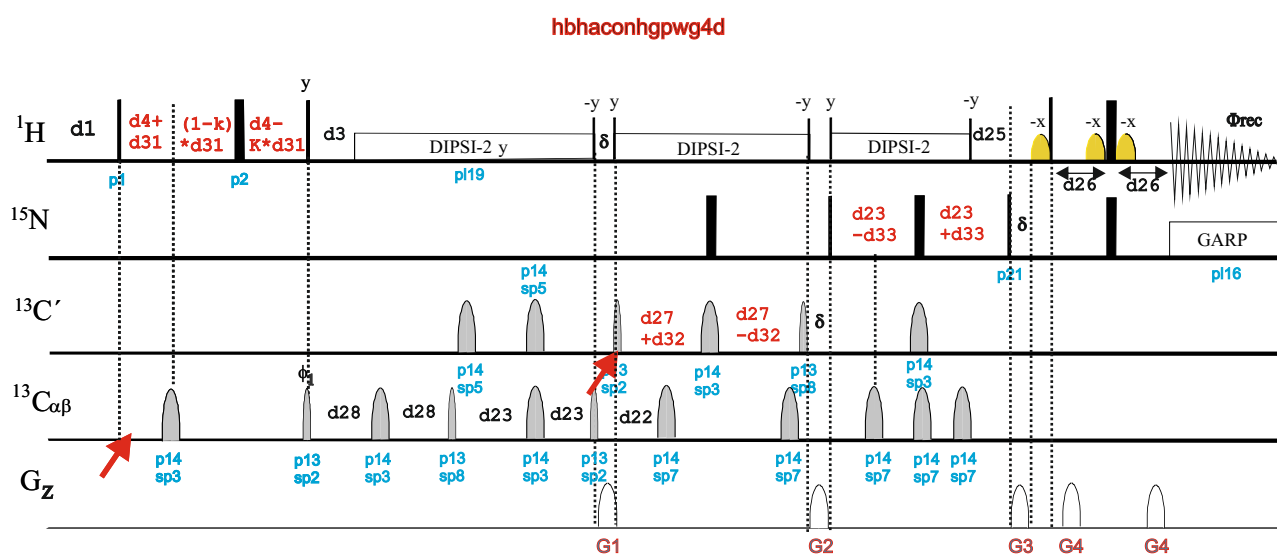
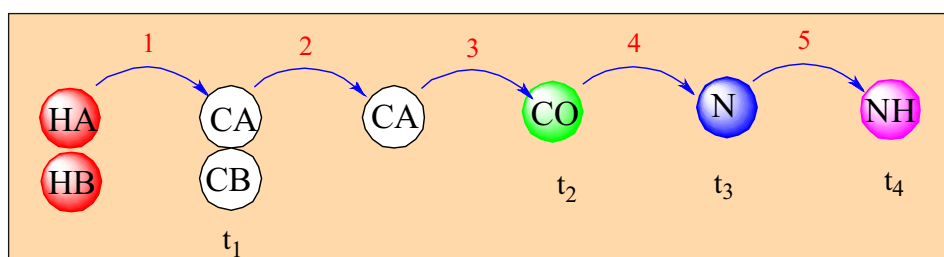
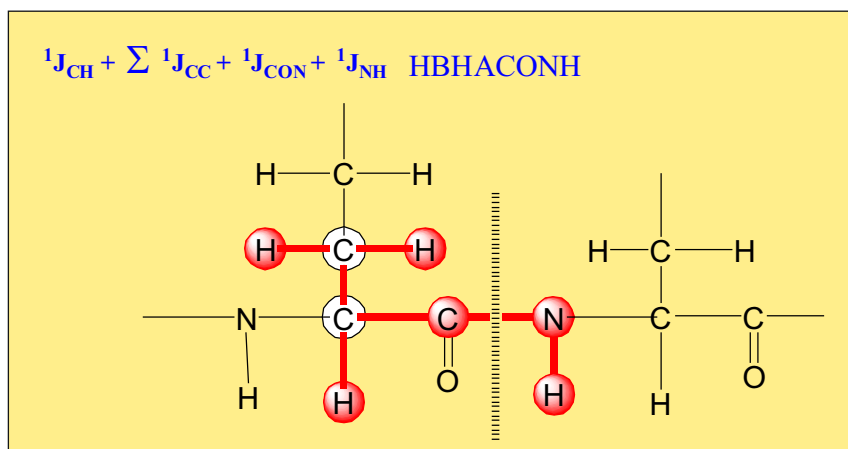


Hali





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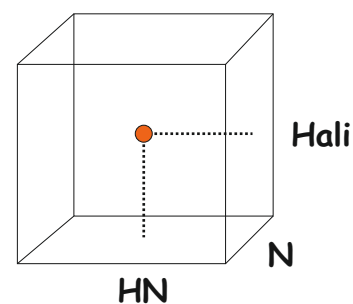
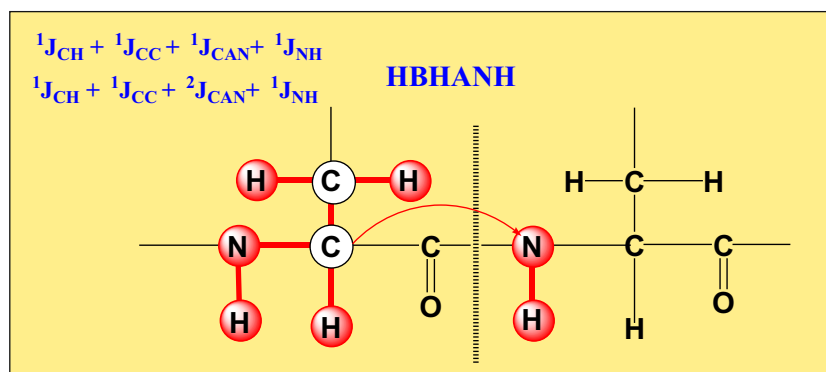
3D HBHANH

3D HBHANH experiment

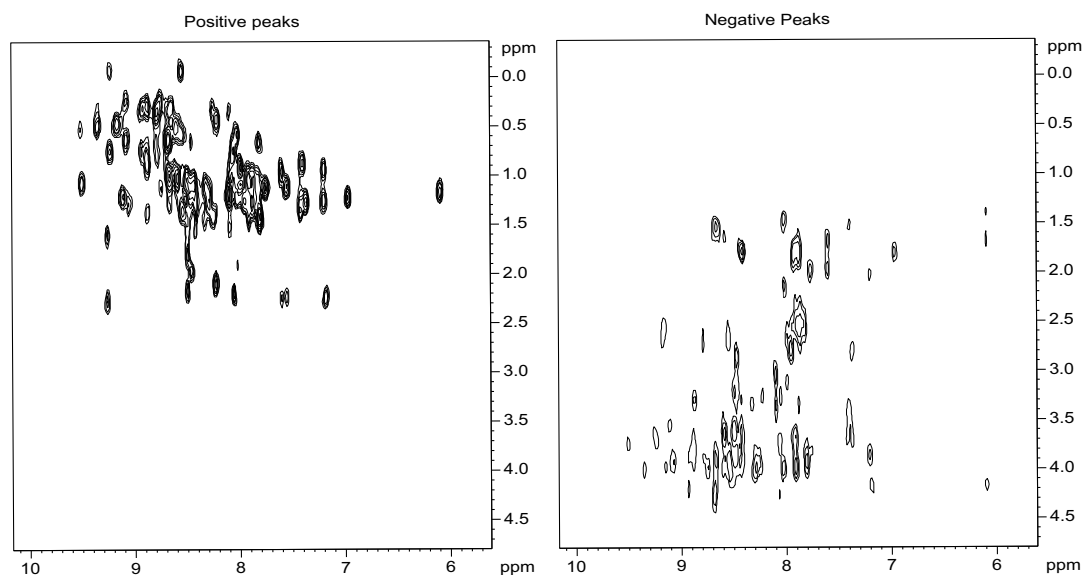
- 3D HBHANH using PEP (**hbhanhgp3d**) | **HBHANHGP3D**)
- 3D HBHANH using WATERGATE (**hbhanhgpwg3d**) | **HBHANHGPWG3D**)
- 3D HBHANH using TROSY (**trhbhanhgp3d**) | **TRHBHANHGP3D**)
- 3D HBHANH using TROSY and gradient echo-antiecho (**trhbhanhetgp3d**) | **TRHBHANHETGP3D**)

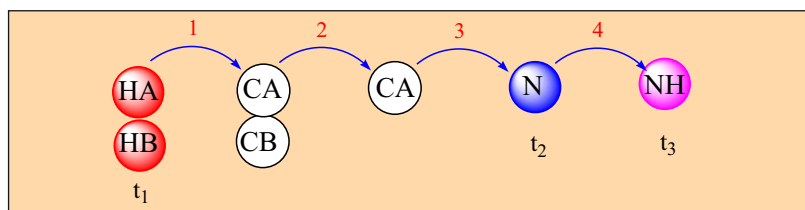
Also see:

3D HBHA(CO)NH experiment



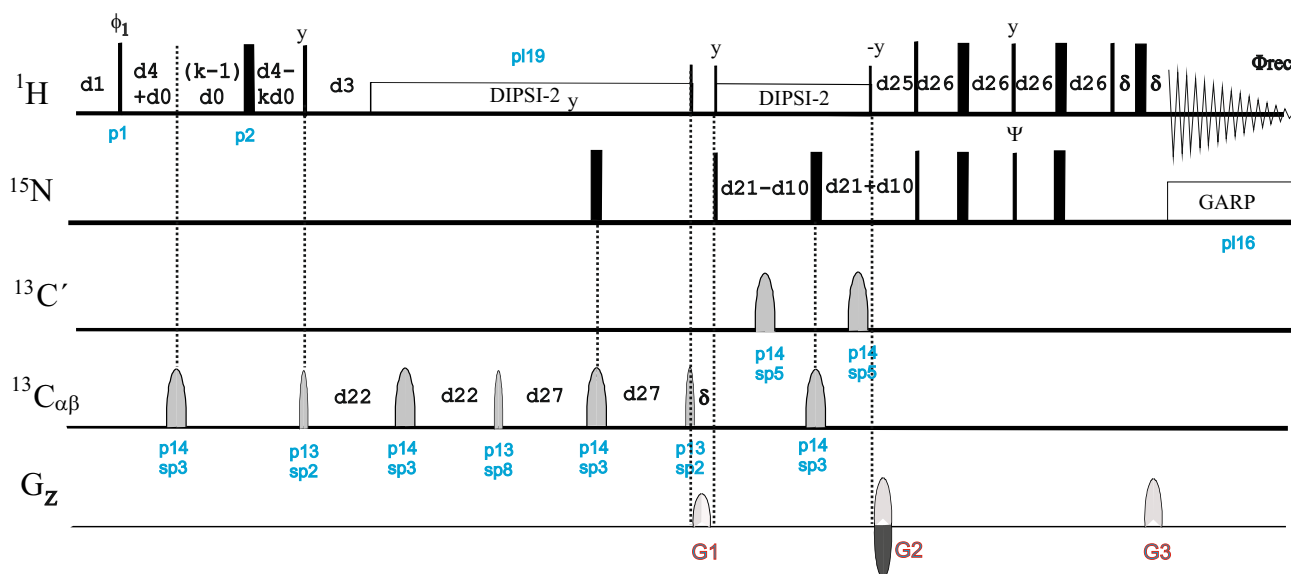
HBHA(N)H



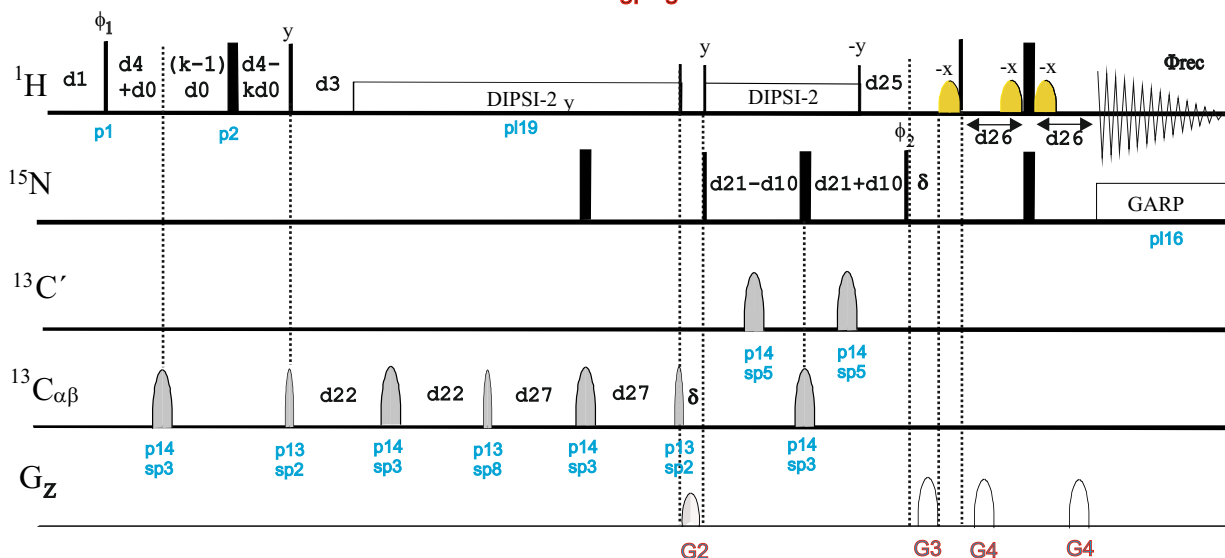


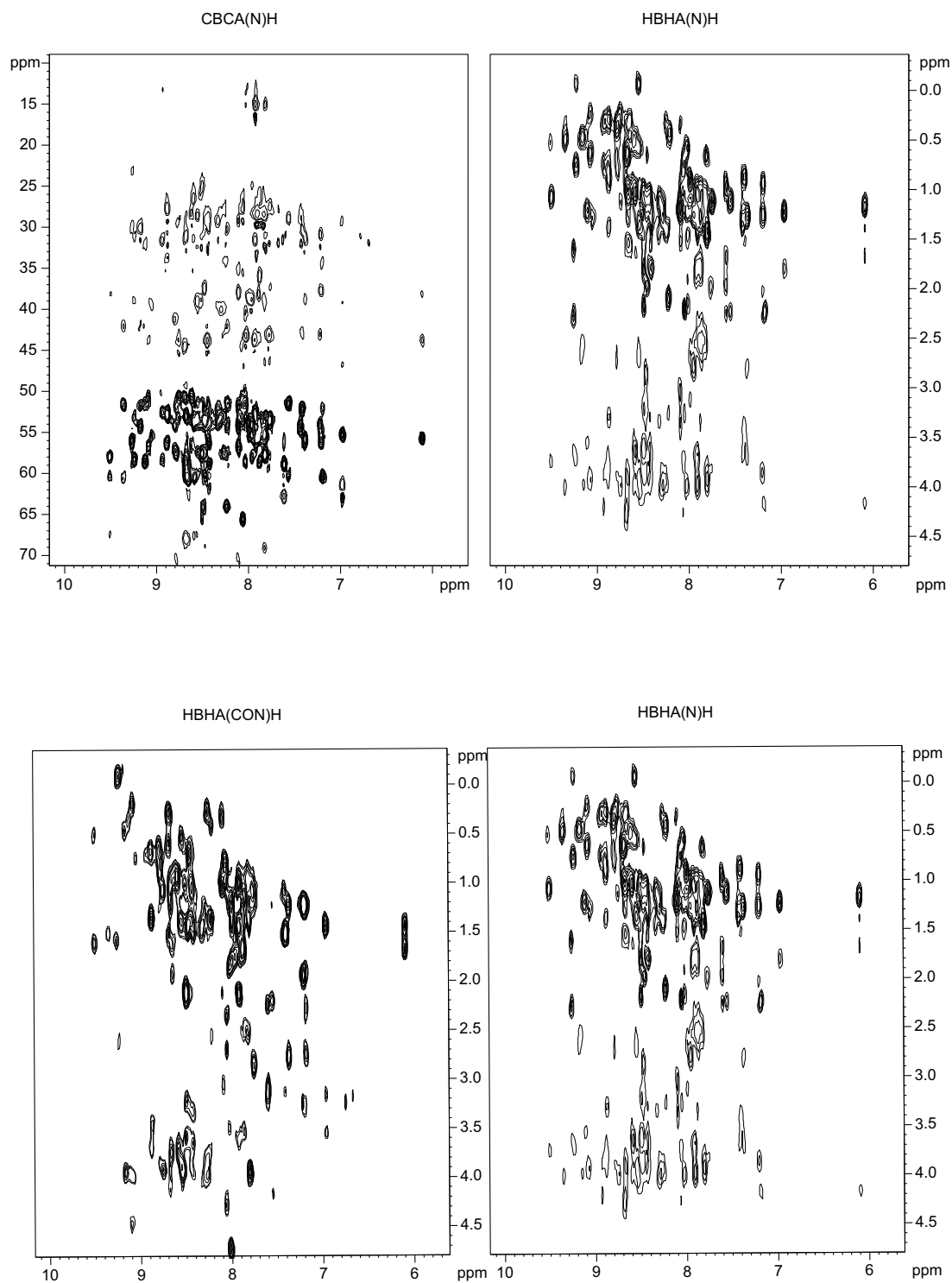
$d4=1/4J(\text{CH})=1.8\text{m}$
 $d3=1/6J(\text{CH})=2.2\text{m}$
 $d21=1/4J(\text{NCO})=12.4\text{m}$
 $d22=1/4J(\text{CACB})=3.6\text{m}$
 $d25=1/2J(\text{NH})=5.5\text{m}$
 $d26=1/4J(\text{NH})=2.3\text{m}$
 $d27=1/4J(\text{NCO})=12.4\text{m}$

hbhanhgp3d



hbhanhgpwg3d







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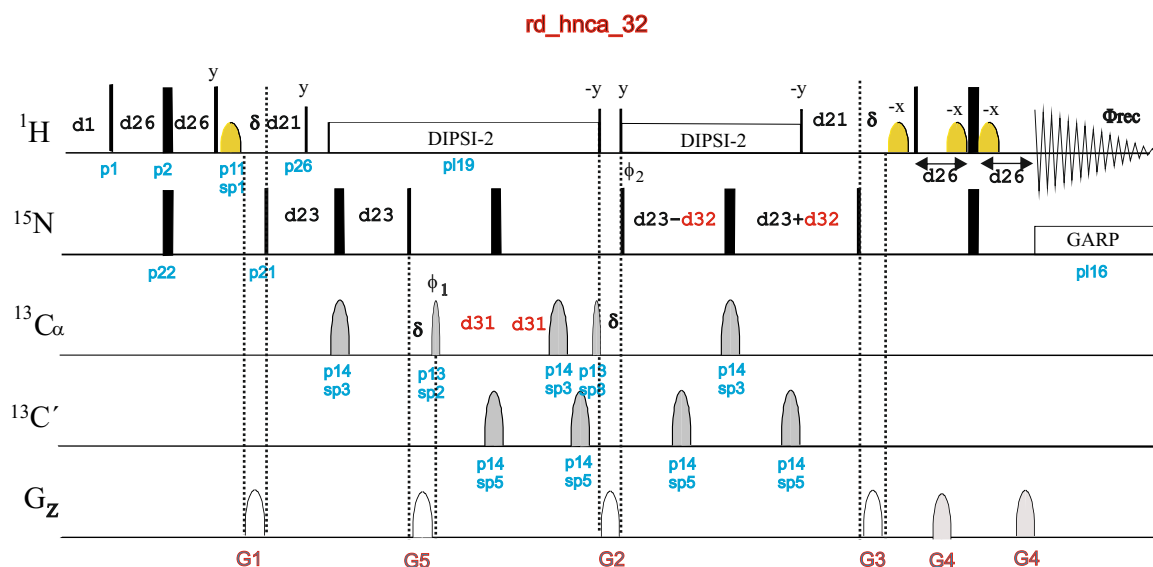
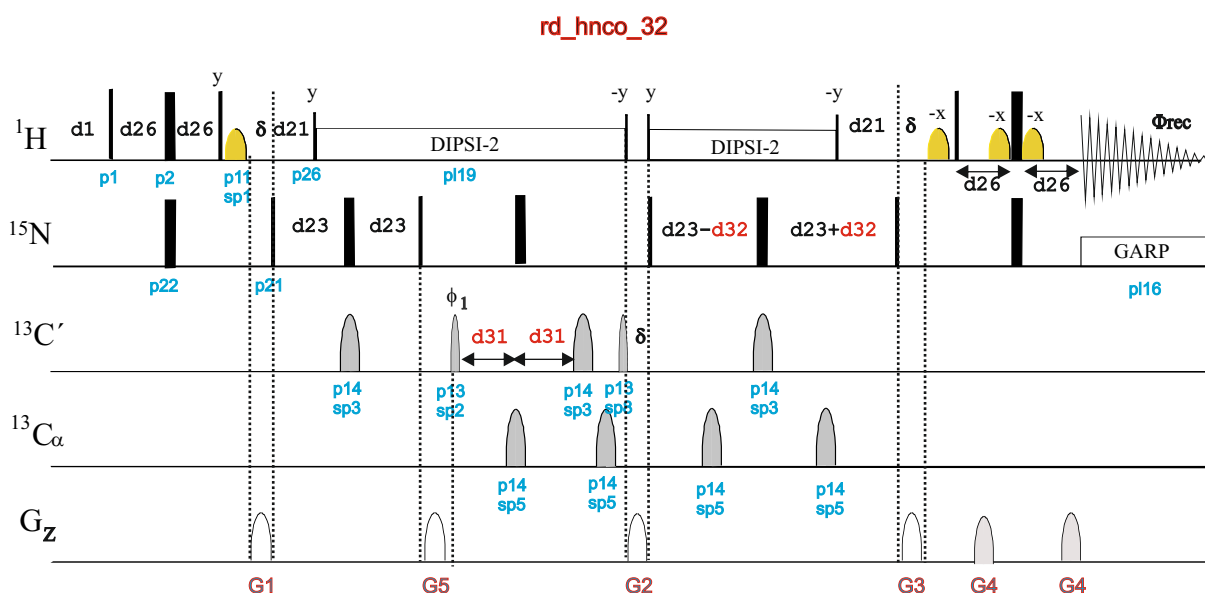
REDUCED-DIMENSIONALITY (APSY) NMR EXPERIMENTS

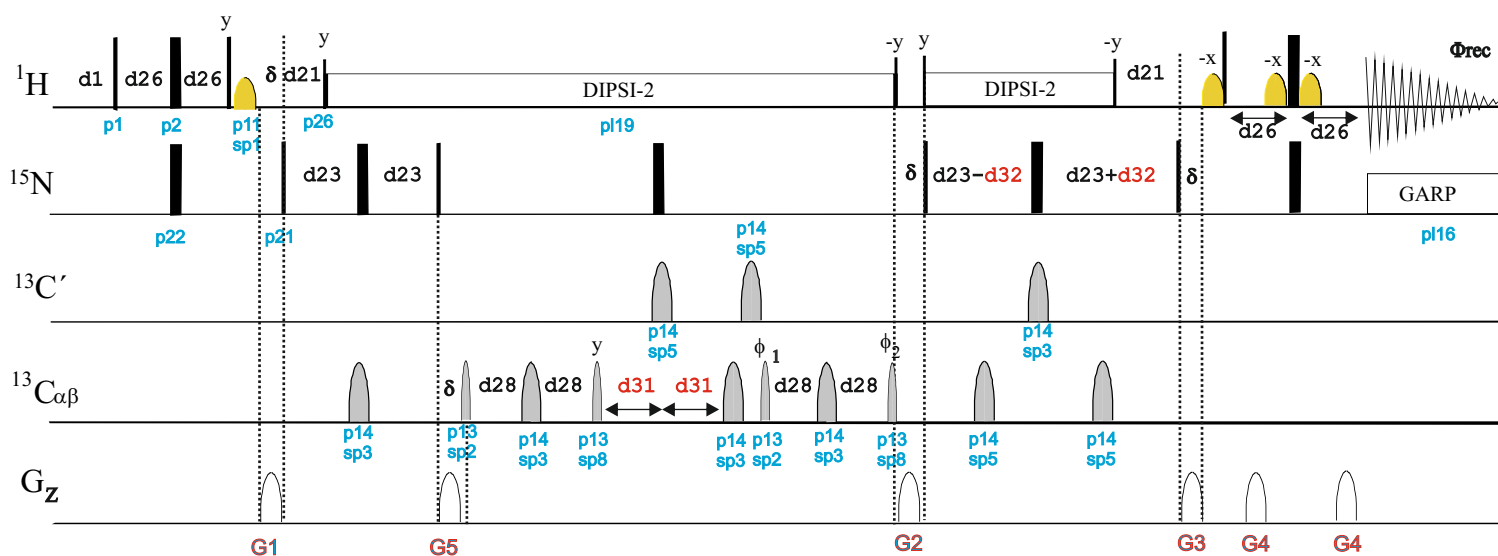
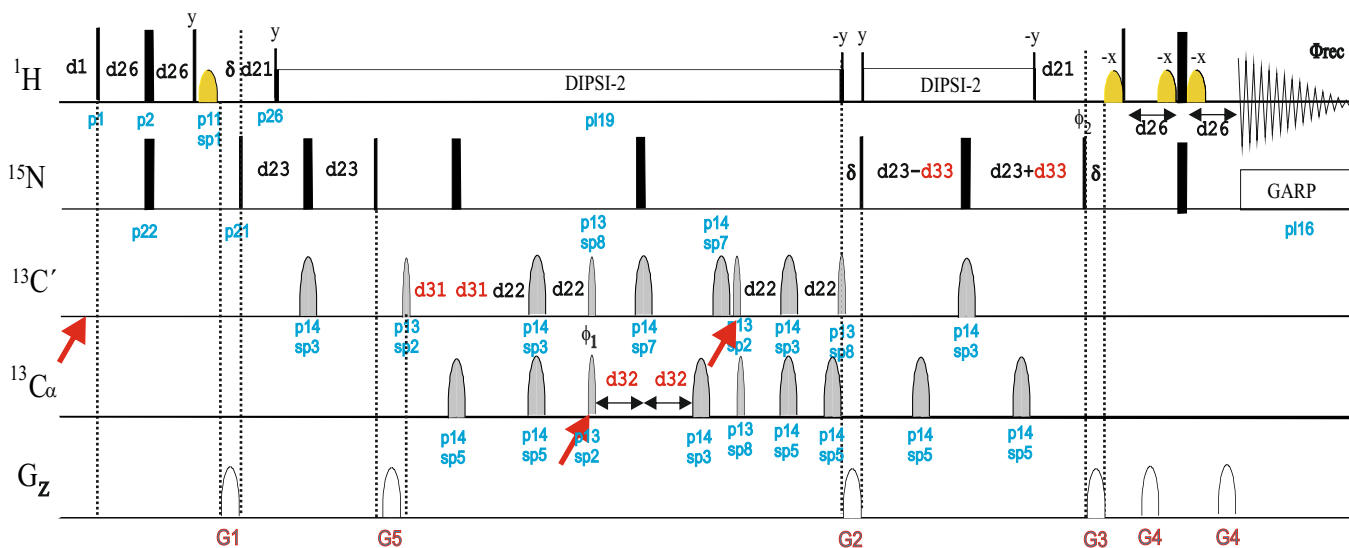
S. Hiller, F. Fiorito, K. Wuethrich & G. Wider, Proc. Natl. Acad. Sci. USA 102, 10876-10881 (2005).
F. Fiorito, S. Hiller, G. Wider & K. Wuethrich, J. Biomol. NMR 35, 27-37 (2006)

Reduced-Dimensionality (RD) / APSY NMR Experiments

- Reduced-Dimensionality (3,2)-HNCA (rd_hnca_32 | APSY_HNCA_32)
- Reduced-Dimensionality (3,2)-HNCACB (rd_hncacb_32 | APSY_HNCACB_32)
- Reduced-Dimensionality (3,2)-HNCOCACB (rd_hncocacb_32 | APSY_HNCOCACB_32)
- Reduced-Dimensionality (6,2)-HNCOCANH (rd_hncocanh_62 | APSY_HNCOCANH_62)
- Reduced-Dimensionality (3,2)-HNCO (rd_hnco_32 | APSY_HNCO_32)
- Reduced-Dimensionality (4,2)-HNCOCA (rd_hncoca_42 | APSY_HNCOCA_42)

See the original experiments





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NMRGuide

2D & 3D
BEST/SOFAST
NMR EXPERIMENTS

SOFAST/BEST NMR Experiments

2D SOFAST/BEST Experiments

- 2D Sofast-HMQC (**sfhmqcf3gp**ph | **SFHMQCF3GPPH**)
- 2D Sofast-HMQC with inversion of water/aliphatic protons (**hetsf hmqcf3gp**ph)
- 2D Sofast-HMQC with sensitivity improved (**sfhmqcf3gp**phias)
- 2D BEST-HSQC (**b_hsqc**etf3gp*si* | **B_HSQCETF3GP**SI)
- 2D BEST-TROSY (**b_trosy**f3gp*ph*)
- 2D BEST-TROSY with sensitivity improved (**b_trosy**etf3gp*si*)

3D SOFAST/BEST Experiments

- 3D BEST-HNCO (**b_hncog**p3d | **B_HNCOGP3D**)
- 3D BEST-HNCO using TROSY (**b_trhncog**p3d)
- 3D BEST-intraHNCO (**b_hncog**p3d | **B_HNCOIGP3D**)
- 3D BEST-intraHNCO using TROSY (**b_trhncog**p3d)
- 3D BEST-HNCA (**b_hncag**p3d | **B_HNCAGP3D**)
- 3D BEST-HNCA using TROSY (**b_trhncag**p3d)
- 3D BEST-intraHNCA (**b_hncag**p3d | **B_HNCAIGP3D**)
- 3D BEST-intraHNCA using TROSY (**b_trhncag**p3d)
- 3D BEST-HN(CO)CA (**b_hncocag**p3d | **B_HNCOCA GP3D**)
- 3D BEST-HN(CO)CA using TROSY (**b_trhncocag**p3d)
- 3D BEST-HN(CA)CO (**b_hncacog**p3d | **B_HNCACOGP3D**)
- 3D BEST-HN(CA)CO using TROSY (**b_trhncacog**p3d)
- 3D BEST-HNCACB (**b_hncacb**gp3d | **B_HNCACBGP3D**)
- 3D BEST-HNCACB using TROSY (**b_trhncacb**gp3d)
- 3D BEST-intraHNCACB (**b_hncacbig**p3d | **B_HNCACBIGP3D**)
- 3D BEST-intraHNCACB using TROSY (**b_trhncacbig**p3d)
- 3D BEST-HN(CO)CACB (**b_hncocacbg**p3d | **B_HNCOCACBGP3D**)
- 3D BEST-HN(CO)CACB using TROSY (**b_trhncocacbg**p3d)

4D SOFAST/BEST Experiments

- 4D BEST-HNCACO (**b_hncacog**p4d)
- 4D BEST-HNCOCA (**b_hncocag**p4d)
- 4D BEST-HNCOCACB (**b_hncocacbg**p4d)

See the original experiments

NH-selective shaped pulses for BEST/Sofast NMR Experiments:



p39
sp23

p39: f1 channel - 120 degree shaped pulse for excitation
sp23= Pc9_4_120.1000 (120o) (3.0ms at 600.13 Mhz)
(or Q5.1000 (90o) (2.0ms at 600.13 MHz))



p40
sp24

p40: f1 channel - 180 degree shaped pulse for refocussing
sp24= Rsnob.1000 (1.0ms at 600.13 Mhz)



p41
sp25

p41: f1 channel - 90 degree shaped pulse for excitation
sp25=sp27= Pc9_4_90.1000 (3.0ms at 600.13 Mhz)



p42
sp26

p42: f1 channel - 180 degree shaped pulse for refocussing
sp26= Reburp.1000 (2.0ms at 600.13 Mhz)



p43
sp28

p43: f1 channel - 90 degree shaped pulse for excitation
sp28= Eburp2.1000 (1.92ms at 600.13 Mhz)
sp29= Eburp2tr.1000 (1.92ms at 600.13 Mhz)



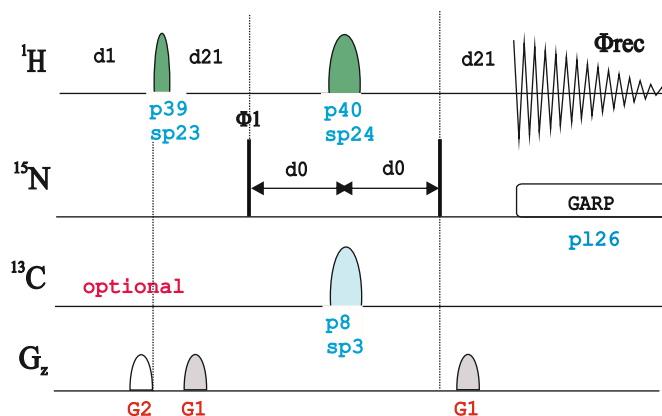
p44
sp30

p44: f1 channel - 180 degree shaped pulse for refocussing
sp30= Bip720,50,20.1 (200us at 600.13 MHz)

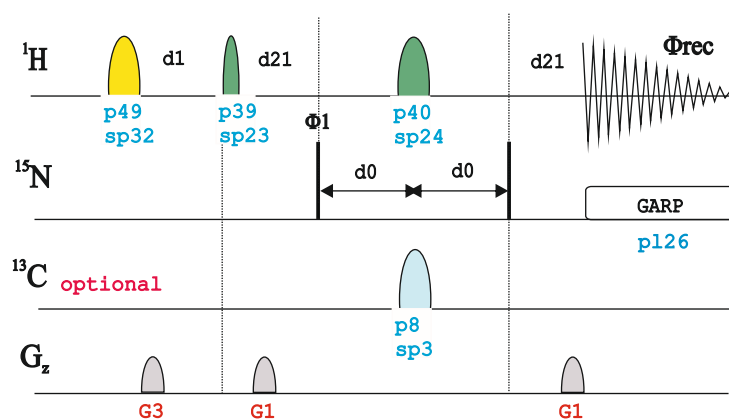
BEST-NMR:

1. P. Schanda, H. v. Melckebeke & B. Brutscher, J. Am. Chem. Soc. 128, 9042-9043 (2006)
2. E. Lescop, P. Schanda & B. Brutscher, J. Magn. Reson. 187 163-169 (2007)

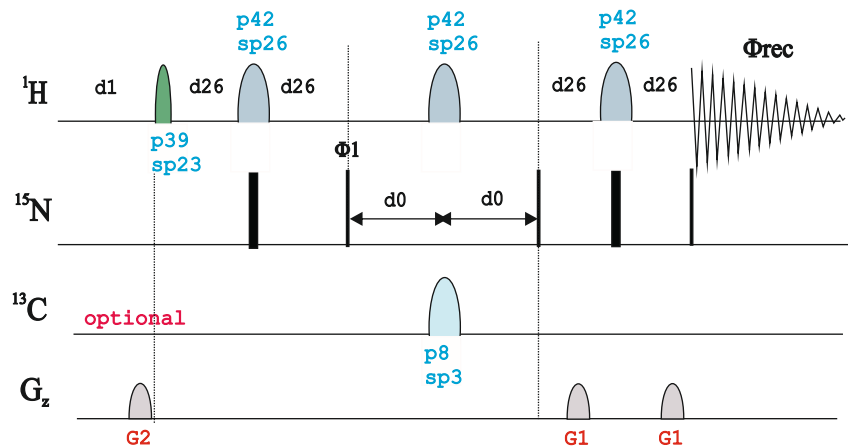
sfhmqcf3gpqh



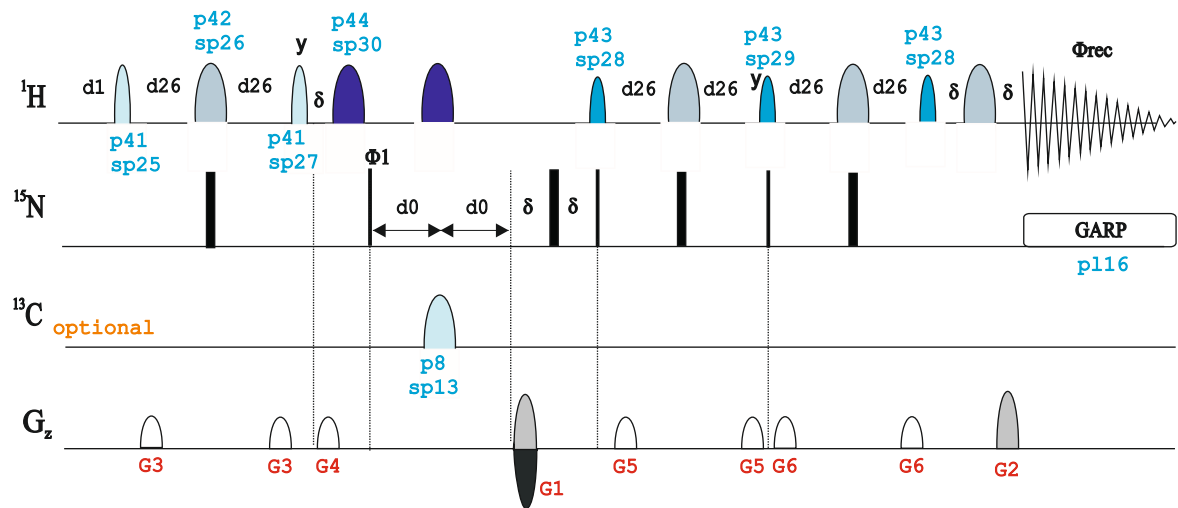
hetsfhmqcf3gpqh



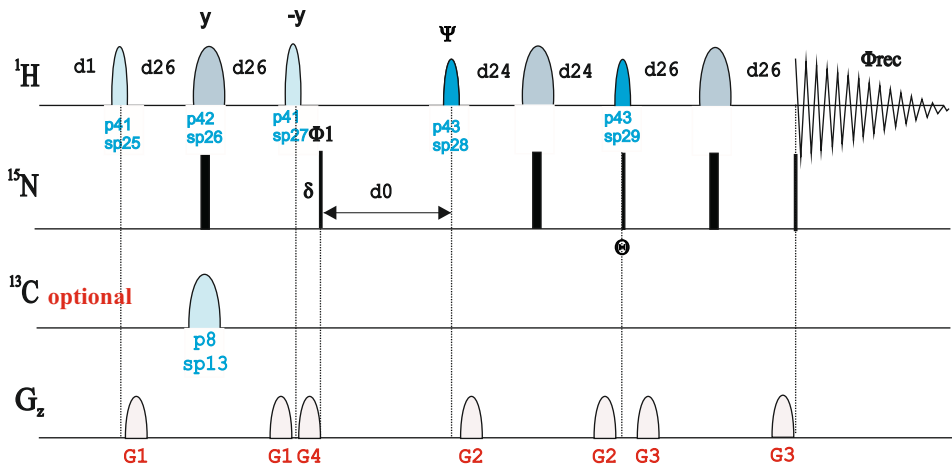
sfhmqcf3gpphiassi



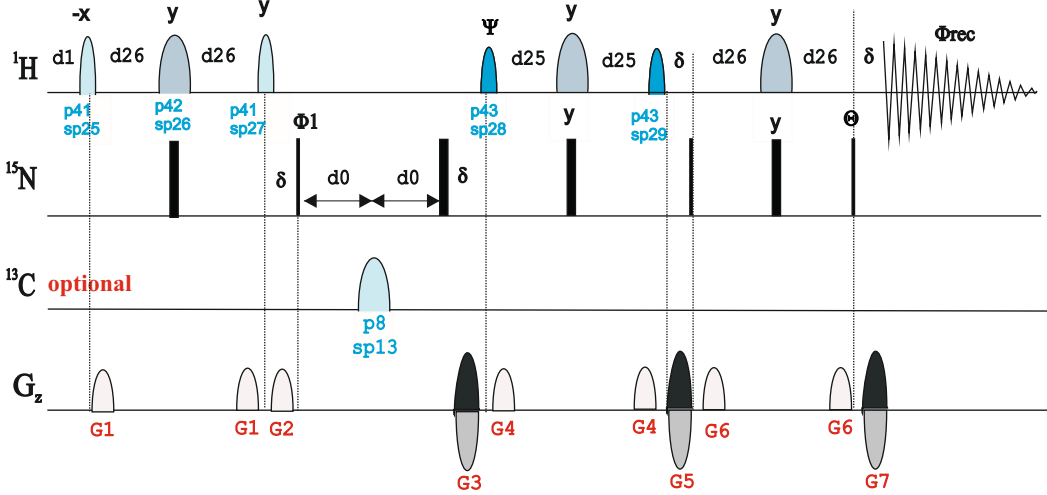
b_hsqcetf3gpsi

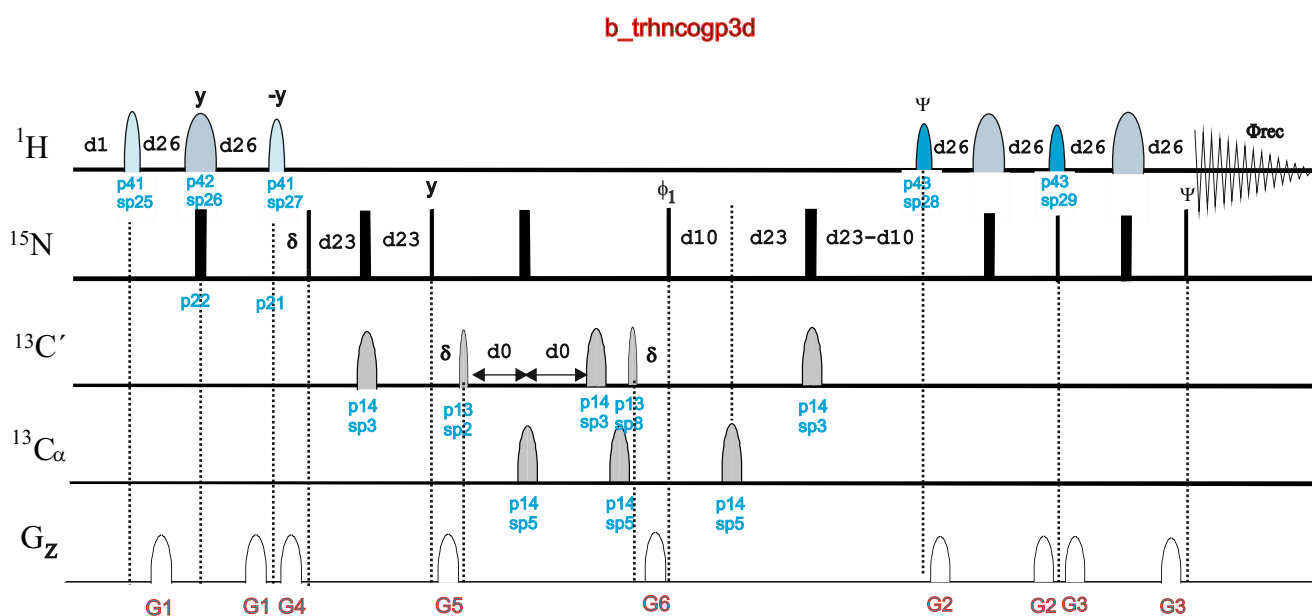
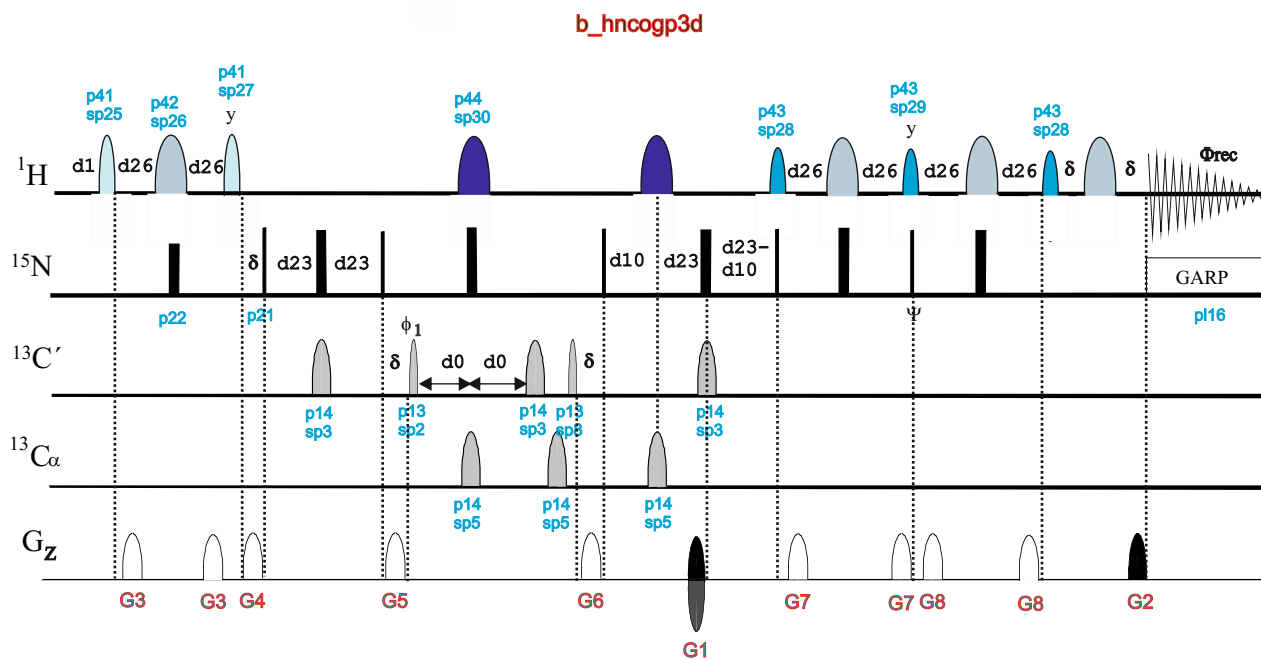


b_trosyf3gpph



b_trosytf3gpsi

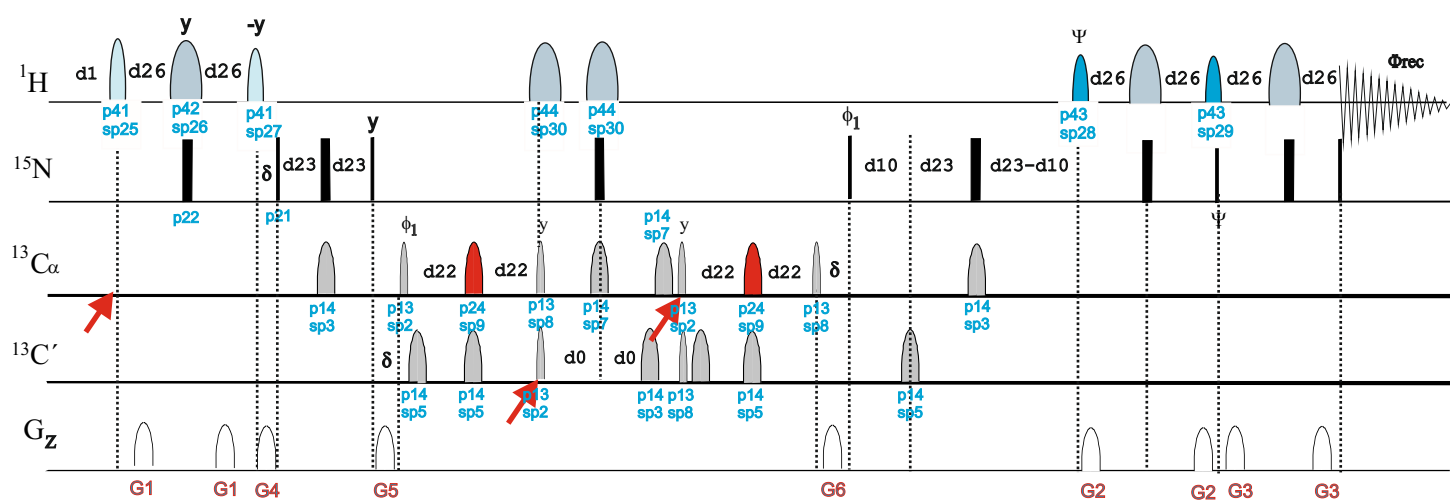


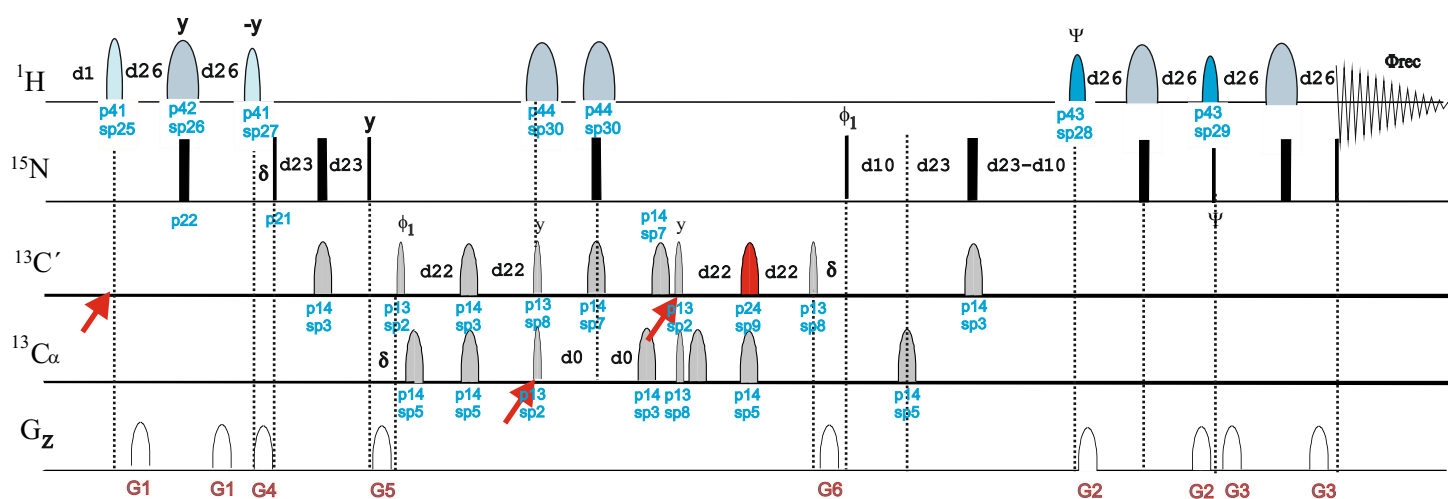


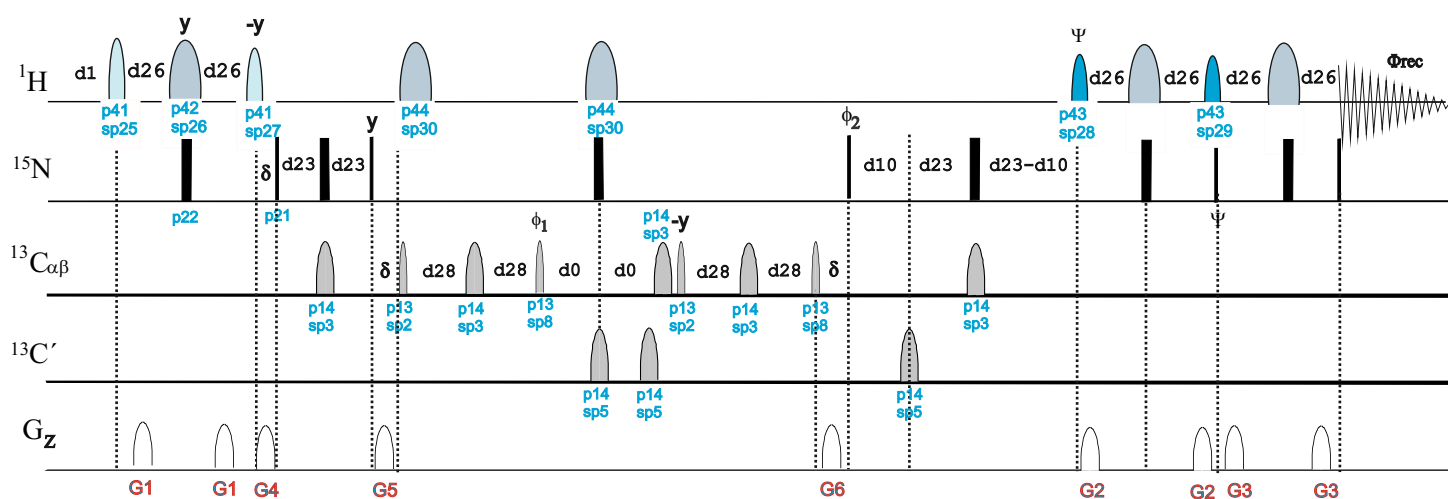


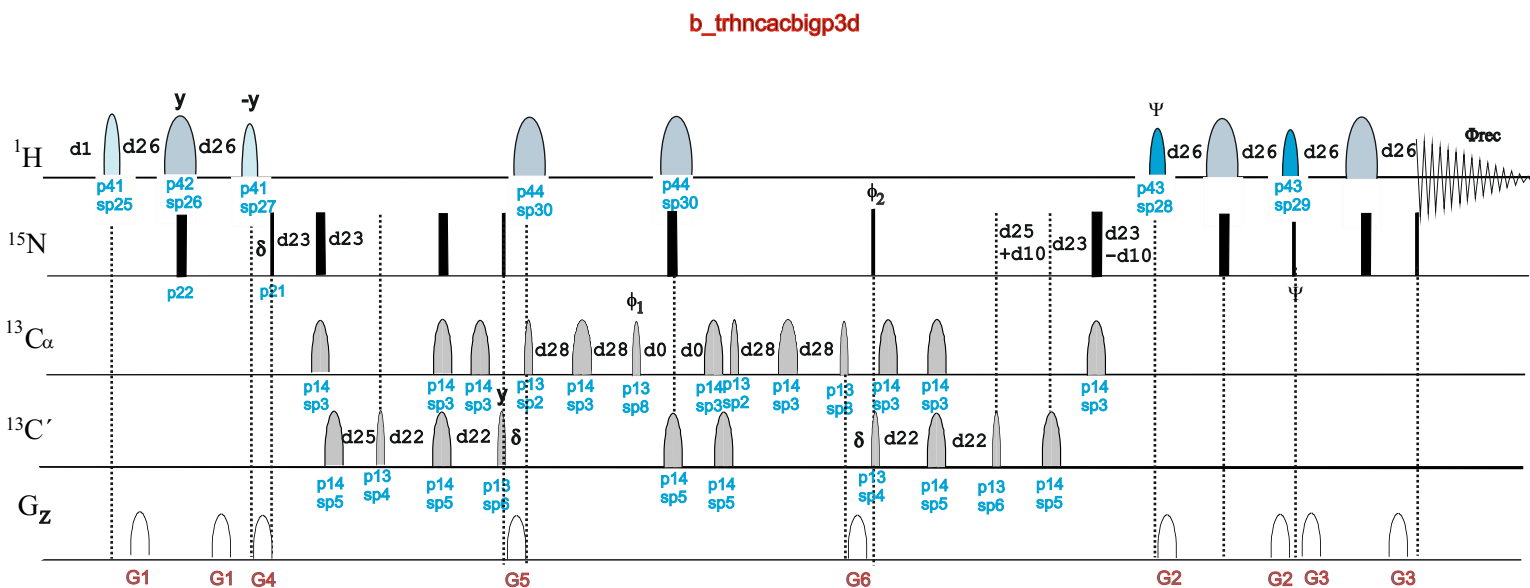
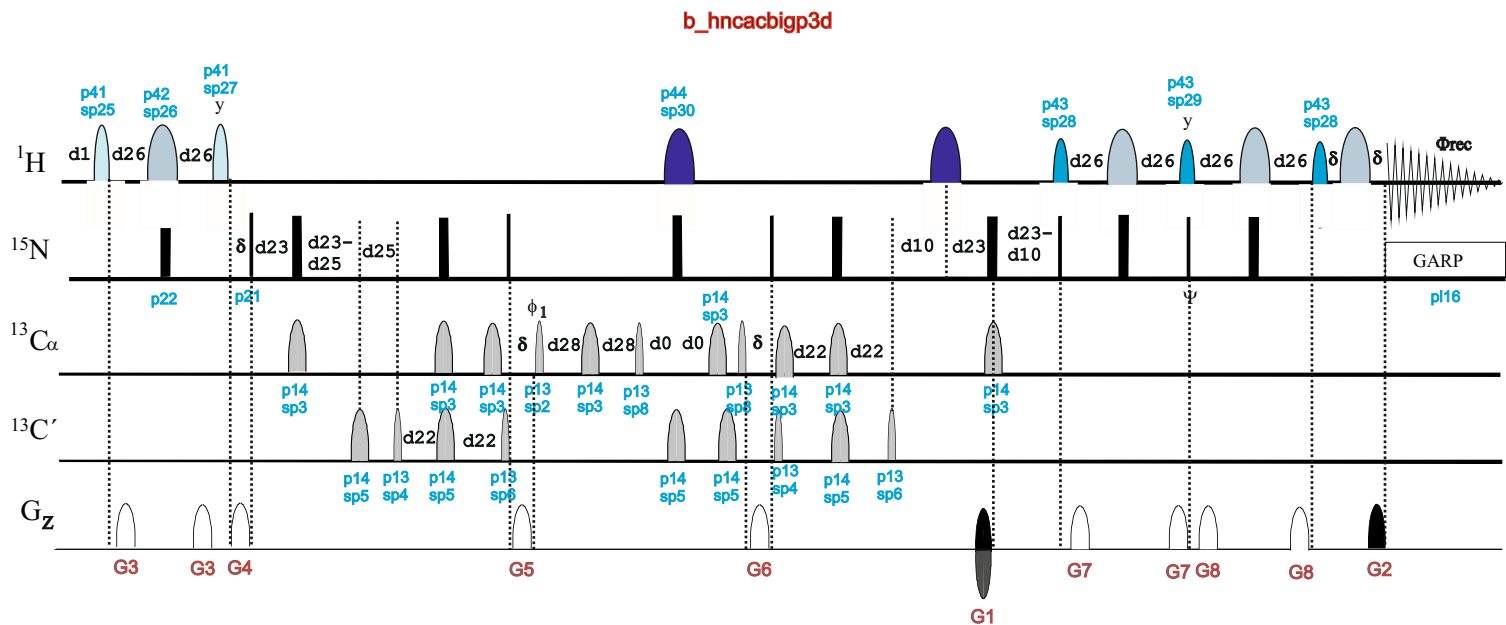
[illegible][illegible]













BRUKER PULSE PROGRAM CATALOGUE

NMRGuide

AMINO-ACID TYPE_SELECTIVE MUSIC EXPERIMENTS

General Description:

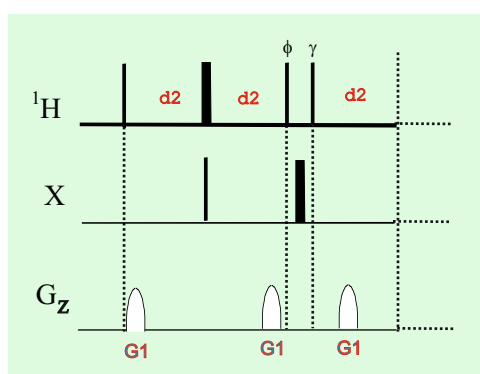
Amino-Acid Type-Selective Experiments are a set of triple-resonance NMR experiments alternatives to the conventional experiments, designed to provide specific information of particular amino-acids. Some of the main features:

1. Sequential and aa-type information is obtained.
2. Reduction of number of peaks and signal overlapping.
3. Unambiguous assignment for some aa.
3. NMR Pulse sequences are mainly based on the original CBCACONH and CBCANH experiments
 - A. CBCACONH-type experiments provide a single cross-peak from the sequential inter-residue $i+1$ correlation due to CO is involved.
 - B. CBCANH-type experiments provide to different cross peaks, from intra- and inter-residue connectivities by means of the similar $1J(NCA)$ and $2J(NCA)$ coupling pathways.
4. They can be recorded as a 2D $1H$ - $15N$ or 3D HNCO- or HNCA-type maps ([see ZGPTNS](#)).
5. Main keys are the initial CH₂-, CH₃- or NH₂-selected transfer steps (see MUSIC element) and the use of specific offset, selective pulses on specific regions and delays optimization.

References of Amino-Acid Type-Selective MUSIC Experiments:

1. P. Schmieder, M. Leidert, M. Kelly & H. Oschkinat, J. magn. Reson. 131, 199-202 (1998).
2. M. Schubert, M. Smalla, P. Schmieder & H. Oschkinat, J. Magn. Reson. 141, 34-43 (1999)
3. M. Schubert, L. Ball, H. Oschkinat & P. Schmieder, J. Biomol. NMR 17, 331-335 (2000)
4. 3. M. Schubert, H. Oschkinat & P. Schmieder, J. Biomol. NMR 20, 379-384 (2001)
5. M. Schubert, H. Oschkinat & P. Schmieder, J. Magn. Reson. 148, 61-72 (2001).
6. M. Schubert, H. Oschkinat & P. Schmieder, J. Magn. Reson. 153, 186-192 (2001)
7. M. Schubert, D. Labudde, D. Leitner, H. Oschkinat & P. Schmieder, J. Biomol. NMR 31, 115-127 (2005).

The MUSIC (Multiplicity Selective In-Phase Coherence Transfer) Element:



Phase Cycles for:

CH₂ or NH₂ selection

ϕ 0°
 γ $45^\circ, 135^\circ, 225^\circ, 315^\circ$
 rec $0^\circ, 180^\circ$

Ch₃ selection

ϕ 0°
 γ $30^\circ, 90^\circ, 150^\circ, 210^\circ, 270^\circ, 330^\circ$
 rec $0^\circ, 180^\circ$

$d2 = 1/2J = 3.6\text{ms}(\text{CH}_2 \text{ or Ch}_3) \text{ or } 5.5\text{ms}(\text{NH}_2)$

AminoAcid-selective (MUSIC) Experiments

- 3D MUSIC Metionine (Met - M) with CH2 selection (**music_cm_3d**)
- 3D MUSIC - Metionine (Met - M) with CH2 selection (**music_cm_3d_2**)

- 3D MUSIC - Glutamic (Glu - E) or Aspartic (Asp - D) with CH2 selection (**music_de_3d**)
- 3D MUSIC - Glutamic (Glu - E) or Aspartic (Asp - D) with CH2 selection (**music_de_3d_2**)

- 3D MUSIC - PhenylAlanine (Phe - F)/Hystidine (His-H)/Tyrosine (Tyr-Y) or Triptophan (Trp - W) with CH2 selection (**music_fhyw_3d**)
- 3D MUSIC - PhenylAlanine (Phe - F)/Hystidine (His-H)/Tyrosine (Tyr-Y) or Triptophan (Trp - W) with CH2 selection (**music_fhyw_3d_2**)

- 3D MUSIC - Glycine (Gly - G) or Asparagine (Asn - N)/Glutamine (Gln - Q) with CH2 selection (**music_gly_3d**)
- 3D MUSIC - Glycine (Gly - G) or Asparagine (Asn - N)/Glutamine (Gln - Q) with CH2 selection (**music_gly_3d_2**)

- 3D MUSIC - Serine (Ser - S) with CH2 selection (**music_ser_3d**)
- 3D MUSIC - Serine (Ser - S) with CH2 selection (**music_ser_3d_2**)

- 3D MUSIC - Lysine (Lys - K) and/or Arginine (Arg- R) (**music_kr_3d**)
- 3D MUSIC - Lysine (Lys - K) and/or Arginine (Arg- R) (**music_kr_3d_2**)

- 3D MUSIC - Isoleucine (Ile - I) with CH3 selection (**music_ile_3d**)
- 3D MUSIC - Isoleucine (Ile - I) with CH3 selection (**music_ile_3d_2**)

- 3D MUSIC - Leucine (Leu - L)/Alanine (Ala-A) or Valine (Val - V)/Isoleucine (Ile-I)/Alanine (Ala-A)with CH3 selection (**music_lavia_3d**)
- 3D MUSIC - Leucine (Leu - L)/Alanine (Ala-A) or Valine (Val - V)/Isoleucine (Ile-I)/Alanine (Ala-A)with CH3 selection (**music_lavia_3d_2**)

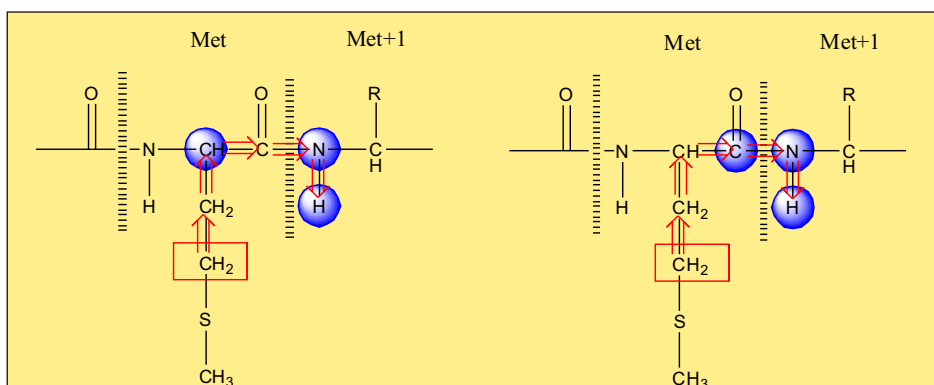
- 3D MUSIC - Valine (Val - V)/Isoleucine (Ile - I) or Theonine (Thr - T)/Alanine (Ala - A)with CH3 selection (**music_tavi_3d**)
- 3D MUSIC - Valine (Val - V)/Isoleucine (Ile - I) or Theonine (Thr - T)/Alanine (Ala - A)with CH3 selection (**music_tavi_3d_2**)

- 3D MUSIC - Proline (Pro - P) (**music_pro_1_3d**)
- 3D MUSIC - Proline (Pro - P) (**music_pro_1_3d.2**)
- 3D MUSIC - Proline (Pro - P) (**music_pro_2_3d**)
- 3D MUSIC - Proline (Pro - P) (**music_pro_2_3d.2**)

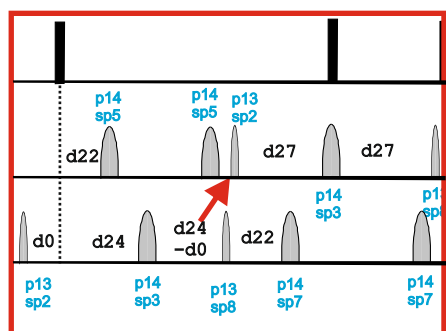
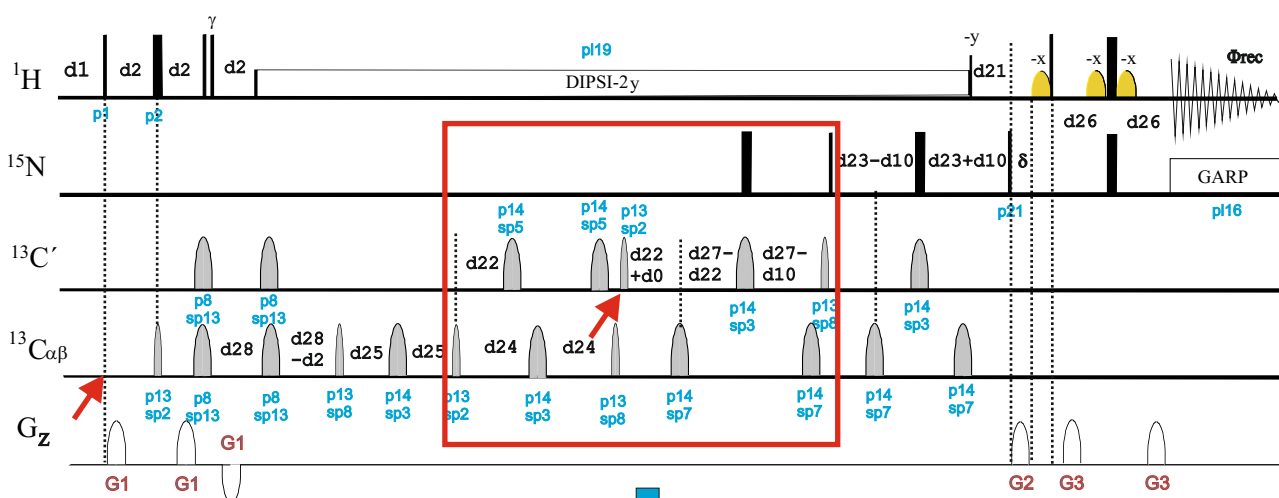
- 3D MUSIC - Glutamine (Gln - Q) or Asparagine (Asn - N) with NH2 selection (**music_qn_3d**)
- 3D MUSIC - Glutamine (Gln - Q) or Asparagine (Asn - N) with NH2 selection (**music_qn_3d_2**)

- 2D MUSIC - Triptophan (Trp - W)(**music_trpe_2d**)

MUSIC-Metionine: $(\text{CH}_2\text{C})\text{CA}(\text{CO})\text{NH}$ and $(\text{CH}_2\text{CCA})\text{CONH}$



music_cm_3d



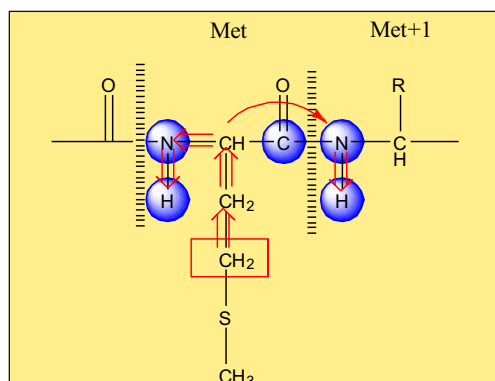
ZGOPTNS:

no option: 3D $(\text{CH}_2\text{C})\text{CA}(\text{CO})\text{NH}$
LABEL CO: 3D $(\text{CH}_2\text{CCA})\text{CONH}$

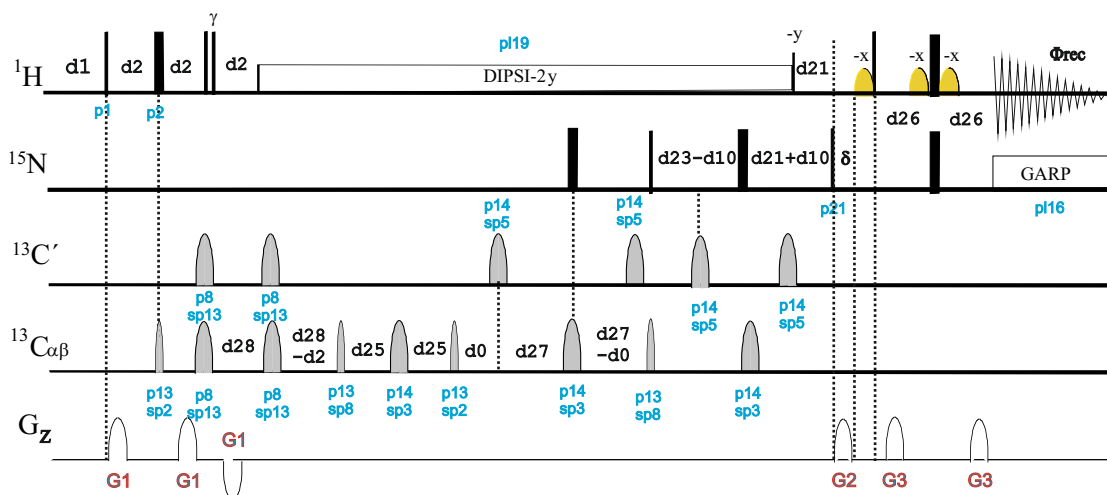
NH(Met+1)
NH(Met+1)

d2 : $1/(2J(\text{CH}))$	[3.5 msec]
d21: $1/(2J(\text{NH}))$	[5.5 msec]
d22: $1/(4J(\text{CaCO}))$	[4.5 msec]
d23: $1/(4J(\text{NCO}))$	[12.4 msec]
d24: $n/(4J(\text{CC}))$	[20 msec]
or $1/(4J(\text{CC}))$ (LABEL_CO)	[5.2 msec]
d25: $1/(4J(\text{CC}))$	[6.0 msec]
d26: $1/(4J(\text{NH}))$	[2.3 msec]
d27: $1/(4J(\text{NCO}))$	[12.4 msec]
d28: $1/(4J(\text{CC}))$	[6.0 msec]
Possible breakthrough: Glu, Gly, Lys, Ser, Val	

MUSIC-Metionine: $(CH_2C)CANH$



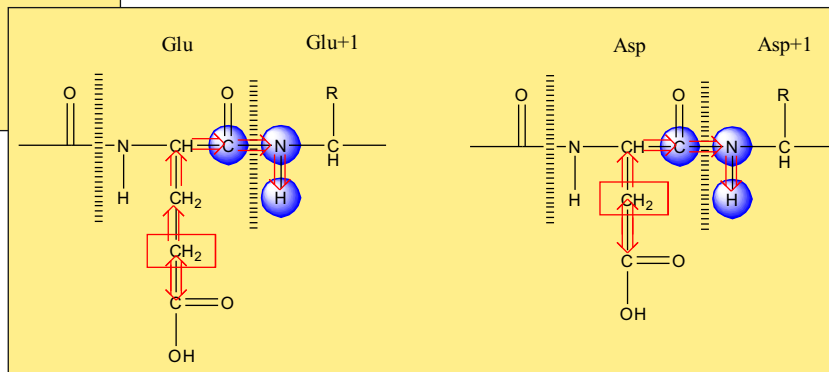
music_cm_3d_2

ZGOPTNS

no option: 3D (CH₂C)CANH NH(Met) and NH(Met+1)

d2 : 1/(2J(CH))	[3.5 msec]
d21: 1/(2J(NH))	[5.5 msec]
d23: 1/(4J(NCα))	[12.4 msec]
d25: 1/(4J(CC))	[6.0 msec]
d26: 1/(4J(NH))	[2.3 msec]
d27: 1/(4J(CβCa)) and 1/(4J(NCα))	[8.2 msec]
d28: 1/(4J(CC))	[6.0 msec]

MUSIC-Glu/Asp: (CH₂COC)CA(CO)NH and (CH₂COCCA)CONH



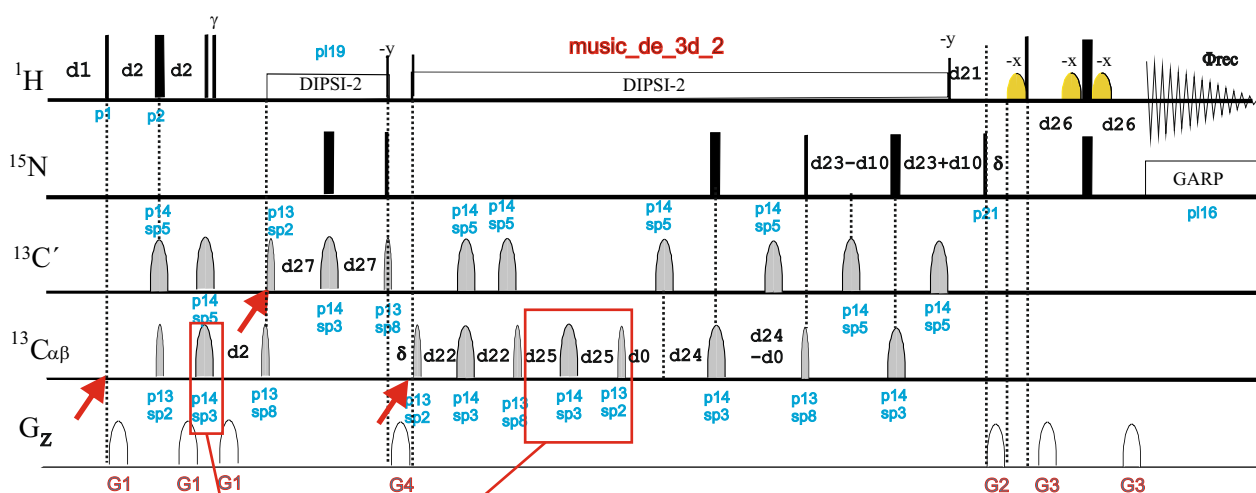
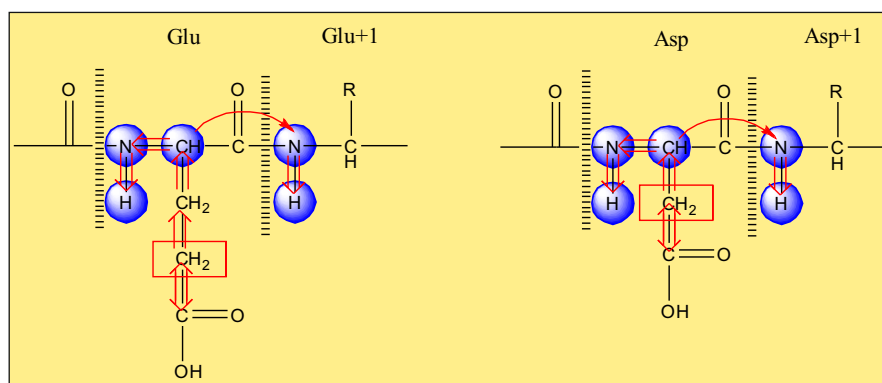
ZGOPTNS: -DLABEL CO



NH(Asp+1)
NH(Glu+1)

d24: $n/(4J(CC)) = [20 \text{ msec}]$
 or $1/(4J(CC) (LABEL_GLU)) = [9.0 \text{ msec}]$
 or $1/(4J(CC) (LABEL_CO)) = [4.5 \text{ msec}]$
 d25: $1/(4J(CC)) = [4.5 \text{ msec}]$
 d26: $1/(4J(NH)) = [2.3 \text{ msec}]$
 d27: $1/(4J(NCO(s))) = [16.0 \text{ msec}]$

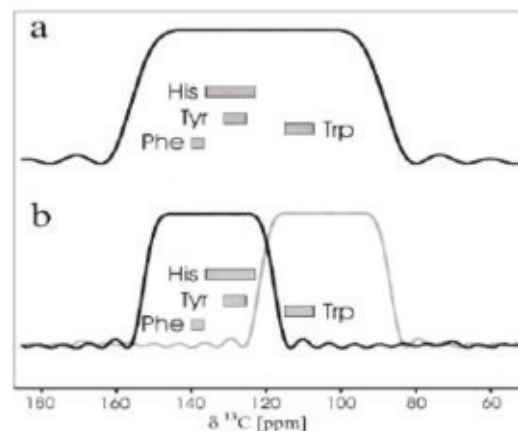
MUSIC-Glu/Asp: (CH₂COC)CANH



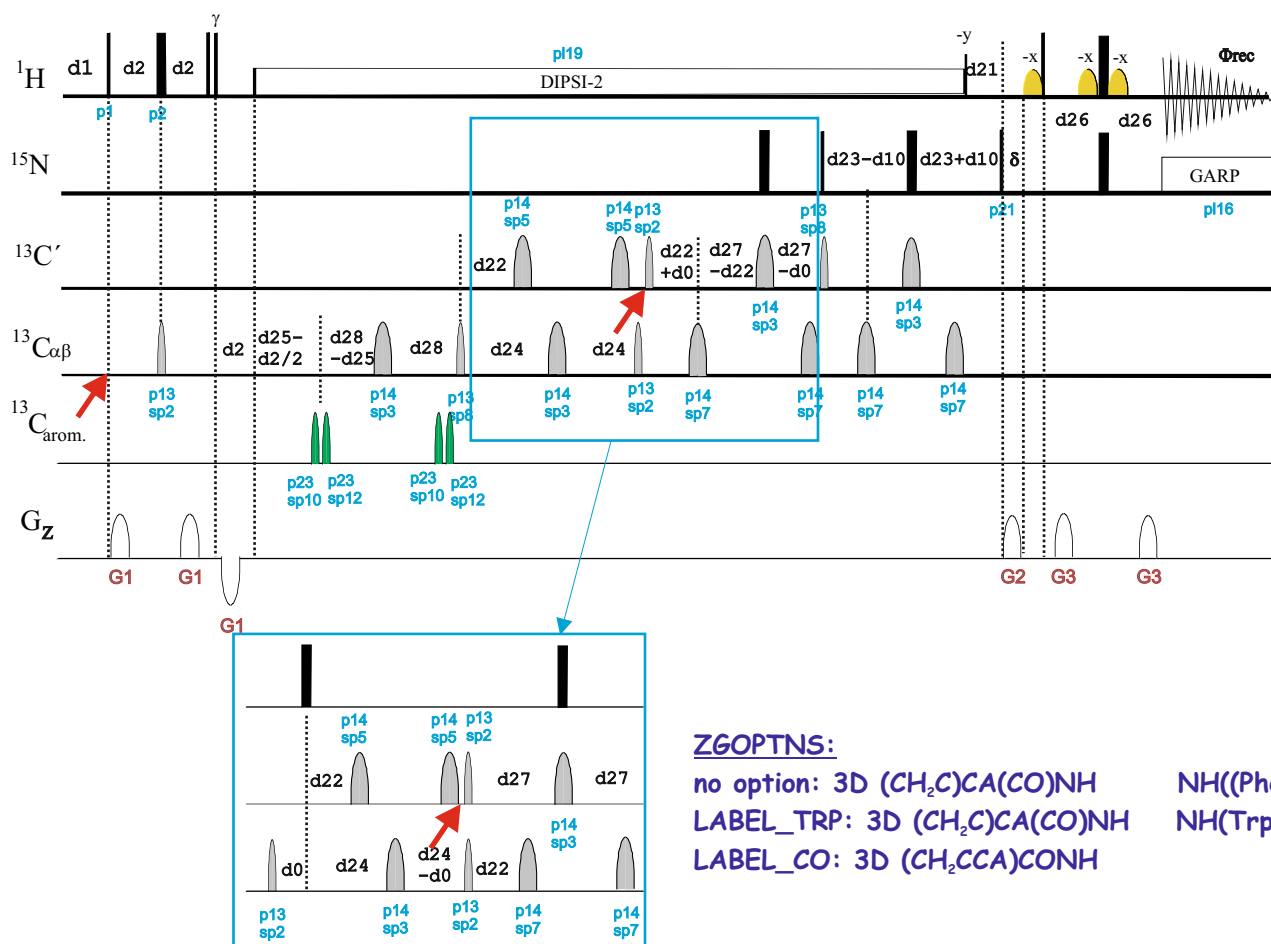
ZGOPTNS
no option: 3D (CH₂COC)CANH NH(Asp+1) and NH(Asp)
LABEL GLU: 3D (CH₂COC)CANH NH(Glu+1) and NH(Glu)

:d2: 1/(2J(CH))	[4.0 msec]
:d21: 1/(2J(NH))	[5.5 msec]
:d22: 1/(4J(CO _{Ca}))	[4.5 msec]
:d23: 1/(4J(N _{Ca}))	[12.4 msec]
:d24: 1/(4J(CC))	[9.0 msec]
:d25: 1/(4J(CC))	[4.5 msec]
:d26: 1/(4J(NH))	[2.3 msec]
:d27: 1/(4J(NCO(s)))	[16.0 msec]

The diagram illustrates the formation of a hydrogen bond between the carbonyl oxygen of residue *aa* and the amide hydrogen of residue *aa+1*. The chemical structures of the two residues are shown, with the hydrogen bond represented by a dashed line. Below the diagram, the chemical structures of the side chains for His, Phe, Tyr, and Trp are shown, indicating their potential to form hydrogen bonds.



music_fhyw_3d

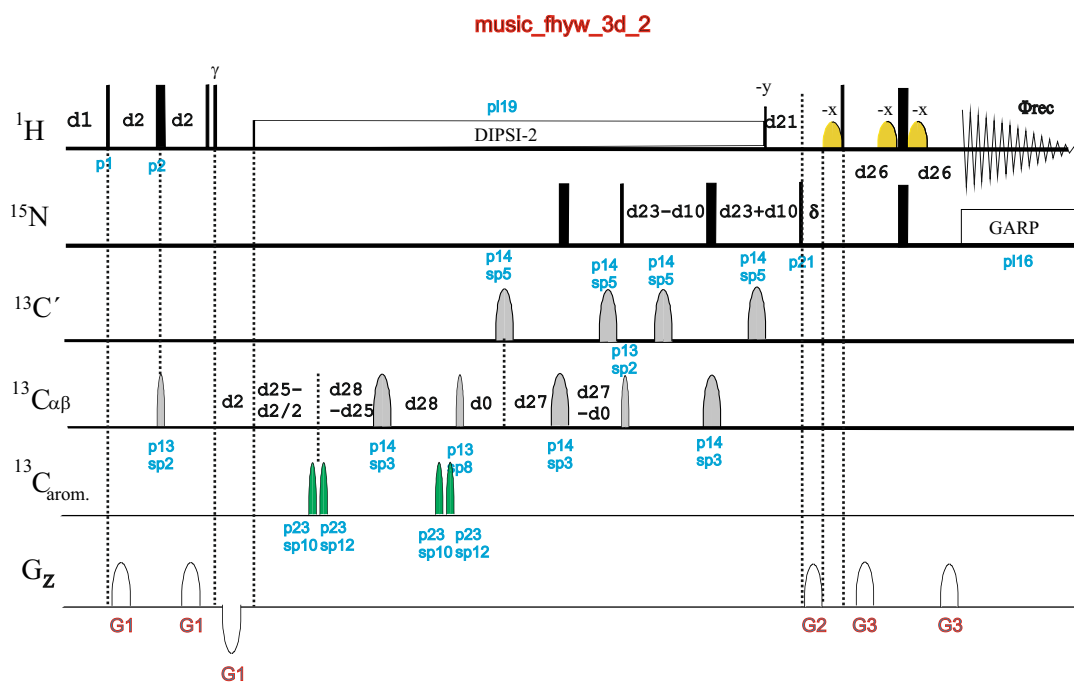
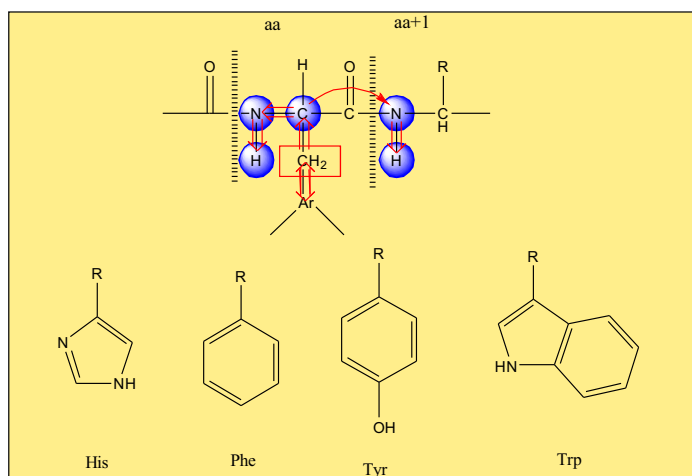


no option: 3D (CH ₂ C)CA(CO)NH	NH((Phe,Tyr,Hys)+1)
LABEL_TRP: 3D (CH ₂ C)CA(CO)NH	NH(Trp+1)
LABEL_CO: 3D (CH ₂ CCA)CONH	

d2: 1/(2J(CH))	[3.5 msec]
d21: 1/(2J(NH))	[5.5 msec]
d22: 1/(4J(CaCO))	[4.5 msec]
d23: 1/(4J(NCO))	[12.4 msec]
d24: n/(4J(CC))	[20 msec]
or 1/(4J(CC) (LABEL_CO))	[4.5 msec]

d25: 1/(4J(CC))	[7.05 msec]
d26: 1/(4J(NH))	[2.3 msec]
d27: 1/(4J(NCO))	[11.4 msec]
d28: 1/(4J(CC))	[7.1 msec]

MUSIC-Aromatic: (CH₂)CANH



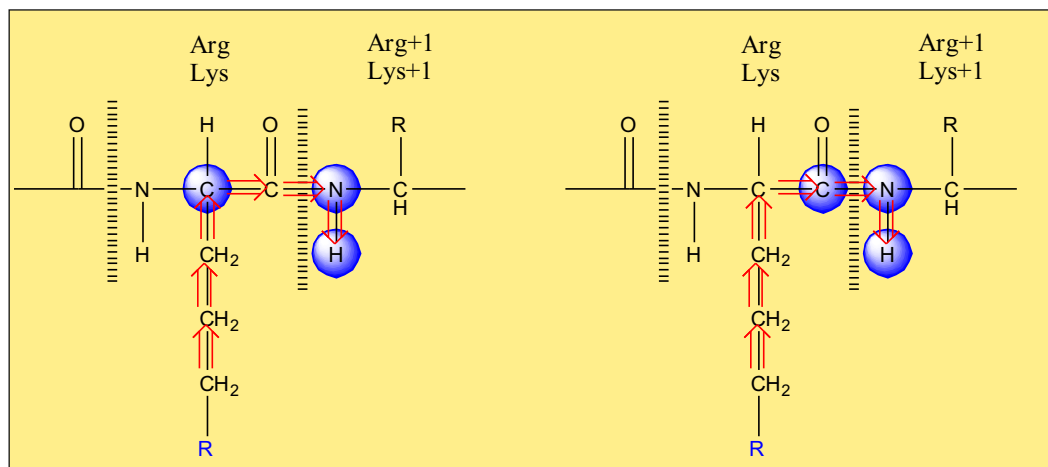
ZGOPTNS:

no option: 3D (CH₂C)CANH
LABEL_TRP: 3D (CH₂C)CANH

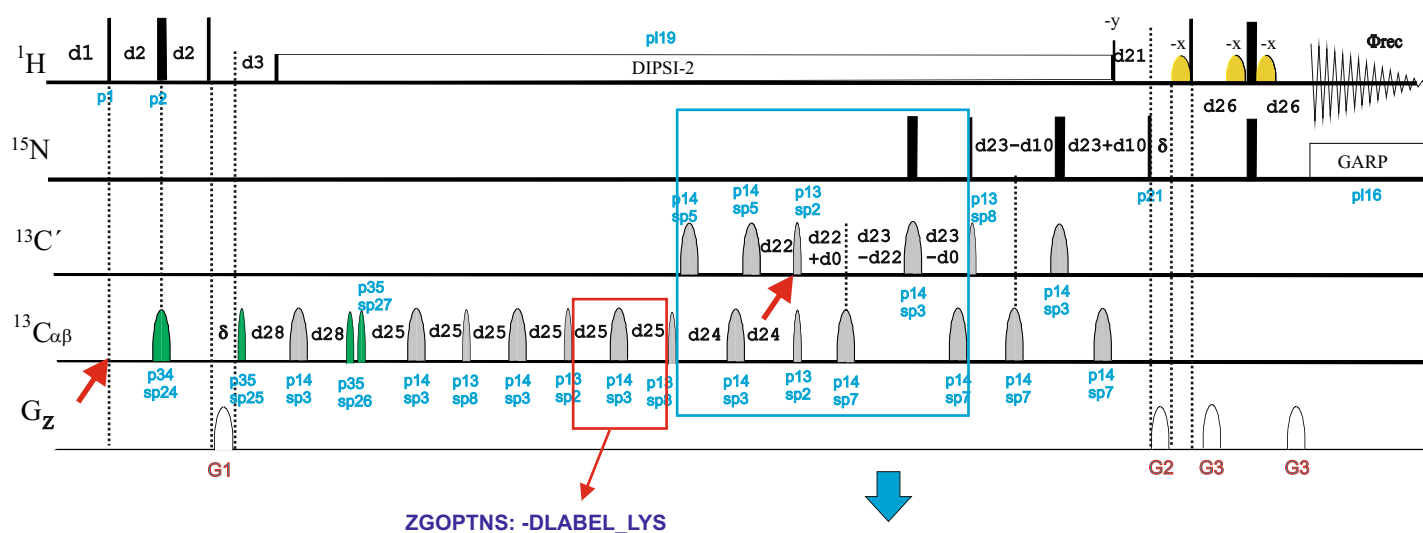
NH((Phe,Tyr,Hys)) and NH((Phe,Tyr,Hys)+1)
NH(Trp) and NH(Trp+1)

d2 : 1/(2J(CH))	[3.5 msec]
d21: 1/(2J(NH))	[5.5 msec]
d23: 1/(4J(NCa))	[12.4 msec]
d25: 1/(4J(CC))	[7.05 msec]
d26: 1/(4J(NH))	[2.3 msec]
d27: 1/(4J(CbCa)) and 1/(4J(NCa))	[9.0 msec]
d28: 1/(4J(CC))	[7.1 msec]

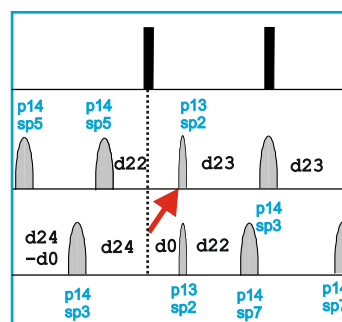
MUSIC-Arg/Lys: $(CH_2C)CA(CO)NH$ and $(CH_2CCA)CONH$



music kr 3d

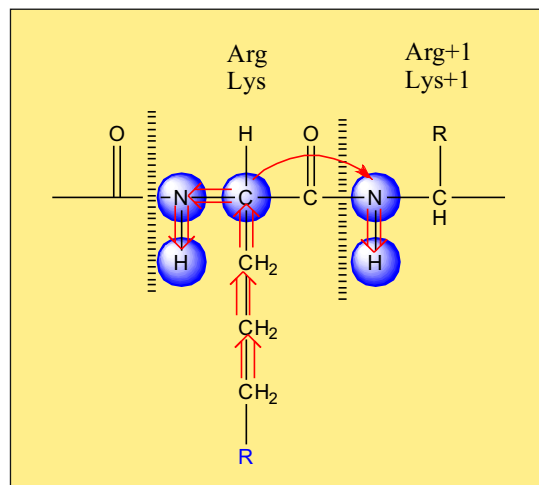


no options: 3D (HC)CA(CO)NH NH(Arg+1)
 LABEL_LYS: 3D (HC)CA(CO)NH NH(Arg+1) and NH(Lys+1)
 LABEL_CO: 3D (HCCA)CONH NH(Arg+1) and NH(Lys+1)

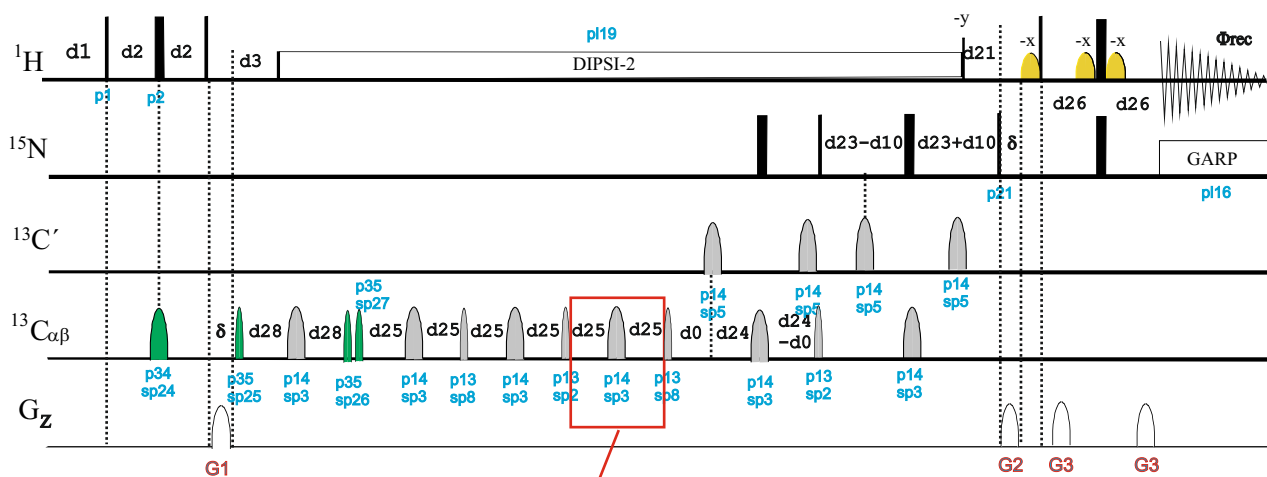


d3 : 1/(4J(CH))	[2.1 msec]	d24: n/(4J(CC)	[19.5m msec]
d4 : 1/(4J(CH))	[2.0 msec]	or 1/(4J(CC) (LABEL_LYS)	[8.8 msec]
d21: 1/(2J(NH)	[5.5 msec]	or 1/(4J(CC) (LABEL_CO)	[4.5 msec]
d22: 1/(4J(CaCO)	[4.5 msec]	d25: 1/(4J(CC)	[5.5 msec]
d23: 1/(4J(NCO)	[12.4 msec]	d26: 1/(4J(NH)	[2.3 msec]
		d28: 1/(8J(CC)	[3.5 msec]

MUSIC-Arg/Lys (CH₂C)CANH



music_kr_3d_2



ZGOPTNS: -DLABEL_LYS

ZGOPTNS

no options: 3D (HC)CANH

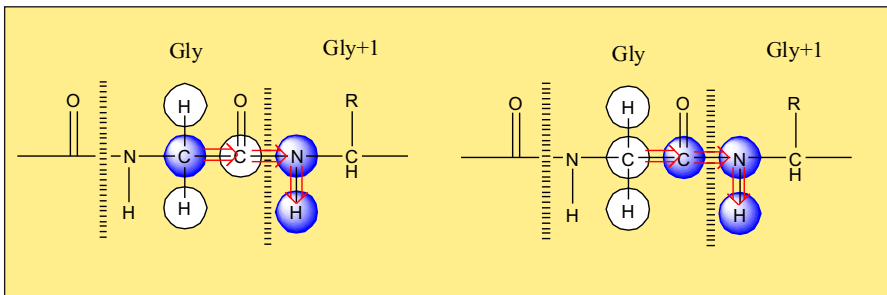
NH(Arg, Arg+1)

LABEL_LYS: 3D (HC)CANH

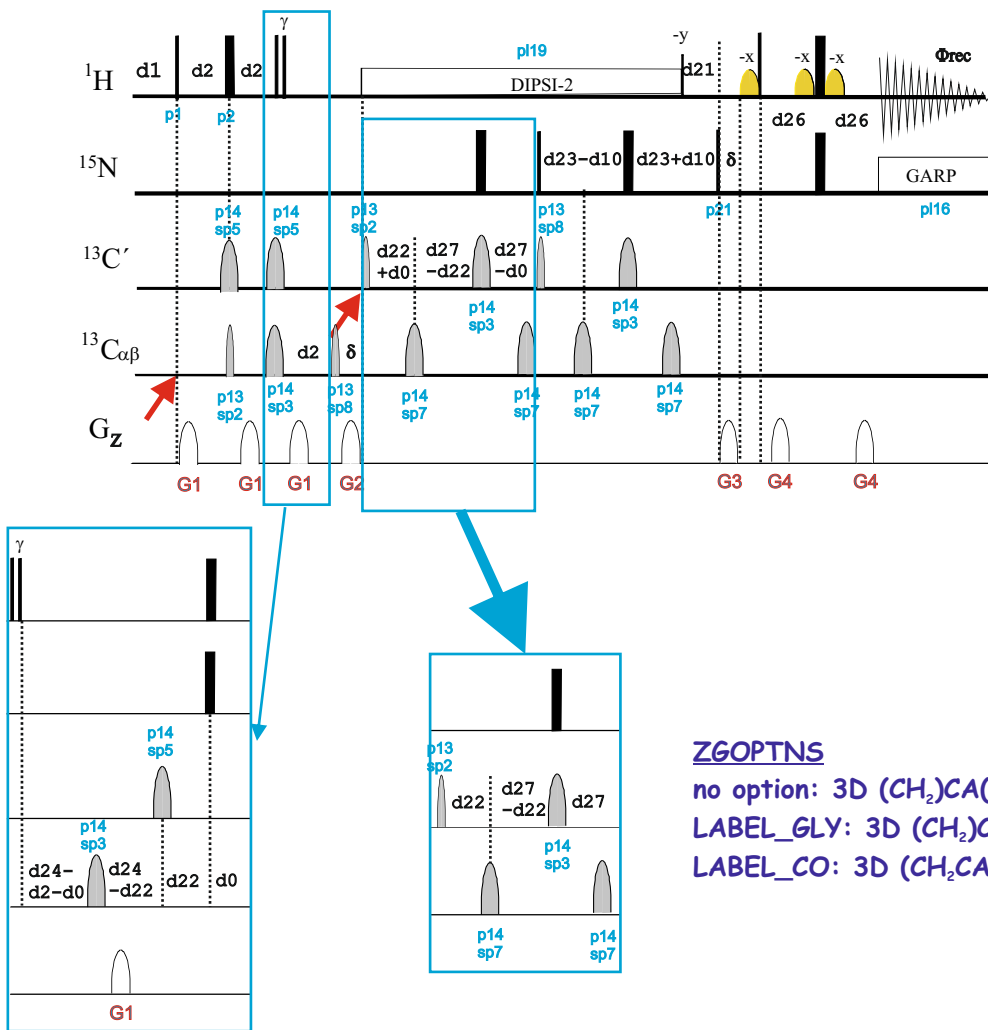
NH(Arg, Arg+1) and NH(Lys, Lys+1)

d3 : 1/(4J(CH))	[2.1 msec]
d4 : 1/(4J(CH))	[2.0 msec]
d21: 1/(2J(NH))	[5.5 msec]
d23: 1/(4J(NCa))	[12.4 msec]
d24: 1/(4J(CbCa)) and 1/(4J(NCa))	[9.0 msec]
d25: 1/(4J(CC))	[5.5 msec]
d26: 1/(4J(NH))	[2.3 msec]
d28: 1/(8J(CC))	[3.5 msec]

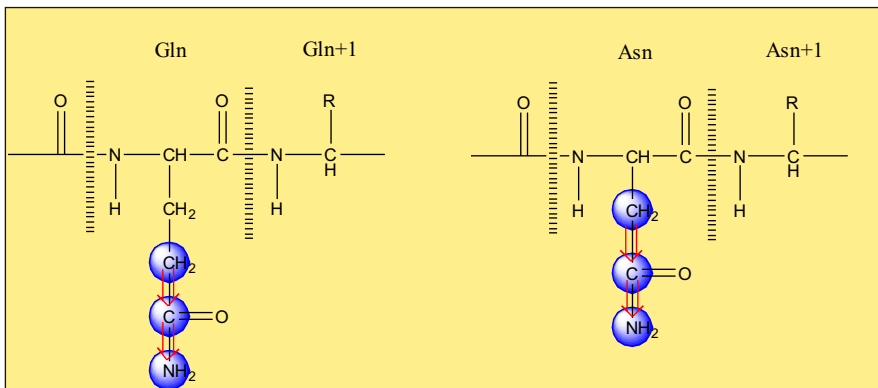
MUSIC-Glycine: $\text{CH}_2(\text{CO})\text{NH}$ and $(\text{CH}_2)\text{CONH}$



music_gly_3d

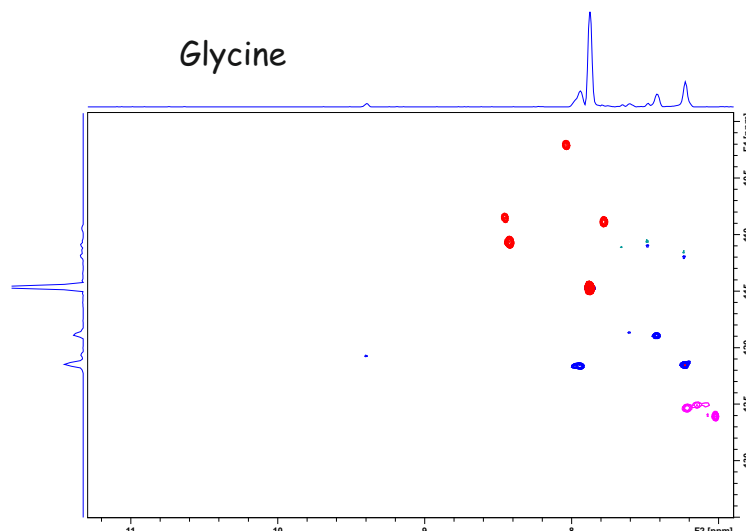


Also can be observed:

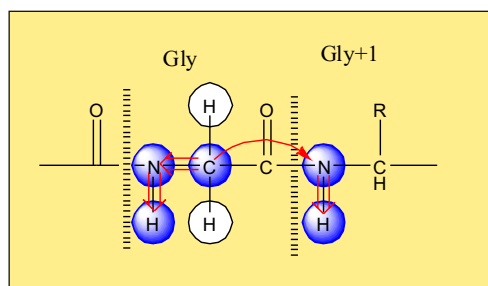


Glycine

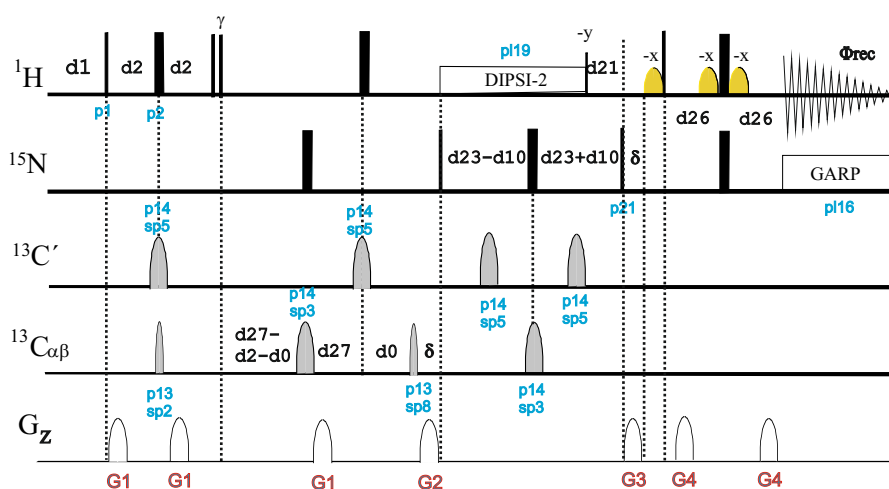
d2 : 1/(2J(CH)) [3.5 msec]
d21: 1/(4J(NH)) [2.9 msec]
or 1/(2J(NH)) (LABEL_GLY) [5.9 msec]
d22: 1/(4J(CaCO)) [4.4 msec]
d23: 1/(4J(NCO)) [12.4 msec]
d24: 1/(4J(NCa)) [13.8 msec]
d26: 1/(4J(NH)) [2.3 msec]
d27: 1/(4J(NCO)) [12.4 msec]



MUSIC-Glycine: CH₂NH



music_gly_3d_2



ZGOPTNS

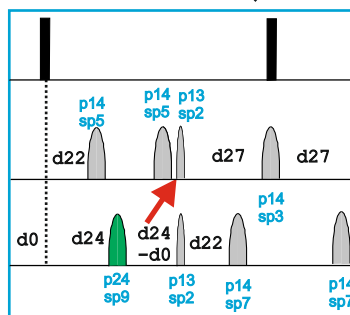
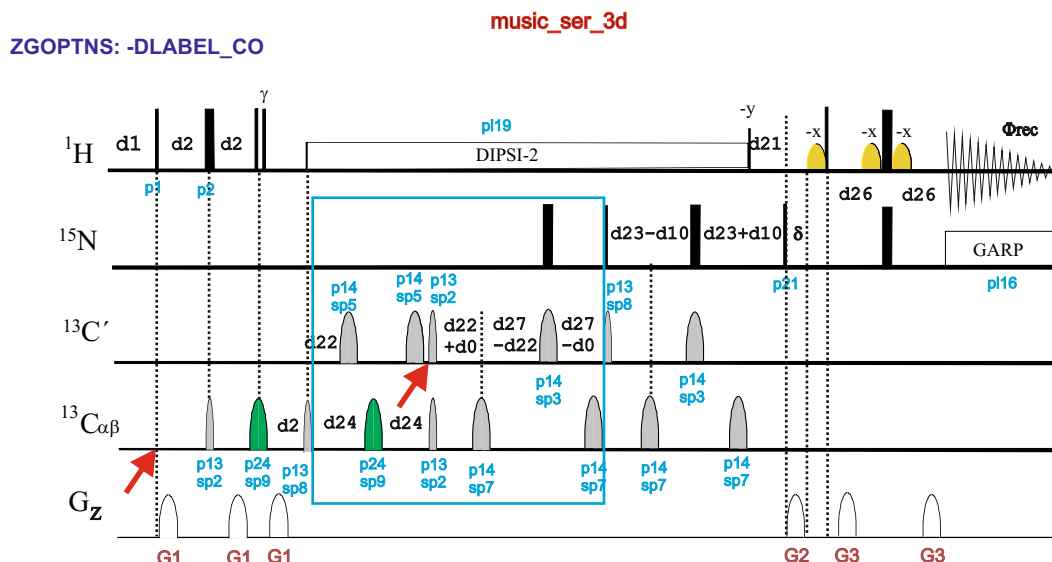
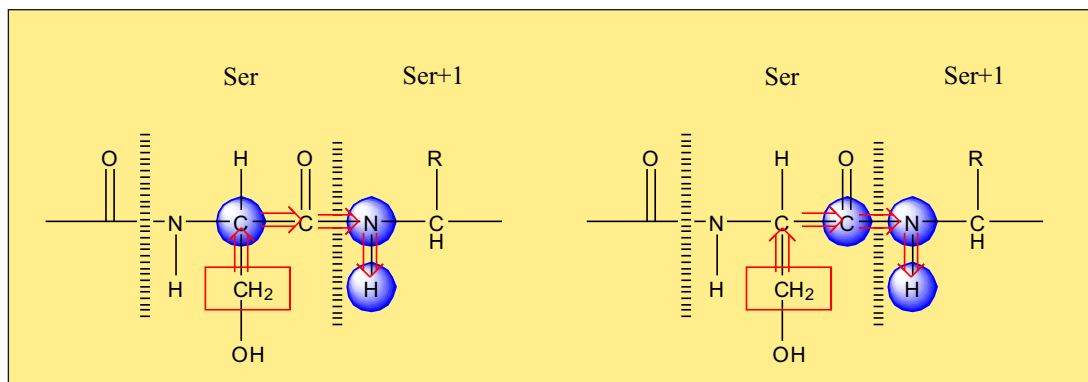
no option: 3D (CH₂)CANH

LABEL_GLY: 3D (CH₂)CANH

NH(Gly+1) and NH(Gly)

NH(Gly+1) and NH(Gly)

MUSIC-SER: $(CH_2)CA(CO)NH$ and $(CH_2CA)CONH$

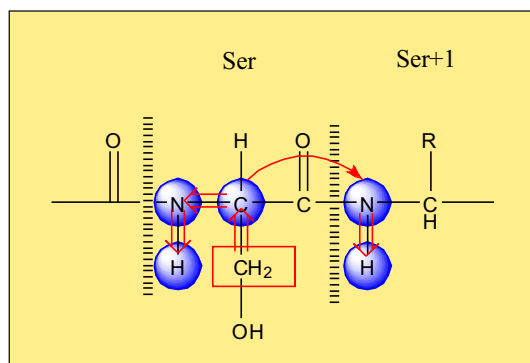


ZGPTNS
no option: 3D $(CH_2C)CA(CO)NH$
LABEL_CO: 3D $(CH_2CCA)CONH$

NH(Ser+1)

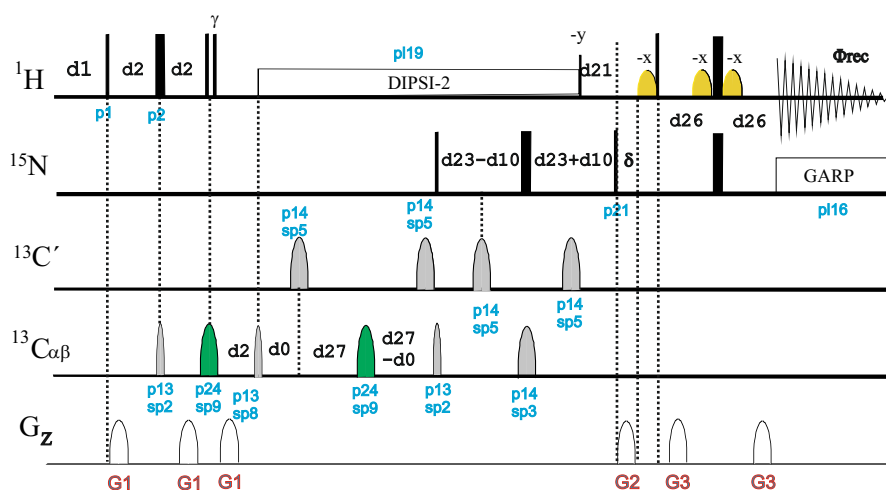
d21: $1/(2J(NH))$	[5.5 msec]
d22: $1/(4J(CaCO))$	[4.5 msec]
d23: $1/(4J(NCO))$	[12.4 msec]
d24: $n/(4J(CC))$	[17 msec]
or $1/(4J(CC) (LABEL_CO))$	[5.3 msec]
d26: $1/(4J(NH))$	[2.3 msec]
d27: $1/(4J(NCO))$	[12.4 msec]

MUSIC-SER: (CH₂)CANH



d2 : 1/(2J(CH))	[3.5 msec]
d21: 1/(2J(NH))	[5.5 msec]
d23: 1/(4J(NCa))	[12.4 msec]
d26: 1/(4J(NH))	[2.3 msec]
d27: 1/(4J(CbCa)) and 1/(4J(NCa))	[8.2 msec]

music_ser_3d_2

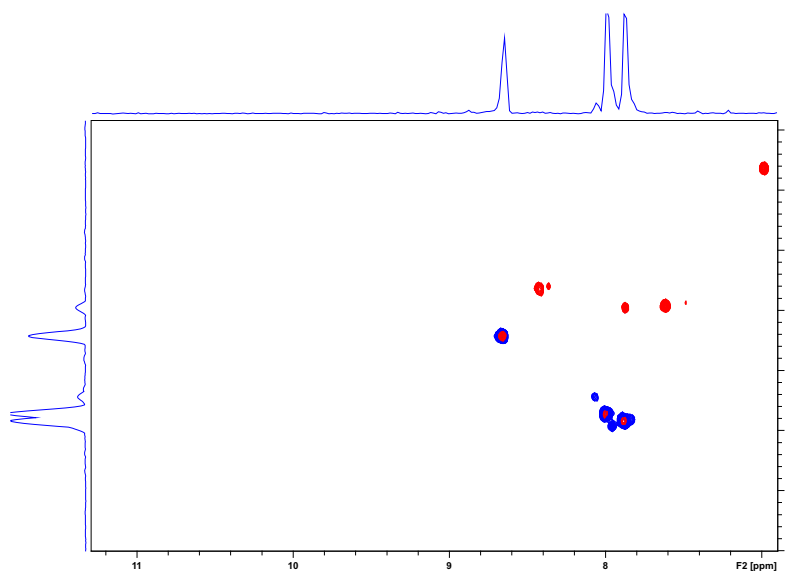


ZGPTNS

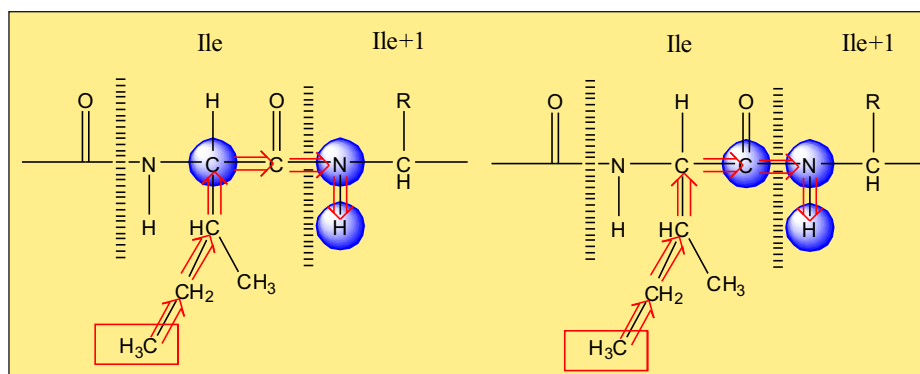
no options: 3D (CH₂C)CANH

NH(Ser+1) and NH(Ser)

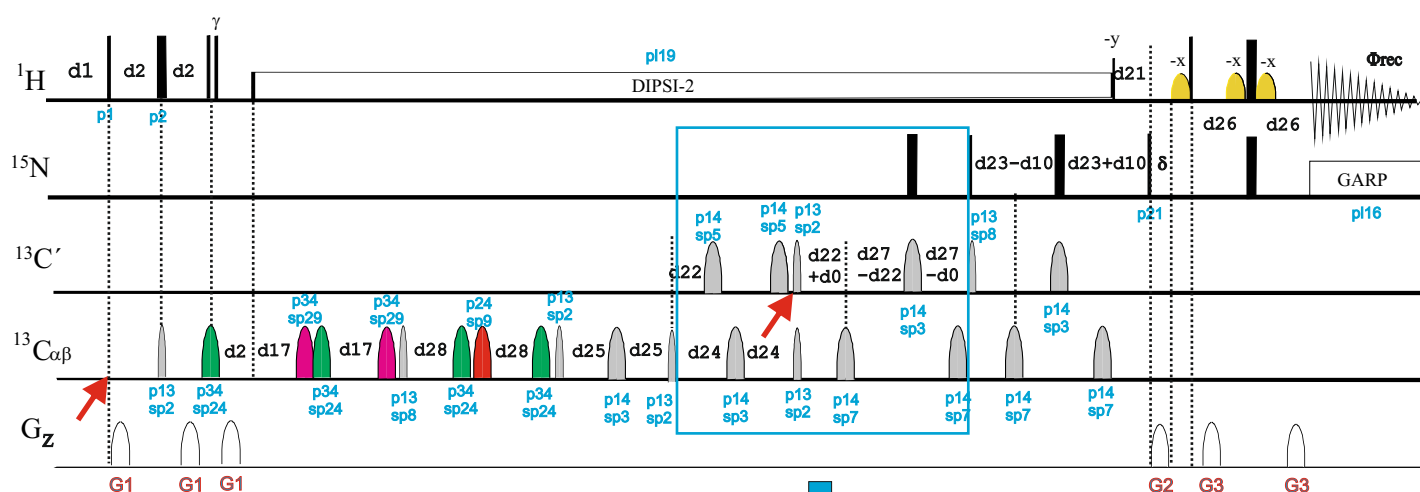
Serine



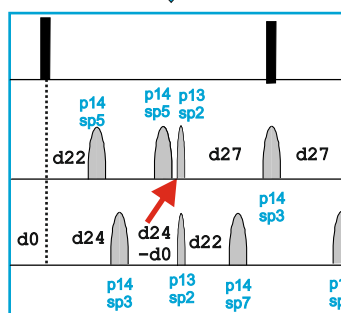
MUSIC-Isoleucine: $(CH_3C)CA(CO)NH$ and $(CH_3CCA)CONH$



music_ile_3d

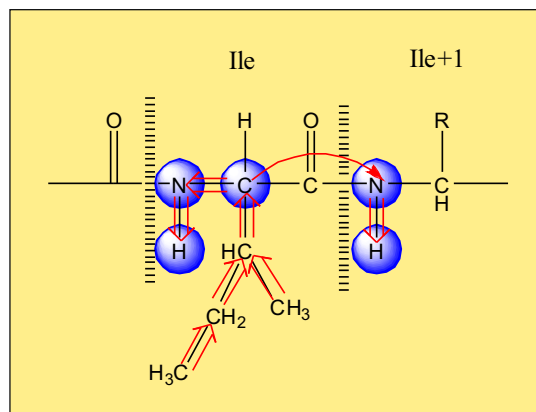


no option: 3D (CH₃C)CA(CO)NH NH(Ile+1)
 LABEL_CO: 3D (CH₃CCA)CONH

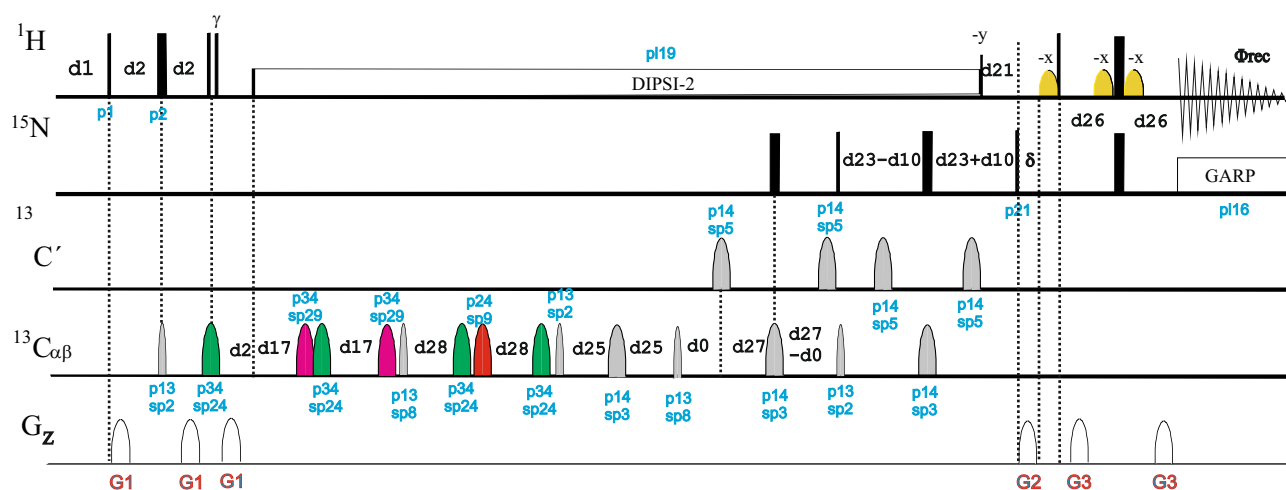


d2 : 1/(2J(CH))	[4.0 msec]
d17: 1/(4J(CC))	[7.0 msec]
d21: 1/(2J(NH))	[5.9 msec]
d22: 1/(4J(CaCO))	[4.5 msec]
d23: 1/(4J(NCO))	[12.4 msec]
d24: n/(4J(CC))	[19 msec]
or 1/(4J(CC) (LABEL_CO))	[4.5 msec]
d25: 1/(4J(CC))	[4.0 msec]
d26: 1/(4J(NH))	[2.3 msec]
d27: 1/(4J(NCO))	[12.4 msec]
d28: 1/(4J(CC))	[7.0 msec]

MUSIC-Isoleucine: $(CH_3)_2CHCH_2CH(NH_2)COOH$



music ile 3d 2



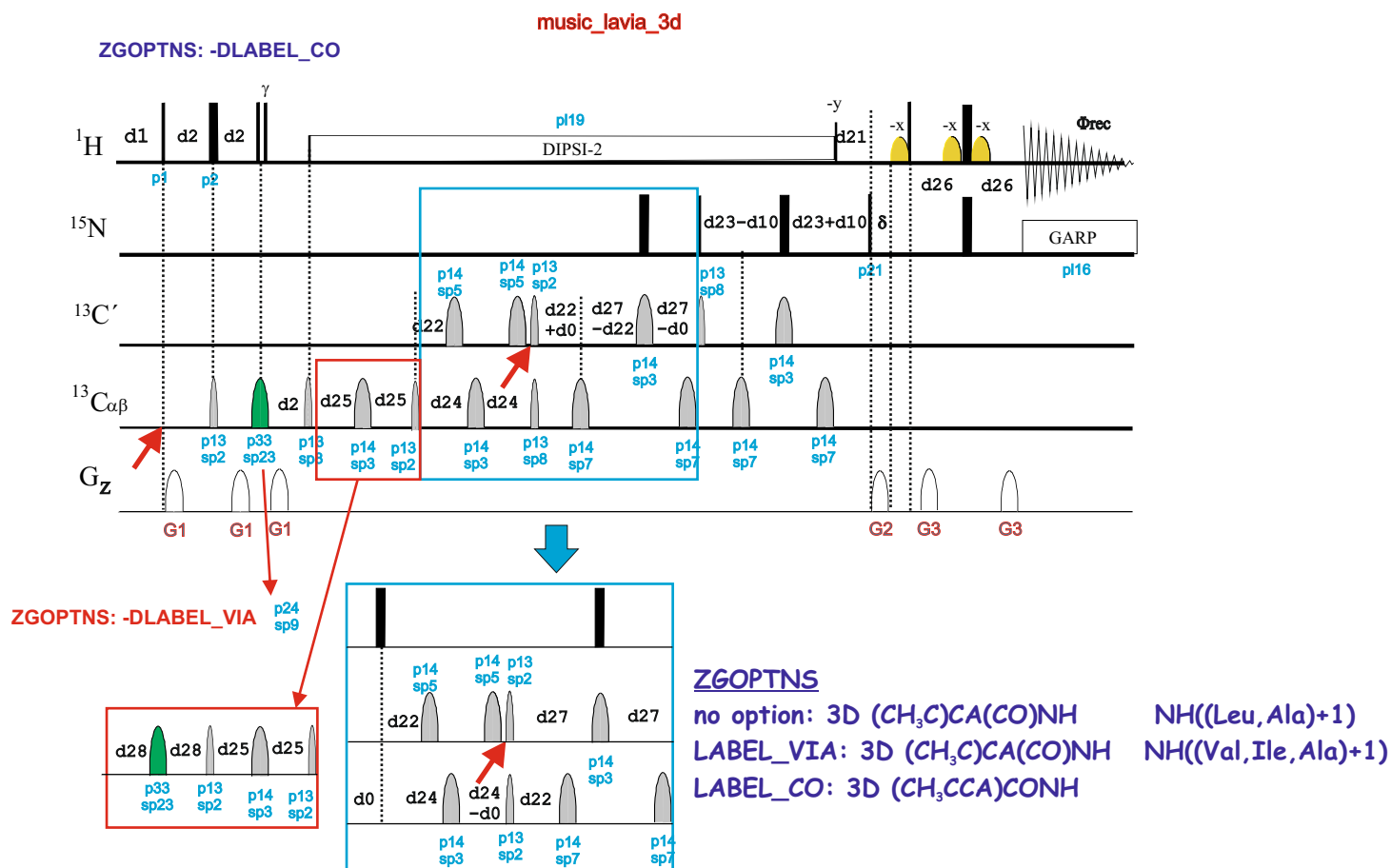
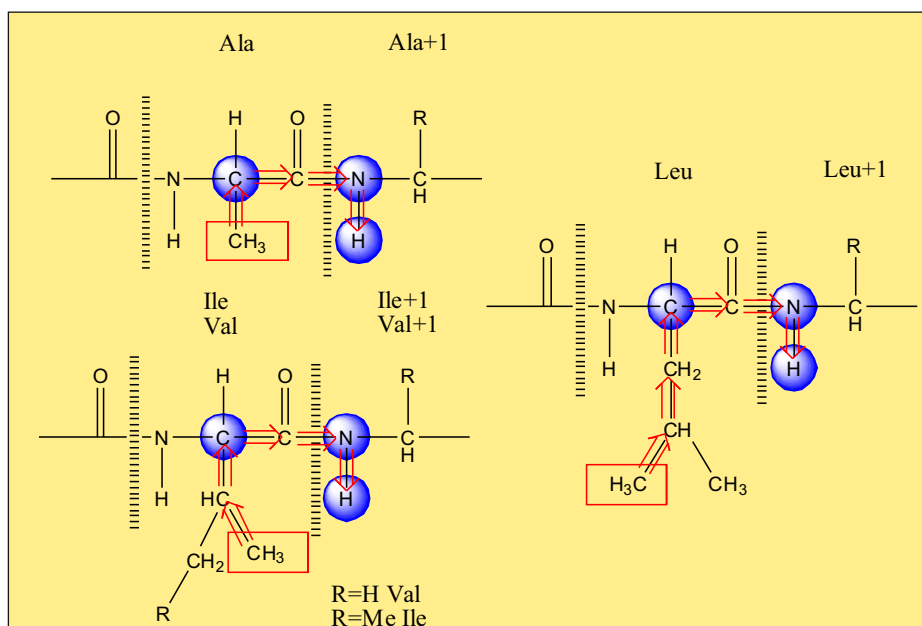
ZGOPTNS

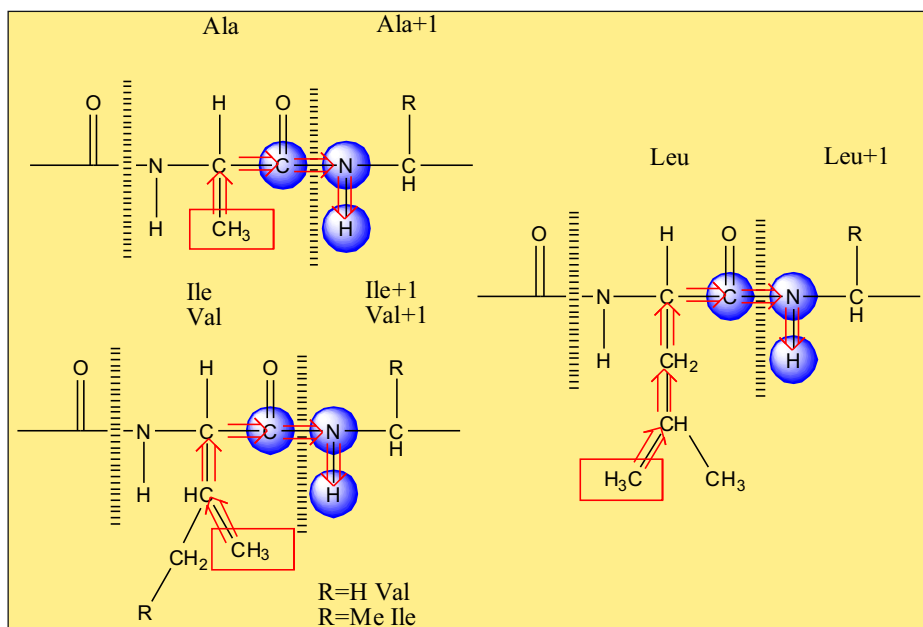
no options: 3D $(\text{CH}_3\text{C})\text{CANH}$

NH(Ile+1) and NH(Ile)

d2 : 1/(2J(CH))	[4.0 msec]
d17: 1/(4J(CC))	[7.0 msec]
d21: 1/(2J(NH))	[5.9 msec]
d23: 1/(4J(NCa))	[12.4 msec]
d25: 1/(4J(CC))	[4.0 msec]
d26: 1/(4J(NH))	[2.3 msec]
d27: 1/(4J(CbCa)) and 1/(4J(NCa))	[9.0 msec]
d28: 1/(4J(CC))	[7.0 msec]

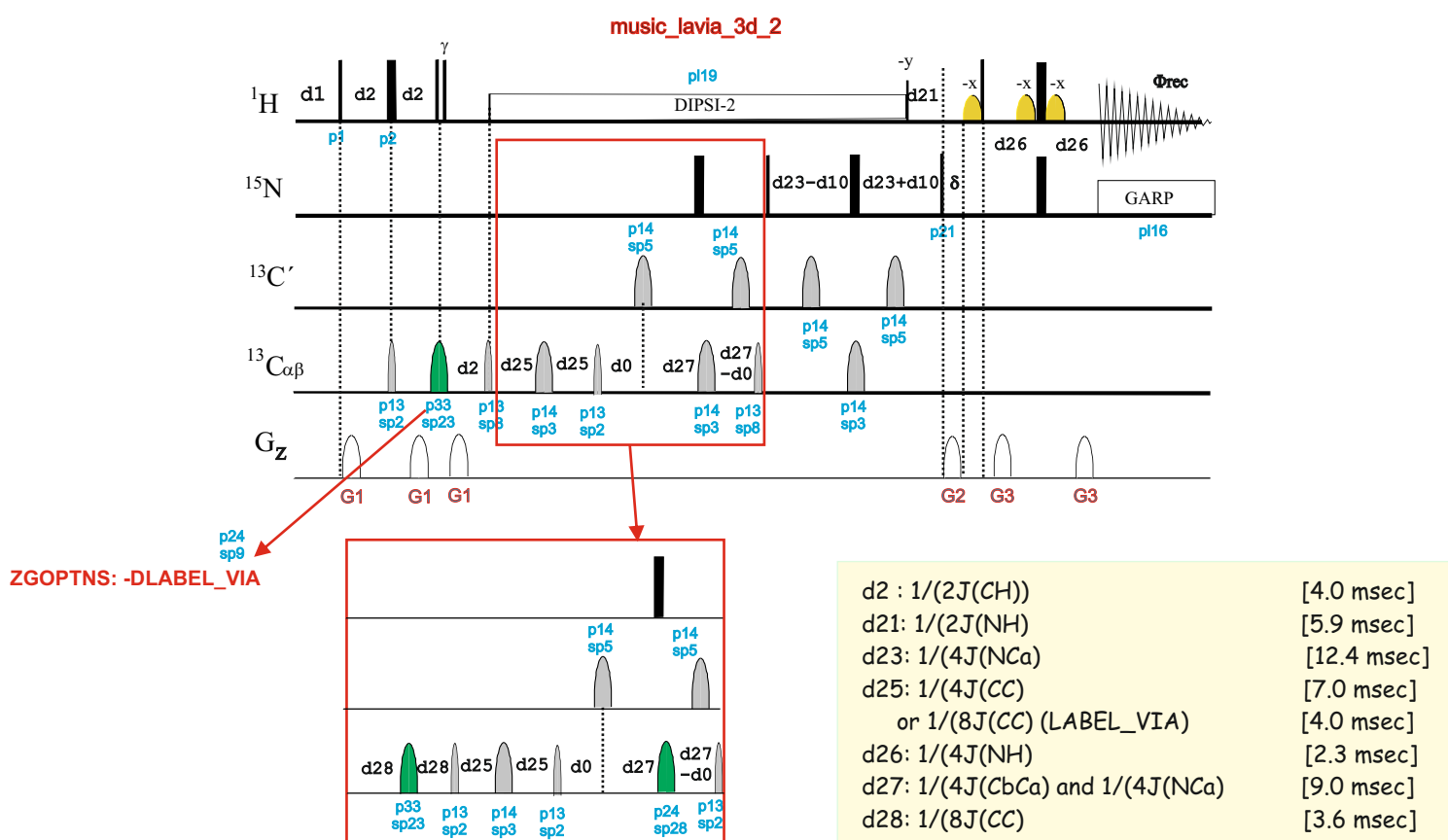
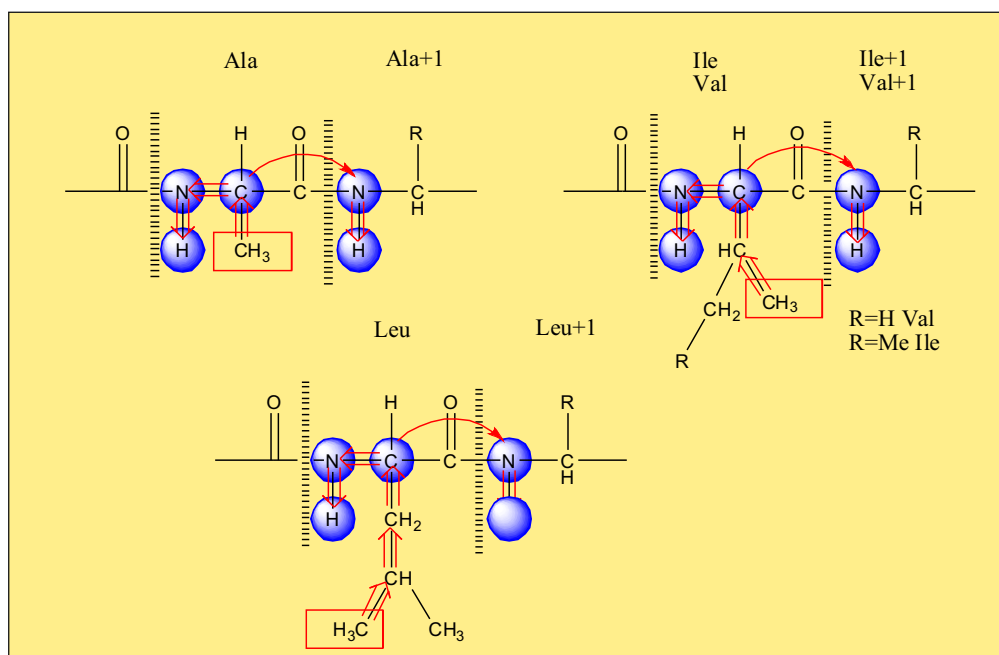
MUSIC-LAVIA: (CH₃C)CA(CO)NH and (CH₃CCA)CONH





d2 : 1/(2J(CH))	[4.0 msec]
d21: 1/(2J(NH))	[5.9 msec]
d22: 1/(4J(CaCO))	[4.5 msec]
d23: 1/(4J(NCO))	[12.4 msec]
d24: n/(4J(CC))	[19 msec]
or n/(4J(CC) (LABEL_VIA))	[17 msec]
or 1/(4J(CC) (LABEL_CO))	[4.5 msec]
d25: 1/(4J(CC))	[7.0 msec]
or 1/(8J(CC) (LABEL_VIA))	[4.0 msec]
d26: 1/(4J(NH))	[2.3 msec]
d27: 1/(4J(NCO))	[12.4 msec]
d28: 1/(8J(CC))	[3.6 msec]

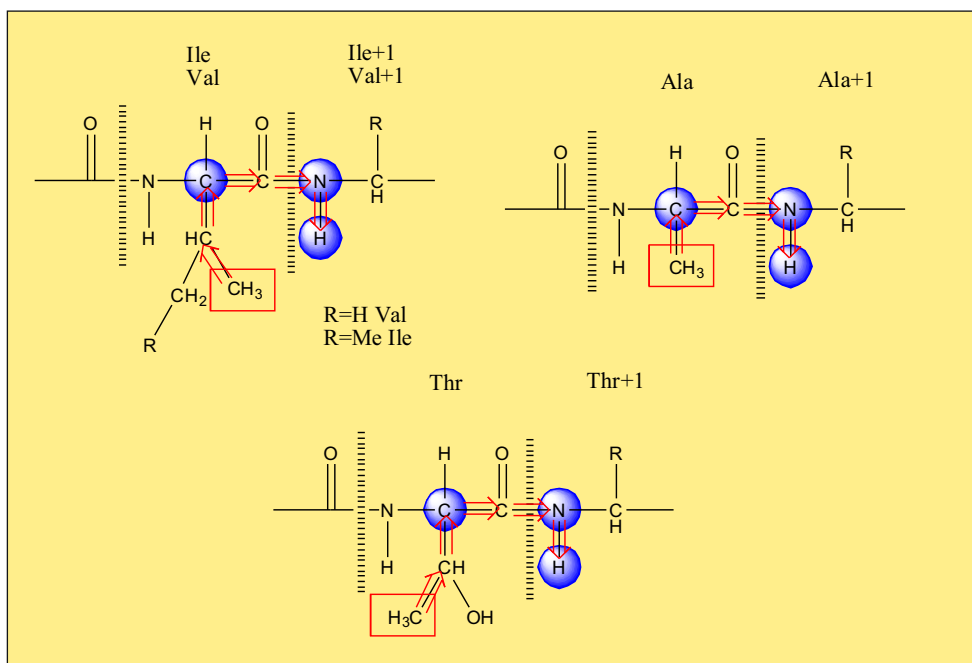
MUSIC-LAVIA: (CH₃C)CANH



ZGOPTNS

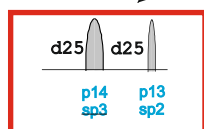
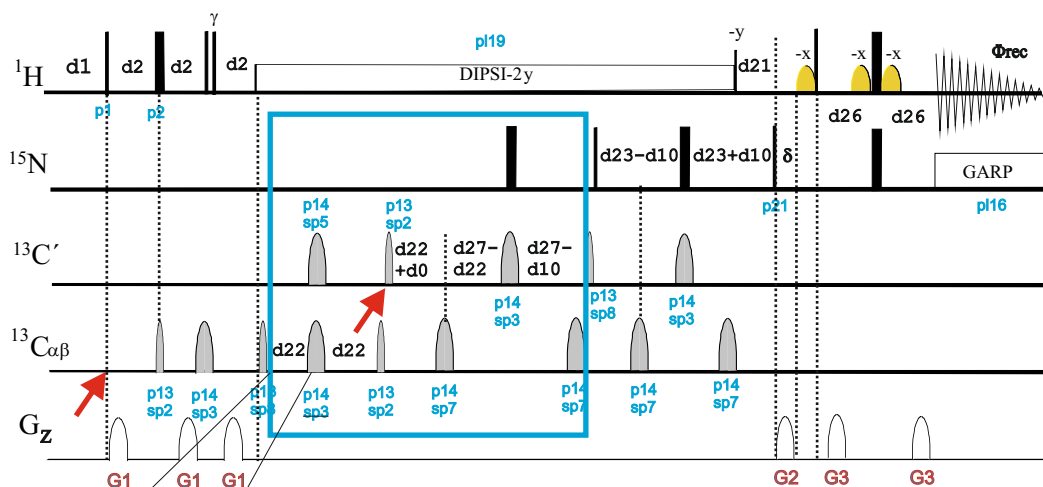
no options: 3D (CH₃C)CANH NH((Leu,Ala)+1) and NH((Leu,Ala))
 LABEL_VIA: 3D (CH₃C)CANH NH((Val,Ile,Ala)+1) and NH((Val,Ile,Ala))

MUSIC-TAVI: $(CH_3C)CA(CO)NH$ and $(CH_3CCA)CONH$



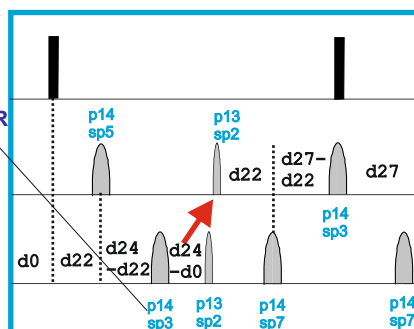
music_tavi_3d

ZGPTNS: -DLABEL_CO, -DLABEL_ALA



no
ZGPTNS:
-DLABEL_ALA

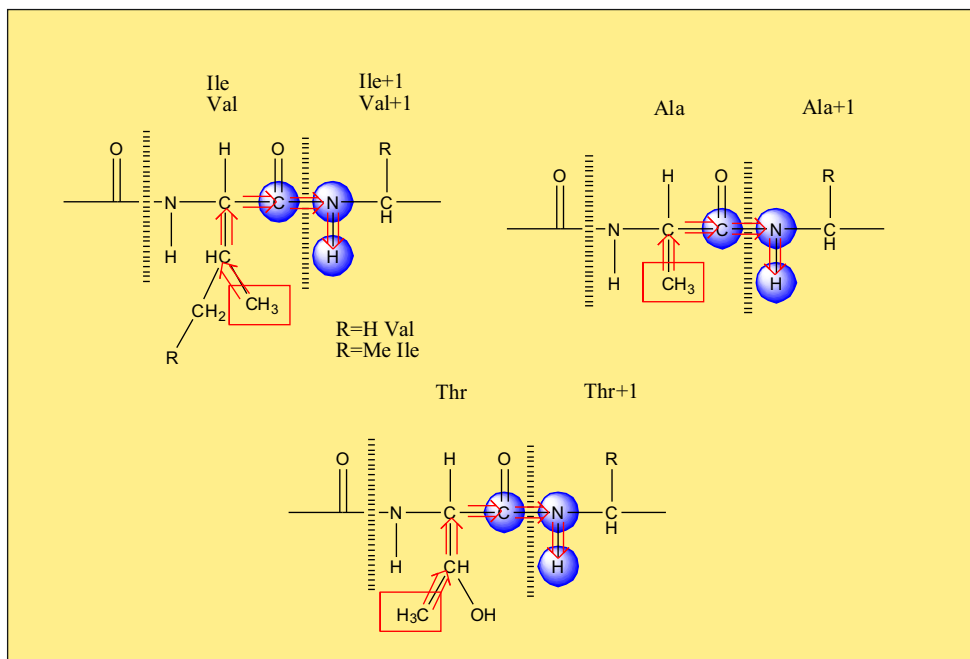
ZGPTNS:
-DLABEL_THR



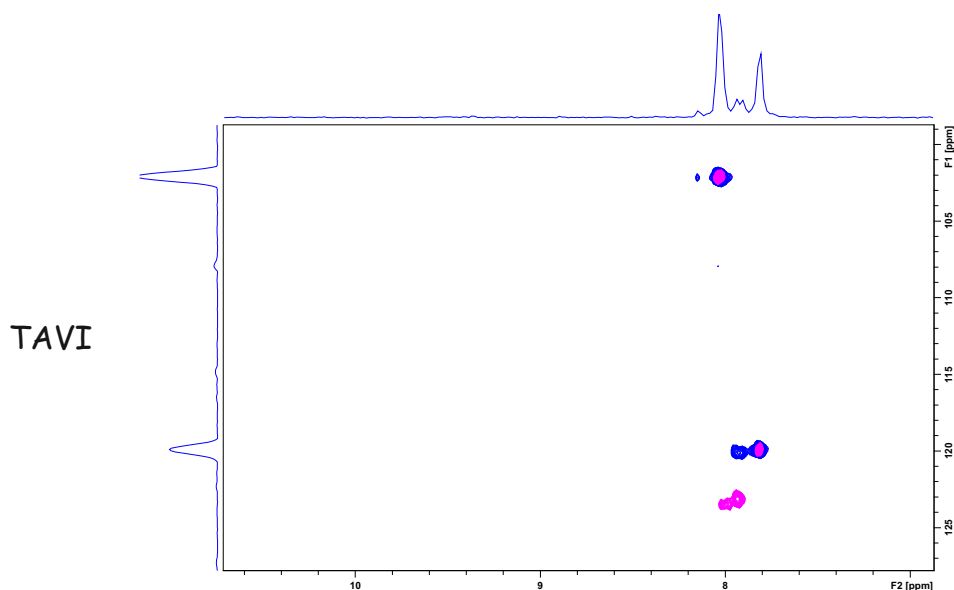
ZGPTNS

no options: 3D $(CH_3C)CA(CO)NH$
LABEL_ALA: 3D $(CH_3C)CA(CO)NH$
LABEL_THR: 3D $(CH_3C)CA(CO)NH$
LABEL_CO: 3D $(CH_3CCA)CONH$

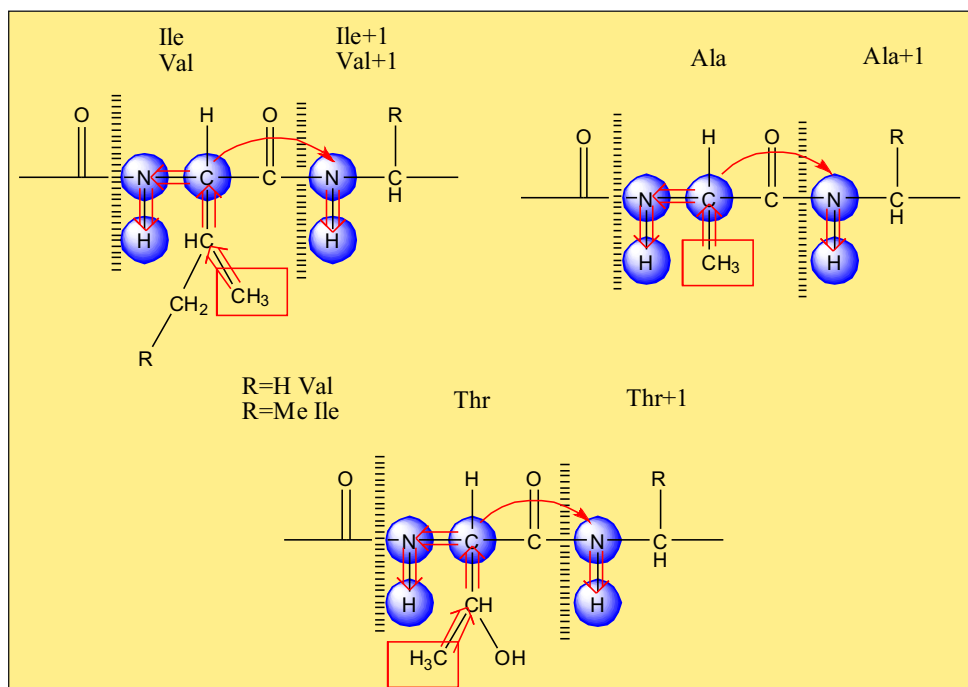
NH((Thr,Ala,Val,Ile)+1)
NH((Ala+1)
NH((Thr,Ala)+1)



d2 : $1/(2J(\text{CH}))$	[4.0 msec]
d21: $1/(2J(\text{NH}))$	[5.9 msec]
d22: $1/(4J(\text{CaCO}))$	[4.4 msec]
d23: $1/(4J(\text{NCO}))$	[12.4 msec]
d24: $n/(4J(\text{CC}))$	[17 msec]
d25: $1/(4J(\text{CC}))$	[5.5 msec]
d26: $1/(4J(\text{NH}))$	[2.3 msec]
d27: $1/(4J(\text{NCO}))$	[12.4 msec]

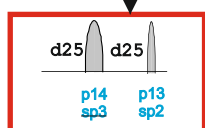
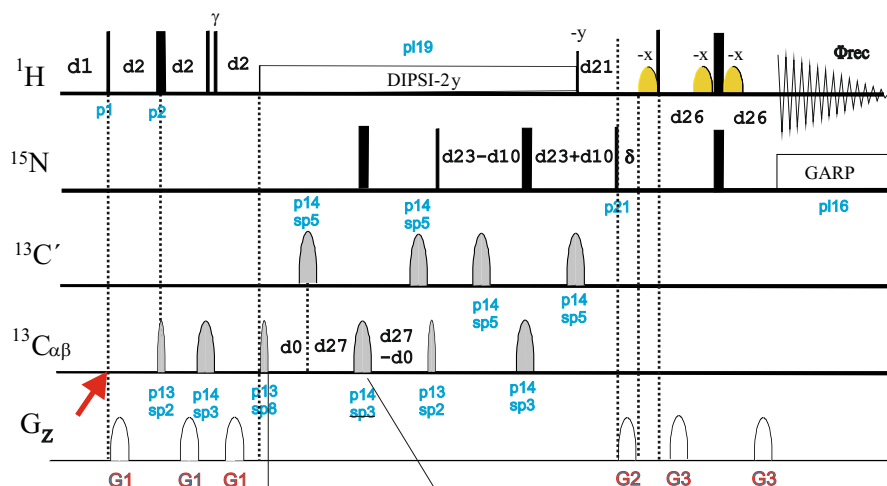


MUSIC-TAVI: (CH₃C)CANH



music_tavi_3d_2

ZGPTNS: -DLABEL_ALA



no
ZGPTNS:
-DLABEL_ALA

ZGPTNS:
-DLABEL_THR

d2 : 1/(2J(CH))	[4.0 msec]
d21: 1/(2J(NH))	[5.9 msec]
d23: 1/(4J(NCa))	[12.4 msec]
d25: 1/(4J(CC))	[5.5 msec]
d26: 1/(4J(NH))	[2.3 msec]
d27: 1/(4J(CbCa)) and 1/(4J(NCa))	[8.2 msec]

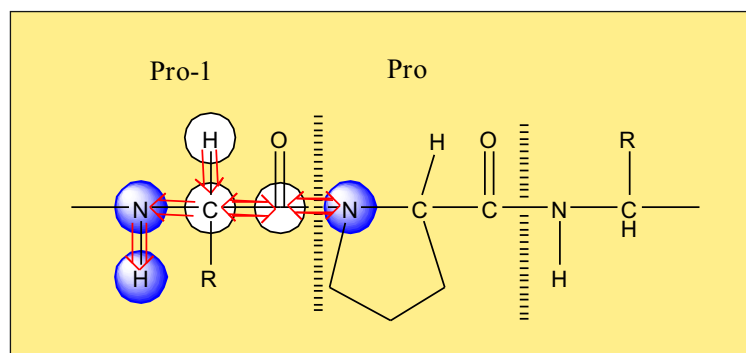
ZGPTNS

no options: 3D (CH₃C)CANH
LABEL_ALA: 3D (CH₃C)CANH
LABEL_THR3D (CH₃C)CANH

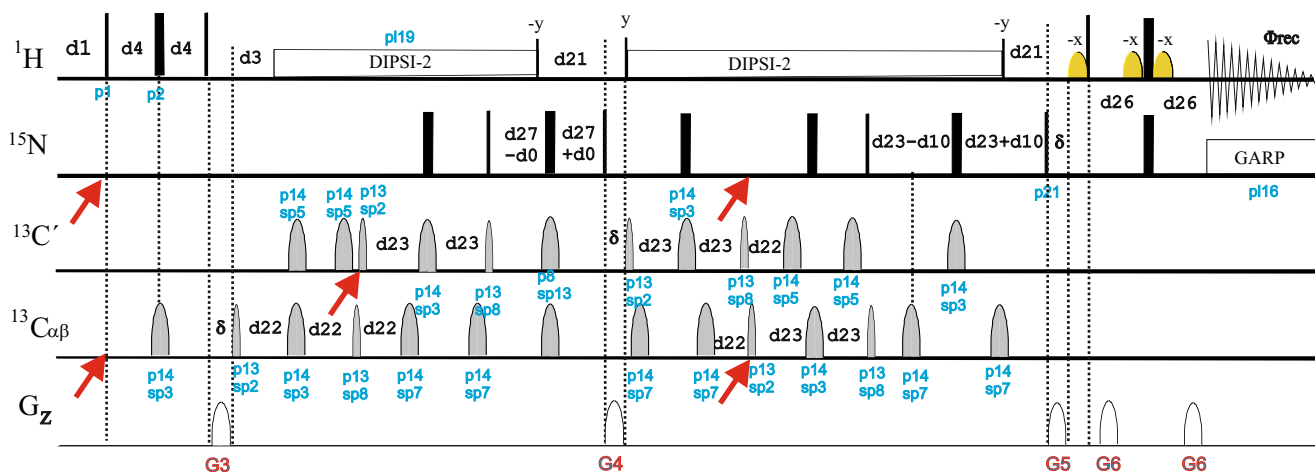
NH((Thr,Ala,Val,Ile)+1) and NH(Thr,Ala,Val,Ile)
NH((Ala+1) and NH(Ala)
NH((Thr,Ala)+1) and NH(Thr,Ala)

MUSIC-Proline: (HACACO)N(COCA)NH

Ref: M. Schubert, L. Ball, H. Oschkinat & P. Schmieder, J. Biomol. NMR 17, 331-335 (2000)



music_pro_1_3d



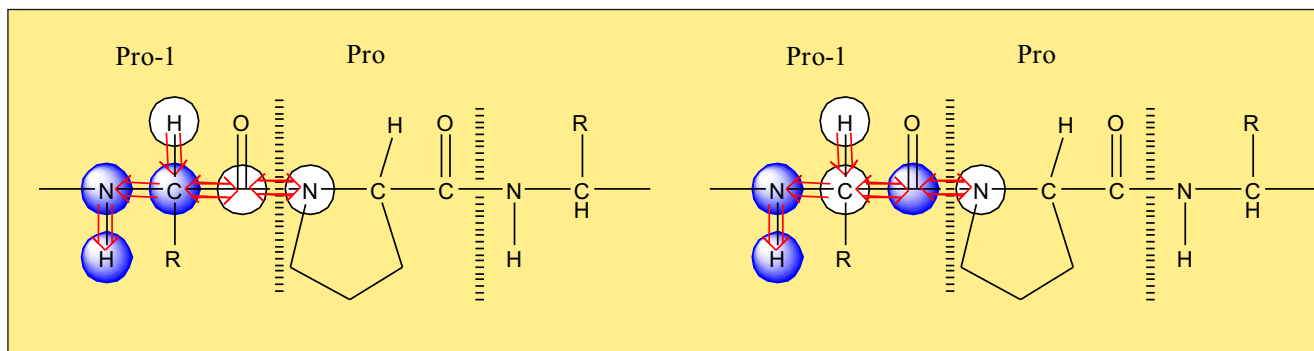
ZGPTNS

no options: 3D (HACACO)N(COCA)NH

NH(Pro-1)

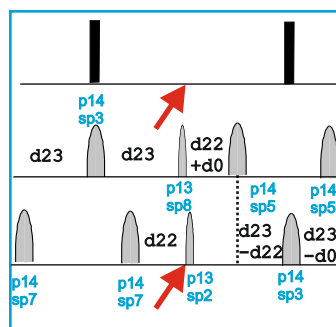
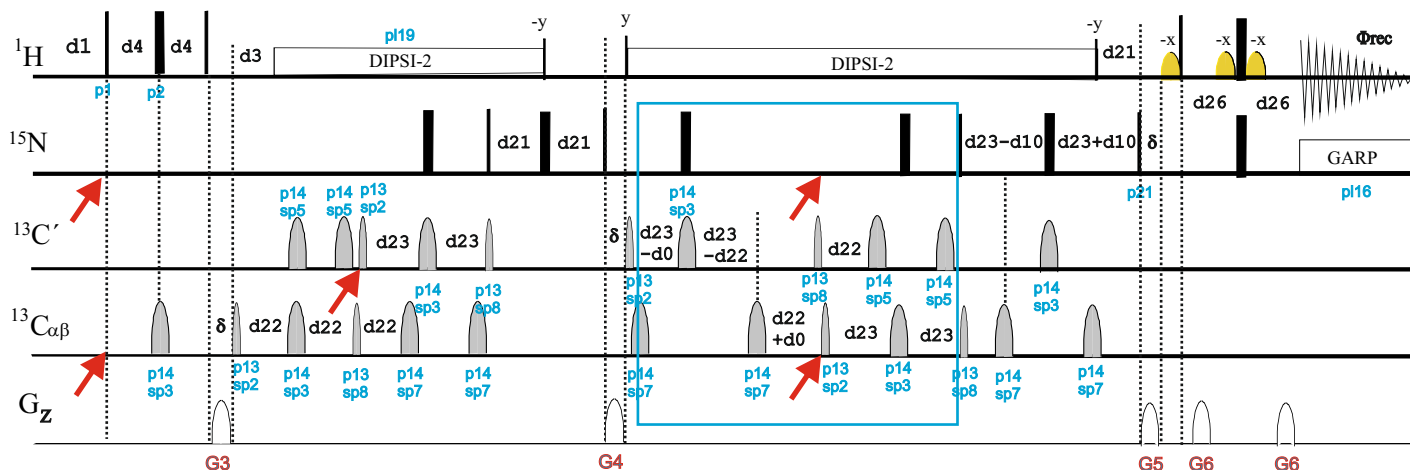
d3 : 1/(4J(CH))	[2.1 msec]
d4 : 1/(4J(CH))	[1.7 msec]
d21: 1/(2J(NH))	[5.5 msec]
d22: 1/(4J(CαCO))	[4.5 msec]
d23: 1/(4J(NC))	[12.4 msec]
d26: 1/(4J(NH))	[2.3 msec]

MUSIC-Proline: (HACACONCO)CANH and (HACACON)CO(CA)NH



music_pro_1_3d.2

ZGOPTNS: -DLABEL_CO



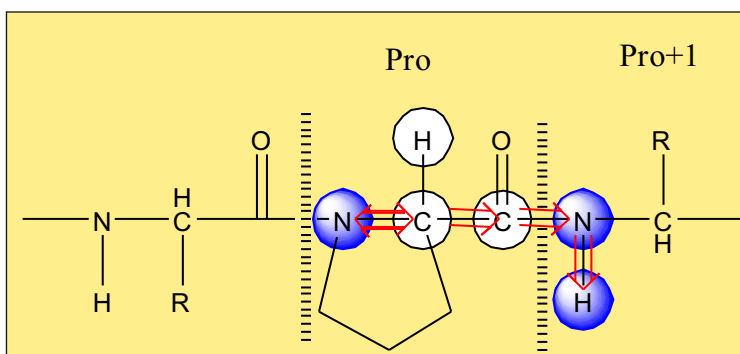
ZGOPTNS

no options: 3D (HACACONCO)CANH
LABEL_CO: 3D (HACACON)CO(CA)NH

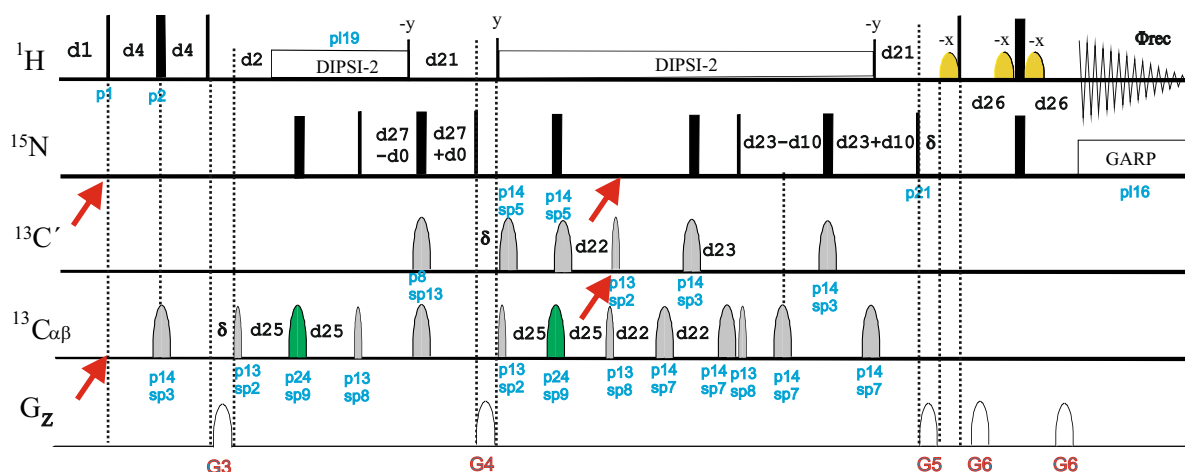
NH(Pro-1)

d3 : $1/(4J(\text{CH}))$	[2.1 msec]
d4 : $1/(4J(\text{CH}))$	[1.7 msec]
d21: $1/(2J(\text{NH}))$	[5.5 msec]
d22: $1/(4J(\text{CaCO}))$	[4.5 msec]
d23: $1/(4J(\text{NC}))$	[12.4 msec]
d26: $1/(4J(\text{NH}))$	[2.3 msec]

MUSIC-Proline: (HACA)N(CACO)NH



music_pro_2_3d



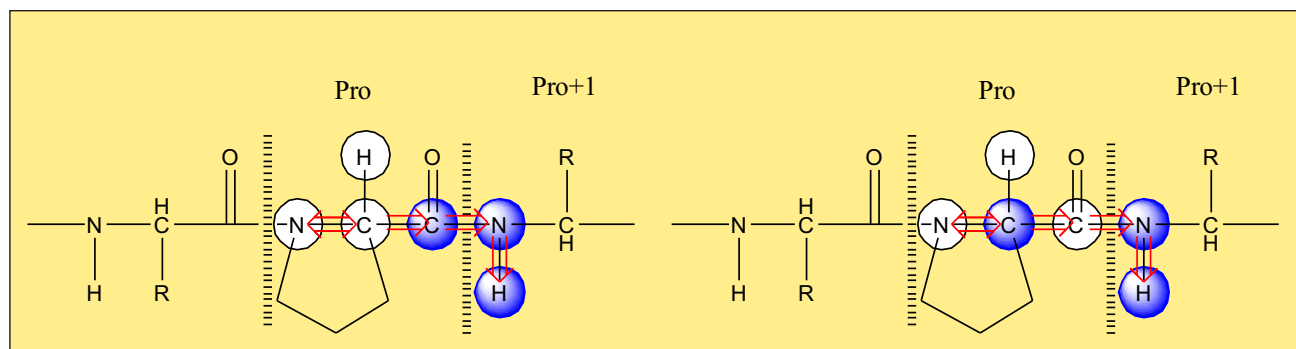
ZGPTNS

no options: 3D (HACA)N(CACO)NH

NH(Pro+1)

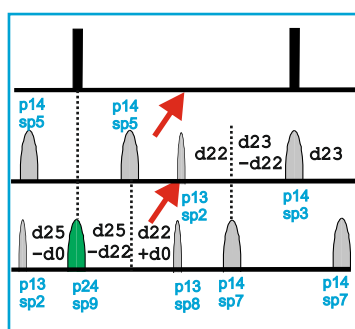
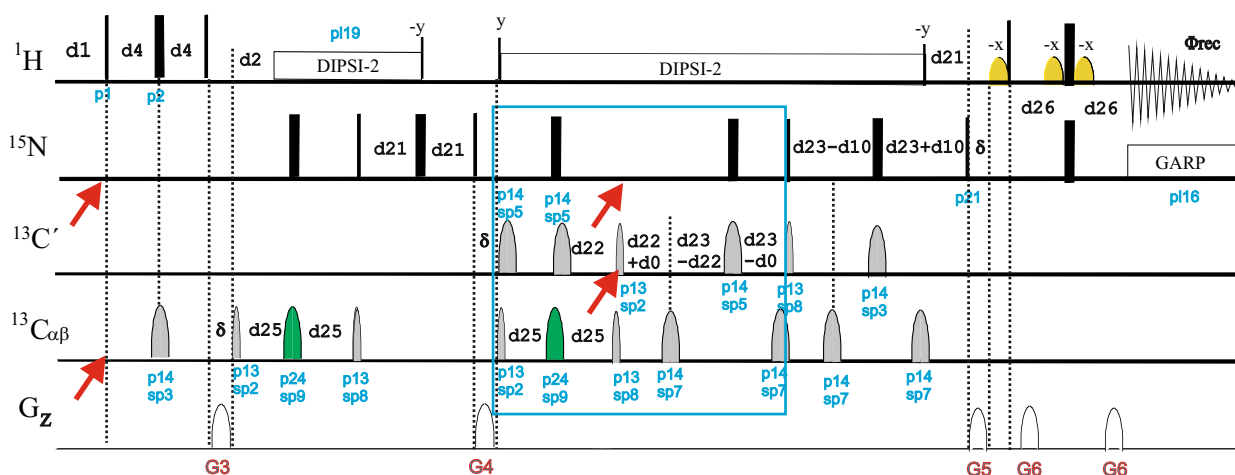
d2 : 1/(2J(CH))	[3.4 msec]
d4 : 1/(4J(CH))	[1.7 msec]
d21: 1/(2J(NH))	[5.5 msec]
d22: 1/(4J(CaCO))	[4.5 msec]
d23: 1/(4J(NCO))	[12.4 msec]
d25: 1/(4J(NCa))	[7.0 msec]
d26: 1/(4J(NH))	[2.3 msec]

MUSIC-Proline: (HACANCA)CONH and (HACAN)CA(CO)NH



music_pro_2_3d.2

ZGPTNS: -DLABEL_CO



ZGPTNS

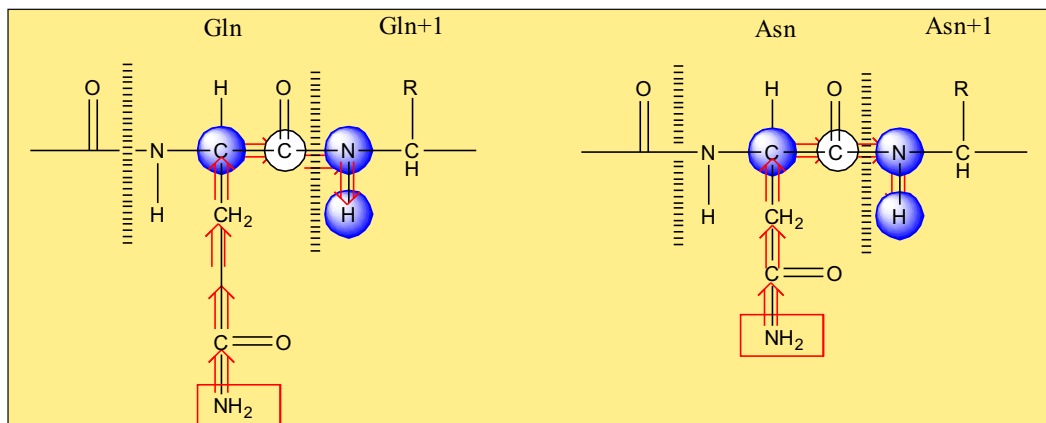
no options: 3D (HACANCA)CONH

NH(Pro+1)

LABEL_CO: 3D (HACAN)CA(CO)NH

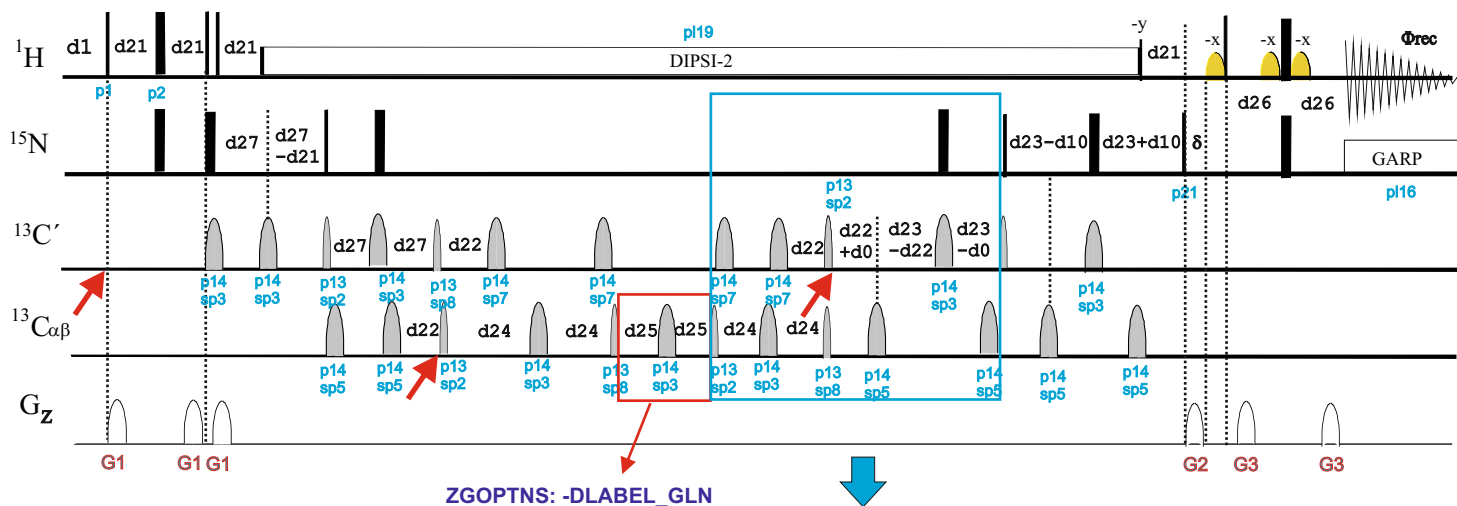
d2 : 1/(2J(CH))	[3.4 msec]
d4 : 1/(4J(CH))	[1.7 msec]
d21: 1/(2J(NH))	[5.5 msec]
d22: 1/(4J(CaCO))	[4.5 msec]
d23: 1/(4J(NCO))	[12.4 msec]
d25: 1/(4J(NCa))	[7.0 msec]
d26: 1/(4J(NH))	[2.3 msec]

MUSIC-GLN/ASN: (NH₂COC)CA(CO)NH and (NH₂COCCA)CONH



music_qn_3d

ZGOPTNS: -DLABEL_CO



ZGOPTNS

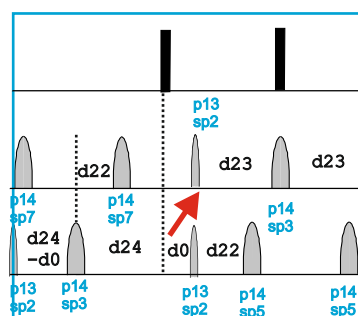
no options: 3D (NH₂COC)CA(CO)NH

LABEL_GLN: 3D (NH₂COC)CA(CO)NH

LABEL_CO: 3D (NH₂COCCA)CONH

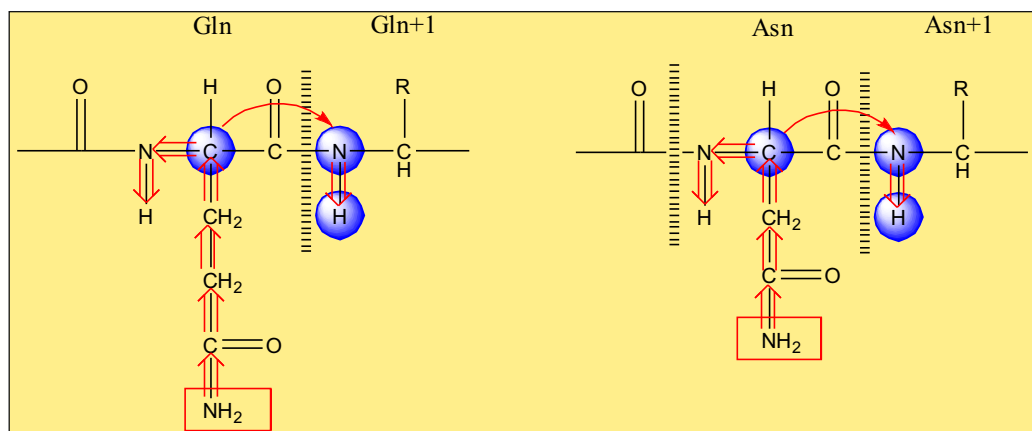
NH(Asn+1)

NH((Gln, Asn)+1)

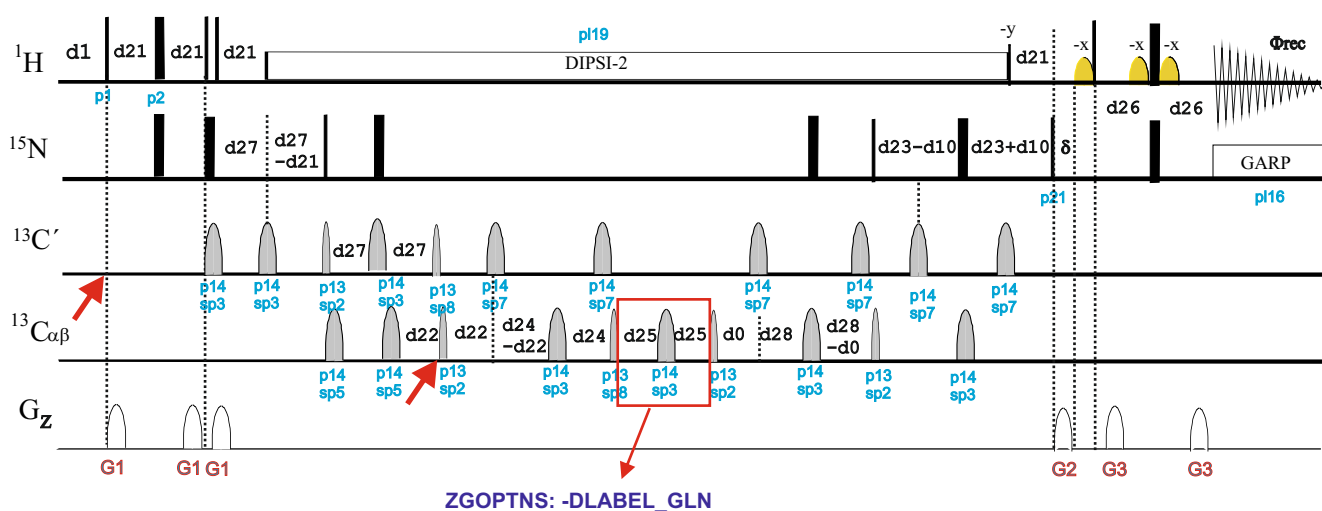


d21: 1/(2J(NH))	[5.5 msec]
d22: 1/(4J(CaCO))	[4.5 msec]
d23: 1/(4J(NCO))	[12.4 msec]
d24: 1/(4J(CC))	[5.2 msec]
d25: 1/(4J(CC))	[6.8 msec]
d26: 1/(4J(NH))	[2.3 msec]
d27: 1/(4J(NCO(s)))	[14.2 msec]

MUSIC-GLN/ASN: (NH₂COC)CANH



music_qn_3d_2



ZGOPTNS

no options: 3D (NH₂COC)CANH
LABEL_GLN: 3D (NH₂COC)CANH

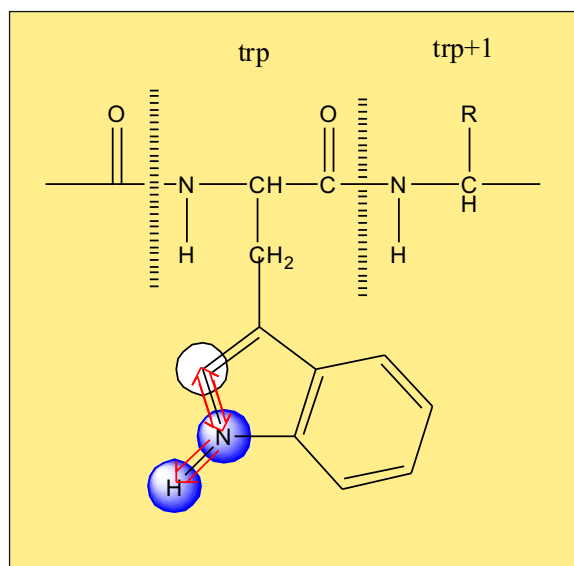
NH(Asn+1)
NH((Gln, Asn)+1)

d21: 1/(2J(NH))	[5.5 msec]
d22: 1/(4J(CaCO))	[4.5 msec]
d23: 1/(4J(NCa))	[12.4 msec]
d24: 1/(4J(CC))	[5.2 msec]
d25: 1/(4J(CC))	[6.8 msec]
d26: 1/(4J(NH))	[2.3 msec]
d27: 1/(4J(NCO(s)))	[14.2 msec]
d28: 1/(4J(CC))	[7.0 msec]
or 1/(4J(CC) (LABEL_GLN))	[9.0 msec]

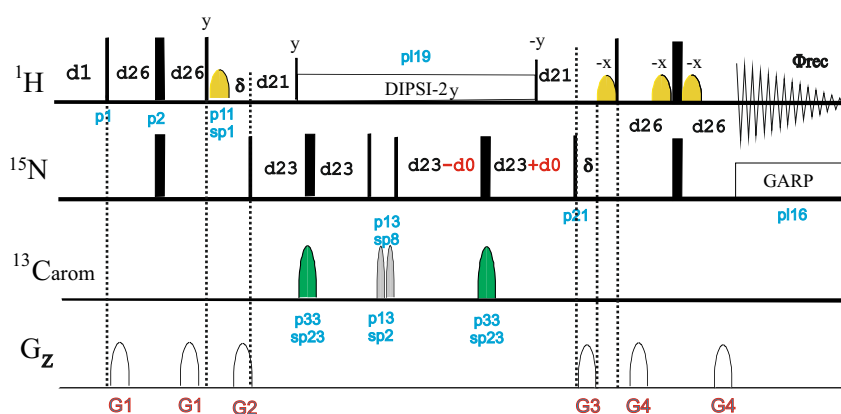
MUSIC-TRP: 2D (HENECE)NH

Reference:

M. Schubert, H. Oschkinat & P. Schmieder, J. Magn. Reson. 153, 186-192 (2001)



music_trpe_2d



d21: $1/(2J(\text{NH}))$ [5.5 msec]
d23: $1/(4J(\text{NC}))$ [12.4 msec]
d26: $1/(4J(\text{NH}))$ [2.3 msec]

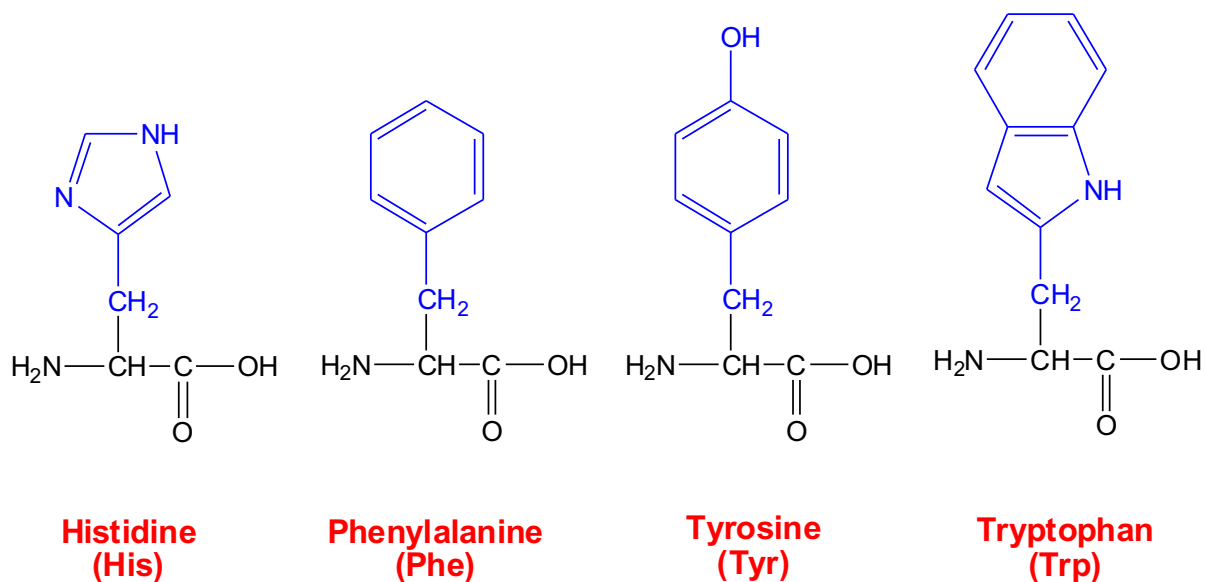
BRUKER PULSE PROGRAM CATALOGUE

NMRGuide

AROMATIC-SPECIFIC NMR EXPERIMENTS

Aromatic-Specific Experiments

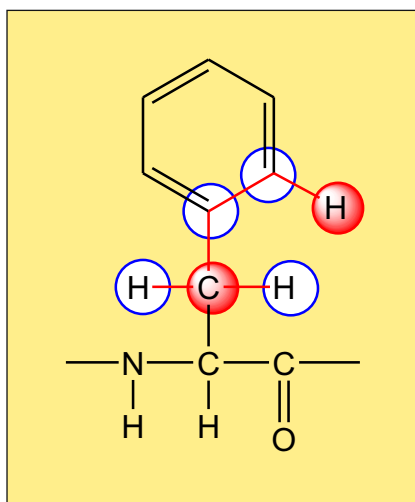
- 2D (HB)CB(CGCD)HD (*hbcbcgcdhdgp*)
- 2D (HB)CB(CGCDCE)HE (*hbcbcgcdcehegp*)
- 2D (HB)CB(CGCC-TOCSY)Har (*hbcbcgccchrgp*)
- 3D Har(CC-TOCSY-CGCBACON)NH (*hcccgcbaconhgp3d*)
- 3D Har(CC-TOCSY-CGCBACON)NH using WATERGATE (*hcccgcbaconhgpwg3d*)
- 3D Har(CC-TOCSY-CGCBACON)NH using TROSY (*trhcccgcbaconhgp3d*)
- 3D Har(CC-TOCSY-CGCBACON)NH using TROSY and echo-antiecho (*trhcccgcbaconhetgp3d*)



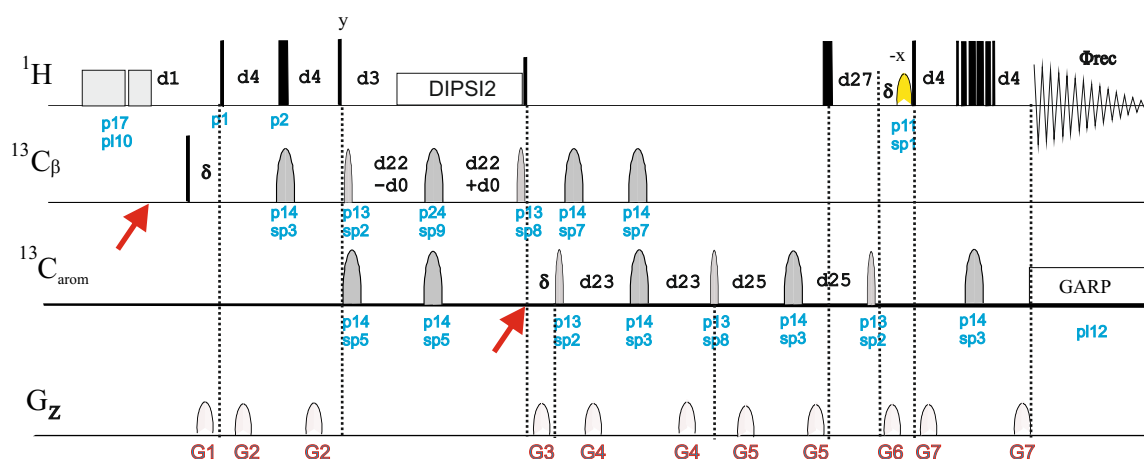
References:

1. T. Yamazaki, J.D. Forman-Kay & L.E. Kay, J. Am. Chem. Soc. 115, 11054-11055 (1993)
2. F. Loehr, R. Haensel, V.V. Rogov & V. Doetsch, J. Biomol. NMR 37, 205-224 (2007)

2D (HB)CB(CGCD)HD

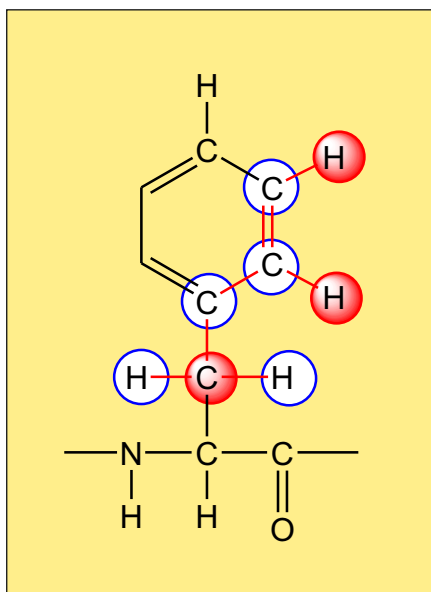


hbcbcgcdhdgp

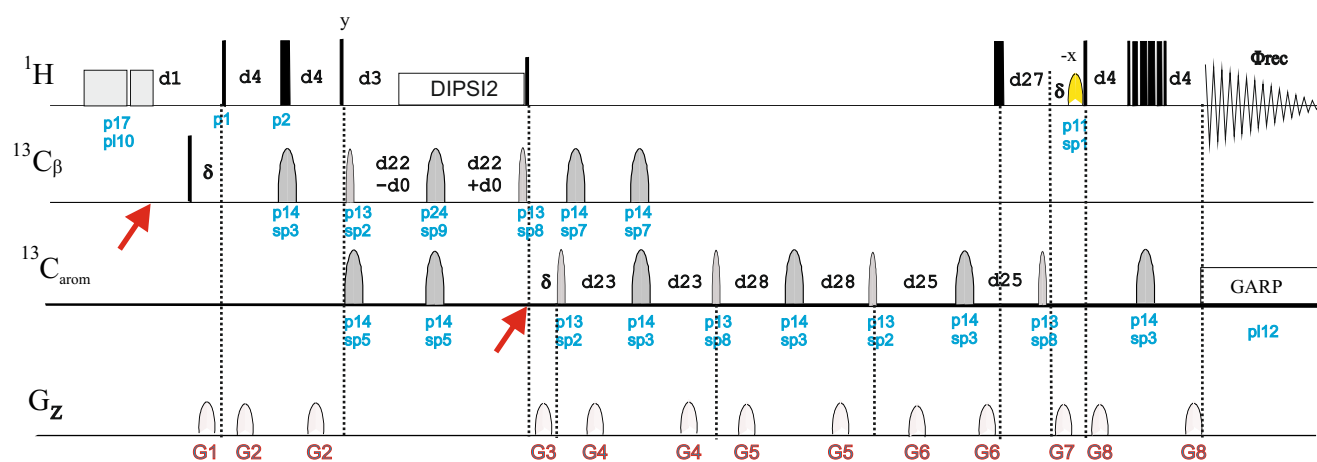


d3 : $1/(3J'(\text{HbCb}))$	[1.8 msec]
d4 : $1/(4J(\text{HbCb}))$	[1.7 msec]
d21: $1/(4J'(\text{HeCe}))$	[1.25 msec]
d22: $1/(4J(\text{CbCg}))$	[4.4 msec]
d23: $1/(4J'(\text{CbCg}))$ and $1/(4J(\text{CgCd}))$	[2.7 msec]
d25: $1/(4J'(\text{CgCd}))$	[2.1 msec]
d27: $1/(4J(\text{HdCd}))$	[1.4 msec]

2D (HB)CB(CGCDCE)HE

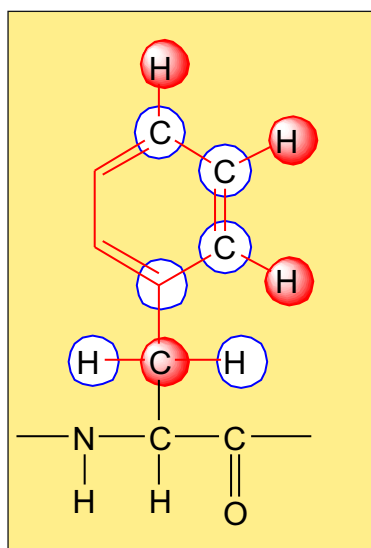


hbcbcgdccehgp

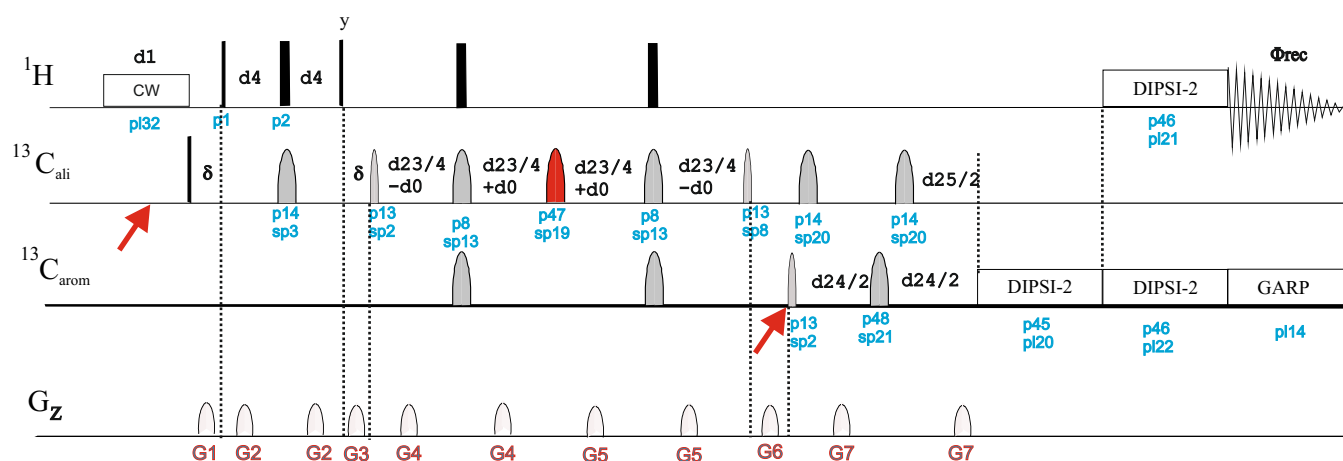


d3 : $1/(3J'(\text{HbCb}))$	[1.8 msec]
d4 : $1/(4J(\text{HbCb}))$	[1.7 msec]
d21: $1/(4J'(\text{HeCe}))$	[1.25 msec]
d22: $1/(4J(\text{CbCg}))$	[4.4 msec]
d23: $1/(4J'(\text{CbCg}))$ and $1/(4J(\text{CgCd}))$	[2.7 msec]
d25: $1/(4J'(\text{CdCe}))$	[2.1 msec]
d27: $1/(4J(\text{HeCe}))$	[1.4 msec]
d28: $1/(4J'(\text{CgCd}))$ and $1/(4J(\text{CdCe}))$	[3.8 msec]

2D (HB)CB(CGCC TOCSY)Har

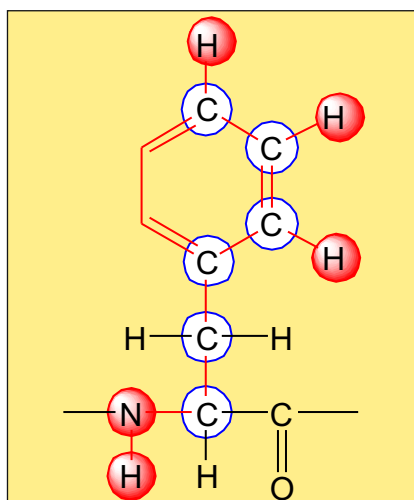


hbcbcgcchargp

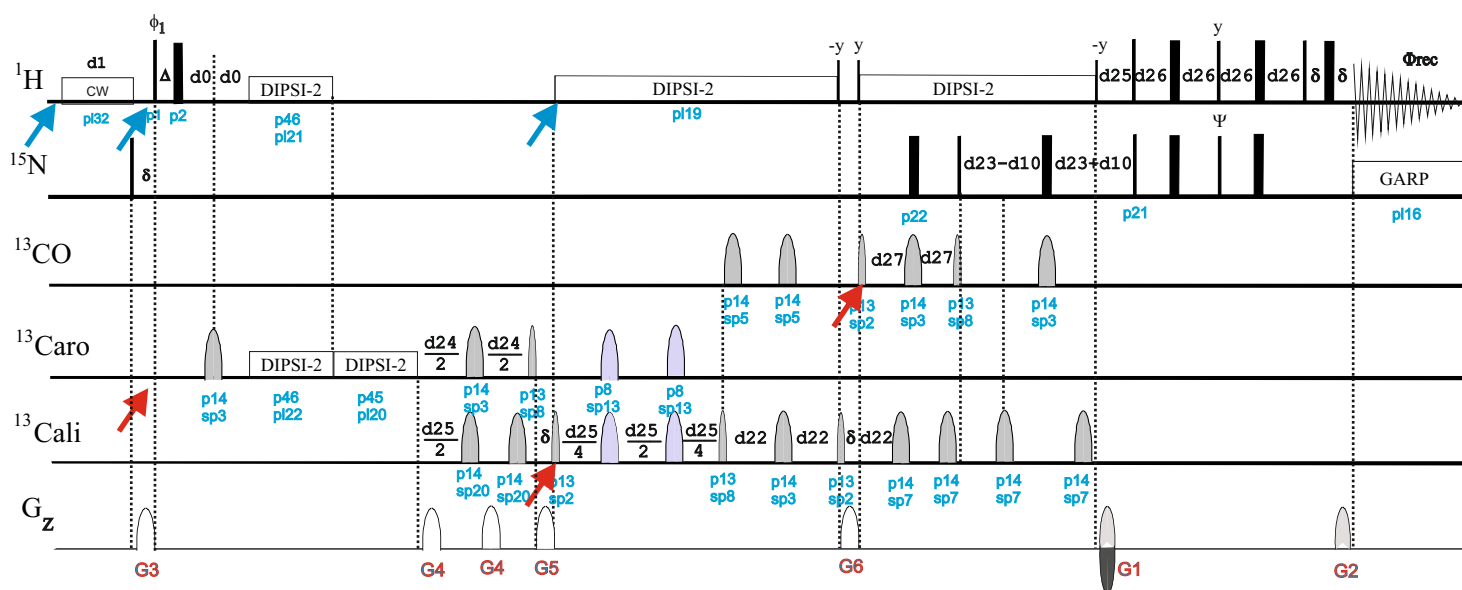


d4 : 1/(4J(HbCb))	[1.7 msec]
d23: 1/(2J'(CbCg)) and 5/(4J'(HbCb))	[9.0 msec]
d24: 1/(J(CgCd))	
Phe, Trp	[11.5 msec]
Tyr	[15.0 msec]
all	[17.4 msec]
d25: 1/(2J(CbCg))	[10.4 msec]
cnst24: Caromatic chemical shift (offset, in ppm)	[130 ppm]
cnst30: Cbeta(aro) chemical shift (offset, in ppm)	[35 ppm]
cnst51: Calpha(aro) chemical shift (offset, in ppm)	[59 ppm]
cnst52: Caromatic chemical shift (offset, in ppm)	
Phe	[141 ppm]
Trp	[111 ppm]
Tyr	[129 ppm]

3D Har(CC-TOCSY-CGCBCACO)NH

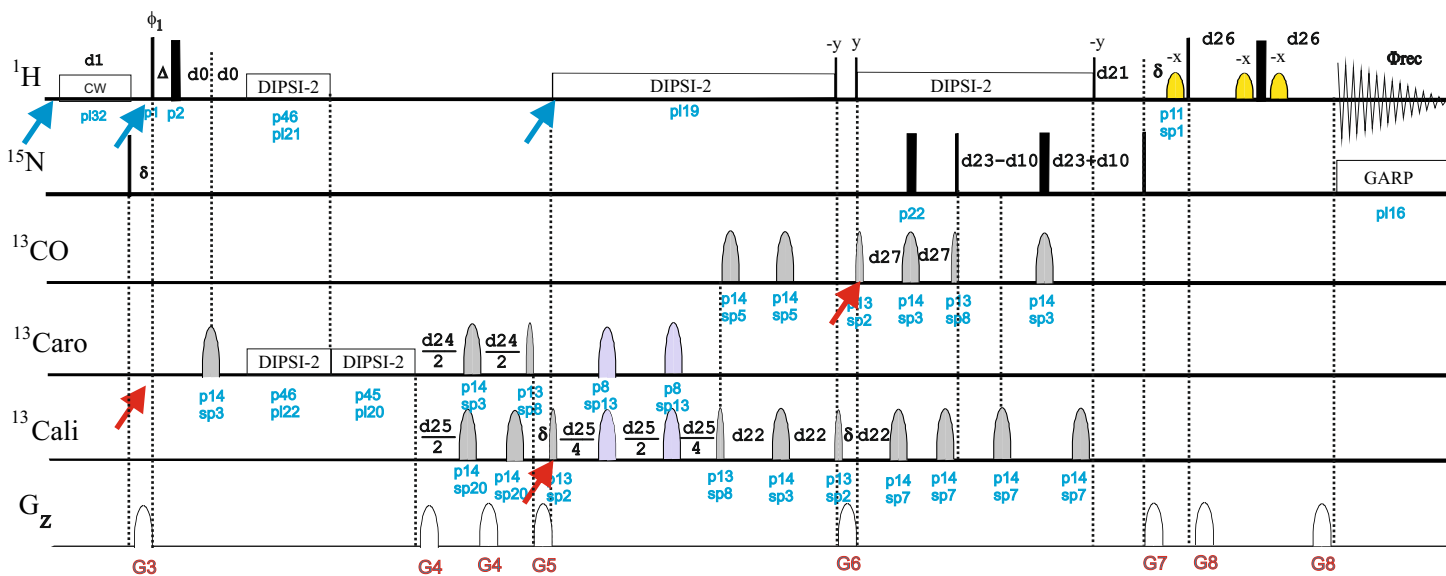


hcccgcbcaconhgp3d

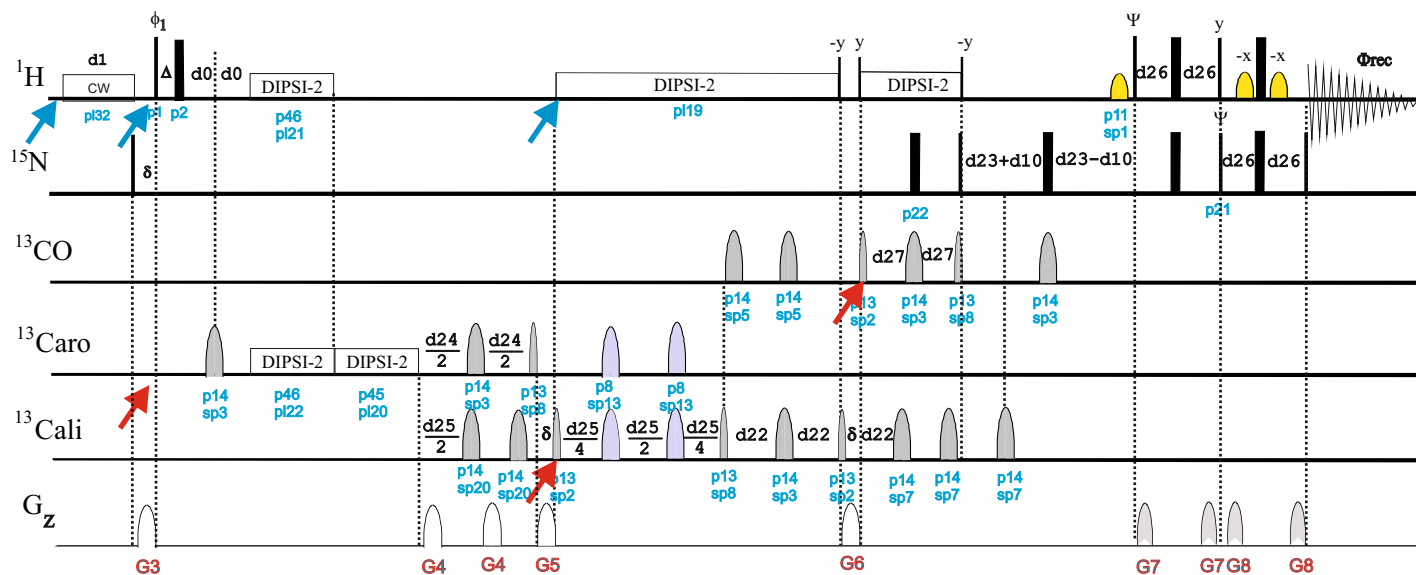


d21: 1/(2J(NH)) [5.5 msec]
d22: 1/(4J(CaCO)) [4.6 msec]
d23: 1/(4J(NCO)) [12.4 msec]
d24: 1/(J(CgCd)) [17.4 msec]
d25: 1/(2J(CbCg)) [10.4 msec]
d26: 1/(4J'(NH)) [2.3 msec]
d27: 1/(4J'(NCO)) [11.0 msec]

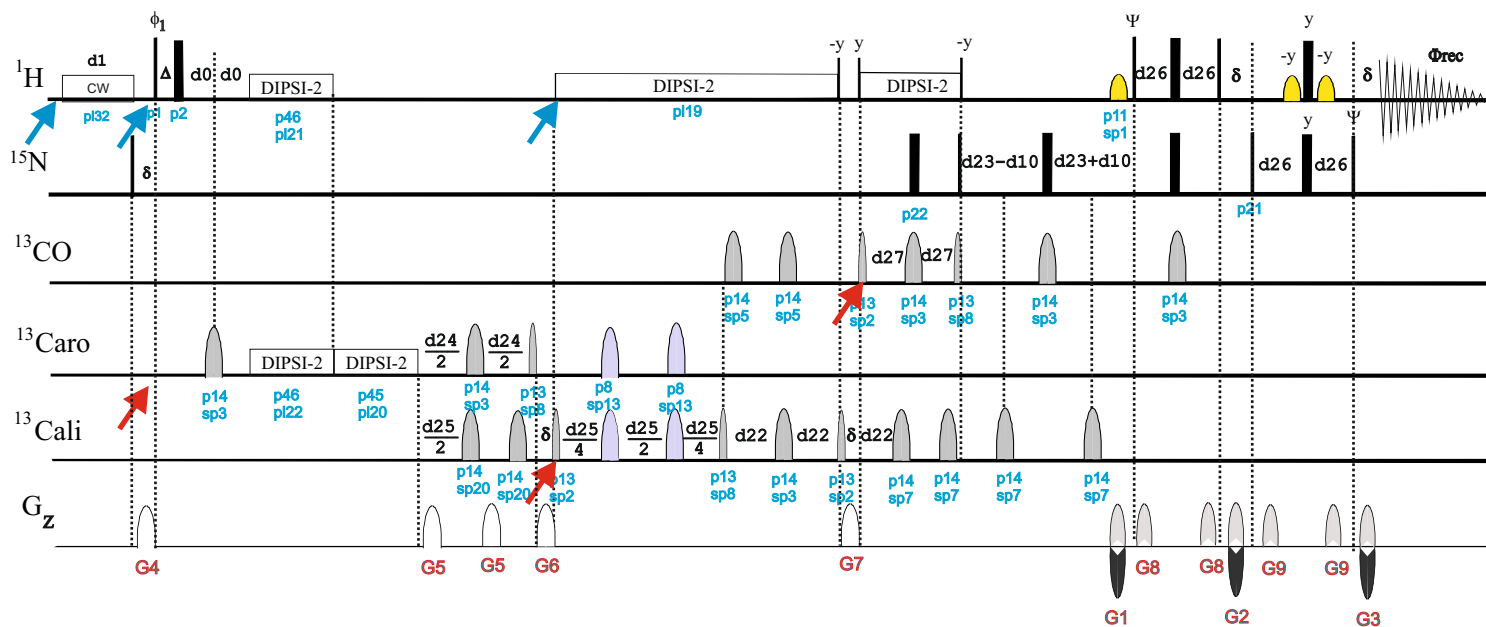
hccccbcacanhgpg3d



trhccccbcacanhgpg3d



trhcccgcbcaconhetgp3d



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METHYL-SELECTIVE NMR EXPERIMENTS

Methyl-selective Experiments

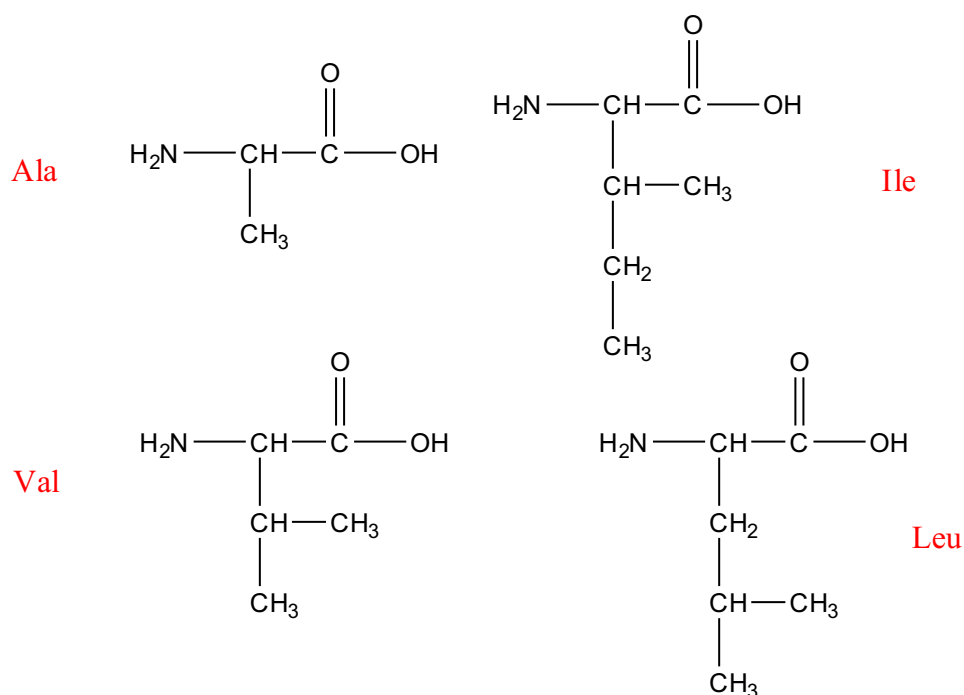
- 3D (Hme)Cme([C])CA experiment using WATERGATE (hmcmbcagpwg3d)
- 3D (Hme)Cme([C]CA)CO experiment using WATERGATE (hmcmbcacogpwg3d)
- 3D (Hme)Cme([C]CA)NH experiment using WATERGATE (hmcmbcanhgpwg3d)
- 3D Hme (Cme[C]CA)NH experiment using WATERGATE (hmcmbcanhgpwg3d.2)
- 3D (Hme)Cme([C]CACO)NH experiment using WATERGATE (hmcmbcaconhgpwg3d)

Also see:

Amino-Acid-Type Experiments with CH₃-selection

All Backbone-Sidechain experiments: (H)CC(CO)NH, CC(CO)NH, CCA(CO)NH, CCANH, CBCACONH, CBCANH

V. Tugarinov & L.E. Kay, J. Am. Chem. Soc. 125, 13868-13878 (2003)



ZGOPTNS options (in eda) In **ALL EXPERIMENTS**:

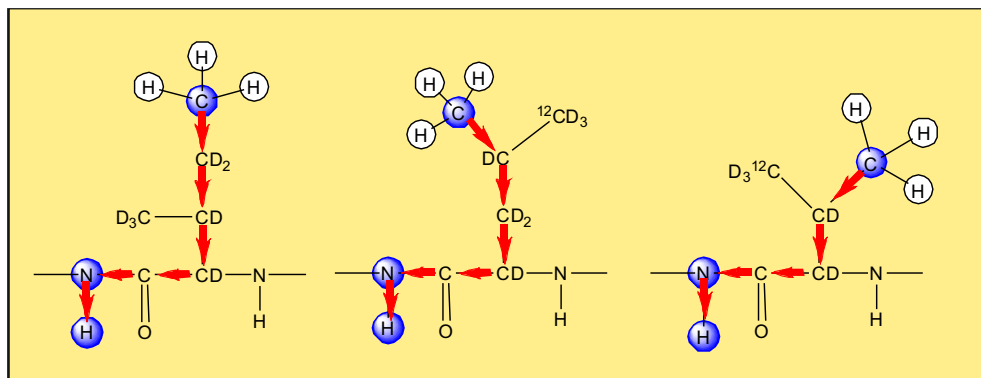
no option all methyl groups

LABEL_ALA: one transfer step along sidechain: methyl groups
in C_β position only (option **-DLABEL_ALA**)

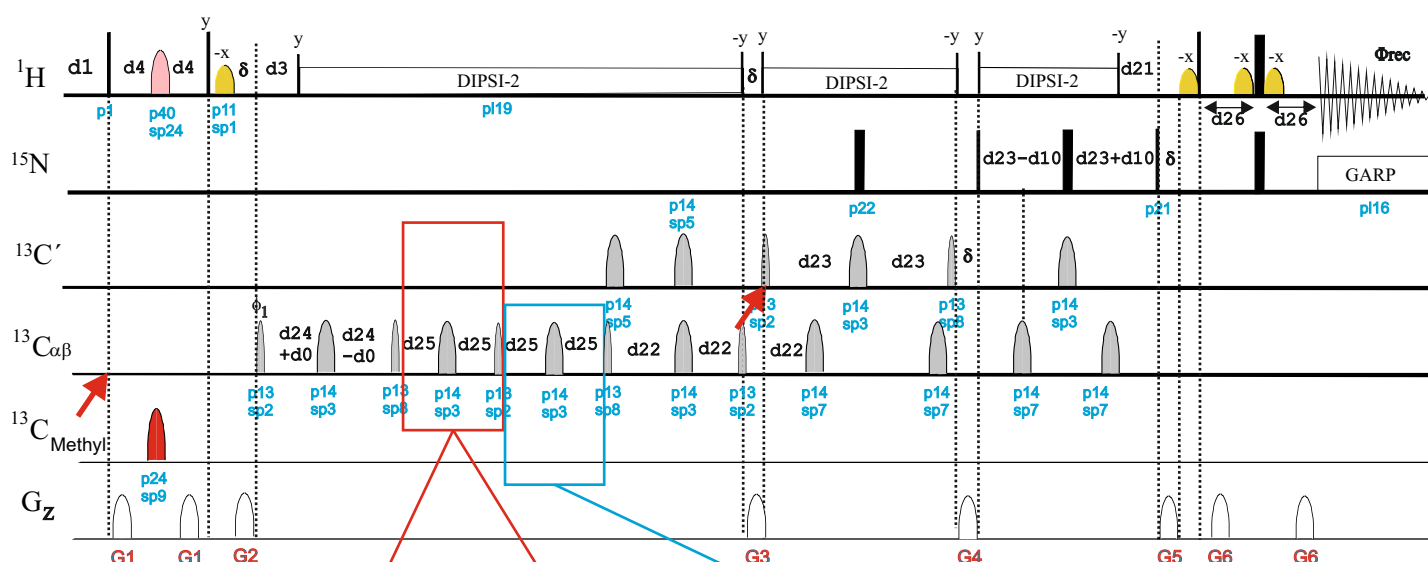
LABEL_VAL: two transfer steps along sidechain: methyl groups
in C_γ position only (option **-DLABEL_VAL**)

LABEL_CG2: refocussing pulse for Ile C_{γ2} (depending on labelling
scheme) (option **-DLABEL_CG2**)

3D (Hme)Cme([C]CACO)NH



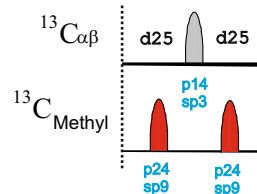
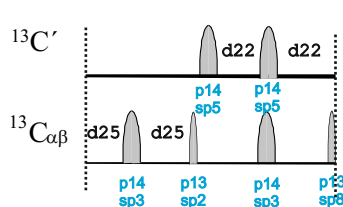
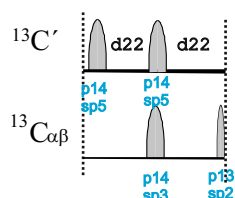
hmcmbcaconhgpwg3d



if "LABEL_ALA"

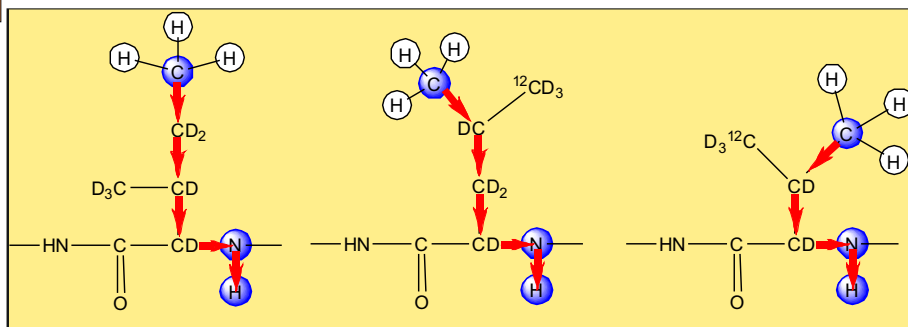
If "LABEL_VAL"

if "LABEL_CG2"

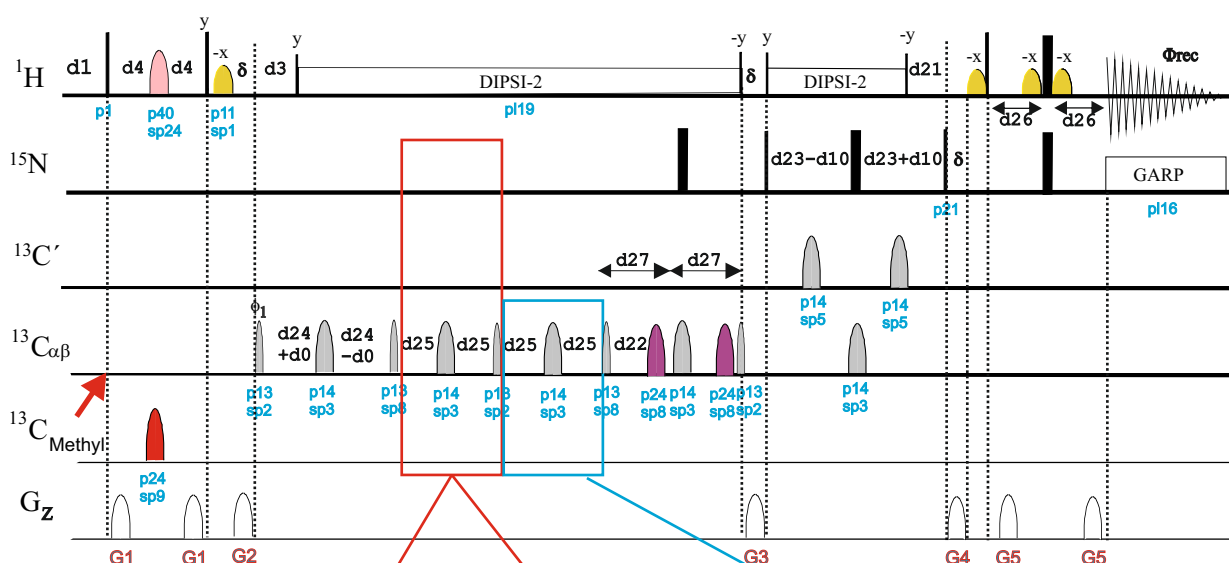


d3 : 1/(6J'(CH))	[1.52 msec]
d4 : 1/(4J(CH))	[1.8 msec]
d21: 1/(2J(NH))	[5.5 msec]
d22: 1/(4J(CaCO))	[4.5 msec]
d23: 1/(4J(NCa))	[12.4 msec]
d24: 1/(4J(CmeC))	[7 msec]
d25: 1/(4J'(CC))	[5 msec]
d26: 1/(4J(NH))	[2.3 msec]

3D (Hme)Cme([C]CA)NH



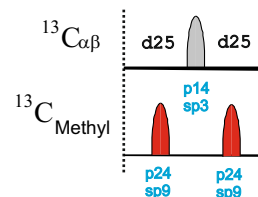
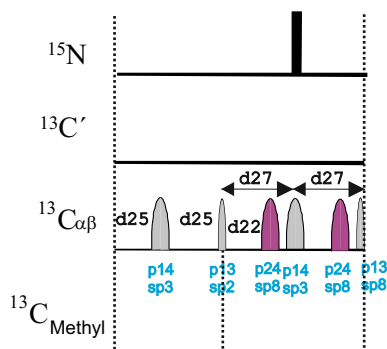
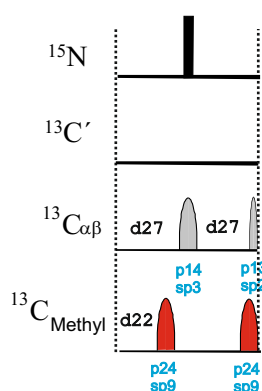
hmcmcbcanhpgwg3d



if "LABEL_ALA"

If "LABEL_VAL"

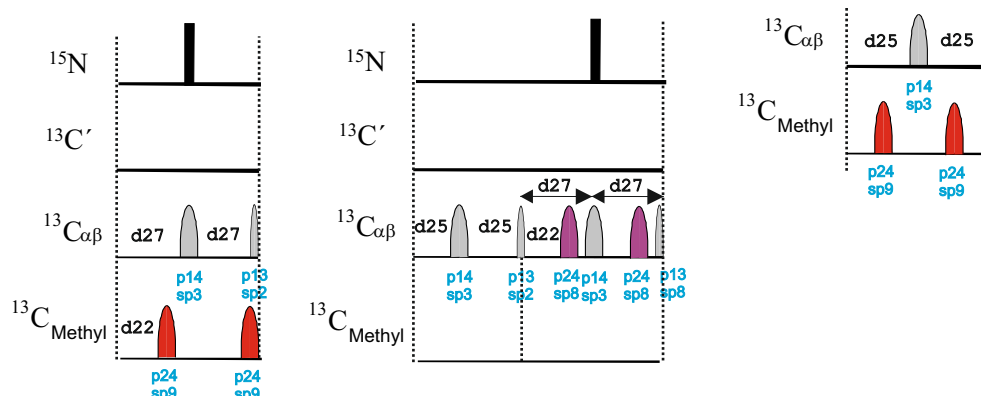
if "LABEL_CG2"



d3 : $1/(6J'(\text{CH}))$	[1.52 msec]
d4 : $1/(4J(\text{CH}))$	[1.8 msec]
d21: $1/(2J(\text{NH}))$	[5.5 msec]
d22: $1/(8J'(\text{CC}))$	[2.7 msec]
d23: $1/(4J(\text{NCa}))$	[12.4 msec]
d24: $1/(4J(\text{CmeC}))$	[7 msec]
d25: $1/(4J'(\text{CC}))$	[5 msec]
d26: $1/(4J(\text{NH}))$	[2.3 msec]
d27: $1/(4J'(\text{NCa}))$	[10.0 msec]

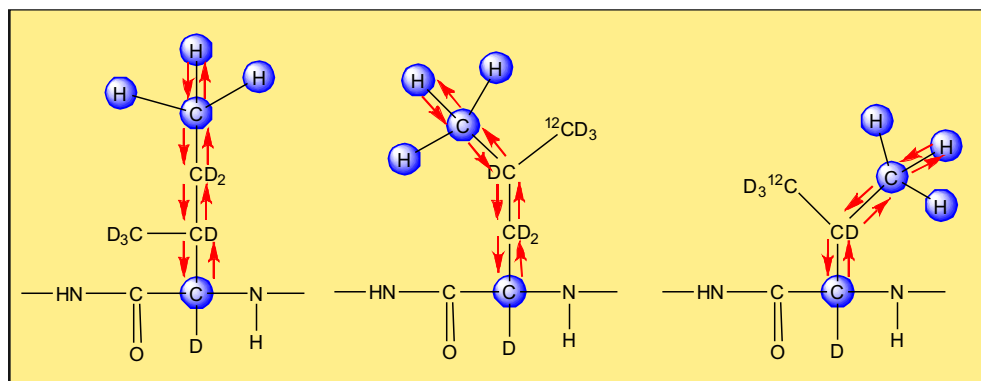
The diagram illustrates the three isotopologues of a peptide backbone, showing the flow of isotopes from the methyl group to the amide group. The left structure shows a ^{12}C backbone with a methyl group (CH_3) and an amide group (NH). The middle structure shows a ^{13}C backbone with a methyl group (CH_3) and an amide group (NH). The right structure shows a ^{15}N backbone with a methyl group (CH_3) and an amide group (NH). Red arrows indicate the flow of isotopes from the methyl group to the amide group.

if "LABEL CG2"

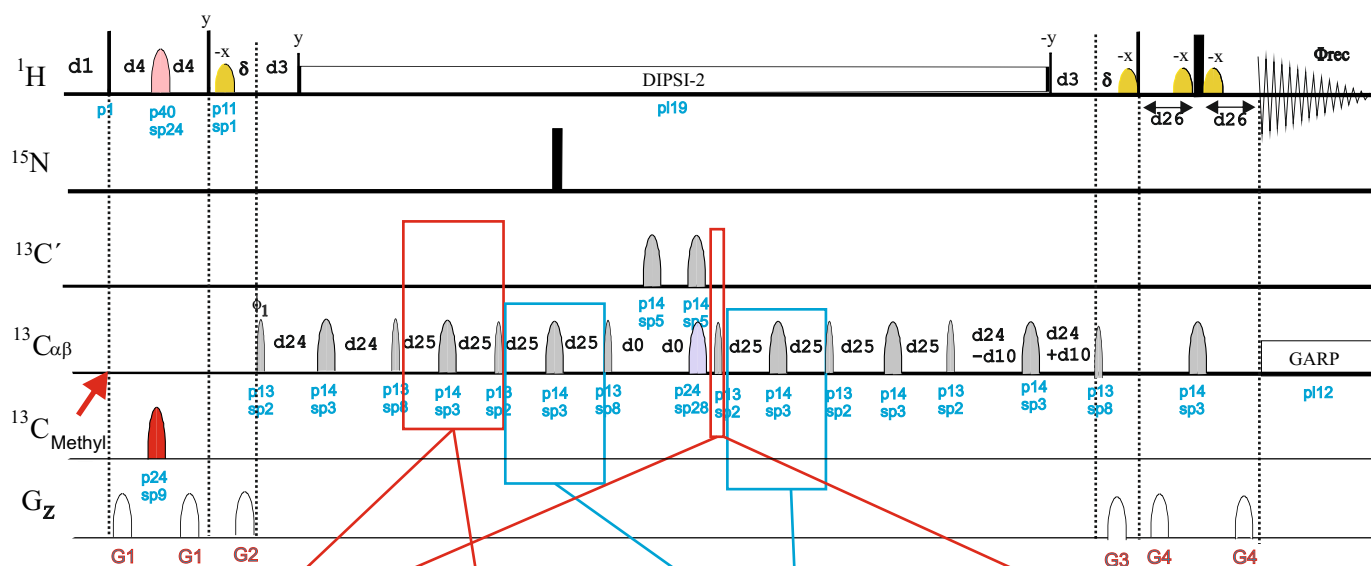


d23: 1/(4J(NCa)	[12.4 msec]
d24: 1/(4J(CmeC))	[7 msec]
d25: 1/(4J'(CC))	[5 msec]
d26: 1/(4J(NH)	[2.3 msec]
d27: 1/(4J'(NCa)	[10.0 msec]

3D (Hme)Cme([C])CA



hmcmbcagpwg3d

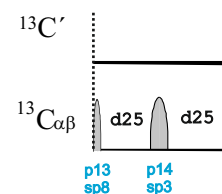
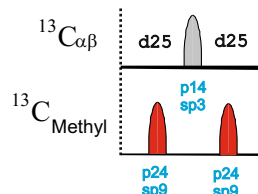
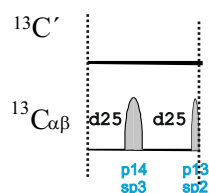


if "LABEL ALA"

If "LABEL VAL"

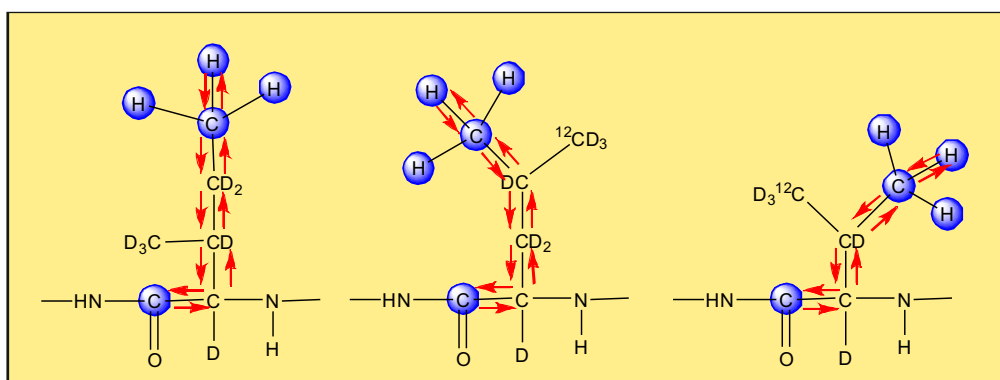
if "LABEL CG2"

If "LABEL VAL"

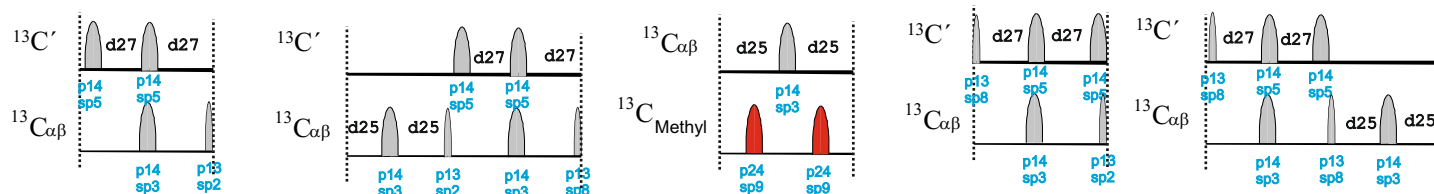
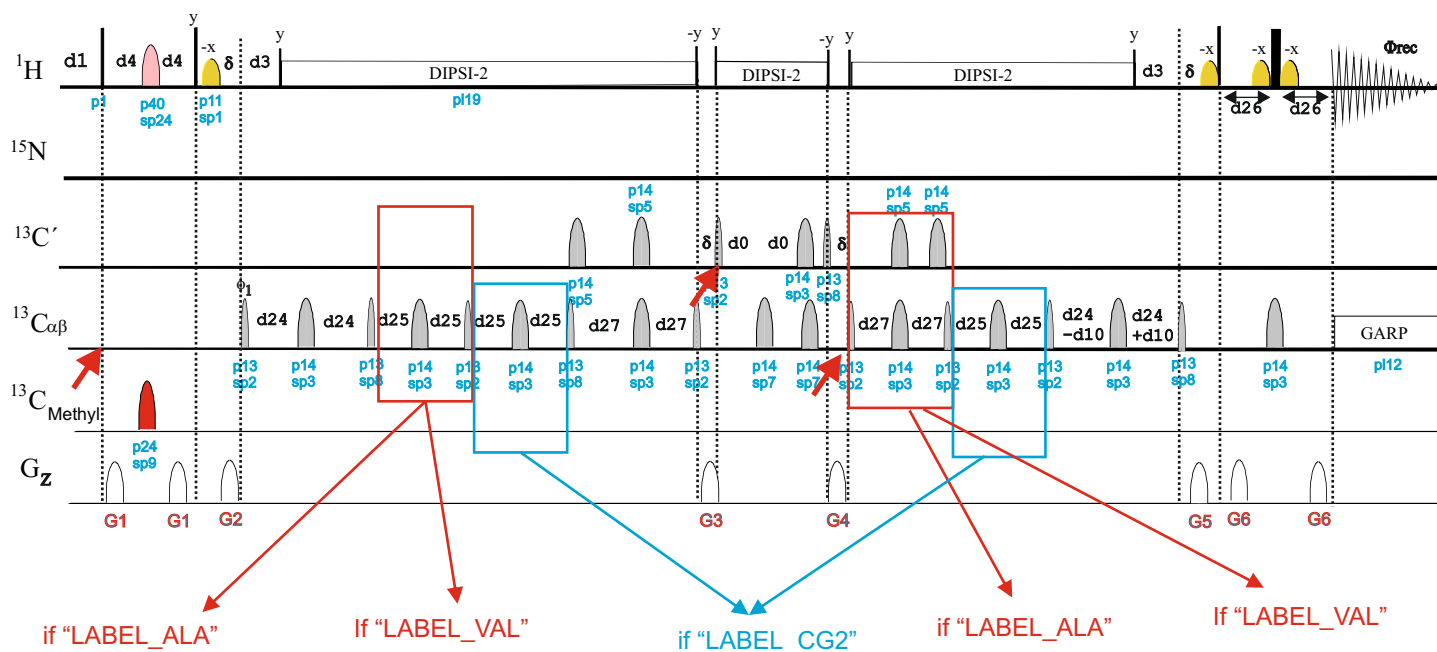


d3 : 1/(6J'(CH))	[1.52 msec]
d4 : 1/(4J(CH))	[1.8 msec]
d24: 1/(4J(CmeC))	[7 msec]
d25: 1/(4J'(CC))	[5 msec]

3D (Hme)Cme([C]CA)CO



hmcmbcacogpwg3d



d3 : 1/(6J'(CH))	[1.52 msec]
d4 : 1/(4J(CH))	[1.8 msec]
d24: 1/(4J(CmeC))	[7 msec]
d25: 1/(4J'(CC))	[5 msec]
d27: 1/(4J''(CC)), 1/(4J(CaCO))	[4.75 msec]

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2D & 3D CARBON-DETECTED EXPERIMENTS

Experimental details for carbon-detected experiments

Offsets

^1H at 4.7ppm (o2p)
 ^{15}N at 118ppm (o3p)
 ^{13}CO at 173ppm (cnst21)
 ^{13}CA at 55 ppm (cnst22)
 $^{13}\text{Cali}$ at 39ppm (cnst23)

Decoupling/Mixing

From f2 channel: ^1H CPD with 3.0KHz Waltz-16 (pcpd2 at pl12)
From f3 channel: ^{15}N CPD with 1KHz GARP-4 (pcpd3 at pl16)

^{13}C TOCSY with 10KHz FLOPSY-16 (pl10)

Spectral Widths

18-24ppm for CO
42 ppm for ^{15}N
48 ppm for CA
75-80 ppm for Cali

Typical ^{13}C pulses from F1 channel (For 600MHz spectrometer)

p11 sp23: 90° Cali/CO on- resonance (320us (Q5 and Q5tr))
p12 sp24: 180° Cali/CO on-resonance (256us (Q3))
p11 sp25: retro 90° Cali/CO on-resonance (320us (Q5 and Q5tr))
p12 sp26: 180° CO/Cali off-resonance with respect to Cali/CO (256us (Q3))
p12 sp27: 180° CO/CA off-resonance with respect to CA/CO (256us (Q3))
p25 sp28: 180° Selective CA on-resonance (1 ms (Q3))
p12 sp29: 180° Cali off-resonance with respect to CA (256us (Q3))
p30 sp30: Simultaneous 180° CA and CO (symmetrically modulated)

p8 sp13: 180° adiabatic for inversion (500us(Chirp))
p24 sp7: 180° adiabatic for refocusing (2000us(Composite chirp))

Very Important!!: In all pulse programs the syntax

prosol relations=<triple_c>

**is included for automated acquisition/set-up using edprosol/getprosol.
This file is defined in the following directory:**

`$TOPSPINHOME/conf/instr/spect/prosol/relations/triple_c`

2D Carbon-Detected Experiments

- 2D CC COSY
 - Conventional (c_cosy)
 - Constant-time (c_cosy_ct / c_cosy2_ct)
- 2D CC NOESY
 - Conventional (c_ccnoesy)
 - 2D CC NOESY (c_ccnoesy2)
 - Constant-time (c_ccnoesy_ct)
- 2D CC TOCSY
 - Conventional (c_ccflopsy16)
 - With DIPAP for virtual decoupling (c_ccflopsy16_ia)
 - Constant-time (c_ccflopsy16_ct)
 - Constant-time with DIPAP for virtual decoupling (c_ccflopsy16_ctia)
- 2D CACO
 - Using HSQC (c_caco)
 - with IPAP for virtual decoupling (c_caco_ia)
 - with S3E for virtual decoupling (c_caco_s3)
 - Using HMQC (c_coca_mq | c_coca_mq.2)
- 2D COCA
 - Using HSQC (c_coca)
 - with DIPAP for virtual decoupling (c_coca_ia)
- 2D CON
 - Using HMQC (c_con_mq)
 - Using HSQC (c_con_sq)
 - Using HSQC with IPAP for virtual decoupling (c_con_iasq)
 - Using HMQC with IPAP for virtual decoupling (c_con_mqia)
- 2D CAN
 - Using HMQC (c_can_mq)
 - Using HMQC (c_can_mq.2)
 - Using HSQC with DIPAP for virtual decoupling (c_can_iasq)

3D Carbon-Detected Experiments For Backbone Assignments

- 3D HCACO
 - (*) With CO detection (**c_hcaco_3d**)
 - With CO detection and with IPAP for virtual decoupling (**c_hcaco_ia3d**)
 - With CO detection and with S3E for virtual decoupling (**c_hcaco_s33d**)
 - With CO detection and using HMQC (**c_hacaco_3d**)
- 3D HCAN
 - (*) With CA detection (**c_hcan_3d**)
 - With CA detection and with DIPAP for virtual decoupling (**c_hcan_ia3d**)
- 3D CANCO
 - (*) With CO detection (**c_canco_3d**)
 - With CO detection and with IPAP for virtual decoupling (**c_canco_ia3d**)
 - With CO detection and with IPAP for virtual decoupling (**c_canco_ia3d.2**)
 - (*) (H)CANCO starting from HA and with CO detection (**c_hcanco_3d**)
 - (H)CANCO starting from HA and with CO detection and with IPAP for virtual decoupling (**c_hcanco_ia3d**)
- 3D intra-CANCO
 - (*) With CO detection (**c_cancoi_3d**)
 - With CO detection and with IPAP for virtual decoupling (**c_cancoi_ia3d**)
 - (*) Intra-(H)CANCO starting from HA and with CO detection (**c_hcancoi_3d**)
 - Intra-(H)CANCO starting from HA and with CO detection and with IPAP for virtual decoupling (**c_hcancoi_ia3d**)
- 3D HNCA
 - (*) With CA detection (**c_hnca_3d**)
 - With CA detection and with DIPAP for virtual decoupling (**c_hnca_ia3d**)
- 3D HNCO
 - (*) With CO detection (**c_hnco_3d**)
 - With CO detection and with IPAP for virtual decoupling (**c_hnco_ia3d**)
- 3D (H)NCACO
 - (*) With CO detection (**c_hncaco_3d**)
 - With CO detection and with IPAP for virtual decoupling (**c_hncaco_ia3d**)
 - With CO detection and with S³E for virtual decoupling (**c_hncaco_s33d**)
- 3D (H)NCOCA
 - (*) With CA detection (**c_hncoca2_3d**)
 - With CA detection and with DIPAP for virtual decoupling (**c_hncoca2_ia3d**)
 - (*) (H)N(CO)CACO with CO detection (**c_hncoca_3d**)
 - (H)N(CO)CACO with CO detection and with IPAP for virtual decoupling (**c_hncoca_ia3d**)

(*) NOTE: These pulse programs have been moved to pp.dextra directory

3D Carbon-Detected Experiments For Sidechain Assignments

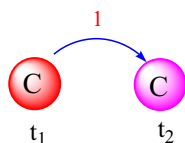
- 3D HCC CT-TOCSY (c_hccflopsy16_3d)
- 3D HBCA
 - (*) With CA detection (c_hbcba_3d)
 - With CA detection and with DIPAP for virtual decoupling (c_hbcba_ia3d)
- 3D HCB(CA)CO
 - (*) With CO detection (c_hcbcaco_3d)
 - With CO detection and with IPAP for virtual decoupling (c_hcbcaco_ia3d)
 - With CO detection and with S³E for virtual decoupling (c_hcbcaco_s33d)
- 3D CBCACO
 - (*) With CO detection (c_cbcaco_3d)
 - With CO detection and with IPAP for virtual decoupling (c_cbcaco_ia3d)
 - With CO detection and with S³E for virtual decoupling (c_cbcaco_s33d)
- 3D CCCO
 - With CO detection and with IPAP for virtual decoupling (c_ccco_ia3d)
 - With CO detection and with S³E for virtual decoupling (c_ccco_s33d)
- 3D CBCACON
 - With CO detection and with IPAP for virtual decoupling (c_cbcacn_ia3d)
- 3D CCCON
 - With CO detection and with IPAP for virtual decoupling (c_cccon_ia3d)
- 3D CBCANCO
 - With CO detection and with IPAP for virtual decoupling (c_cbcanco_ia3d)
- 3D (H)CBCAN
 - (*) With CA detection (c_hbcnan_3d)
 - With CA detection with DIPAP for virtual decoupling (c_hbcnan_ia3d)

(*) NOTE: These pulse programs have been moved to pp.dextra directory

2D ^{13}C - ^{13}C COSY Experiment

Experiment Description

The 2D CC COSY experiment allows to obtain a homonuclear CC correlation map to trace out through-bond carbon-carbon connectivities in ^{13}C -labeled proteins

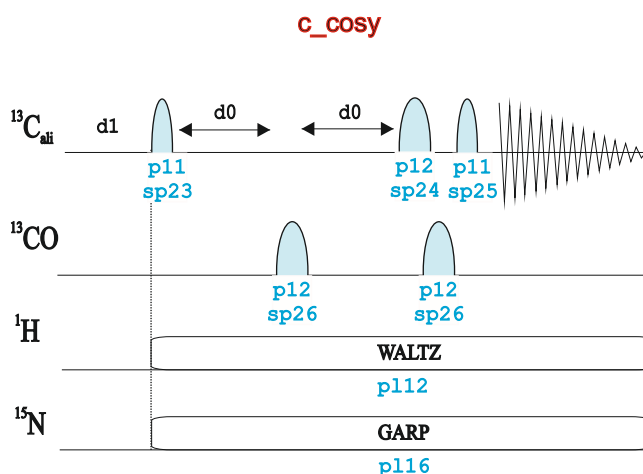
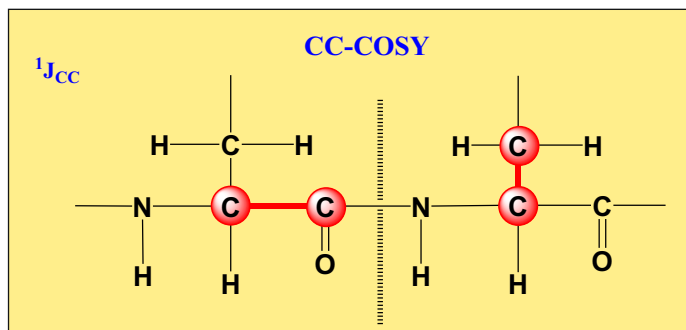


Related Experiments

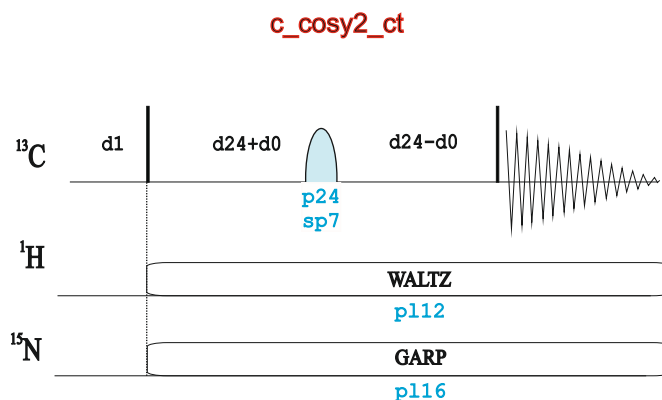
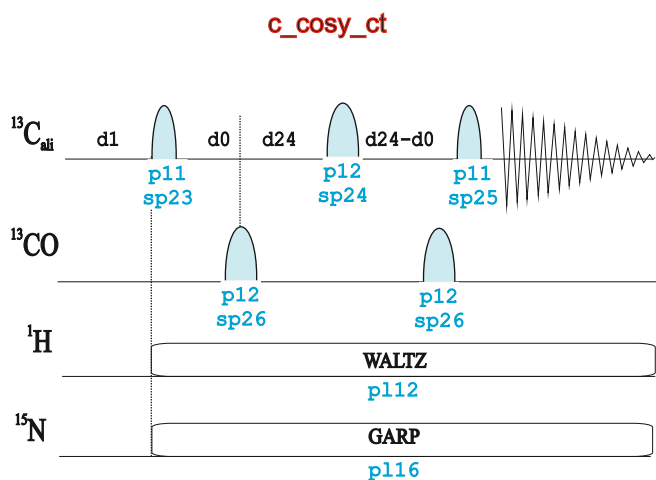
2D COCA
2D CC and 3D HCC TOCSY

References:

1. T.E. Machonkin, W.M. Westler & J.L. Markley, J. Am. Chem. Soc. 124, 3204-3205 (2002)
2. W. Bermel, I. Bertini, I.C. Felli, R. Kuemmerle & R. Pierattelli, J. Am. Chem. Soc. 125, 16423-16429 (2003)



$$d24 = 1/4J(\text{CC}) = 5\text{ms}$$



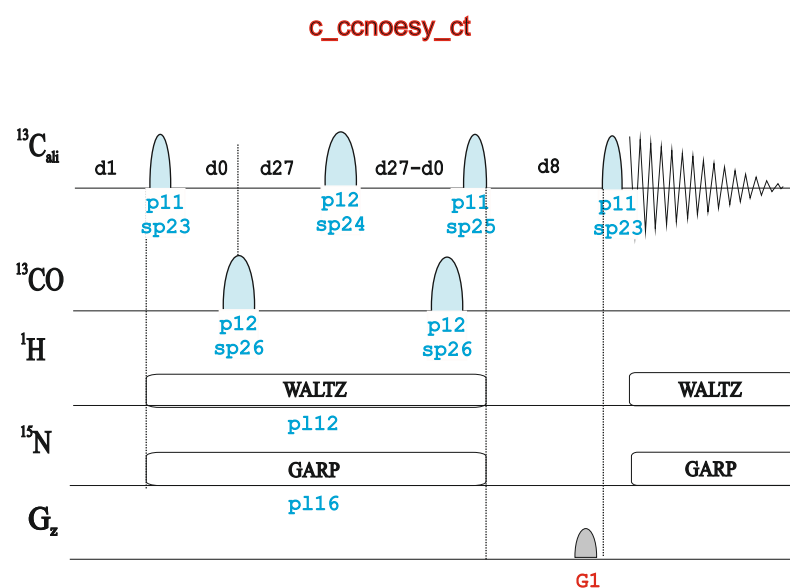
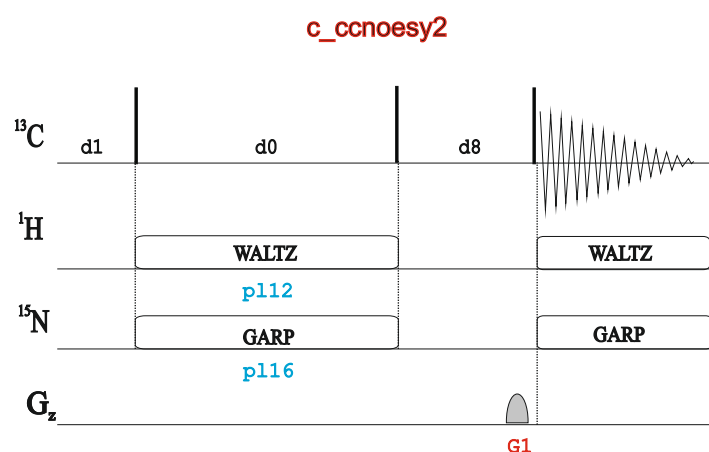
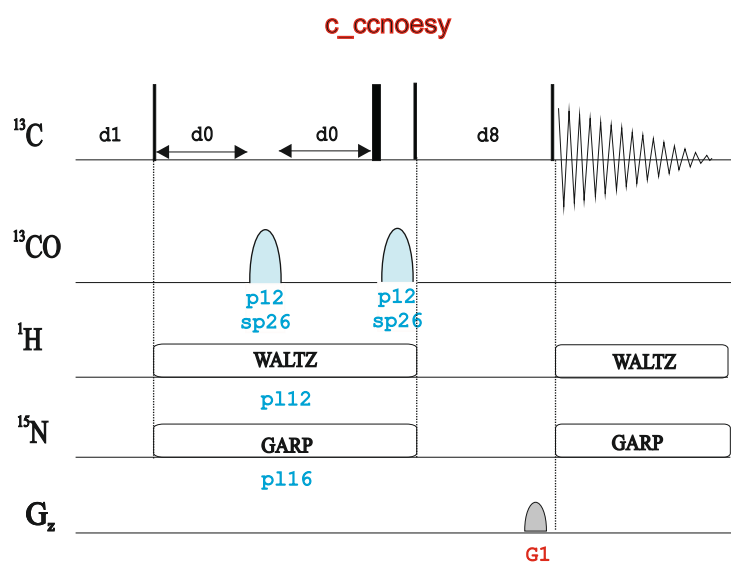
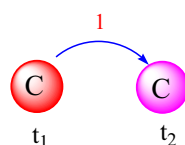
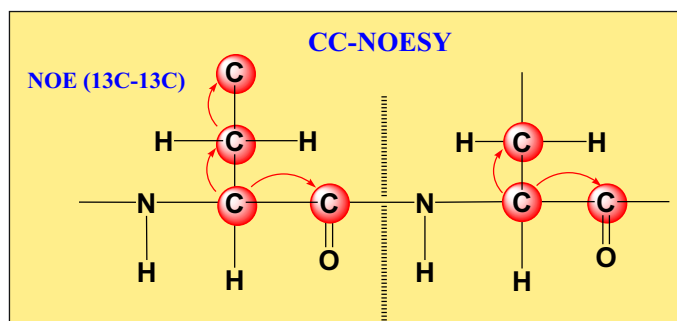
2D ^{13}C - ^{13}C NOESY Experiment

Experiment Description

The 2D CC NOESY experiment allows to obtain a homonuclear CC correlation map to trace out through-space carbon-carbon interactions in ^{13}C -labeled proteins

Related Experiments

2D CC COSY and 2D CC TOCSY



d8=NOE mixing time
d27=1/2J(CACB)=13.3ms

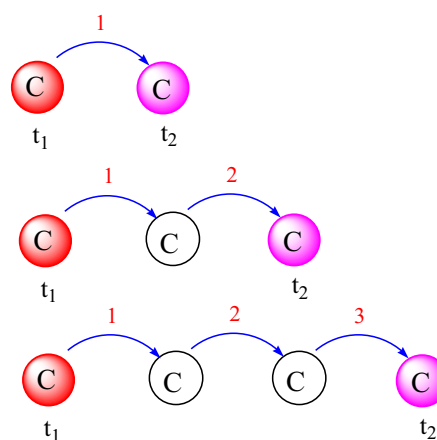
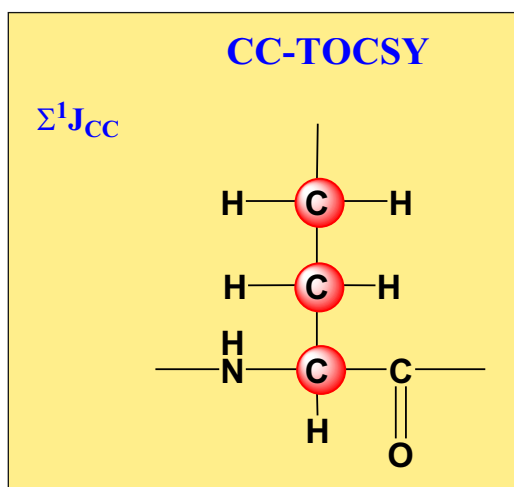
References:

1. W. Bermel, I. Bertini, I.C. Felli, R. Kuemmerle & R. Pierattelli, J. Am. Chem. Soc. 125, 16423-16429 (2003)
2. I. Bertini, I.C. Felli, R. Kuemmerle, D. Moskau & R. Pierattelli, J. Am. Chem. Soc. 126, 464-465 (2004)

2D ^{13}C - ^{13}C TOCSY Experiment

Experiment Description

The 2D CC TOCSY experiment is a ^{13}C -start, ^{13}C -detected TOCSY scheme that allows to trace out through-bond CC connectivities via $1J(\text{CC})$ in ^{13}C -labeled proteins. Homonuclear CC splitting in the acquisition dimension can be removed by selective homonuclear decoupling during acquisition or virtually using the DIPAP approach (05JMR404).



NMR Spectrum

The experiment provides a 2D correlation map in which each cross-peak displays a doublet in the acquisition dimension due to $1J(\text{CC})$ coupling.

References:

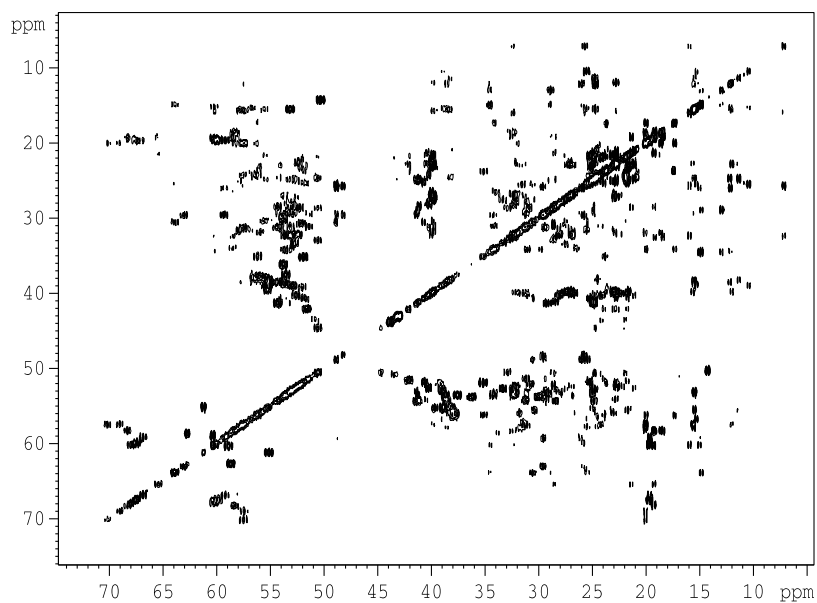
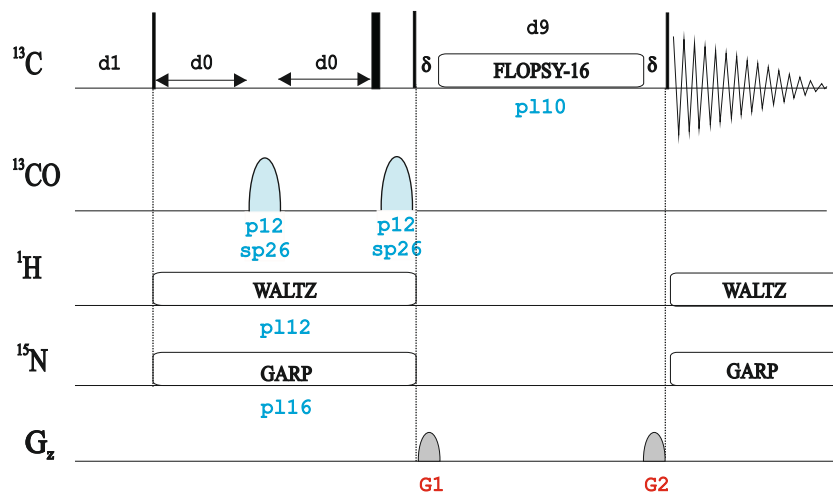
1. A. Eletsky, O. Moreira, H. Kovacs & K. Pervushin, J. Biomol. NMR 26, 167-179 (2003)
2. W. Bermel, I. Bertini, L. Duma, I. C. Felli, L. Emsley, R. Pierattelli, P. R. Vasos, Angew. Chem. Int. Ed. 44, 3089-3092 (2005)
3. L. Duma, S. Hediger, A. Lesage & L. Emsley, J. Magn. Reson. 164, 187-195 (2003)

Related Experiments

2D CC COSY and 2D CC NOESY
3D carbon-detected HCC TOCSY

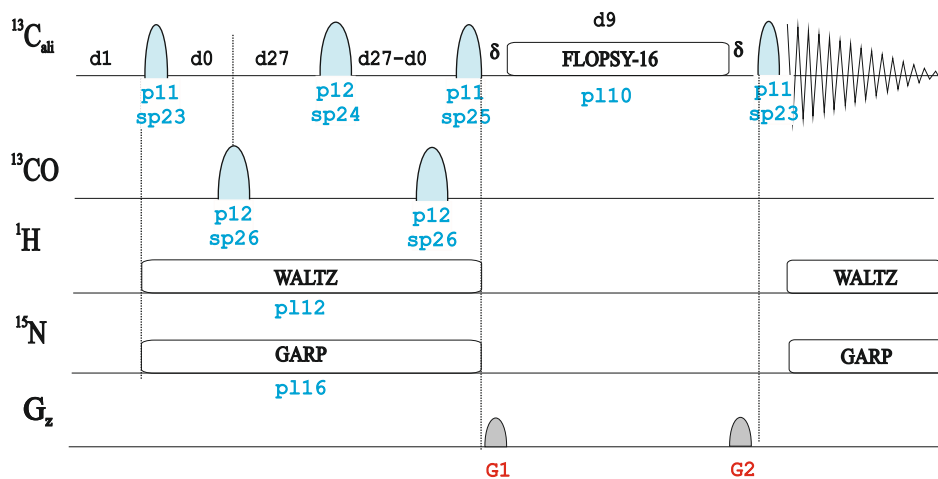
3D HCCH-type experiments

c_ccflopsy16

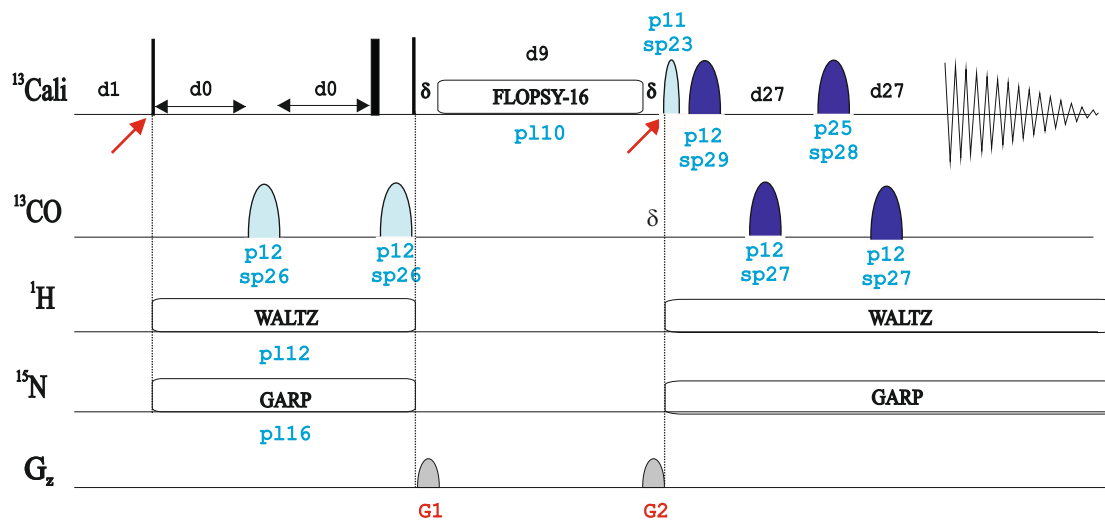


$d9$ =TOCSY mixing time
 $d27=1/2J(\text{CACB})=13.3\text{ms}$
 or $=1/8J(\text{CACB})=3.6\text{ms}$ (DIPAP)
 $d22=1/4J(\text{COCA})=4.5\text{ms}$
 $d23=1/2J(\text{CACB})=13.3\text{ms}$ (DIPAP)

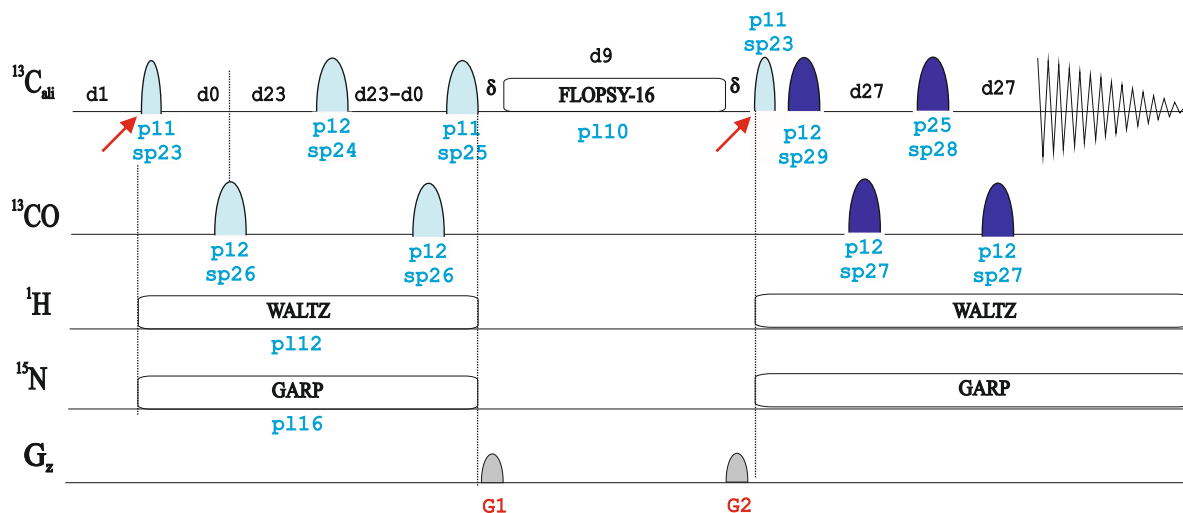
c_ccflopsy16_ct



c_ccflopsy16_ia



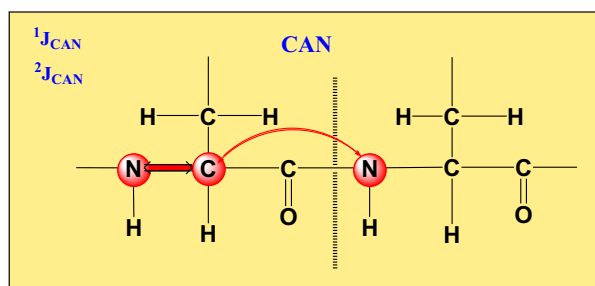
c_ccflopsy16_ctia



2D CAN Experiment

Experiment Description

The 2D CAN experiment is a CA-detected experiment that allows the correlation between the chemical shifts of the CA(i) carbon with the Nitrogen of the same (i) and the next (i+1) residue in doubly-labeled $^{13}\text{C}/^{15}\text{N}$ proteins. Homonuclear CO-CA splitting in the acquisition dimension can be removed by homonuclear decoupling during acquisition or virtually using the IPAP approach (05JMR404).



NMR Spectrum

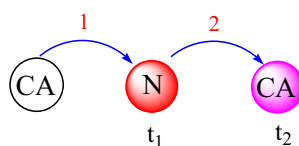
The experiment provides a 2D correlation map in which each CA in the acquisition dimension is correlated to two different N chemical shifts.

Related Experiments

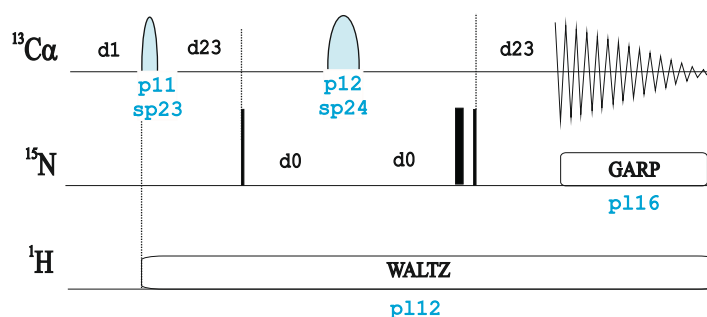
3D HCAN

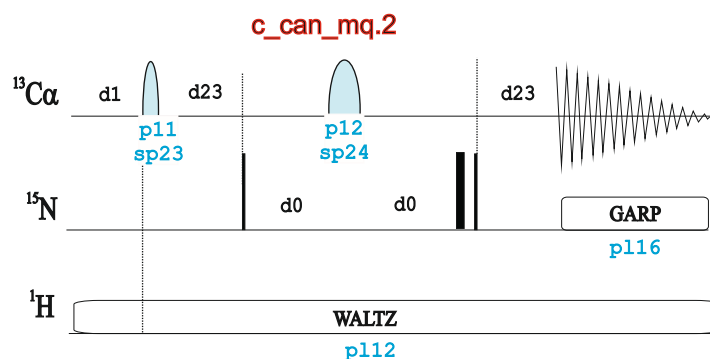
References:

W. Bermel, I. Bertini, L. Duma, I.C. Felli, L. Emsley, R. Pierattelli, P.R. Vasos, *Angew. Chem. Int. Ed* 44, 3089-3092 (2005)

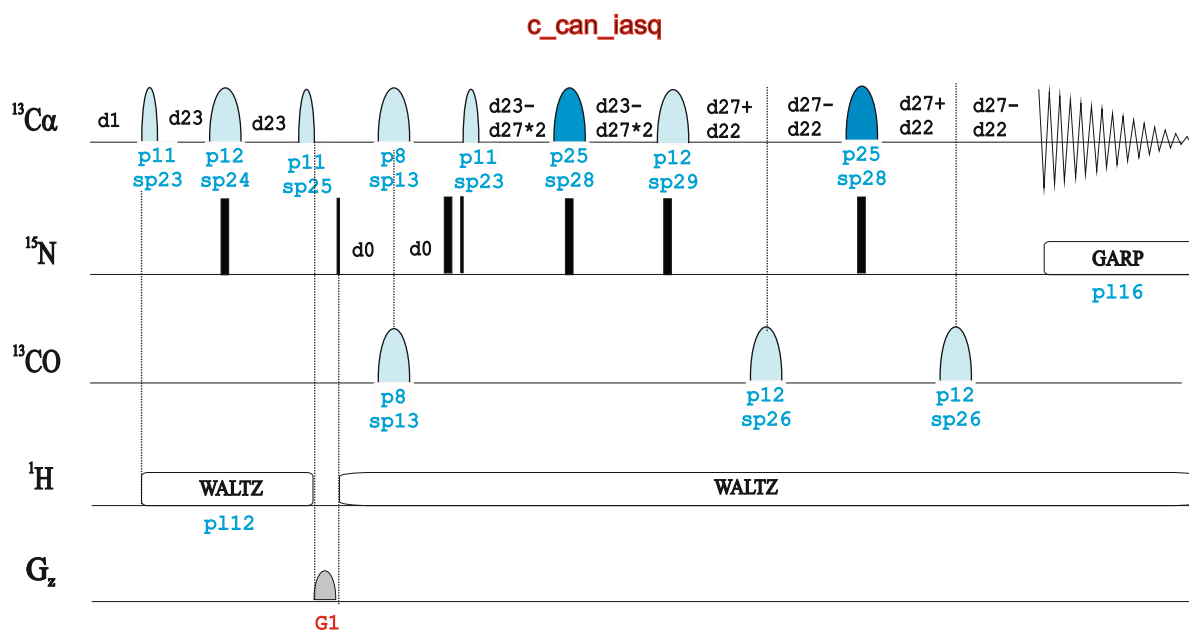


c_can_mq





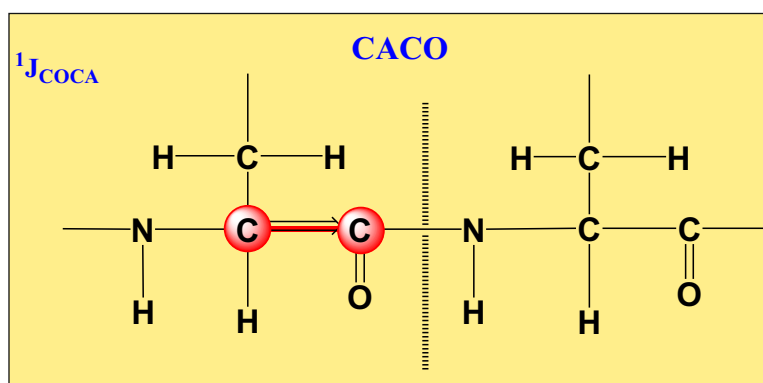
$d27 = 1/8J(CACB) = 3.6\text{ms}$
 $d22 = 1/4J(COCA) = 4.5\text{ms}$
 $d23 = 1/2J(CAN) = 25\text{ms}$ (in mq experiments)
 or $= 1/4J(CAN) = 12.4\text{ms}$ (in sq experiments)



2D CACO Experiment

Experiment Description

The 2D CACO experiment is a CO-detected that allows the correlation between the chemical shifts of the CA and CO carbons of the same residue in ^{13}C -labeled proteins. Homonuclear CO-CA splitting in the acquisition dimension can be removed by homonuclear decoupling during acquisition or virtually using the IPAP approach (05JMR404).



The CACO experiment can be driven in a out-and-stay way (c_caco) or using a out-and-back transfer (c_coca_mq).

NMR Spectrum

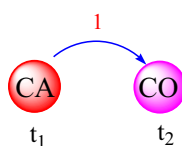
The experiment provides a 2D correlation map in which each cross-peak displays a doublet in the acquisition dimension due to $1J(\text{CACO})$ coupling

References:

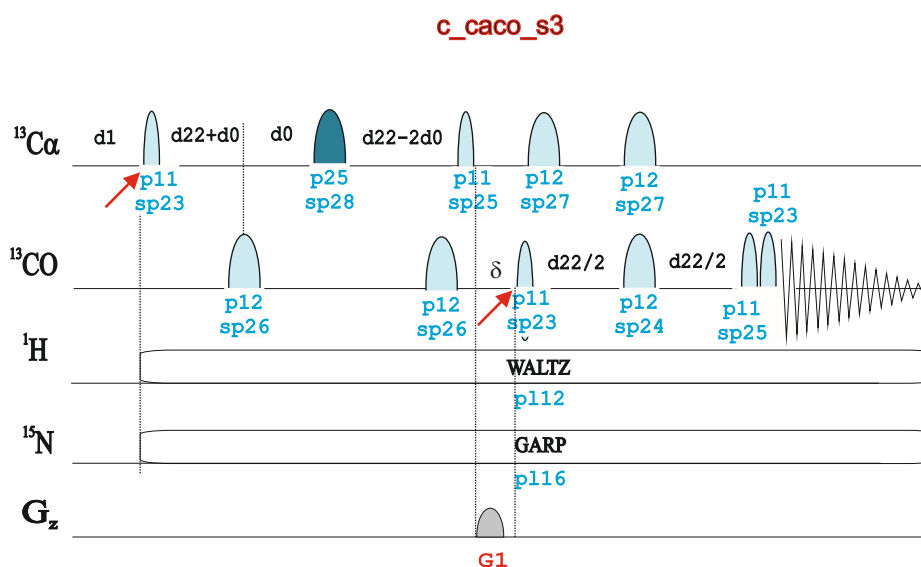
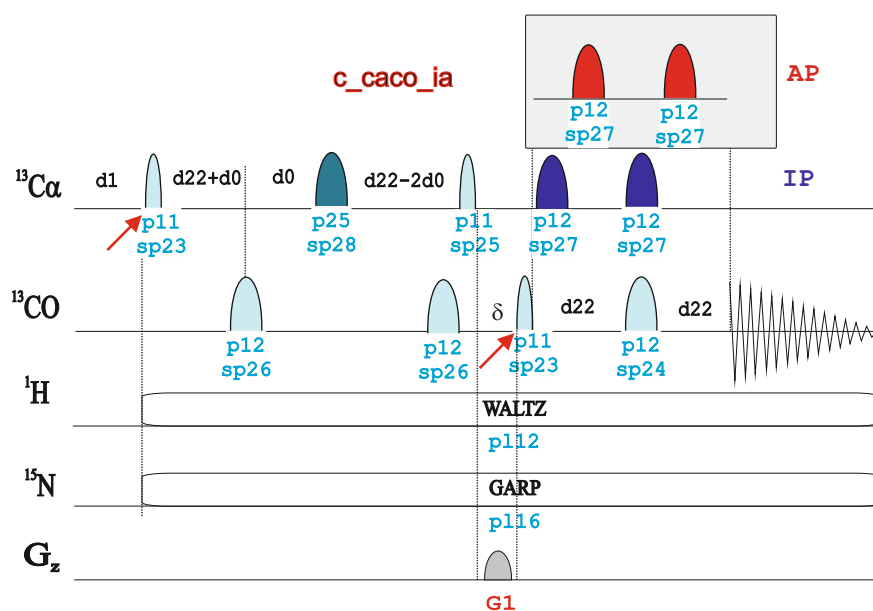
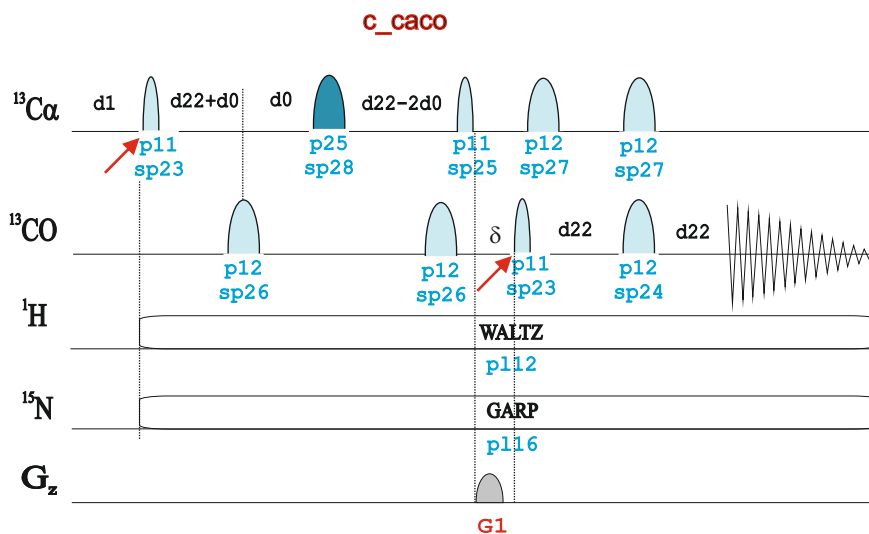
W. Bermel, I. Bertini, L. Duma, I.C. Felli, L. Emsley, R. Pierattelli, P.R. Vasos, Angew. Chem. Int. Ed. 44, 3089-3092 (2005)

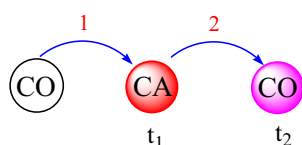
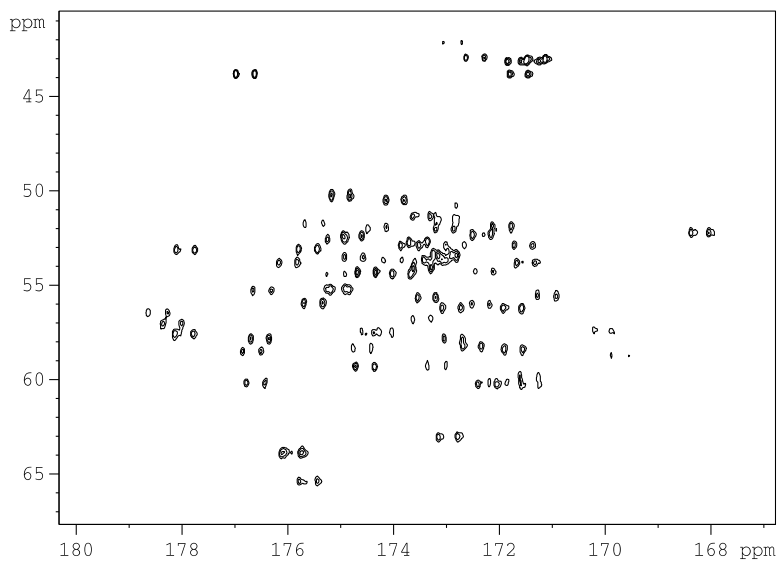
Related Experiments

2D COCA
3D HCACO



$$d_{22} = 1/4J(\text{COCA}) = 4.5\text{ms}$$

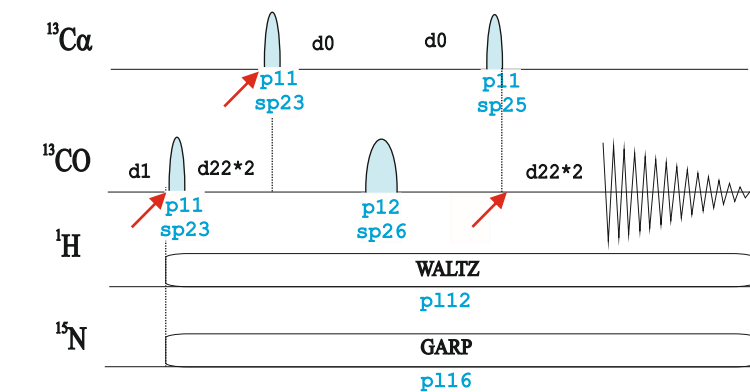




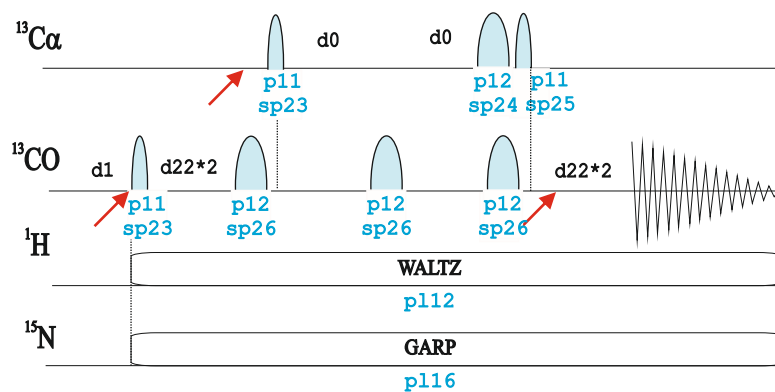
References:

1. M. Kostic, S.S. Pochapsky & T.C. Pochapsky, J. Am. Chem. Soc. 124, 9054-9055 (2002)
2. W. Bermel, I. Bertini, I.C. Felli, R. Kuemmerle & R. Pierattelli, J. Am. Chem. Soc. 125, 16423-16429 (2003)

c_coca_mq



c_coca_mq.2



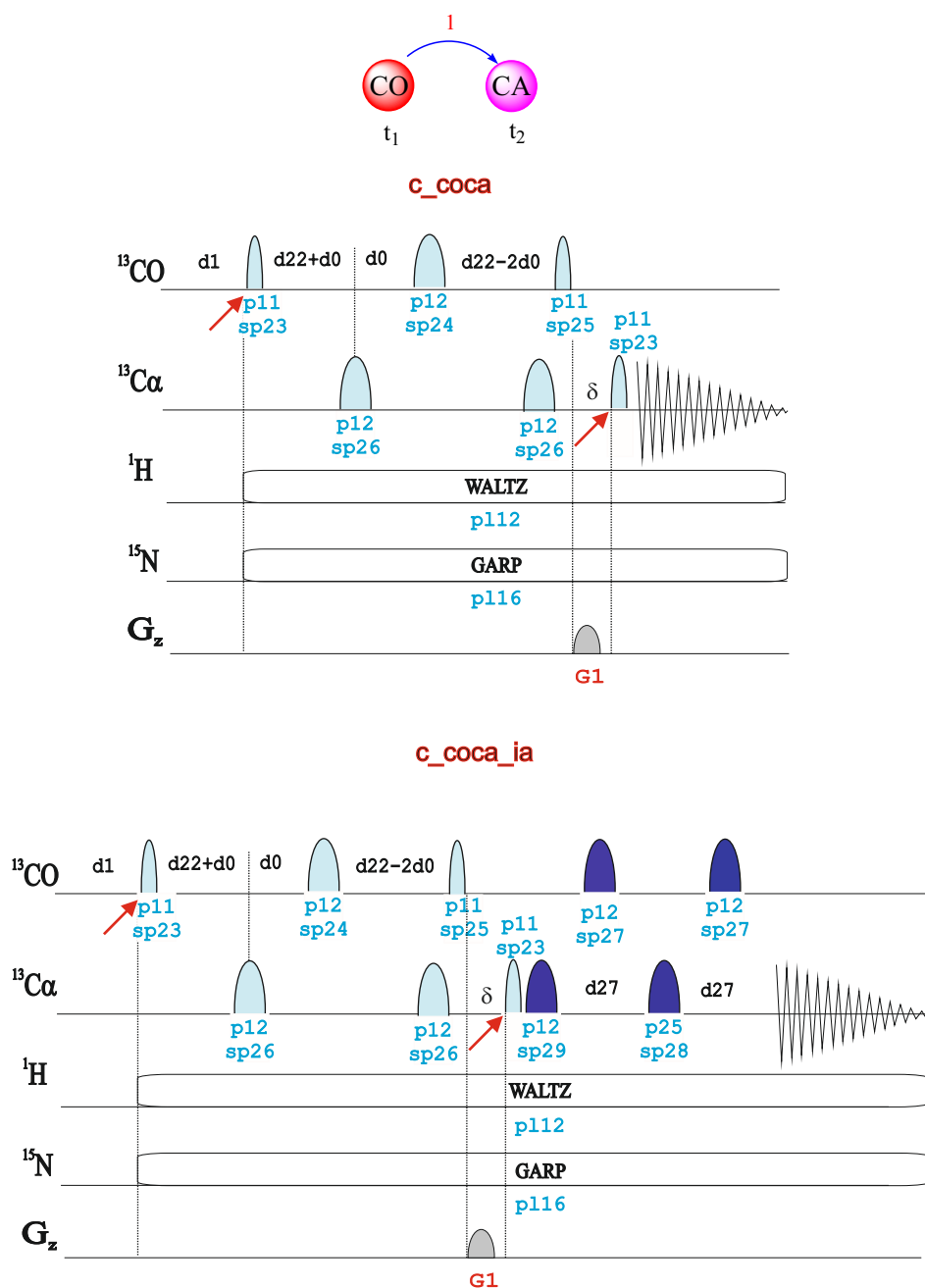
2D COCA Experiment

Experiment Description

The 2D COCA experiment is the equivalent CA-detected experiment of the CO-detected CACO experiment

References:

W. Bermel, I. Bertini, L. Duma, I.C. Felli, L. Emsley, R. Pierattelli, P.R. Vasos, Angew. Chem. Int. Ed. 44, 3089-3092 (2005)



$$d27 = 1/8J(CACB) = 3.6\text{ms}$$

$$d22 = 1/4J(COCA) = 4.5\text{ms}$$

2D CON Experiment

Experiment Description

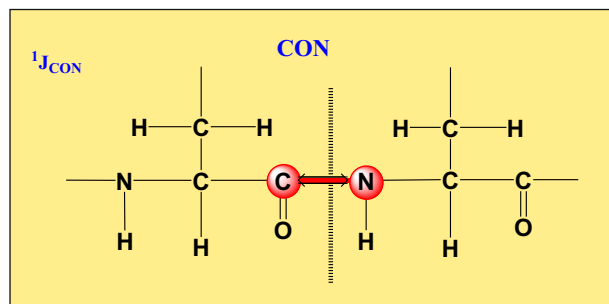
The 2D CON experiment is a CO-detected experiment that allows the correlation between the chemical shifts of the carbonyl CO carbo and the amide N of the next residue in doubly $^{13}\text{C}/^{15}\text{N}$ -labeled proteins. Homonuclear CO-CA splitting (55Hz) in the acquisition dimension can be removed by homonuclear decoupling during acquisition or virtually using the IPAP approach.

Related Experiments

3D HNCO

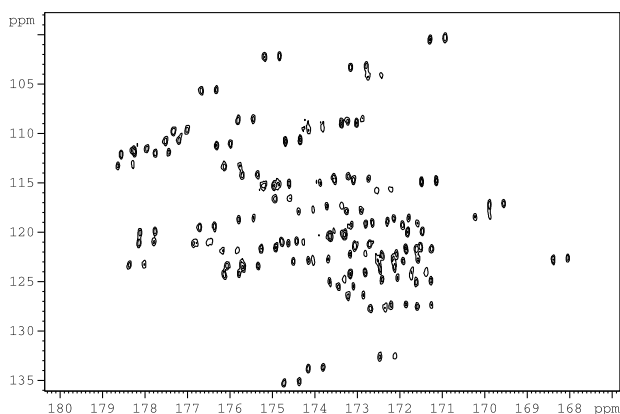
NMR Spectrum

The experiment provides a 2D correlation map in which each cross-peak corresponds to the CO-N bond connectivity

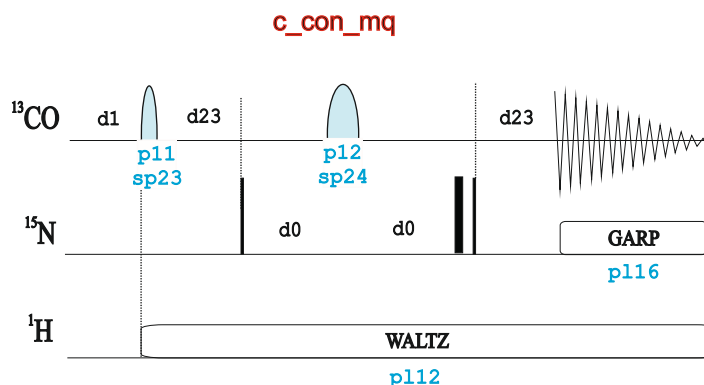
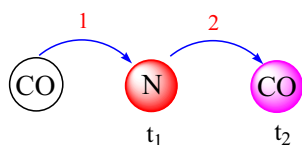


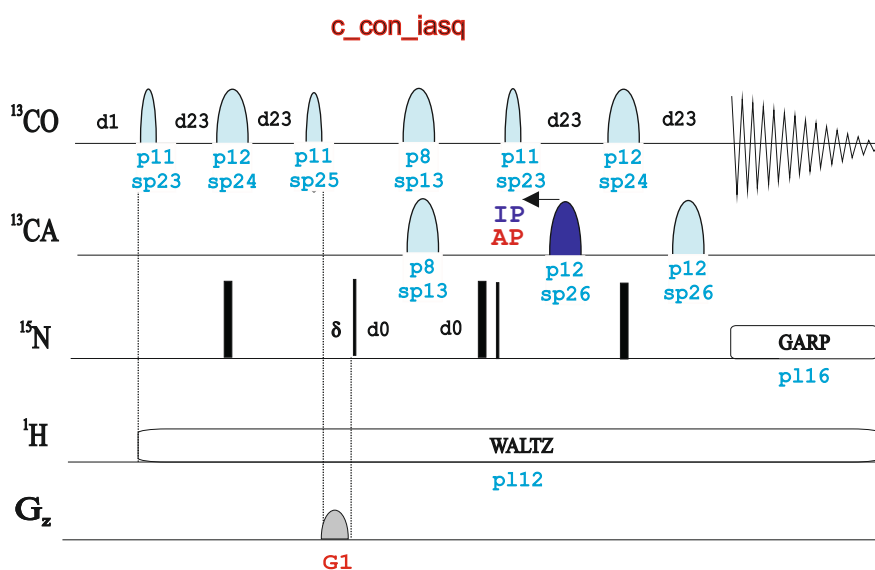
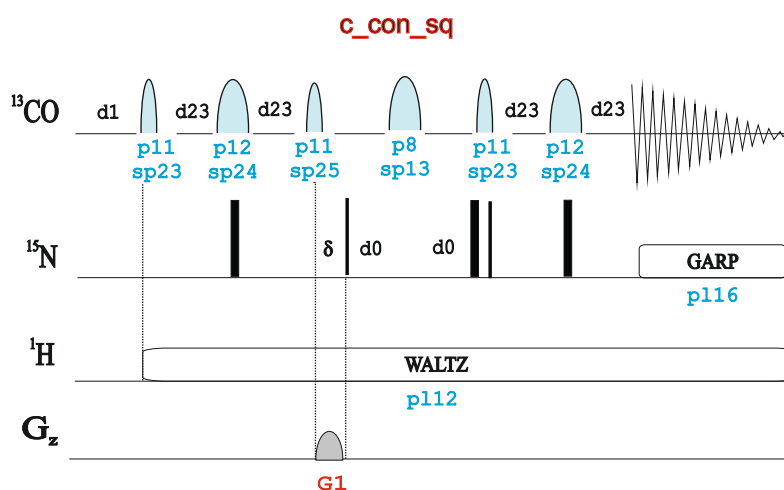
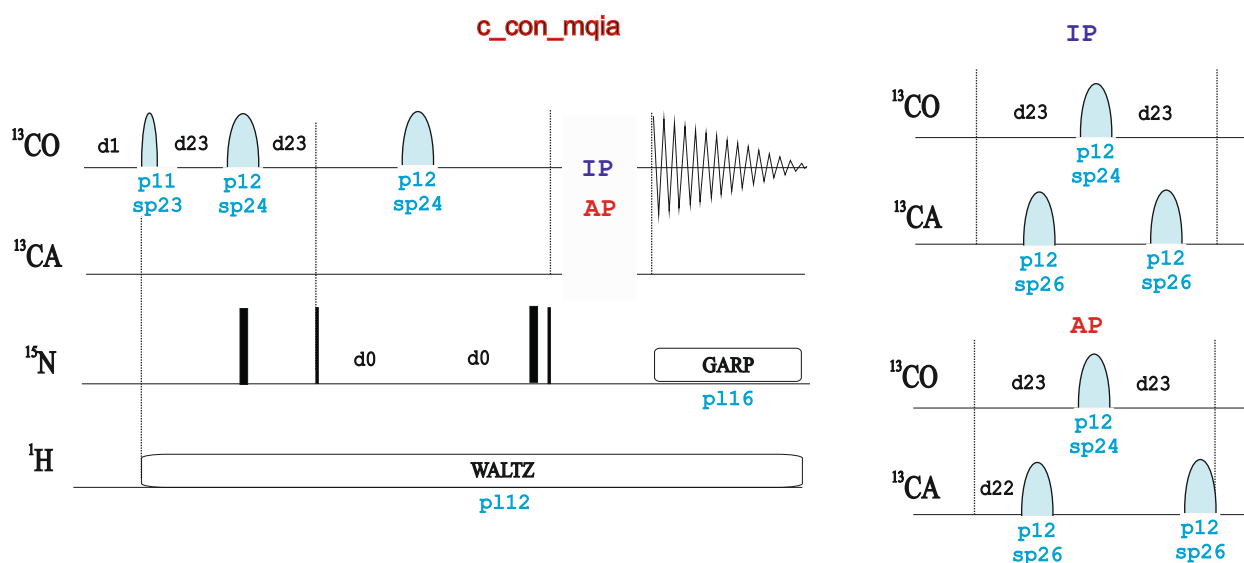
References:

1. M. Kostic, S.S. Pochapsky & T.C. Pochapsky, J. Am. Chem. Soc. 124, 9054-9055 (2002)
2. W. Bermel, I. Bertini, L. Duma, I.C. Felli, L. Emsley, R. Pierattelli, P.R. Vasos, Angew. Chem. Int. Ed. 44, 3089-3092 (2005))



$d23 = 1/2J(\text{NCO}) = 25\text{ms}$ (in mq experiments)
or $= 1/4J(\text{NCO}) = 12.5\text{ms}$ (in sq experiments)
 $d22 = 1/4J(\text{COCA}) = 4.5\text{ms}$

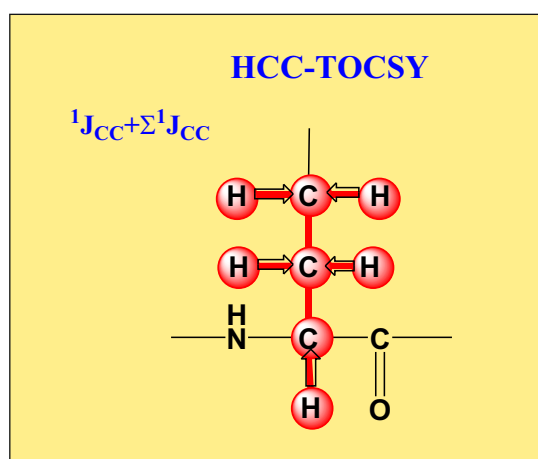




3D HCC-TOCSY Experiment

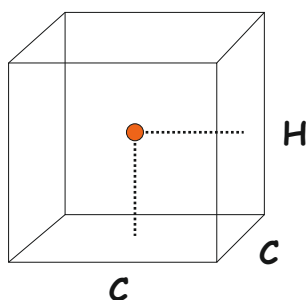
Experiment Description

The 3D HCC-TOCSY experiment is a C-detected experiment that allows the correlation between all sidechain ^1H and aliphatic ^{13}C of the same residues in ^{13}C -labeled proteins.



NMR Spectrum

The experiment provides a 3D correlation map in which each cross-peak correspond to a HC-C connectivity.

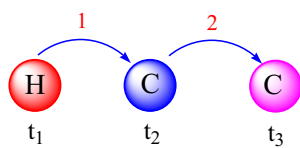


References:

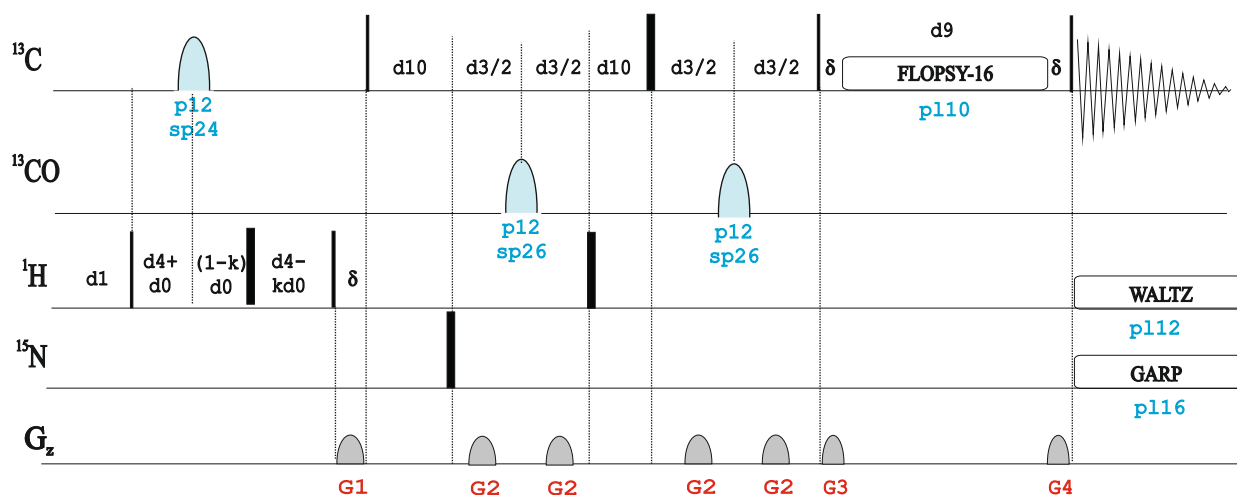
Z. Serber, C. Richter & V. Doetsch, ChemBioChem. 2, 247-251 (2001)

Related Experiments

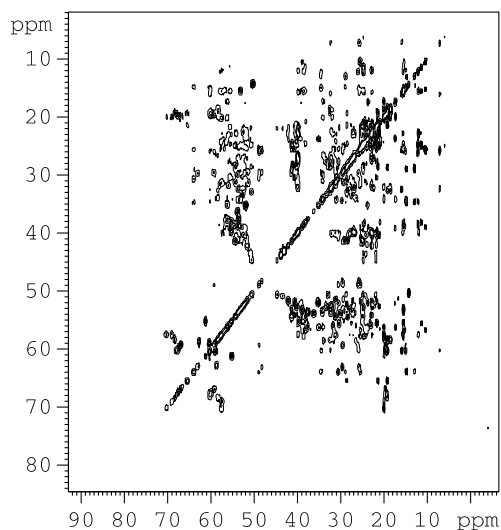
2D CC COSY and CC-TOCSY experiment



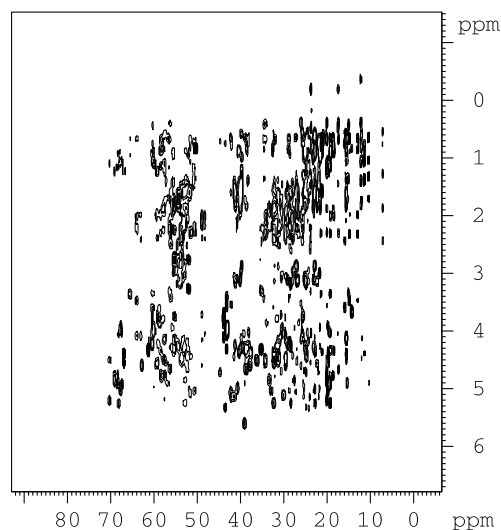
c_hccflopsy16_3d



2D (H)CC



2D H(C)C

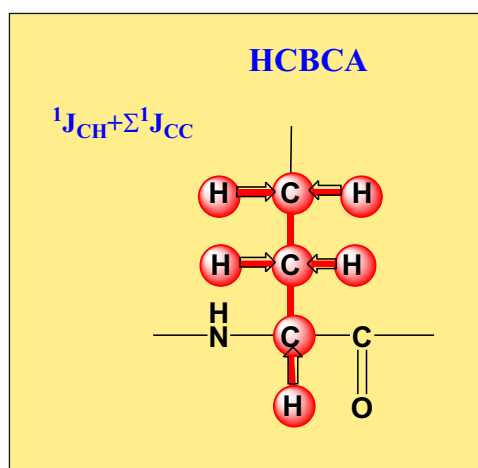


d9 is the TOCSY mixing time
 $d3 = 1/6J(\text{CH}) = 0.95\text{ms}$
 $d4 = 1/4J(\text{CH}) = 1.8\text{ms}$

3D HCBCA Experiment

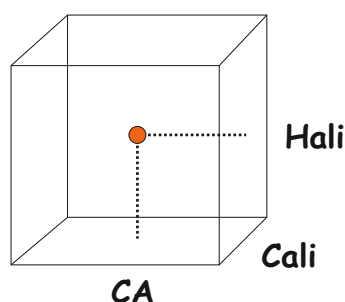
Experiment Description

The 3D HCBCA experiment is a carbon-detected experiment that allows to obtain the sidechain H, CB and CA connectivities in ^{13}C -labeled proteins. Homonuclear CO-CA splitting in the acquisition dimension can be removed by homonuclear decoupling during acquisition or virtually using the IPAP approach (05JMR404).



NMR Spectrum

The experiment provides a 3D correlation map in which each cross-peak displays a doublet in the acquisition dimension due to $1J(\text{CACO})$ coupling

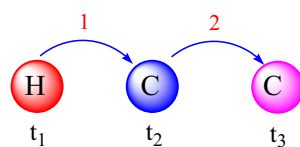


References:

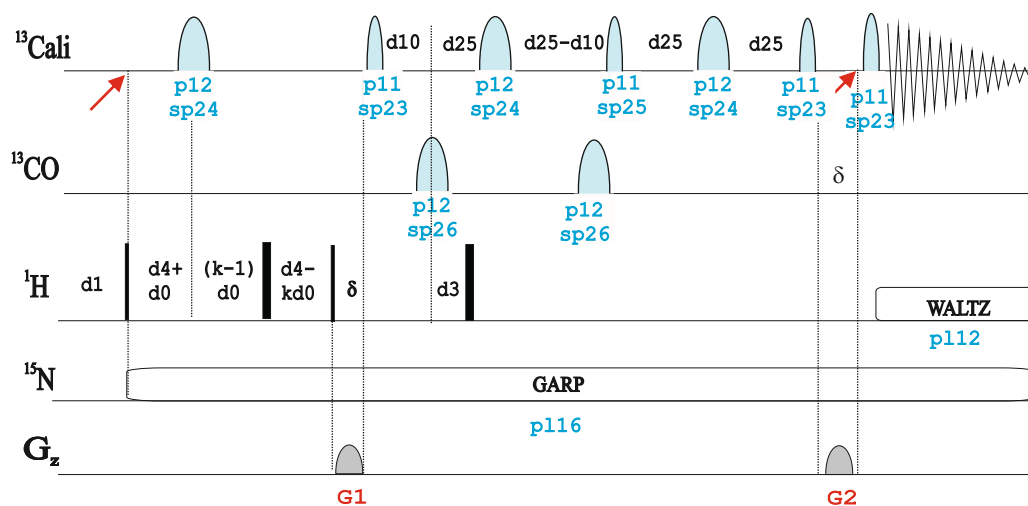
1. W. Bermel, I. Bertini, L. Duma, I.C. Felli, L. Emsley, R. Pierattelli, P.R. Vasos, *Angew. Chem. Int. Ed.* 44, 3089-3092 (2005)
2. L. Duma, S. Hediger, A. Lesage & L. Emsley, *J. Magn. Reson.* 164, 187-195 (2003)

Related Experiments

2D CC TOCSY
3D HCC TOCSY

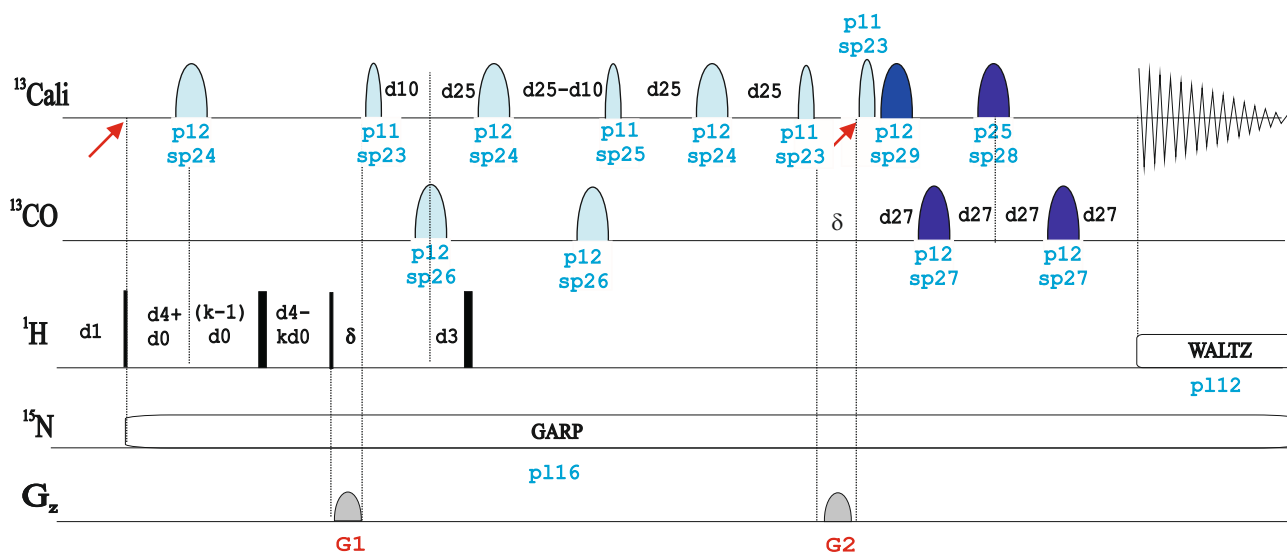


c_hcbca_3d



$d25 = 1/8J(CACB) = 4.0\text{ms}$
 $d22 = 1/4J(COCA) = 4.5\text{ms}$
 $d27 = 1/4J(CACB) = 7.2\text{ms}$
 $d3 = 1/6J(CHA) = 1.1\text{ms}$
 $d4 = 1/4J(CHA) = 1.8\text{ms}$

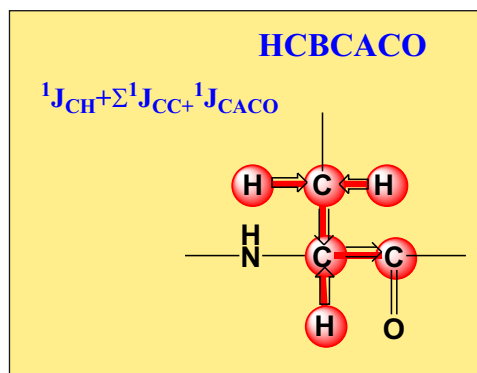
c_hcbca_ia3d



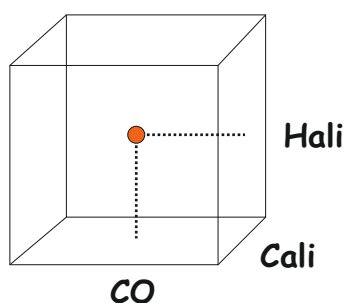
3D HCBCACO Experiment

Experiment Description

The 3D HCBCACO experiment is a CO-detected that allows the correlation between the chemical shifts of the sidechain protons and the CB, CA and CO carbons of the same residue in ^{13}C -labeled proteins. Homonuclear CO-CA splitting in the acquisition dimension can be removed by homonuclear decoupling during acquisition or virtually using the IPAP approach.



NMR Spectrum



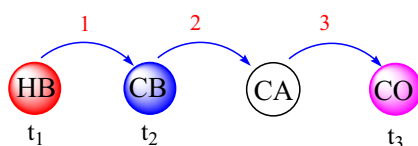
References:

W. Bermel, I. Bertini, L. Duma, I.C. Felli, L. Emsley, R. Pierattelli, P.R. Vasos, *Angew. Chem. Int. Ed.* 44, 3089-3092 (2005)

Related Experiments

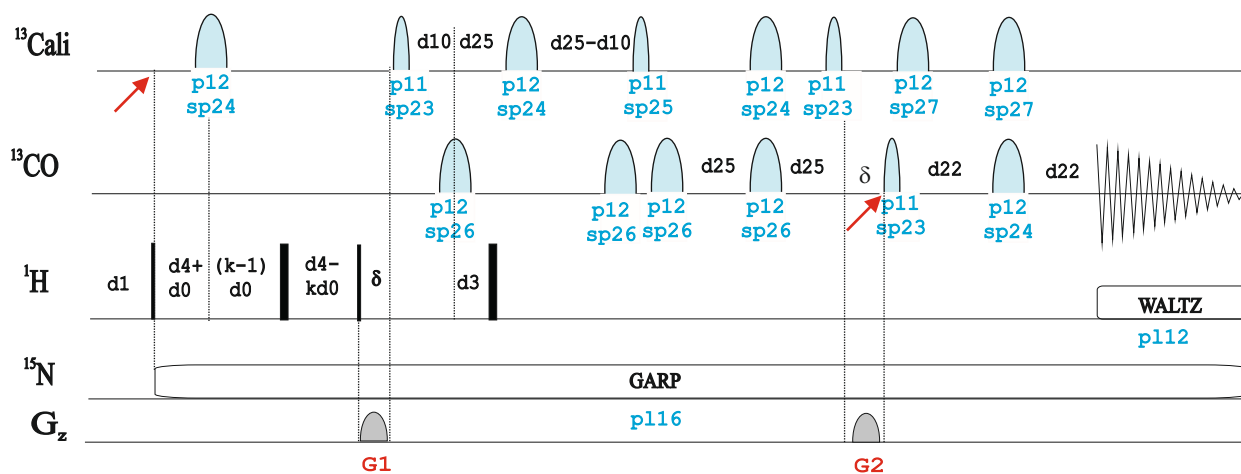
2D CC TOCSY

3D HCC TOCSY and HCBCA experiments

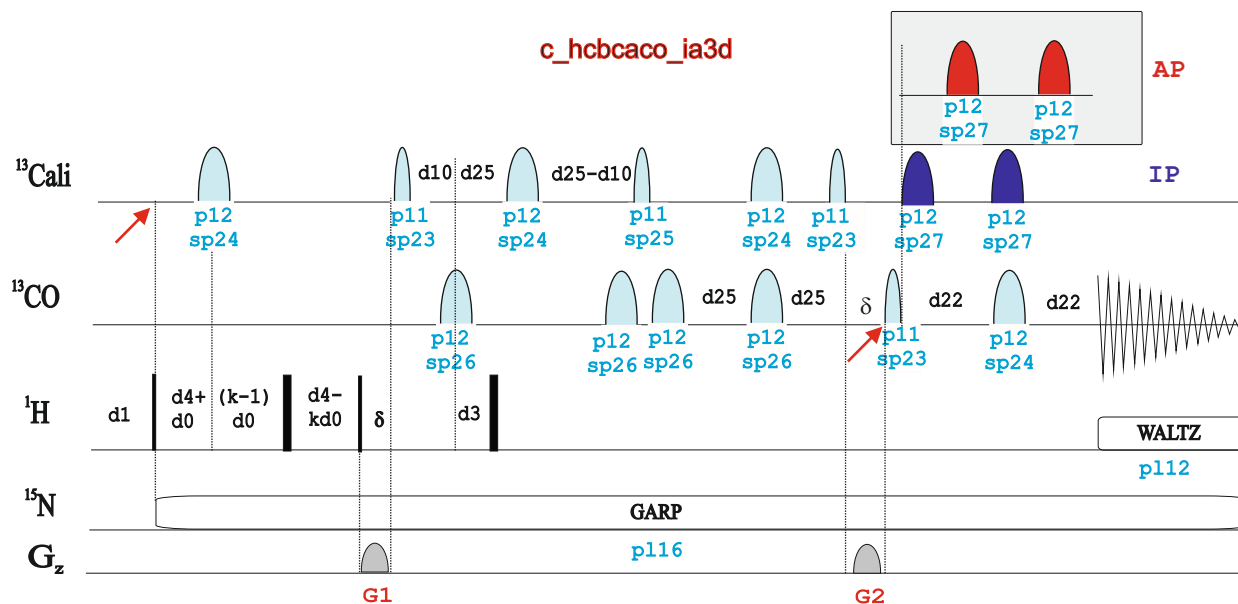


$$\begin{aligned} d25 &= 1/8J(\text{CACB}) = 4.0\text{ms} \\ d22 &= 1/4J(\text{COCA}) = 4.5\text{ms} \\ d3 &= 1/6J(\text{CHA}) = 1.1\text{ms} \\ d4 &= 1/4J(\text{CHA}) = 1.8\text{ms} \end{aligned}$$

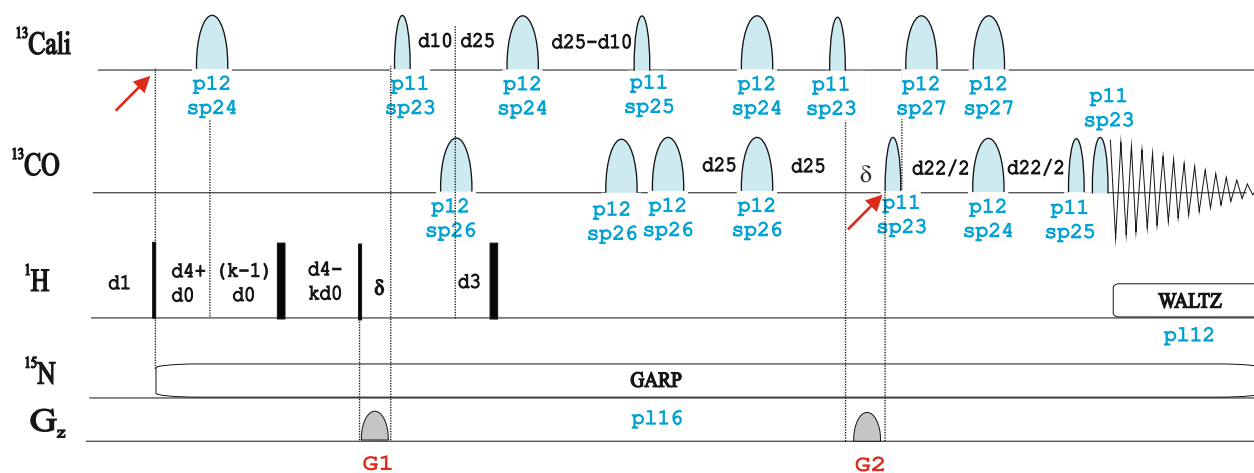
c_hcbcac0_3d



c_hcbcac0_ia3d



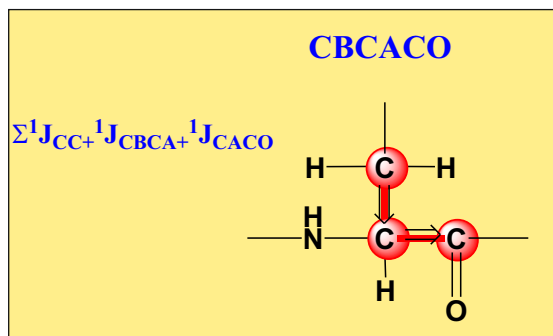
c_hcbcac0_s33d



3D CBCACO Experiment

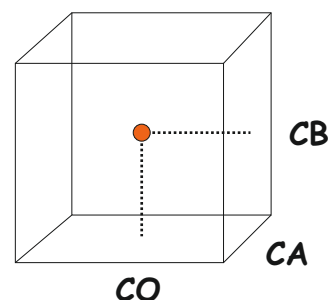
Experiment Description

The 3D CBCACO experiment is a CO-detected experiment that allows the correlation between the chemical shifts of the sidechain CB, CA and CO carbons of the same residue in ^{13}C -labeled proteins. Homonuclear CO-CA splitting in the acquisition dimension can be removed by homonuclear decoupling during acquisition or virtually using the IPAP approach (05JMR404)



NMR Spectrum

The experiment provides a 3D correlation map in which each cross-peak displays a doublet in the acquisition dimension due to $1J(\text{CACO})$ coupling

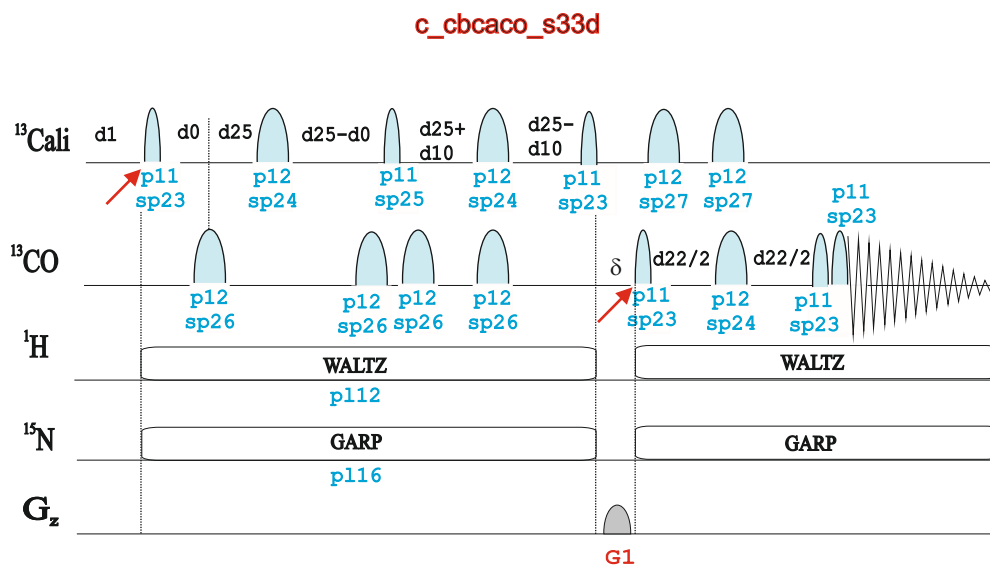


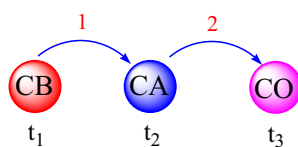
References:

W. Bermel, I. Bertini, L. Duma, I.C. Felli, L. Emsley, R. Pierattelli, & P.R. Vasos, *Angew. Chem. Int. Ed.* 44, 3089-3092 (2005)

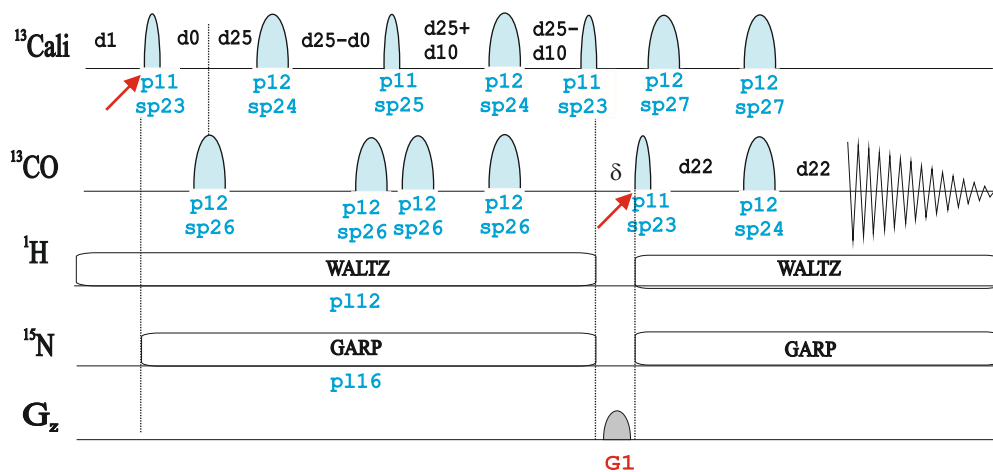
Related Experiments

2D CC COSY and TOCSY
2D CACO
3D HCAO





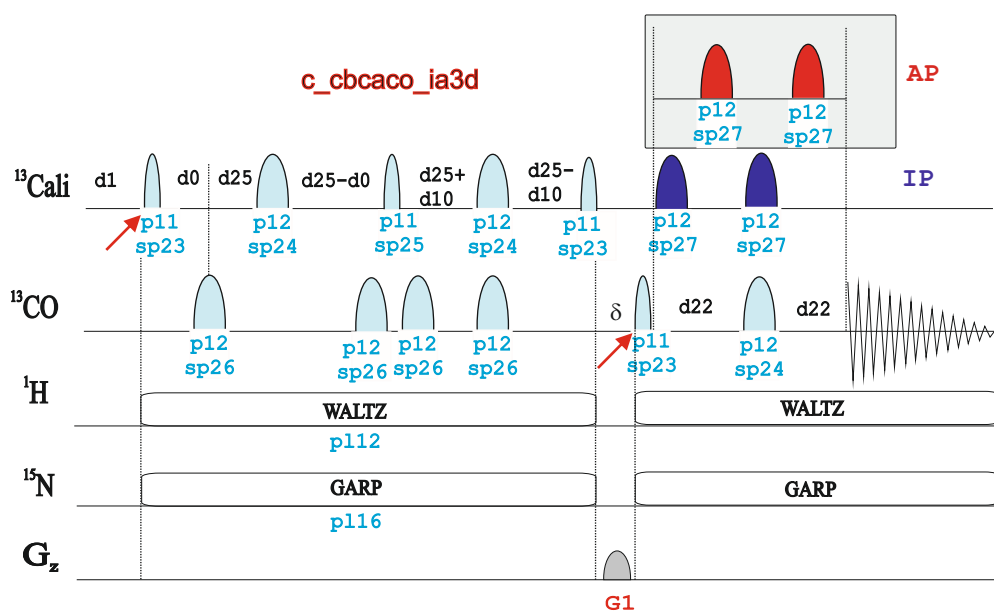
c_cbcaco_3d



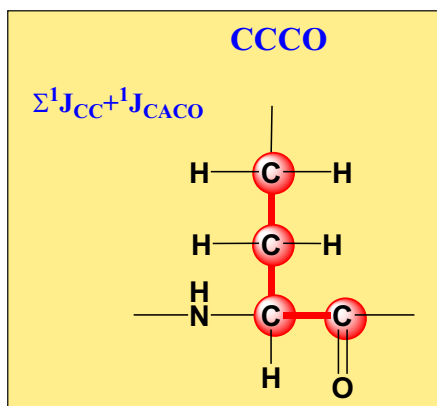
$$d22 = 1/4J(COCA) = 4.5\text{ms}$$

$$d25 = 1/8J(CACB) = 5.0\text{ms}$$

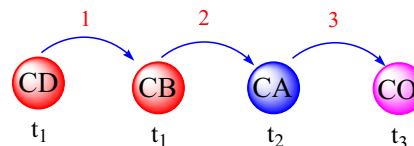
c_cbcaco_ia3d



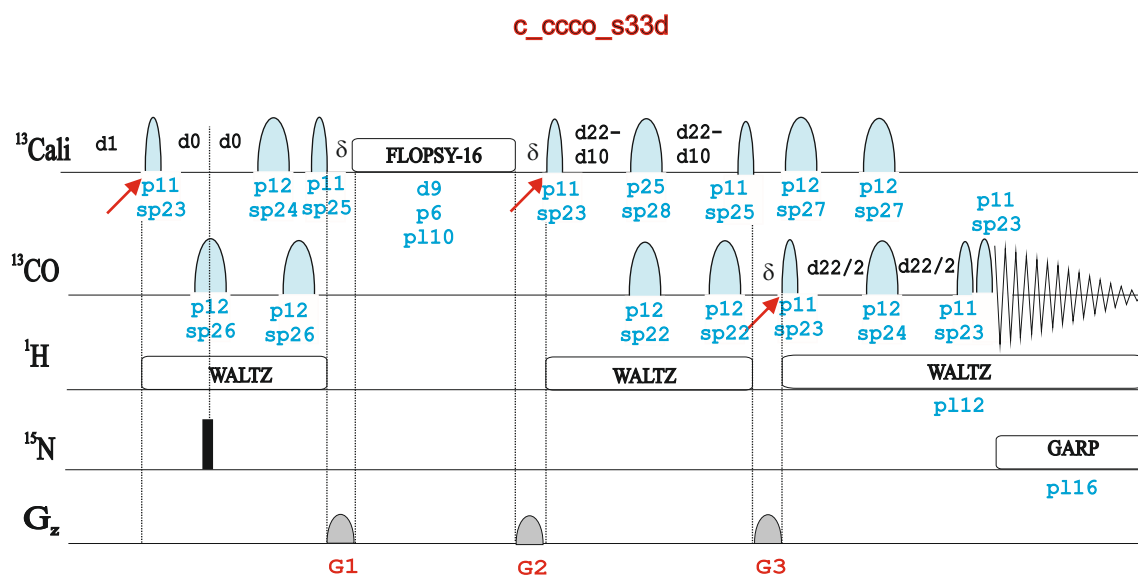
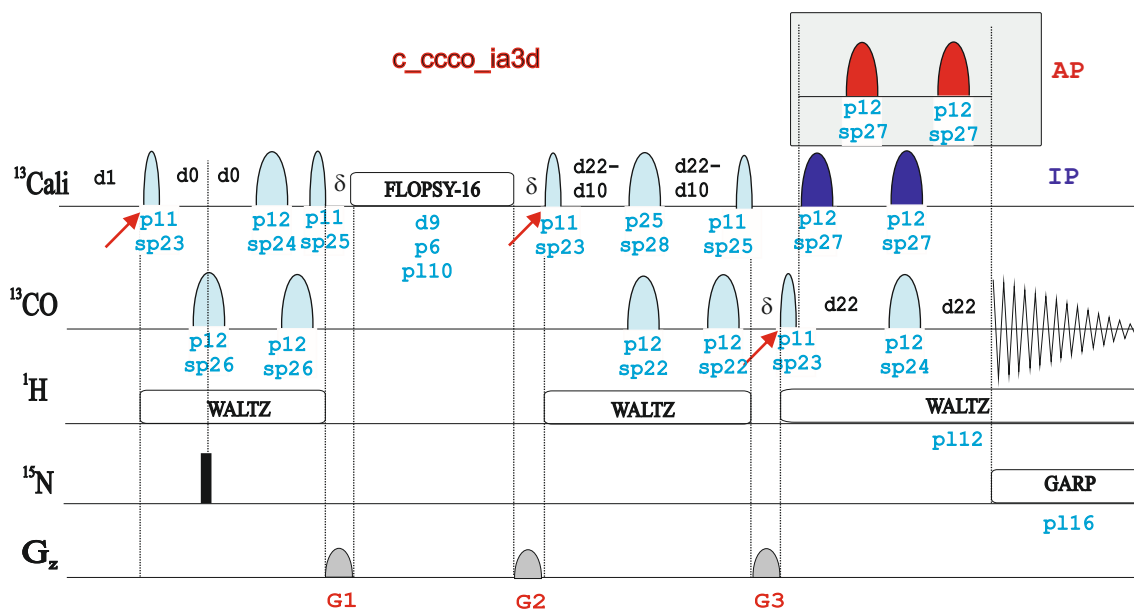
3D CCCO Experiment



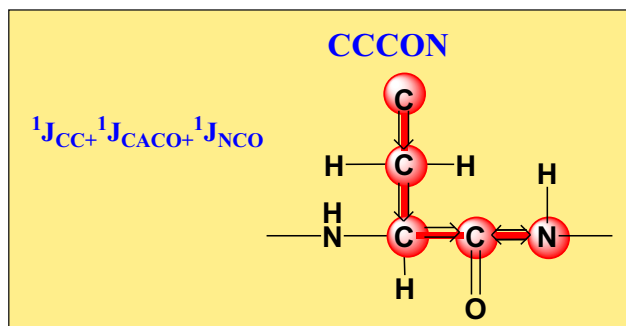
W. Bermel, I. Bertini, I.C. Felli, R. Kuemmerle
& R. Pierattelli, J. Magn. Reson. 178, 56-64 (2006)



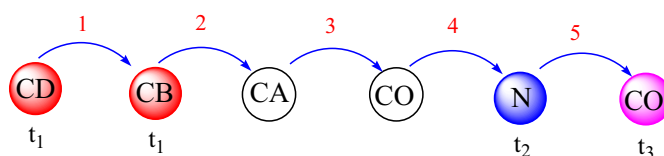
d22: $1/(4J(COCa))$ [4.5 msec]



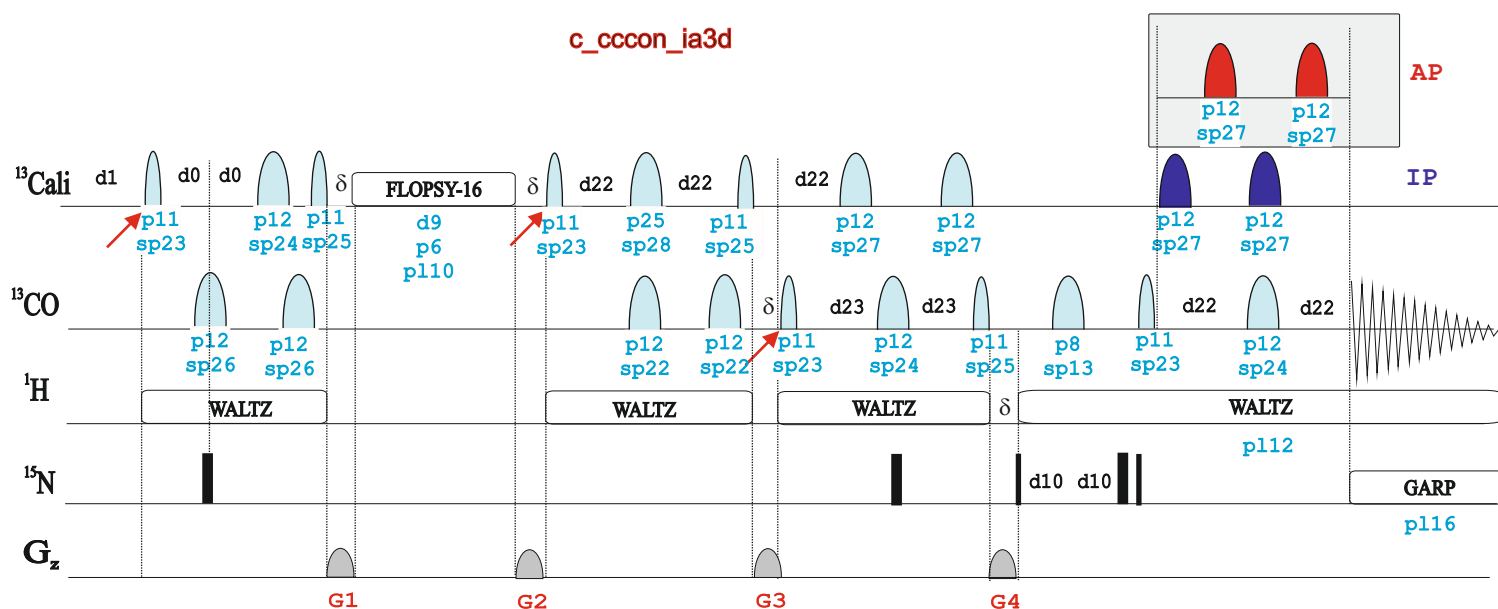
3D CCON Experiment



W. Bermel, I. Bertini, I.C. Felli, R. Kuemmerle
& R. Pierattelli, J. Magn. Reson. 178, 56-64 (2006)



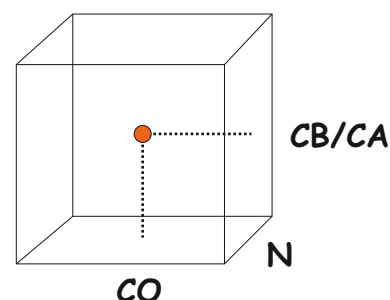
c_cccon_ia3d



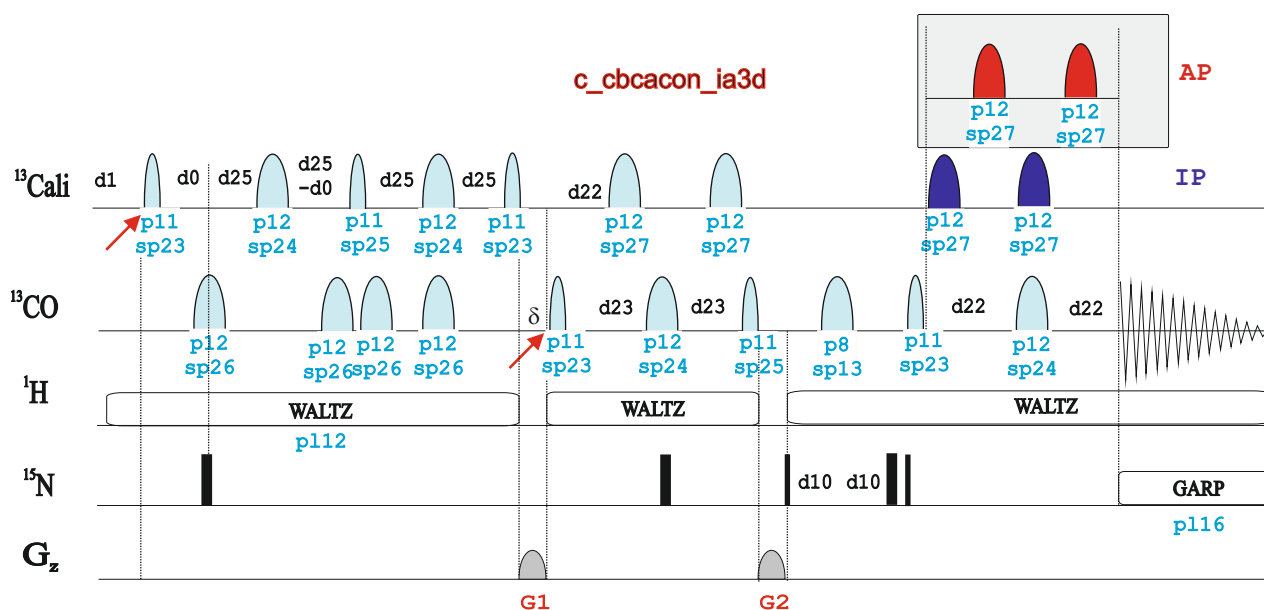
d22: $1/(4J(CO\alpha))$ [4.5 msec]
d23: $1/(4J(NCO))$ [12.5 msec]
d9 : TOCSY mixing time [12 msec]

Experiment Description

W. Bermel, I. Bertini, I.C. Felli, R. Kuemmerle & R. Pierattelli, *J. Magn. Reson.* 178, 56-64 (2006)



$d_{22} = 1/4J(COCA) = 4.5\text{ms}$
 $d_{23} = 1/4J(CON) = 12.5\text{ms}$
 $d_{25} = 1/8J(CACB) = 5.0\text{ms}$



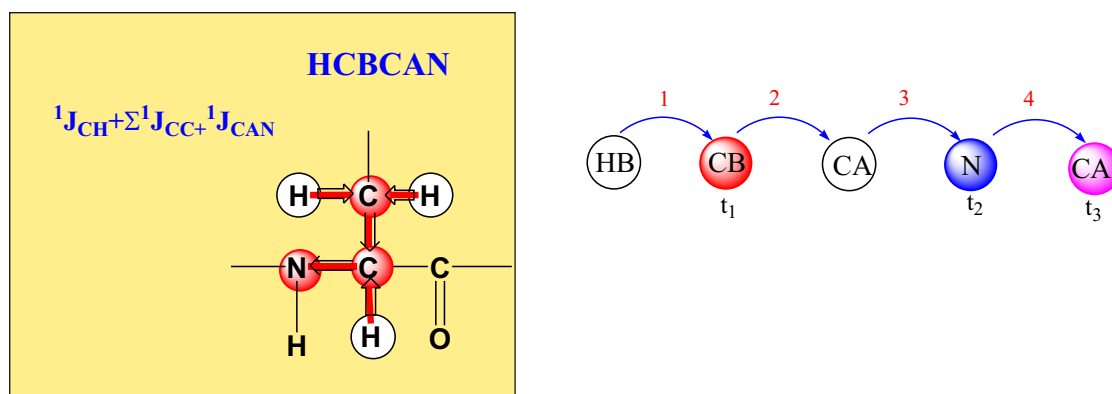
3D (H)CBCAN Experiment

Experiment Description

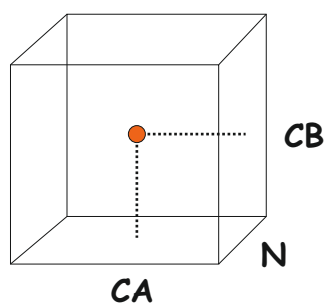
The 3D (H)CBCAN experiment is a CA-detected experiment that allows to assign intra-residue CA, CB and N chemical shifts in doubly-labeled $^{13}\text{C}/^{15}\text{N}$ proteins. Homonuclear CO-CA splitting in the acquisition dimension can be removed by homonuclear decoupling during acquisition or virtually using the IPAP approach.

References:

W. Bermel, I. Bertini, L. Duma, I.C. Felli, L. Emsley, R. Pierattelli, P.R. Vasos, *Angew. Chem. Int. Ed.* 44, 3089-3092 (2005)



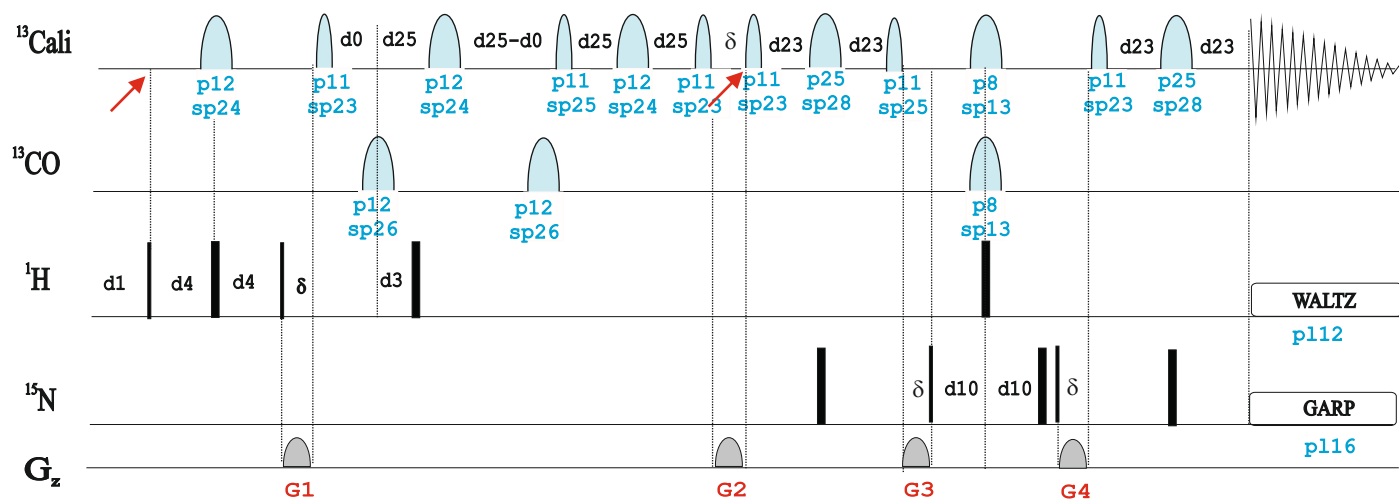
NMR Spectrum



Related Experiments

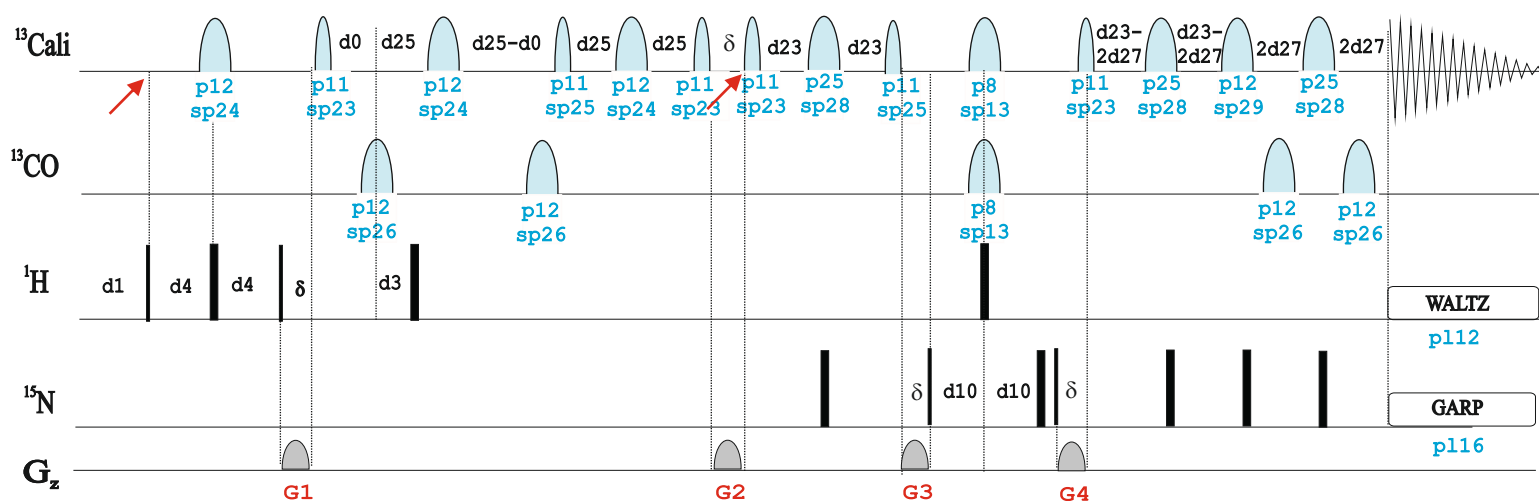
3D HCC TOCSY

c_hcbcan_3d



$d22 = 1/4J(\text{COCA}) = 4.5\text{ms}$
 $d25 = 1/8J(\text{CACB}) = 4.0\text{ms}$
 $d23 = 1/4J(\text{NCA}) = 12.4\text{ms}$
 $d27 = 1/8(\text{CACB}) = 3.6\text{ms}$
 $d3 = 1/6J(\text{CHA}) = 1.1\text{ms}$
 $d4 = 1/4J(\text{CHA}) = 1.8\text{ms}$

c_hcbcan_ia3d



3D CO-Detected HCACO Experiment

Experiment Description

The 3D HCACO experiment is a CO-detected experiment that allows the correlation between the chemical shifts of the CA and CO carbons of the same residue in ^{13}C -labeled proteins. Homonuclear CO-CA splitting in the acquisition dimension can be removed by homonuclear decoupling during acquisition or virtually using the IPAP approach (05JMR404).

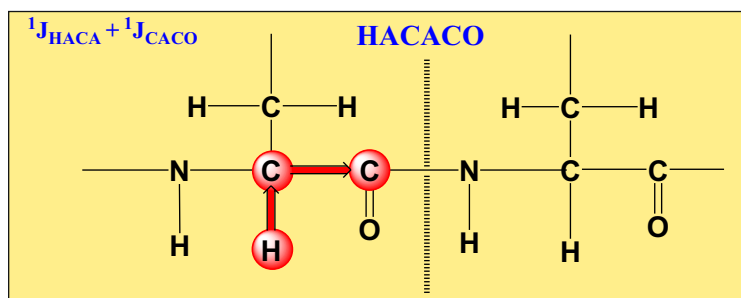
Related Experiments

2D COCA

3D HA-detected HCACO

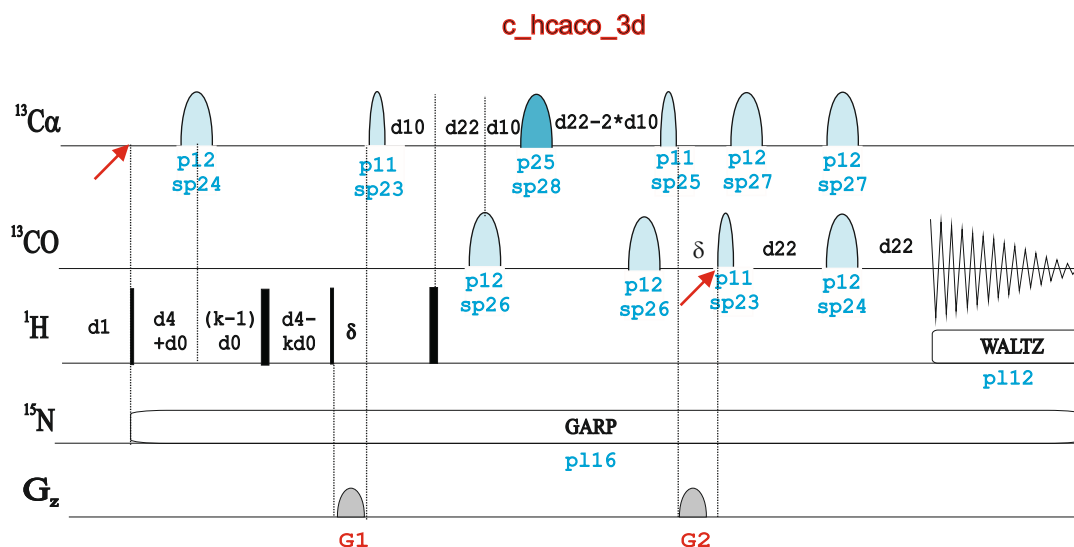
NMR Spectrum

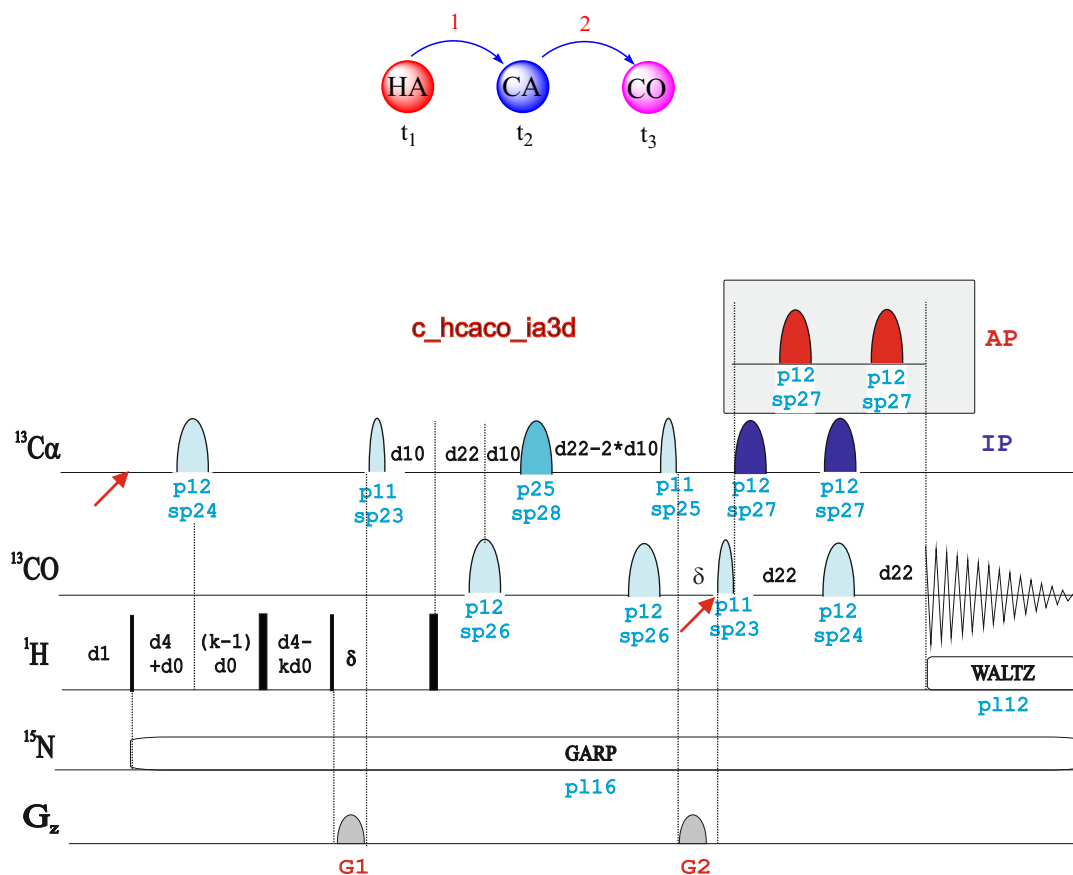
The experiment provides a 3D correlation map in which each cross-peak displays a doublet in the acquisition dimension due to $1J(\text{CACO})$ coupling.



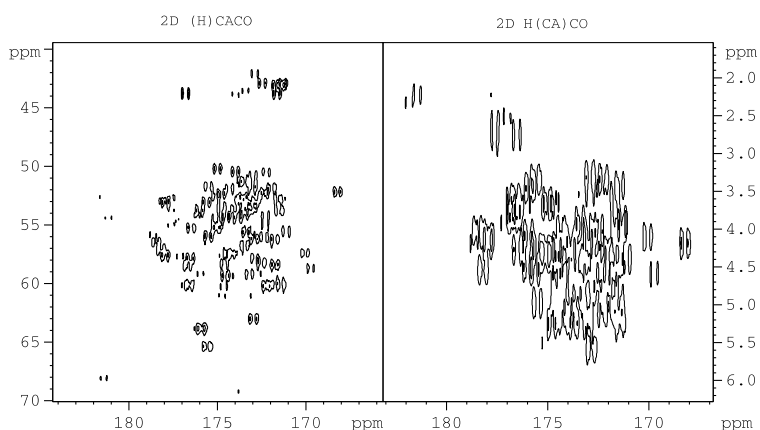
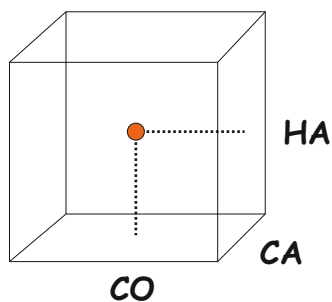
References:

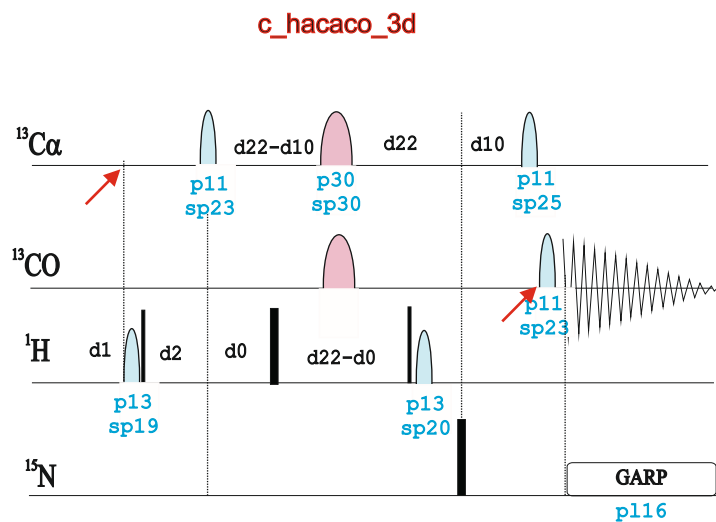
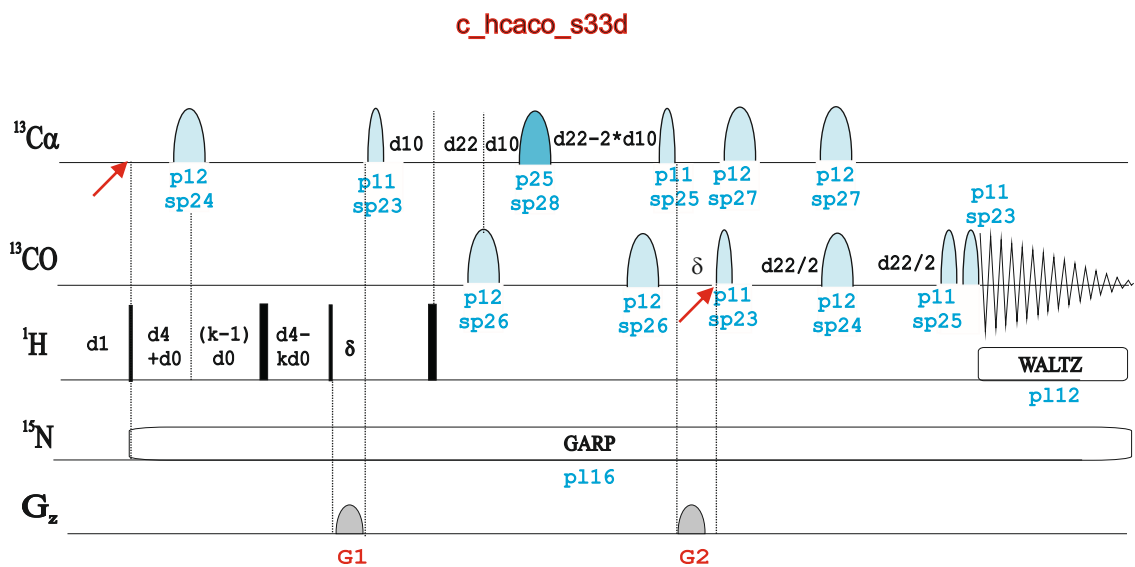
1. Z. Serber, C. Richter, D. Moskau, J.-M. Boehlen, T. Gerfin, D. Marek, M. Haeberli, L. Baslgia, F. Laukien, A.S. Stern, J.C. Hoch & V. Doetsch, J. Am. Chem. Soc. 122, 3554-3555 (2000)
2. W. Bermel, I. Bertini, L. Duma, I.C. Felli, L. Emsley, R. Pierattelli, P.R. Vasos, Angew. Chem. Int. Ed. 44, 3089-3092 (2005).
3. K. Pervushin & A. Eletsky, J. Biomol. NMR 25, 147-152 (2003)





$d22 = 1/4J(\text{COCA}) = 4.5\text{ms}$
 $d2 = 1/2J(\text{CHA}) = 3.2\text{ms}$
 $d3 = 1/6J(\text{CHA}) = 1.1\text{ms}$
 $d4 = 1/4J(\text{CHA}) = 1.8\text{ms}$

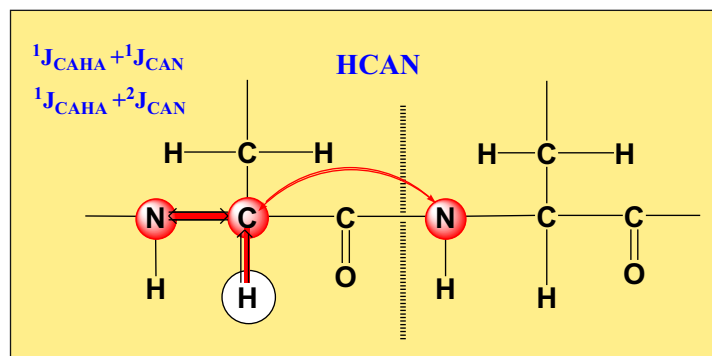




3D HCAN Experiment

Experiment Description

The 3D HCAN experiment is a CA-detected experiment that correlates the CA-HA of a given residue with the N chemical shift of the same and the next residue in doubly-labeled $^{13}\text{C}/^{15}\text{N}$ proteins.

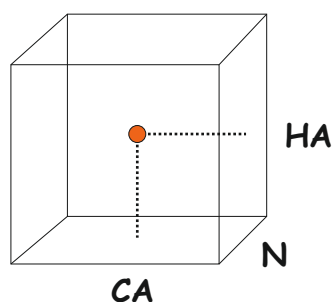


Related Experiments

2D CAN
3D HNCA

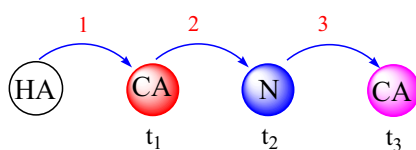
NMR Spectrum

A 3D H,N,C map is obtained

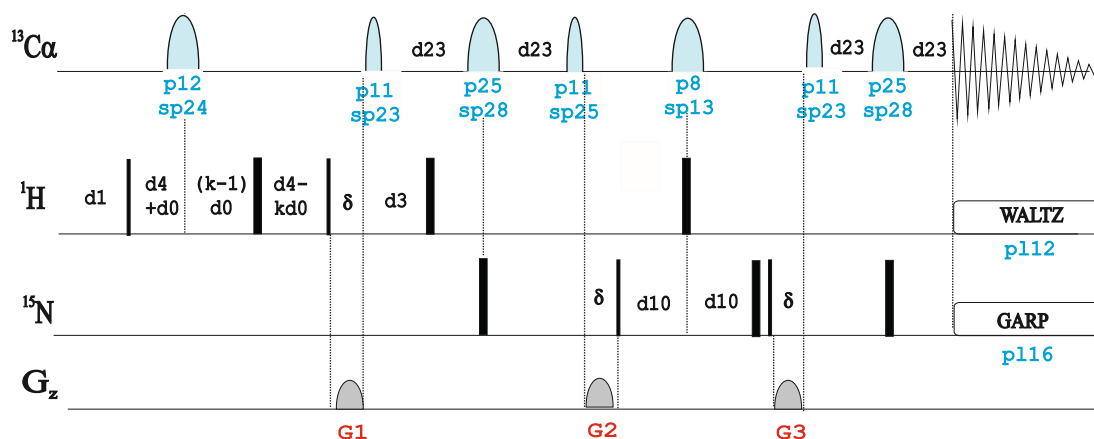


References:

1. W. Bermel, I. Bertini, L. Duma, I.C. Felli, L. Emsley, R. Pierattelli, P.R. Vasos, *Angew. Chem. Int. Ed.* 44, 3089-3092 (2005)

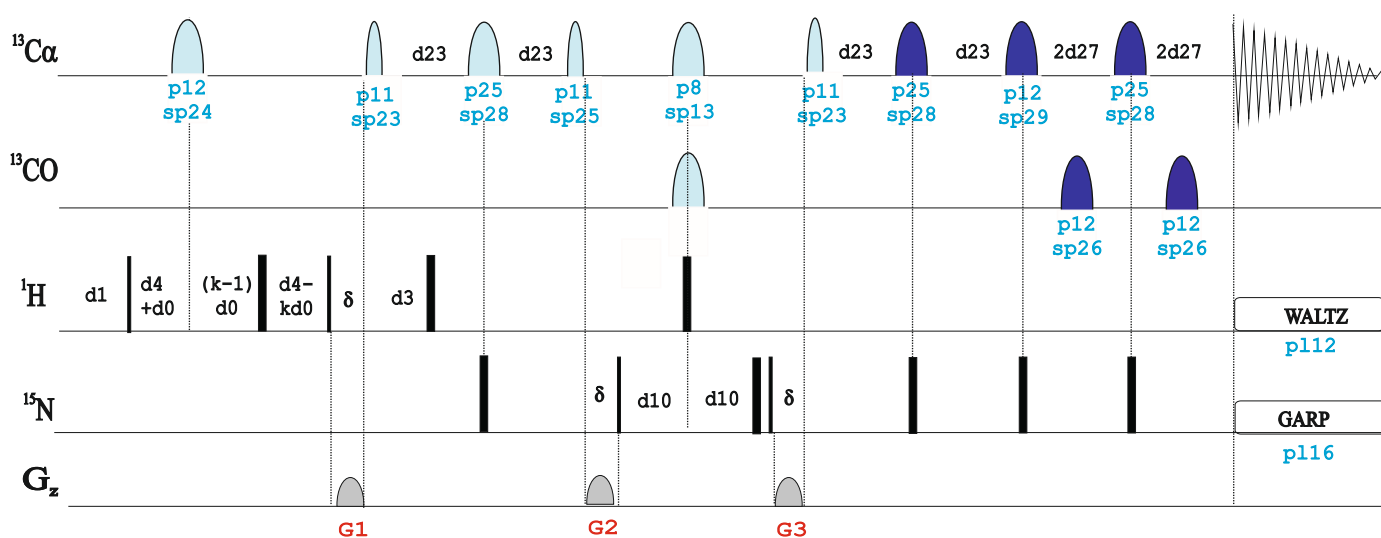


c_hcan_3d



$d23 = 1/4J(NCA) = 12.4\text{ms}$
 $d22 = 1/4J(COCA) = 4.5\text{ms}$
 $d27 = 1/8J(CACB) = 3.6\text{ms}$
 $d3 = 1/6J(CHA) = 1.1\text{ms}$
 $d4 = 1/4J(CHA) = 1.8\text{ms}$

c_hcan_ia3d

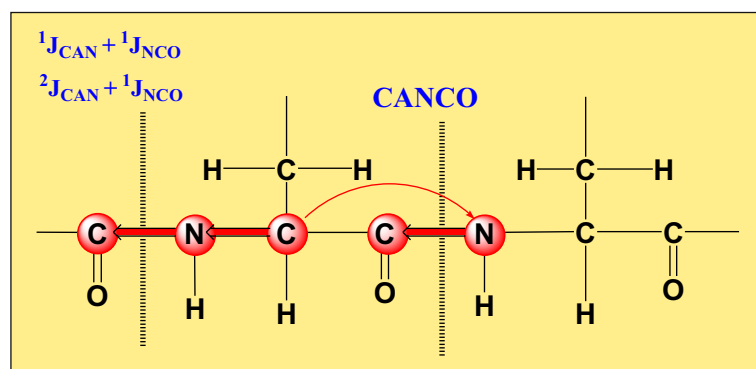


3D CANCO Experiment

Experiment Description

The 3D CANCO experiment is a CO-detected experiment that allows the correlation between the chemical shifts of the CA and the CO of the same and the previous residues and the N of the same and the next residue in doubly-labeled $^{13}\text{C}/^{15}\text{N}$ proteins.

Homonuclear CO-CA splitting in the acquisition dimension can be removed by homonuclear decoupling during acquisition or virtually using the IPAP approach.

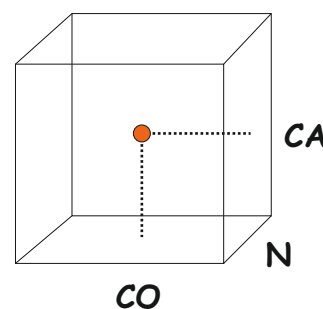


Related Experiments

3D HNCACO experiment
3D intra-CANCO and (H)CANCO experiments

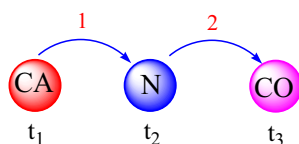
NMR Spectrum

The experiment provides a 3D correlation map in which each CA nucleus displays two different connectivities



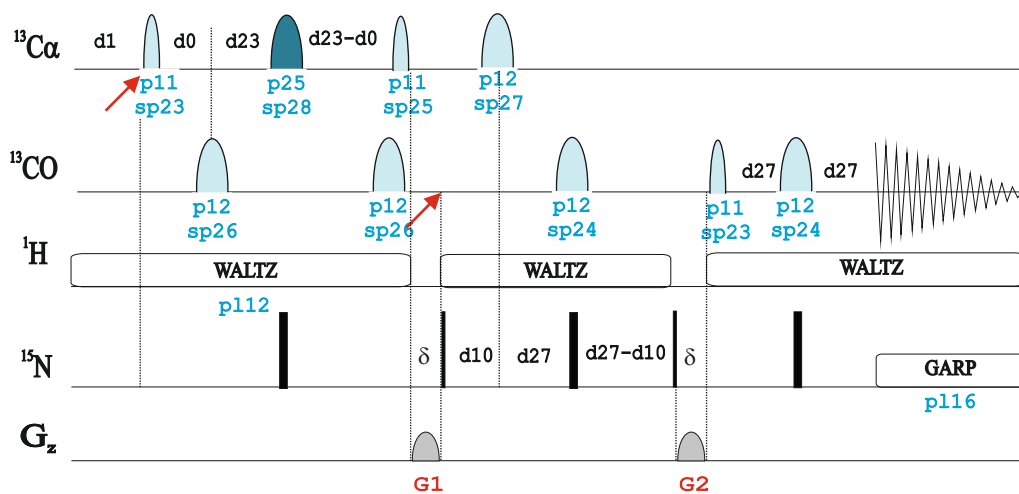
References:

1. I. Bertini, L. Duma, I.C. Felli, M. Fey, C. Luchinat, R. Pierattelli & P. Vasos, *Angew. Chem. Int. Ed.* 43, 2257-2259 (2004)
2. W. Bermel, I. Bertini, L. Duma, I.C. Felli, L. Emsley, R. Pierattelli, P.R. Vasos, *Angew. Chem. Int. Ed.* 44, 3089-3092 (2005)

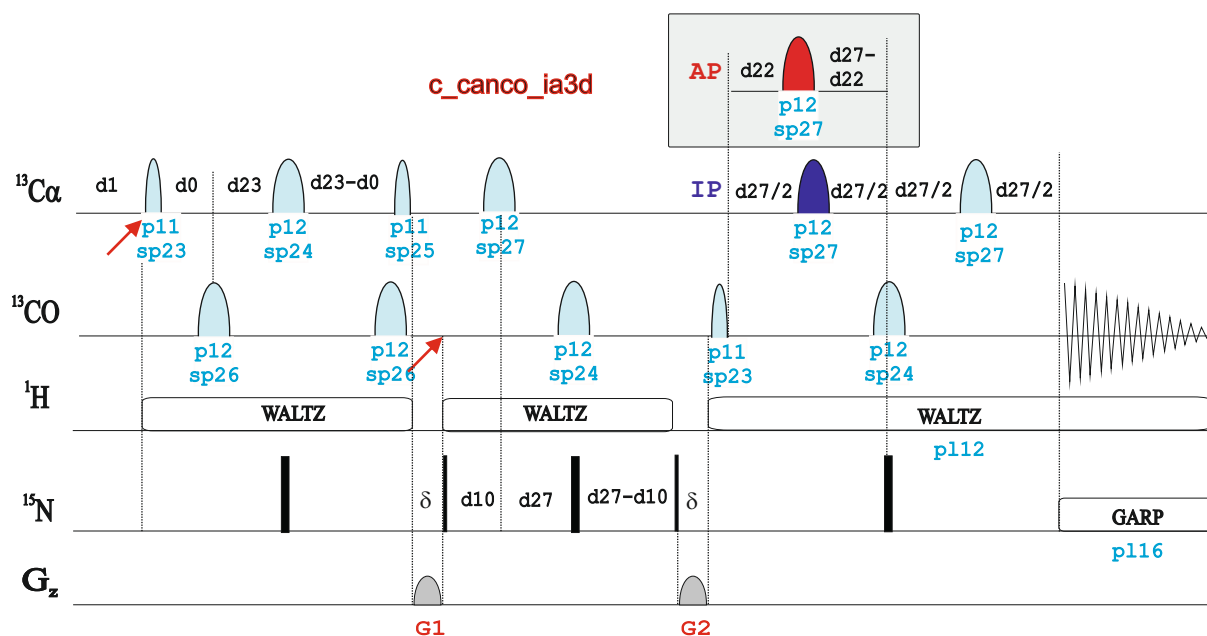


$$\begin{aligned} d23 &= 1/4J(\text{NCA}) = 12.4\text{ms} \\ d22 &= 1/4J(\text{COCA}) = 4.5\text{ms} \\ d27 &= 1/4J(\text{NCO}) = 16.0\text{ms} \\ d3 &= 1/6J(\text{CHA}) = 1.1\text{ms} \\ d4 &= 1/4J(\text{CHA}) = 1.8\text{ms} \end{aligned}$$

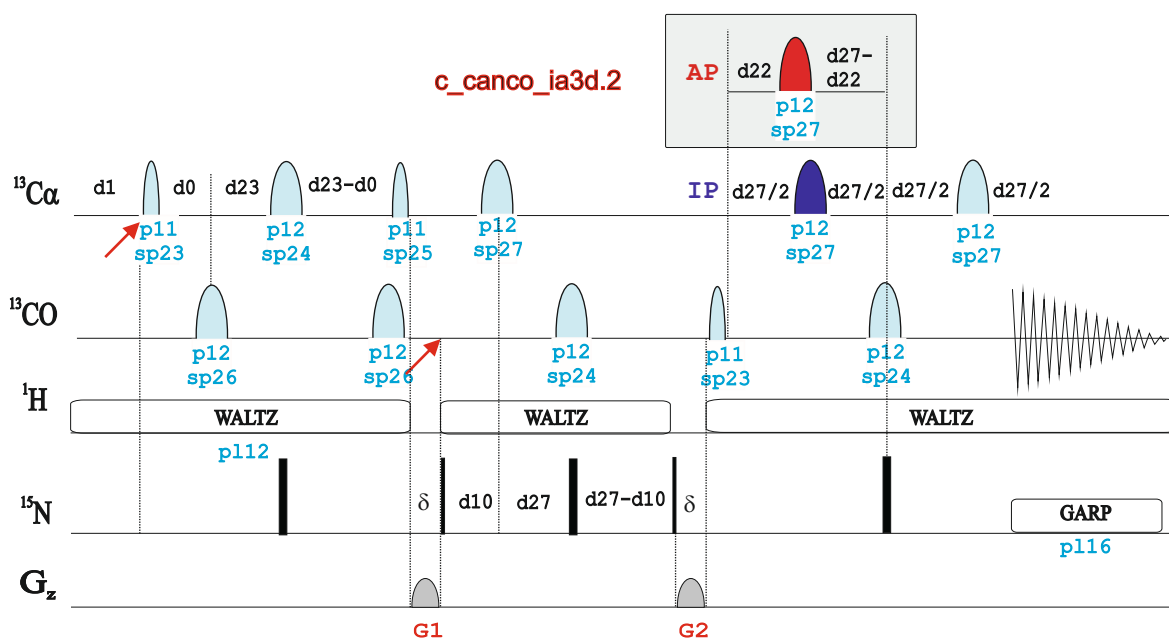
c_canco_3d



c_canco_ia3d



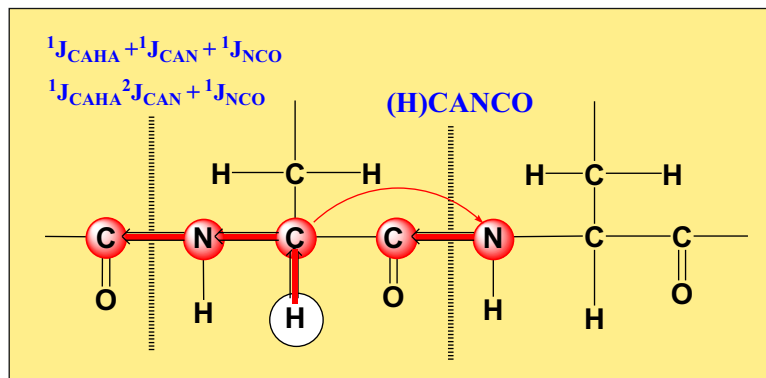
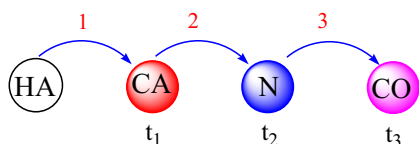
c_canco_ia3d.2



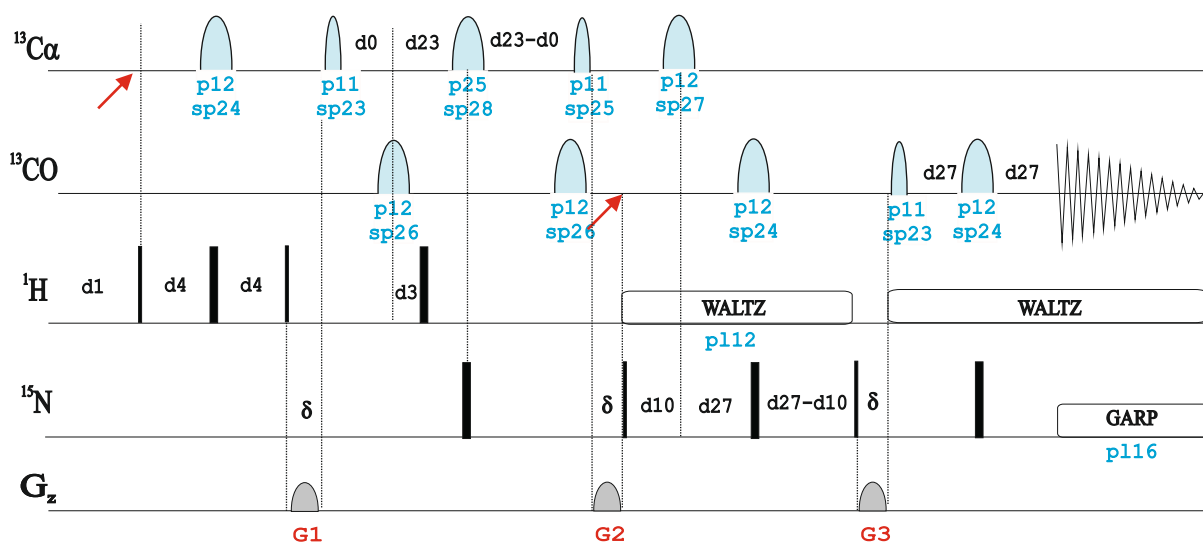
3D (H)CANCO Experiment

Experiment Description

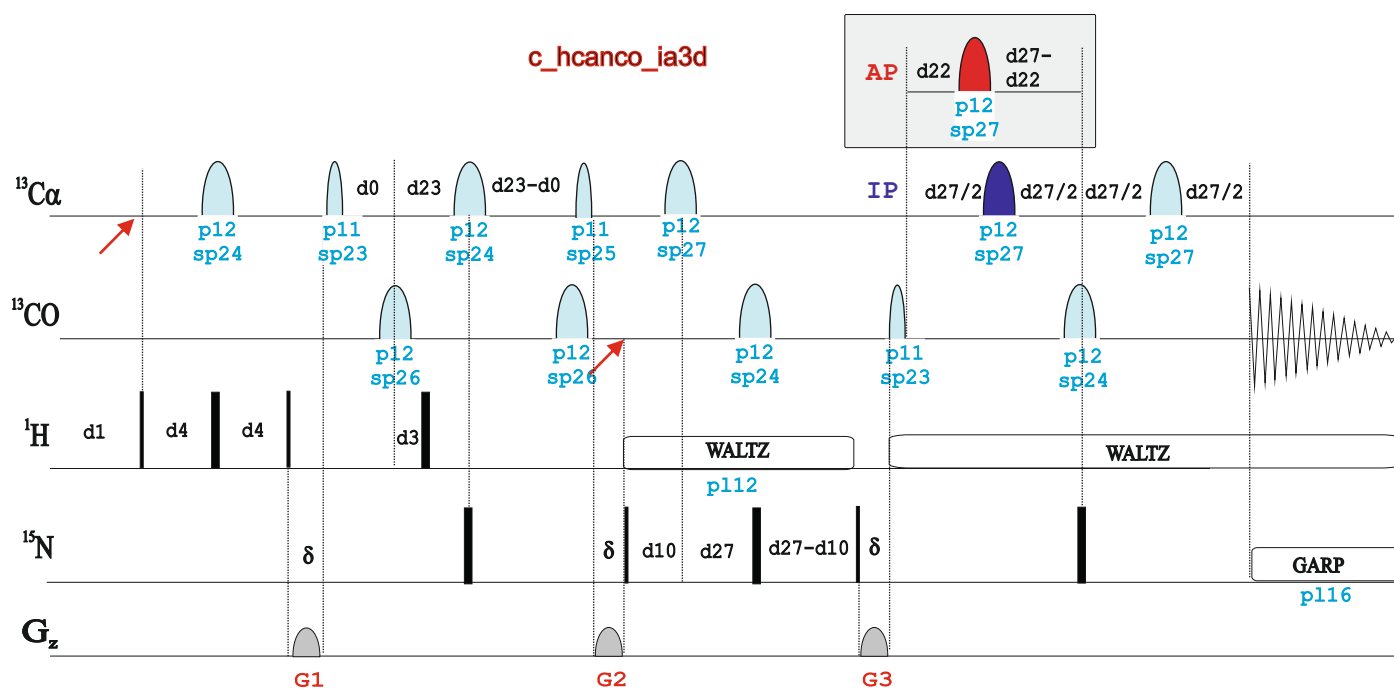
Variant of the CANCO experiment that starts from the HA protons.



c_hcanco_3d



c_hcanco_ia3d

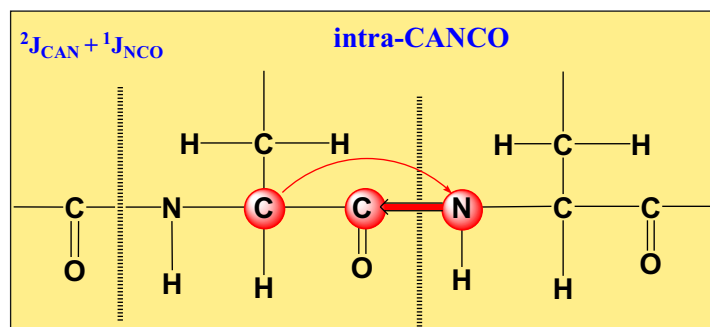
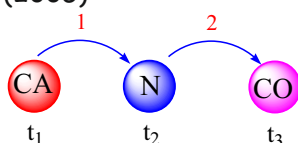


3D intra-CANCO Experiment

Experiment Description

Variant of the CANCO experiment that provides exclusively intra-residue CANCO connectivities.

1. W. Bermel, I. Bertini, I.C. Felli, R. Pierattelli & P. Vasos, *J. Magn. Reson.* 172, 324-328 (2005)
2. W. Bermel, I. Bertini, L. Duma, I.C. Felli, L. Emsley, R. Pierattelli, P.R. Vasos, *Angew. Chem. Int. Ed.* 44, 3089-3092 (2005)

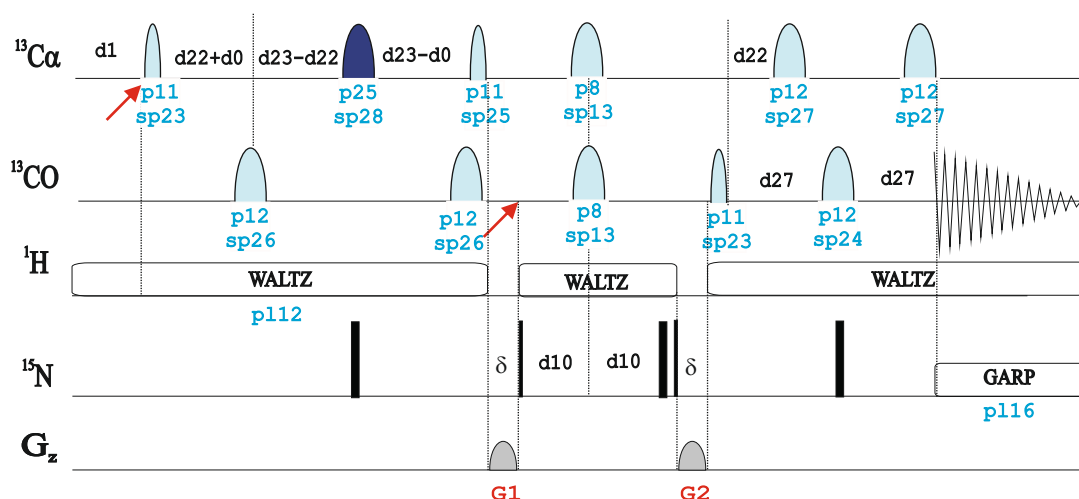


$$d22: 1/(4J(CO\text{Ca})) = [4.5 \text{ msec}]$$

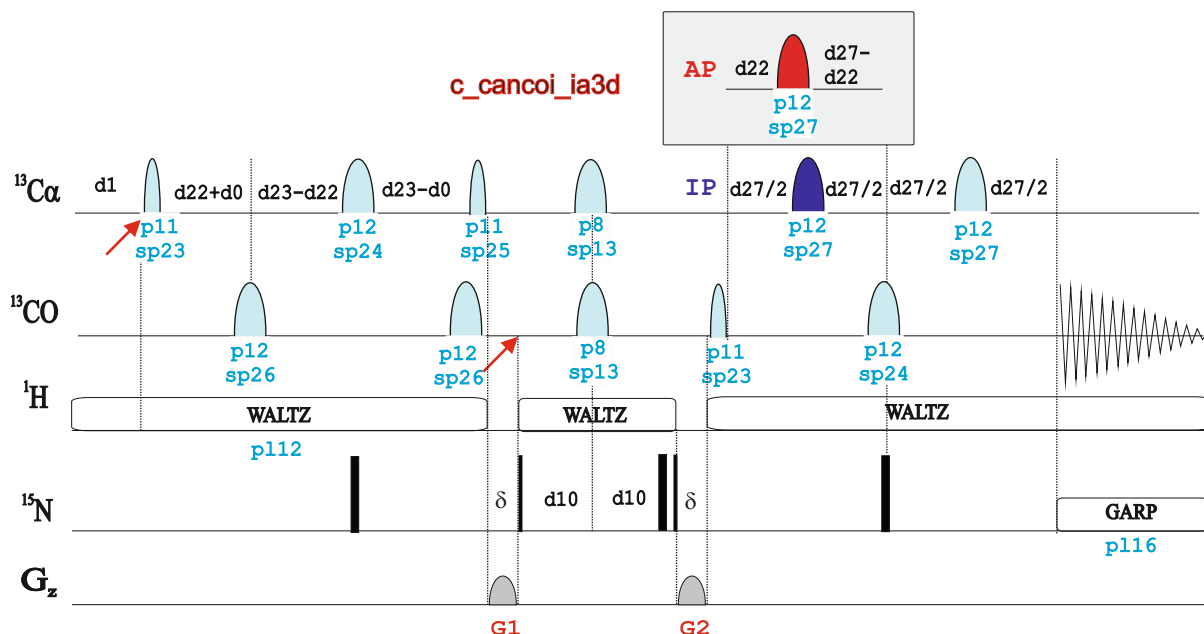
$$d23: 1/(4J(N\text{Ca})) \text{ and } 1/(2J(\text{CaCb})) = [13.3 \text{ msec}]$$

$$d27: 1/(4J(N\text{CO})) = [16.0 \text{ msec}]$$

c_cancoi_3d



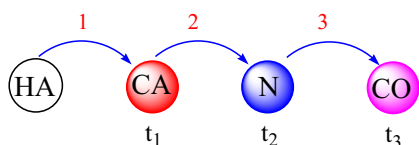
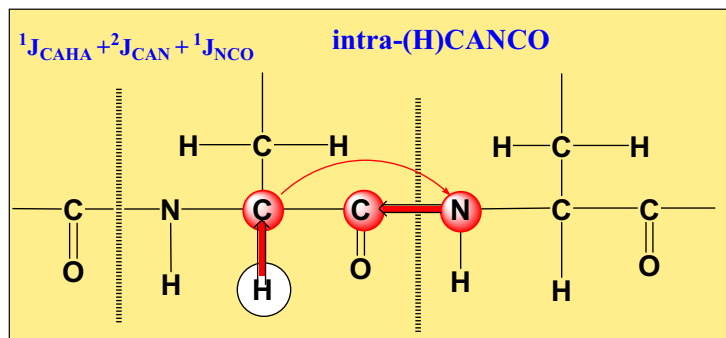
c_cancoi_ia3d



3D intra-(H)CANCO Experiment

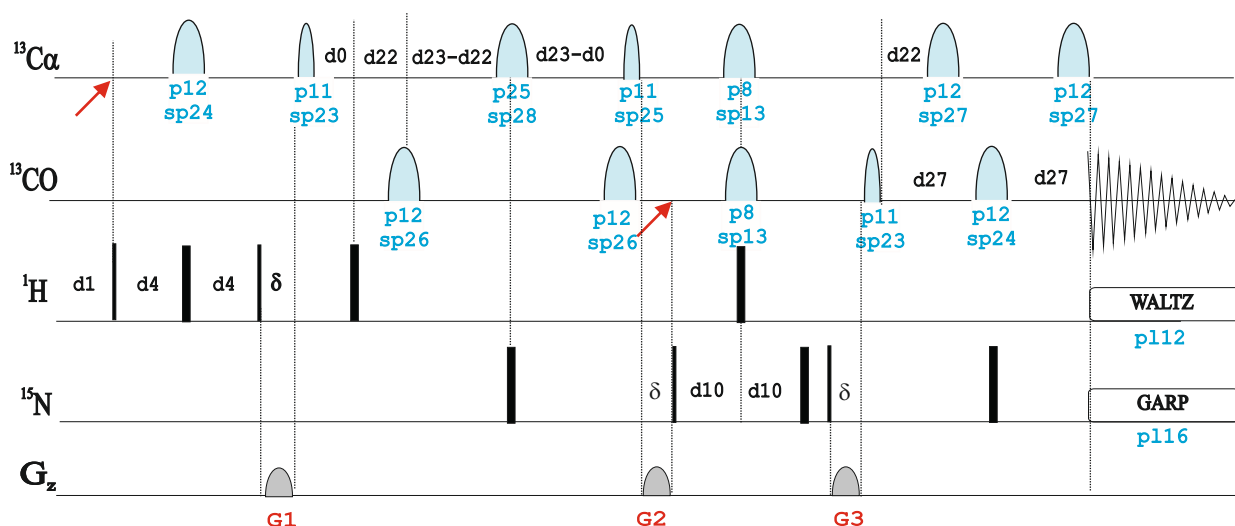
Experiment Description

Variant of the intra-CANCO experiment that starts from the HA protons.

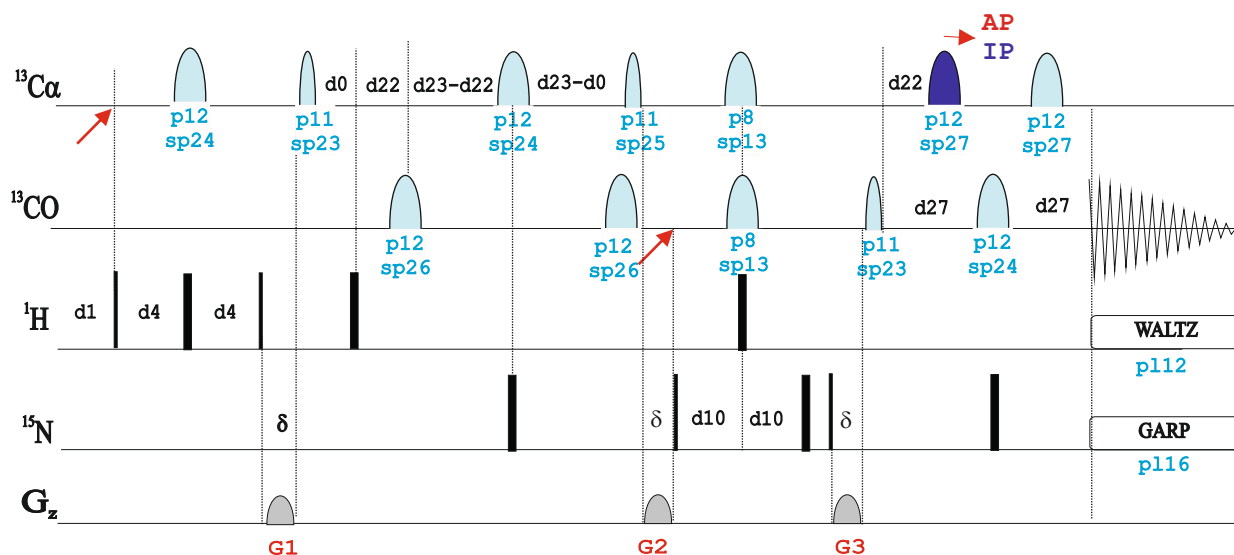


$d3 : 1/(6J(\text{HCA}))$ [1.1 msec]
 $d4 : 1/(4J(\text{HCA}))$ [1.8 msec]
 $d22 : 1/(4J(\text{COCa}))$ [4.5 msec]
 $d23 : 1/(4J(\text{NCa}))$ and $1/(2J(\text{CaCb}))$ [13.3 msec]
 $d27 : 1/(4J(\text{NCO}))$ [16.0 msec]

c_hcancoi_3d



c_hcancoi_ia3d



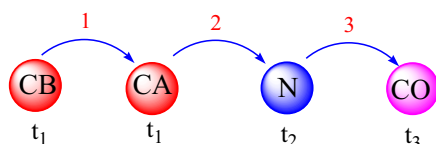
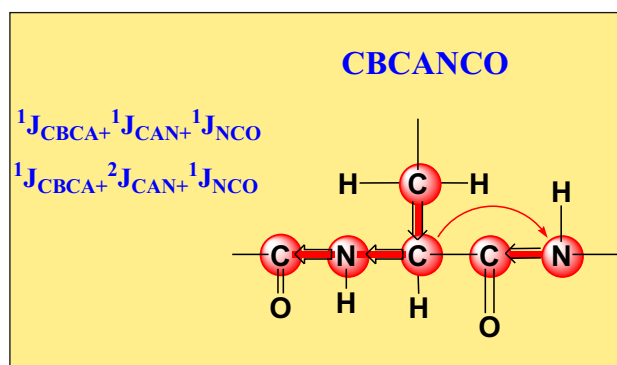
3D CBCANCO Experiment

Experiment Description

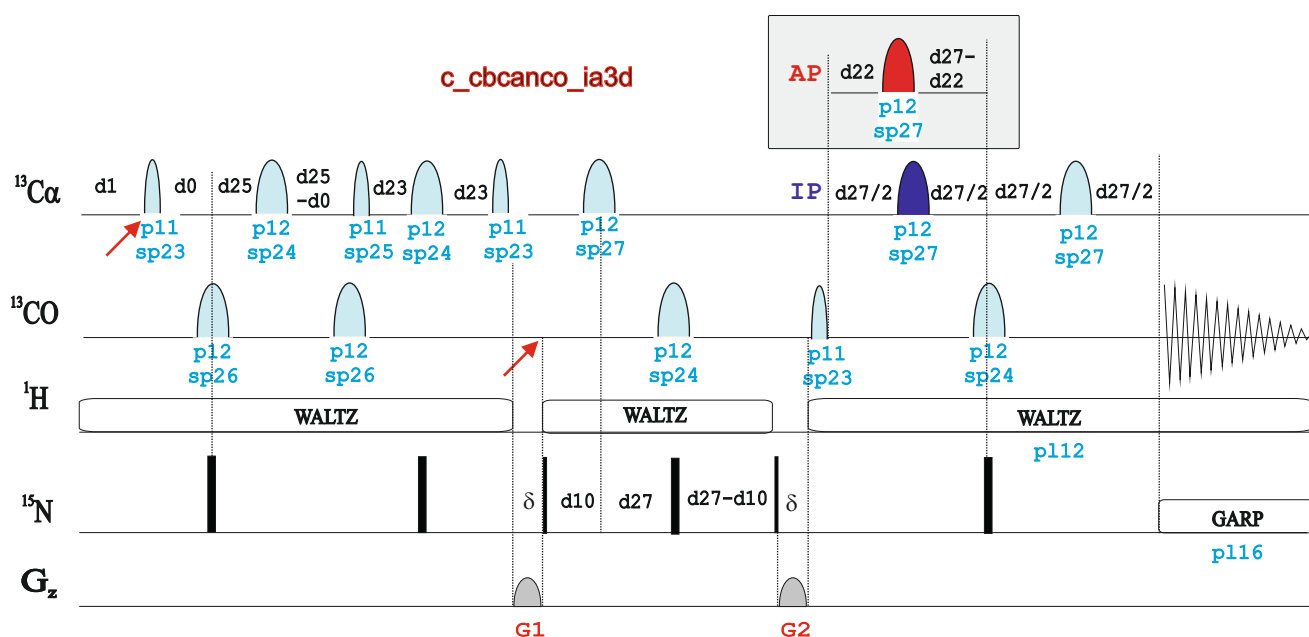
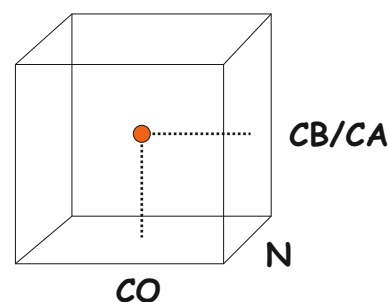
Variant of the CANCO experiment
incorporating an initial CB-CA transfer
The experiment
provides intra- and inter-residue
between CB,CA and CO,N connectivities

References:

W. Bermel, I. Bertini, I.C. Felli, R. Kuemmerle
& R. Pierattelli, J. Magn. Reson. 178, 56-64 (2006)



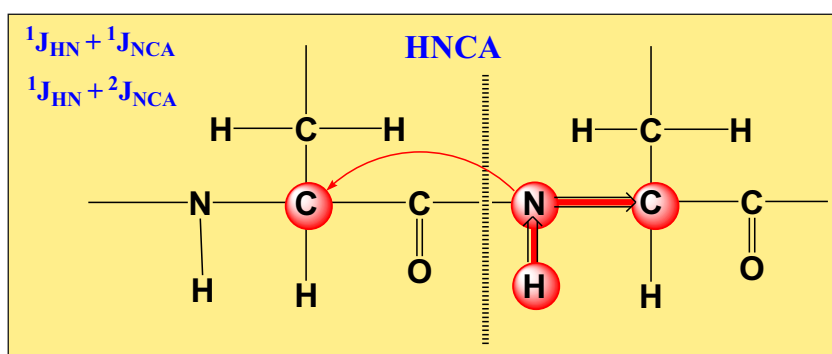
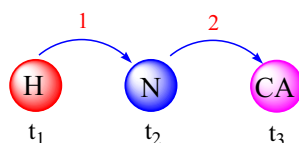
$d23 = 1/4J(\text{NCA}) = 12.4\text{ms}$
 $d22 = 1/4J(\text{COCA}) = 4.5\text{ms}$
 $d27 = 1/4J(\text{NCO}) = 16.0\text{ms}$
 $d3 = 1/6J(\text{CHA}) = 1.1\text{ms}$
 $d4 = 1/4J(\text{CHA}) = 1.8\text{ms}$



3D CA-detected HNCA Experiment

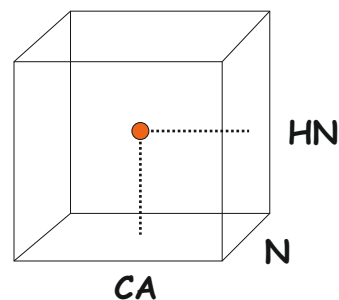
Experiment Description

The 3D CA-detected HNCA experiment is an out-and-stay version of the conventional HNCA experiment



NMR Spectrum

The experiment provides the same 3D HNCA correlation map



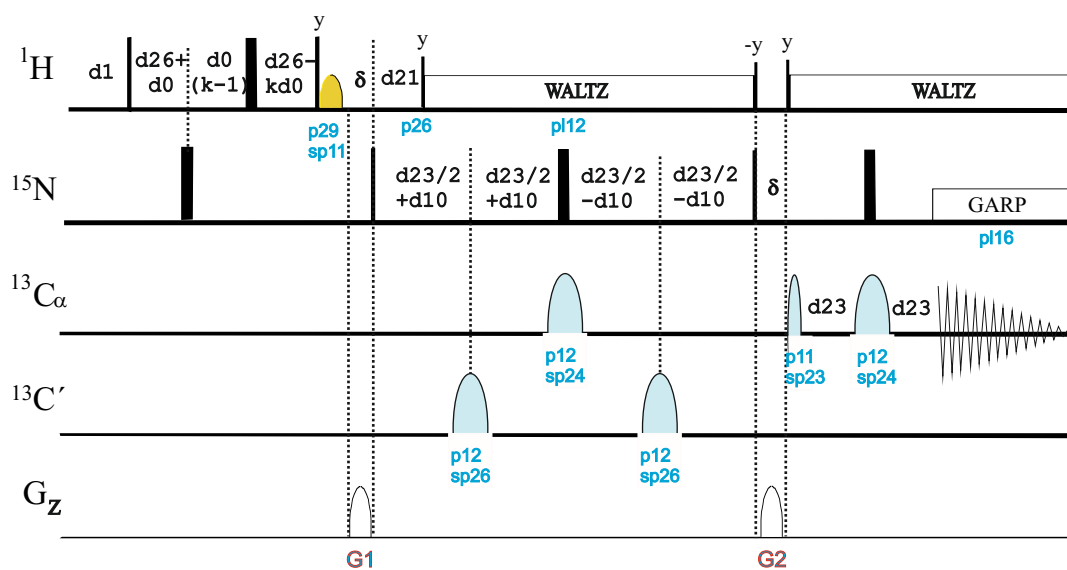
References:

W. Bermel, I. Bertini, L. Duma, I.C. Felli, L. Emsley, R. Pierattelli, P.R. Vasos, *Angew. Chem. Int. Ed.* 44, 3089-3092 (2005)

Related Experiments.

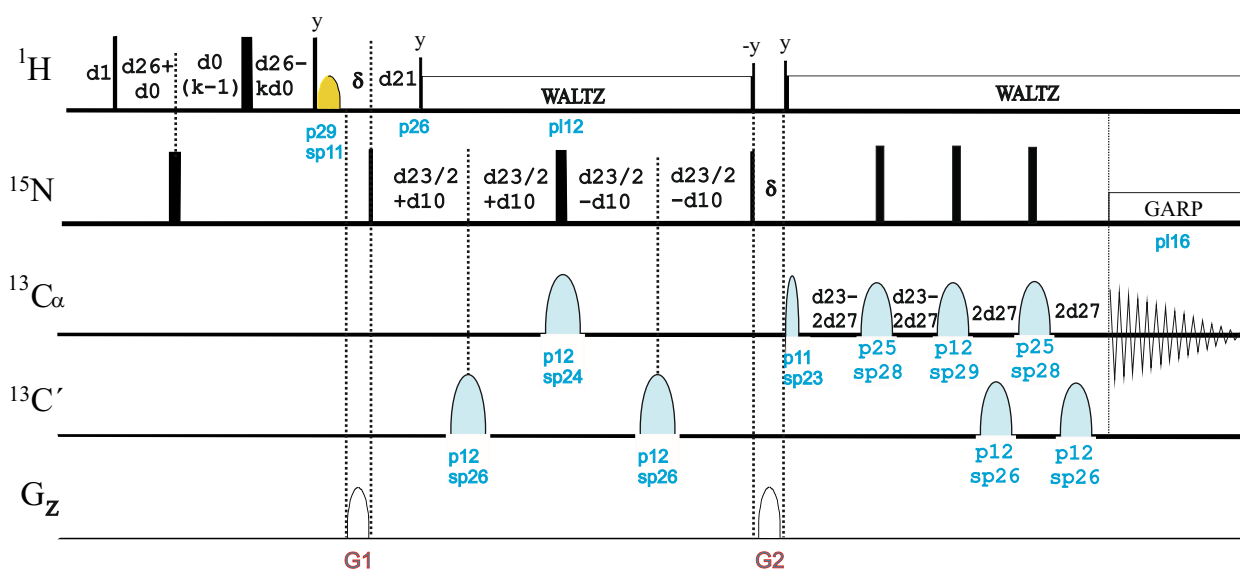
3D HA-Detected HNCA

c_hnca_3d



$d21 = 1/2J(NH) = 5.5ms$
 $d22 = 1/4J(COCA) = 4.5ms$
 $d23 = 1/4J(NCA) = 12.4ms$
 $d26 = 1/4J(NH) = 2.3ms$
 $d27 = 1/8(CACB) = 3.6ms$

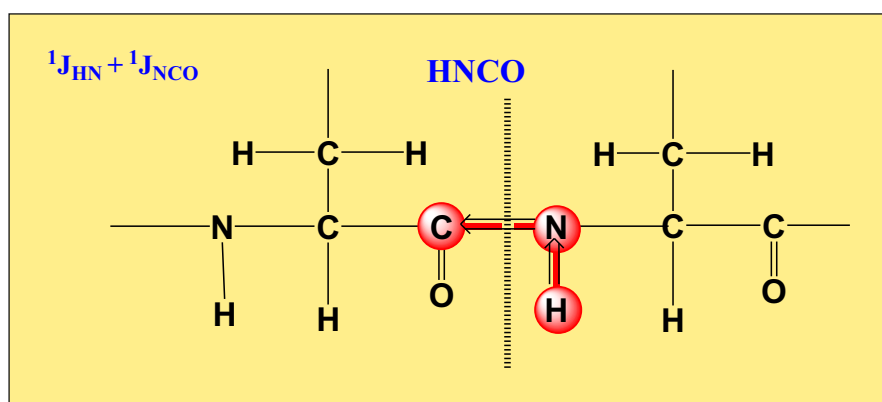
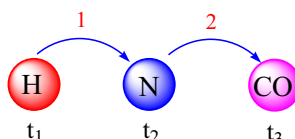
c_hnca_ia3d



3D CO-detected HNCO Experiment

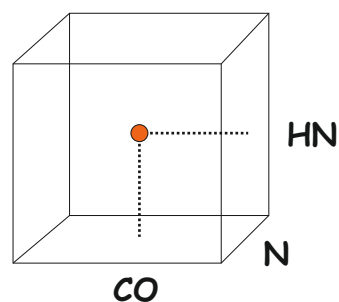
Experiment Description

The 3D CO-detected HNCO experiment is an out-and-stay version of the conventional HNCO experiment



NMR Spectrum

The experiment provides the same 3D HNCO correlation map



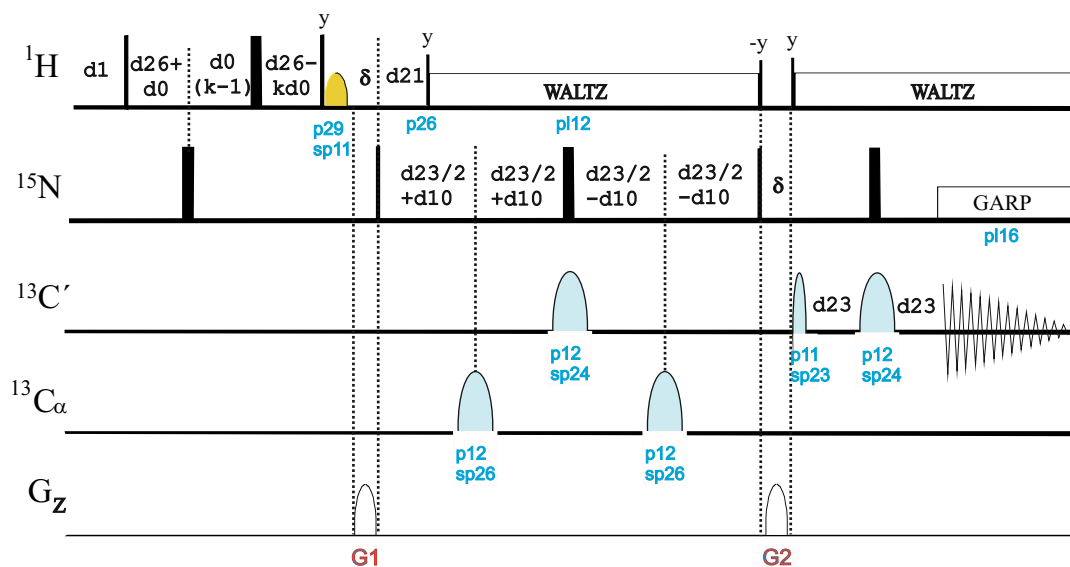
References:

W. Bermel, I. Bertini, L. Duma, I.C. Felli, L. Emsley, R. Pierattelli, P.R. Vasos, *Angew. Chem. Int. Ed.* 44, 3089-3092 (2005)

Related Experiments.

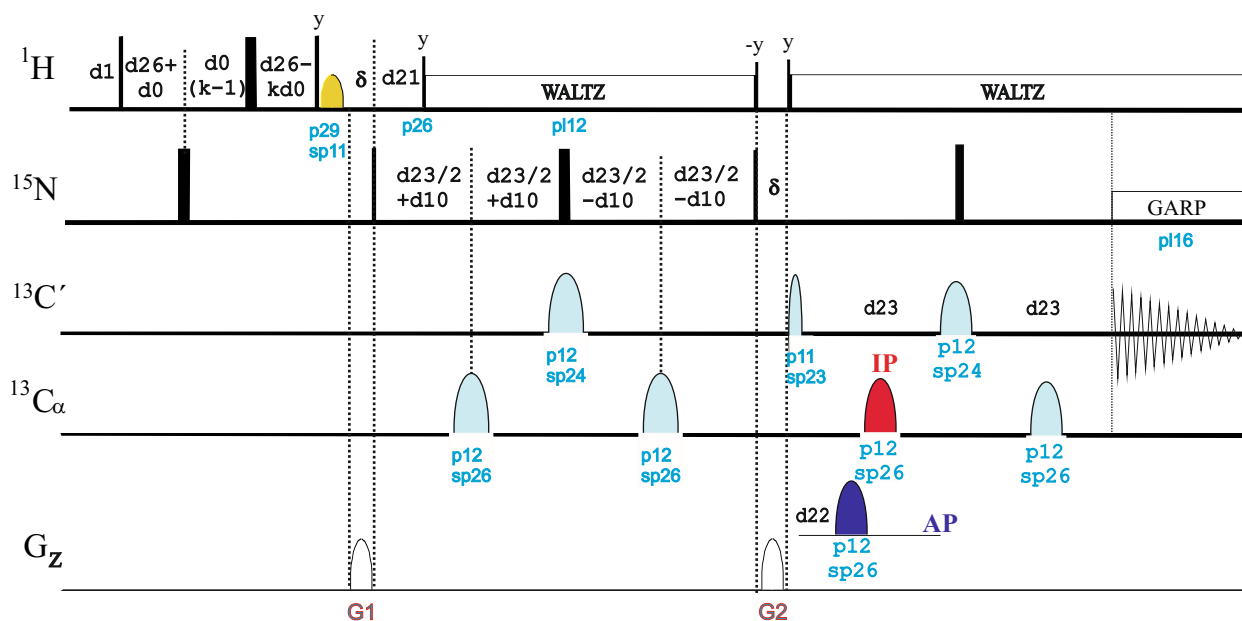
3D HN-Detected HNCO

c_hnco_3d



$d21=1/2J(\text{NH})=5.5\text{ms}$
 $d22=1/4J(\text{COCA})=4.5\text{ms}$
 $d23=1/4J(\text{NCA})=12.4\text{ms}$
 $d27=1/8(\text{CACB})=3.6\text{ms}$

c_hnco_ia3d



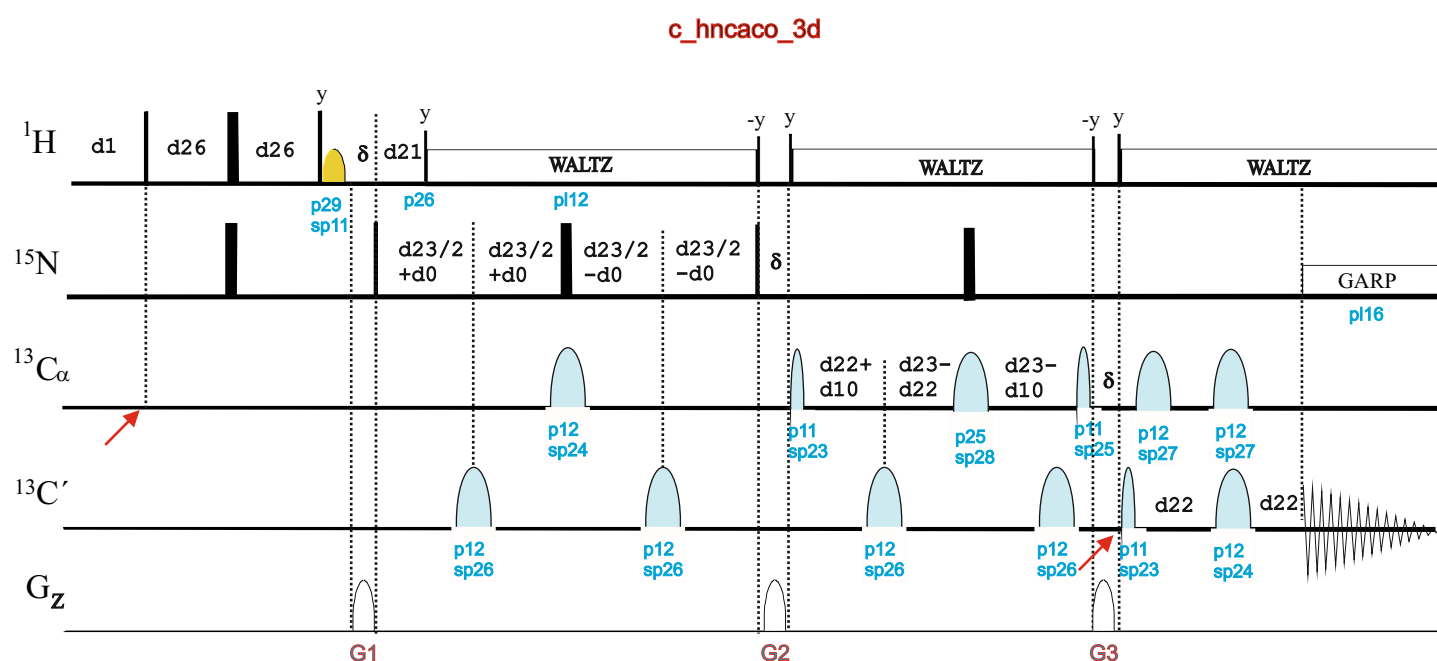
Experiment Description

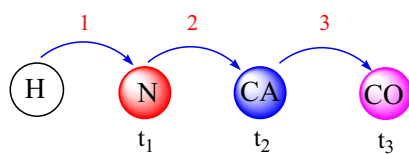
$^1J_{HN} + ^1J_{NCA} + ^1J_{COCA}$
 $^1J_{HN} + ^2J_{NCA} + ^1J_{COCA}$

(H)NCACO

W. Bermel, I. Bertini, L. Duma, I.C. Felli, L. Emsley, R. Pierattelli, P.R. Vasos, *Angew. Chem. Int. Ed.* 44, 3089-3092 (2005)

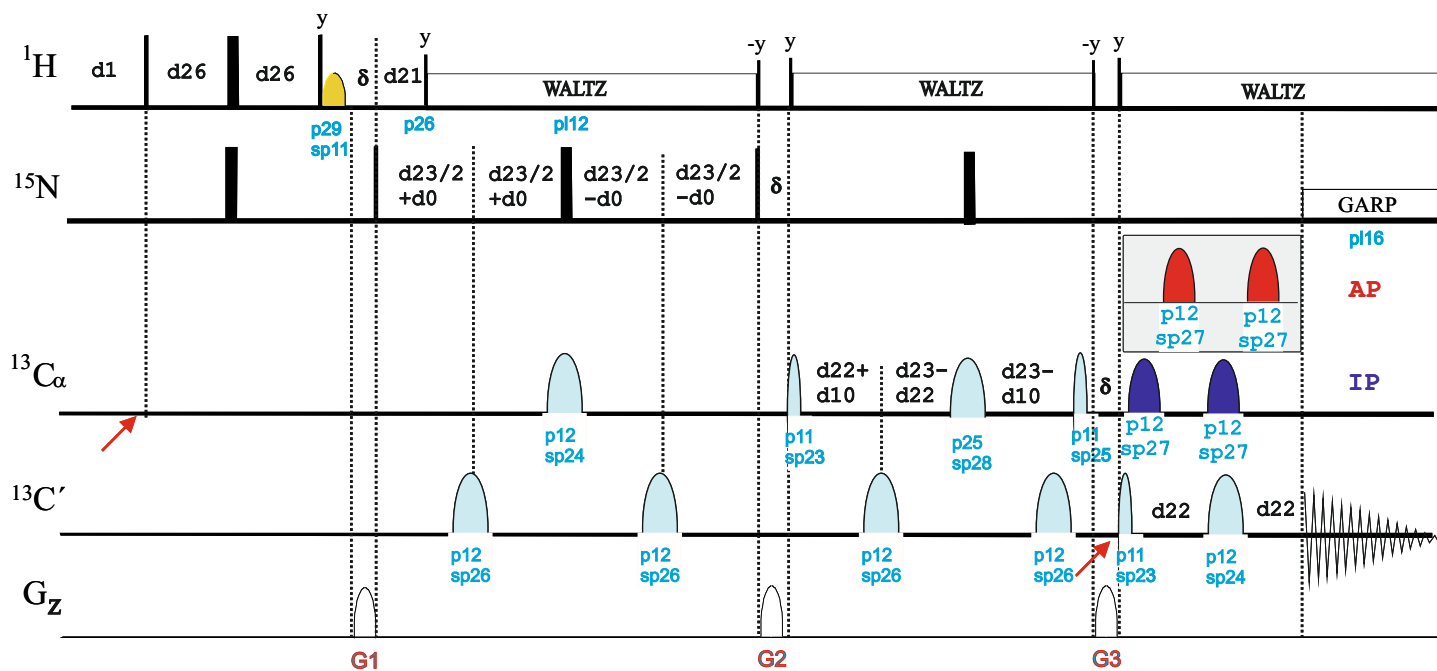
3D HN-Detected HNCACO



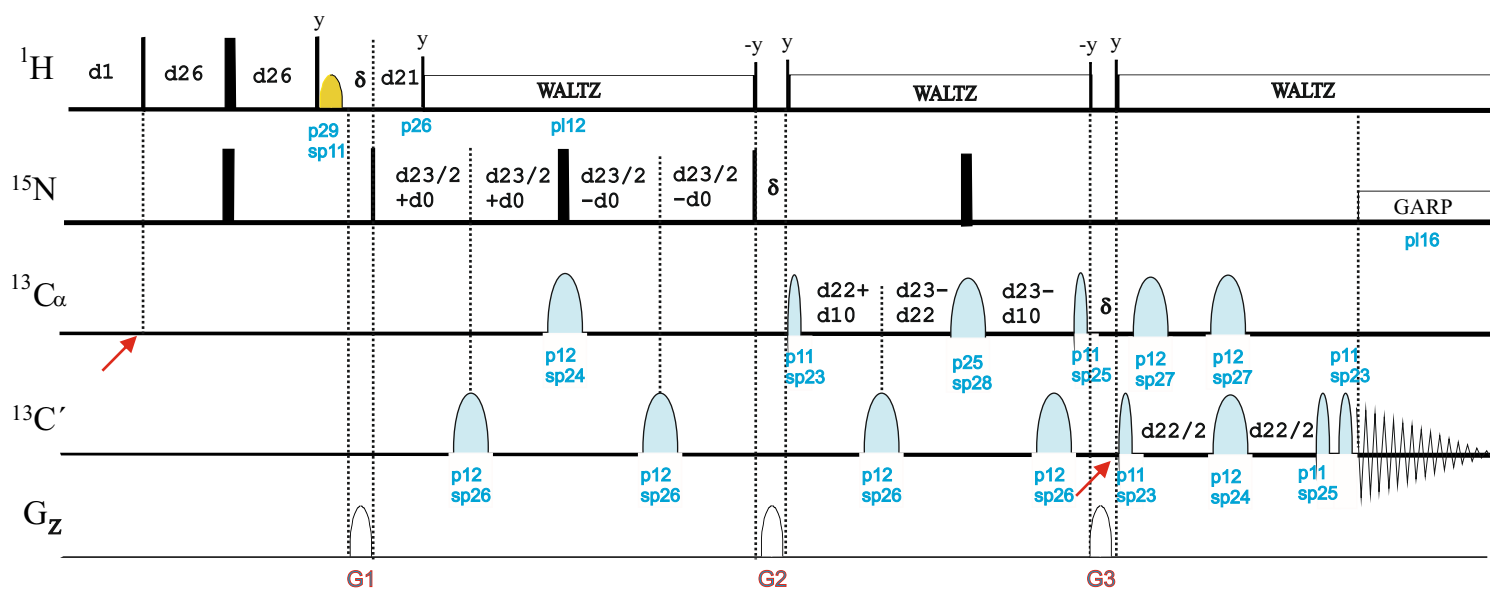


$d21=1/2J(\text{NH})=5.5\text{ms}$
 $d22=1/4J(\text{COCA})=4.5\text{ms}$
 $d23=1/4J(\text{NCA})=12.4\text{ms}$
 $d26=1/4J(\text{NH})=2.3\text{ms}$

c_hncaco_la3d



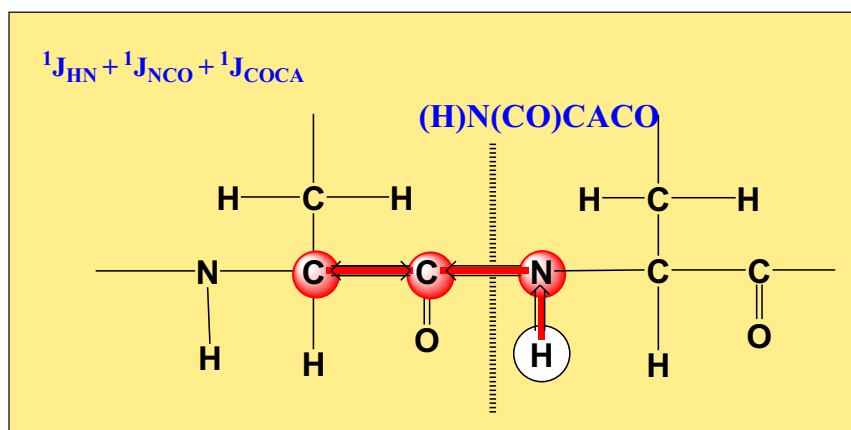
c_hncaco_s33d



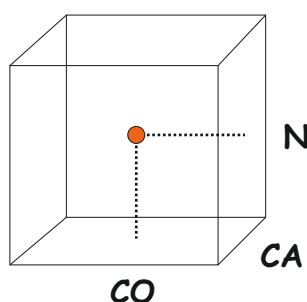
3D CO-detected (H)NCOCA Experiment

Experiment Description

The 3D (H)N(CO)CACO is the CO-detected equivalent of the HNCOCA experiment, in which a nitrogen nucleus is correlated to the CO and CA carbons of the previous residue.



NMR Spectrum

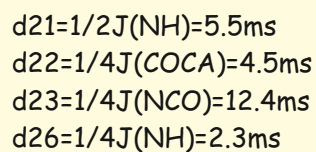


References:

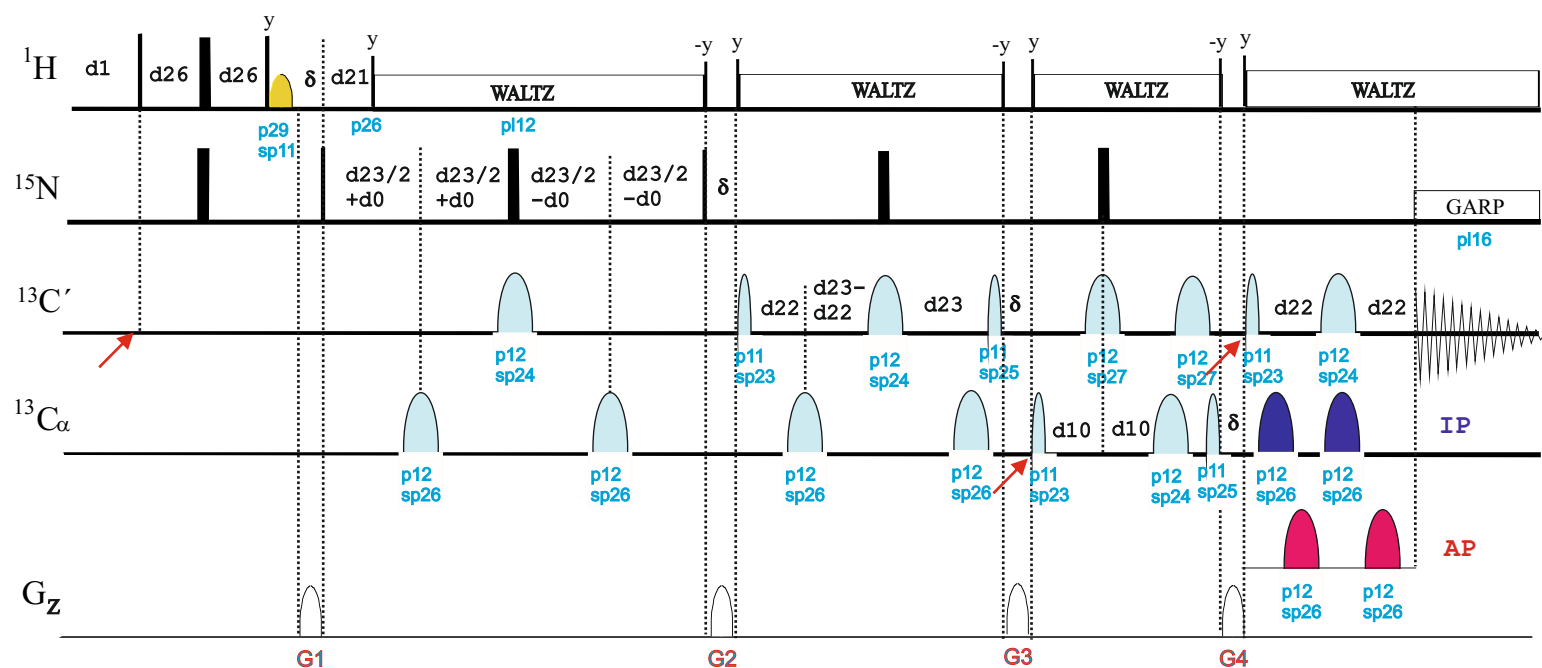
W. Bermel, I. Bertini, L. Duma, I.C. Felli, L. Emsley, R. Pierattelli, P.R. Vasos, *Angew. Chem. Int. Ed.* 44, 3089-3092 (2005)

Related Experiments.

3D HN-Detected HNCOCA
CA-detected (H)NCOCA



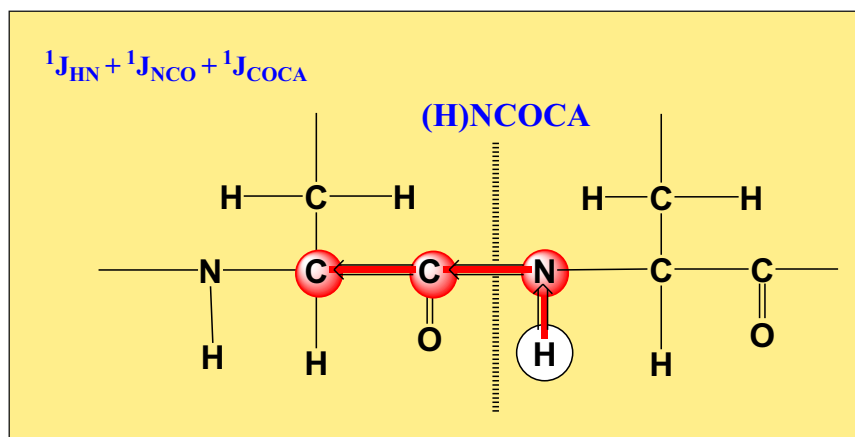
c_hncoca_ia3d



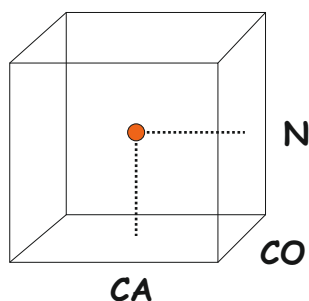
3D CA-detected (H)NCOCA Experiment

Experiment Description

The 3D CA-detected HNCOCA experiment is an out-and-stay version of the conventional ^1H -detected HNCOCA experiment. Each nitrogen is correlated to CA and CO carbons of the same and the previous residue.



NMR Spectrum

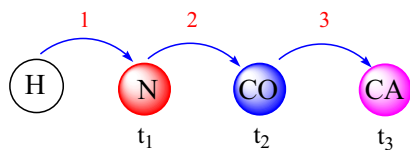


References:

W. Bermel, I. Bertini, L. Duma, I.C. Felli, L. Emsley, R. Pierattelli, P.R. Vasos, *Angew. Chem. Int. Ed.* 44, 3089-3092 (2005)

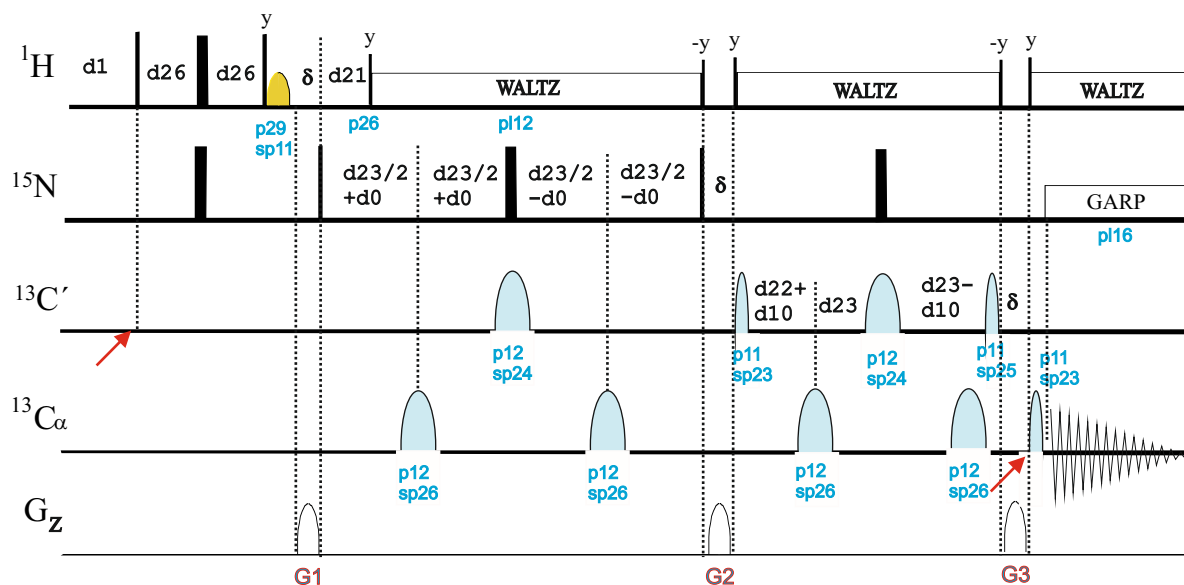
Related Experiments

^1H -detected HNCOCA
CO-detected (H)NCOCA
CANCO and i-CANCO

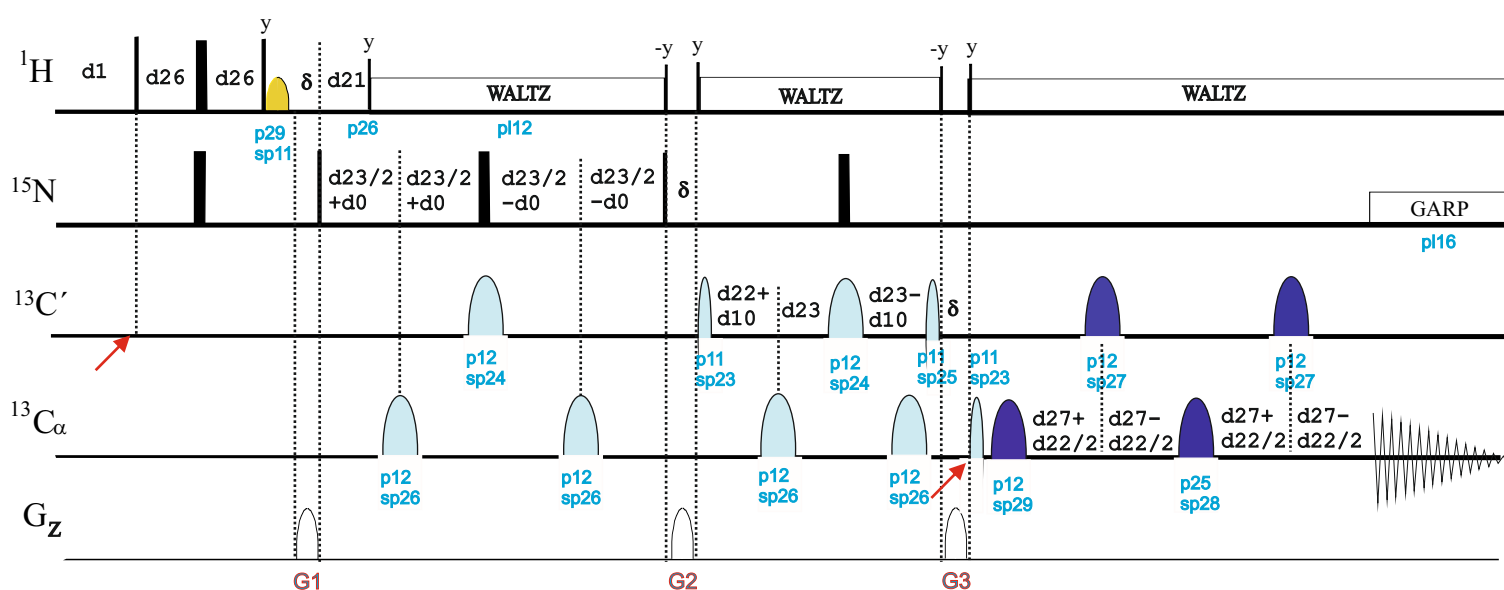


$d21=1/2J(NH)=5.5\text{ms}$
 $d22=1/4J(COCA)=4.5\text{ms}$
 $d23=1/4J(NCA)=12.4\text{ms}$
 $d26=1/4J(NH)=2.3\text{ms}$
 $d27=1/8(CACB)=3.6\text{ms}$

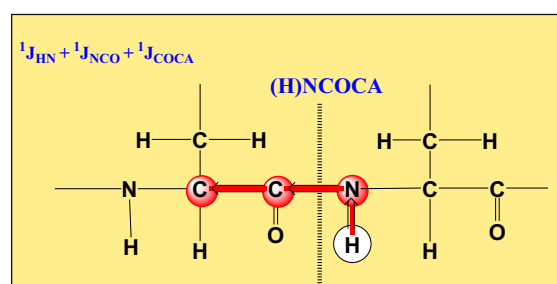
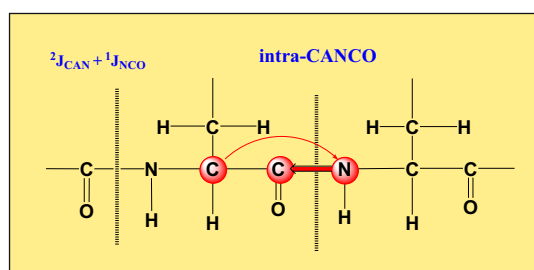
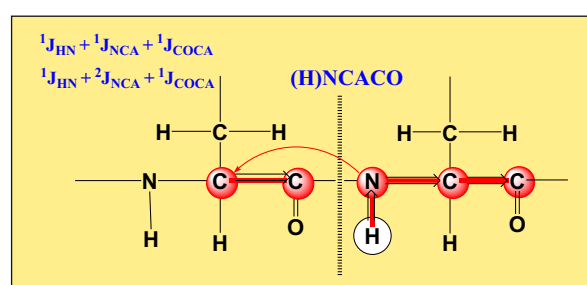
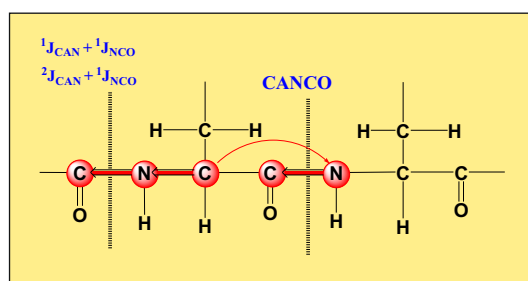
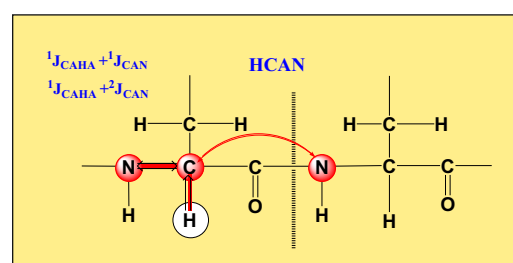
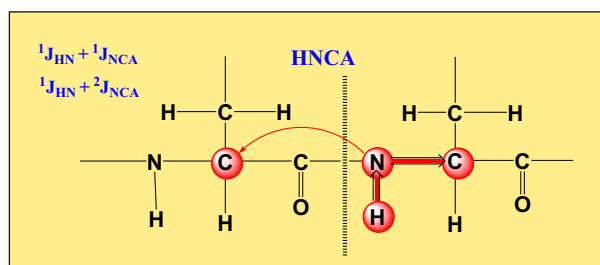
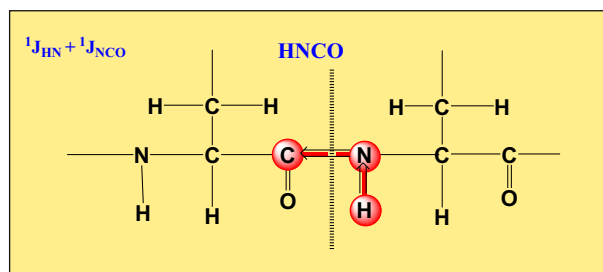
c_hncoca2_3d



c_hncoca2_ia3d



Summary of C-detected backbone CN experiments



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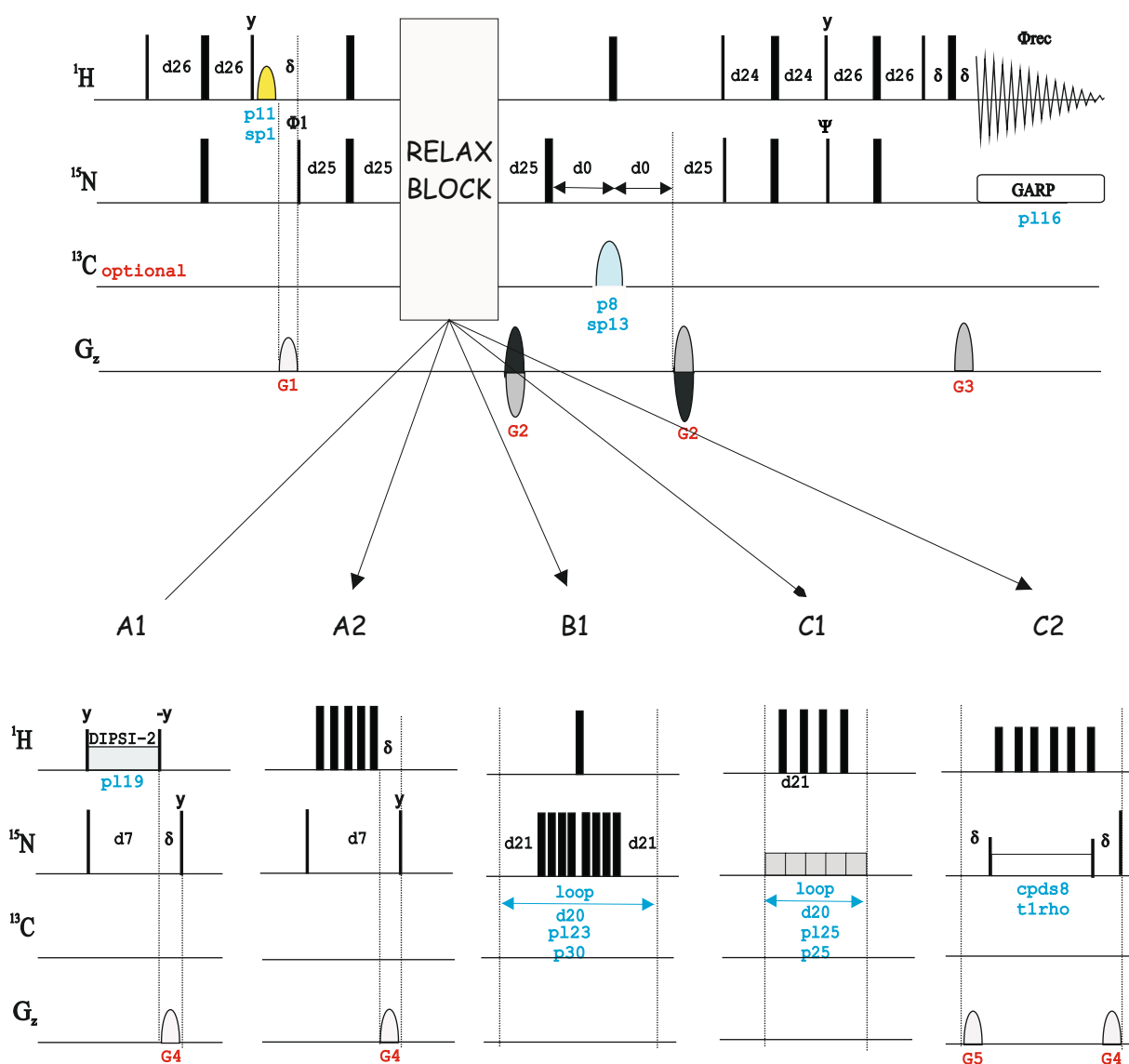
NMRGuide

2D HSQC EXPERIMENTS FOR
THE MEASUREMENT OF T₁, T₂, T₁RHO
RELAXATION TIMES AND
HETERONUCLEAR NOEs.

NMR Experiment: Relaxation Rates Measurement

Pulprog (3D mode)	Parameter Set	pp (2D mode)	TROSY version
A1. hsqct1etf3gpsi3d	HSQCT1ETF3GPSI3D	hsqct1etf3gpsi3d	trt1etf3gpsi3d
A2. hsqct1etf3gpsi3d.2	HSQCT1ETF3GPSI3D.2	hsqct1etf3gpsi3d.2	
B1. hsqct2etf3gpsi3d	HSQCT2ETF3GPSI3D	hsqct2etf3gpsi3d	trt2etf3gpsi3d
C1. hsqctretf3gpsi3d	HSQCTRETF3GPSI3D	hsqctretf3gpsi3d	
C2. hsqctretf3gpsi3d.2	HSQCTRETF3GPSI3D.2		

General Scheme



2D HSQC experiments for ^{13}C Relaxation Measurements (from f2 channel)

- Heteronuclear ^{13}C - ^1H NOEs:

Phase sensitive ge-2D ^1H - ^{13}C HSQC to measure heteronuclear ^{13}C - ^1H NOEs using PEP
(**hsqcnoegpsi** | **HSQCNOEGPSI**)

Phase sensitive ge-2D ^1H - ^{13}C HSQC to measure heteronuclear ^{13}C - ^1H NOEs using PEP and
refocusing adiabatic ^{13}C pulses (**hsqcnoegpsi.2** | **HSQCNOEGPSI**)

- T_1 (C):

Phase-sensitive ge-2D ^1H - ^{13}C HSQC to measure ^{13}C T_1 relaxation times using PEP, 180° ^1H pulses
and acquired as pseudo-3D (**hsqct1etgpsi3d**).

Phase-sensitive ge-2D ^1H - ^{13}C HSQC to measure ^{13}C T_1 relaxation times using PEP, 180° ^1H pulses,
refocusing adiabatic ^{13}C pulses and acquired as pseudo-3D (**hsqct1etgpsi3d.2**).

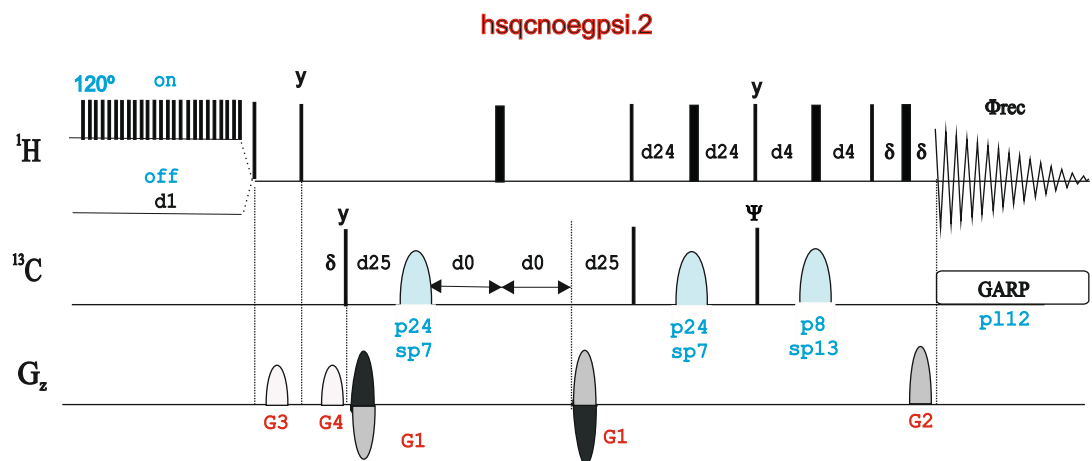
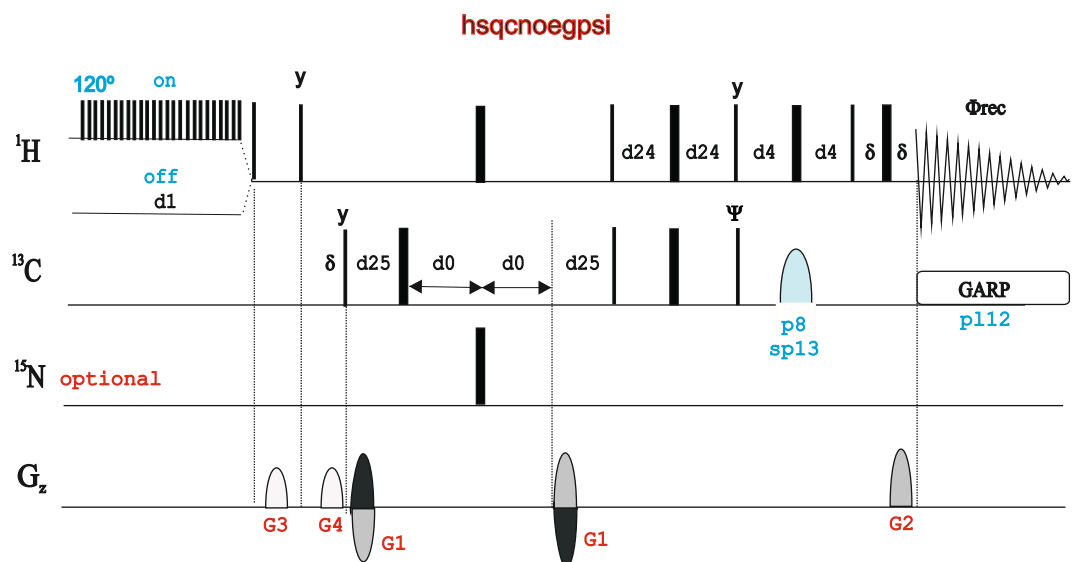
- T_2 (C):

Phase-sensitive ge-2D ^1H - ^{15}N HSQC to measure ^{13}C T_2 relaxation times using PEP and refocusing
adiabatic ^{13}C pulses (**hsqct2etgpsi3d.2**)

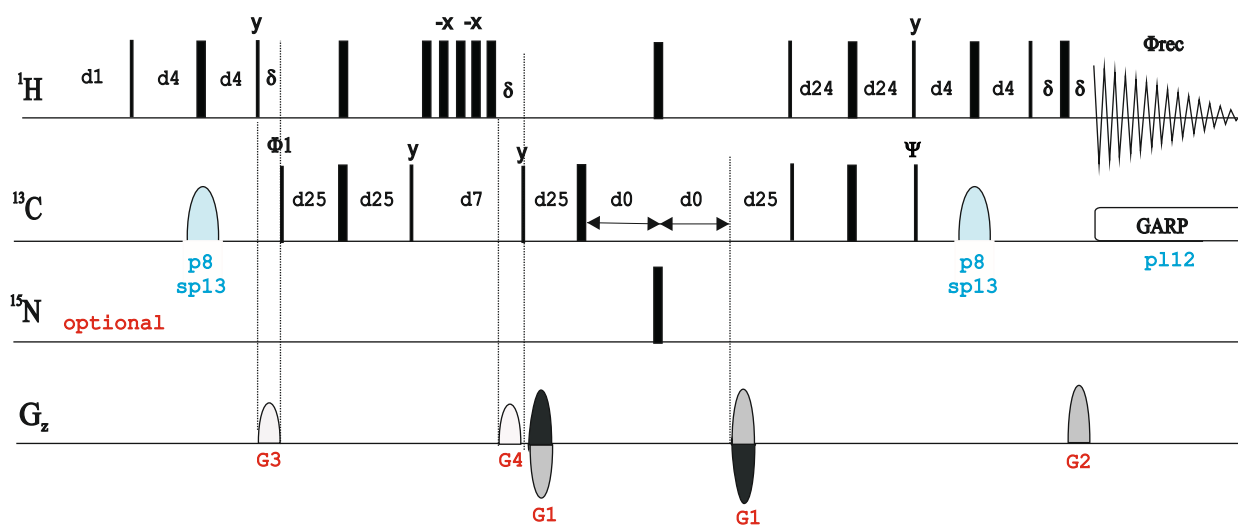
Also see:

T1 & T2 Relaxation

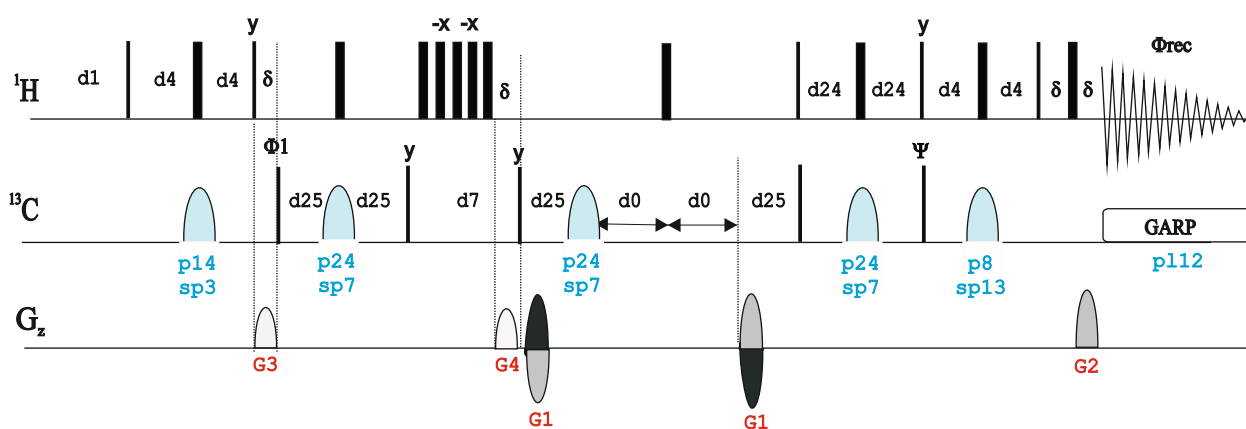
3D HNCO for Relaxation Measurements



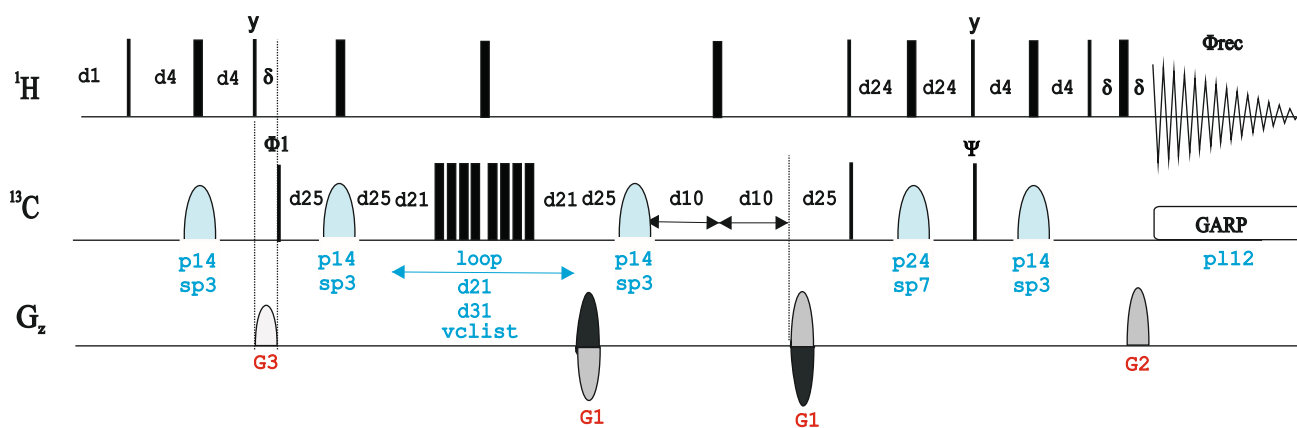
hsqct1etgpsi3d



hsqct1etgpsi3d.2



hsqct2etgpsi3d.2



2D HSQC experiments for ^{15}N Relaxation Measurements (from f3 channel)

- Heteronuclear ^{15}N - ^1H NOEs:

Phase sensitive ge-2D ^1H - ^{15}N HSQC to measure heteronuclear ^{15}N - ^1H NOEs using PEP
(**hsqcnoef3gpsi** | **HSQCNOEF3GPSI**)

Phase sensitive ge-2D ^1H - ^{15}N HSQC to measure heteronuclear ^{15}N - ^1H NOEs using TROSY
(**trnoef3gpsi** | **TRNOEF3GPSI**)

- T_1 (N):

Phase-sensitive ge-2D ^1H - ^{15}N HSQC to measure ^{15}N T_1 relaxation times using PEP:

Using 1H-decoupling (**hsqct1etf3gpsi** | **HSQCT1ETF3GPSI**)

Using 1H-decoupling acquired as pseudo-3D (**hsqct1etf3gpsi3d** | **HSQCT1ETF3GPSI3D**)

Using 180 1H pulses (**hsqct1etf3gpsi.2** | **HSQCT1ETF3GPSI.2**)

Using 180 1H pulses acquired as pseudo-3D (**hsqct1etf3gpsi3d.2** | **HSQCT1ETF3GPSI3D.2**)

Phase sensitive ge-2D ^1H - ^{15}N HSQC to measure ^{15}N T_1 relaxation times using TROSY:

Using 1H-decoupling (**trt1etf3gpsi** | **TRT1ETF3GPSI**)

Using 1H-decoupling acquired as pseudo-3D (**trt1etf3gpsi3d**)

Using 180 1H pulses acquired as pseudo-3D (**trt1etf3gpsi3d.2**)

- T_2 (N):

Phase-sensitive ge-2D ^1H - ^{15}N HSQC to measure ^{15}N T_2 relaxation times using PEP:

Acquired as individual 2D data (**hsqct2etf3gpsi** | **HSQCT2ETF3GPSI**):

Acquired as pseudo-3D (**hsqct2etf3gpsi3d** | **HSQCT2ETF3GPSI3D**)

Phase sensitive ge-2D ^1H - ^{15}N HSQC to measure ^{15}N T_2 relaxation times using TROSY:

Acquired as individual 2D (**trt2etf3gpsi** | **TRT2ETF3GPSI**)

Acquired as pseudo-3D (**trt2etf3gpsi3d**)

- $T_{1\rho}$ (N):

Phase-sensitive ge-2D ^1H - ^{15}N HSQC to measure ^{15}N $T_{1\rho}$ relaxation times using PEP:

Acquired as individual 2D data (**hsqctretf3gpsi** | **HSQCTRETF3GPSI**)

Acquired as pseudo-3D (**hsqctretf3gpsi3d** | **HSQCTRETF3GPSI3D**)

With adiabatic ramping and acquired as pseudo-3D (**hsqctretf3gpsi3d.2** |

HSQCTRETF3GPSI3D.2)

Phase-sensitive ge-2D ^1H - ^{15}N HSQC to measure ^{15}N $T_{1\rho}$ relaxation times using TROSY:

Acquired as pseudo-3D (**trtretf3gpsi3d**)

- R_{exchange} (N):

Phase sensitive ge-2D ^1H - ^{15}N HSQC to measure ^{15}N -R(exchange) using PEP and Relaxation-dispersion (**hsqcrexetf3gpsi3d** | **HSQCTREXETF3GPSI3D**)

Phase sensitive ge-2D ^1H - ^{15}N HSQC to measure ^{15}N -R(exchange) using TROSY and Relaxation-dispersion (**trrexetf3gpsi3d**)

Phase sensitive ge-2D ^1H - ^{15}N HSQC to measure ^{15}N -exchange

Using PEP (**hsqcetexf3gp**)

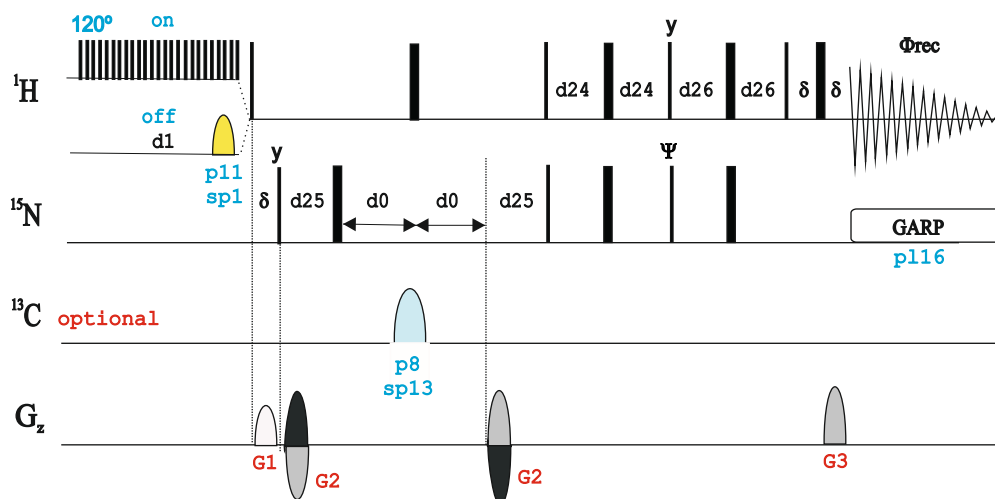
Using WATERGATE (**hsqcexf3gpwgh**)

Using TROSY (**tretexf3gp**)

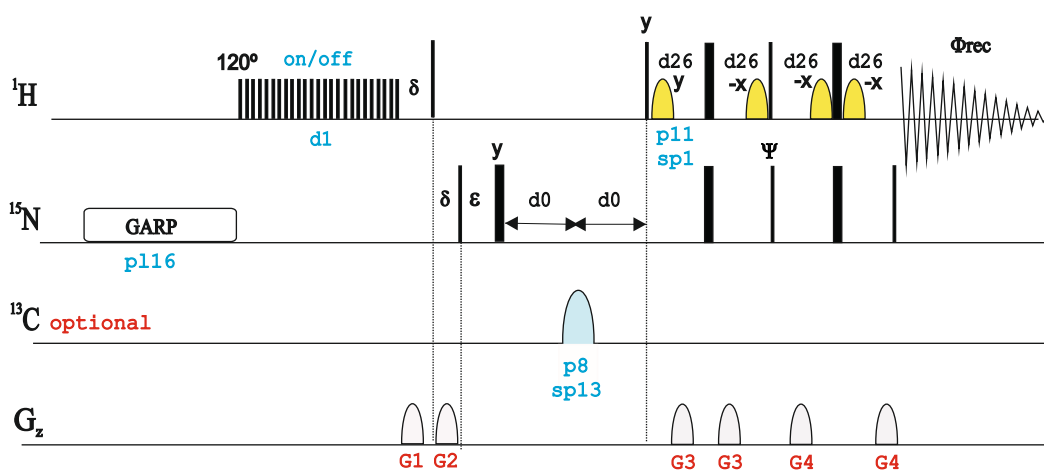
- Cross-correlation:

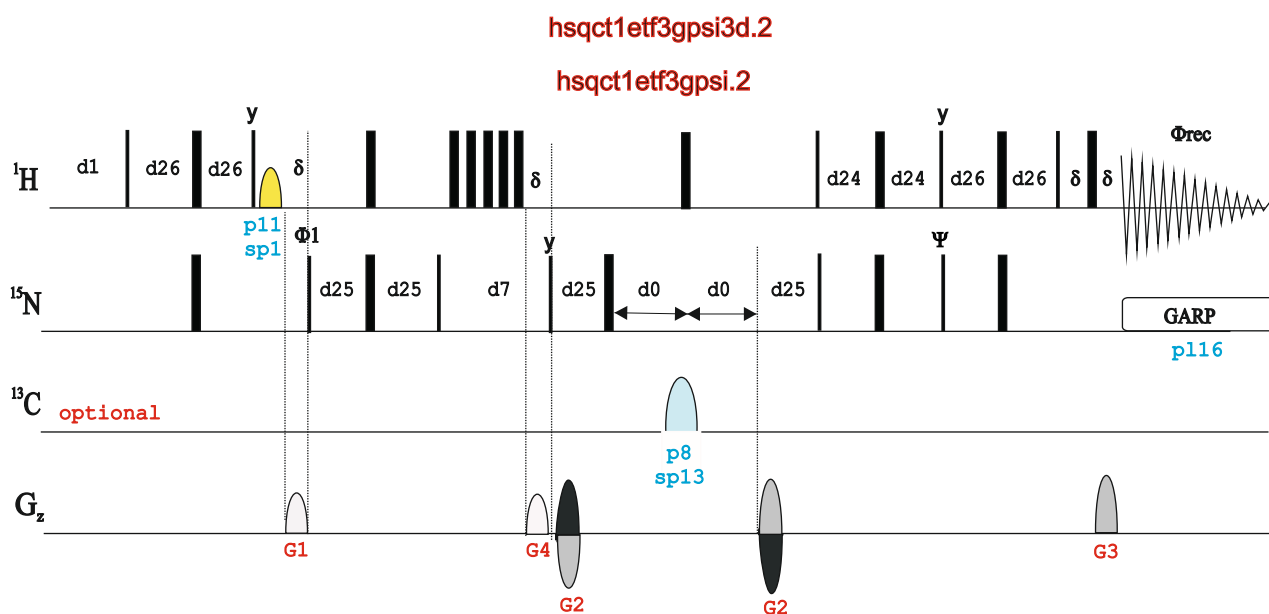
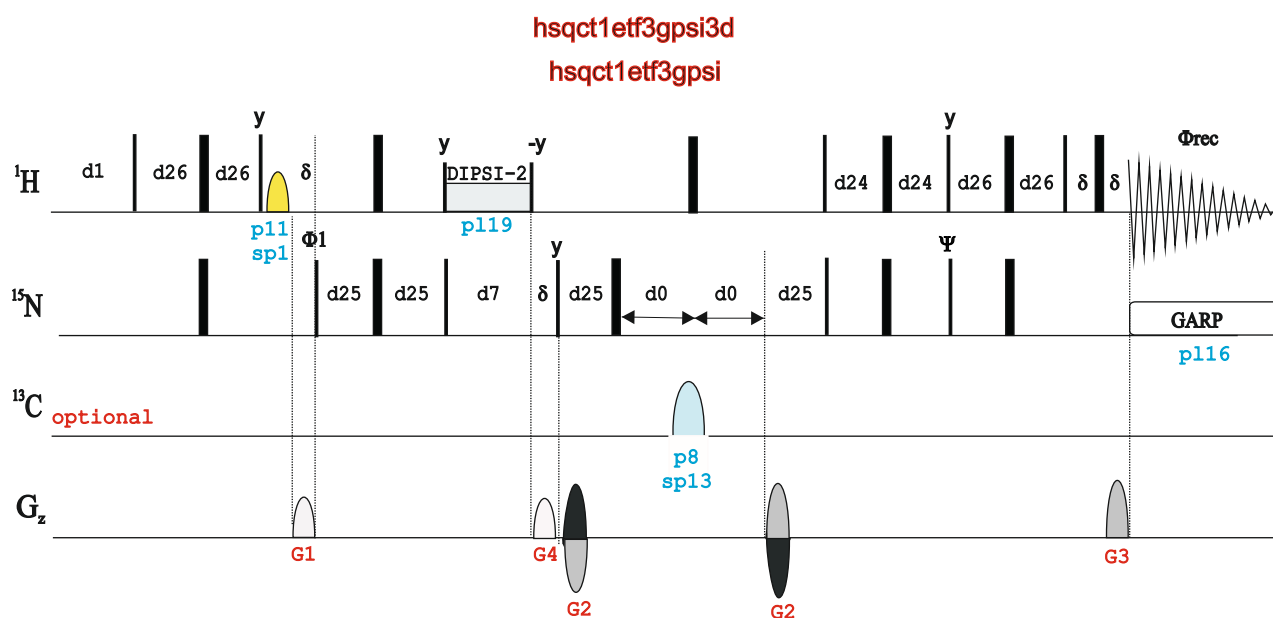
Phase-sensitive ge-2D ^1H - ^{15}N HSQC to measure N-15 / H-1 cross correlation (**hsqcccf3gpwhg**)

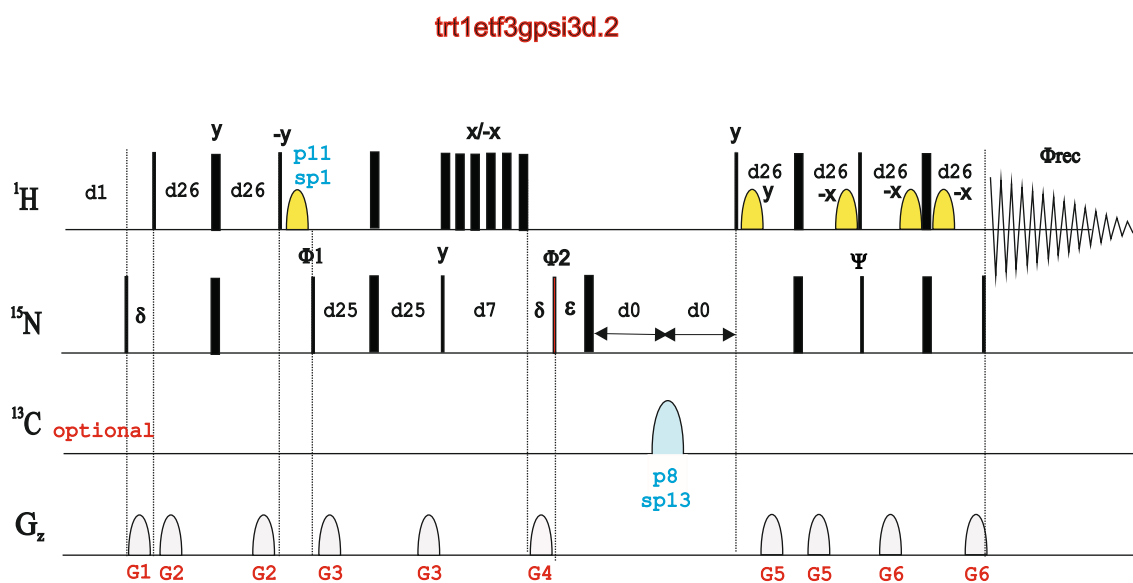
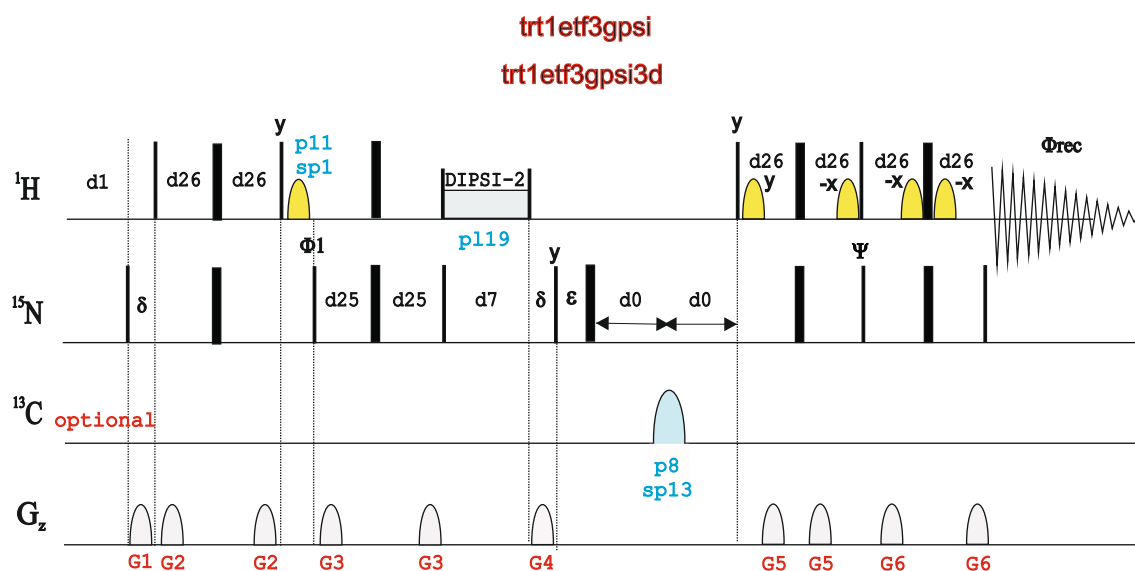
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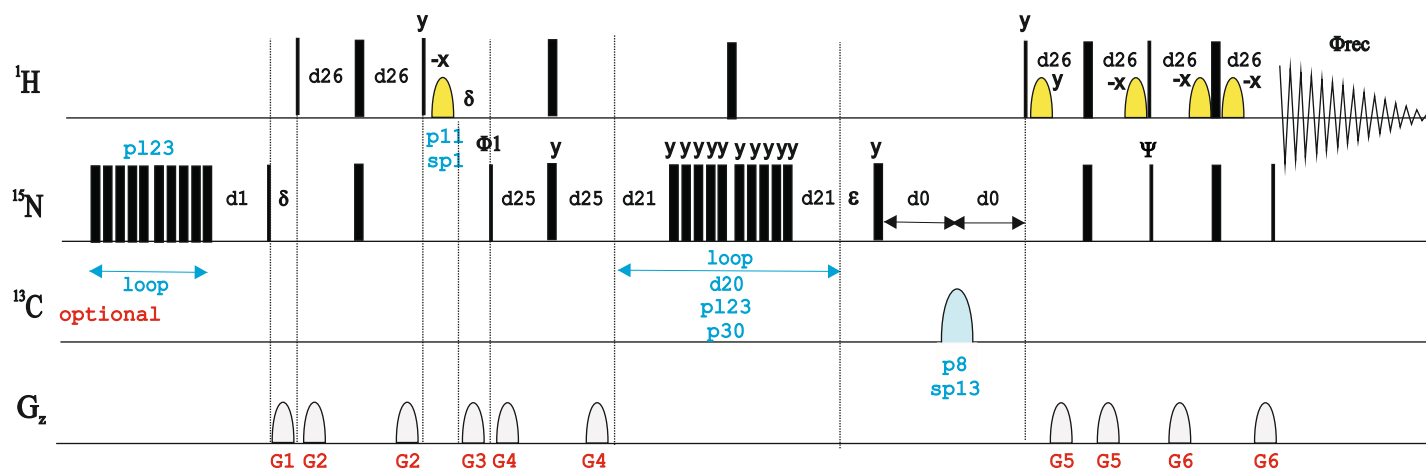
trnoef3gpsi



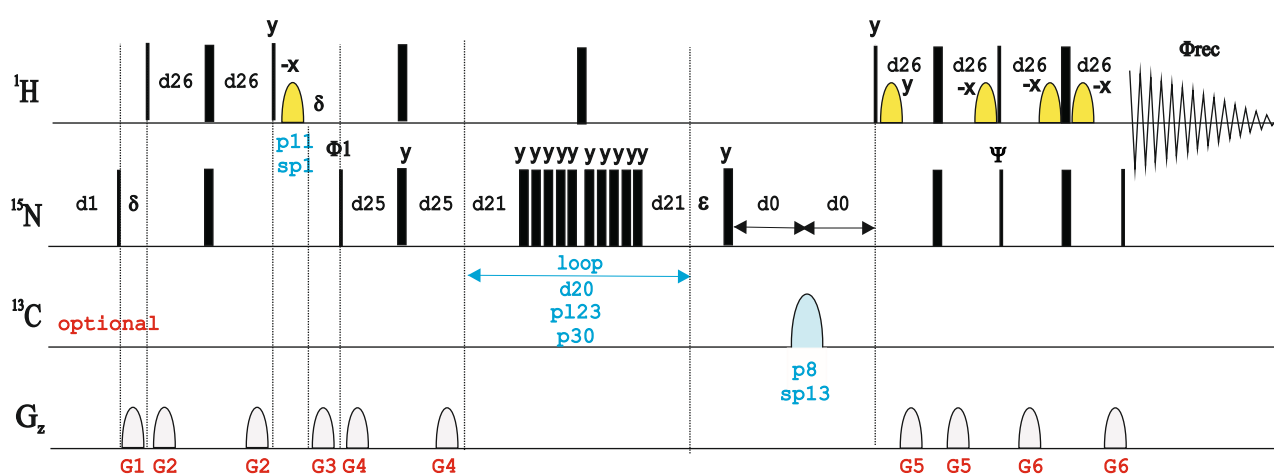


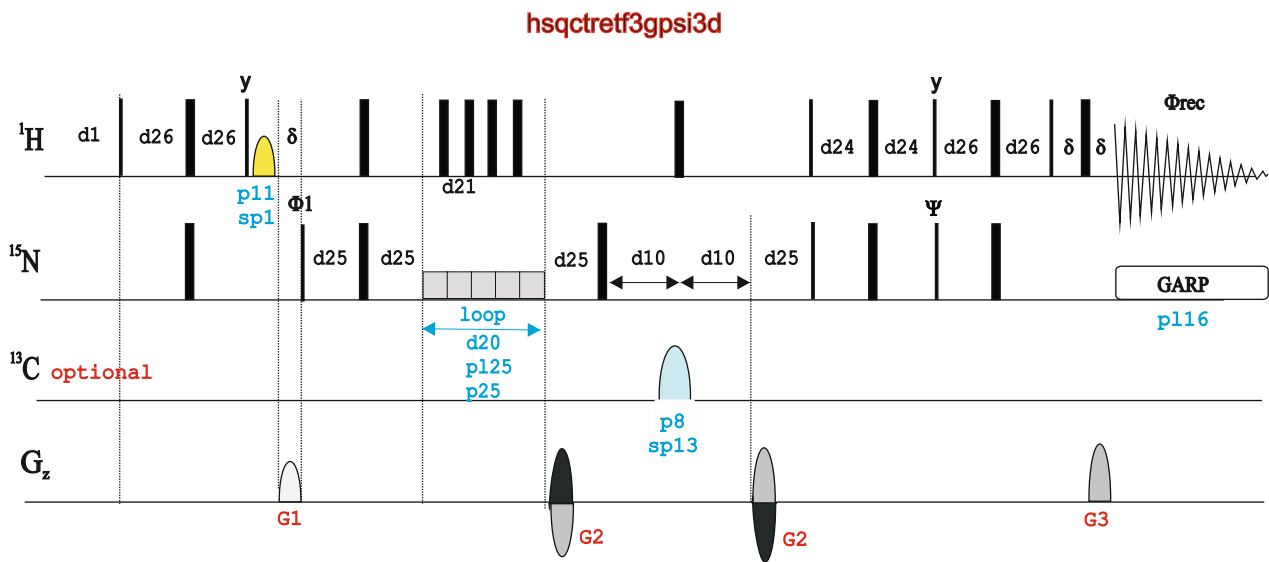
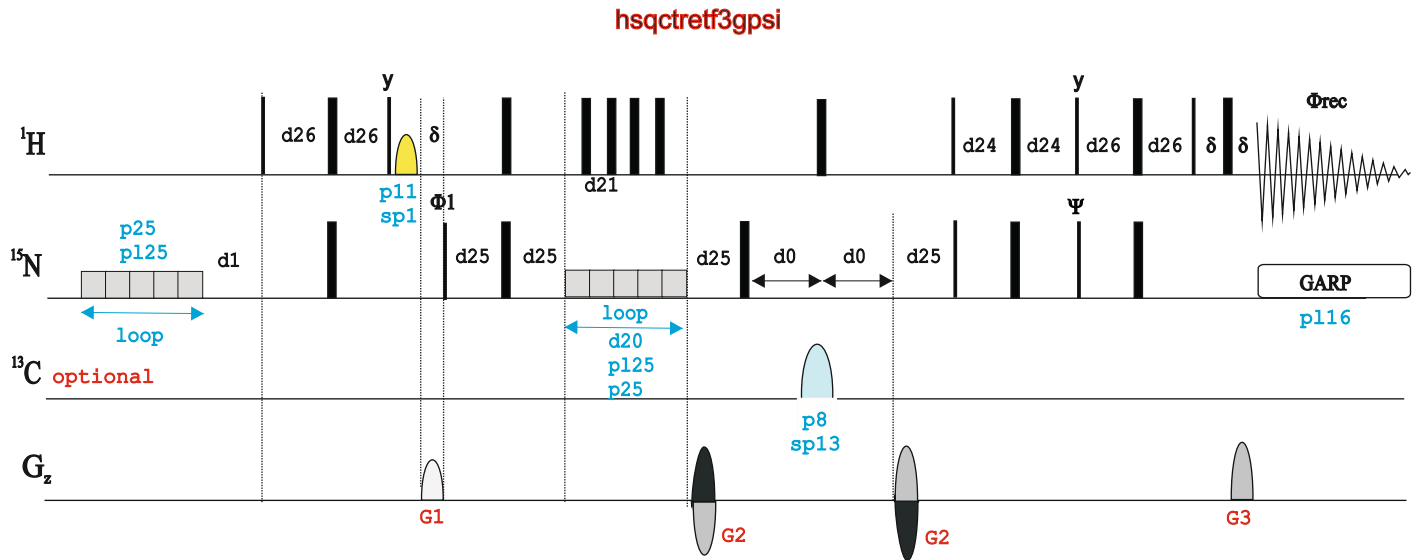


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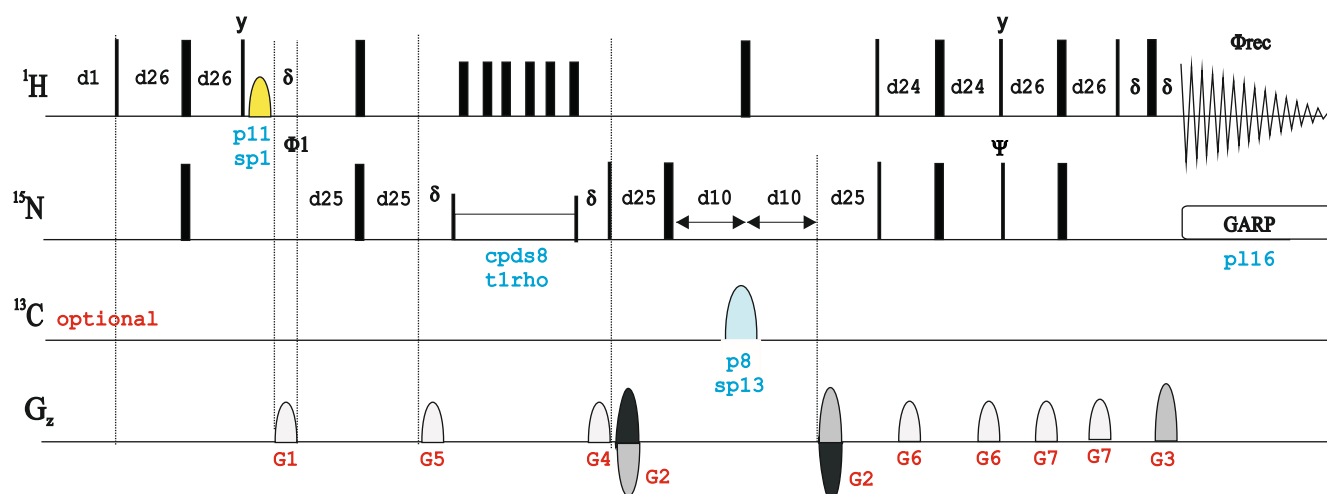


trt2etf3gpsi3d

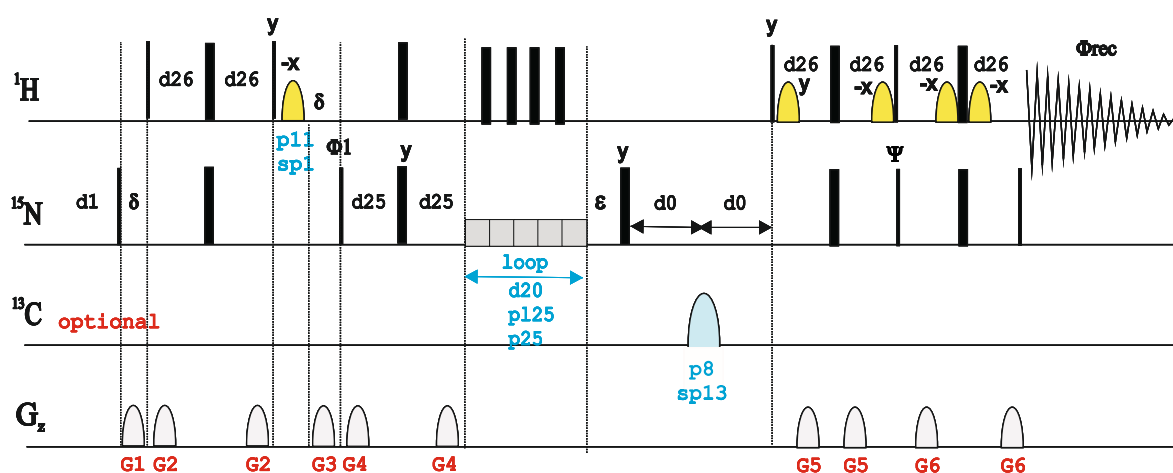




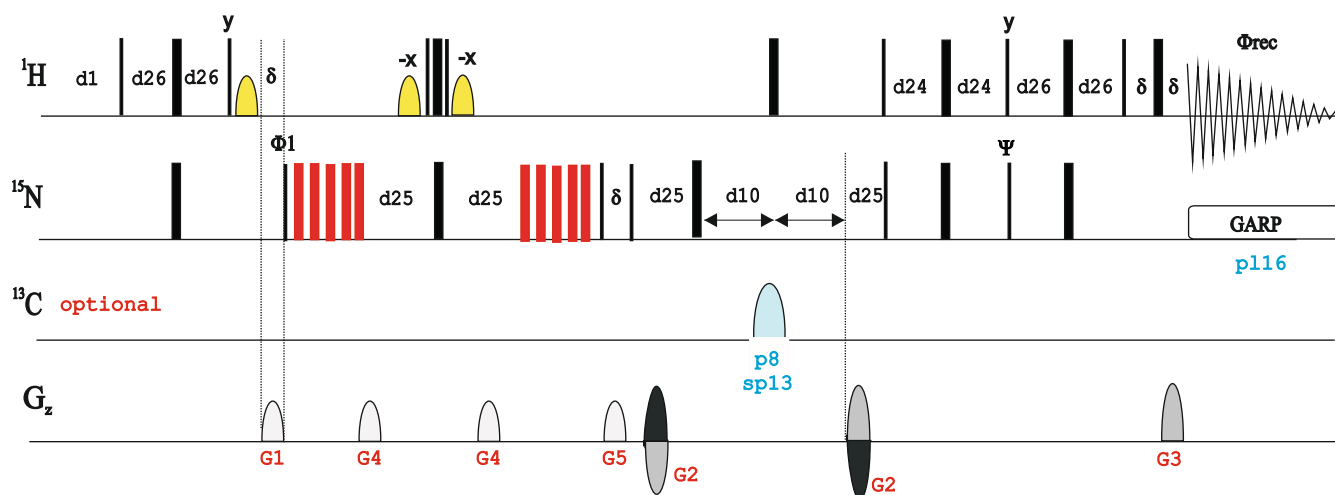
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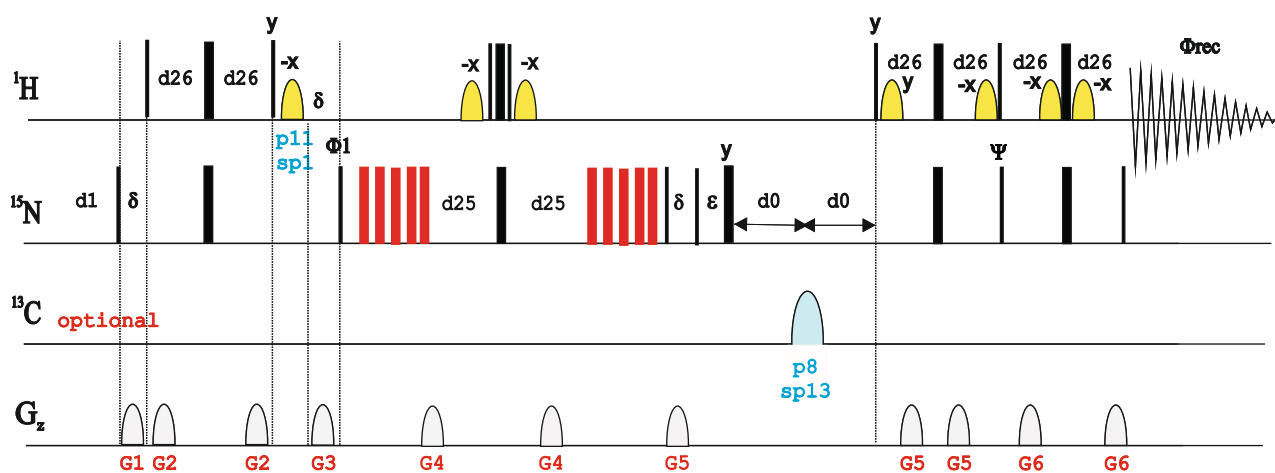
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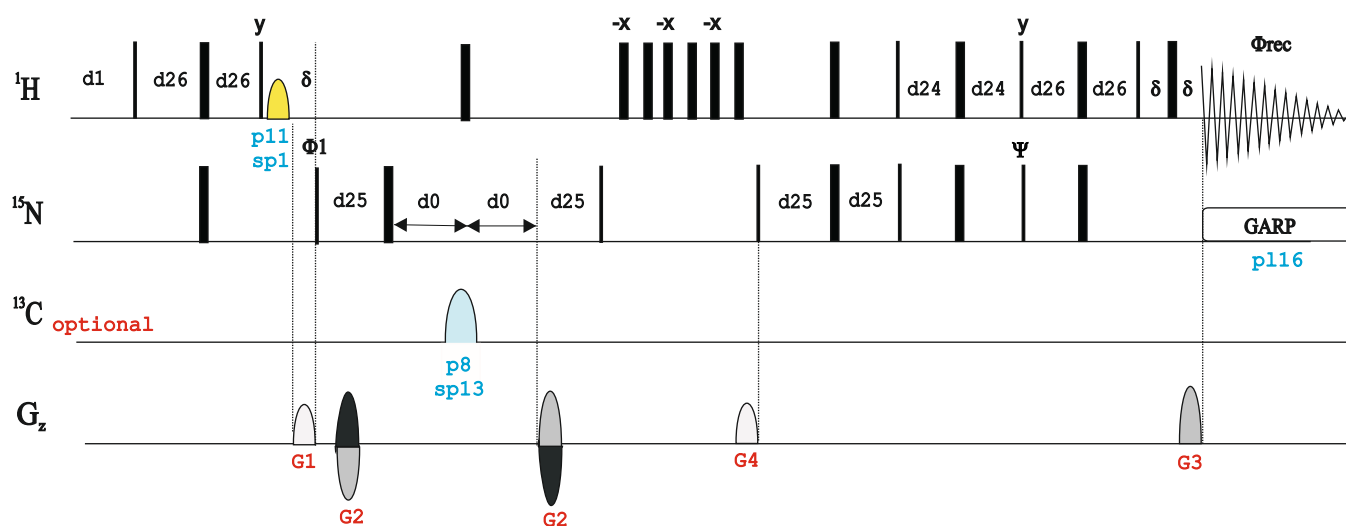
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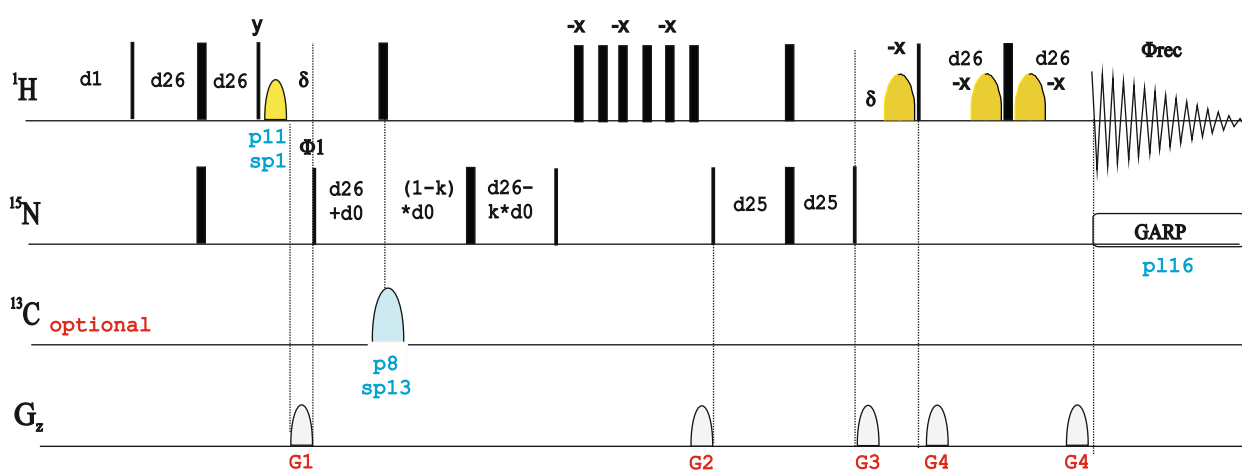
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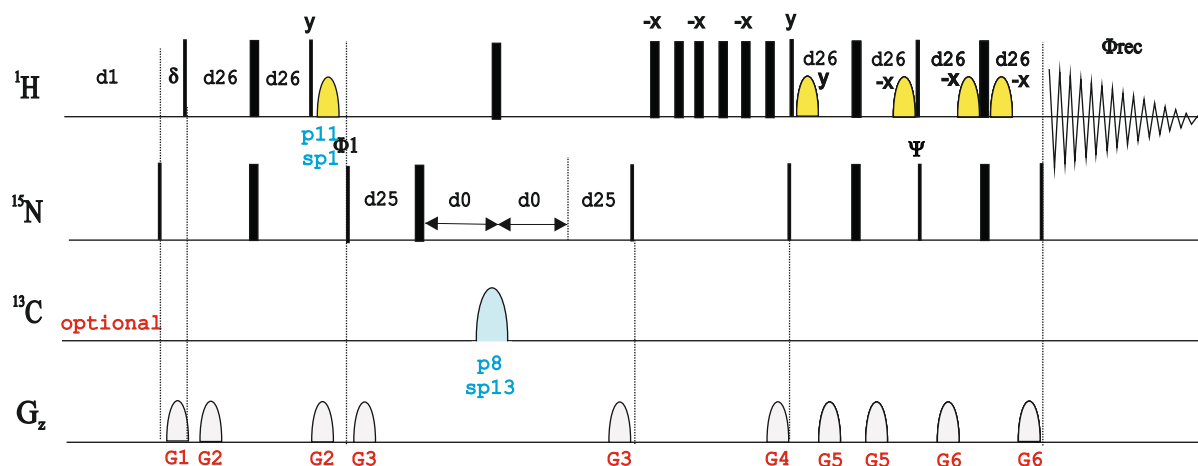
hsqcetextf3gp



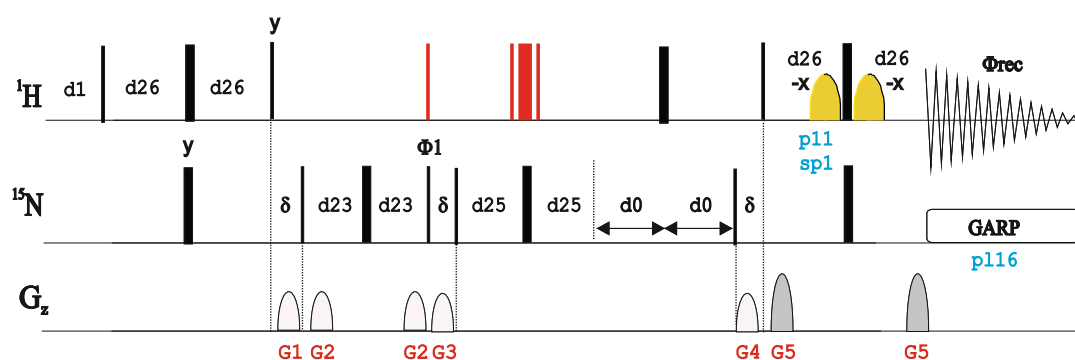
hsqcexf3gpwgph



tretef3gp



hsqccc3gp phwg



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NMRGuide

3D HNCO EXPERIMENTS FOR
THE MEASUREMENT OF T₁, T₂ AND T₁RHO
RELAXATION TIMES.

3D HNCO experiments for ^{15}N Relaxation Measurements

- Heteronuclear ^{15}N - ^1H NOEs:

3D HNCO to measure heteronuclear ^{15}N - ^1H NOEs using PEP (hnconoef3gpsi)

- T_1 (N):

3D HNCO to measure ^{15}N T_1 relaxation times

Using PEP (hncot1f3gpsi)

Using TROSY (trhncot1f3gp)

- T_2 (N):

3D HNCO to measure ^{15}N T_2 relaxation times

Using PEP (hncot2f3gpsi)

Using TROSY (trhncot2f3gp)

- $T_{1\rho}$ (N):

3D HNCO to measure ^{15}N $T_{1\rho}$ relaxation times

Using PEP (hncotr1f3gpsi)

Using TROSY (trhncotr1f3gp)

- R_{exchange} (N):

3D HNCO to measure ^{15}N R_{exchange}

Using PEP (hncorex1f3gpsi)

Using TROSY (trhncorex1f3gp)

Also see:

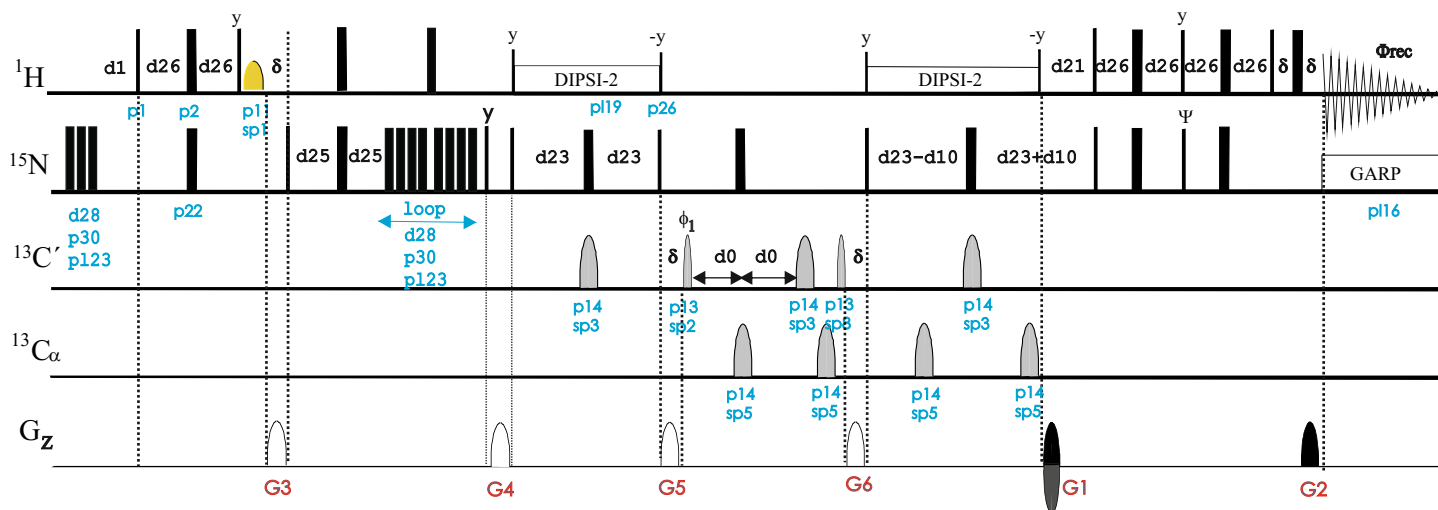
T1 & T2 Relaxation

2D HSQC Experiments for Relaxation Measurements

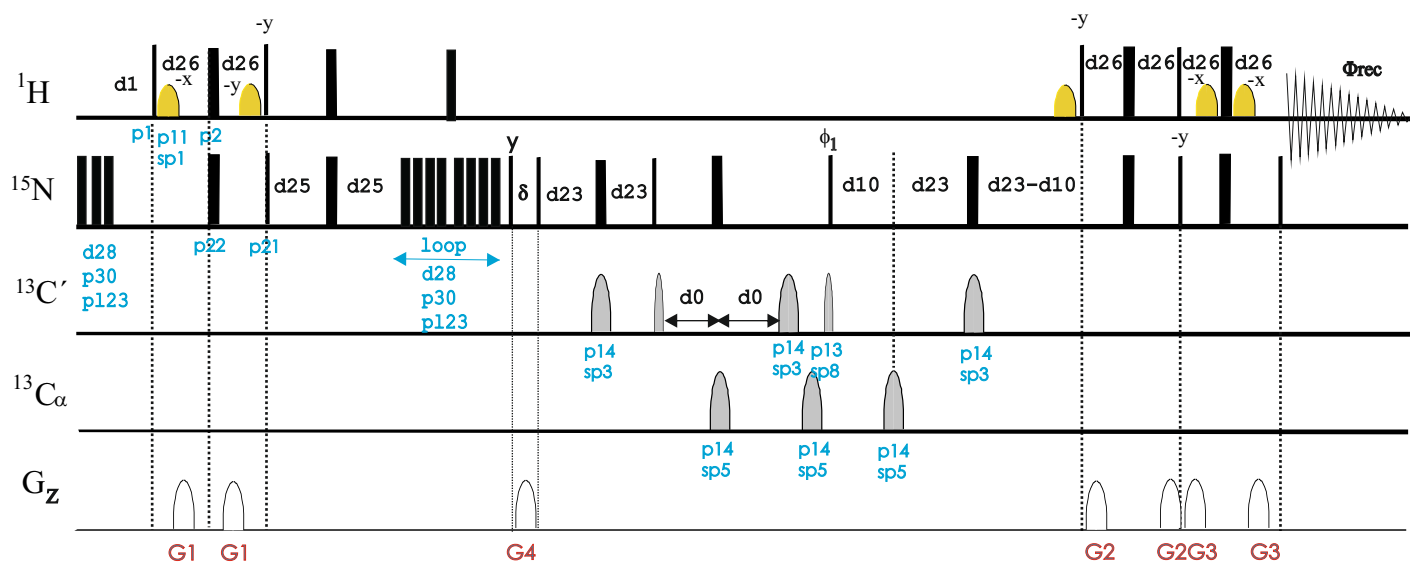


V. Tugarinov, W.-Y. Choy, E. Kupce & L.E. Kay, J. Biomol. NMR 30, 347-352 (2004)

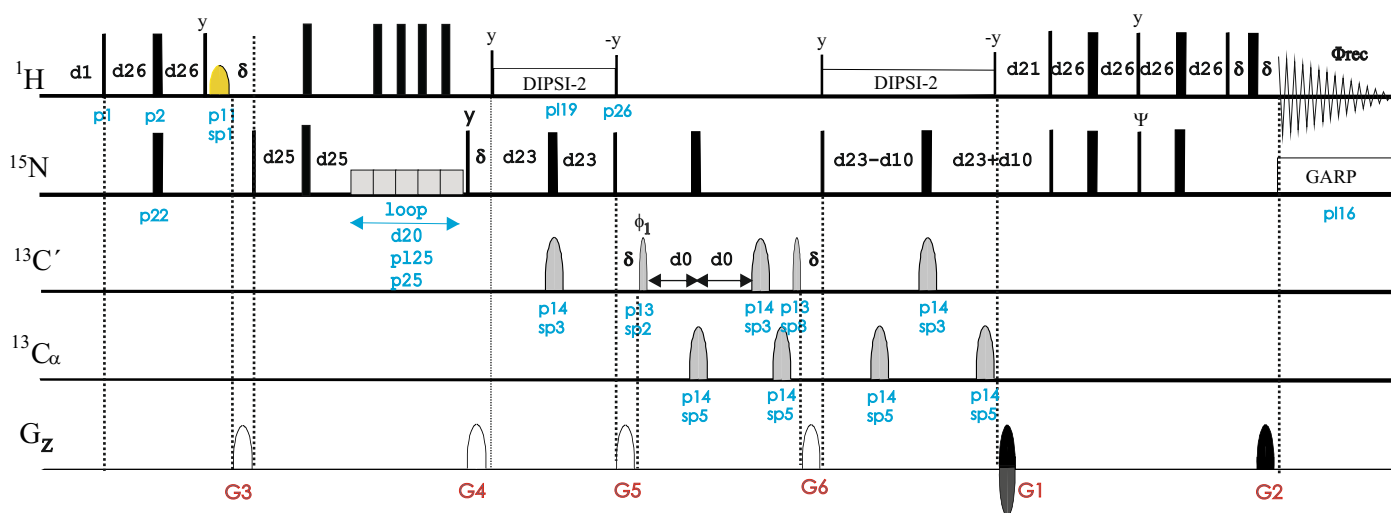
hncot2f3gpsi



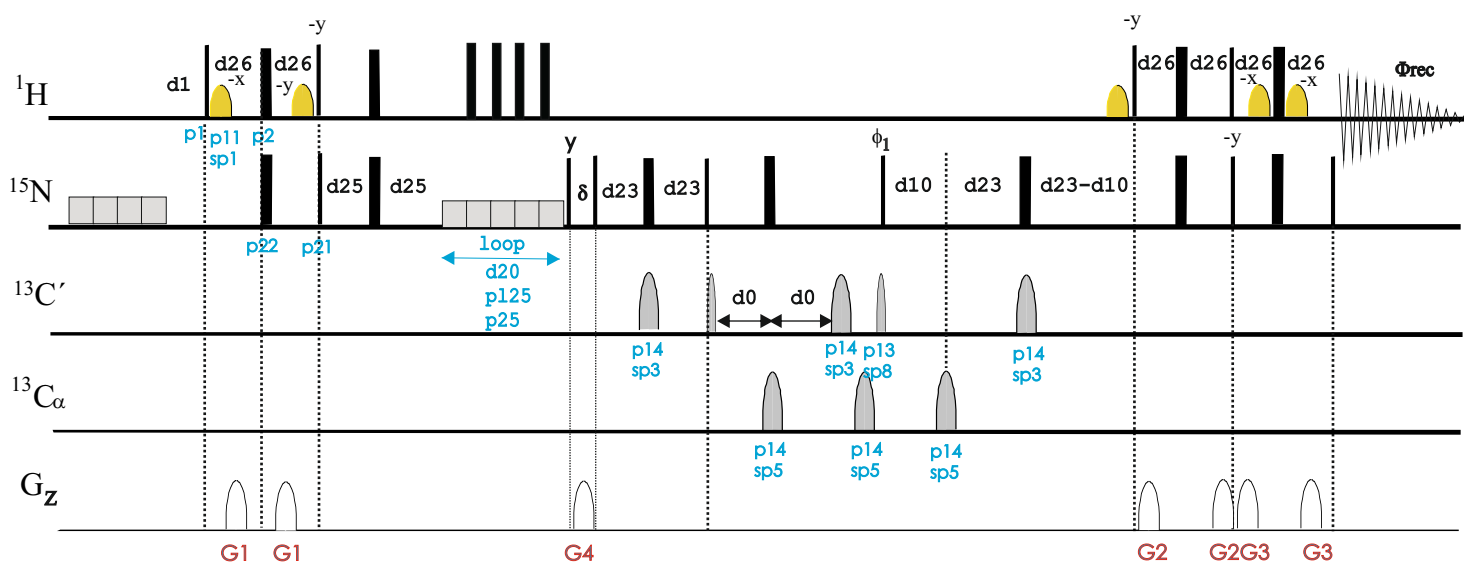
trhncot2f3gp



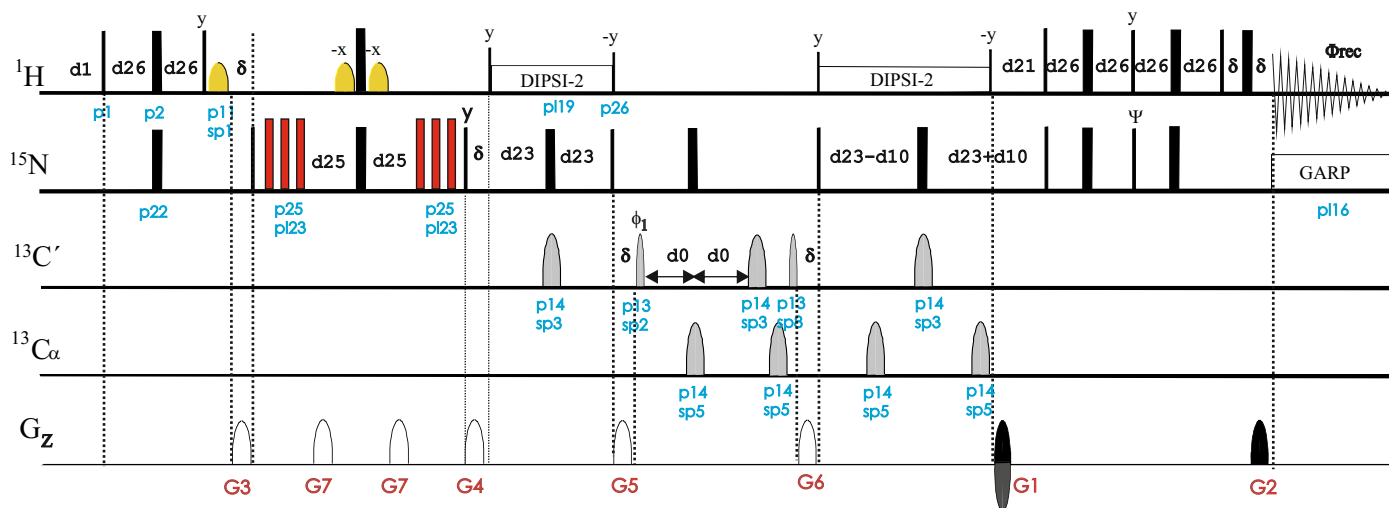
hncotr3gpsi



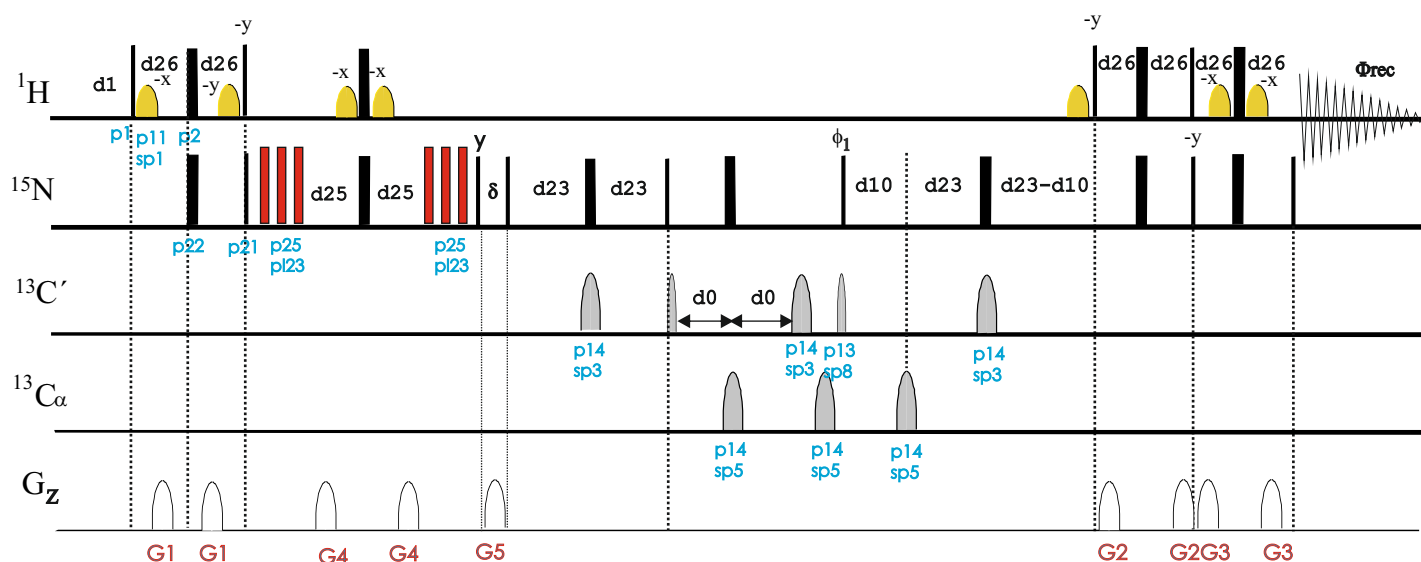
trhncotr3gp



hncorexf3gpsi



trhncorexf3gp



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NMRGuide

PROTEIN NMR COUPLING CONSTANTS

Protein NMR Coupling Constants

[Tutorials: J Backbone](#)
[Tutorials: J Sidechain](#)
[Tutorials: J Miscellaneous](#)

NMR Experiments

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[Determination](#)
[J-Resolved](#)
[Spin-State Selective](#)
[E.COSY](#)
[TROSY/antiTROSY](#)
[J-scaling](#)
[J-Quantitative](#)
[DQ-ZQ](#)

Scalar Couplings (J)

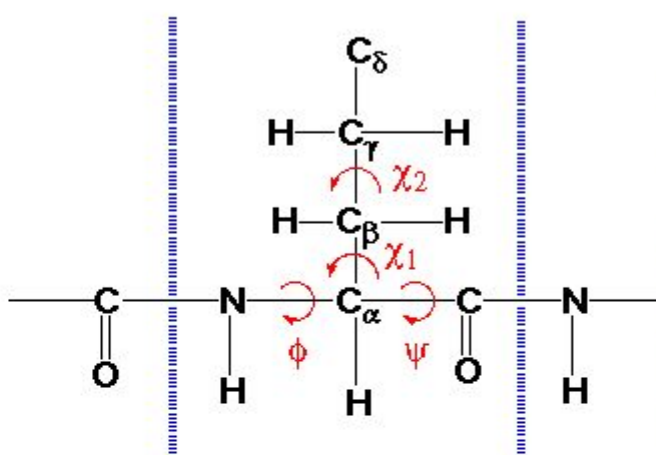
[One-bond](#)
[Two-bond](#)
[Three-bond](#)

[Backbone Three-bond \$\phi\$](#)
[Backbone Three-bond \$\omega\$](#)
[Backbone Three-bond \$\psi\$](#)
[Sidechain Three-bond \$\chi_1\$](#)
[Sidechain Three-bond \$\chi_2\$](#)

Dipolar Couplings (D)

[Introduction](#)
[Anisotropic Media](#)
[NMR Experiments](#)
[Structure Calculation](#)

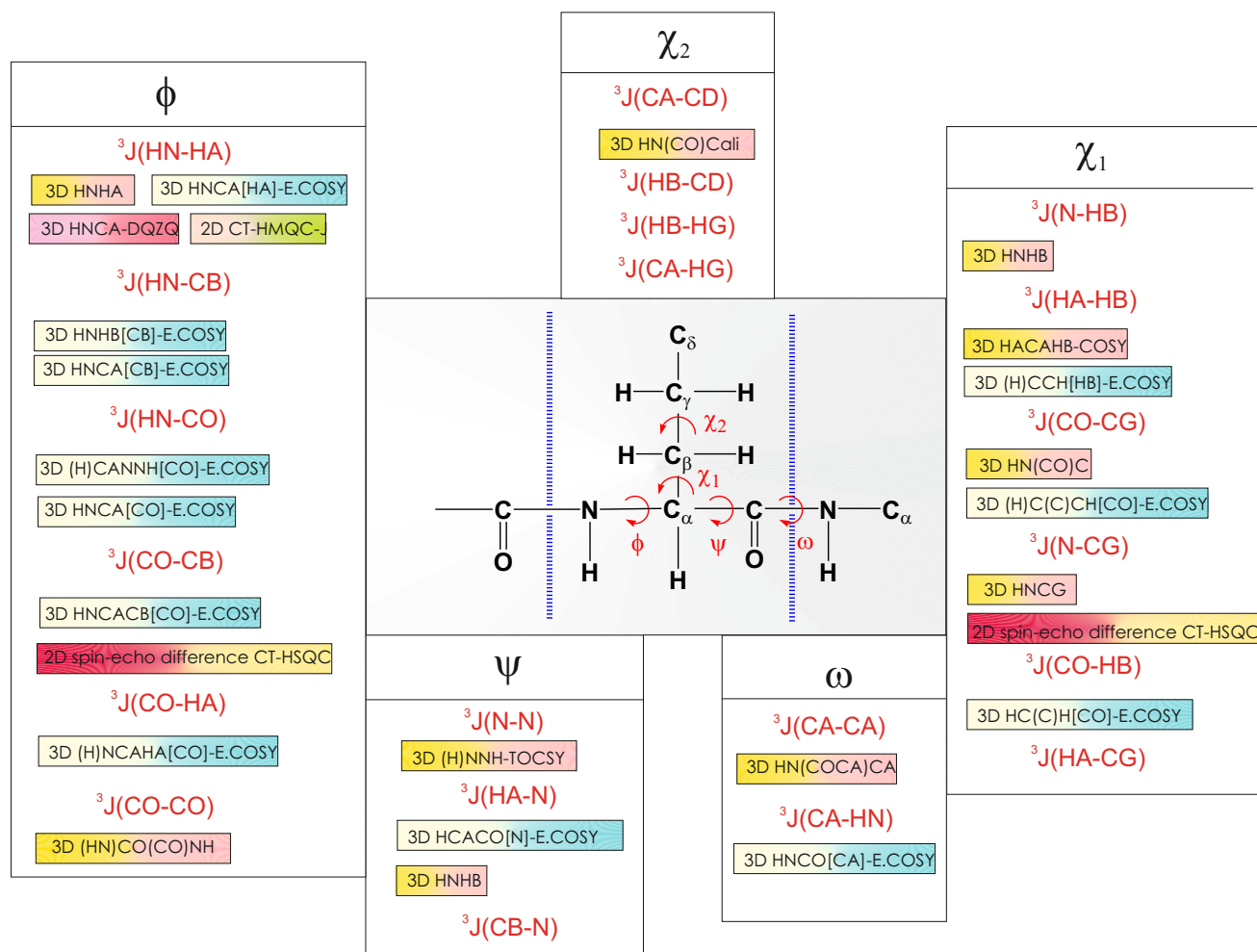
[Cross-Hydrogen Bond \(\$^hJ\$ \)](#)
[Introduction](#)
[NMR Experiments](#)
[Applications](#)



Applications

[2D Experiments](#) | [3D Double-Resonance Experiments](#)
[3D Triple-Resonance Experiments](#)

General Reading: [76PROG41](#), [B03ZER147](#)



PROTEIN NMR COUPLING CONSTANTS

Phi Backbone Coupling Constant

- 3D HNHA experiment (**hnhagp3d** | **HNHAGP3D**) - $3J(\text{HN-HA})$ via quantitative-J
- 3D HNCA[HA,CB]-E.COSY (**hncaecosgp3d** | **HNCAECOSGP3D**) - $3J[\text{H(N)-HA}]$ and $3J[\text{H(N)-CB}]$ via E.COSY
- 3D HNCA[HA]-E.COSY (**hncaecosgp3d2** | **HNCAECOSGP3D2**) - $3J[\text{H(N)-HA}]$ via E.COSY
- 3D DQ/ZQ HNCA (**hncadqzqgp3d** | **HNCADQZQGP3D**) - $3J[\text{H(N)-HA}]$ and $3J[\text{H(N)-CB}]$ via DQ/ZQ
- 2D CT-HMQC-J (**hmqcjpg** | **HMQCJGP**) - $3J[\text{H(N)-HA}]$ via J-modulation
- 3D HNHB[CB]-E.COSY (**hnhbecosgp3d** | **HNHBECOSGP3D**) - $3J[\text{H(N)-CB}]$ via E.COSY
- 3D HNCA[CB]-E.COSY (**hncajcgp3d** | **HNCAJCGP3D**) - $3J[\text{H(N)-CB}]$ via E.COSY
- 3D (H)CANNH[CO]-E.COSY (**hcannhgp3d** | **HCANNHGP3D**) - $3J[\text{H(N)-CO}]$ via E.COSY
- 3D HNCA[CO]-E.COSY (**hncacosygp3d** | **HNCA COSYGP3D**) - $3J[\text{H(N)-CO}]$ via E.COSY
- 3D HNACB[CO]-E.COSY (**hncacbgpjc3d** | **HNACBGPJC3D**) - $3J[\text{CO-CB}]$ via E.COSY
- 2D spin-echo difference CT-HSQC (**hsqccte tgpjclr** | **HSQCCTETGPJCLR**) - $3J[\text{CO-CB}]$ via spin-echo difference
- 3D (H)NCAHA[CO]-E.COSY (**hncahagp3d** | **HNCAHAGP3D**) - $3J[\text{HA-CO}]$ via E.COSY
- 3D (HN)CO(CO)NH (**hncocogp3d** | **HNCOCOGP3D**) - $3J[\text{CO-CO}]$ via quantitative-J

Psi Backbone Coupling Constant

- 3D (H)NNH-TOCSY (**hnnhdigp3d** | **HNNHDI GP3D**) - $3J[\text{N-N}]$ via quantitative-J
- 3D HCACO[N]-E.COSY (**hcacogpjc3d** | **HCACOGPJ C3D**) - $3J[\text{HA-N}]$ via E.COSY
- 3D HNHB (**hnhbgp3d** | **HNHBGP3D**) - $3J[\text{HN-HA}]$ and $3J[\text{HN-HB}]$ via quantitative-J

Omega Backbone Coupling Constant

- 3D HN(CO)CA (**hncocacagp3d** | **HNCOACAGP3D**) - $3J[\text{CA-CA}]$ via quantitative-J
- 3D HNCO[CA]-E.COSY (**hncoccosgp3d** | **HNCOECOSGP3D**) - $3J[\text{H(N)-CA}]$ via E.COSY

Chi1 Sidechain Coupling Constant

- 3D HNHB (**hnhbgp3d** | **HNHBGP3D**) - $3J[\text{HN-HA}]$ and $3J[\text{HN-HB}]$ via quantitative-J
- 3D HACAHB-COSY (**hacahbcosygp3d** | **HACAHBCOSYGP3D**) - $3J[\text{HA-HB}]$ via quantitative-J
- 3D HN(CO)C (**hncocgp3d** | **HNCOGP3D**) - $3J[\text{CG-CO}]$ via quantitative-J
- 3D HC(C)H[HA]-E.COSY (**hcchecosgp3d** | **HCCHECOSGP3D**) - $3J[\text{HA-HB}]$ via E.COSY
- 3D HC(C)H[CO]-E.COSY (**hcchcosygp3d** | **HCCHCOSYGP3D**) - $3J[\text{CO-HB}]$ via E.COSY
- 3D (H)C(C)CH[CO]-E.COSY (**hccccosygp3d** | **HCCCCOSYGP3D**) - $3J[\text{CG-CO}]$ via E.COSY
- 3D HNCG (**hncggp3d.1** | **HNCGGP3D.1**) - $3J[\text{N-CG}]$ via quantitative-J
- 3D HNCG (**hncggp3d.2** | **HNCGGP3D.2**) - $3J[\text{N-CG}]$ via quantitative-J
- 2D spin-echo difference CT-HSQC (**hsqcetf pf3gpjcsi** | **HSQCETFPF3GPJCSI**) - $3J[\text{N-CG}]$ via spin-echo difference

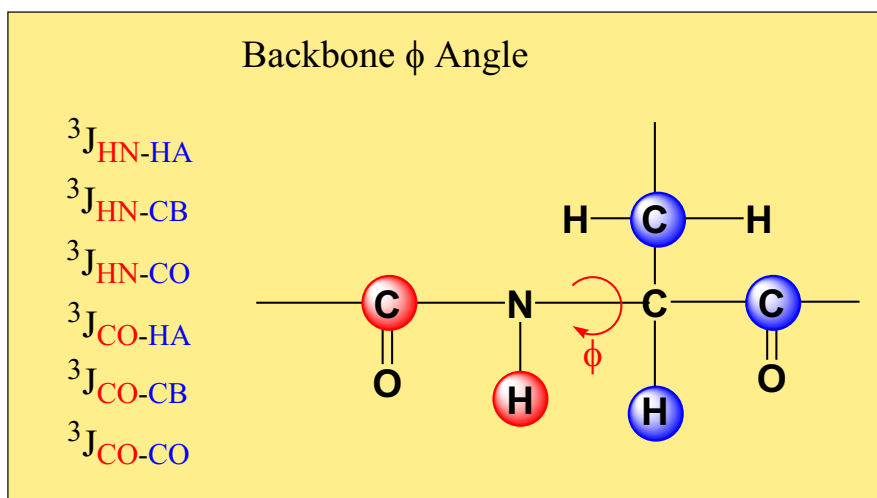
Chi2 Sidechain Coupling Constant

- 3D HN(CO)CAlI (**hncocacgp3d** | **HNCOACGP3D**) - $3J[\text{CA-CD}]$ via quantitative-J

BRUKER PULSE PROGRAM CATALOGUE

NMRGuide

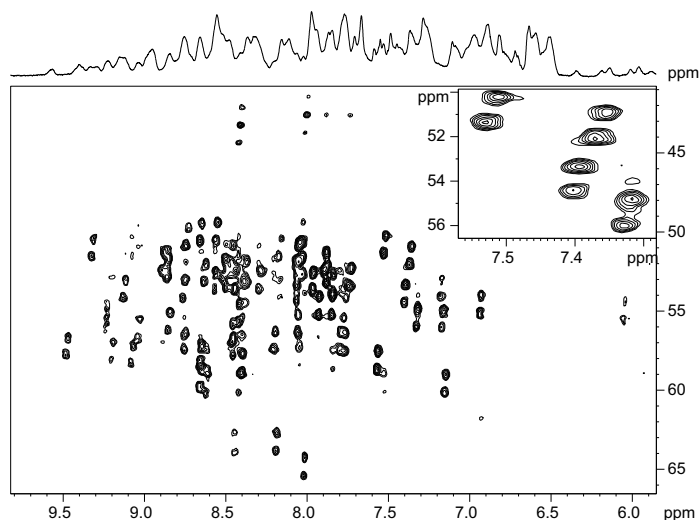
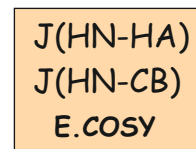
PROTEIN NMR
COUPLING CONSTANTS
PHI BACKBONE ANGLE



Phi Backbone Coupling Constant

- 3D HNHA experiment (**hnhagp3d** | **HNHAGP3D**) - $^3J(\text{HN-HA})$ via quantitative-J
- 3D HNCA[HA,CB]-E.COSY (**hncacosgp3d** | **HNCAECOSGP3D**) - $^3J[\text{H(N)-HA}]$ and $^3J[\text{H(N)-CB}]$ via E.COSY
- 3D HNCA[HA]-E.COSY (**hncacosgp3d2** | **HNCAECOSGP3D2**) - $^3J[\text{H(N)-HA}]$ via E.COSY
- 3D DQ/ZQ HNCA (**hncadqzqgp3d** | **HNCADQZQGP3D**) - $^3J[\text{H(N)-HA}]$ and $^3J[\text{H(N)-CB}]$ via DQ/ZQ
- 2D CT-HMQC-J (**hmqcjgp** | **HMQCJGP**) - $^3J[\text{H(N)-HA}]$ via J-modulation
- 3D HNHB[CB]-E.COSY (**hnhbecosgp3d** | **HNHBECOSGP3D**) - $^3J[\text{H(N)-CB}]$ via E.COSY
- 3D HNCA[CB]-E.COSY (**hncajcgp3d** | **HNCAJCGP3D**) - $^3J[\text{H(N)-CB}]$ via E.COSY
- 3D (H)CANNH[CO]-E.COSY (**hcannhgp3d** | **HCANNHGP3D**) - $^3J[\text{H(N)-CO}]$ via E.COSY
- 3D HNCA[CO]-E.COSY (**hncacosygp3d** | **HNCACOSYGP3D**) - $^3J[\text{H(N)-CO}]$ via E.COSY
- 3D HNACB[CO]-E.COSY (**hncacbgpj3d** | **HNACBGPJC3D**) - $^3J[\text{CO-CB}]$ via E.COSY
- 2D spin-echo difference CT-HSQC (**hsqcctetgpcjclr** | **HSQCCTETGPJCLR**) - $^3J[\text{CO-CB}]$ via spin-echo difference
- 3D (H)NCAHA[CO]-E.COSY (**hncahagp3d** | **HNCAHAGP3D**) - $^3J[\text{HA-CO}]$ via E.COSY
- 3D (HN)CO(CO)NH (**hncocogp3d** | **HNCOCOGP3D**) - $^3J[\text{CO-CO}]$ via quantitative-J

3D HNCA[HA,CB]-E.COSY Experiment



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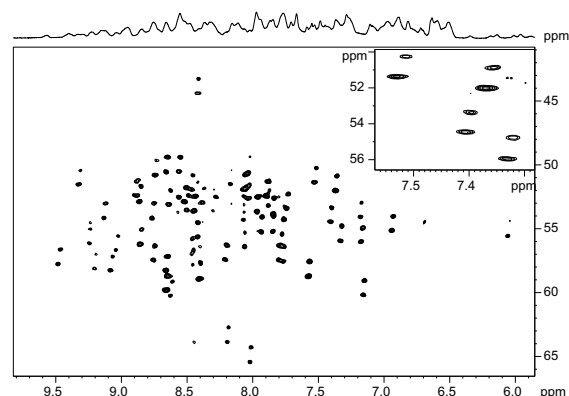
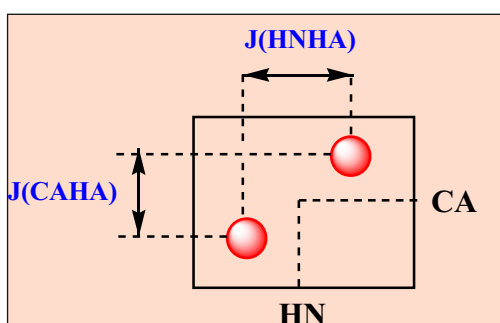
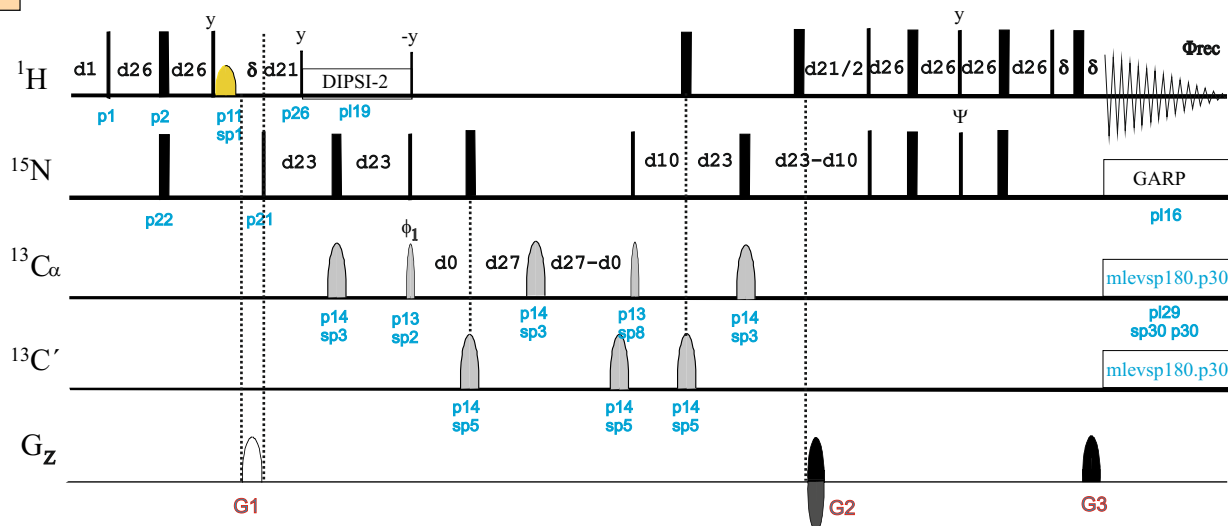
HNCA[HA]

$^1J_{HN} + ^1J_{NCA}$
 $^1J_{HN} + ^2J_{NCA}$

Chemical structure diagram illustrating the HNCA[HA] experiment. The structure shows two adjacent amino acid residues. The first residue (left) has a methyl group (CH₃) and an amide group (NH). The second residue (right) has a methyl group (CH₃) and an amide group (NH). A red arrow indicates the transfer of magnetization from the α -carbon of the first residue to the nitrogen of the second residue. The diagram is labeled with $^1J_{HN} + ^1J_{NCA}$ and $^1J_{HN} + ^2J_{NCA}$.

d21: 1/(2J(NH)	[5.5 msec]
d23: 1/(4J(NCa)	[12 msec]
d26: 1/(4J'(NH)	[2.3 msec]
d27: constant time delay T(C)	[13.3 msec]

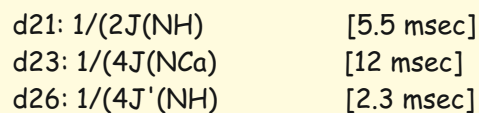
hncaecosgp3d2



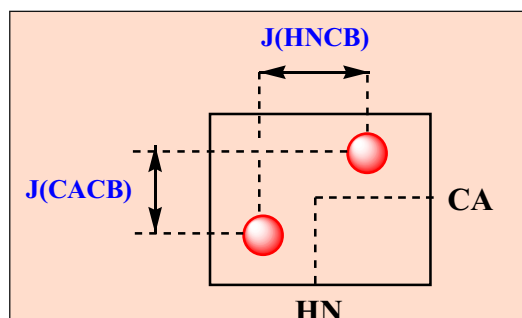
Related Experiments:

© 2010, BRUKER Biospin, Teodor Parella

3D HNCA[CB]-E.COSY Experiment



J(HN-CB)
E.COSY



A.C. Wang & A. Bax, *J. Am. Chem. Soc.* 118, 2483-2494 (1996)

Related Experiments:

See original 3D HNCA Experiment

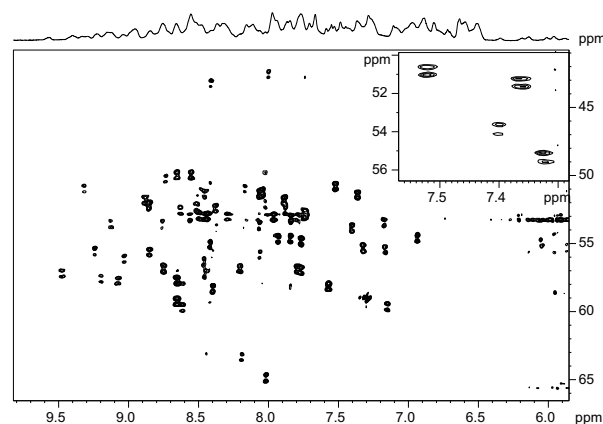
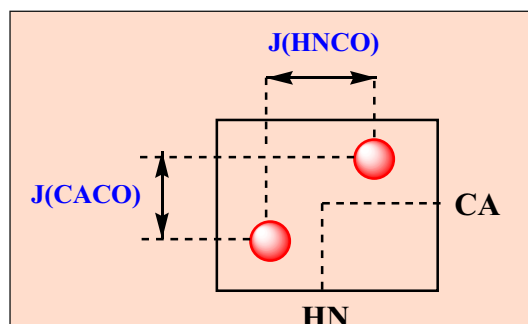
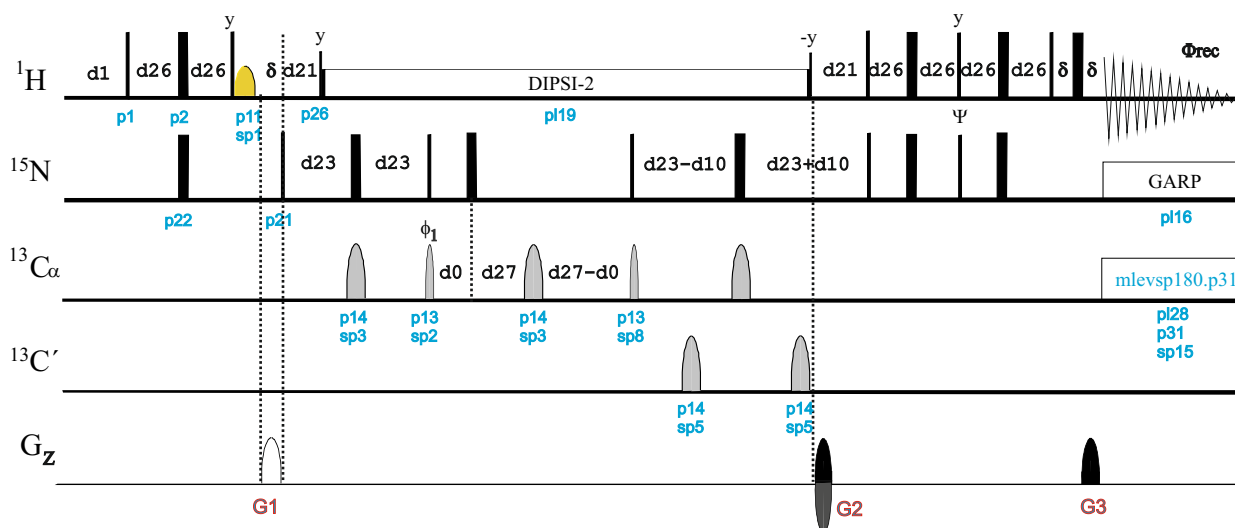
HNCA[CO]

$^1J_{HN} + ^1J_{NCA}$
 $^1J_{HN} + ^2J_{NCA}$

Diagram illustrating the HNCA[CO] experiment. The structure shows a protein backbone fragment (left) and a side chain (right). The HNCA[CO] experiment is used to correlate the chemical shifts of the ^1H and ^{13}C atoms in the backbone and side chain. The diagram shows the transfer of magnetization from the ^1H and ^{13}C atoms in the backbone to the ^1H and ^{13}C atoms in the side chain.

d21: 1/(2J(NH)	[5.5 msec]
d23: 1/(4J(NCa)	[12 msec]
d26: 1/(4J'(NH)	[2.3 msec]
d27: constant time delay T(C)	[13.3 msec]

hncacosygp3d

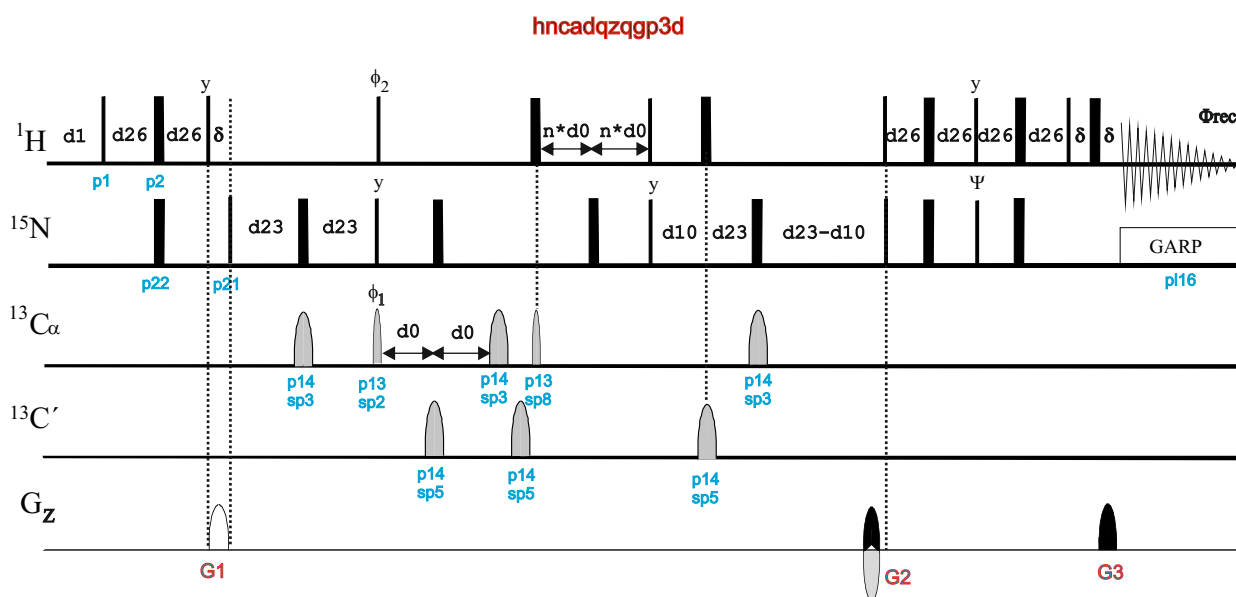


R.Weisemann, H. Rueterjans, H. Schwalbe, J. Schleucher, W. Bermel & C. Griesinger, J. Biomol. NMR 4, 231-240 (1994)

See original 3D HNCA experiment

3D DQ/ZQ-HNCA Experiment

$J(\text{HN-HA})$ and $J(\text{HN-CB})$
DQ/ZQ



d23: $1/(4J(\text{NCa}))$ [13.5 msec]
d26: $1/(4J'(\text{NH}))$ [2.6 msec]

Acquisition and Processing

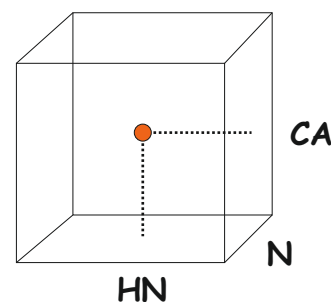
DQ+ZQ and DQ-ZQ Data are recorded in interleaved mode
Processing:
use AU-program split [ipap 2]

References:

A. Rexroth, P. Schmidt, S. Salma, T. Geppert, H. Schwalbe &
C. Griesinger, J. Am. Chem. Soc. 117, 10389-10390 (1995)

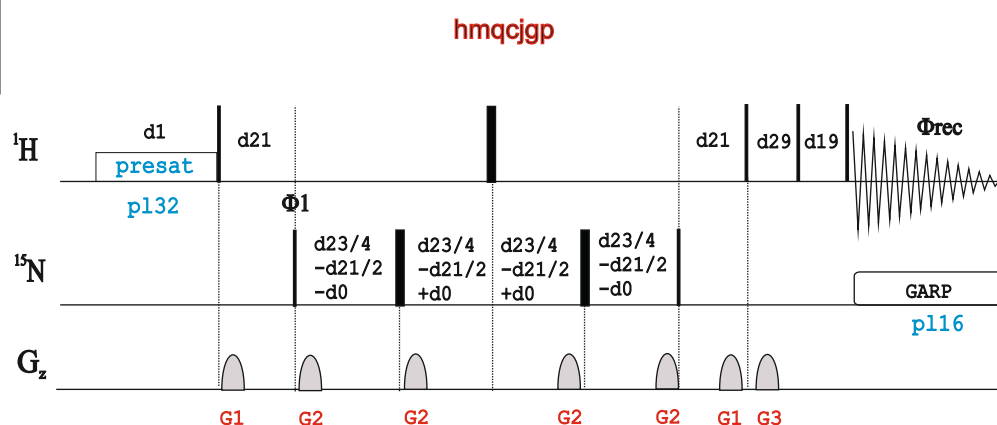
Related Experiments:

See original 3D HNCA Experiment



2D J-Modulated CT-HMQC Experiment

J(HN-HA)
J-modulation



d21: $1/(2J(\text{NH}))$ [5.3 msec]
d23: overall constant time for J-modulation : $4 \cdot T + 2 \cdot d21$
d29: z-filter delay (delta) [2 msec]

References:

H. Kuboniwa, S. Grzesiek, F. Delaglio & A. Bax, J. Biomol NMR 4, 871-878 (1994)

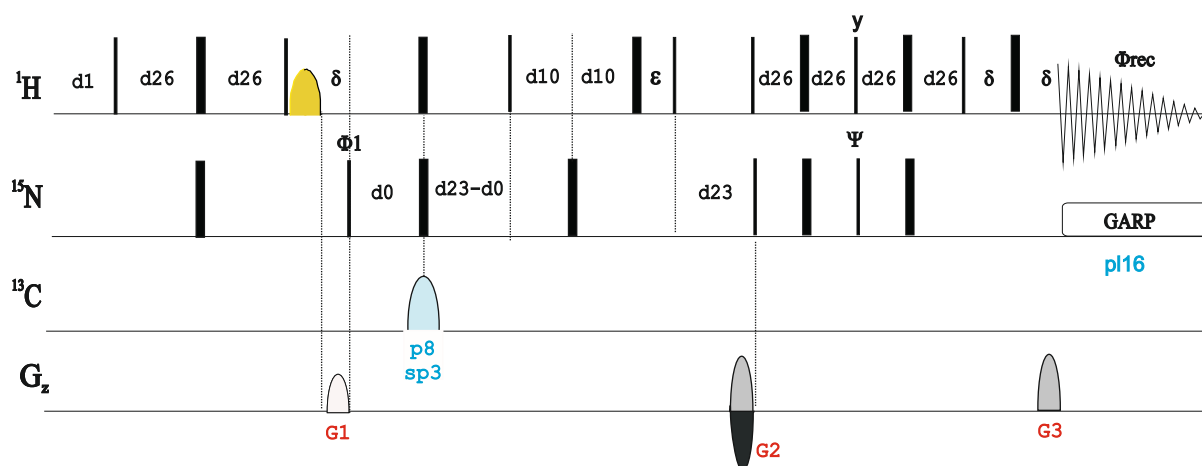
Related Experiments:

See original 2D HMQC and CT-HMQC experiments

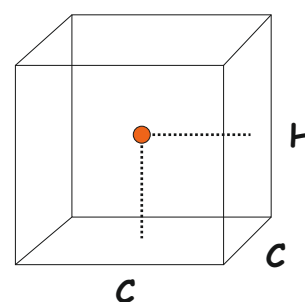
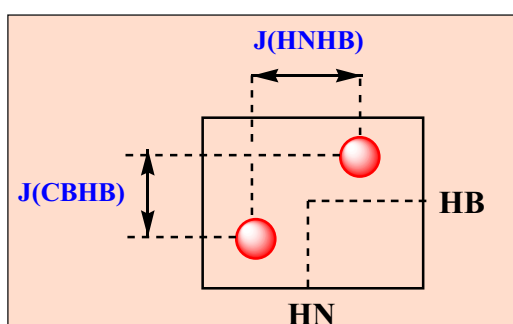
3D HNHB[CB]-E.COSY Experiment

J(HN-CB)
E.COSY

hnhbecosgp3d



d23: constant time delay T(N) [37.8 msec]
d26: $1/(4J'(\text{NH}))$ [2.3 msec]



References:

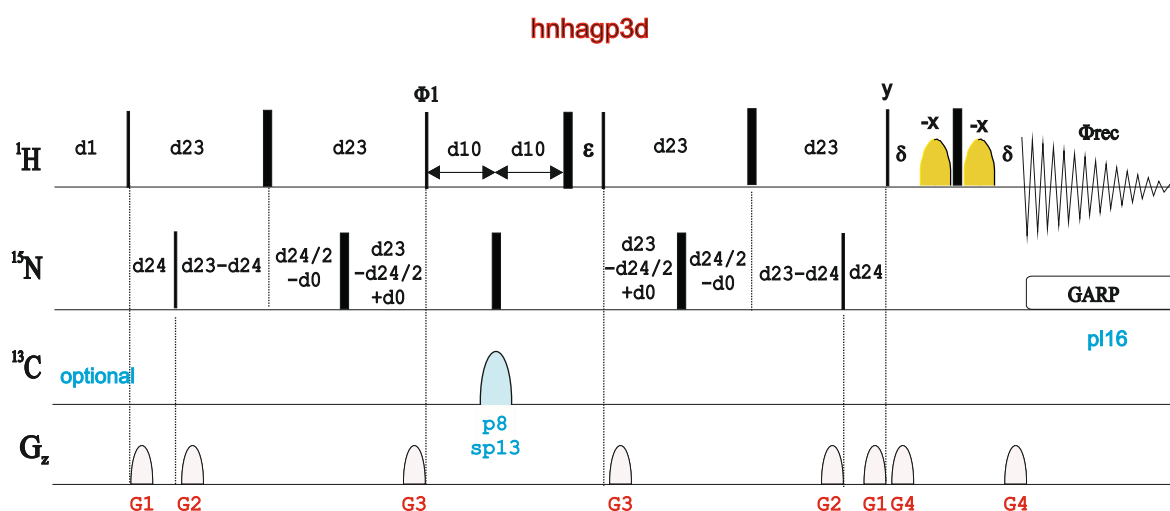
F. Loehr & H. Rueterjans, J. Biomol. NMR 13, 263 - 274 (1999)

Related Experiments:

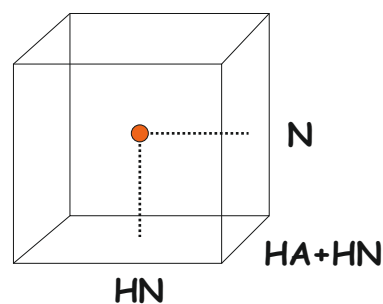
See original 3D HNHB experiment

3D HNHA Experiment

J(HN-HA)
J-quantitative



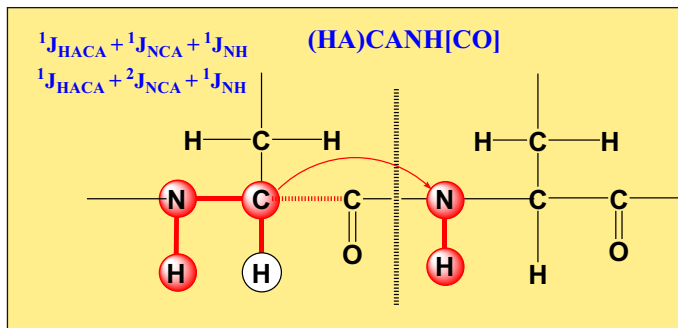
d23: $1/(4J(\text{HNHa}))$ [13.05 msec]
d24: $1/(2J(\text{NH}))$ [4.5 msec]



References:

1. G.W. Vuister & A. Bax, J. Am. Chem. Soc. 115, 7772-7777 (1993)
2. G.W. Vuister & A. Bax, J. Biomol NMR 4, 193-200 (1994)

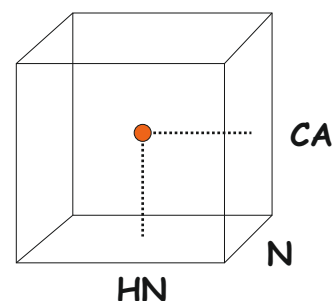
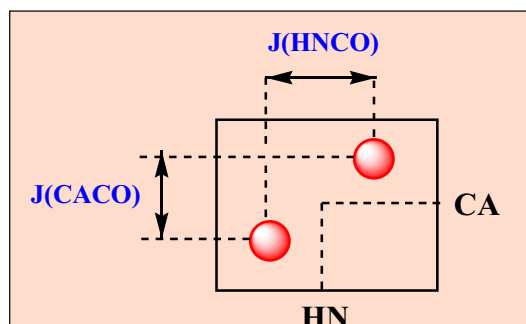
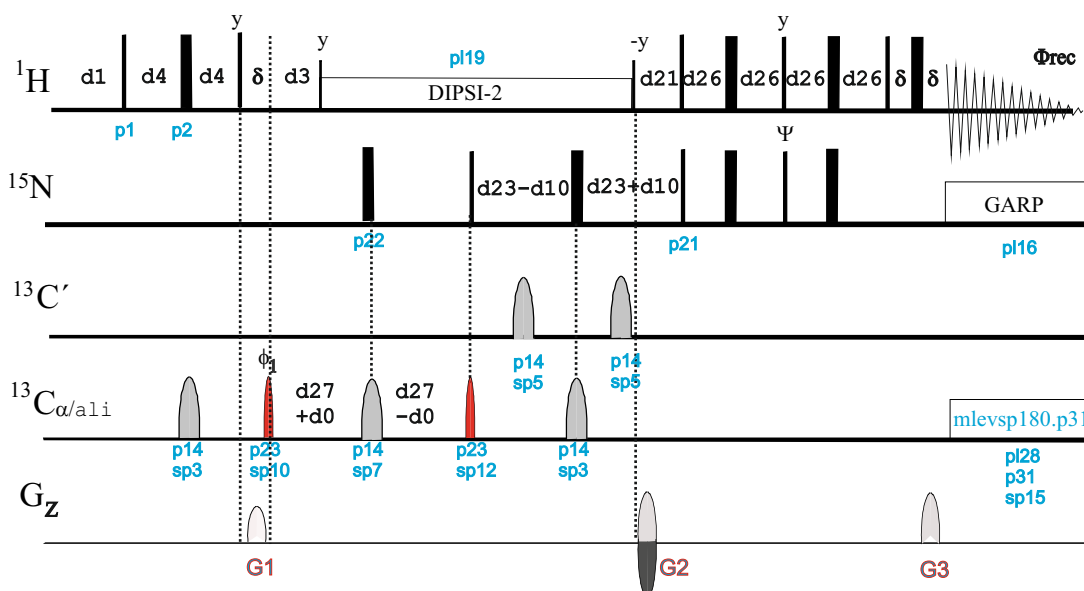
3D (H)CANNH[CO]-E.COSY Experiment



d3 : $1/(3.4J(\text{CH}))$ [2.0 msec]
d4 : $1/(4J(\text{CH}))$ [1.7 msec]
d21: $1/(2J(\text{NH}))$ [5.5 msec]
d23: $1/(4J(\text{NCA}))$ [12 msec]
d26: $1/(4J'(\text{NH}))$ [2.3 msec]
d27: constant time delay $T(\text{C})$ [13.3 msec]

J(HN-CO) E.COSY

hcannhgp3d



References:

F. Loehr & H. Rueterjans, J. Biomol. NMR 5, 25-36 (1995)

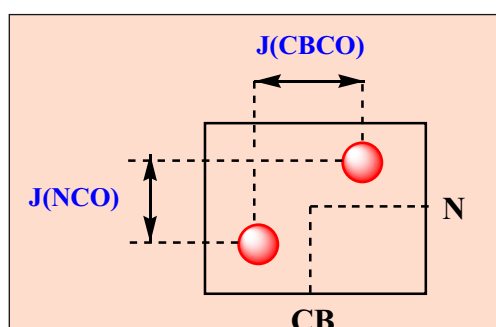
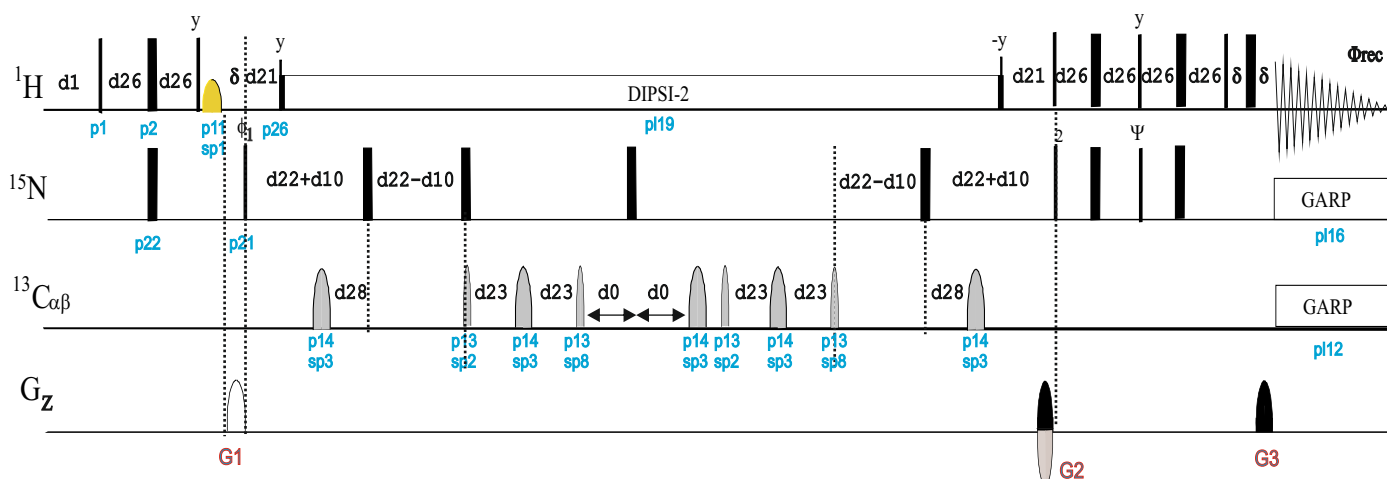
Related Experiments:

See original 3D HACANH experiment

$^1J_{NH} + ^1J_{CAN} + ^1J_{CC}$
 $^1J_{NH} + ^2J_{CAN} + ^1J_{CC}$

HNCACB[CO]

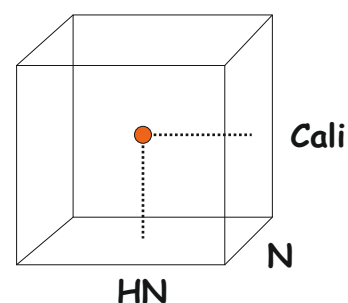
hncacbgpjc3d



d21: 1/(2J(NH))	[5.5 msec]
d22: T(N)	[17.6 msec]
d23: 1/(4J(CaCb))	[6.7 msec]
d26: 1/(4J'(NH))	[2.3 msec]
d28: T(N) - [1/(4J(NCa)opt]	[2.1 msec]

F. Loehr & H. Rueterjans, J. Biomol. NMR 13, 263-274 (1999)
J.-S. Hu & A. Bax, J. Biomol. NMR 11, 199-203 (1998)

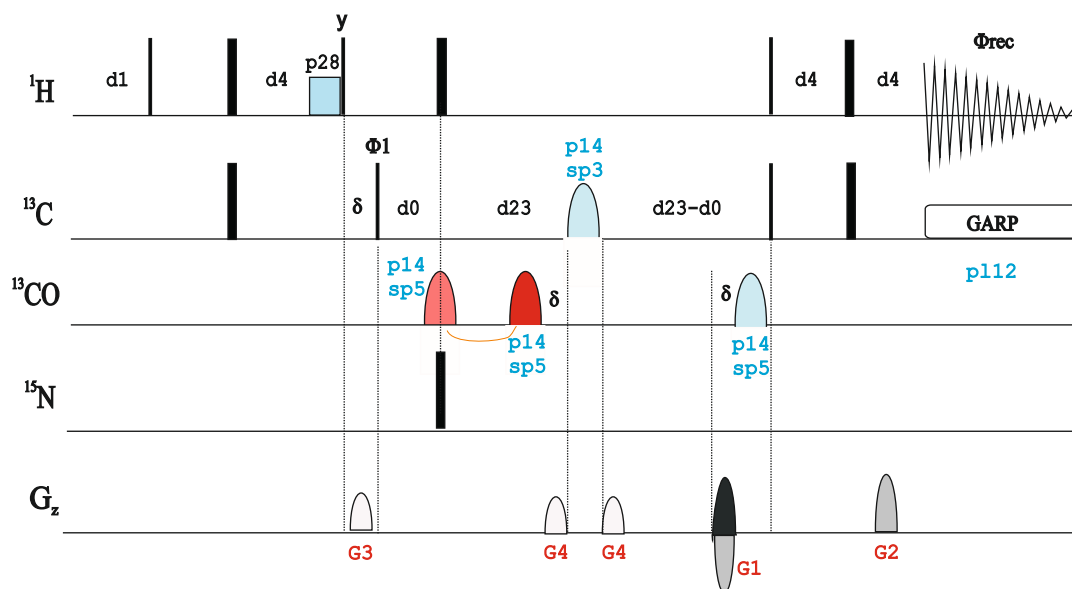
See original 3D HNCACB experiment



2D Spin-echo Difference CT-HSQC Experiment

$J(\text{CO-CB})$
spin-echo difference

hsqcctetgpcjr



d4 : $1/(4J)\text{CH}$ [1.7 msec]
d23: constant time delay $T(\text{C})$ [28.7 msec]
 $2T = n/1J(\text{CC})$
d31: effective delay for J-evolution

References:

S. Grzesiek, G.W. Vuister & A. Bax, J. Biomol. NMR 3, 487-493 (1993)

Related Experiments:

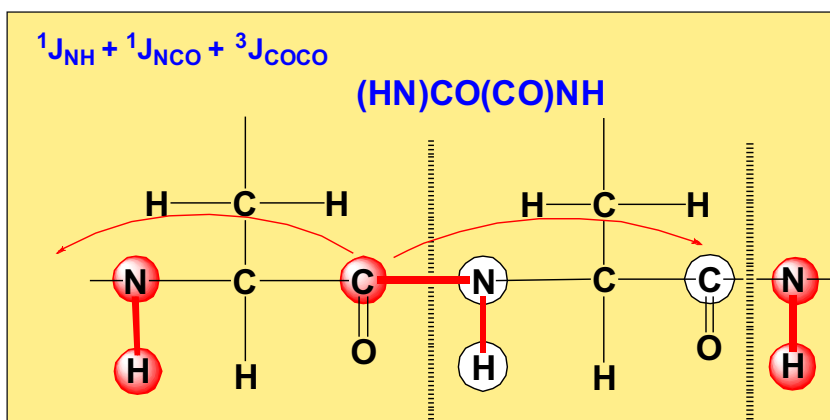
See original 2D CT-HSQC experiment

Processing:

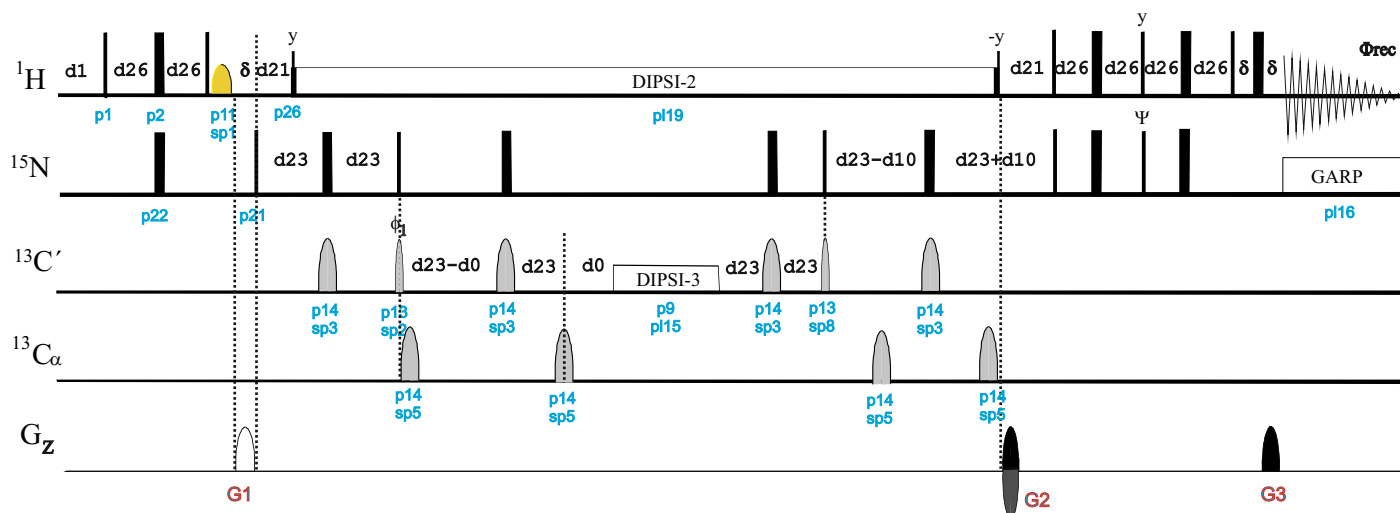
Two data are recorded in an interleaved mode.
Use AU-program split [2] to split data

3D (HN)CO(CO)NH Experiment

$J(\text{CO-CO})$
J-quantitative



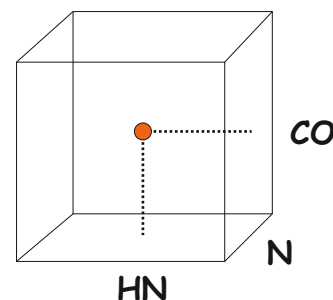
hncocogp3d



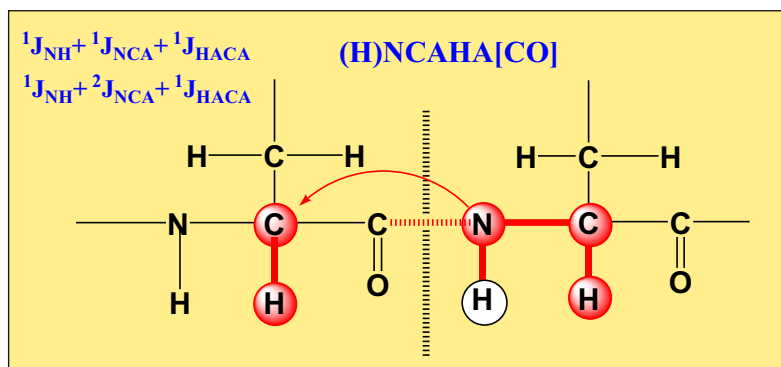
d21: $1/(2J(\text{NH}))$ [5.5 msec]
d23: $1/(4J(\text{NCO}))$ [13.5 msec]
d26: $1/(4J'(\text{NH}))$ [2.3 msec]
d31: length of DIPSI-3 cycle

References:

S. Grzesiek & A. Bax, J. Biomol. NMR 9, 207-211 (1997)
J.-S. Hu & A. Bax, J. Am. Chem. Soc. 118, 8170-8171 (1996)

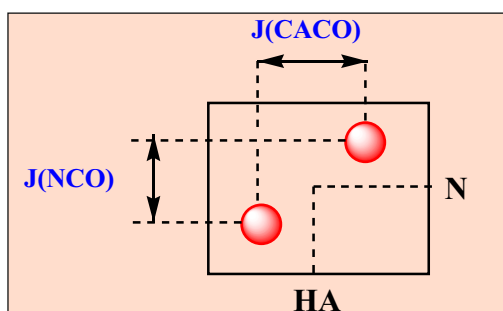
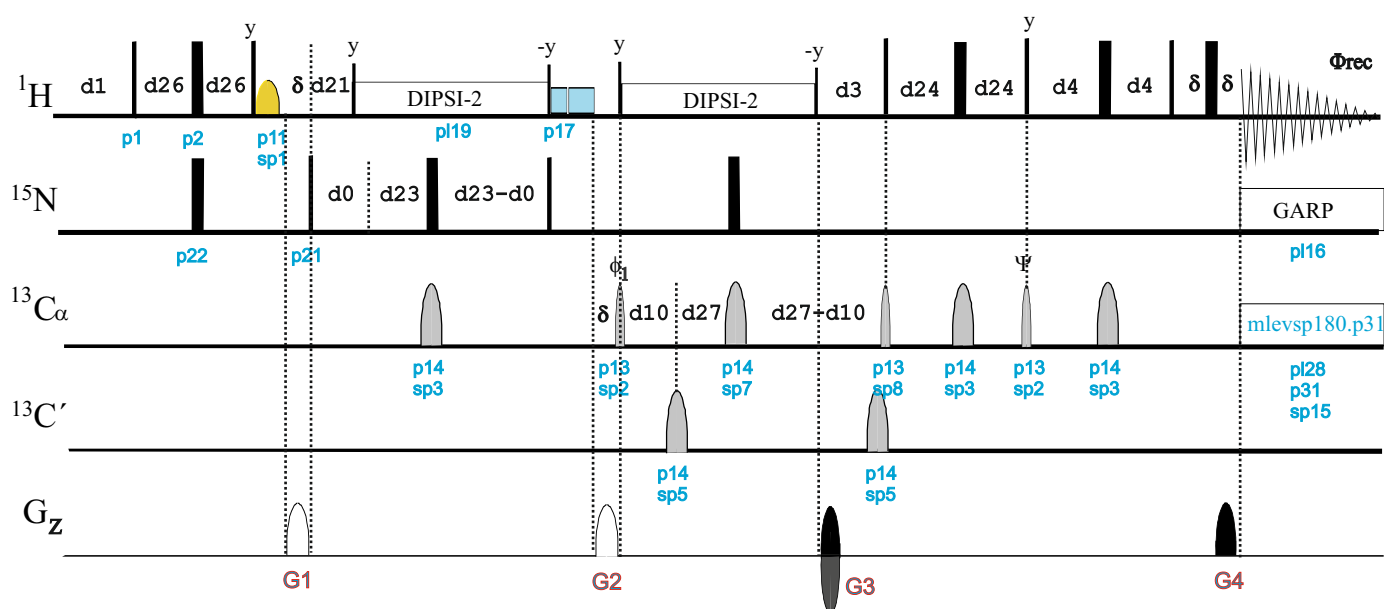


3D (H)NCAHA[CO]-E.COSY Experiment



J(HA-CO)
E.COSY

hncahgp3d



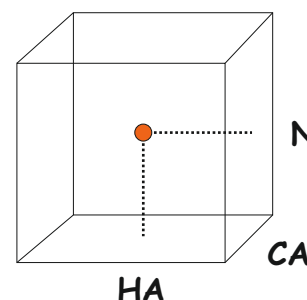
d3 : $1/(3.2J(CH))$ [2.1 msec]
d4 : $1/(4J(CH))$ [1.7 msec]
d21: $1/(2J(NH))$ [5.5 msec]
d23: $1/(4J(NCa))$ [15.5 msec]
d24: $1/(8J)CH$ for all multiplicities
 $1/(4J)CH$ for CH
d26: $1/(4J'(NH))$ [2.3 msec]
d27: constant time delay T(C) [13.3 msec]

References:

F. Loehr & H. Rueterjans, J. Biomol. NMR 5, 25 - 36 (1995)

Related Experiment:

See the original HNCAHA Experiment

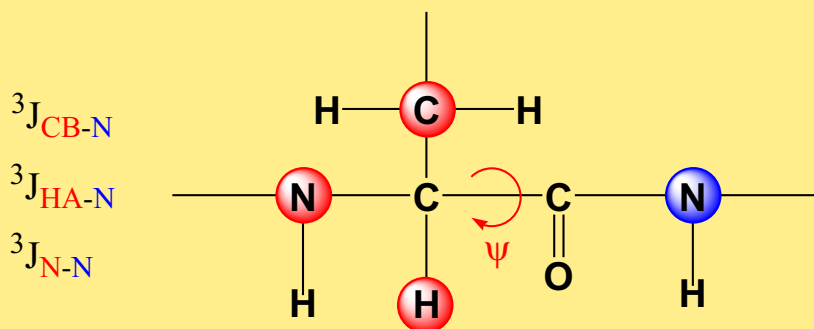


BRUKER PULSE PROGRAM CATALOGUE

NMRGuide

PROTEIN NMR
COUPLING CONSTANTS
PSI BACKBONE ANGLE

Backbone ψ Angle

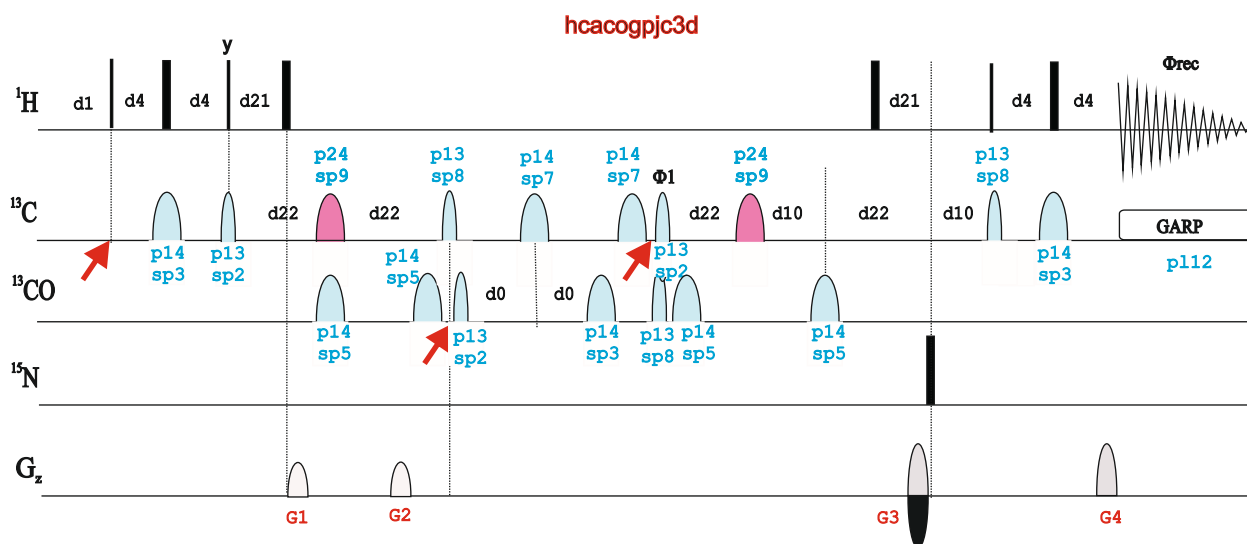
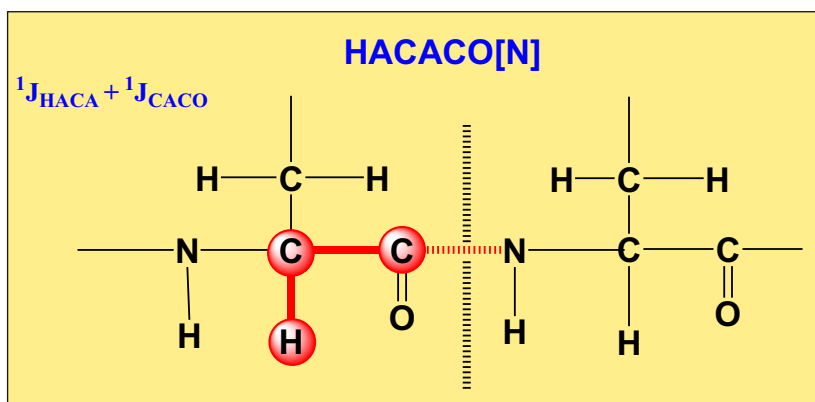


Psi Backbone Coupling Constant

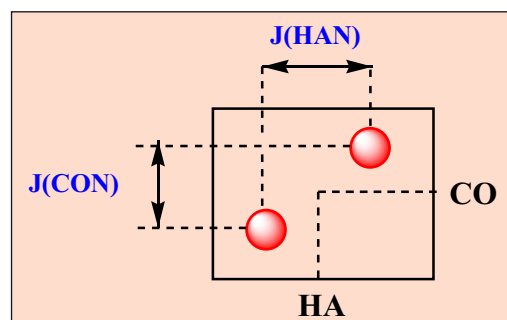
- 3D (H)NNH-TOCSY (**hnnhdigp3d** | **HNNHDI6P3D**) - $3J[N-N]$ via quantitative-J
- 3D HCACO[N]-E.COSY (**hcacogpjc3d** | **HCACOGPJC3D**) - $3J[HA-N]$ via E.COSY
- Also see in Ch1 Sidechain Coupling Constants:
3D HNHB (**hnhbgp3d** | **HNHBGP3D**) - $3J[HN-HA]$ and $3J[HN-HB]$ via quantitative-J

3D HACACO[N]-E.COSY Experiment

$J(\text{HA-N})$
E.COSY



d4 : $1/(4J(\text{HCA}))$ [1.7 msec]
d21: $1/(4J'(\text{HCA}))$ for CH [1.7 msec]
 $1/(6J'(\text{HCA}))$ for CH and CH2 [1.2 msec]
d22: $1/(4J(\text{CaCO}))$ [4.5 msec]

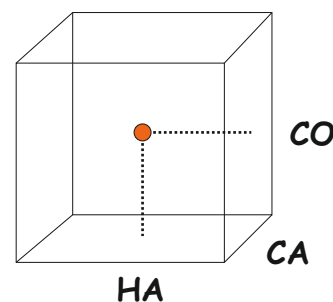


References:

A.C. Wang & A. Bax, J. Am. Chem. Soc. 117, 1810-1813 (1995))
;(L.E. Kay et al., J. Magn. Reson 89, 496 - 514 (1990)

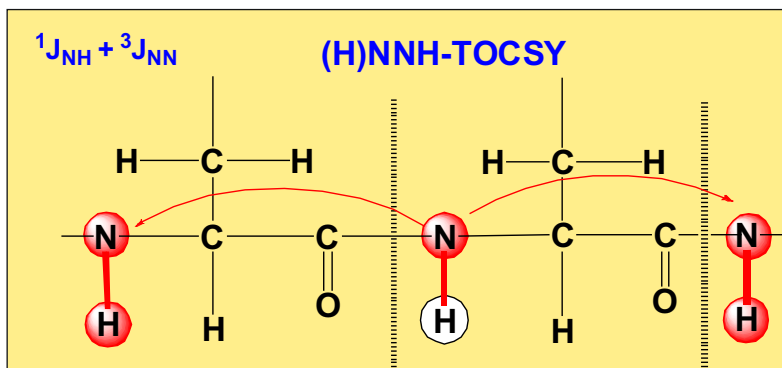
Related Experiments:

See the original 3D HCACO Experiment

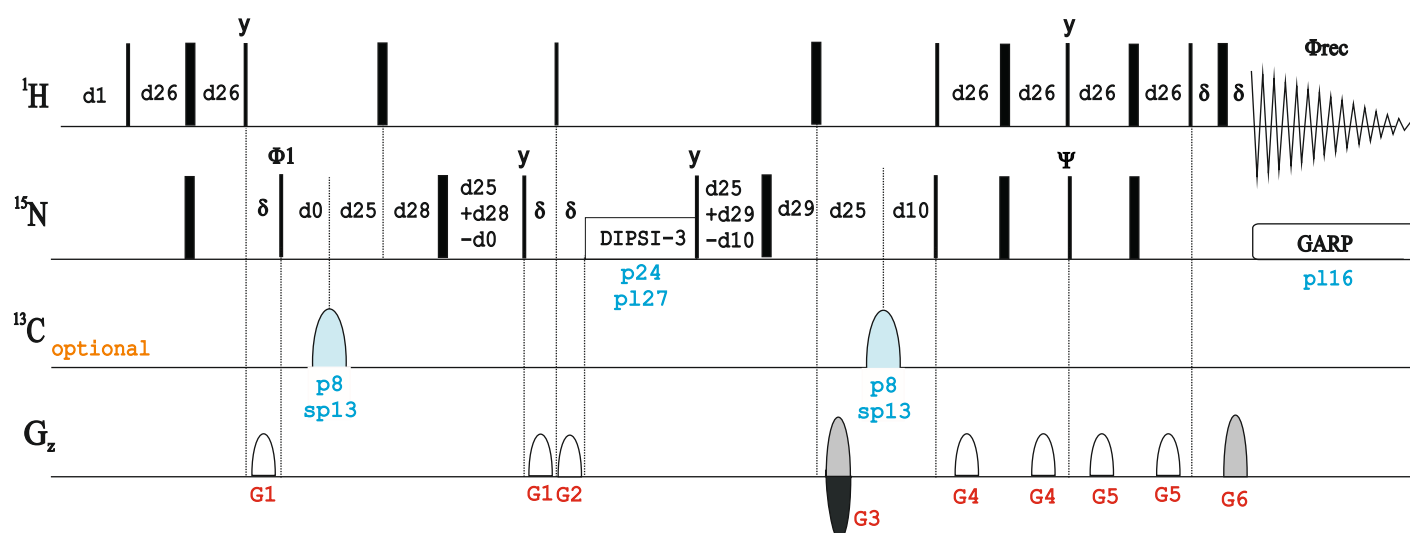


3D (H)NNH-TOCSY Experiment

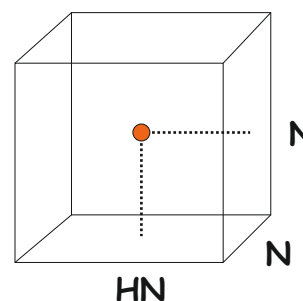
$J(N-N)$
J-quantitative



hnnhdigp3d



d25: $1/(4J(NH))$ [2.75 msec]
d26: $1/(4J'(NH))$ [2.3 msec]
d31: length of DIPSI-3 cycle



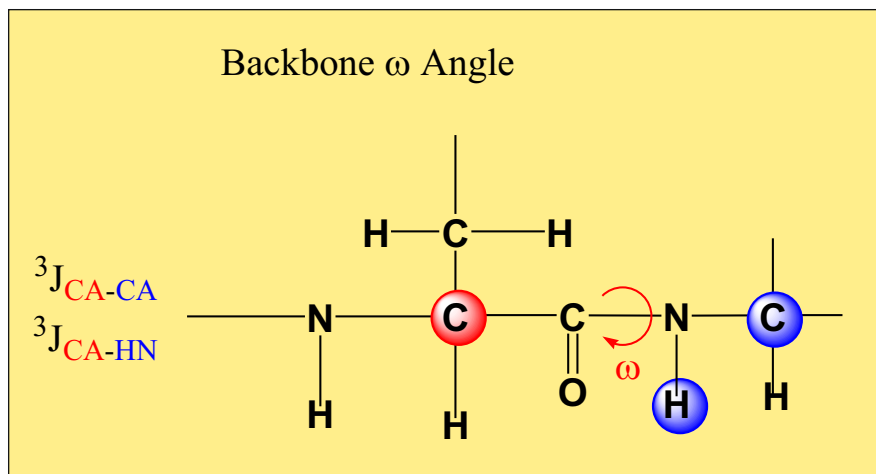
References:

- F. Loehr & H. Rueterjans, *J. Magn. Reson.* 132, 130-137 (1998)
K. Theis, A.J. Dingley, A. Hoffmann, J.G. Omichinski & S. Grzesiek, *J. Biomol. NMR* 10, 403-408 (1997)

BRUKER PULSE PROGRAM CATALOGUE

NMRGuide

PROTEIN NMR
COUPLING CONSTANTS
OMEGA BACKBONE ANGLE



Omega Backbone Coupling Constant

- 3D HN(COCA)CA (*hncocacagp3d* | *HNCOCACAGP3D*) - $3J[\text{CA-CA}]$ via quantitative-J
- 3D HNCO[CA]-E.COSY (*hncoccosgp3d* | *HNCOECOSGP3D*) - $3J[\text{H(N)-CA}]$ via E.COSY

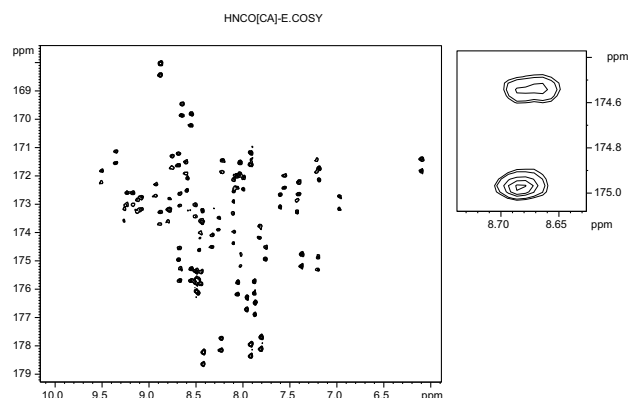
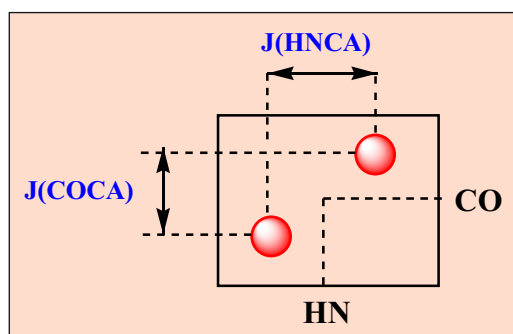
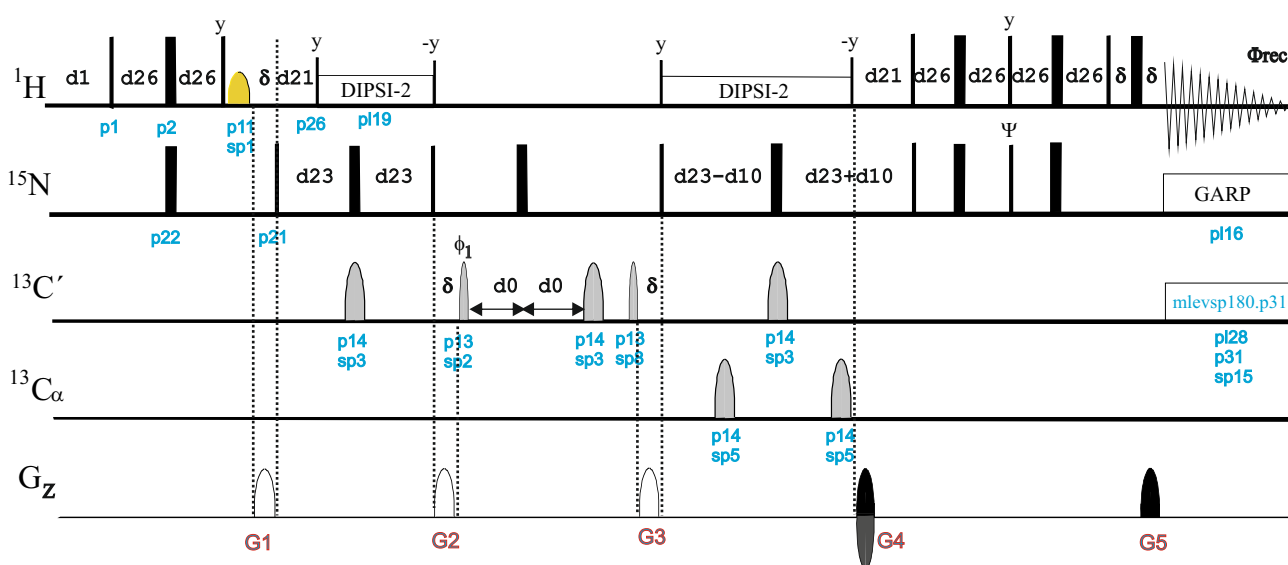
$^1J_{HN} + ^1J_{NCO}$

HNCO[CA]

The diagram illustrates the chemical structure of the HNCO[CA] experiment. It shows two molecules connected by a dashed line. The left molecule is an amide (H₂N-C(=O)-CH₃) and the right molecule is a carbamate (H₂N-C(=O)-O-CH₃). The dashed line connects the carbonyl carbon of the amide to the carbonyl carbon of the carbamate. The amide nitrogen is labeled with $^1J_{HN}$ and the carbamate nitrogen is labeled with $^1J_{NCO}$.

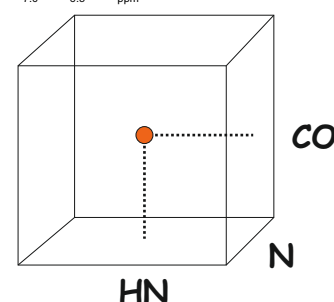
d21: $1/(2J(\text{NH}))$	[5.5 msec]
d23: $1/(4J(\text{NCO}))$	[12 msec]
d26: $1/(4J'(\text{NH}))$	[2.3 msec]

hncoecosgp3d



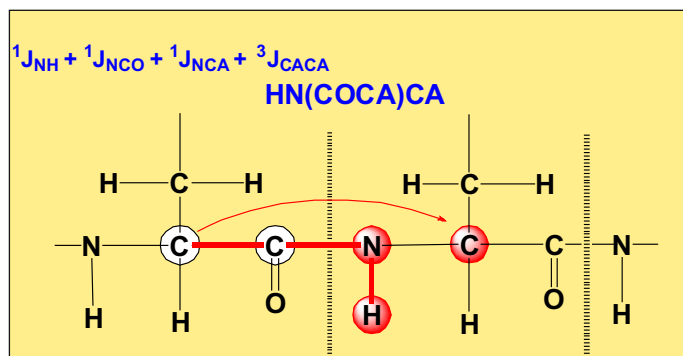
M. Hennig, W. Bermel, H. Schwalbe & C. Griesinger, *J. Am. Chem. Soc.* 122, 6268-6277 (2000)

See original 3D HNCO experiment

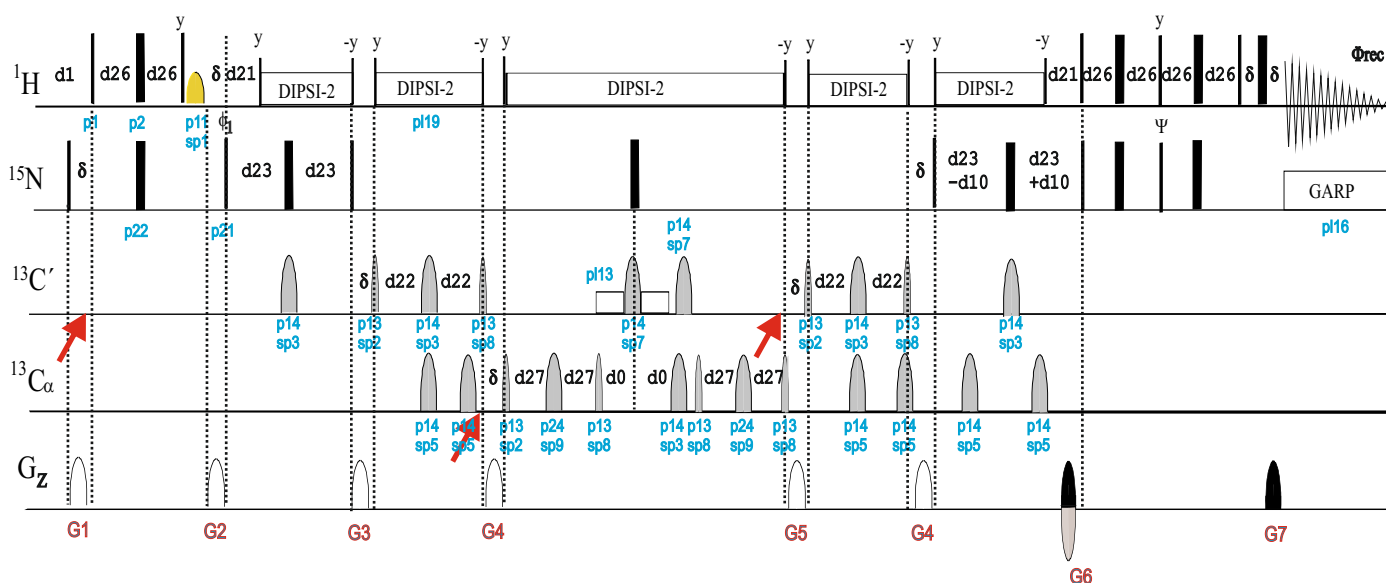


3D HN(COCA)CA Experiment

$J(\text{CA}-\text{CA})$
J-quantitative



hncocacagp3d



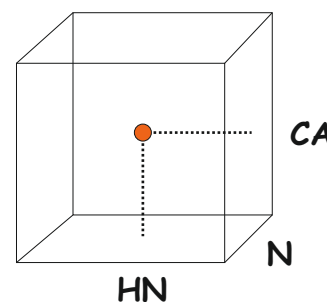
d21: $1/(2J(\text{NH}))$	[5.5 msec]
d22: $1/(4J(\text{COCa}))$	[4.55 msec]
d23: $1/(4J(\text{NCO}))$	[12.8 msec]
d26: $1/(4J'(\text{NH}))$	[2.4 msec]
d27: $1/(4J'(\text{CaCa}))$	[28.6 msec]

References:

M. Hennig, W. Bermel, H. Schwalbe & C. Griesinger, J. Am. Chem. Soc. 122, 6268-6277 (2000)

Related Experiments:

See original 3D HNCOCA experiment



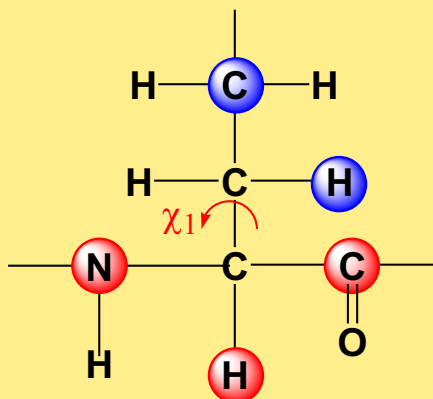
BRUKER PULSE PROGRAM CATALOGUE

NMRGuide

PROTEIN NMR
COUPLING CONSTANTS
CHI1 SIDECHAIN ANGLE

Side Chain χ_1 Angle

$^3J_{\text{N-HB}}$
 $^3J_{\text{N-CG}}$
 $^3J_{\text{HA-HB}}$
 $^3J_{\text{HA-CG}}$
 $^3J_{\text{CO-HB}}$
 $^3J_{\text{CO-CG}}$



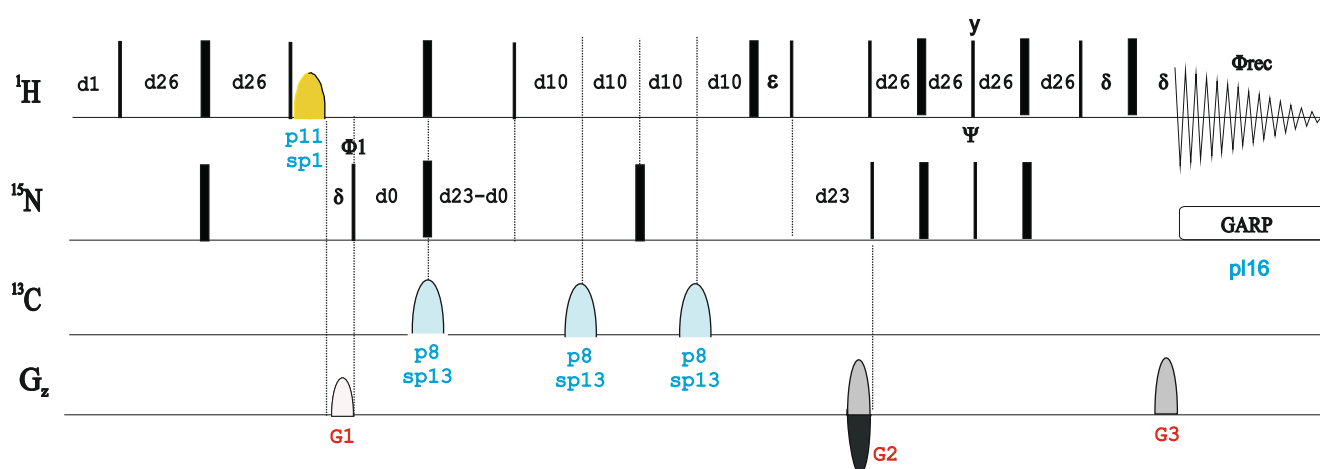
Chi1 Sidechain Coupling Constant

- 3D HNHB (**hnhbgp3d** | **HNHBGP3D**) - $^3J[\text{HN-HA}]$ and $^3J[\text{HN-HB}]$ via quantitative-J
- 3D HACAHB-COSY (**hacahbcosygp3d** | **HACAHBcosyGP3D**) - $^3J[\text{HA-HB}]$ via quantitative-J
- 3D HN(CO)C (**hncocgp3d** | **HNCOCGP3D**) - $^3J[\text{CG-CO}]$ via quantitative-J
- 3D HC(C)H[HA]-E.COSY (**hcchecosgp3d** | **HCCHecosGP3D**) - $^3J[\text{HA-HB}]$ via E.COSY
- 3D HC(C)H[CO]-E.COSY (**hcchcosygp3d** | **HCCHcosyGP3D**) - $^3J[\text{CO-HB}]$ via E.COSY
- 3D (H)C(C)CH[CO]-E.COSY (**hccccosygp3d** | **HCCCCosyGP3D**) - $^3J[\text{CG-CO}]$ via E.COSY
- 3D HNCG (**hncg3d.1** | **HNCGP3D.1**) - $^3J[\text{N-CG}]$ via quantitative-J
- 3D HNCG (**hncg3d.2** | **HNCGP3D.2**) - $^3J[\text{N-CG}]$ via quantitative-J
- 2D spin-echo difference CT-HSQC (**hsqcetfpf3gpjcsi** | **HSQCETFPF6PJCSI**) - $^3J[\text{N-CG}]$ via spin-echo difference

3D HNHB Experiment

$J(N-HB)$, $J(N-HA)$
J-quantitative

hnhbgp3d



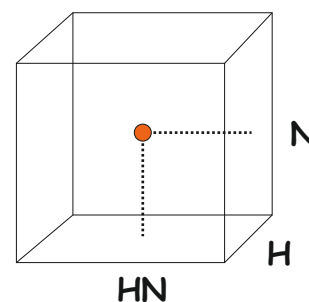
d23: constant time delay $T(N)$ [37.8 msec]
d26: $1/(4J'(NH))$ [2.3 msec]

References:

1. S.J. Archer, M. Ikura, D.A. Torchia & A. Bax, J. Magn. Reson. 95, 636-641 (1991)
2. P. Duex, B. Whitehead, R. Boelens, R. Kaptein & G.W. Vuister, J. Biomol. NMR 10, 301-306 (1997)
3. F. Loehr & H. Rueterjans, J. Biomol. NMR 13, 263 - 274 (1999)

Related Experiments:

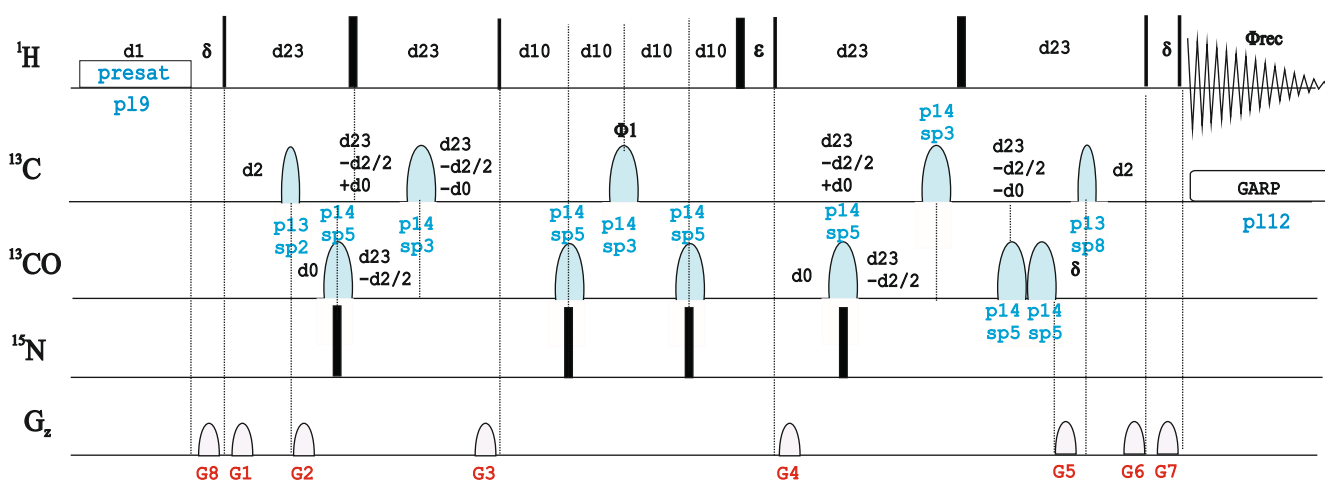
See also: 3D HNHB-E.COSY experiment



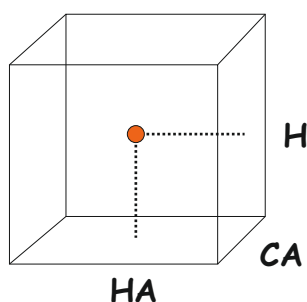
3D HACAHB-COSY Experiment

$J(\text{HA-HB})$
J-quantitative

hacahbcosygp3d



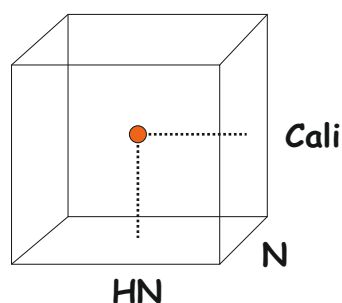
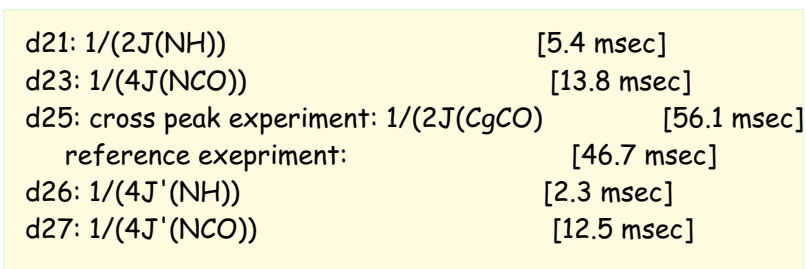
$d2 : 1/(2J(\text{CH}))$ [3.4 msec]
 $d23 : 1/(4J'(\text{HaHb}))$ [8.7 msec]



References:

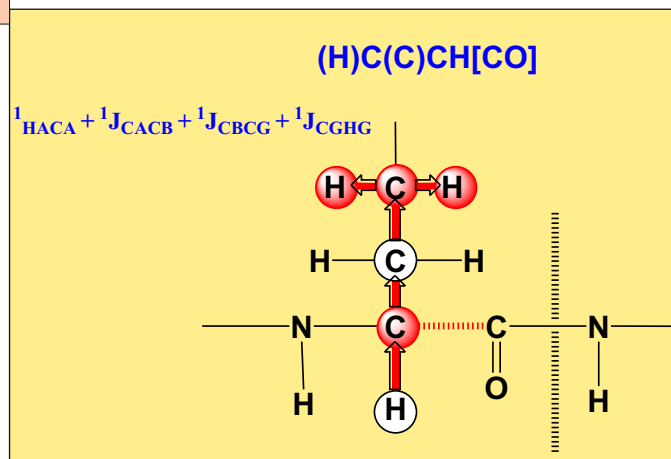
S. Grzesiek, H. Kuboniwa, A.P. Hinck & A. Bax, J. Am. Chem. Soc.
117, 5312-5315 (1995)

J(CG-CO)
J-quantitative



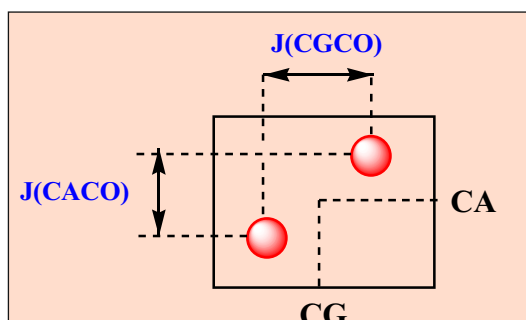
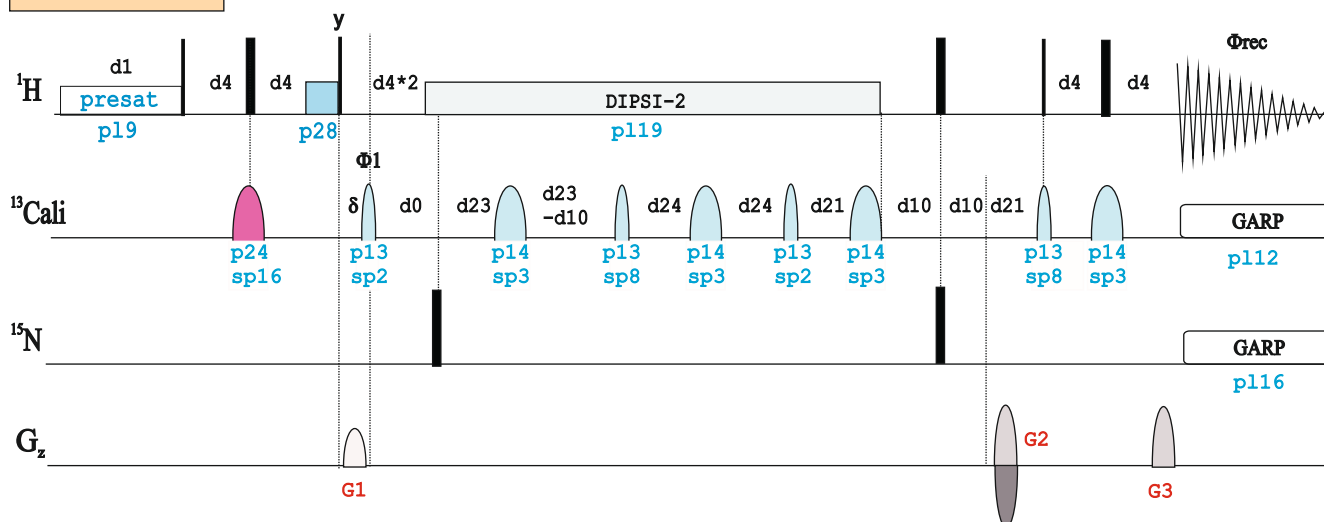
J.-S. Hu & A. Bax, *J. Am. Chem. Soc.* 119, 6360 - 6368 (1997)

3D (H)C(C)CH[CO]-E.COSY Experiment



J(CG-CO) E.COSY

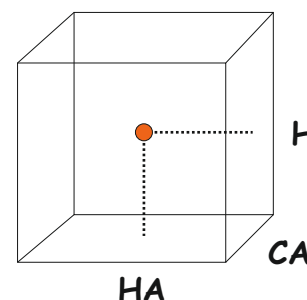
hccccosygp3d



d21: $1/(5J'(CH))$	[1.38 msec]
d23: $1/(4J(CC))$	[7.2 msec]
d24: $1/(6.65J'(CC))$	[4.3 msec]

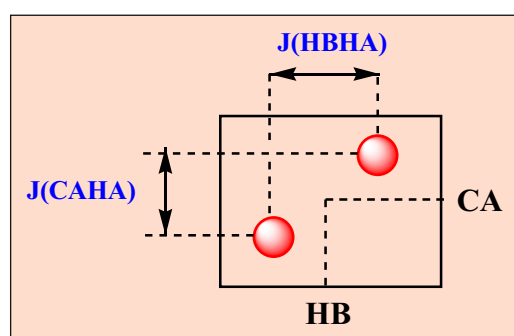
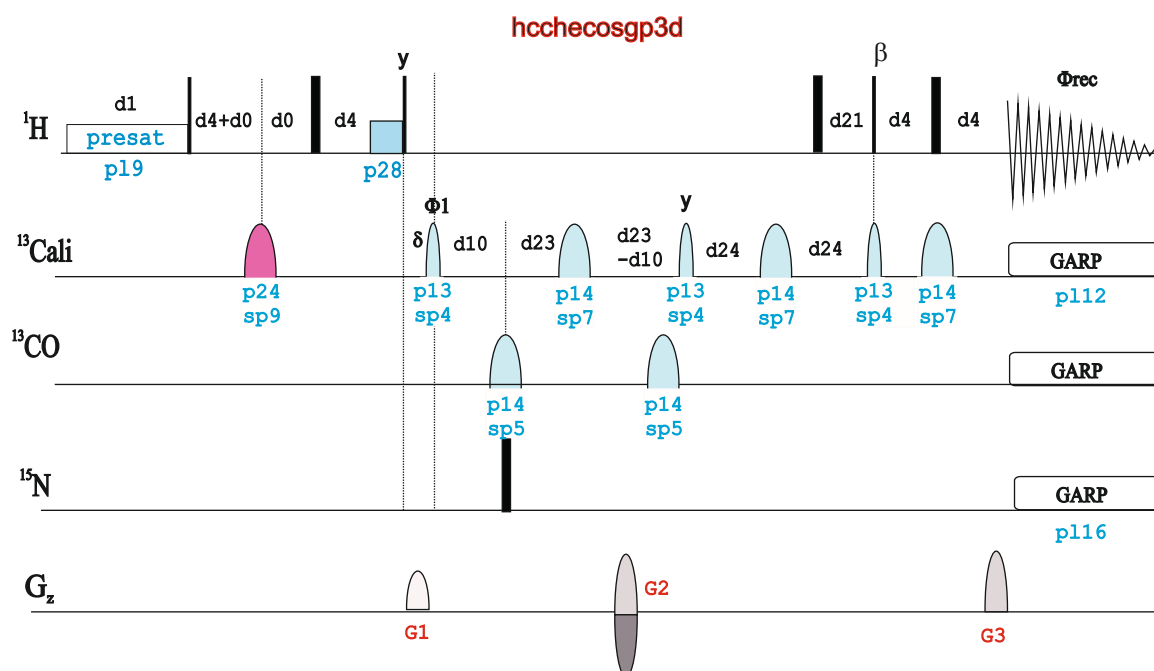
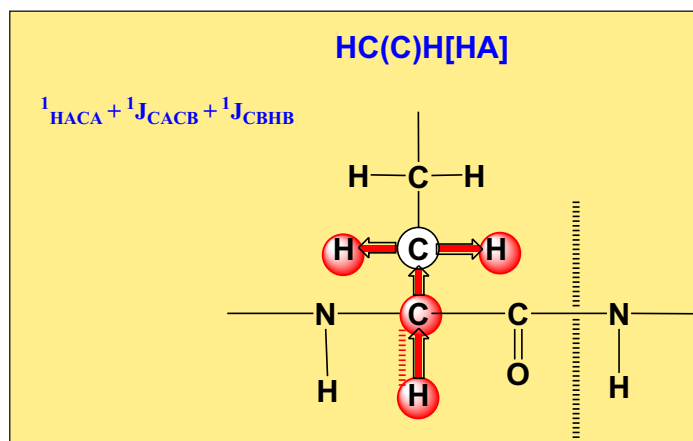
References:

1. H. Schwalbe, A. Rexroth, U. Eggenberger, T. Geppert & C. Griesinger, J. Am. Chem. Soc. 115, 7878-7879 (1993)
2. Y. Karimi-Nejad, J.M. Schmidt, H. Rueterjans, H. Schwalbe & C. Griesinger, Biochemistry 33, 5481-5492 (1994)



3D HC(C)H[HA]-E.COSY Experiment

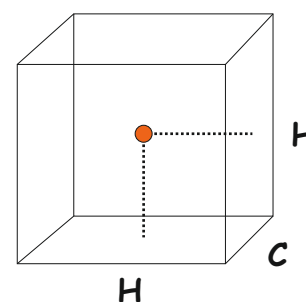
J(HB-HA)
E.COSY



d4 : $1/(4J(\text{CH}))$ [1.7 msec]
d21: $1/(8J'(\text{CH}))$ [0.85 msec]
d23: $1/(4J(\text{CC}))$ [7.2 msec]
d24: $1/(4J'(\text{CC}))$ [3.6 msec]

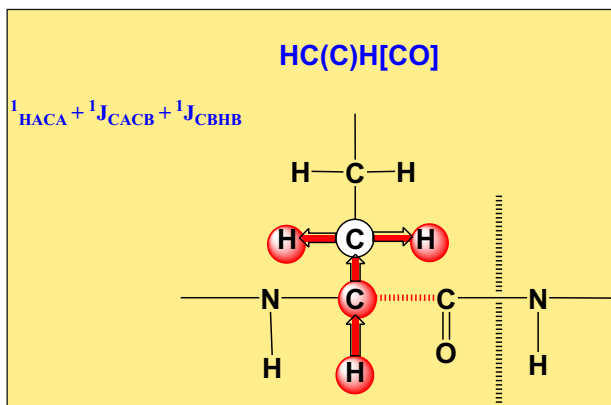
References:

1. Y. Karimi-Nejad, J.M. Schmidt, H. Rueterjans, H. Schwalbe & C. Griesinger, Biochemistry 33, 5481-5492 (1994)
2. U. Eggenberger, Y. Karimi-Nejad, H. Thuring, H. Rueterjans & C. Griesinger, J. Biomol. NMR 2, 583-590 (1992)

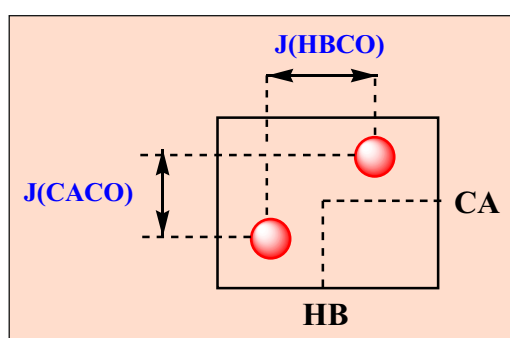
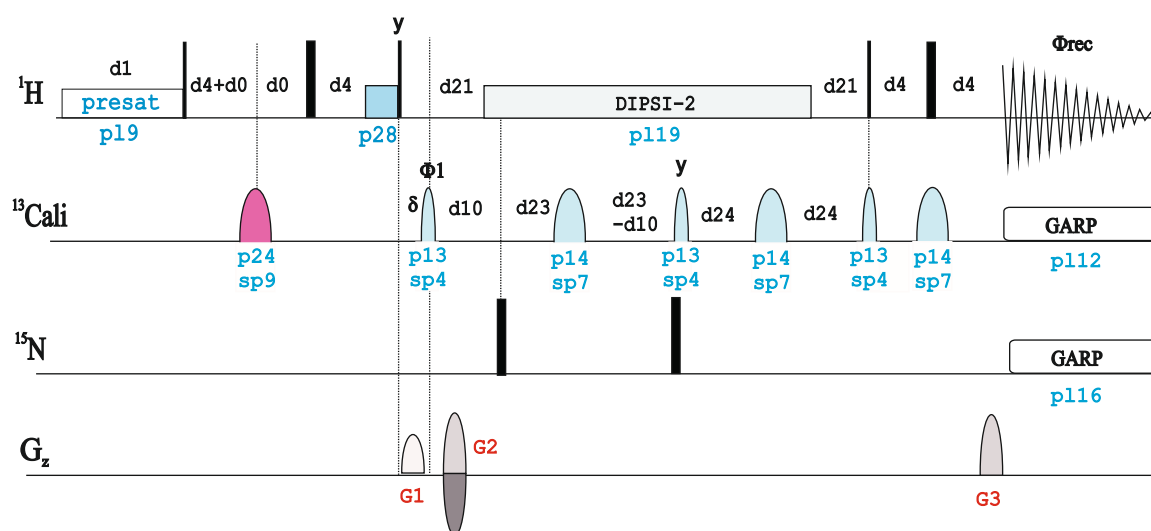


3D HC(C)H[CO]-E.COSY Experiment

$J(\text{HB-CO})$
E.COSY



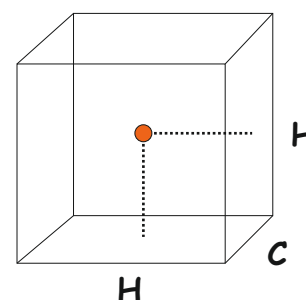
hcchcosygp3d



d4 : $1/(4J(\text{CH}))$	[1.7 msec]
d21: $1/(4J'(\text{CH}))$	[1.7 msec]
d23: $1/(4J(\text{CC}))$	[7.2 msec]
d24: $1/(4J'(\text{CC}))$	[3.6 msec]

References:

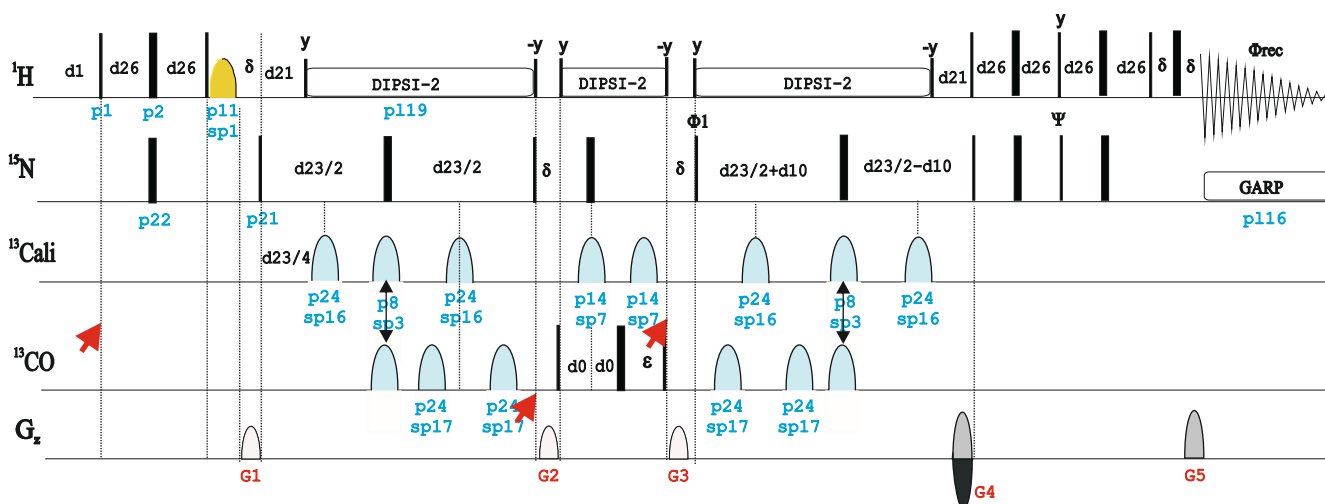
1. Y. Karimi-Nejad, J.M. Schmidt, H. Rueterjans, H. Schwalbe & C. Griesinger, Biochemistry 33, 5481-5492 (1994)
2. U. Eggenberger, Y. Karimi-Nejad, H. Thuerling, H. Rueterjans & C. Griesinger, J. Biomol. NMR 2, 583-590 (1992)



3D HNCg Experiment

hncg3d.1

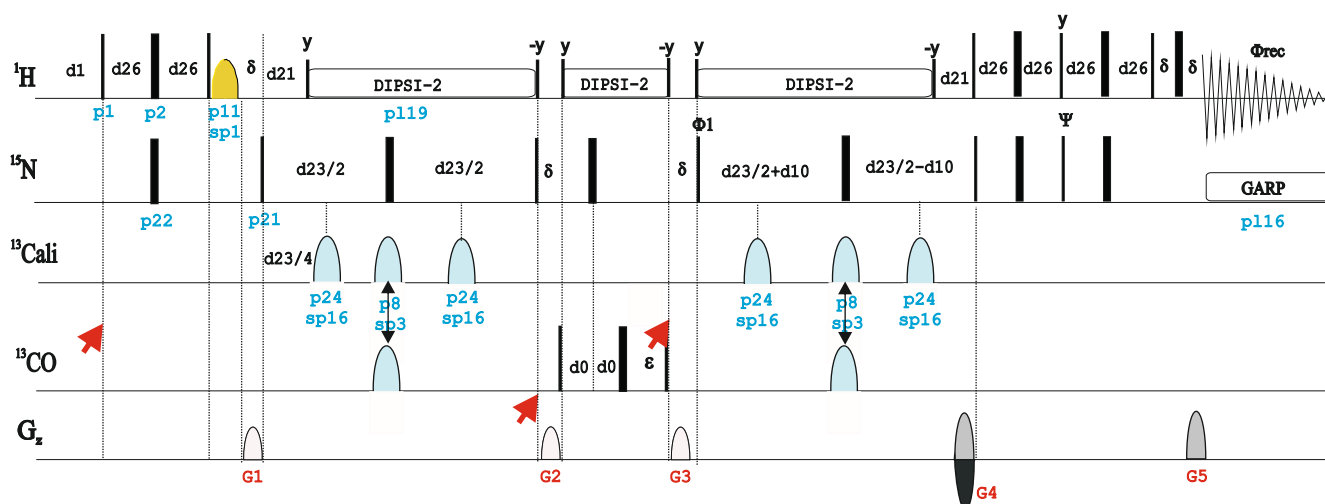
J(N-CG)
J-quantitative
Reference experiment



d21: $1/(2J(\text{NH}))$ [5.5 msec]
d23: $1/(2J(\text{NCg}) = 2 \cdot T(\text{N}))$ [66.6 msec]
d26: $1/(4J'(\text{NH}))$ [2.3 msec]

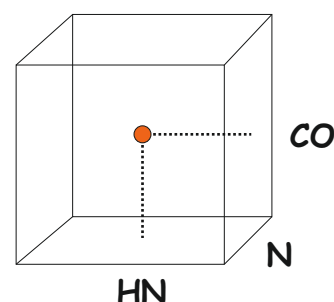
hncg3d.2

J(N-CG)
J-quantitative
Cross-peak experiment

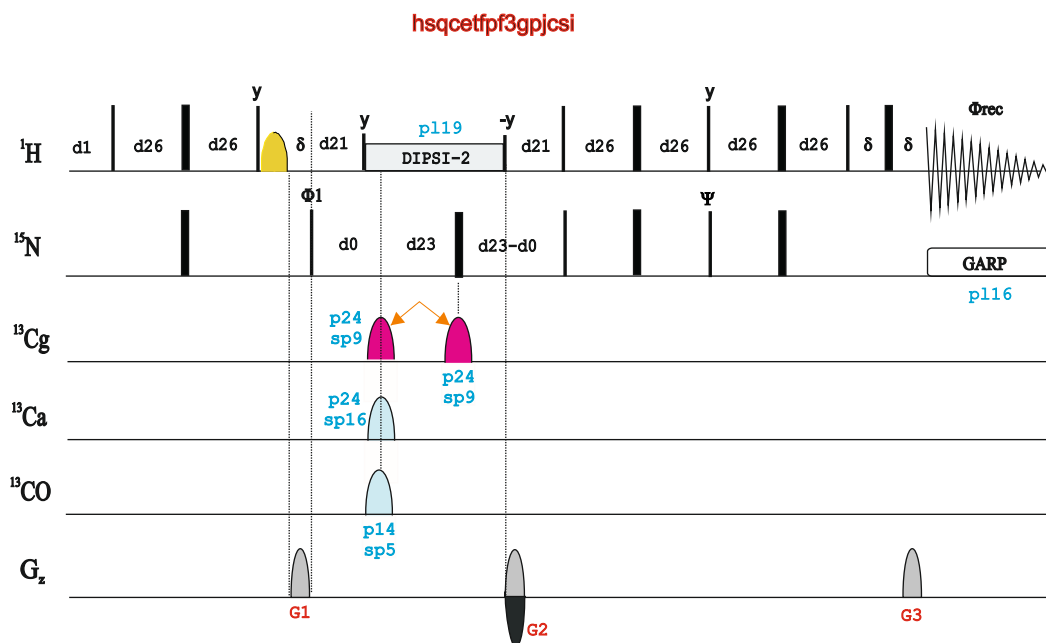


References:

1. J.-S. Hu & A. Bax, J. Biomol. NMR 9, 323-328 (1997)
2. R. Konrat, D.R. Muhandiram, N.A. Farrow & L.E. Kay, J. Biomol. NMR 9, 409-422 (1997)



J(N-CG)
spin-echo difference



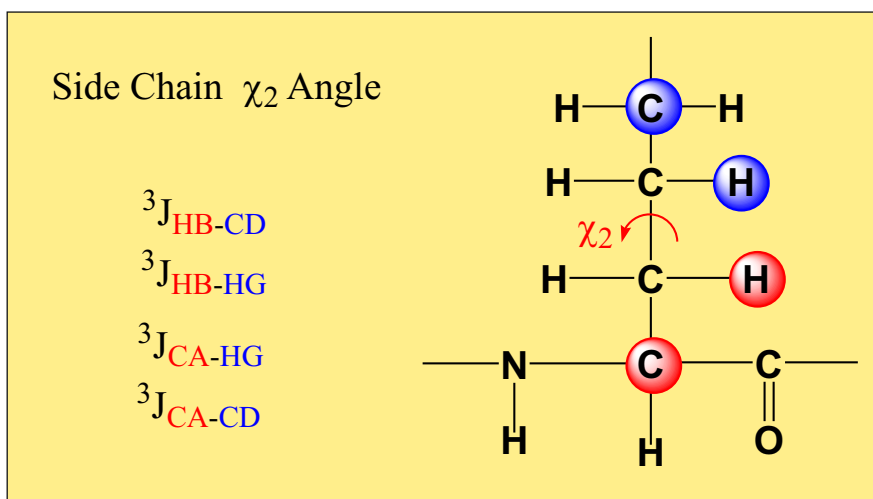
d21: 1/(2J(NH))	[5.5 msec]
d23: constant time delay T(N)	[100 msec]
d26: 1/(4J'(NH))	[2.3 msec]

Two data are recorded in a interleaved mode
Use AU-program split [2] to split data

BRUKER PULSE PROGRAM CATALOGUE

NMRGuide

PROTEIN NMR
COUPLING CONSTANTS
CHI2 SIDECHAIN ANGLE

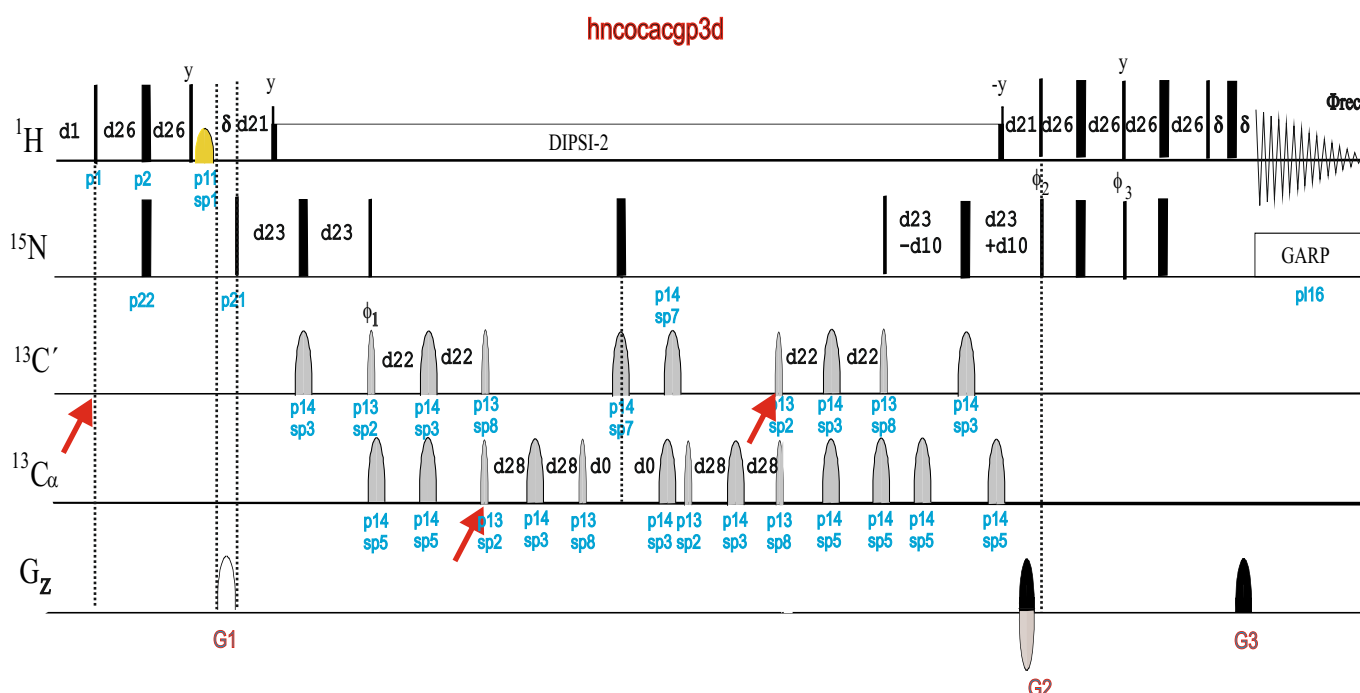


Chi2 Sidechain Coupling Constant

- 3D HN(CO)CACali (**hncocacgp3d** | HNCOCACGP3D) - $3J_{\text{CA-CD}}$ via quantitative-J

J(CA-CD)
J-quantitative

d21: $1/(2J(\text{NH}))$	[5.5 msec]
d22: $1/(4J(\text{COCa}))$	[4.5 msec]
d23: $1/(4J(\text{NCO}))$	[15 msec]
d26: $1/(4J'(\text{NH}))$	[2.5 msec]
d28: $1/(4J(\text{CaCd}))$	[28.2 msec]



References:

M. Hennig, D. Ott, P. Schulte, R. Loewe, J. Krebs, T. Vorherr,
W. Bermel, H. Schwalbe & C. Griesinger, J. Am. Chem. Soc. 119, 5055-5056 (1997)

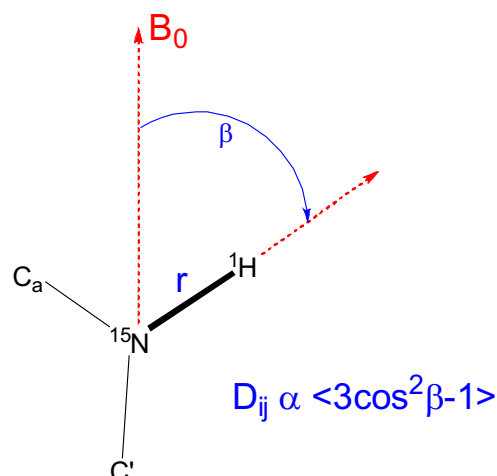
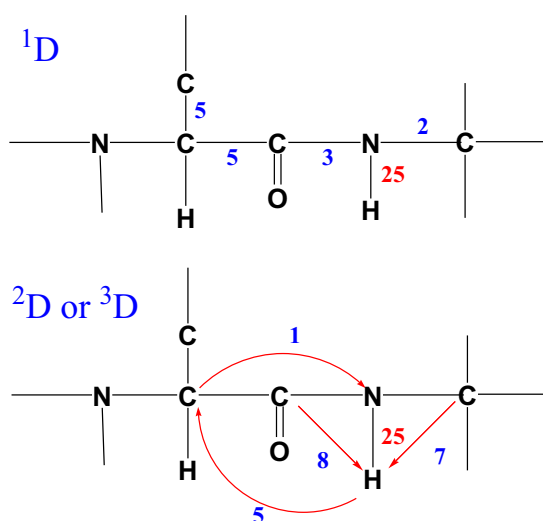
BRUKER PULSE PROGRAM CATALOGUE

NMRGuide

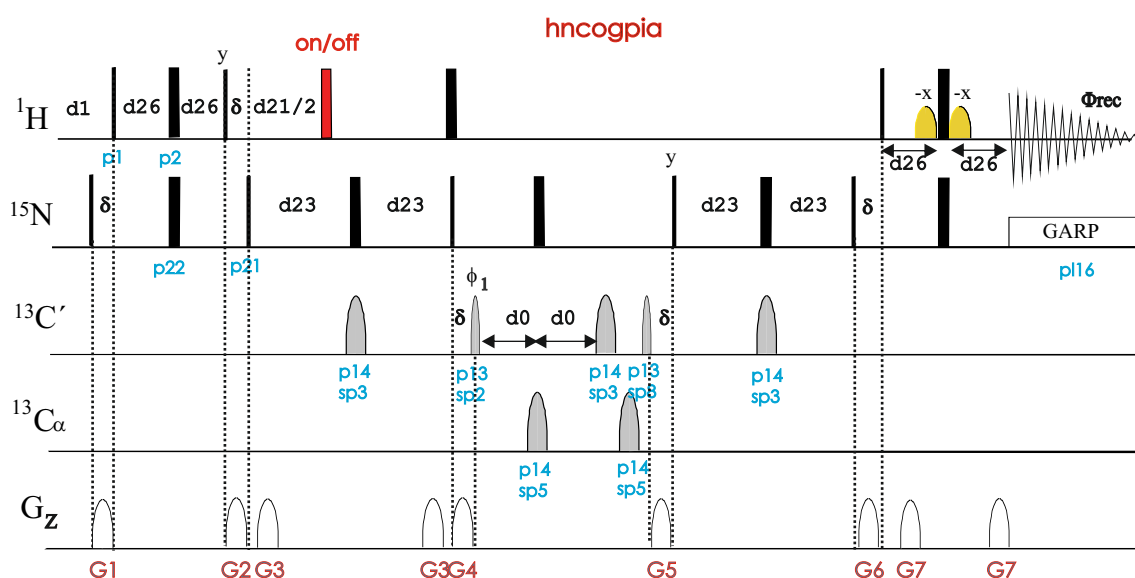
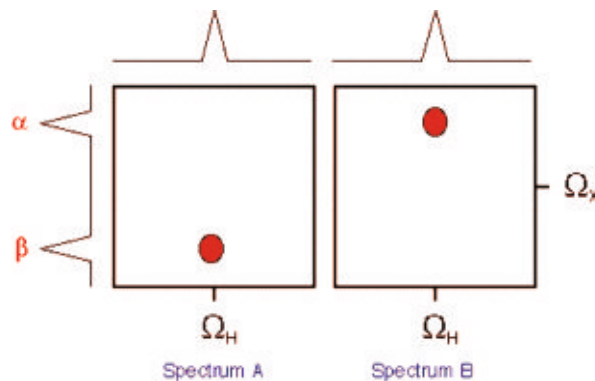
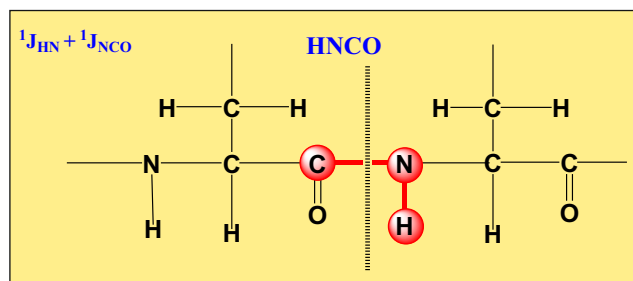
3D IPAP-HNCO & -IPAP-HNCA
FOR RDC MEASUREMENTS

3D HNCO and HNCA experiments for RDC measurements:

- 3D IPAP-HNCO to measure $^1J(\text{NH})$ (**hncogpia**)
- 3D IPAP-J-HNCO to measure $^1J(\text{CA-CO})$ and $^3J(\text{HN-CA})$:
Using PEP (**hncogprc3d1** | HNC06RPC3D1)
Using WATERGATE (**hncogprcw3d1** | HNC06RPCW63D1)
Using TROSY (**trhncogprc3d1** | TRHNC06RPC3D1)
- 3D IPAP-J-HNCO to measure $^{1,2}J(\text{N-CA})$ and $^3J(\text{HN-CA})$:
Using PEP (**hncogprc3d2** | HNC06RPC3D2)
Using WATERGATE (**hncogprcw3d2** | HNC06RPCW63D2)
Using TROSY (**trhncogprc3d2** | TRHNC06RPC3D2)
- 3D IPAP-J-HNCO to measure $^1J(\text{N-CO})$:
Using PEP (**hncogprc3d3** | HNC06RPC3D3)
Using WATERGATE (**hncogprcw3d3** | HNC06RPCW63D3)
Using TROSY (**trhncogprc3d3** | TRHNC06RPC3D3)
- 3D J-HNCO (CA) to measure $^1J(\text{CA-CB})$:
Using PEP (**hncogprc3d4** | HNC06RPC3D4)
Using WATERGATE (**hncogprcw3d4** | HNC06RPCW63D4)
Using TROSY (**trhncogprc3d4** | TRHNC06RPC3D4)
- 3D IPAP-J-HNCO (CA) to measure $^1J(\text{CA-HA})$ and $^1J(\text{CA-CB})$:
Using PEP (**hncogprc3d5** | HNC06RPC3D5)
Using WATERGATE (**hncogprcw3d5** | HNC06RPCW63D5)
Using TROSY (**trhncogprc3d5** | TRHNC06RPC3D5)
- 3D IPAP-J-HNCO to measure $^1J(\text{H-N})$ and $^3J(\text{HN-CA})$:
Using PEP (**hncogprc3d6** | HNC06RPC3D6)
Using WATERGATE (**hncogprcw3d6** | HNC06RPCW63D6)
Using TROSY (**trhncogprc3d6** | TRHNC06RPC3D6)
- 3D IPAP-J-HNCO to measure $^1J(\text{N-CO})$:
Using PEP (**hncogprc3d7**)
Using WATERGATE (**hncogprcw3d7**)
Using TROSY (**trhncogprc3d7**)
- 3D IPAP-J-HNCA to measure $^1J(\text{CA-HA})$:
Using PEP (**hncagprc3d1**)
Using WATERGATE (**hncagprcw3d1**)
Using TROSY (**trhncagprc3d1**)



3D IPAP-HNCO: J(NH)



Processing:

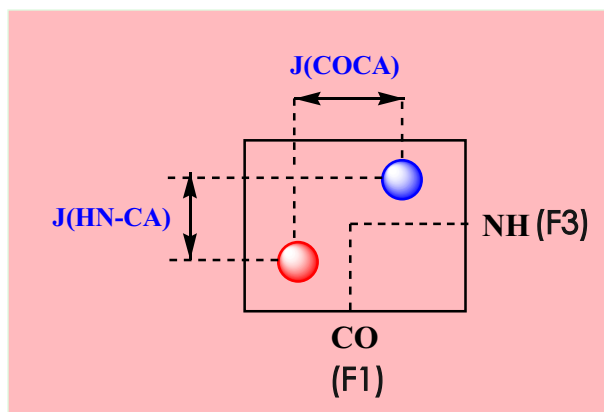
Two data are recorded in a interleaved mode.
Use AU-program split [ipap 2] to split data

Reference:

M.Ottiger, F. Delaglio & A. Bax, J. Magn. Reson.
131, 373-378 (1998)

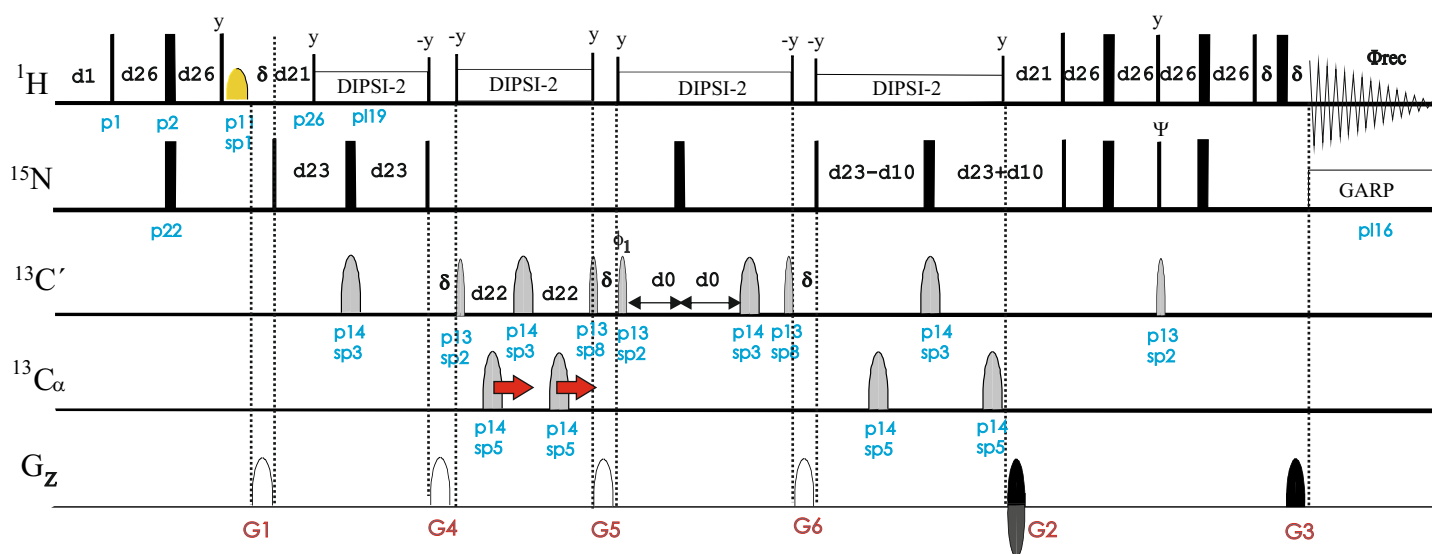
d21: $1/(2J(\text{NH}))$	[5.3 msec]
d23: $1/(4J(\text{NCO}))$	[13.5 msec]
d26: $1/(4J'(\text{NH}))$	[2.5 msec]

3D IPAP-J-HNCO: 1J(CA-CO) and 3J(HN-CA)



$d_{26} = 1/4 J(\text{NH}) = 2.3\text{m}$
 $d_{21} = 1/2 J(\text{NH}) = 5.5\text{m}$
 $d_{23} = 1/4 J(\text{NCO}) = 12\text{m}$
 $d_{22} = 1/4 J(\text{COCA}) = 4.3\text{m}$

hncogprc3d1



S3 Editing of CA prior to CO evolution

$$F1(H) \rightarrow F3(N) \rightarrow F2(C=O, J(Ca), t1) \rightarrow F3(N, t2) \rightarrow F1(H, t3).$$

Processing:

Two data (IP and AP) are recorded in a interleaved mode.

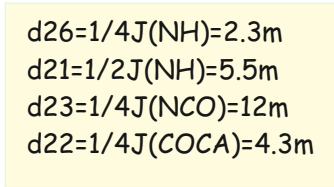
Use AU-program split [ipap 2] to split data (IP+AP and IP-AP)

Reference:

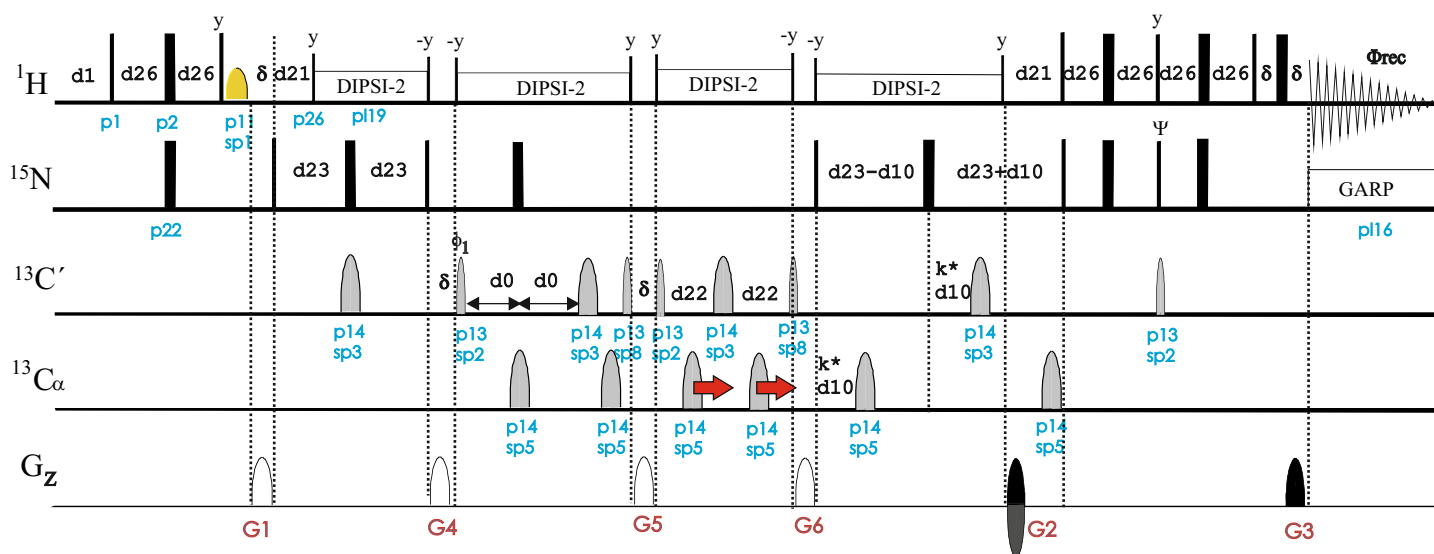
P. Permi, P.R. Rosevear & A. Annala, *J. Biomol. NMR* 17, 43-54 (2000)

[illegible][illegible]

3D IPAP-J-HNCO: 1J(N-CA), 2J(N-CA) and 2J(HN-CA), 3J(HN-CA)



hncogprc3d2



S3 Editing of CA prior to NH evolution.
 $F1(H) \rightarrow F3(N) \rightarrow F2(C=O, t_1) \rightarrow F3(N, t_2, J(C\alpha)) \rightarrow F1(H, t_3)$

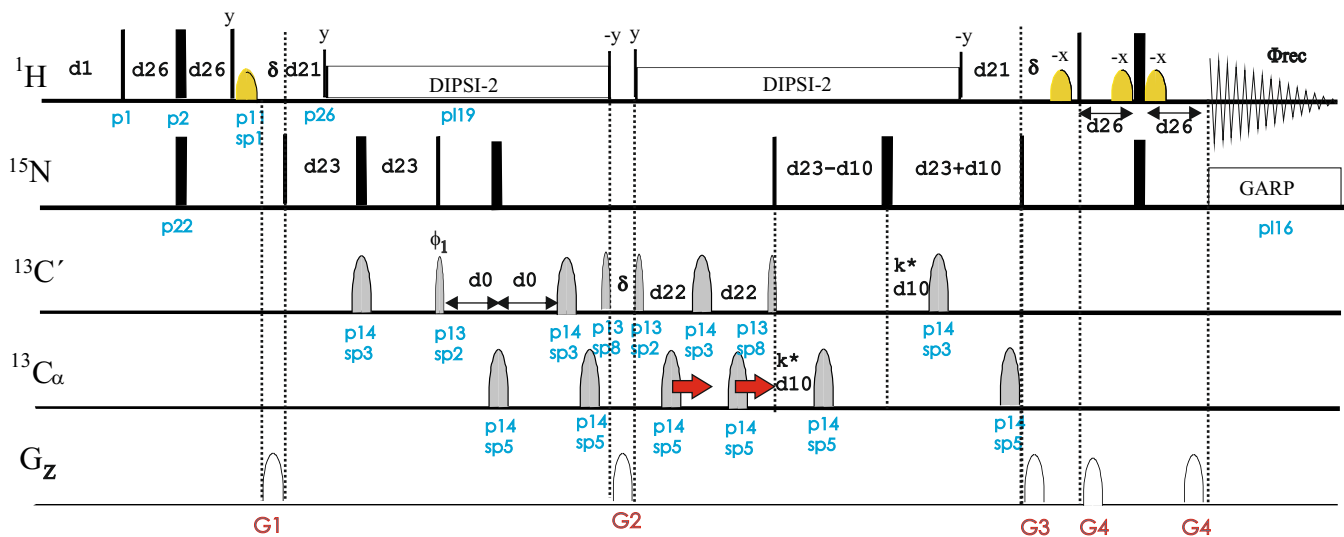
Processing:

Two data (IP and AP) are recorded in a interleaved mode.
Use AU-program split [ipap 2] to split data (IP+ap and IP-AP)

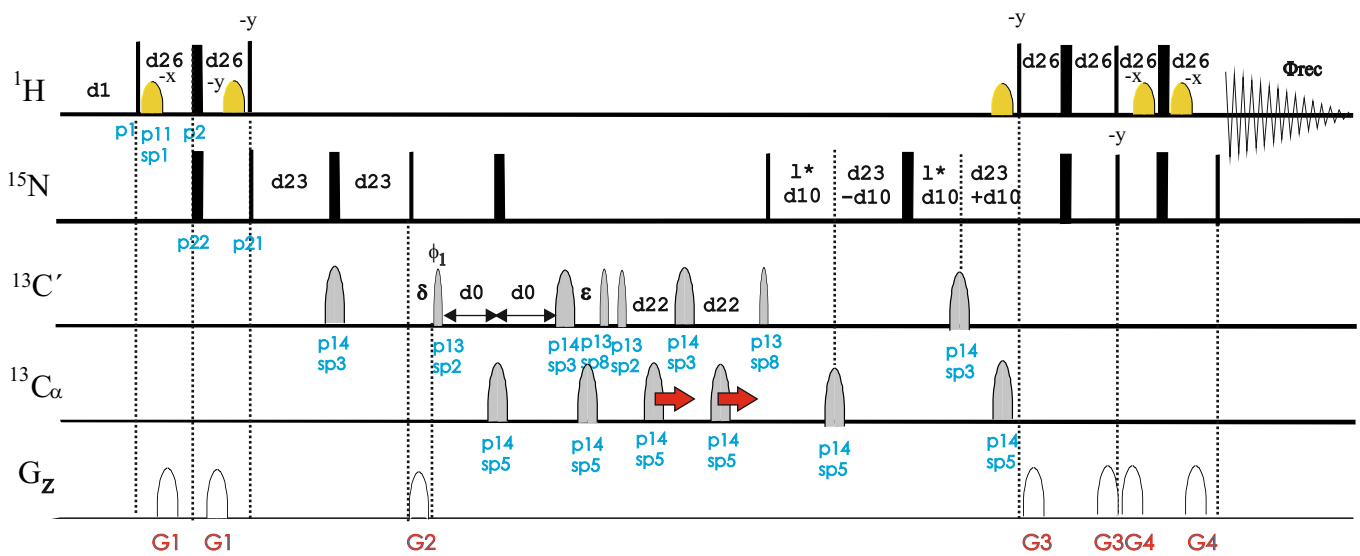
Reference:

P. Permi, P.R. Rosevear & A. Annala, *J. Biomol. NMR* 17, 43-54 (2000)

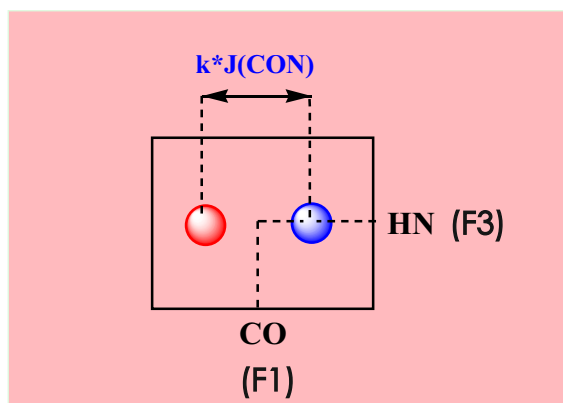
hncogprcw3d2



trhncogprc3d2

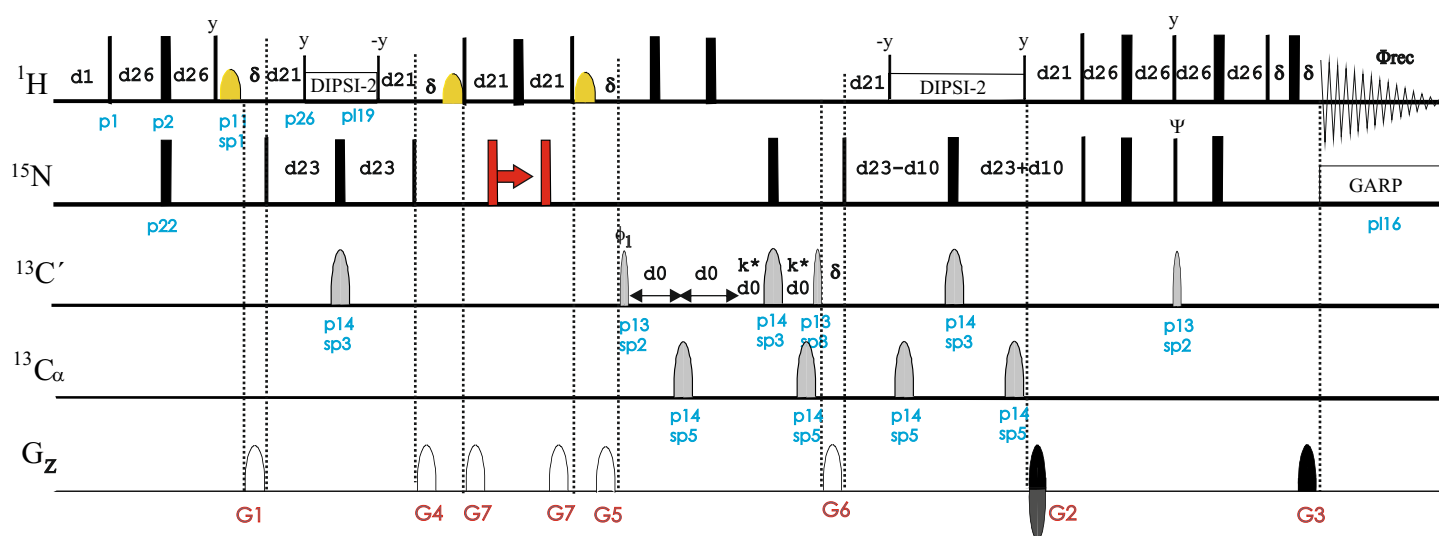


3D IPAP-J-HNCO: 1J(N-CO)



d21: $1/(2J(\text{NH}))$	[5.5 msec]
d23: $1/(4J(\text{NCO}))$	[12 msec]
d26: $1/(4J'(\text{NH}))$	[2.3 msec]

hncogprc3d3



Editing of N prior to CO evolution.

$\text{F1(H)} \rightarrow \text{F3(N)} \rightarrow \text{F1(H, J(N))} \rightarrow \text{F2(C=O, t1)} \rightarrow \text{F3(N, t2)} \rightarrow \text{F1(H, t3)}$

Processing:

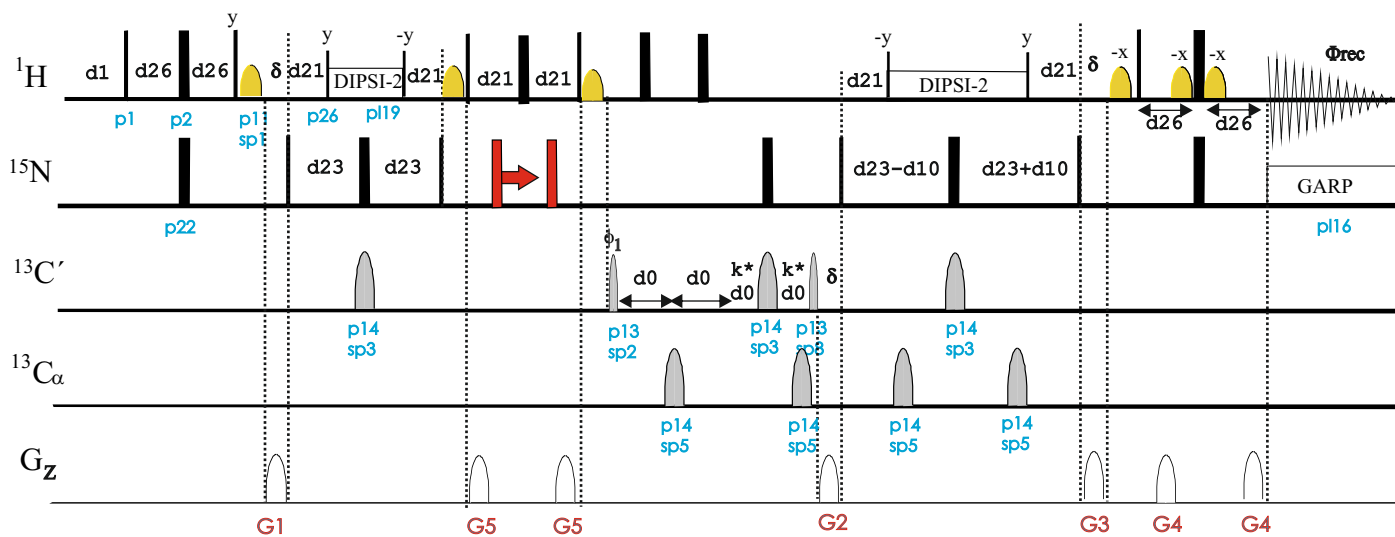
Two data (IP and AP) are recorded in a interleaved mode.

Use AU-program split [ipap 2] to split data (IP+ap and IP-AP)

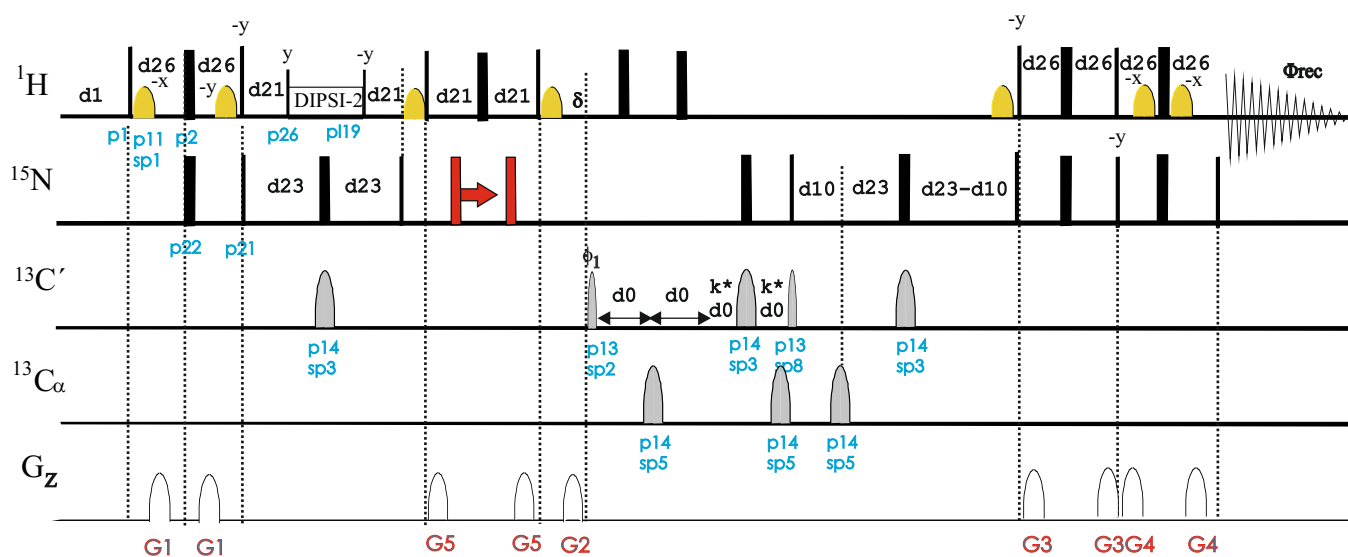
Reference:

P. Permi, P.R. Rosevear & A. Annala, J. Biomol. NMR 17, 43-54 (2000)

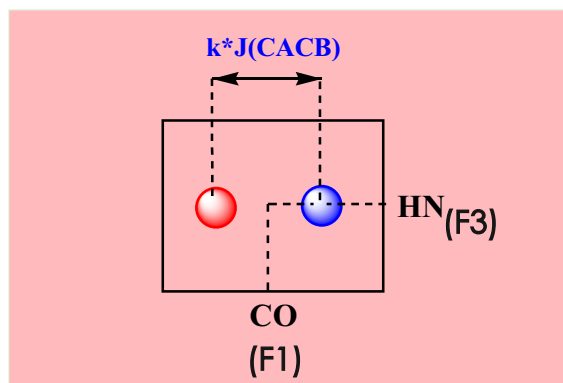
hncogprcw3d3



trhncogprc3d3

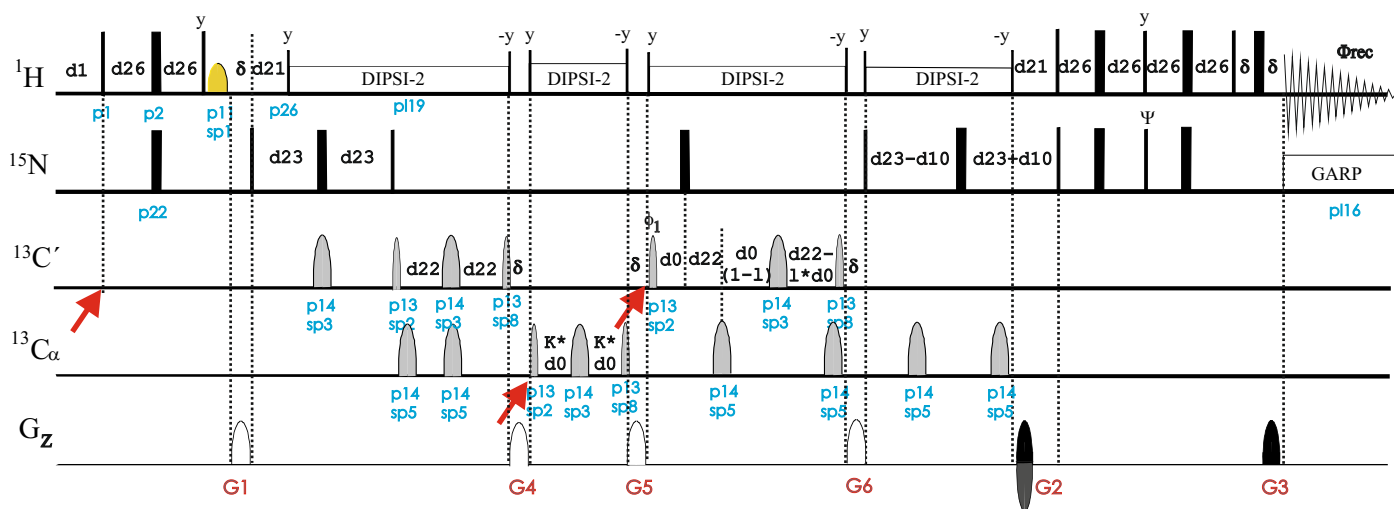


3D J-HNCO: 1J(CA-CB)



d21: $1/(2J(\text{NH}))$	[5.5 msec]
d22: $1/(4J(\text{CO}\alpha))$	[4.5 msec]
d23: $1/(4J(\text{NCO}))$	[12 msec]
d26: $1/(4J'(\text{NH}))$	[2.3 msec]

hncogprc3d4



Editing of N prior to CO evolution.

$\text{F1(H)} \rightarrow \text{F3(N)} \rightarrow \text{F2(C=O)} \rightarrow \text{F2(C}\alpha, J(\text{Cb})) \rightarrow \text{F2(C=O, t1)} \rightarrow \text{F3(N, t2)} \rightarrow \text{F1(H, t3)}$

Processing:

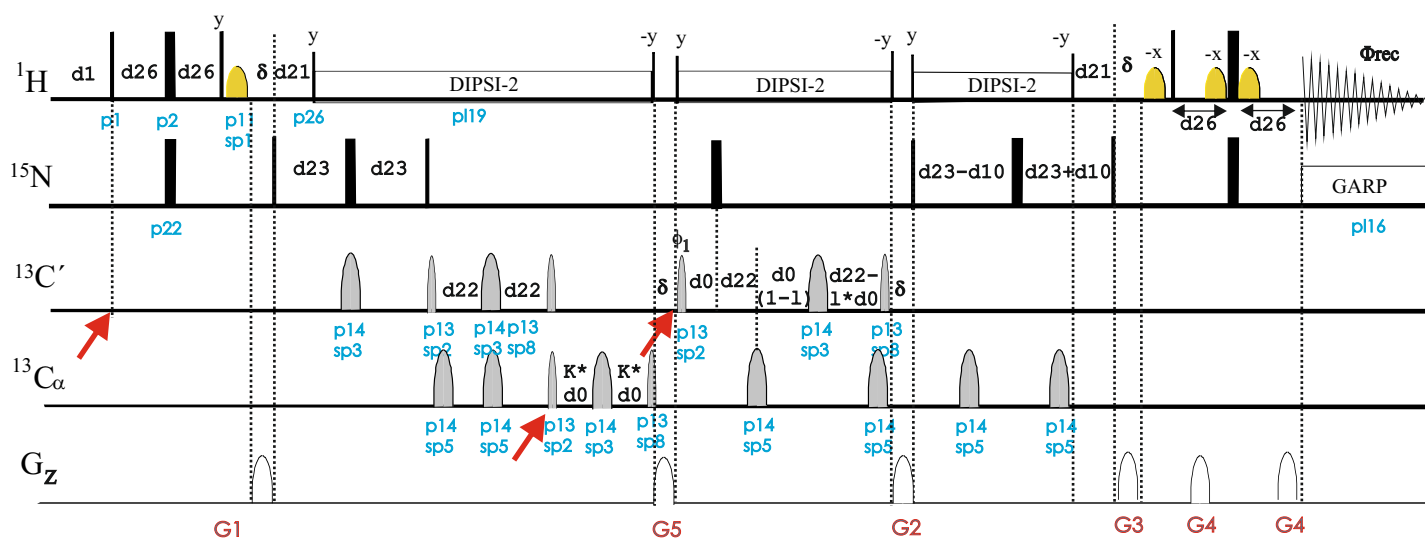
Two data (IP and AP) are recorded in a interleaved mode.

Use AU-program split [ipap 2] to split data (IP+ap and IP-AP)

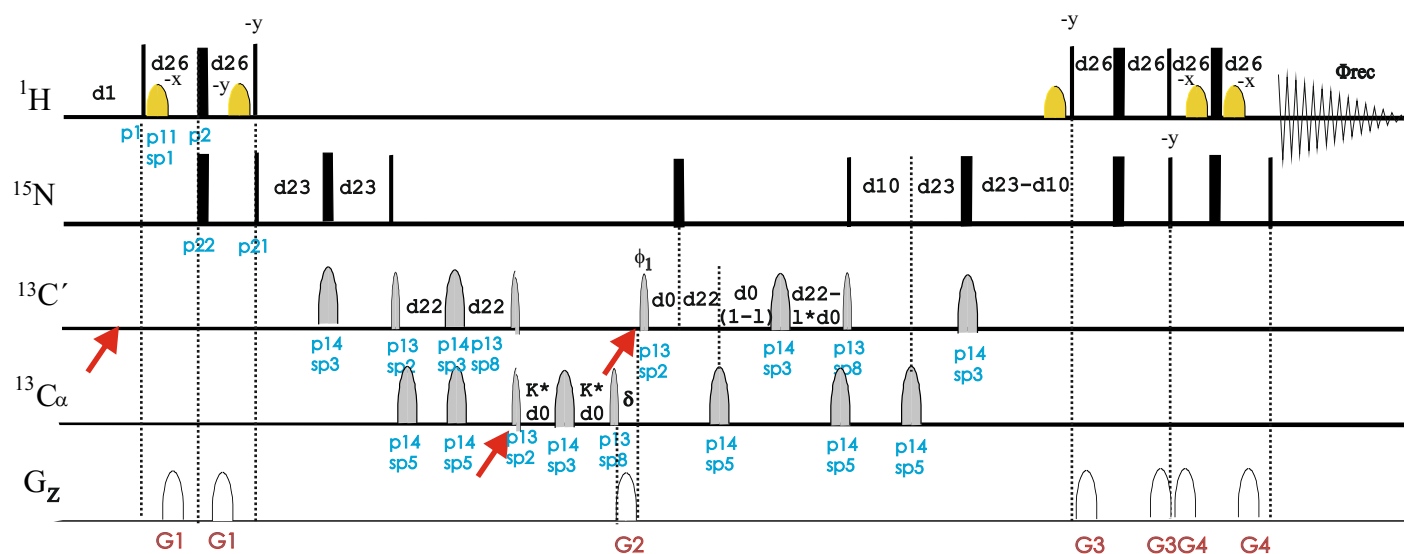
Reference:

P. Permi, P.R. Rosevear & A. Annala, J. Biomol. NMR 17, 43-54 (2000)

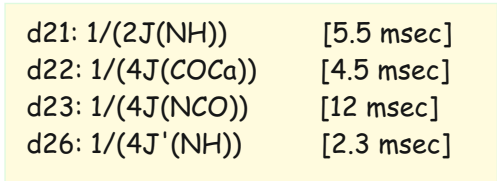
hncogprcw3d4



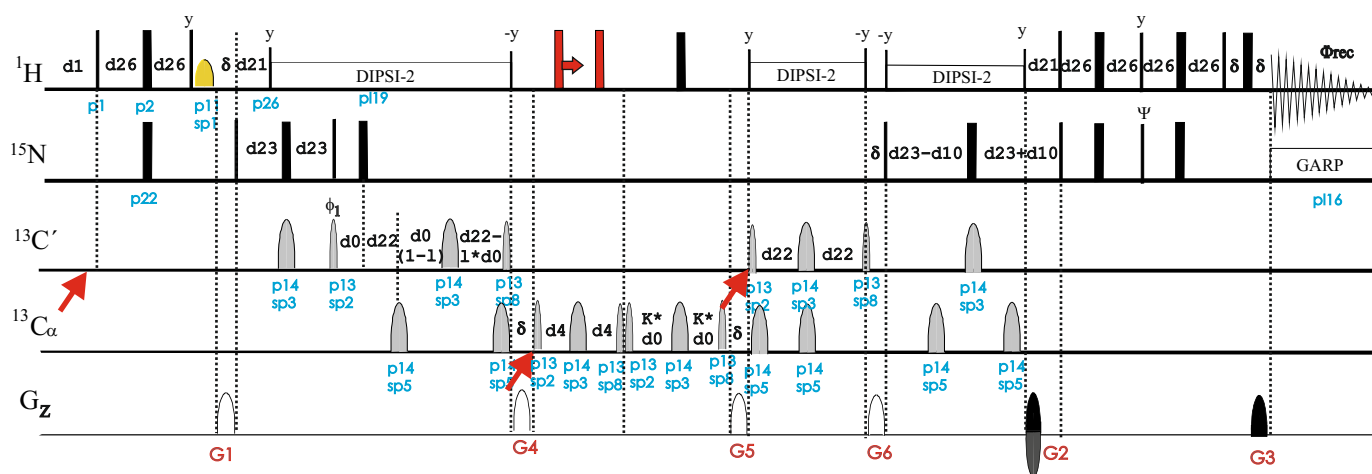
trhncogprc3d4



3D IPAP-J-HNCO: $1J(CA-HA)$ and $1J(CA-CB)$



hncogprc3d5



Editing of CA after the CO evolution.

$$F1(H) \rightarrow F3(N) \rightarrow F2(C=O, t_1) \rightarrow F2(Ca, J(Ha)) \rightarrow F2(C=O) \rightarrow F3(N, t_2) \rightarrow F1(H, t_3)$$

Processing:

Two data (IP and AP) are recorded in a interleaved mode.

Use AU-program split [ipap 2] to split data (IP+ap and IP-AP)

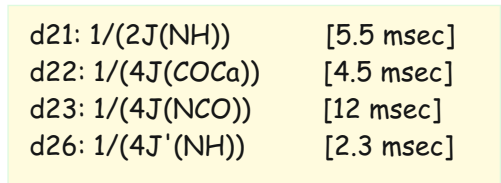
Reference:

D. Yang, J.R. Tolman, N.K. Goto & L.E. Kay, J. Biomol. NMR 12, 325-332 (1998)

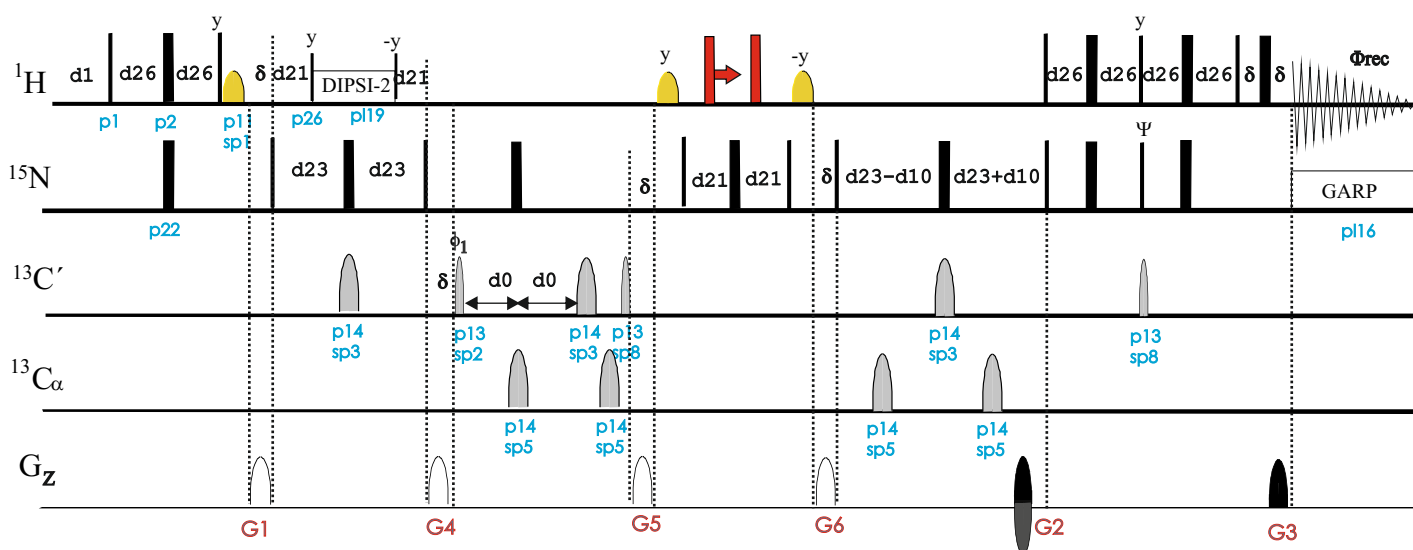
[illegible]

The schematic shows four horizontal tracks representing different nuclei: ^1H , ^{15}N , $^{13}\text{C}'$, and G_Z . The ^1H track includes pulses labeled d1, d26_{-x}, d26_{-y}, and a series of d26 pulses followed by a Φ_{rec} signal. The ^{15}N track shows pulses d23, d23, d10, d23, d23-d10, and -y. The $^{13}\text{C}'$ track displays various peaks labeled with p14 sp3, p13 sp2, p13 sp8, d4, K* d0, d22, and others. The G_Z track at the bottom shows Gaussian-like shapes corresponding to the time points G1, G2, G3, G3G4, and G4. Vertical dashed lines indicate synchronization between the different channels.

3D IPAP-J-HNCO: 1J(HN)



hncogprc3d6



Editing of HN prior to N evolution.

$$F1(H) \rightarrow F3(N) \rightarrow F2(C=O, t1) \rightarrow F3(N, J(H(N), t2) \rightarrow F1(H, t3)$$

Processing:

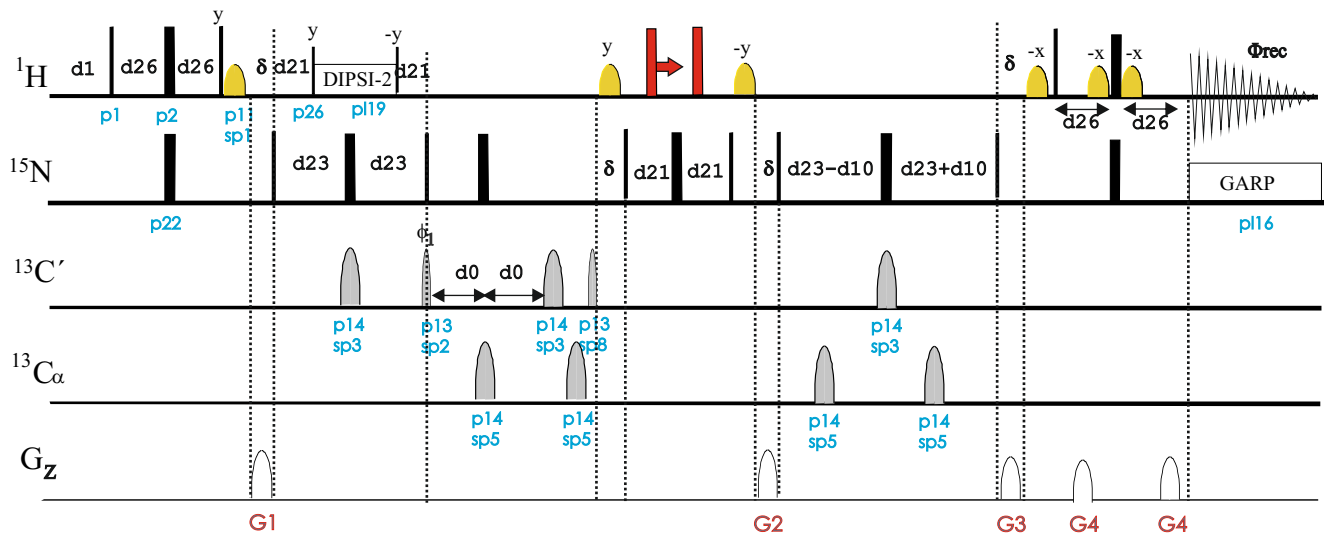
Two data (IP and AP) are recorded in a interleaved mode.

Use AU-program split [ipap 2] to split data (IP+ap and IP-AP)

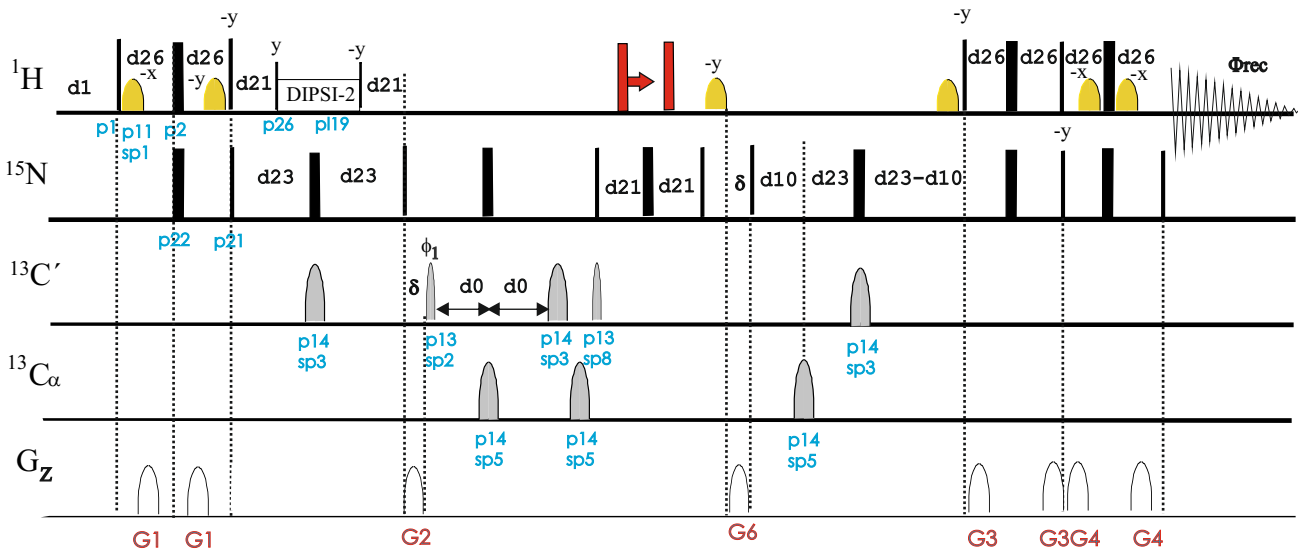
Reference:

P. Permi, P.R. Rosevear & A. Annila, *J. Biomol. NMR* 17, 43-54 (2000)

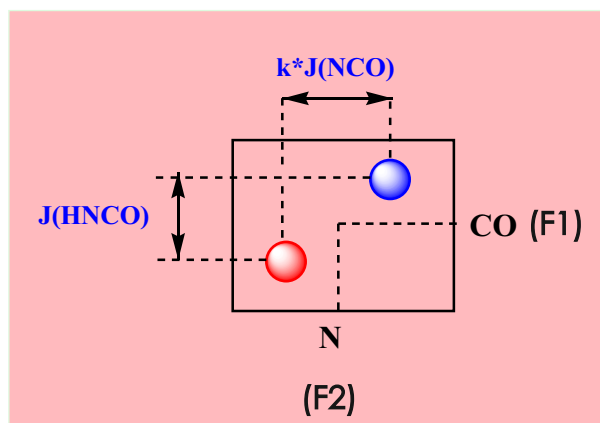
hncogprcw3d6



trhncogprc3d6

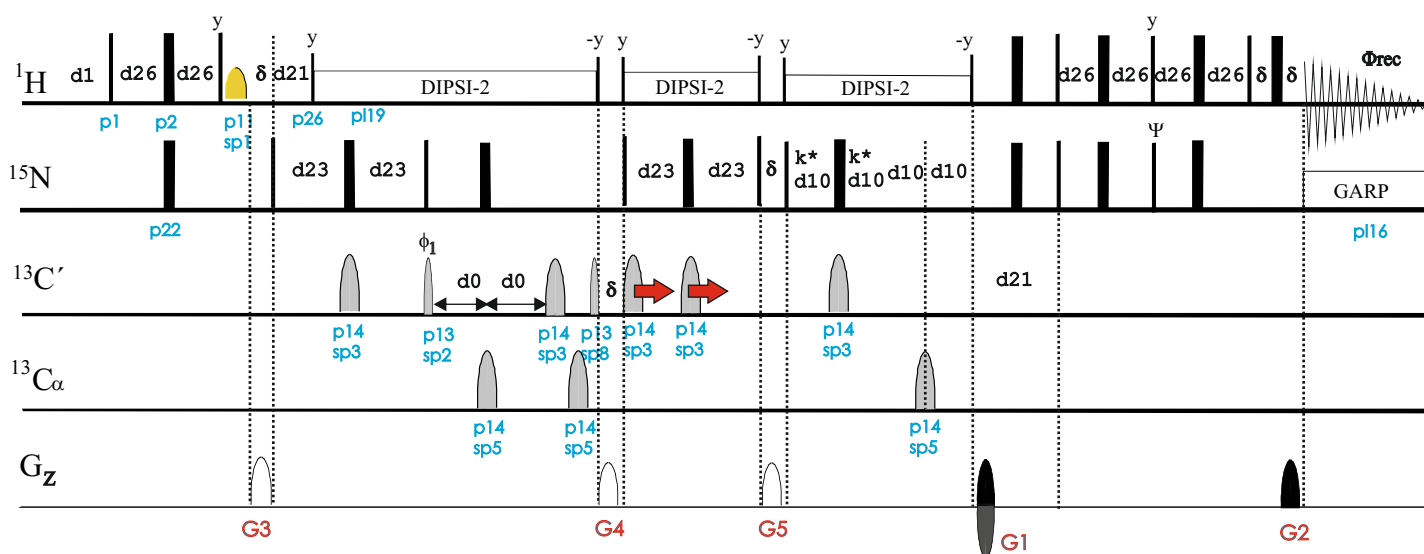


3D IPAP-J-HNCO: 1J(NCO) and 2J(HNCO)



d21: 1/(2J(NH))	[5.5 msec]
d23: 1/(4J(NCO))	[12 msec]
d26: 1/(4J'(NH))	[2.3 msec]

hncogprc3d7



Editing of CO prior to N evolution.

$$F1(H) \rightarrow F3(N) \rightarrow F2(C=O, +1) \rightarrow F3(N, J(C'), +2) \rightarrow F1(H, +3)$$

Processing:

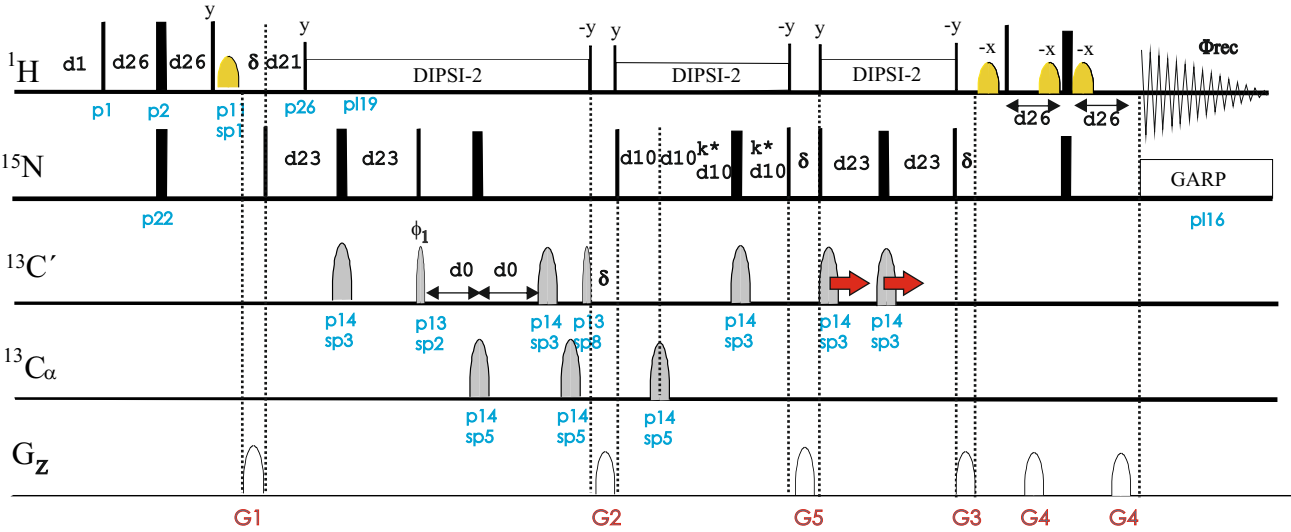
Two data (IP and AP) are recorded in a interleaved mode.

Use AU-program split [ipap 2] to split data (IP+ap and IP-AP)

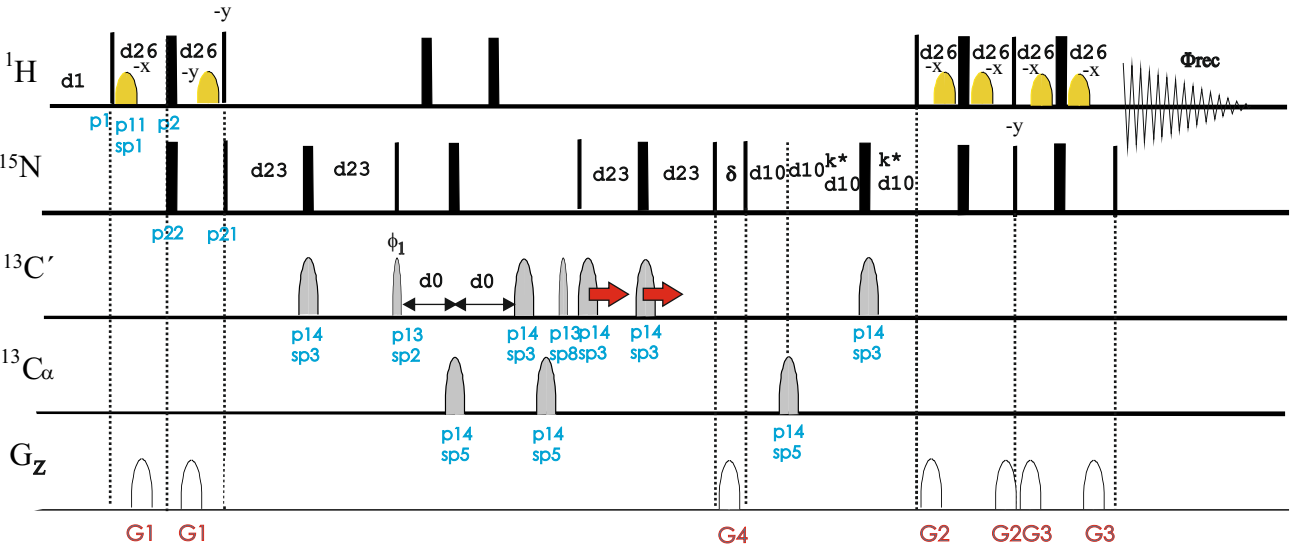
Reference:

P. Permi, P.R. Rosevear & A. Annila, *J. Biomol. NMR* 17, 43-54 (2000)

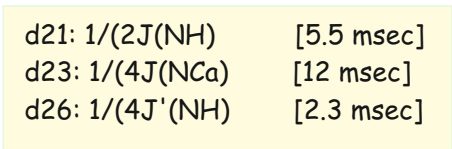
hncogprcw3d7



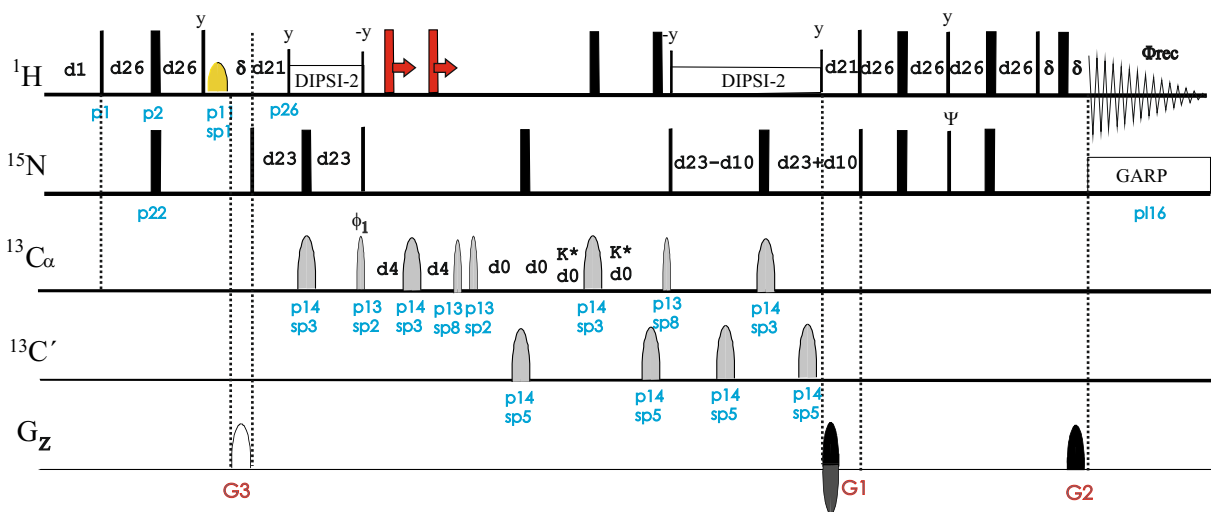
trhncogprc3d7



3D IPAP-J-HNCA: $1J(\text{CA-HA})$ and $1J(\text{CACB})$



hncagprc3d1



S3 Editing of HA prior to CA evolution.

$$F1(H) \rightarrow F3(N) \rightarrow F2(Ca, J, t+1) \rightarrow F3(N, t+2) \rightarrow F1(H, t+3)$$

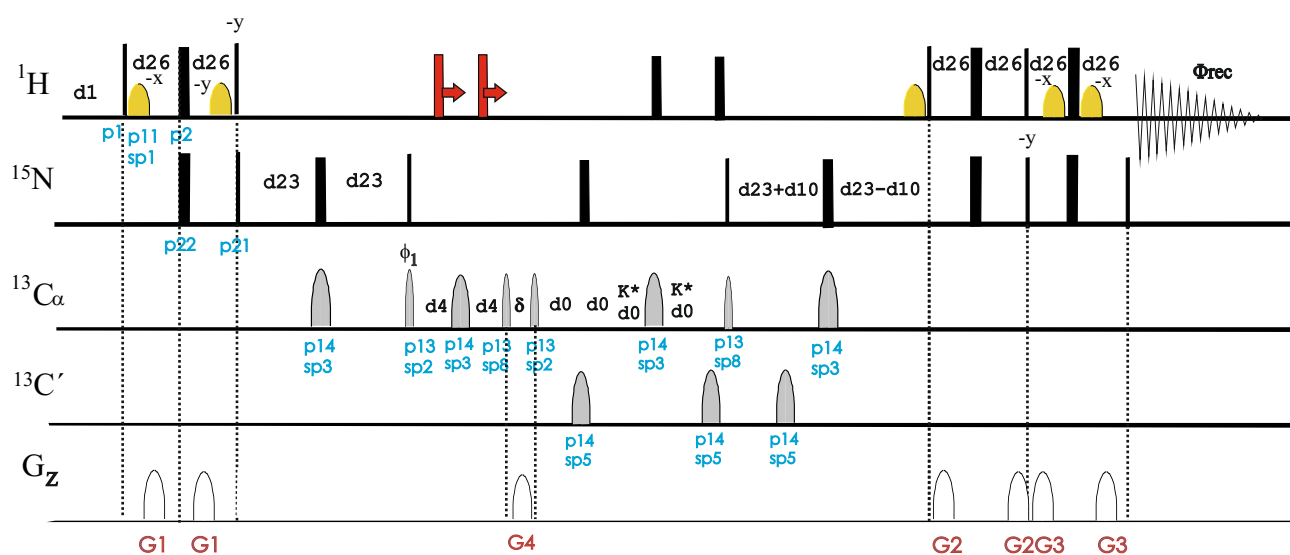
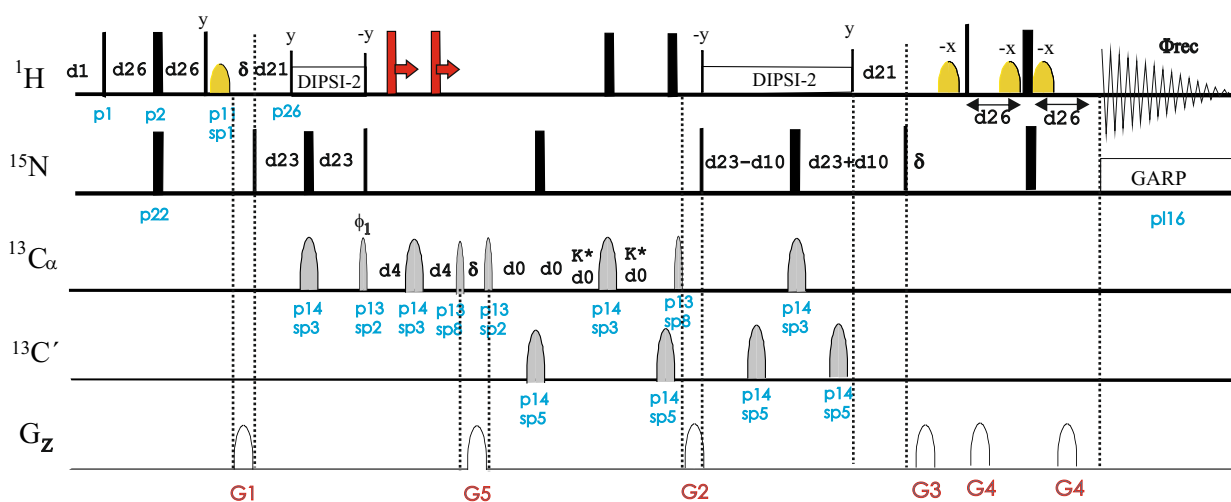
Processing:

Two data (IP and AP) are recorded in a interleaved mode.

Use AU-program split [ipap 2] to split data (IP+ap and IP-AP)

Reference:

P. Permi, J. Biomol. NMR 27, 341-349 (2003)



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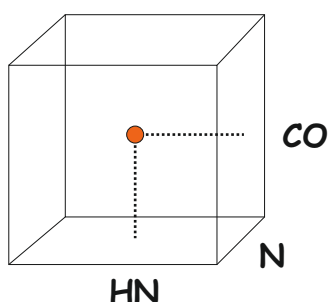
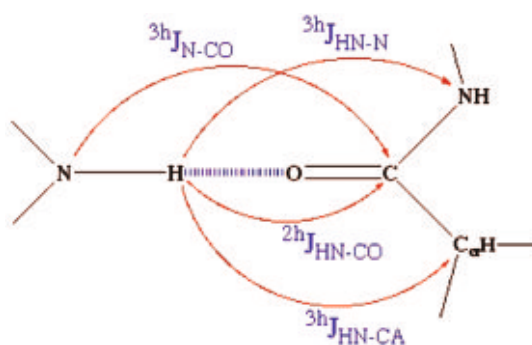
PROTEIN NMR COUPLING CONSTANTS THROUGH-HYDROGEN BONDS

Through-Hydrogen-bond 3D HNCO experiments

- 3D Hydrogen bond-HNCO (**hncogphb3d** | **HNCOGPHB3D**)
- 3D Hydrogen bond-HNCO with ^{13}C decoupling (**hncogphb3d.2**)
- 3D Hydrogen bond-HNCO without decoupling to enhance TROSY effect without spin-state selection (**hncogphb3d2** | **HNCOGPHB3D2**)
- 3D Hydrogen bond-HNCO using TROSY (**trhncogphb3d**)

Also see:

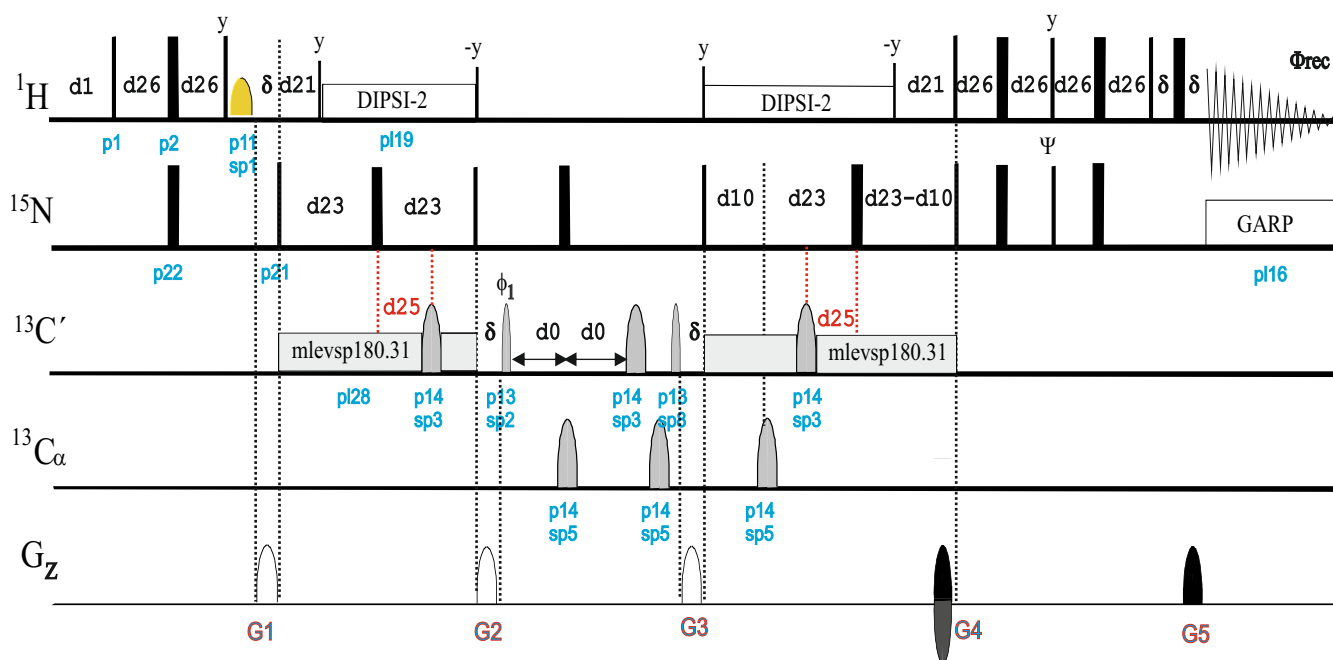
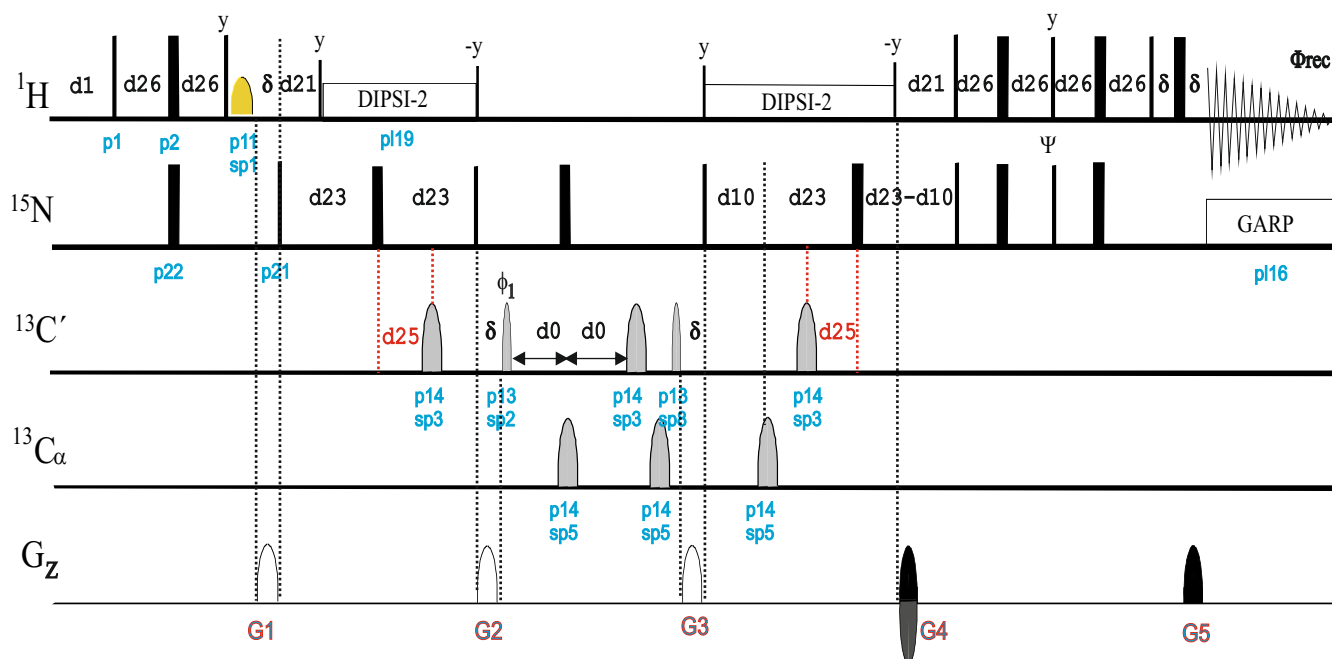
The original 3D HNCO Experiment.



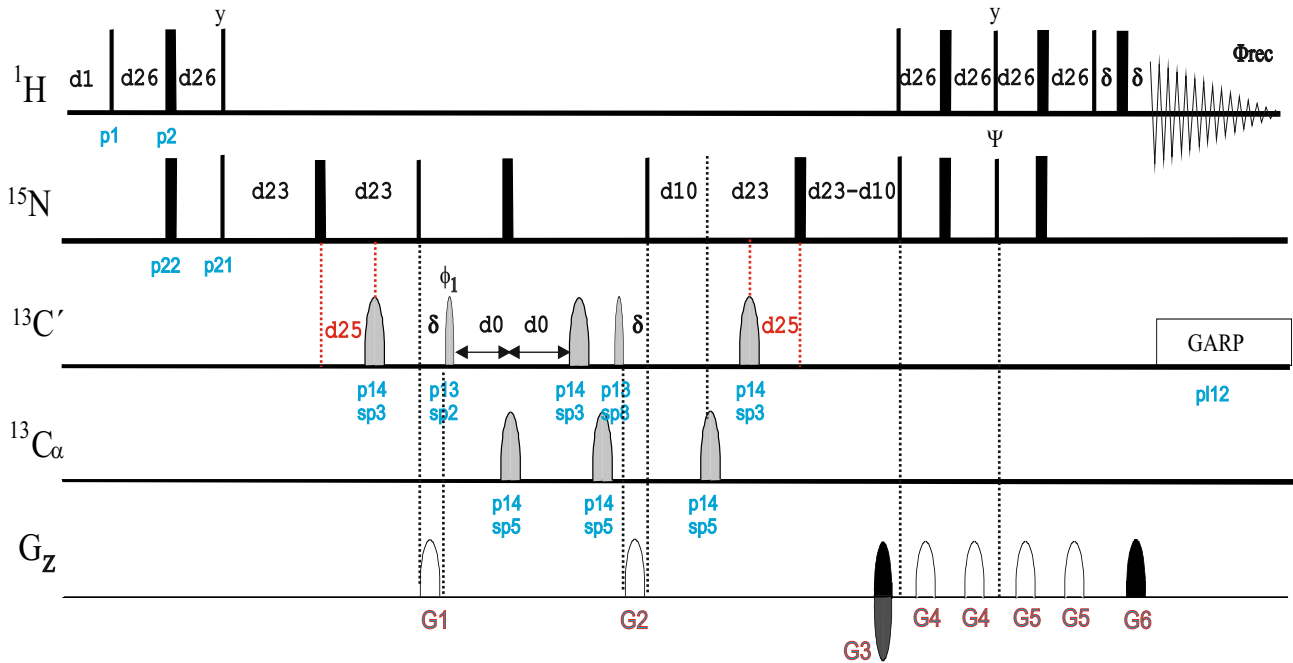
d21: $1/(2J(\text{NH}))$	[5.5 msec]
d23: $1/(1J(\text{NCO}))$	[66.6 msec]
d25: $1/(4J(\text{NCO}))$	[16.6 msec]
d26: $1/(4J'(\text{NH}))$	[2.3 msec]

References:

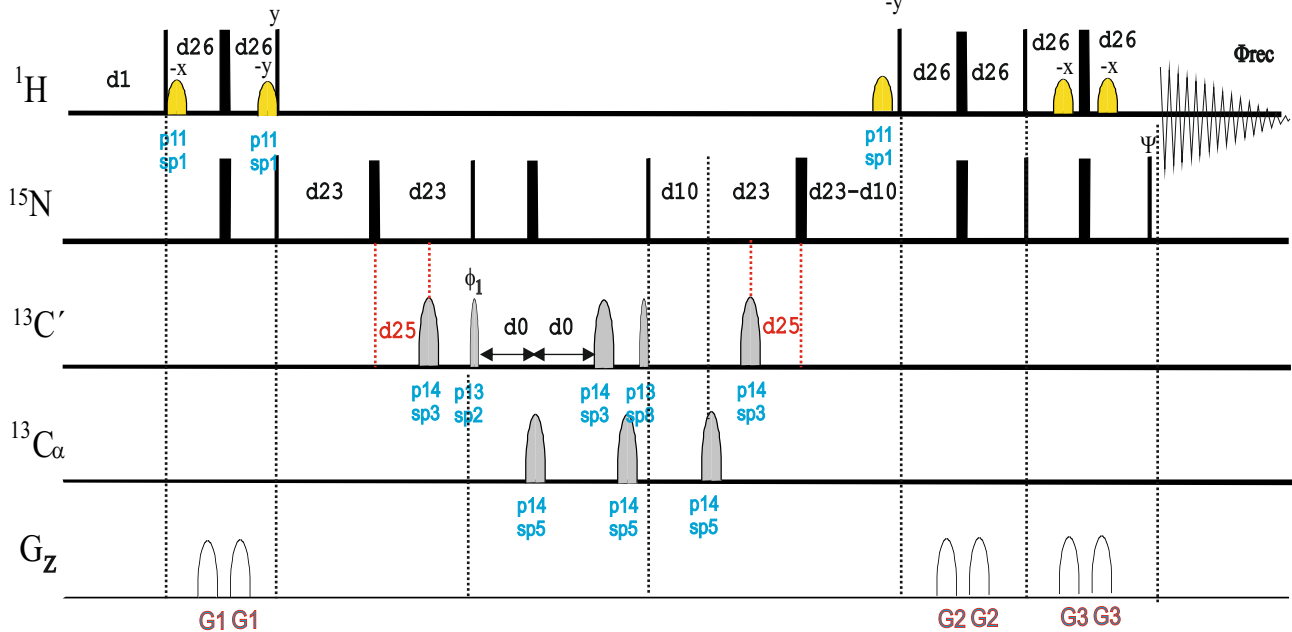
1.F. Cordier & S. Grzesiek, J. Am. Chem. Soc. 121, 1601-1602 (1999)



hncogphb3d2



trhncogphb3d



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2D & 3D NUCLEIC-ACID NMR EXPERIMENTS. INTRODUCTION

References:

1. S.S. Wijmenga and B.N.M. van Buuren, "The use of NMR methods for conformational studies of nucleic acids, *Prog. Nucl. Magn. Reson.*, 32, 287-387 (1998).
2. B. Fürtig, C. Richter, J. Wöhnert, and H. Schwalbe, "NMR of RNA", *ChemBioChem*, 4, 936-962(2003).

1. Sugar Assignment

H and H/C experiments
Sugar puckering
Measurement of J(CH) and J(HH)

2. Sequential assignment via phosphodiester linkage

H/P and H/C/P experiments
Measurement of J(PH) and J(PC)
NOE contacts

3. Sugar-to-base connectivities

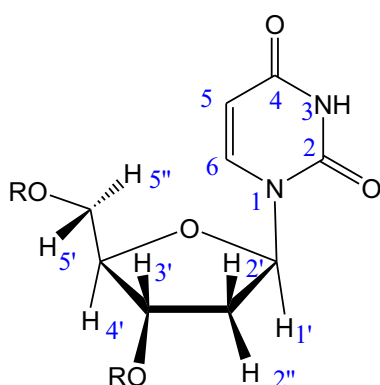
H/C/N experiments
NOE contacts

4. Intra-base assignment

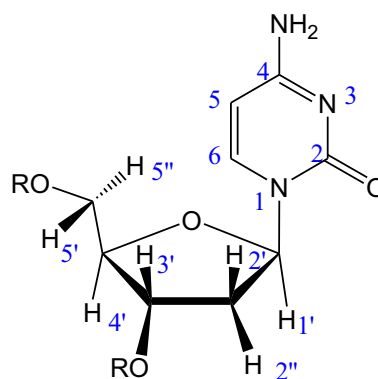
H/N, H/C and H/C/N experiments

5. Base-pairing identification

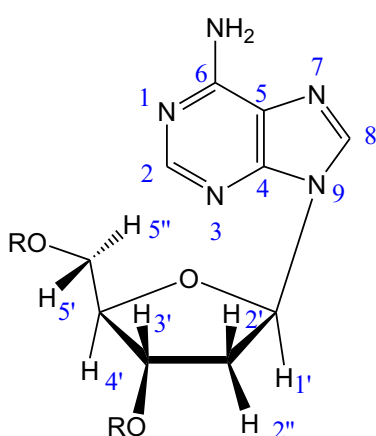
Through-hydrogen-bond H/N experiments
NOE contacts



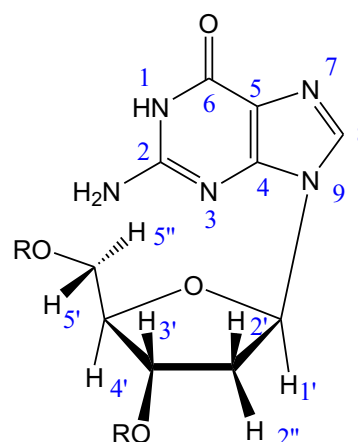
Uridine



Cytosine, C



Adenine, A



Guanine, G

	<u>N1</u>	<u>C2</u>	<u>N3(H)</u>	<u>C4</u>	<u>C5(H5)</u>	<u>C6(H6)</u>	<u>N(H2)</u>			
<u>U</u>	142-146	154	156-162 (13-14)	169	102-107 (5.0-6.0)	137-144 (6.9-7.9)	-			
<u>C</u>	150-156	159	210	166-168	94-99 (5.0-6.0)	136-144 (6.9-7.9)	94-98 (6.7-7.0 & 8.1-8.8)			
	<u>N1(H)</u>	<u>C2(H2)</u>	<u>N3</u>	<u>C4</u>	<u>C5</u>	<u>C6</u>	<u>N7</u>	<u>C8(H8)</u>	<u>N9</u>	<u>N(H2)</u>
<u>A</u>	214-216	152-156 (7-8)	220-226	149-151	119-121	157-158	224-232	137-142 (7.7-8.5)	166-172	82-84 (5-6 & 7.8)
<u>G</u>	146-149 (12-13.6)	156	167	152-154	117-119	161	228-238	131-138 (7.5-8.3)	166-172	72-76 (5-6 & 8-9)
	<u>C1'</u>	<u>C2'</u>	<u>C3'</u>	<u>C4'</u>	<u>C5'</u>					
Sugar	87-94 (5-6	70-78 4.4-5.0	70-78 4.4-5.0	82-86 3.8-4.3	63-68 3.8-4.3)					

Main Features of nucleic acid (NA) experiments

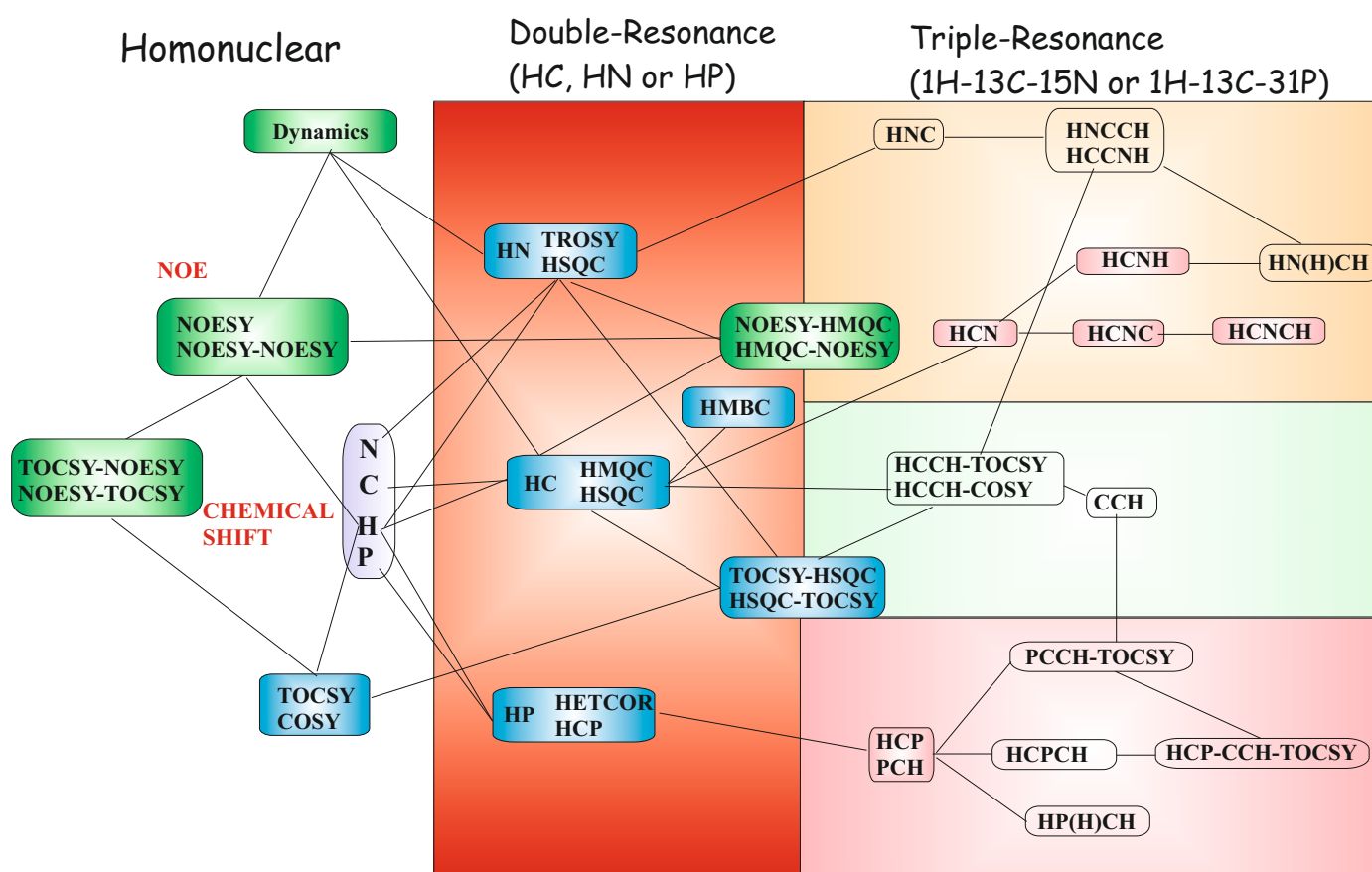
NAs usually present poor degeneracy and important conformational flexibility. Thus, ^1H NMR spectra of NAs can be difficult to analyze because of their low proton density and important resonance overlapping due to poor ^1H chemical shift dispersion. However, small NAs can be studied using the same 1D and 2D NMR experiments dedicated to study natural-abundance organic molecules. Higher NAs would require double- and triple-resonance NMR experiments involving low-sensitive ^{13}C or ^{15}N nuclei.

Sample Requirements

Unlabeled NAs can be analyzed with typical 1D and 2D NMR homo- and heteronuclear NMR experiments. In complex NAs, more sophisticated and specifically designed ^{15}N and Triple-resonance HCX experiments can require selective $^{13}\text{C}/^{15}\text{N}$ labeling or $^{13}\text{C}/^{15}\text{N}$ -doubly labeled samples.

Hardware Requirements

NAs experiments are best recorded on triple-resonance $^1\text{H}, ^{13}\text{C}, ^{15}\text{N}$ or $^1\text{H}, ^{13}\text{C}, ^{31}\text{P}$ inverse probeheads with z-gradients capabilities.



Experimental details for nucleic-acid experiments

Offsets

F1 channel: ^1H (o1p)
F2 channel: ^{13}C (o2p)
F3 channel: ^{15}N (o3p) in HN-type or HCN-type experiments
F3 channel: ^{31}P (o3p) in HP-type or HCP-type experiments

Mixing/Decoupling

From f2 channel:
13C CPD with GARP (pcpd2=80us at pl12)
13C-13C TOCSY with FLOPSY-16 (p9 at pl15)

From f3 channel:
15N CPD with GARP (pcpd3=200us at pl16)
31P CPD with GARP (pcpd3 at pl16)

Typical 13C pulses from F2 channel

p13 sp2: 90° C on- resonance (320us , sptam2=Q5.1000)
P14 sp3: 180° C on-resonance (256us, sptam3= Q3.1000)
p13 sp8: retro- 90° C on-resonance (320us, sptam8= Q5tr.1000)
p14 sp5: 180° C off-resonance (256us, sptam5=Q3.1000)

p8 sp13: 180° adiabatic for inversion (500us using CHIRP , sptam13=Crp60,0.5,20.1)

Typical 15N pulses from F3 channel

p30 sp9: 180° N1/N9 on- resonance (700us , sptam9=Q3.1000)

Very Important!!: In all pulse programs the syntax

prosol relations=<triple_na>

is included for automated acquisition/set-up using edprosol/getprosol.
This file is defined in the following directory:

$\$TOPSPINHOME/conf/instr/spect/prosol/relations/triple_na$

Specific Nucleic Acid NMR

- **3D HC and HN NOESY Experiments:**

3D ^1H - ^{13}C NOESY-CT-HSQC using echo-antiecho (na_noesyhsqccetg3d)

3D ^1H - ^{13}C NOESY-HSQC using WATERGATE and refocusing of $J(\text{C}5\text{C}6)$ during t_1 (na_c6noesyhsqcg3d)

3D ^1H - ^{15}N NOESY-HSQC using WATERGATE (na_noesyhsqcf3gpgw3d)

- **2D and 3D HCN-Type Experiments:**

HCN experiment

3D using echo-antiecho (na_hcnetgpsi3d | NA_HCNETGPSI3D)

3D using echo-antiecho and selective pulses (na_hcnetgpsisp3d | NA_HCNETGPSISP3D)

3D using MQ (na_hcnmq3d)

3D using MQ and selective ^1H pulses (na_hcnmqsp3d)

3D using TROSY (na_trhcnph3d)

3D using TROSY and gradient selection (na_trhcnetsi3d)

2D H(C)N using TROSY (na_trhcnph)

2D H(C)N using TROSY and gradient selection (na_trhcnnet)

2D H(C)N using MQ (na_hcnmqgpphpr | NA_HCNMQGPPHPR)

HCNCH experiment

2D H(CNC)H (na_hcnchgpjrphsp | NA_HCNCHGPTJRPSP)

3D H(C)N(C)H using MQ (na_hcnchgmqs3d)

3D H(C)N(C)H using MQ and TROSY (na_trhcnchmqsp3d)

3D H(C)N(C)H using MQ, TROSY and WATERGATE (na_trhcnchmqspwg3d)

3D (H)CN(C)H using MQ, TROSY and WATERGATE (na_trhcnchmqspwg3d2)

3D (HC)N(C)CH-COSY using MQ (na_hcnchcomq3d)

3D (HC)N(C)CH-TOCSY using MQ (na_hcnchdimq3d)

2D H(CN)H using WATERGATE (na_hcnhgpph19 | NA_HCNHGPPH19)

2D H(CN)C (na_h68c68n19c42)

HCCNH experiment

3D H(6/8)(CCC)NH (na_hccnhdigpwg3d | NA_HCCNHDI6PWG3D)

3D H(CC)NH-COSY (na_h5c5c4n3h_3d)

3D H(CC)NH-TOCSY (na_h56c56c4n3h_3d)

3D (H)C(C)NH-TOCSY (na_h56c56c4n3h_3d2)

2D H(NC6)C5 (na_hnc6c5etgpsi)

3D (H)N(C)CH (na_hncch3d)

3D TROSY-(H)CCH-COSY for intra-base correlation (na_trhcchco3d)

- **Observation HN-N hydrogen bonds:**

2D HNN-COSY (na_hnncosygpphwg | NA_HNNCOSYGPPHWG)

2D HNN-COSY using shaped ^{15}N 180° pulses (na_hnncosygpphspwg)

2D HNN-COSY using TROSY and shaped ^{15}N 180° pulses (na_trhnncosygpphspwg)

- **2D and 3D HC Experiments to determine $J(\text{HH})$ and $J(\text{CH})$:**

3D H(C)CH-E.COSY experiment (na_hcchecgp3d | NA_HCCHGCP3D)

3D HCC-TOCSY-CCH-COSY experiment (na_hcchfwdigp3d | NA_HCCHFWDIGP3D)

3D HCC-TOCSY-CCH-E.COSY experiment (na_hcchfwdiecg3d | NA_HCCHFWDIEGCP3D)

3D HCC-TOCSY-CCH-E.COSY experiment using jump-and-return (11) (na_hcchfwdiecgj3d)

3D forward directed quantitative gamma HCC-TOCSY (na_ghcchfwdigp3d | NA_GHCCHFWDIGP3D)

2D ^1H - ^{13}C HSQC for measuring J_{CH} in sugars (na_hsqcetgpjcsf | NA_HSQCETGPJCSP)

- **2D and 3D HP Experiments:**

2D CT HH- $\{^3\text{P}\}$ -COSY with presaturation to measure $J(\text{H}3'\text{-P})$ (na_hpcosyphpr | NA_HPCOSYPHPR)

2D ^1H - ^3P HETCOR experiment

Using echo-antiecho (na_xhcoetf3gp)

Constant-time using echo-antiecho (na_xhcoctetf3gp)

Constant-time without gradient selection (na_hpctco)

Constant-time without gradient selection using jr (na_hpctcojr)

2D ^1H - ^3P HSQC experiment

Using CPMG (na_hsqctf3gpxy)

Using CPMG and jump-and-return (na_hsqcf3gpjrphxy)

2D ^1H - ^3P Hetero-TOCSY using cross-polarization (na_hpdi)

2D ^1H - ^3P HSQC-NOESY using CPMG (na_hsqcf3gnophxy)

2D ^1H - ^3P Hetero-TOCSY-NOESY

Using cross-polarization (na_hpdino)

Using WATERGATE and cross-polarization (na_hpdino19)

3D using cross-polarization (na_hpdino3d)

3D using WATERGATE and cross-polarization (na_hpdino193d)

- **2D and 3D HCP Experiments:**

HCP Experiment

3D HCP using sensitivity-enhancement (na_hcpetgpsi3d | NA_HCPETGPSI3D)

3D HCP-TOCSY

Using CC TOCSY and presaturation (na_hcpdigp3d)

Using CC TOCSY and jump-and-return (11) (na_hcpdigpjr3d)

Using CC TOCSY and echo-antiecho (na_hcpdietgp3d)

Using CC TOCSY and sensitivity-enhancement (na_hcpdietgpsi3d | NA_HCPDIETGPSI3D)

PHCH Experiment

3D P(H)CH using HMQC and echo-antiecho (na_hpccoetf3gp3d)

3D Constant-time P(H)CH using HMQC (na_hpcctco3d)

3D Constant-time P(H)CH using HMQC and echo-antiecho (na_hpccoctetf3gp3d)

3D Hetero-TOCSY-COSY using HMQC and cross-polarization (na_hpdico3d)

PCH Experiment

2D P(C)H using HC INEPT transfer (na_pcchco)

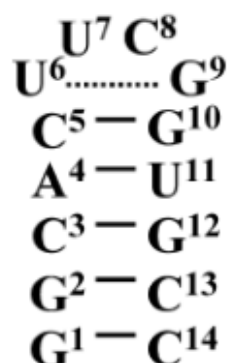
2D P(C)H using HC cross-polarization (na_pcchdi)

2D P(CCC)H using CC TOCSY and HC cross-polarization (na_pcchdi2)

2D quantitative HC(P) for determination of $J(\text{CP})$ (na_hcpqetgpsi.1 | NA_HCPQETGPSI.1 and na_hcpqetgpsi.2 | NA_HCPQETGPSI.2)

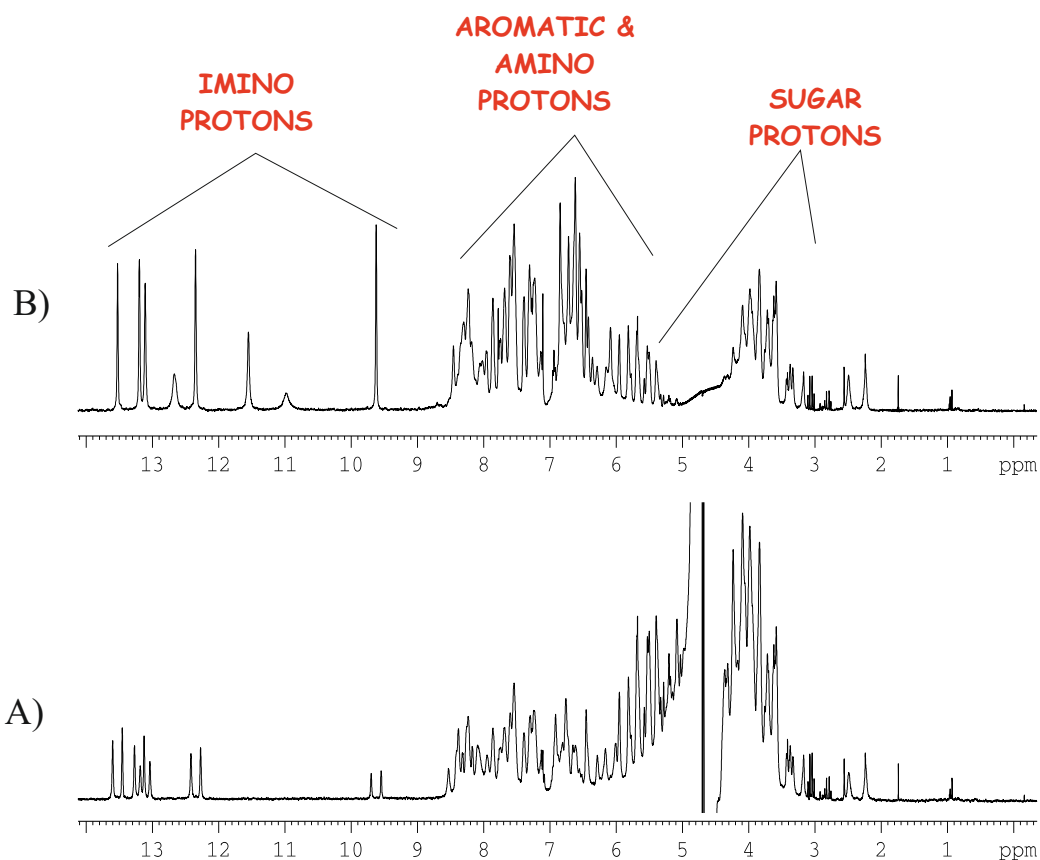
2D P-FIDS experiment to measure $J(\text{HP})$ and $J(\text{CP})$ (na_pfidsetgpsi | NA_PFIDSETGPSI)

All NMR spectra shown in this chapter correspond to a 1mM sample of doubly-labeled $^{13}\text{C}/^{15}\text{N}$ RNA 14-mer 5'-GGCACUUCGGUGCC-3' (commercially available from Silantes) dissolved in 90% $\text{H}_2\text{O}/10\%$ D_2O (courtesy from Dr. W. Bermel - Bruker Biospin, Kalshruhe). Experiments were recorded in a 600MHz AVANCE spectrometer equipped with a 5mm TXI probehead.

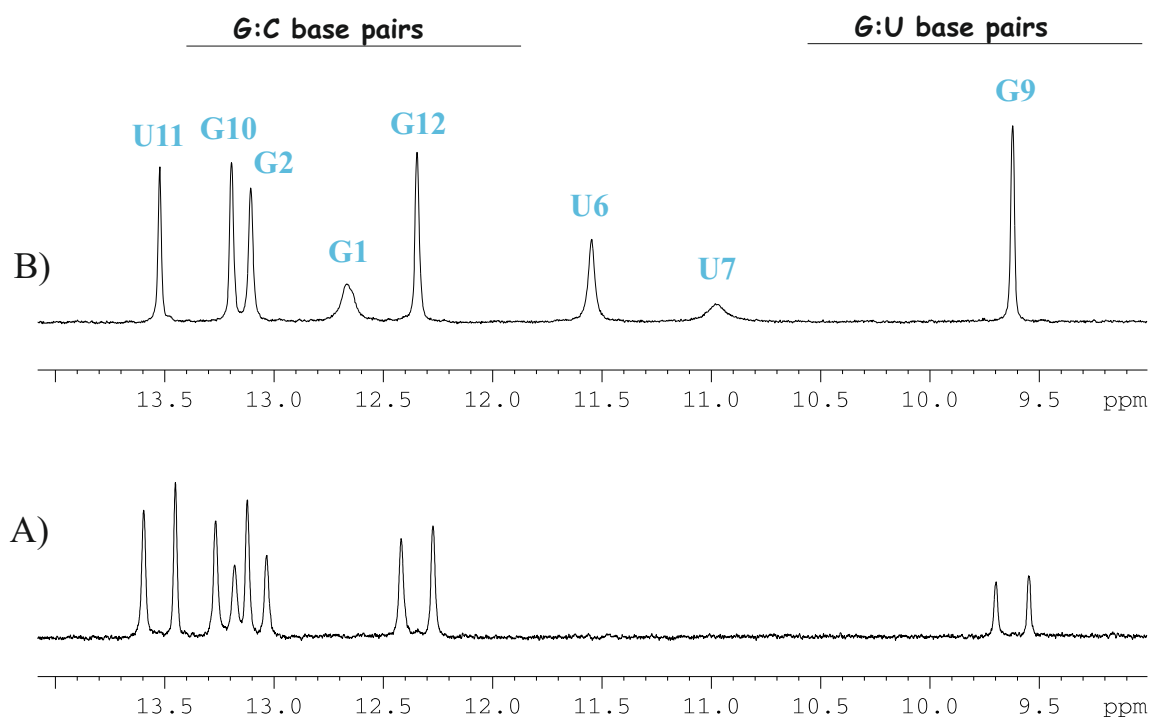


A) ^1H spectrum using presaturation (zgpr)

B) ^1H spectrum using water suppression using WATERGATE and heteronuclear ^{15}N decoupling during ^1H acquisition.



Expansions of the lowfield imino NH region.



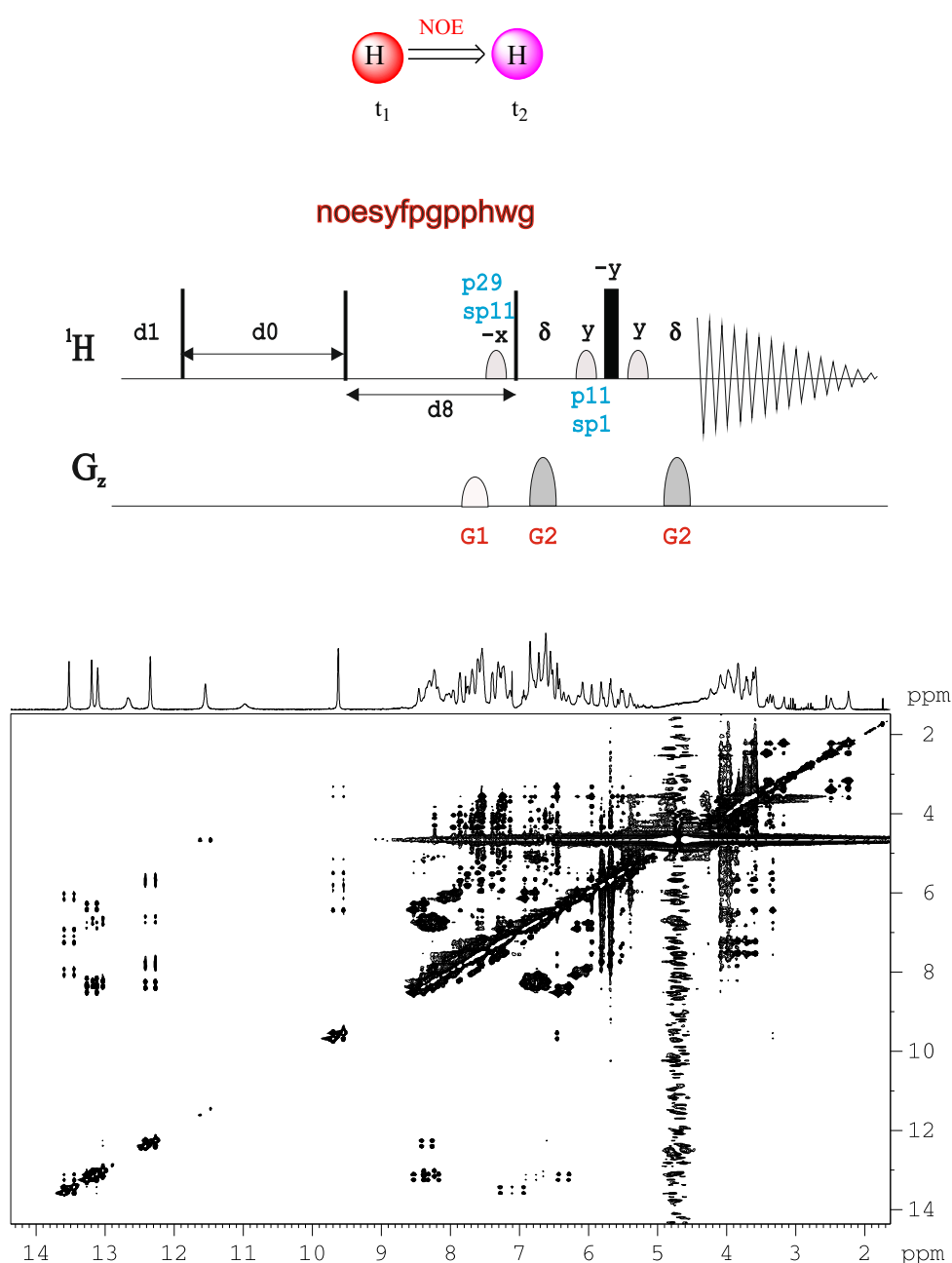
Important classical 2D experiments to study NAs:

- 2D ^1H - ^1H COSY and TOCSY experiments for assignment of ribose spin systems
- 2D ^1H - ^1H NOESY experiment for intra- and inter-residue connectivities, and also for base pairing
- 2D ^1H - ^{13}C and ^1H - ^{15}N HMQC i HSQC experiments to identify directly-attached CH and NH spin systems.
- 2D ^1H - ^{13}C HMBC and 2D long-range optimized HSQC to trace out two- and three-bond away proton-carbon and proton-nitrogen connectivities. Very useful for the assignment of non-protonated carbon and nitrogen in the base moiety.

2D NOESY Experiment

NOESY experiment is an important tool for conformational studies of nucleic acids. It can be run on unlabeled and labeled nucleic acids. Important NOE contacts for sequential assignments are imino-to-imino, imino-to-amino, and imino-to-nonexchangeable proton regions. Information on base pairing and hydrogen bonding can be also extracted from NOE imino cross-peaks.

See all available NOESY schemes in the 2D NOESY chapter or also 3D X-edited NOESY experiments.



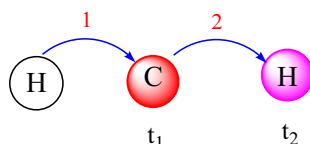
BRUKER PULSE PROGRAM CATALOGUE

NMRGuide

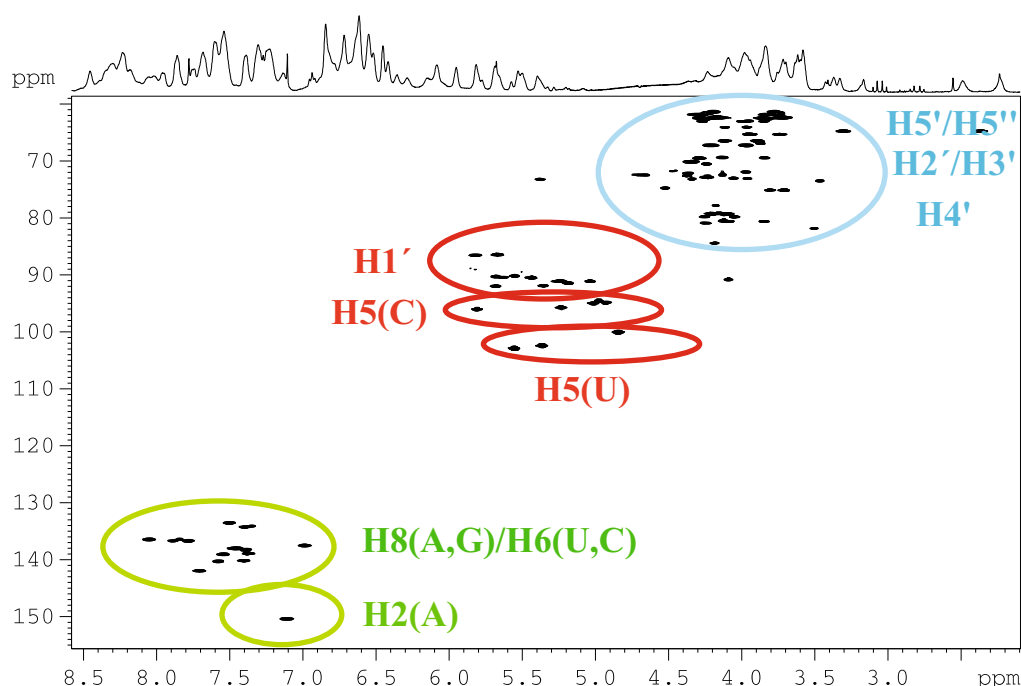
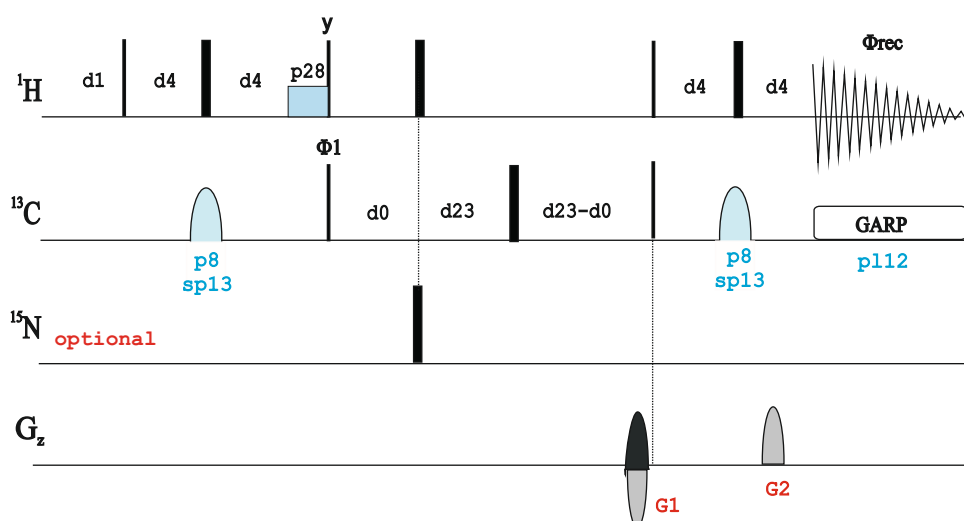
NUCLEIC-ACID NMR 2D & 3D HCN EXPERIMENTS

2D Constant-time HSQC/HMQC Experiment

^1H - ^{13}C correlation experiments can be recorded as usual for both unlabeled and ^{13}C -labeled NAs. In the later, constant-time experiments are recommended to refocus $J(\text{CC})$ during the indirect F_1 dimension. See the corresponding 2D HSQC and HMQC chapters for all available pulse programs.



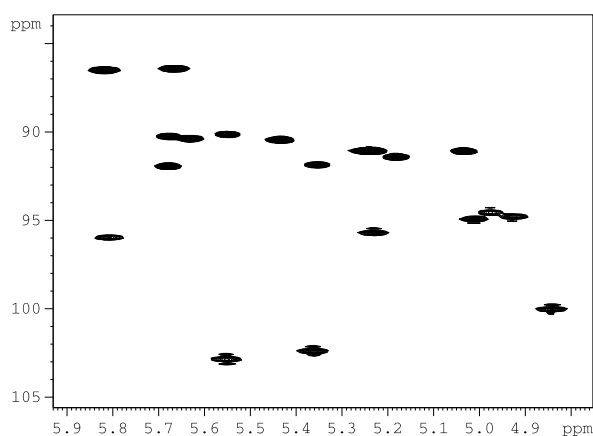
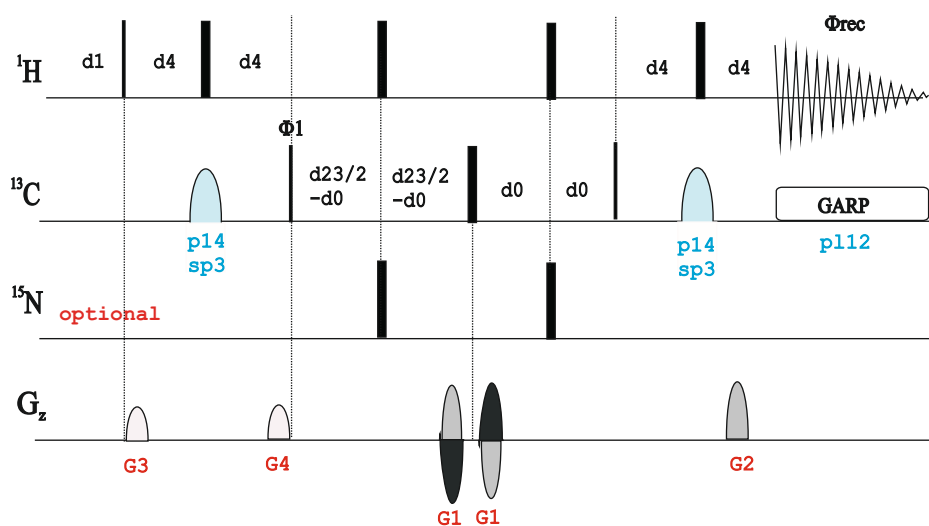
hsqcctetgsp.2



$d1=1.5\text{s}$
 $d4=1/4J(\text{CH})=1.72\text{ms}$
(optimized to $\text{cns}2=145\text{Hz}$)
 $d23=\text{CT}(\text{C}) \text{ period}=8.8\text{ms}$

For a complete assignment,
See Fig. 6 in 04jb69-28

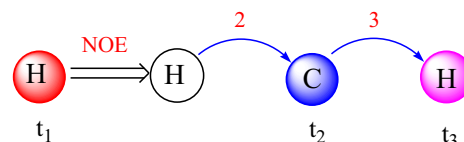
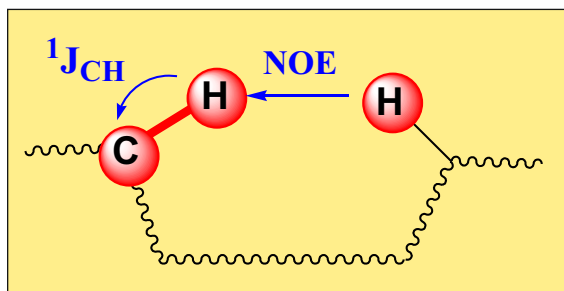
hmqcctetgp



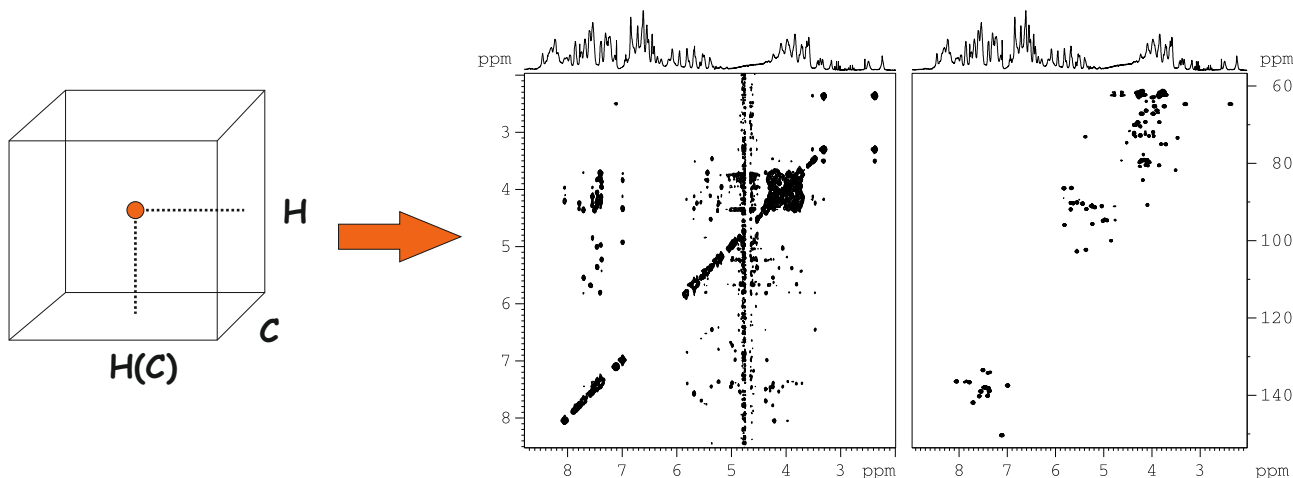
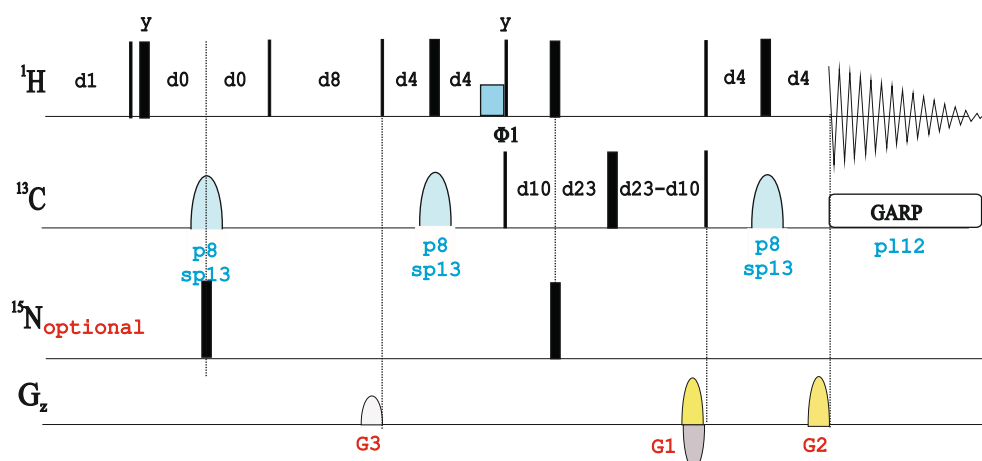
d1=1.5s
d4=1/4J(CH)=1.72ms
(optimized to cnst2=145Hz)
d23=CT(C) period=8.8ms

3D Constant-time ^1H - ^{13}C NOESY-HSQC Experiment

Constant-time version of the 3D NOESY-HSQC experiment to be applied on ^{13}C -labeled NAs. Useful to remove $J(\text{CC})$ splitting from the indirect C dimension. The experiment allows to detect intra-residue 1H - 1H NOE contacts between individual sugar rings and their connected bases.

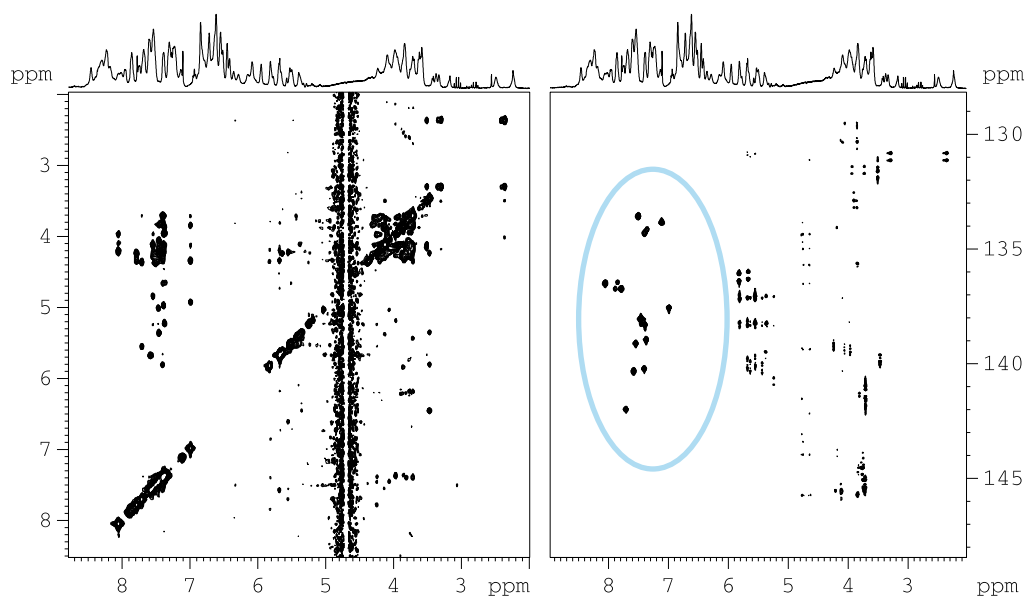
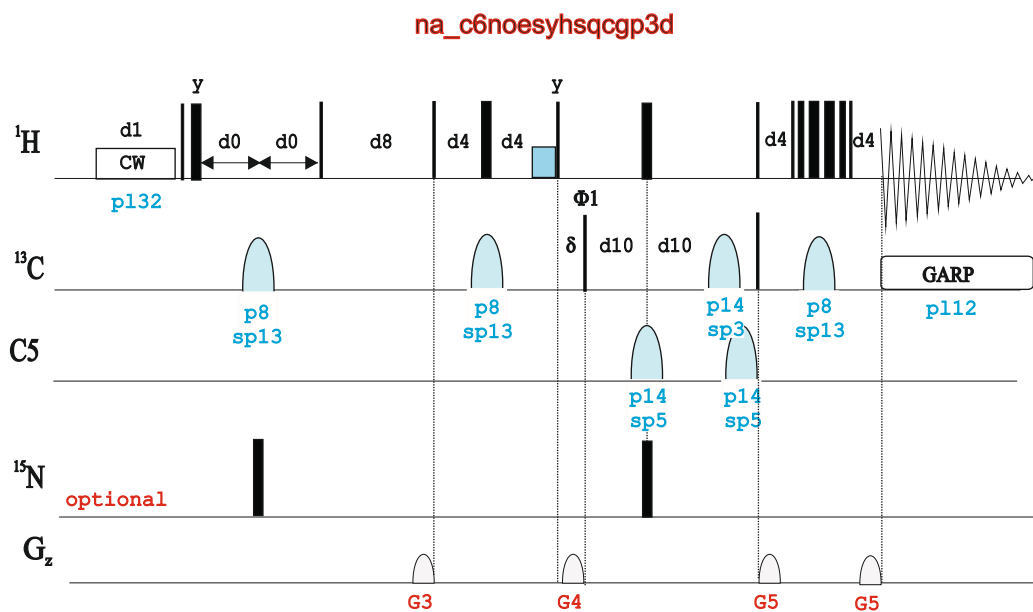


na_noesyhsqcctetgp3d



d1=1.5s
d8=NOESY mixing time=100ms
d4=1/4J(CH)=1.72ms
(optimized cst2=145Hz)
d23=CT(C) period=8.8ms

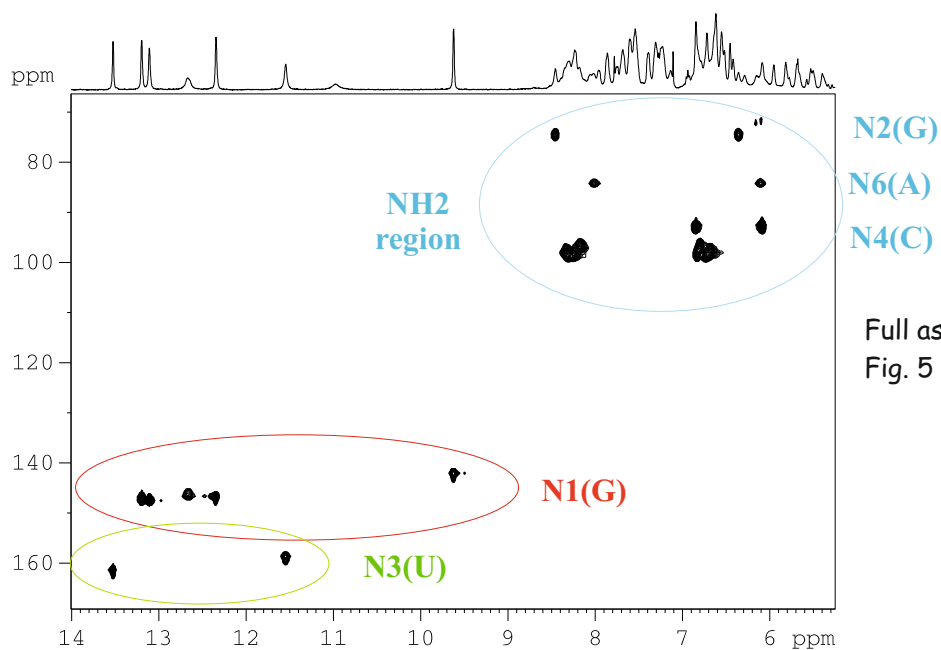
Non-constant-time version of the 3D NOESY-HSQC experiment with selective refocusing of the H(C6C5) coupling constant by means of 180° ¹³C selective pulses (p14=1ms, spnam=Q3)) on C5 during the indirect d10 period.



d1=1.5s
d8=NOESY mixing time=100ms
d4=1/4J(CH)=1.25ms (optimized to cnst2=200Hz)
SW in the C dimension reduced to 16.5ppm

Experiment Description

A diagram illustrating a Markov chain with three states: H (white circle), N (red circle), and H (pink circle). Transitions are labeled 1 and 2. State N is labeled t_1 and the final state H is labeled t_2 .

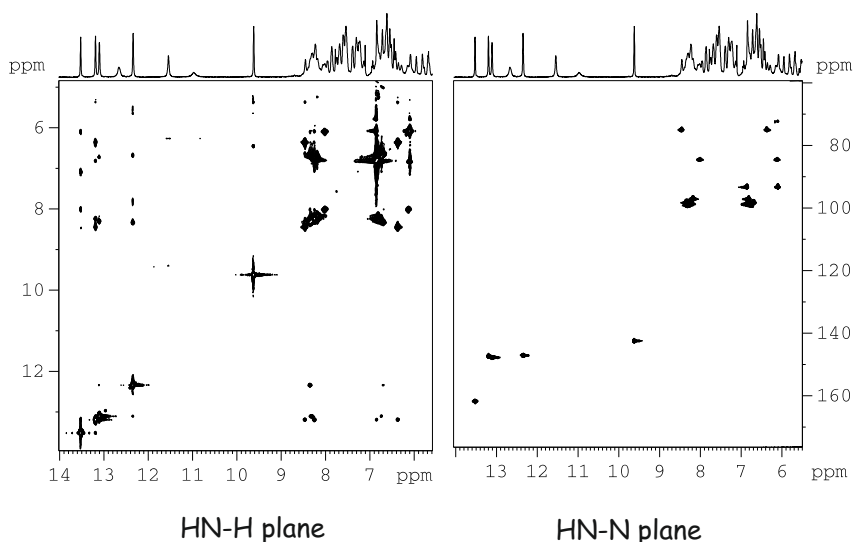
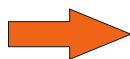
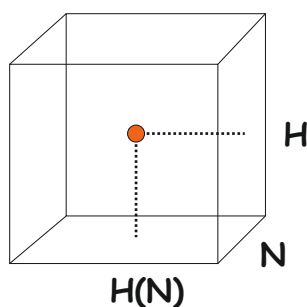
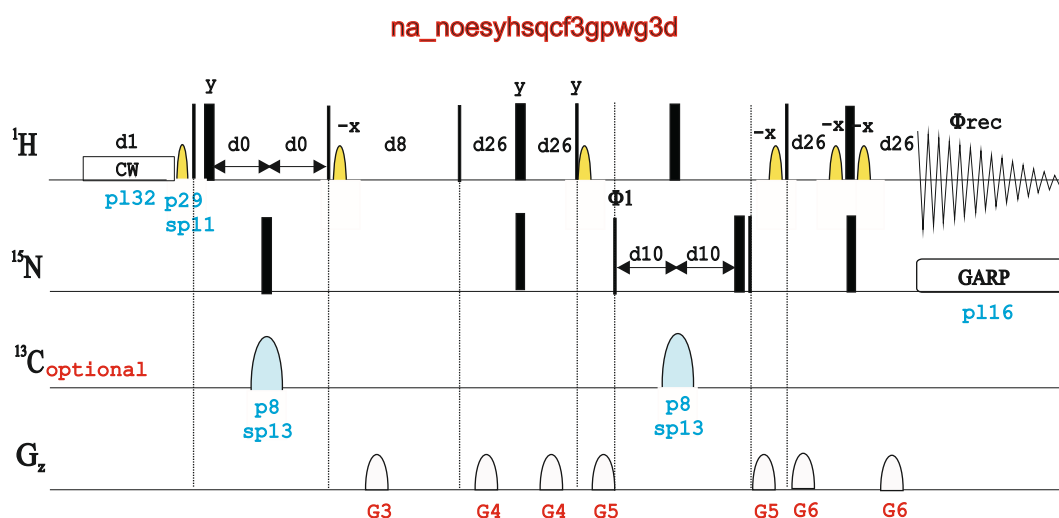
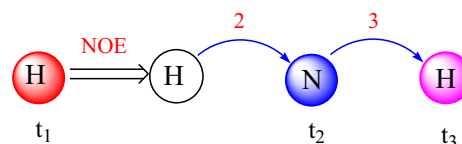
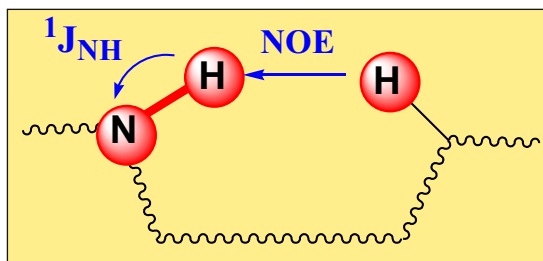


Full assignment:
Fig. 5 in 04jb69-28

d1=1.5s
p11=90° water selective=1ms (Squa100.1000)
d26=1/4J(NH)=2.77ms
(optimized cnst4=90Hz)

3D ^1H - ^{15}N NOESY-HSQC Experiment

Sequential assignment of exchangeable imino and amino groups via NOE contacts. Three important connectivities: imino-to-imino, imino-to-amino, and amino-to-non exchangeable aromatic and sugar protons

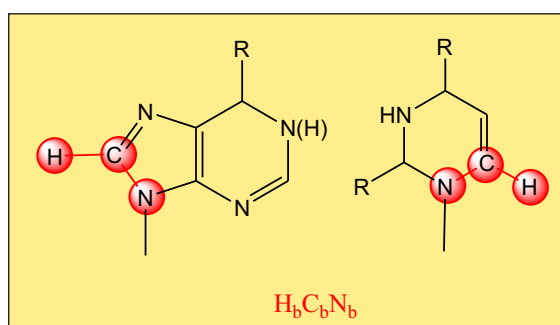
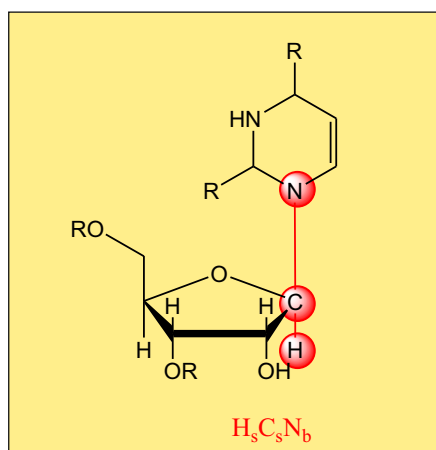


d1=1.5s
d8=NOE mixing time=100ms
p11=water selective=1ms (Squa100.1000)
p29=water selective=2ms (sinc1.1000)
d26=1/4J(NH)=2.77m
(optimized cnst4=90Hz)
ZGOPTNS=-DLABEL_CN

3D HCN Experiment

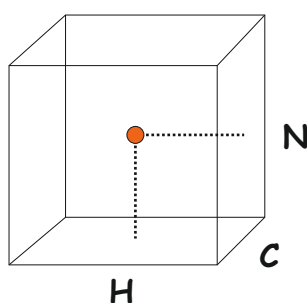
Experiment Description:

This experiment provides sugar-to-base and intrabase HCN connectivities in isotopically labeled nucleotides. Several 2D and 3D versions of this out-and-back HCN experiment incorporating SQC, MQC and TROSY effects are available.



NMR Spectrum

The experiment provides a 3D correlation map. As a function of experimental conditions, both type of correlations can be observed in the same spectrum. Otherwise, selective HsCsNb or HbCbNb spectra can also be obtained.

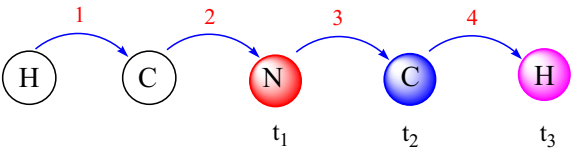


References:

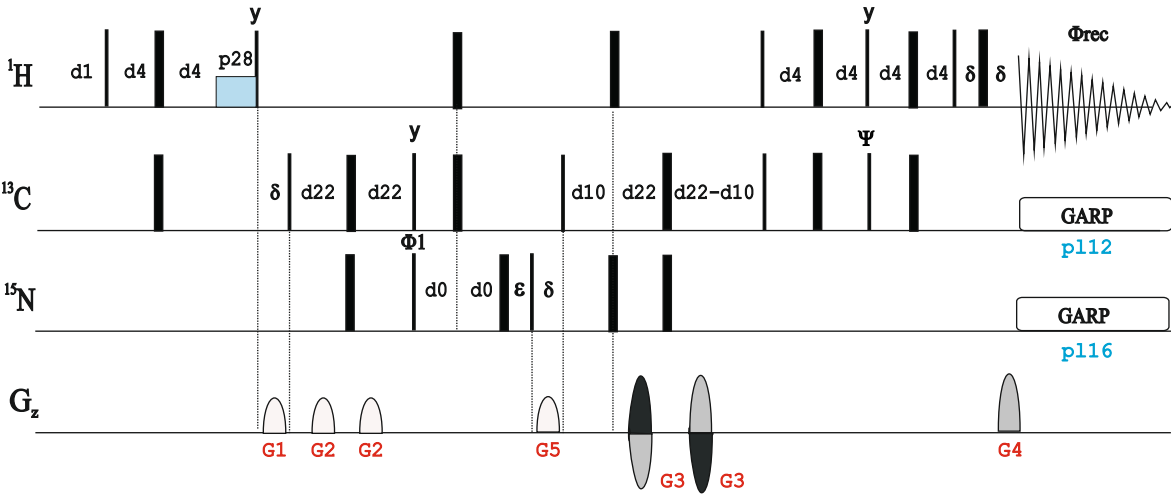
V. Sklenar, R.D. Peterson, M.R. Rejante & J. Feigon, J. Biomol. NMR 3, 721 - 727 (1993)

Related Experiments

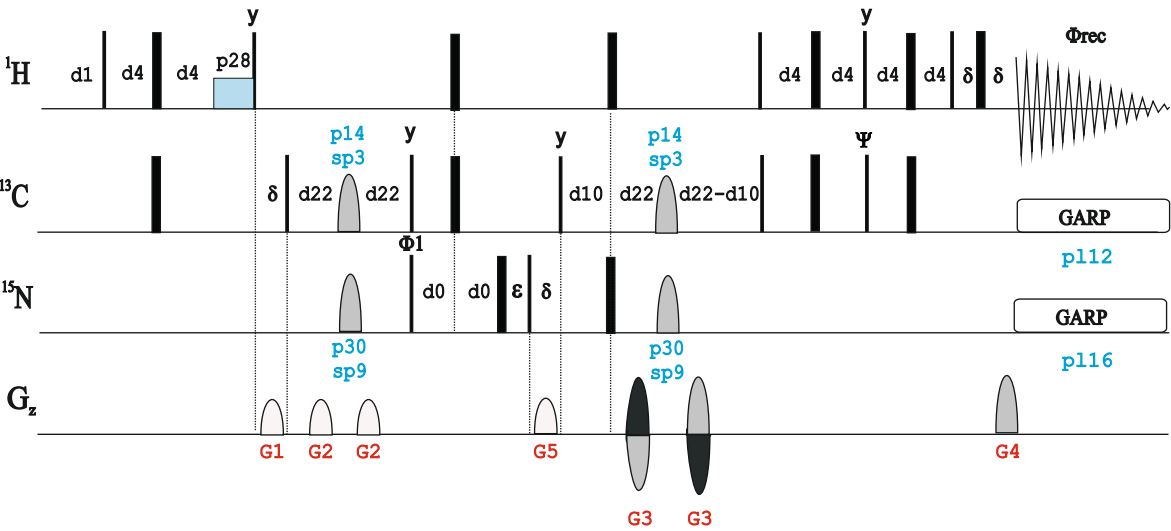
HCNCH
HCNH



na_hcnetgpsi3d

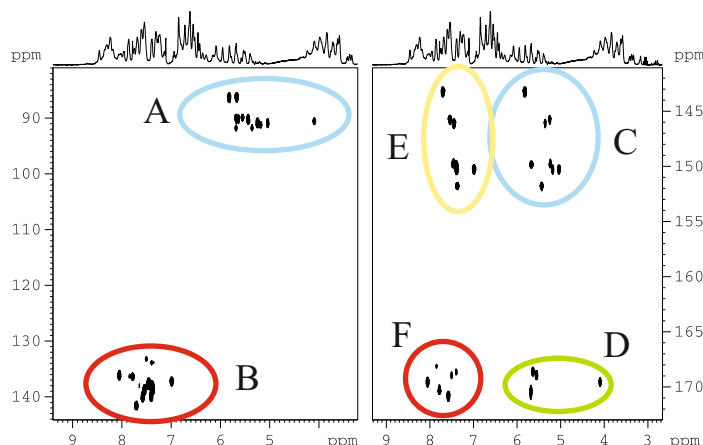


na_hcnetgpsisp3d

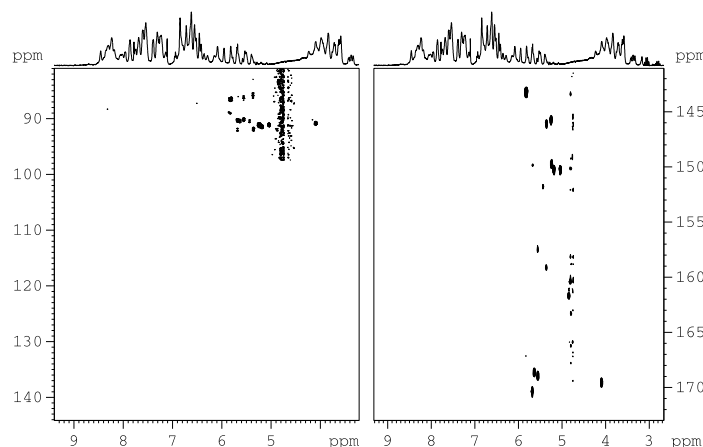


The 2D HC(N) plane can be separated in two areas: A) sugar area (blue) displaying the anomeric H1'-C1' correlations; and B) base area (red) displaying the olefinic H6C6(U,C) and H8C8(A,G) correlations.

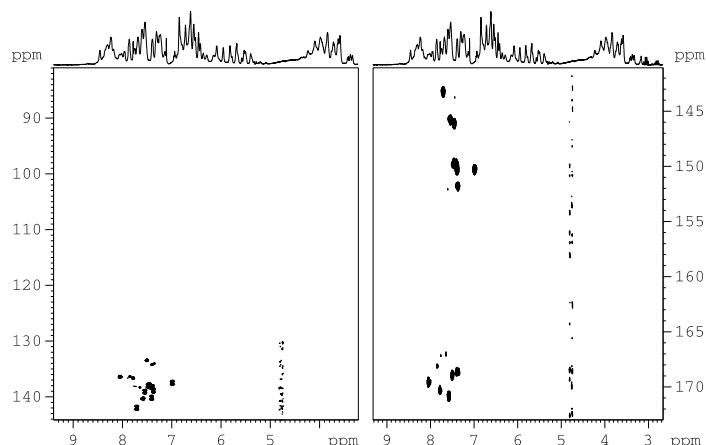
The 2D H(C)N plane displays four different sugar-to-base correlations C) H1'-to-N1(U,C) (blue area); D) H1'-to-N9(A,G) (green area); E) H6(U,C)-to-N1(U,C) (yellow area); and F) H8(A,G)-to-N9(A,G) (red area).



d1=1.5s
d4=1/4J(CH)=1.40ms for all J(HC) ,
J(H8C8) and J(H6C6)
d22=1/4J(CN)=17.5ms for all J(N1C1'), J(N9C1'),
J(N1C6), and J(N9C8)
p14=2.6ms (spnam3=q3_rna_c68c1.256)
o2p=113.45ppm
p30=700us(spnam9=Q3.1000)



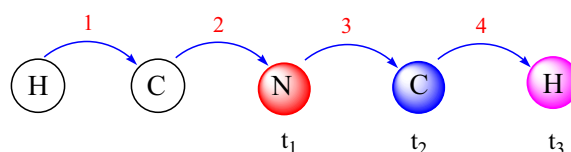
d1=1.5s
d4=1/4J(CH)=1.56ms for J(H1'C1')
d22=1/4J(CN)=15ms for J(N1C1'), J(N9C1')
p14=1.0ms (spnam3=Q3.1000)
o2p=89.19ppm
p30=700us(spnam9=Q3.1000)
Reduced SW in the C dimension=16.5ppm



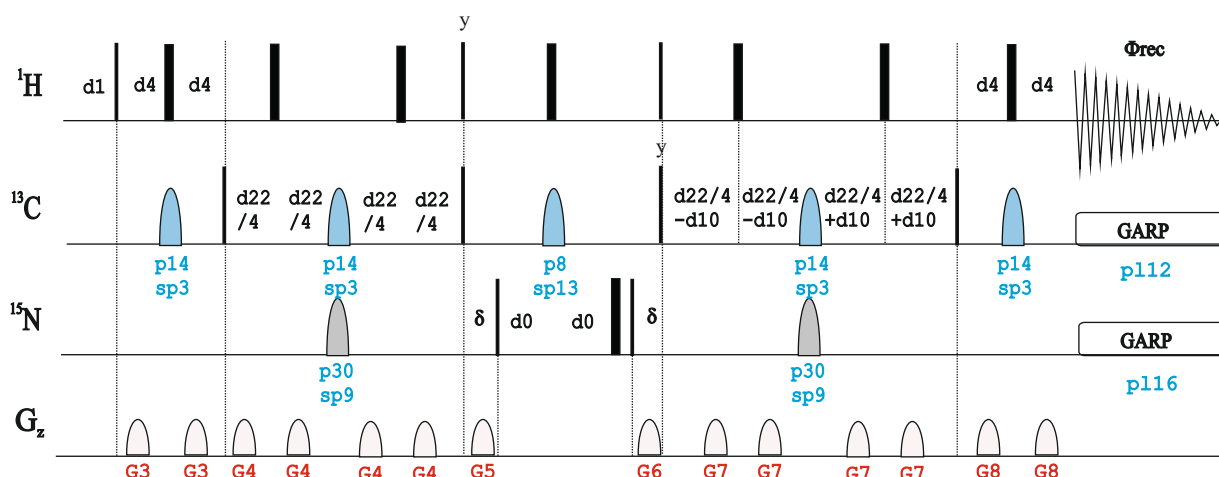
d1=1.5s
d4=1/4J(CH)=1.25ms for J(H8C8) and J(H6C6)
d22=1/4J(CN)=15ms for J(N1C6), and J(N9C8)
p14=1.0ms (spnam3=Q3.1000)
o2p=137.7ppm
p30=700us(spnam9=Q3.1000)
Reduced SW in the C dimension=16.5ppm

Experiment Description:

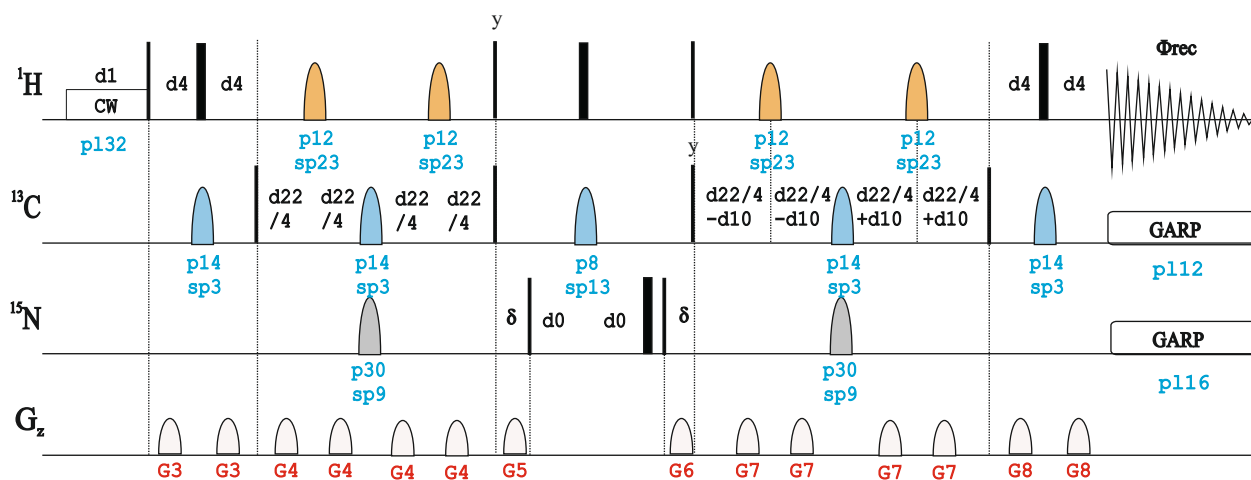
J.P. Marino, J.L. Diener, P.B. Moore & C. Griesinger, *J. Am. Chem. Soc.* 119, 7361-7366 (1997)

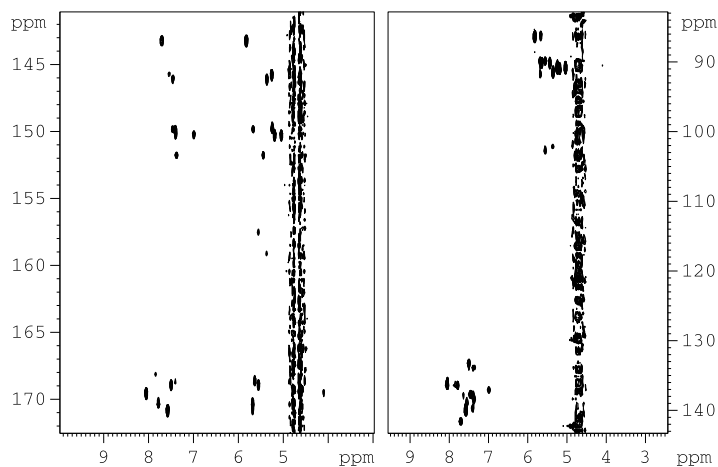


na_hcnmq3d

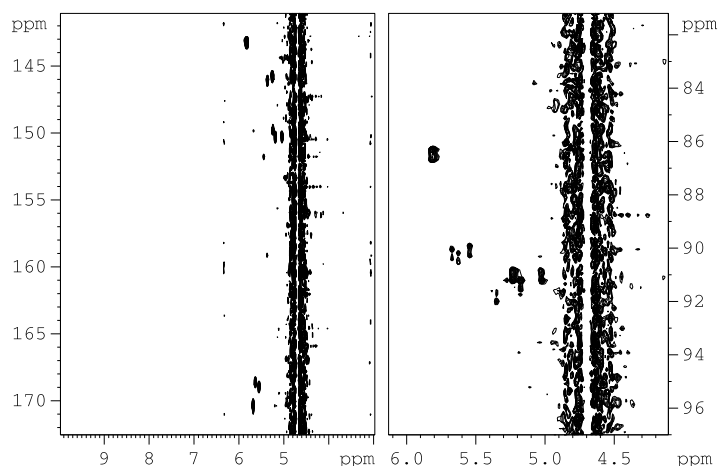


na_hcnmqsp3d

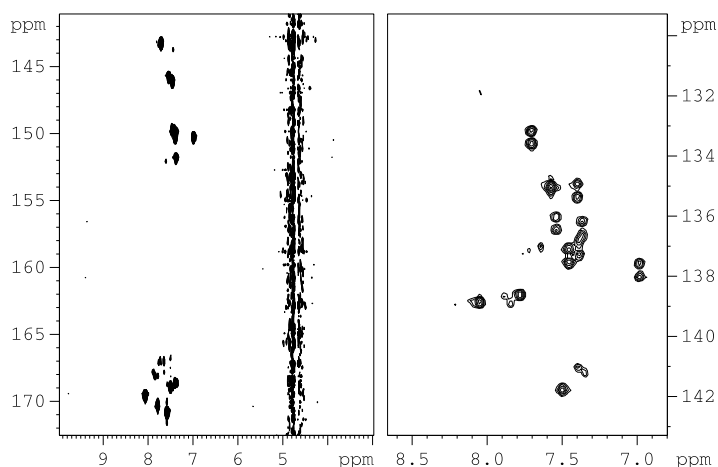




d1=1.5s
d4=1/4J(CH)=1.40ms for all J(H1'C1'), J(H8C8) and J(H6C6)
d22=1/4J(CN)=16.0ms for all J(N1C1'), J(N9C1'), J(N1C6), and J(N9C8)
p14=2.6ms (spnam3=q3_rna_c68c1.256)
o2p=113.45ppm
p30=700us(spnam9=Q3.1000)
p12=1.65ms (spnam23=reburp.1000)



d1=1.5s
d4=1/4J(CH)=1.56ms for J(H1'C1')
d22=1/4J(CN)=16ms for J(N1C1'), J(N9C1')
p14=1.0ms (spnam3=Q3.1000)
o2p=89.19ppm
p30=700us(spnam9=Q3.1000)
p12=3.30ms (spnam23=reburp.1000)
Reduced SW in the C dimension=16.5ppm

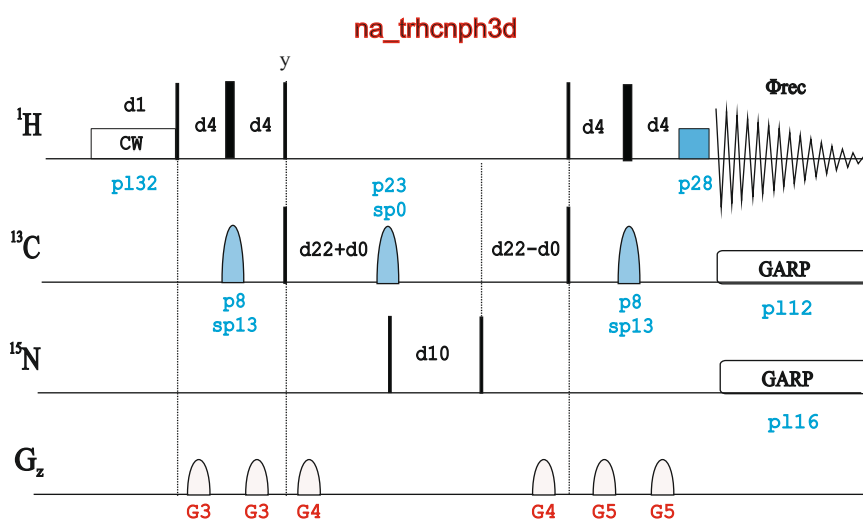
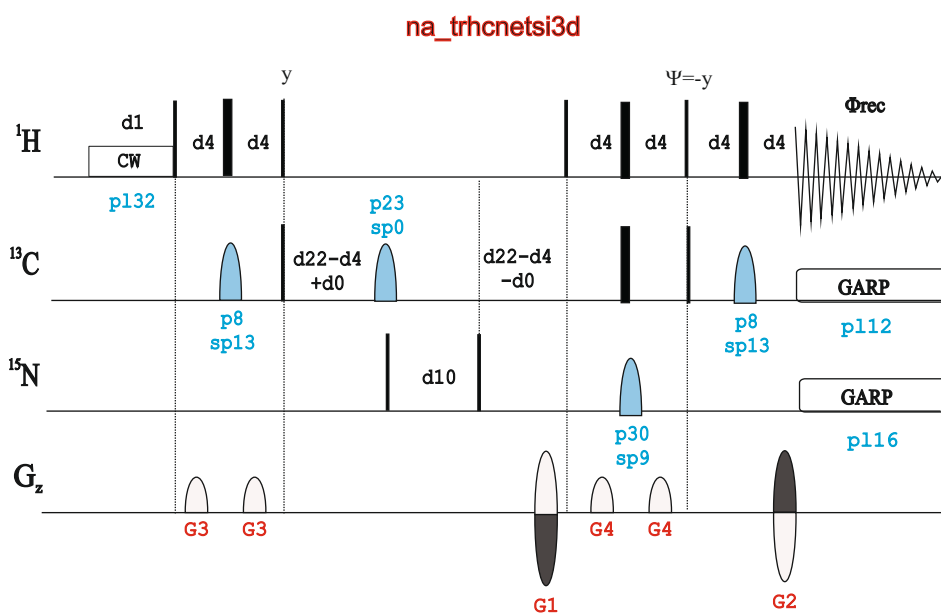


d1=1.5s
d4=1/4J(CH)=1.25ms for J(H8C8) and J(H6C6)
d22=1/4J(CN)=16ms for J(N1C6), and J(N9C8)
p14=1.0ms (spnam3=Q3.1000)
o2p=137.7ppm
p30=700us(spnam9=Q3.1000)
p12=3.30ms (spnam23=reburp.1000)
Reduced SW in the C dimension=16.5ppm

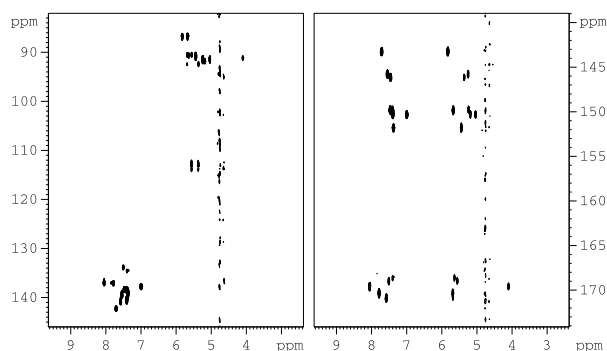
3D TROSY-HCN Experiment

Version of the HCN experiment that involves multiple-quantum coherences (MQC) and TROSY effects instead of SQC to enhance relaxation features.

1. R. Fiala, J. Czernek & V. Sklenar, J. Biomol. NMR 16, 291-302 (2000)
2. R. Riek, K. Pervushin, C. Fernandez, M. Kainosho & K. Wuethrich, J. Am. J. Chem. Soc. 123, 658-664 (2001)
3. B. Brutscher & J.-P. Simorre, J. Biomol. NMR 21, 367-372 (2001)



d1=1.5s
d4=1/4J(CH)=1.40ms for all J(H1'C1'), J(H8C8) and J(H6C6)
d22=1/2J(CN)=30ms for all J(N1C1'), J(N9C1'), J(N1C6), and J(N9C8)
p23=0ms (spnam3=q3_rna_c68c1.256)
o2p=113.45ppm
p30=700us (spnam9=Q3.1000)



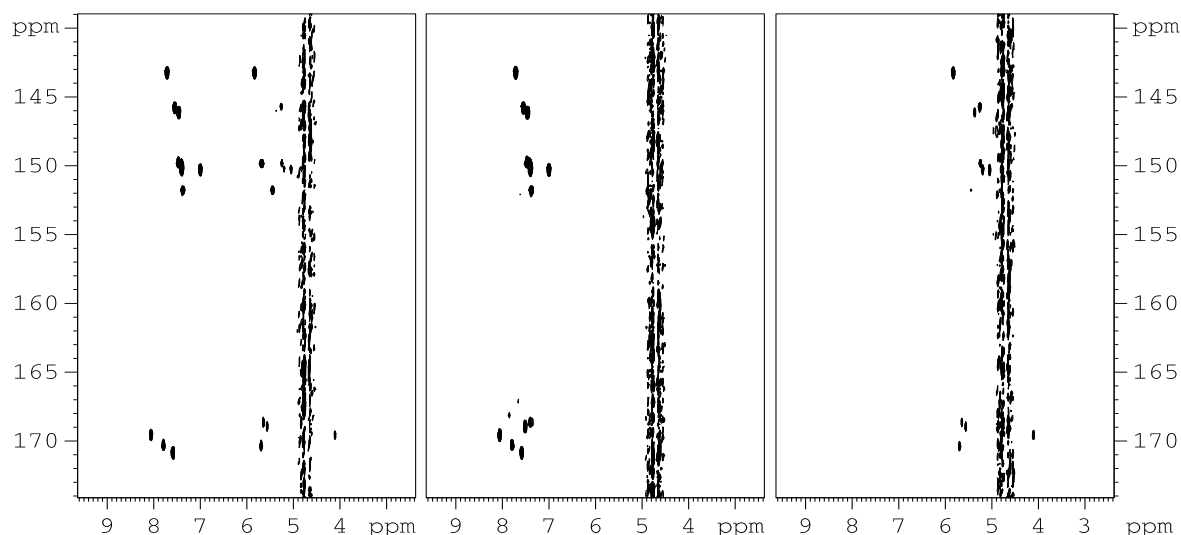
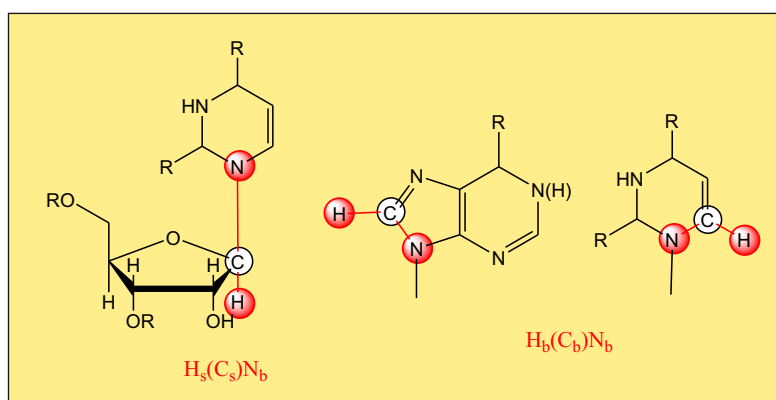
2D TROSY-H(C)N Experiment

Experiment Description:

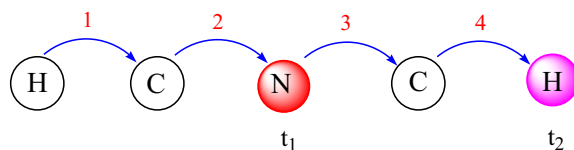
2D TROSY version of the HCN experiment in which the 2D H(C)N plane is obtained

References:

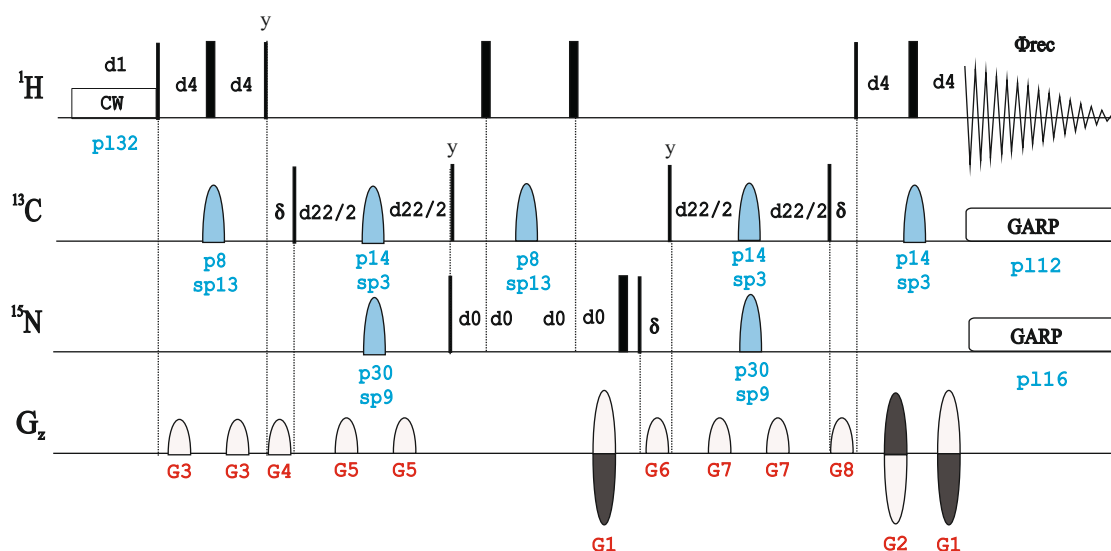
R. Fiala, J. Czernek & V. Sklenar, J. Biomol. NMR 16, 291-302 (2000)



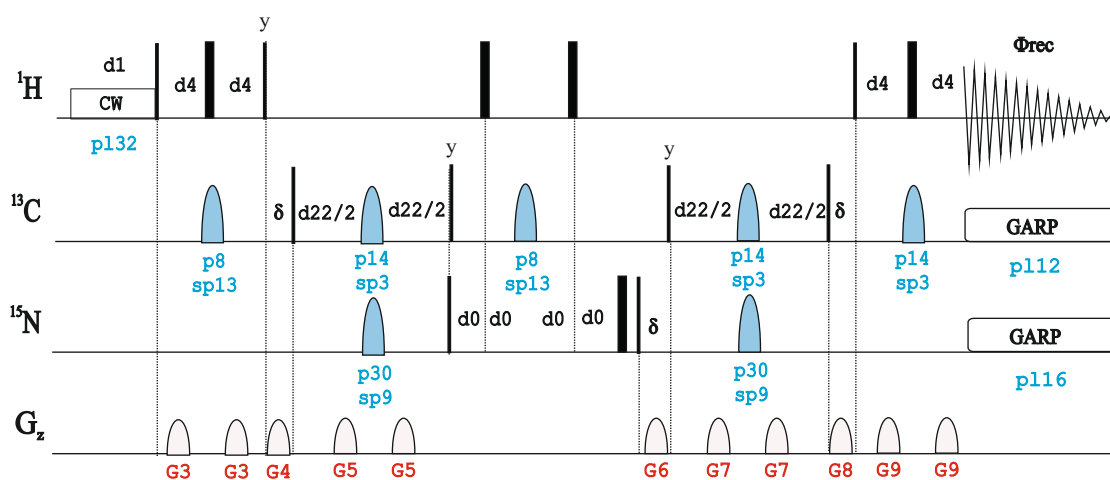
The same acquisition parameters as discussed in the 3D HCN experiments



na_trhcnph



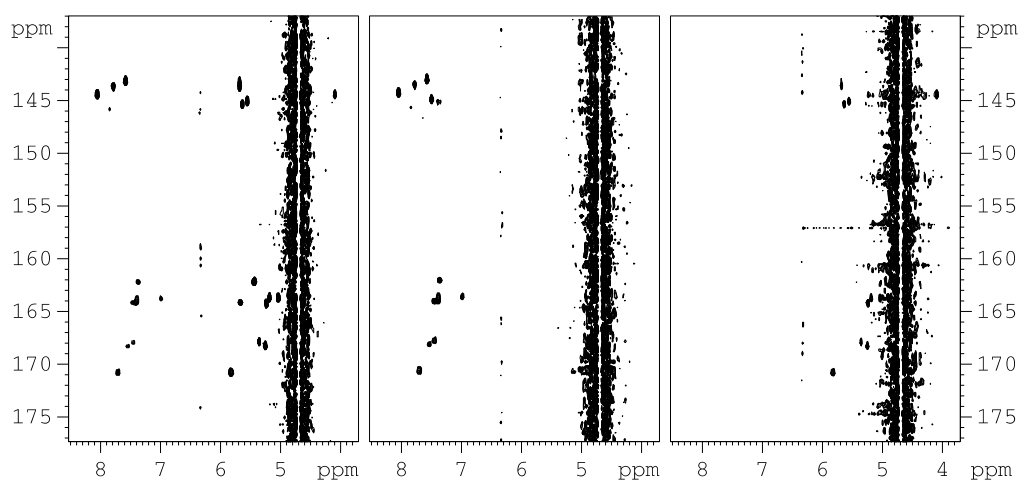
na_trhcnph



Experiment Description:

References:

-



936

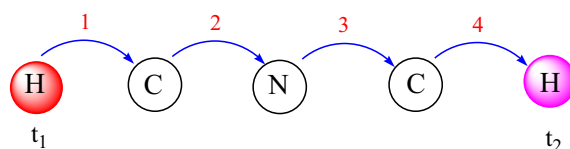
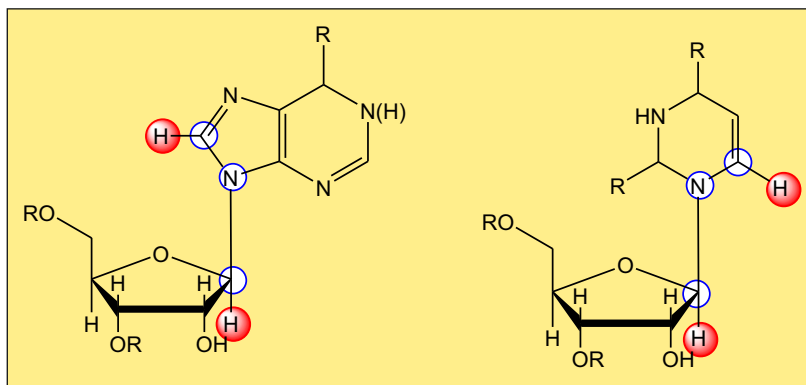
2D H(CNC)H Experiment

Experiment Description

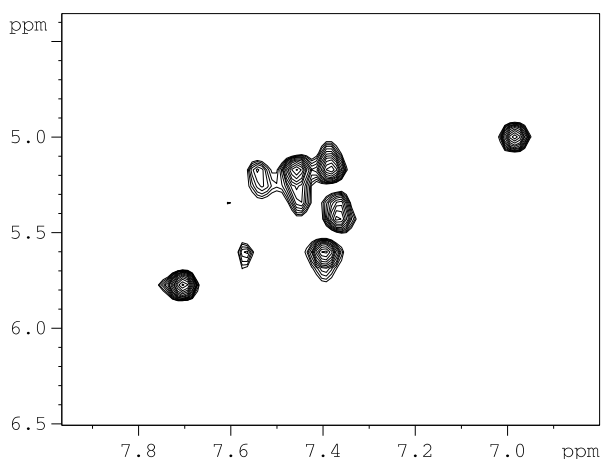
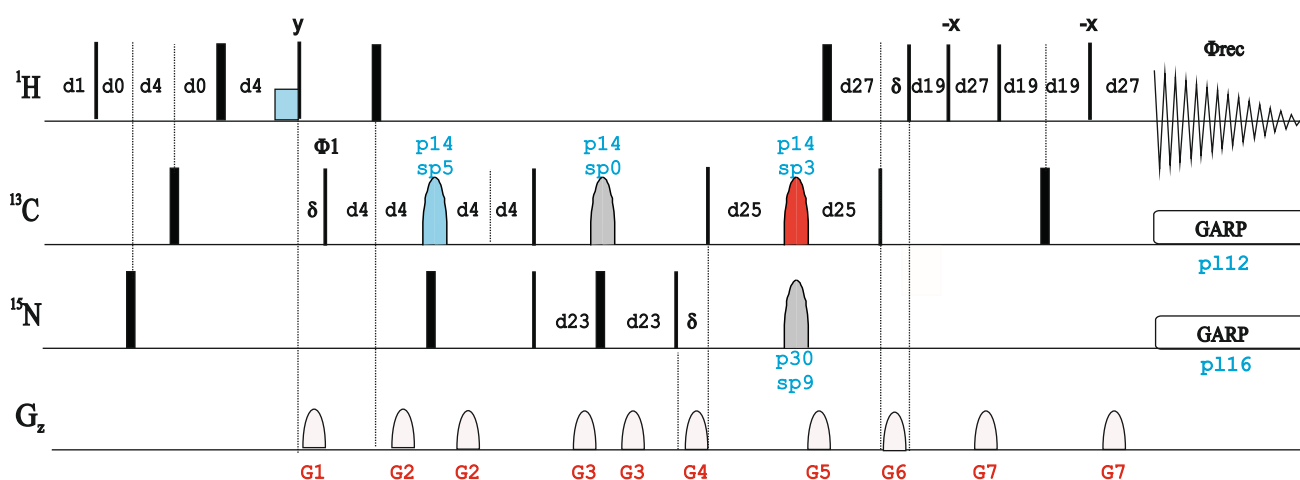
2D version of the HCNCH experiment that allows to correlate the anomeric proton of the sugar ring with the H6/H8 of the connected base in isotopically labeled oligonucleotides.

References:

V. Sklenar, R.D. Peterson, M.R. Rejante, E. Wang & J. Feigon,
J. Am. Chem. Soc. 115, 12181 - 12182 (1993)



na_hcnchgpjrphsp

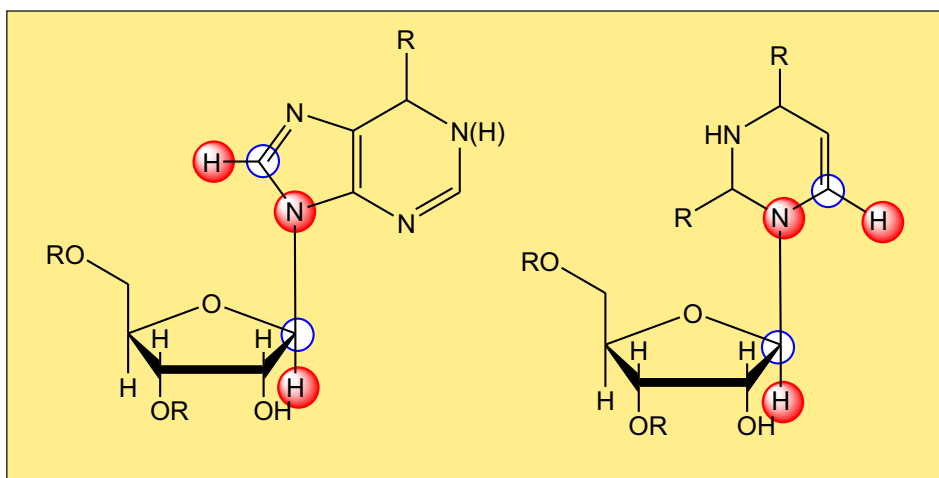


d1=1.5s
d4=1/4J(CH)=1.56ms
d23=1/4J(CN)=17ms
d25=1/4J(CN)=16ms
d27=1/4J(CH)=1.25ms
d19=134us
p14=1ms (spnam3=spnam5=Q3.1000
and spnam0=q3_rna_c68c1.1000)
o2p=113.5 ppm

3D H(C)N(C)H Experiment

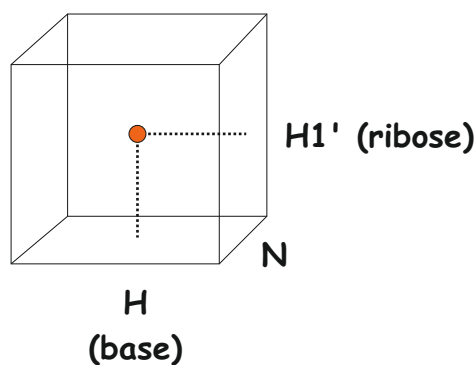
Experiment Description:

3D version of the HCNCH experiment that allows to correlate the two different HCN correlations observed in the HCN experiment. The experiment starts from the H1'-C1' ribose pair, N1/9 is allowed to evolve in an indirect dimension and finally the H6C6/H8C8 base proton is detected.



NMR Spectrum

The experiment provides a 3D correlation map

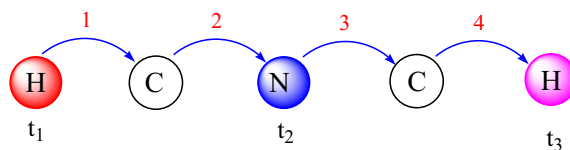


References:

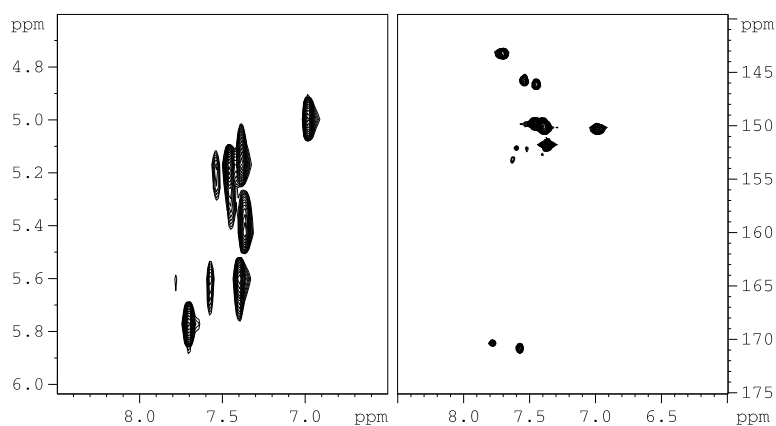
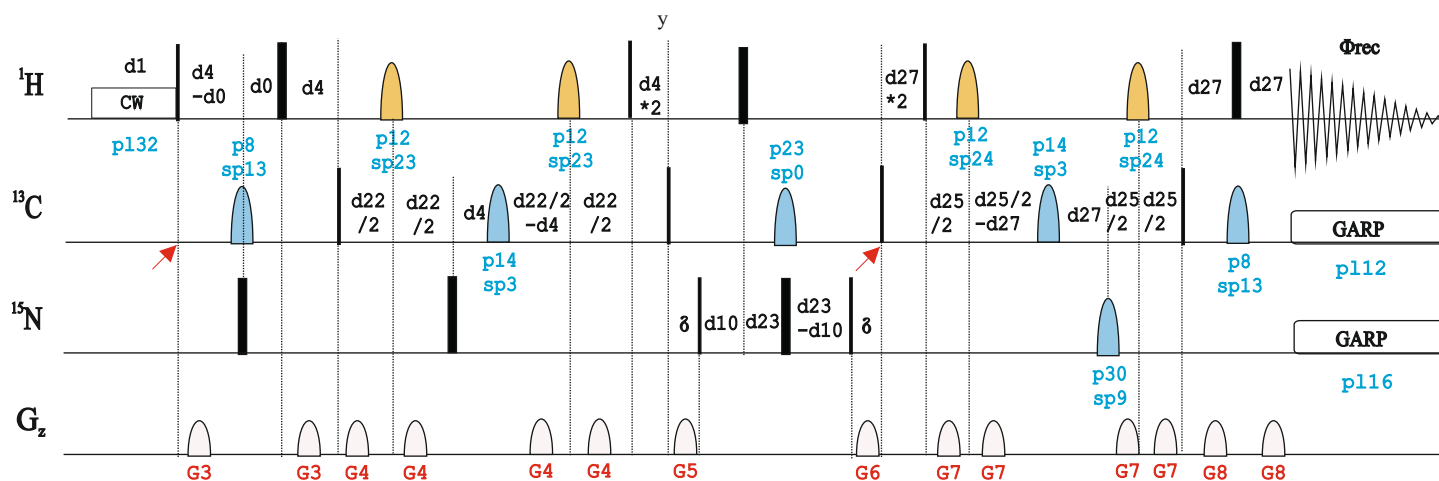
R. Fiala, F. Jiang & V. Sklenar, J. Biomol. NMR 12, 373-383 (1998)

Related Experiments

HCN experiment



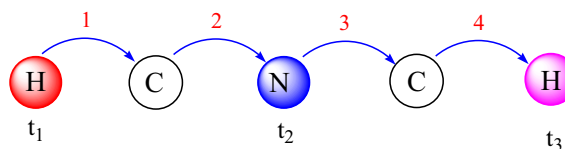
na_hcnchmqsp3d



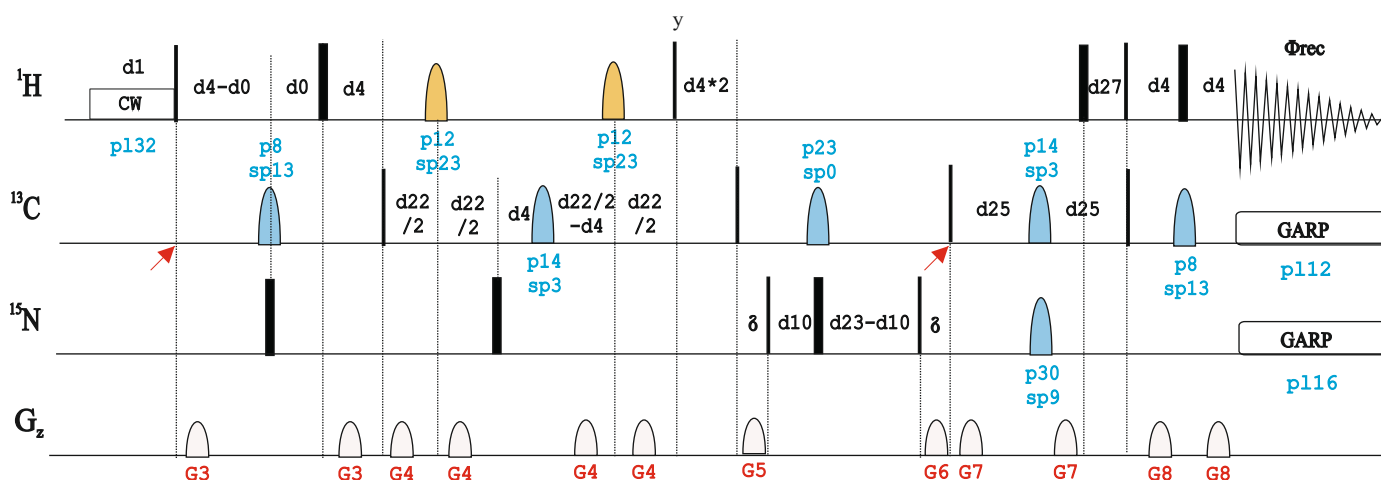
d1=1.5s
 d4=1/4J(C1'H1')=1.6ms
 d22=1/4J(C1'N)=18ms
 d23=1/4J(C1'N, C6/8N)=17ms
 d25=1/4J(C6/8N)=16ms
 d27=1/4J(C6/8H6/8)=1.25ms
 p12=3.3ms (spnam23=spnam24=reburp.1000)
 p14=1ms (spnam3=spnam5=Q3.1000)
 p23=0 (spnam0=q3_rna_c68c1.1000)
 cnst21=89.19 (C1' chemical shift)
 cnst22=137.7 (C6C(chemical shift)

3D TROSY MQ-H(C)N(C)H Experiment

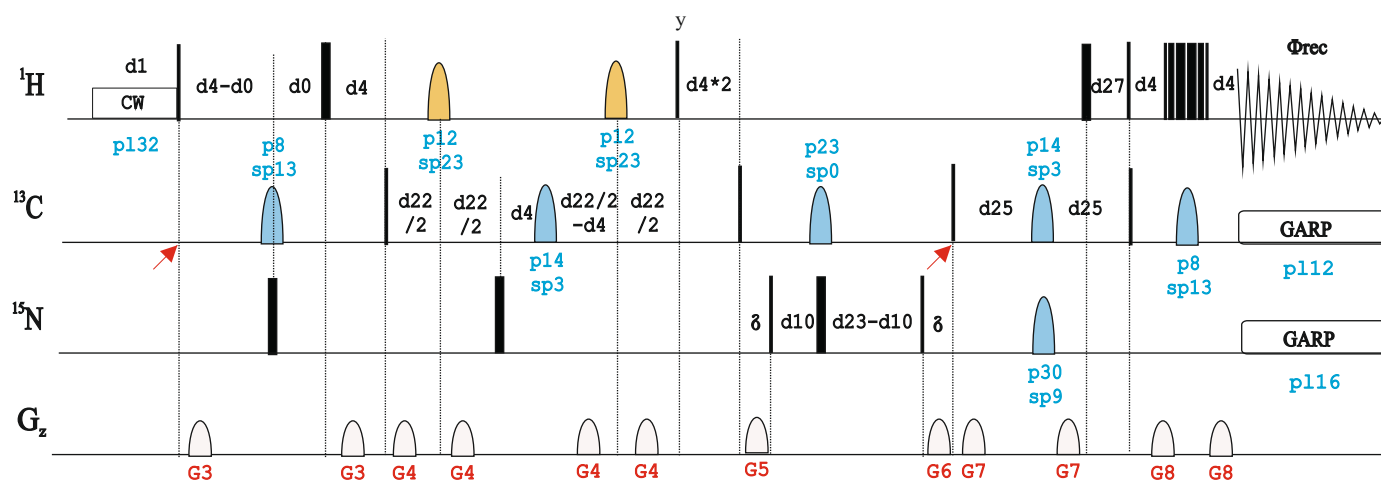
R. Fiala, J. Czernek & V. Sklenar, J. Biomol. NMR 16, 291-302 (2000)



na_trhcnchmqsp3d



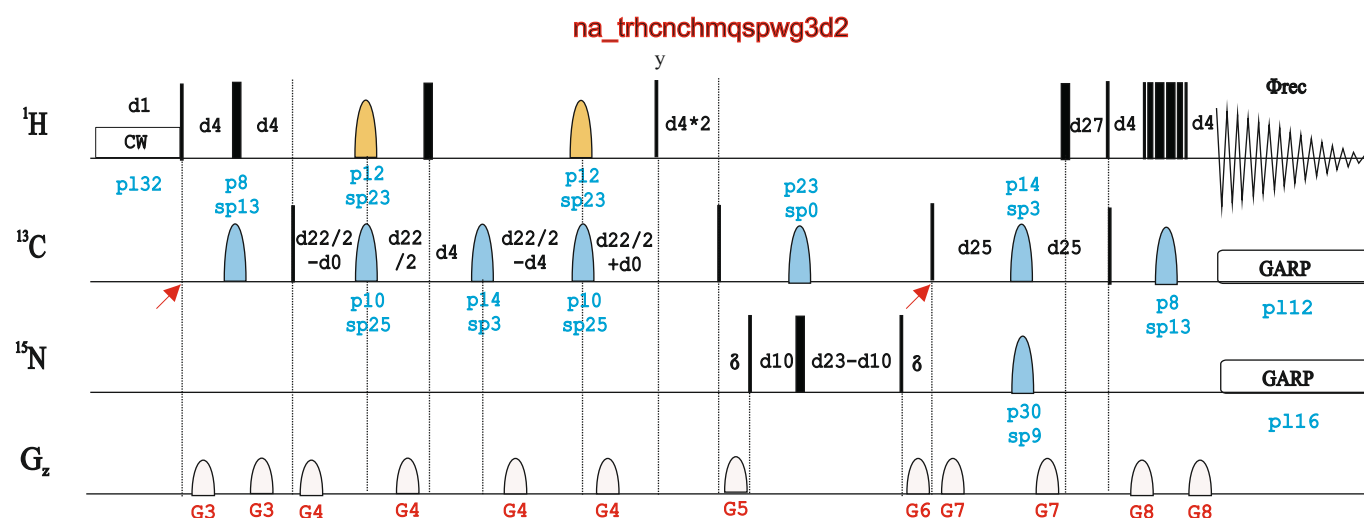
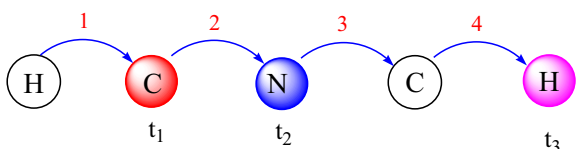
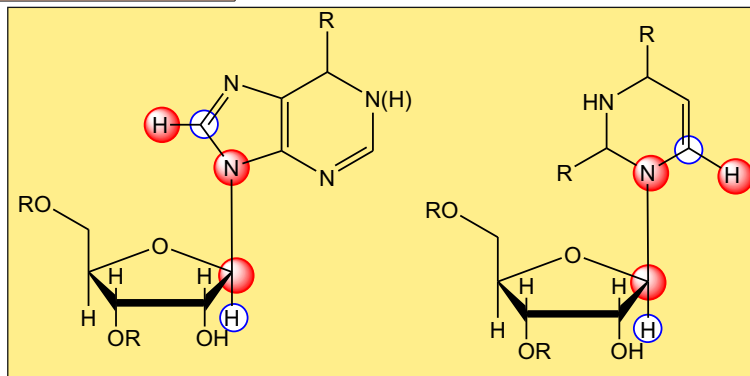
na_trhcnchmqspwg3d



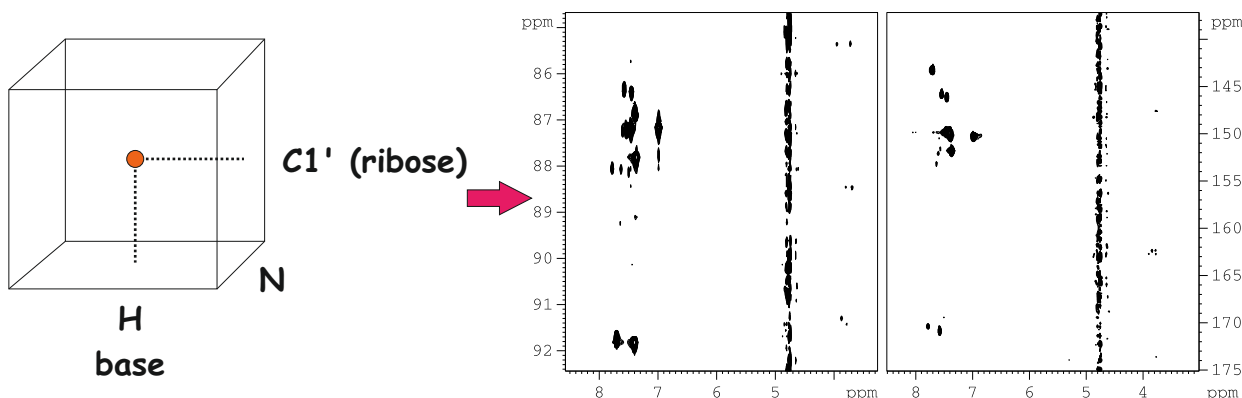
3D TROSY (H)CN(C)H Experiment

TROSY version of the 3D HCNCH experiment in which C1' chemical shift evolves instead of the H1' chemical shift.

R. Fiala, J. Czernek & V. Sklenar,
J. Biomol. NMR 16, 291-302 (2000)



The experiment yields a 3D map correlation the sugar C1' carbno with the N1/N9 nitrogen and the H2/H8 protons of the connected base.



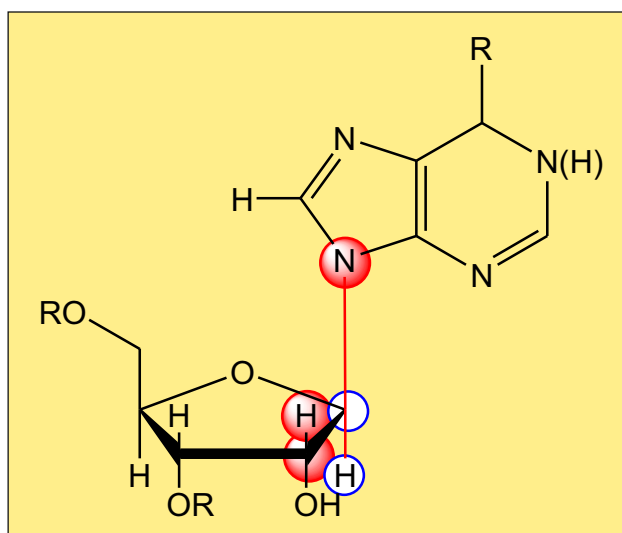
d1=1.5s
d4=1/4J(C1'H1')=1.6ms
d22=1/4J(C1'N)=18ms
d23=1/4J(C1'N, C6/8N)=17ms
d25=1/4J(C6/8N)=16ms
d27=1/4J(C6/8H6/8)=1.25ms

p12=3.3ms (spnam23=spnam24=reburp.1000)
p14=1ms (spnam3=spnam5=Q3.1000)
p23=0 (spnam0=q3_rna_c68c1.1000)
cnst21=89.19 (C1' chemical shift)
cnst22=137.7 (C6C8 chemical shift)
cnst23=72 (C2' chemical shift)

3D MQ-(HC)N(C)CH-COSY Experiment

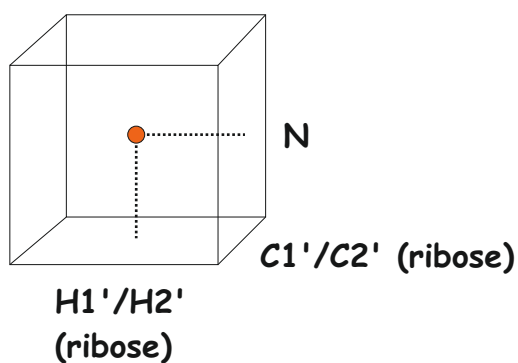
Experiment Description:

This experiment (HCN-CCH COSY) uses the good chemical shift dispersion of N1/N9 to assign the ribose spin system via a C1' to C2' COSY transfer after an initial HCNC transfer.



NMR Spectrum

The experiment provides a 3D correlation map

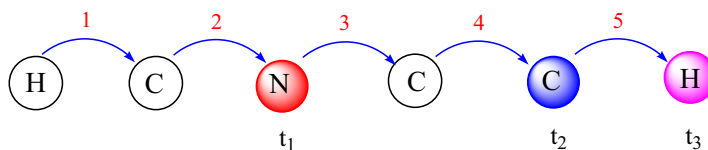


References:

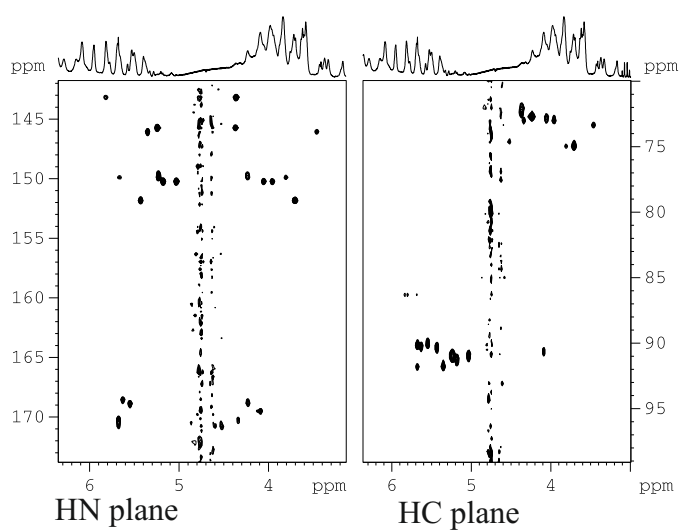
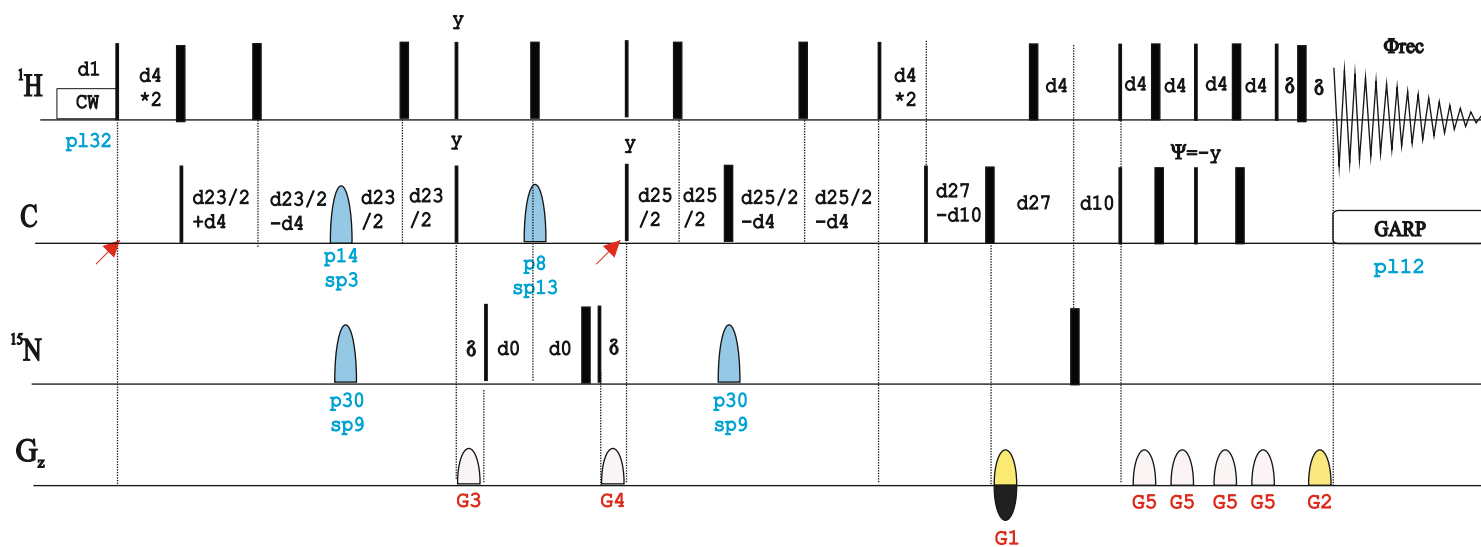
W. Hu, L. Jiang & Y.Q. Gossler, J. Magn. Reson. 145, 147-151 (2000)

Related Experiments

HCN-CCH TOCSY



na_hcncchcomq3d

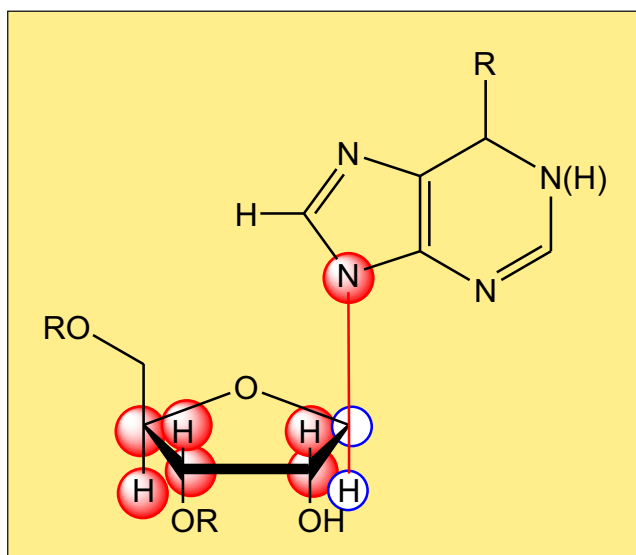


$d1=1.5s$
 $d4=1/4J(C1'H1')=1.56ms$
 $d23=1/4J(C1'N)=18ms$
 $d25=1/4J(C1'N)=15ms$
 $d27=1/8J(C1'C2')=3.25ms$
 $cnst21=C1'$ chemical shift=90ppm
 $cnst23=C2'$ chemical shift=72 ppm
 $o2p=79ppm$
 $p14=1ms$ (spnam3=Q3.1000)
 $o3p=160$ ppm
 $p30=700us$ (spnam9=Q3.1000)

3D MQ-(HC)N(C)CH-TOCSY Experiment

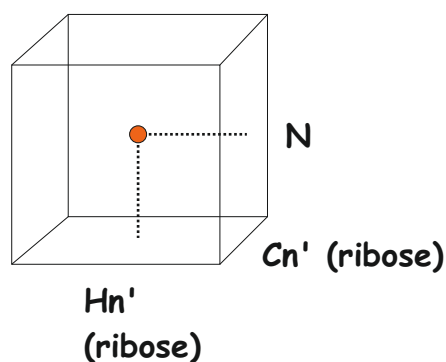
Experiment Description:

This experiment (HCN-CCH TOCSY) uses the good chemical shift dispersion of N1/N9 to assign the ribose spin system via a C1' to Cn' TOCSY transfer after an initial HCNC transfer.



NMR Spectrum

The experiment provides a 3D correlation map

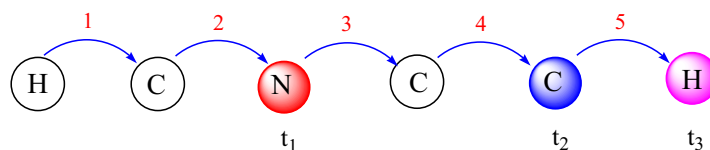


References:

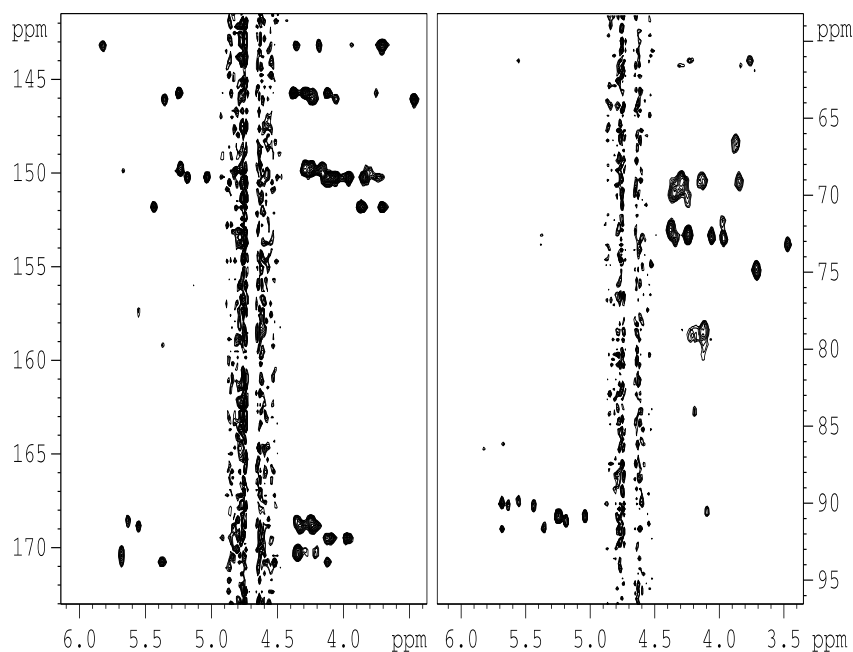
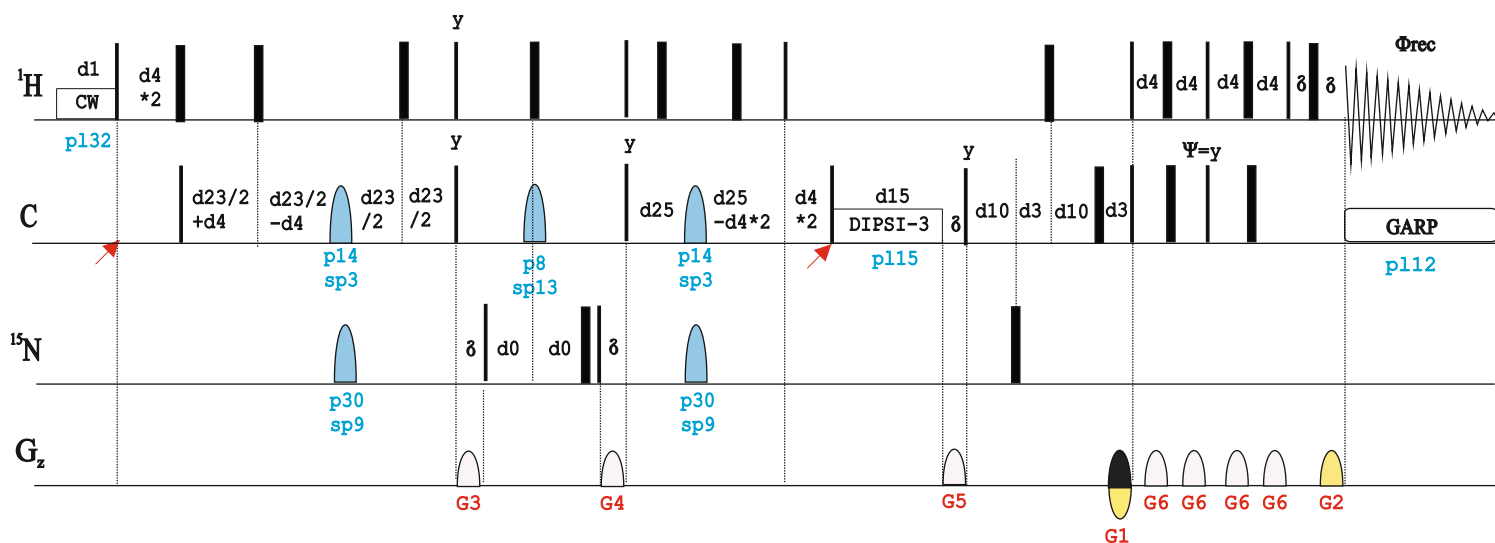
W. Hu, L. Jiang & Y.Q. Gossler, J. Magn. Reson. 145, 147-151 (2000)

Related Experiments

HCN-CCH COSY



na_hcncchdimq3d



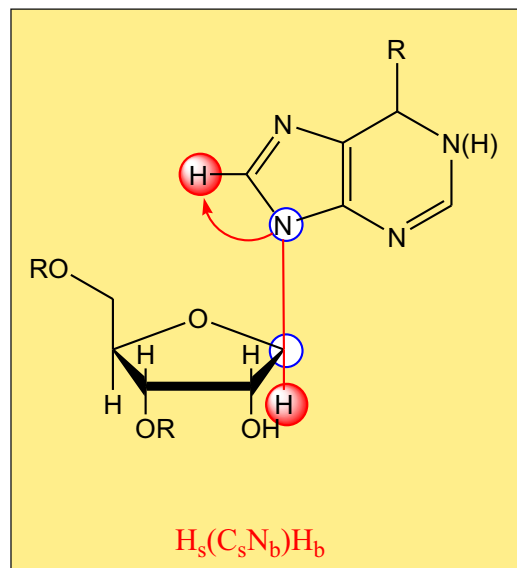
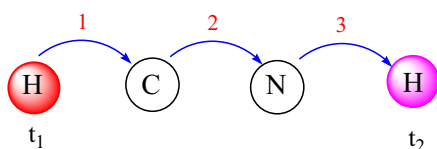
d1=1.5s
 d4=1/4J(C1'H1')=1.56ms
 d3=1/4J(C'H')=0.95ms
 d15= CC TOCSY= 12 ms
 d23=1/4J(C1'N)=18ms
 d24=1/8J(C'H')=0.78ms
 d25=1/4J(C1'N)=15ms
 d27=1/8J/C1'C2')=3.25ms
 cnst21=C1' chemical shift=90ppm
 cnst23=C2' chemical shift=72 ppm
 o2p=79ppm
 p14=1ms (spnam3=Q3.1000)
 o3p=160 ppm
 p30=700us (spnam9=Q3.1000)

2D H(CN)H Experiment

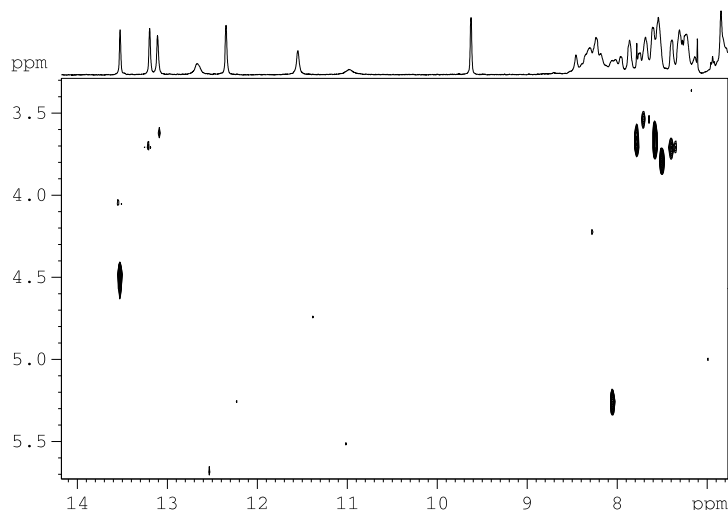
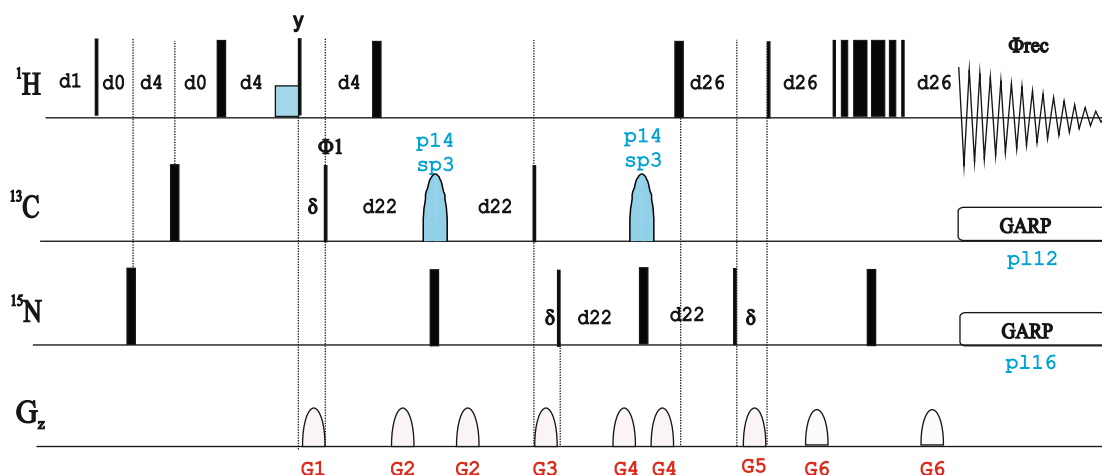
Experiment Description:

Experiment alternative to the HCNCH experiment that allows to correlate the H1' ribose proton with the base H6/8 protons via $2J(N1/9-H6/8)$ coupling constant

S. Tate, A. Ono & M. Kainosho, J. Am. Chem. Soc. 116, 5977 - 5978 (1994).



na_hcnhgpph19

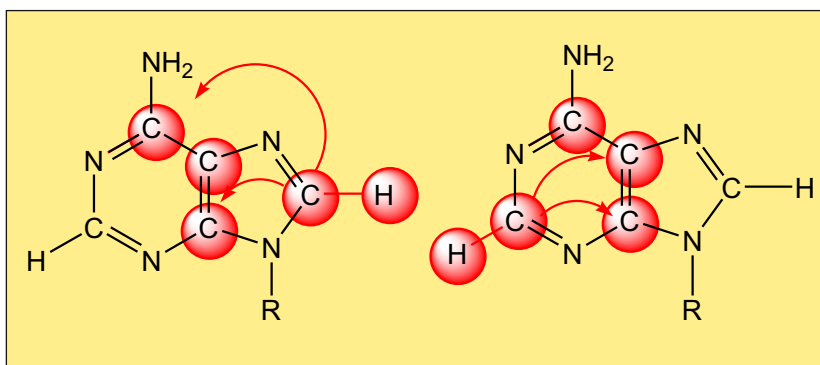


d1=1.5s
d4=1/4J(CH)=1.56ms
d22=1/4J(CN)=18.0ms
d26=1/4J(NH)=15ms (long-range)
p14=1ms (spnam3=Q3.1000)
o2p=89.19ppm

3D TROSY-(H)CCH-COSY Experiment

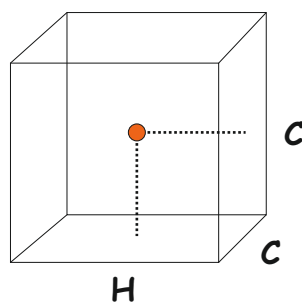
Experiment Description:

Experiment that correlates the adenine H2 and H8 protons in ^{13}C -labeled NAs molecules. The experiment provides ^{13}C chemical shifts of all carbon nuclei in the adenine base and also the long-range H8-C4/C5/C8 correlation in guanines (01jb173-20).



NMR Spectrum

The experiment provides a 3D correlation map

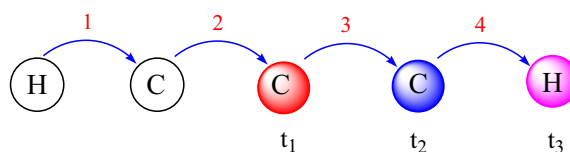


References:

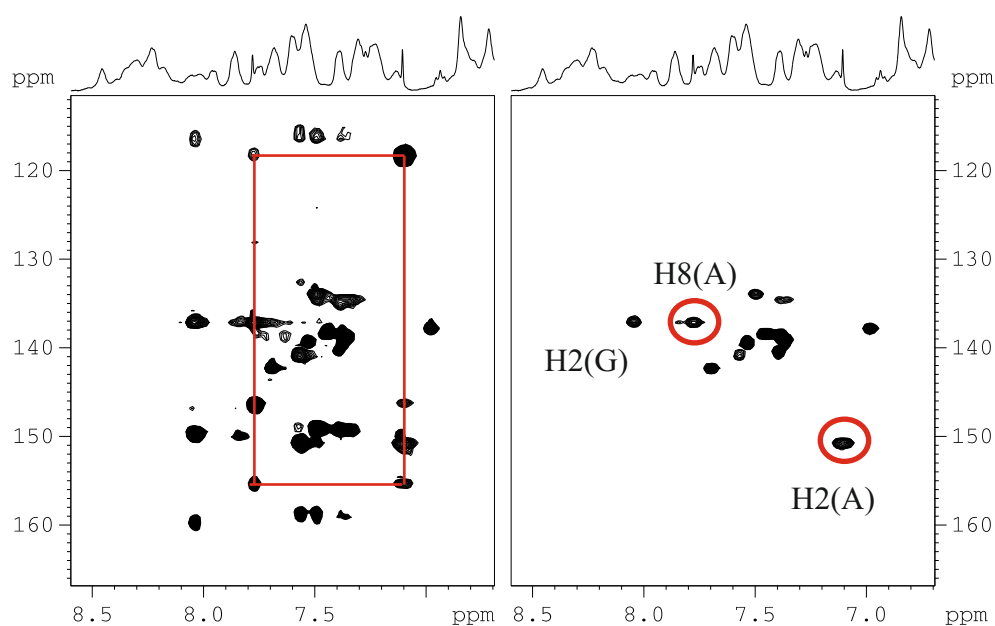
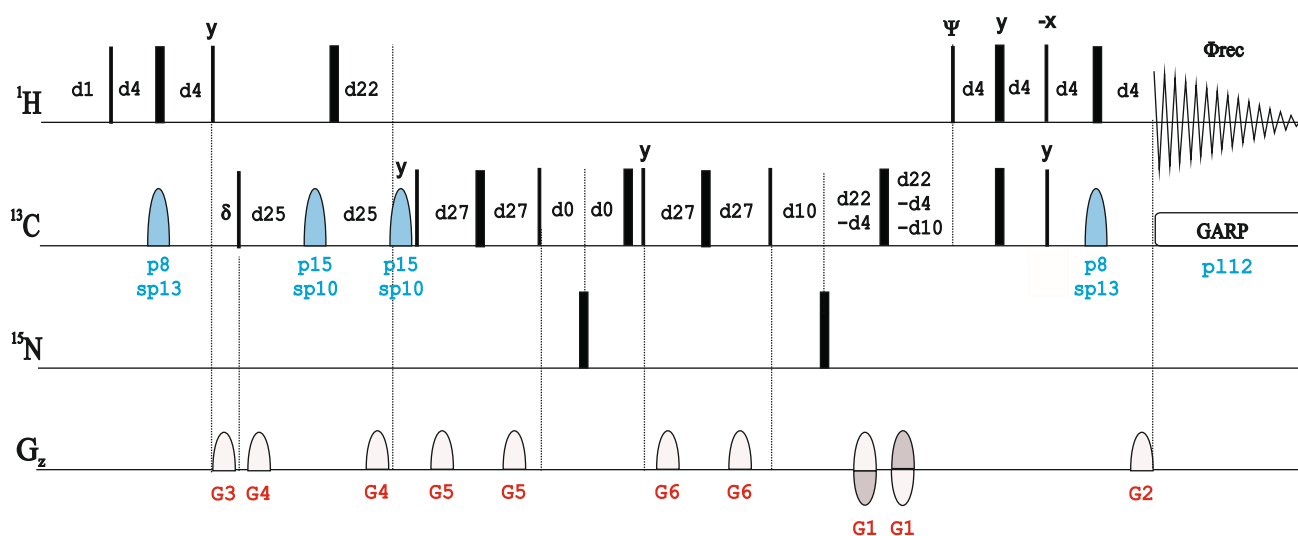
B. Simon, K. Zanier & M. Sattler, J. Biomol. NMR 20, 173-176 (2001)

Related Experiments

2D ^1H - ^{13}C HMBC



na_trhcchco3d



d1=1.5s
d4=1.25ms
cnst28=4.69 C5 offset
d22=1/4J(C2C5) and
1/4(C8C4/C6)=14.2ms
d25=1/2J(C5C6)=7.12ms
d27=1/4J(C5C4/C6)=1ms
o2p=140ppm
p15=90 pulse C5 off-resonance

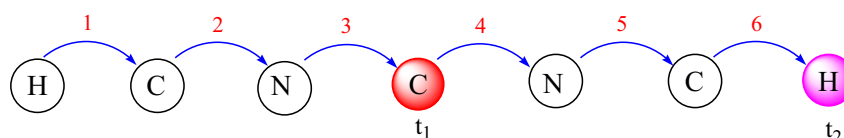
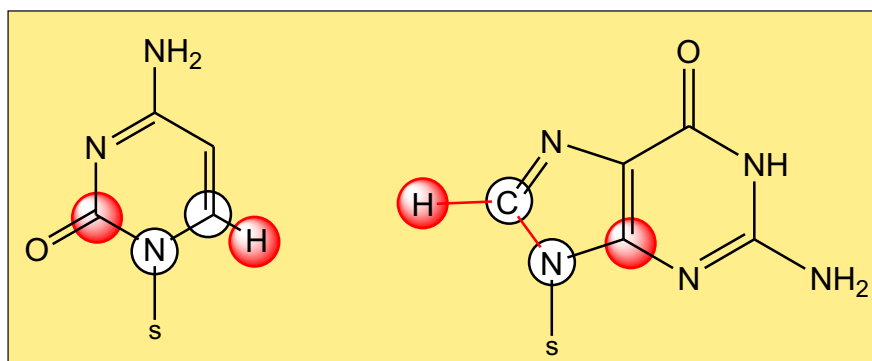
2D H(CN)C Experiment

Experiment Description:

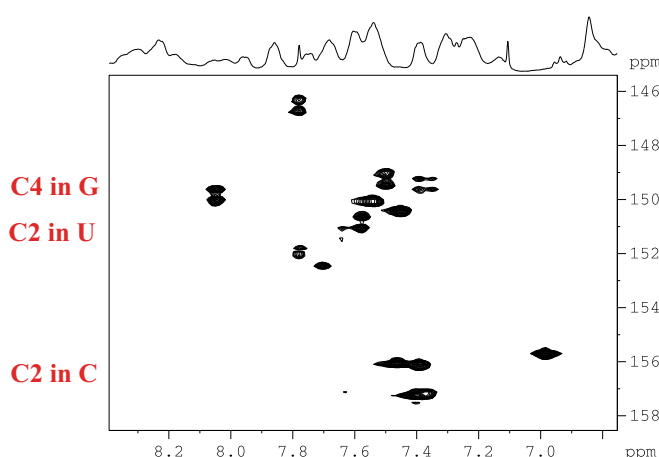
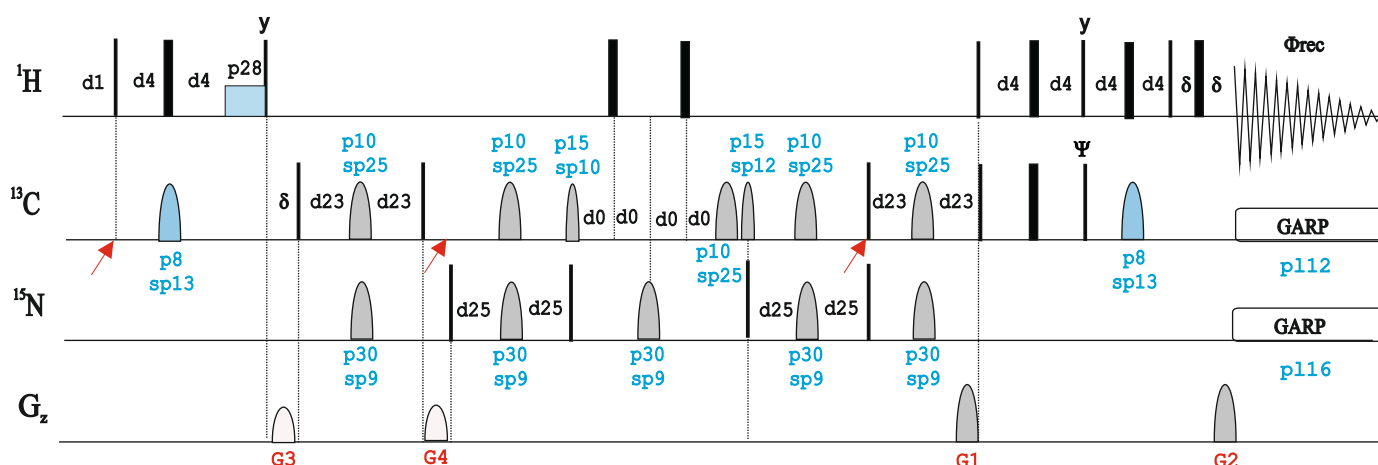
The H(CN)C experiment (also referred as H(6/8)C(6/8)N(1/9)C(2/4)) correlates the aromatic H6/8 protons of the base with the non-protonated C2/4 carbons via the C6/8 and N1/9 centers.

References:

B. Fuertig, C. Richter, W. Bermel & H. Schwalbe,
J. Biomol. NMR 28, 69-79 (2004)



na_h68c68n19c42



d1=1.5s
d4=1/4J(CH)=1.25ms for J(H8C6) and J(H6C6)
d23=1/4J(CN)=15ms for J(N1C6), and J(N9C8)
d25=1/4J(CN)=15ms for J(N1C2), and J(N9C4)
o2p=cnst27=152ppm
cnst22=137.7=chemical shift C6(CU)/C8(AG)
p30=700us(spnam9=Q3.1000)
p10=
p15=
Reduced SW in the C dimension=16.5ppm

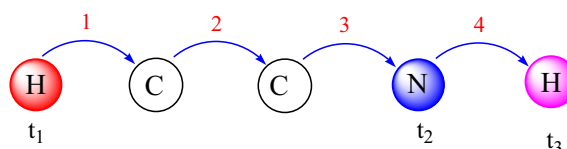
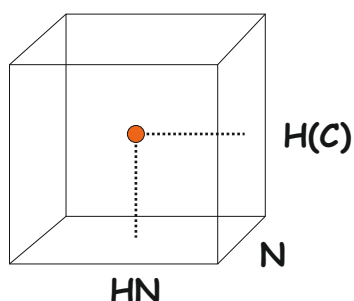
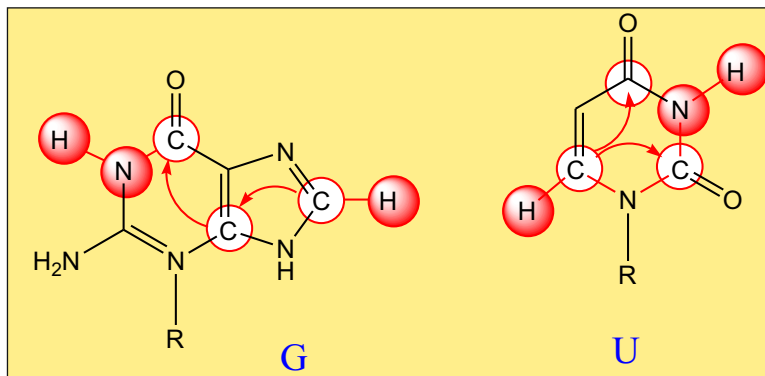
3D H(6/8)(CCC)NH Experiment

Experiment Description:

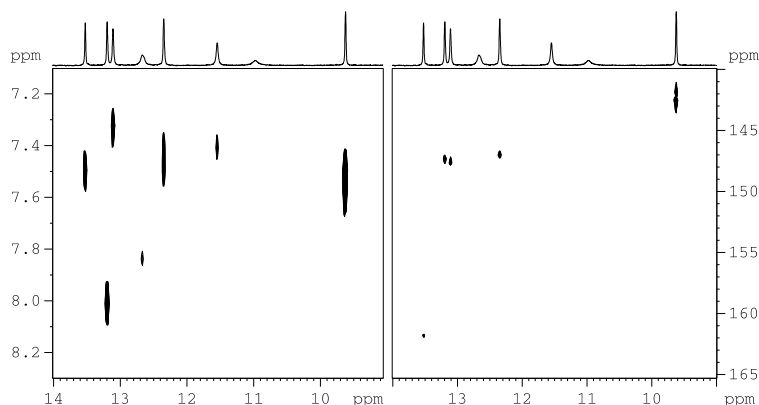
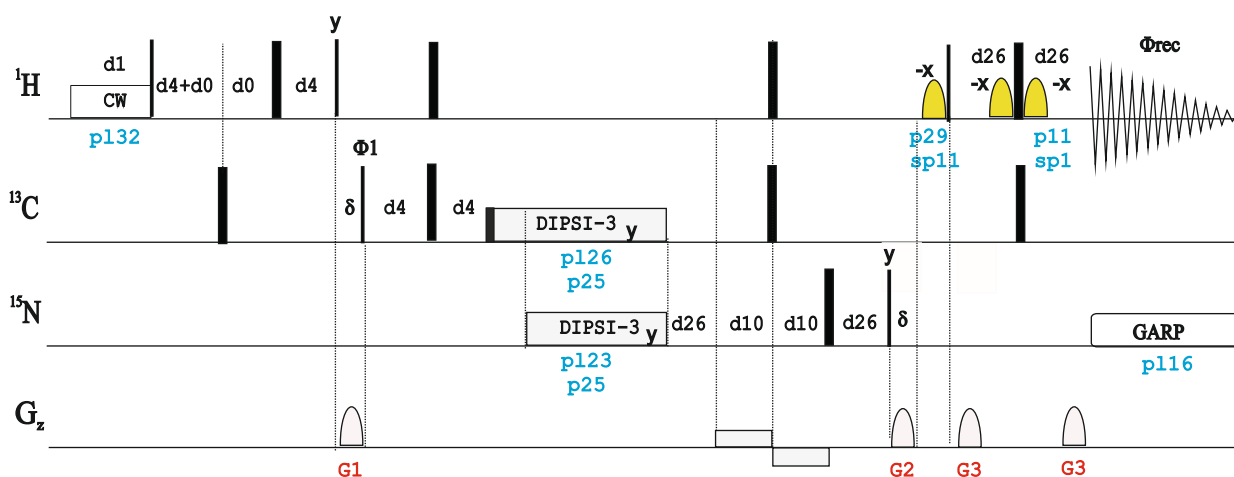
The HCCNH-TOCSY experiment allows the correlation between the exchangeable imino NH groups with H8 in guanines and H6 in uridines.

References:

V. Sklenar, T. Dieckmann, S. E. Butcher & J. Feigon,
J. Biomol. NMR 7, 83 - 87 (1996)



na_hccnhdigpwg3d



d1=1.5s
d4=1/4J(CH)=12.5ms
optimized for cnst2=200Hz
d26=1/4J(NH)=2.77ms
optimized for cnst4=90Hz
p29=p11=1ms (Squa100.1000)
p25=245us
l1=1
l1=3
o2p=149 ppm

3D H(CC)NH-COSY Experiment

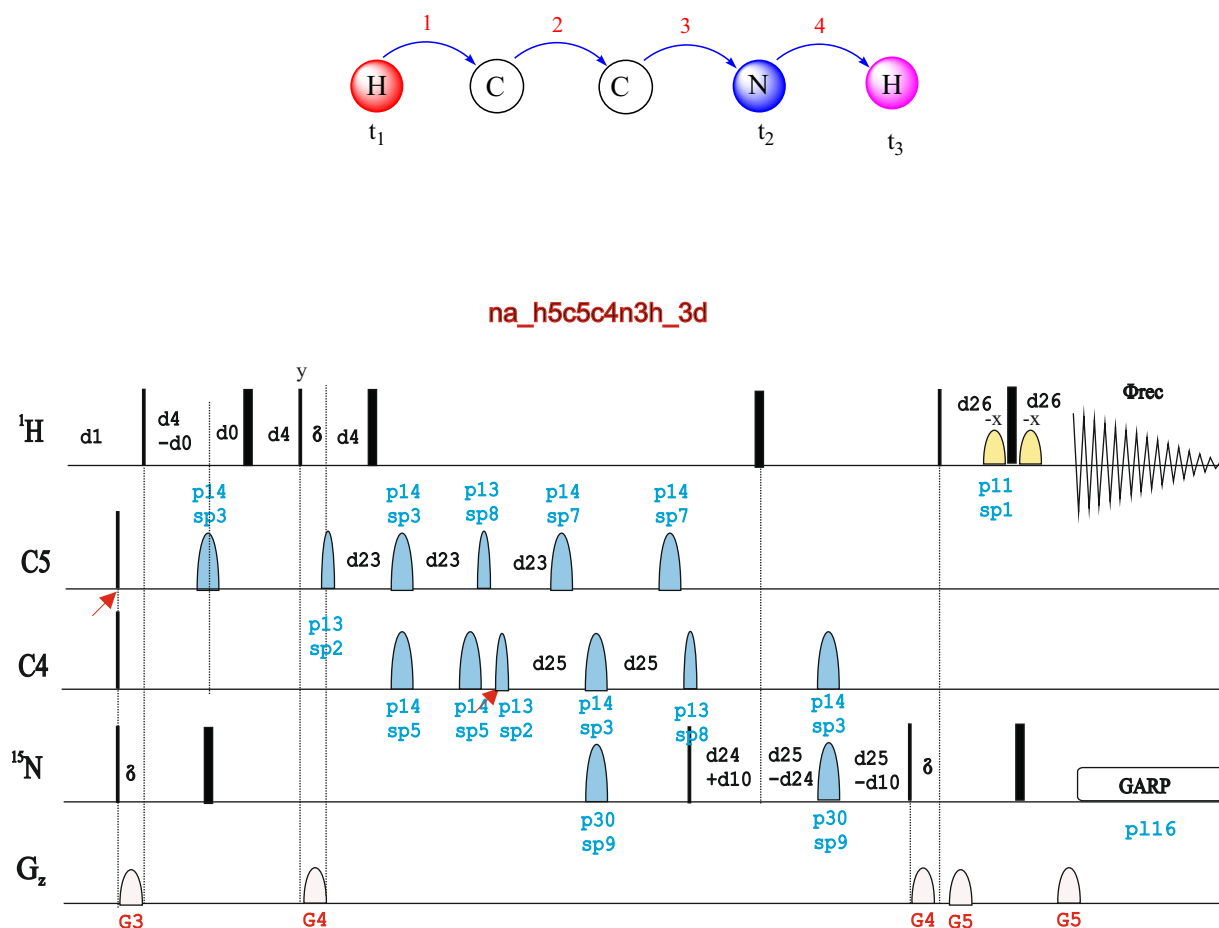
Experiment Description:

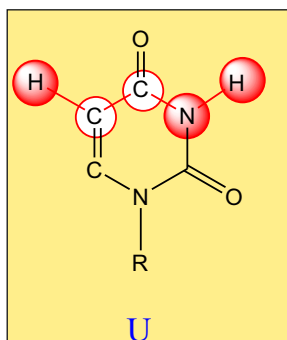
The HCCNH experiment allows the correlation of the exchangeable NH and NH₂ spin systems with the H₅ and H₆ protons in U and C via a CC COSY transfer.

The experiment starts from the aromatic CH spin system and detects H(N). It can be separately optimized for imino NH or for amino NH₂ groups.

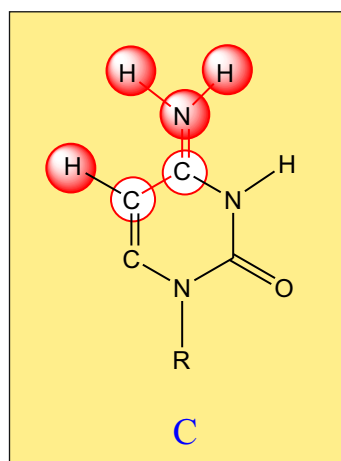
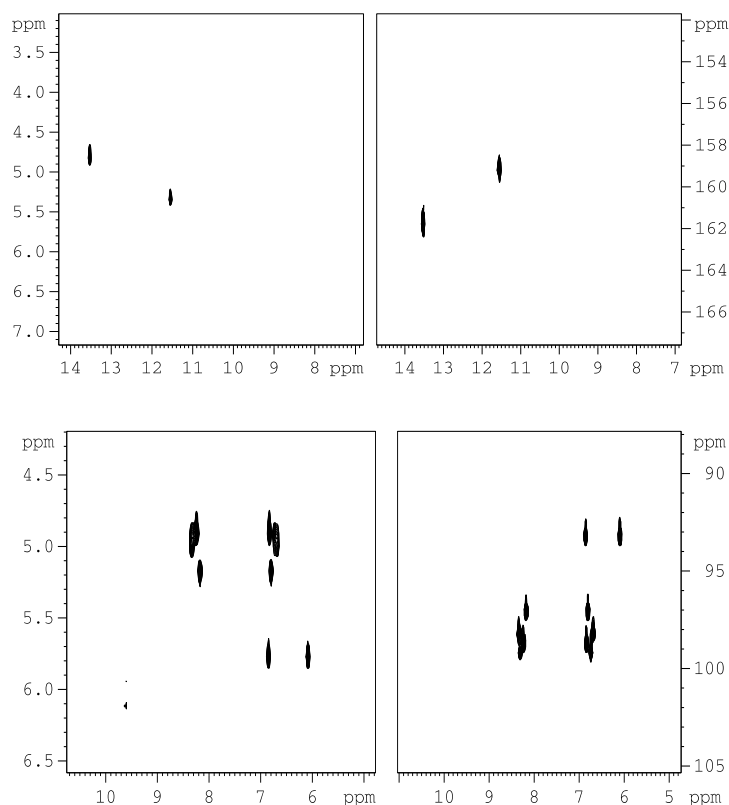
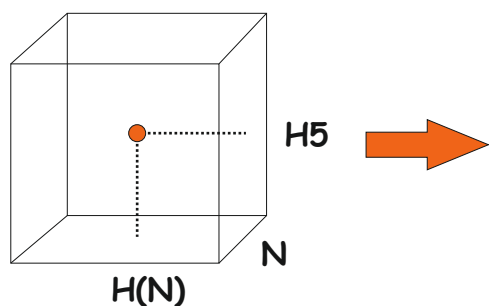
References:

J. Woehnert, R. Ramachandran, M. Goerlach & L.R. Brown, J. Magn. Reson. 139, 430-433 (1999)





$d1=1.5s$
 $d4=1/4J(C5H5)=1.25ms$
 $d23=1/4J(C5C4)=4.1ms$
 $d24=1/4J(NH)$ for $U=2.78ms$
 $d25=1/4J(C4N)=10ms$
 $d26=1/4J(NH)=2.5ms$
 $p11=1\ ms\ (spnam1=Squa100.1000)$
 $p13=1ms\ (spnam2=Q5.1000\ and\ spnam8=Q5tr.1000)$
 $p14=1ms\ (spnam3/5/7=Q3.1000)$
 $cnst24=C4(C/U)$ chemical shift=169ppm
 $cnst28=C5(C/U)$ chemical shift=105ppm
 $o3p=160ppm$ (for U)
 $p30=700us\ (spnam9=Q3.1000)$



$d1=1.5s$
 $d4=1/4J(C5H5)=1.25ms$
 $d23=1/4J(C5C4)=4.1ms$
 $d24=1/8J(NH)$ for $C=1.39ms$
 $d25=1/4J(C4N)=10ms$
 $d26=1/4J(NH)=2.5ms$
 $p11=1\ ms\ (spnam1=Squa100.1000)$
 $p13=1ms\ (spnam2=Q5.1000\ and\ spnam8=Q5tr.1000)$
 $p14=1ms\ (spnam3/5/7=Q3.1000)$
 $cnst24=C4(C/U)$ chemical shift=169ppm
 $cnst28=C5(C/U)$ chemical shift=105ppm
 $o3p=100ppm$ (for C)
 $p30=700us\ (spnam9=Q3.1000)$

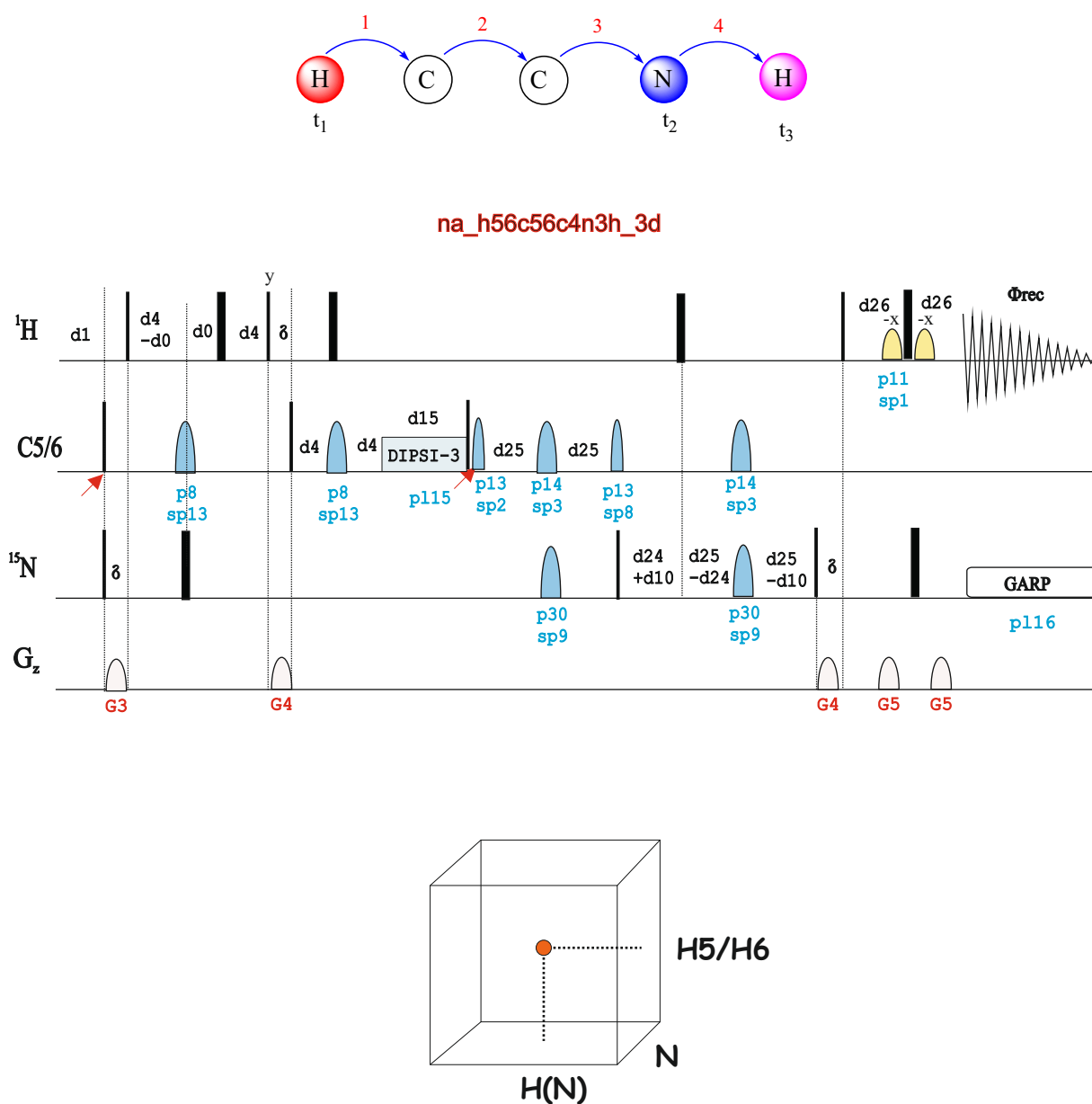
3D H(CC)NH-TOCSY Experiment

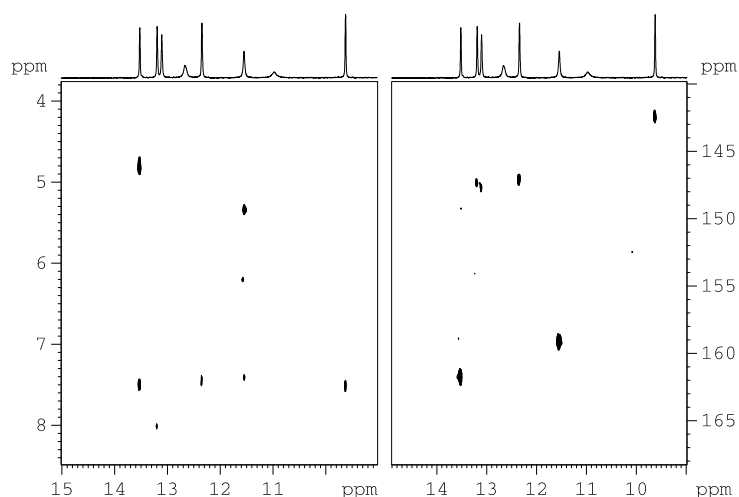
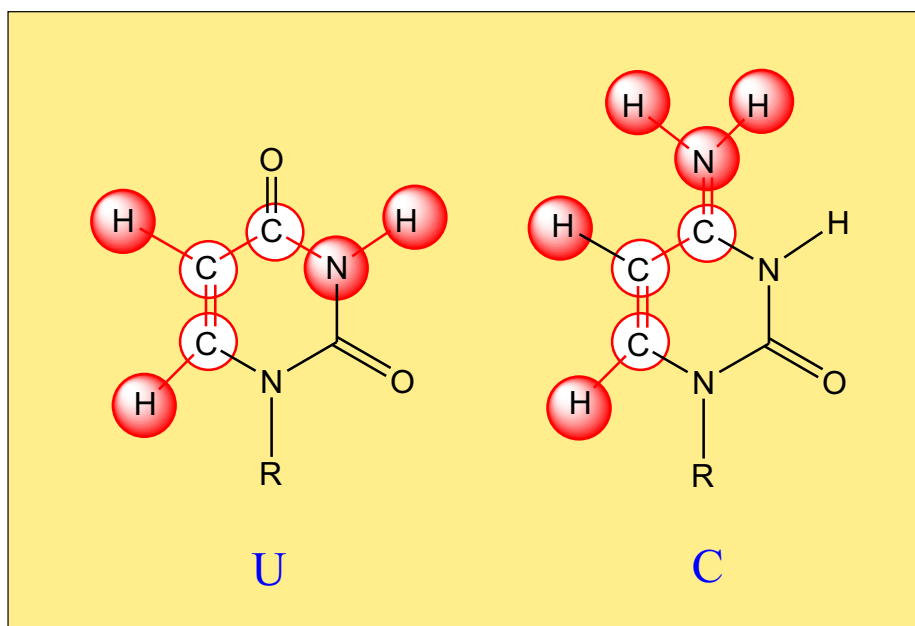
Experiment Description:

The HCCNH-TOCSY experiment allows the correlation of the exchangeable NH and NH spin systems with the H5 and H6 protons in U and C via a CC TOCSY transfer. The experiment starts from the aromatic CH spin system and detects H(N). It can be separately optimized for imino NH or for amino NH₂ groups.

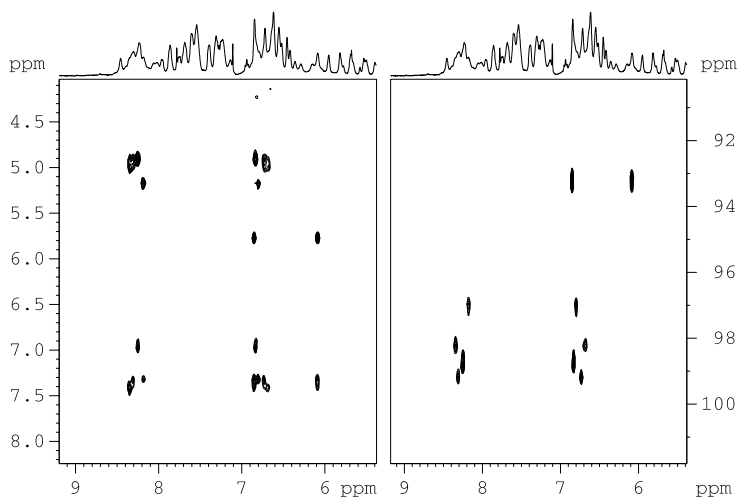
References:

J. Woehnert, M. Goerlach & H. Schwalbe, J. Biomol. NMR 26, 79-83 (2003).





$d_{24}=1/4J(\text{NH})$ for U=2.78ms
 $o_{3p}=160\text{ppm}$ (for U)



$d_1=1.5\text{s}$
 $d_4=1/4J(\text{C}5\text{H}5)=1.25\text{ms}$
 $d_{24}=1/4J(\text{NH})$ for U or $1/8J(\text{NH})$ for C
 $d_{25}=1/4J(\text{C}4\text{N})=10\text{ms}$
 $d_{26}=1/4J(\text{NH})=2.5\text{ms}$
 $d_{15}=\text{CC TOCSY}=19.5\text{ms}$
 $p_{13}=1\text{ms}$ (spnam2=Q5.1000 and spnam8=Q5tr.1000)
 $p_{14}=1\text{ms}$ (spnam3=Q3.1000)
 $p_{30}=700\text{us}$ (spnam9=Q3.1000)
 $cnst_{24}=169\text{ppm}$ (C4 in C/U)
 $cnst_{28}=105\text{ppm}$ (C5 in C/U)
 $o_{2p}=89.19\text{ppm}$
 $o_{3p}=160\text{ppm}$ (for U) or 100ppm (for C)

$d_{24}=1/8J(\text{NH})$ for U=1.39ms
 $o_{3p}=100\text{ppm}$ (for C)

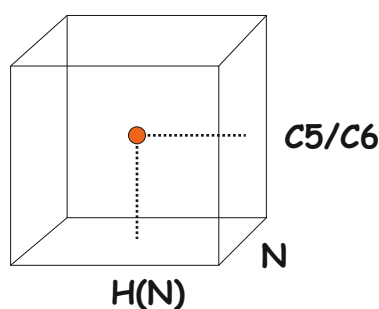
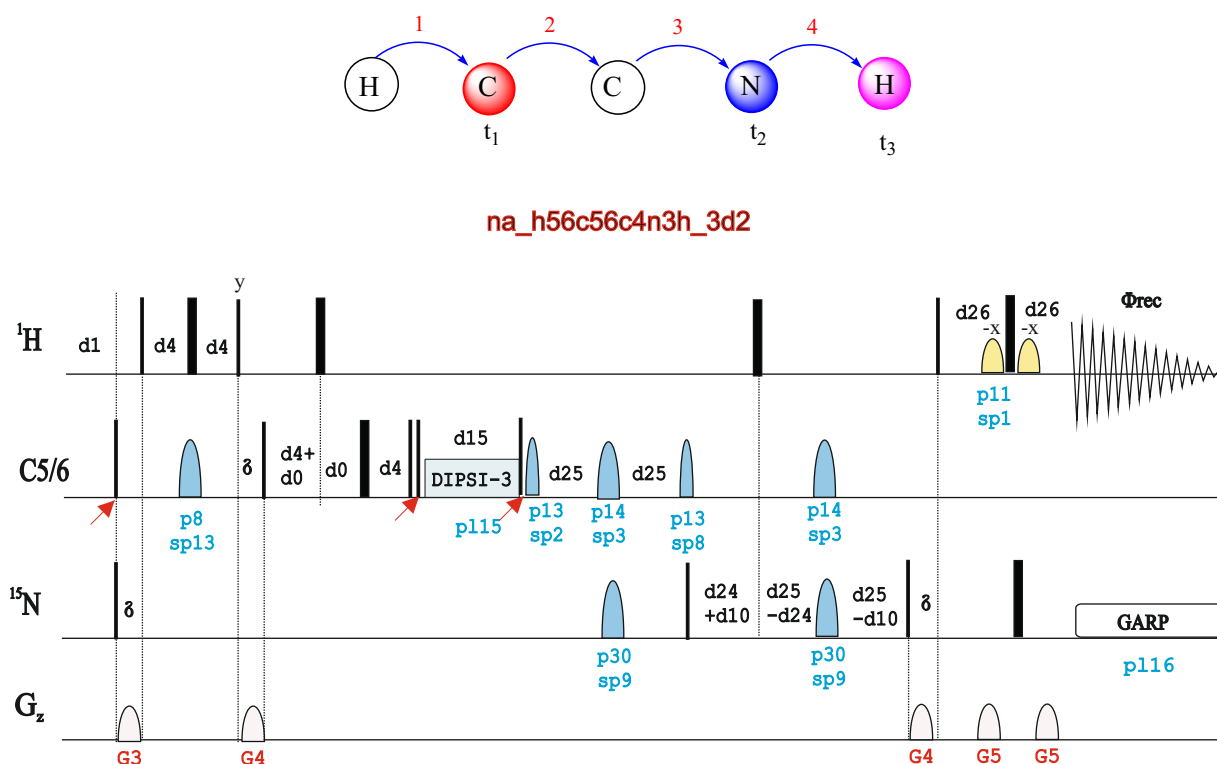
3D (H)C(C)NH-TOCSY Experiment

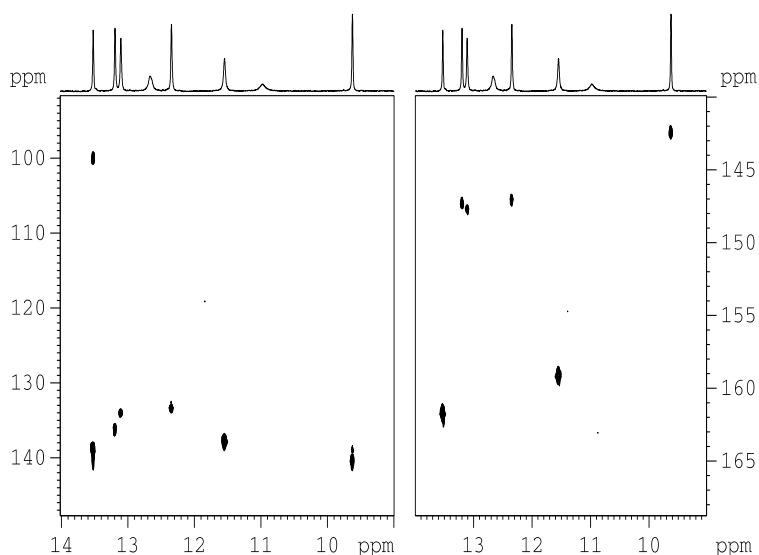
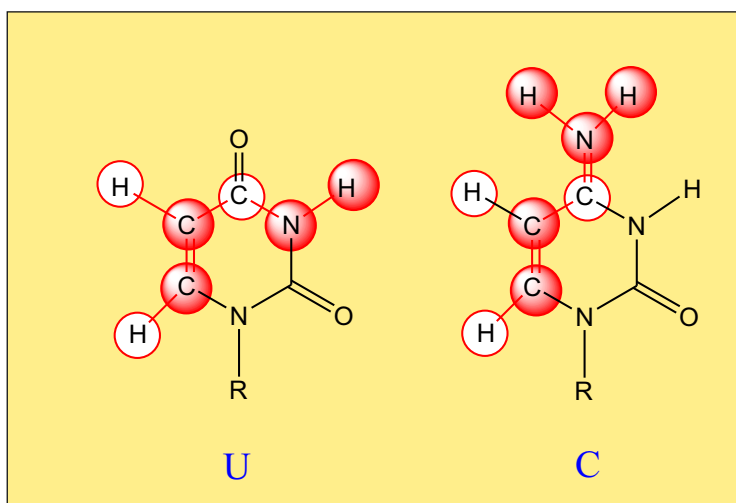
Experiment Description:

The HCCNH-TOCSY experiment allows the correlation of the exchangeable NH and NH spin systems with the C6 carbons in U and C via a CC TOCSY transfer. The experiment starts from the aromatic CH spin system and detects H(N). It can be separately optimized for imino NH or for amino NH₂ groups.

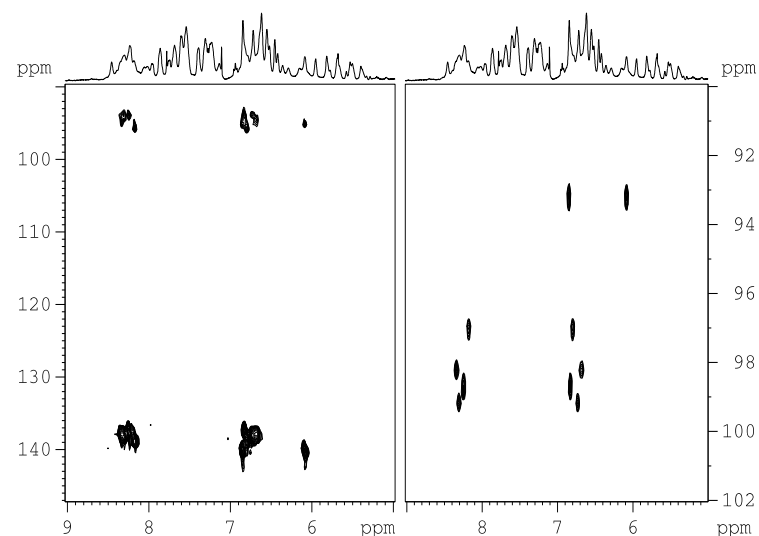
References:

J. Woehnert, M. Goerlach & H. Schwalbe, J. Biomol. NMR 26, 79-83 (2003)





$d24=1/4J(\text{NH})$ for U=2.78ms
 $o3p=160\text{ppm}$ (for U)



$d1=1.5\text{s}$
 $d4=1/4J(\text{C}5\text{H}5)=1.25\text{ms}$
 $d25=1/4J(\text{C}4\text{N})=10\text{ms}$
 $d26=1/4J(\text{NH})=2.5\text{ms}$
 $d15=\text{CC TOCSY}=19.5\text{ms}$
 $p13=1\text{ms}$ (spnam2=Q5.1000 and spnam8=Q5tr.1000)
 $p14=1\text{ms}$ (spnam3=Q3.1000)
 $p30=700\text{us}$ (spnam9=Q3.1000)
 $cnst22=137\text{ppm}$ (C6 in C7U)
 $cnst24=169\text{ppm}$ (C4 in C/U)
 $cnst28=105\text{ppm}$ (C5 in C/U)
 $o2p=121.35\text{ppm}$

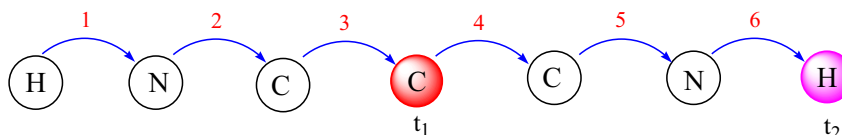
$d24=1/8J(\text{NH})$ for C=1.39ms
 $o3p=100\text{ppm}$ (for C)

Experiment Description:

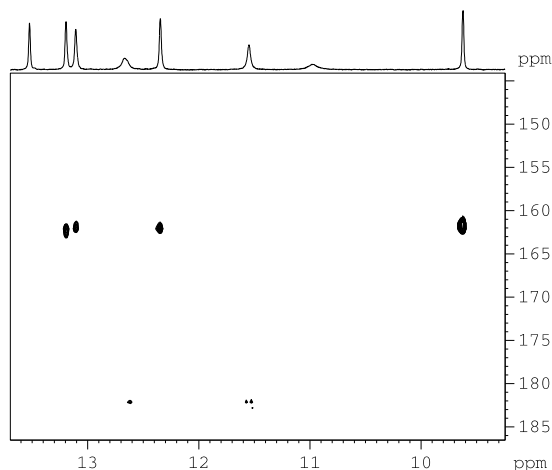
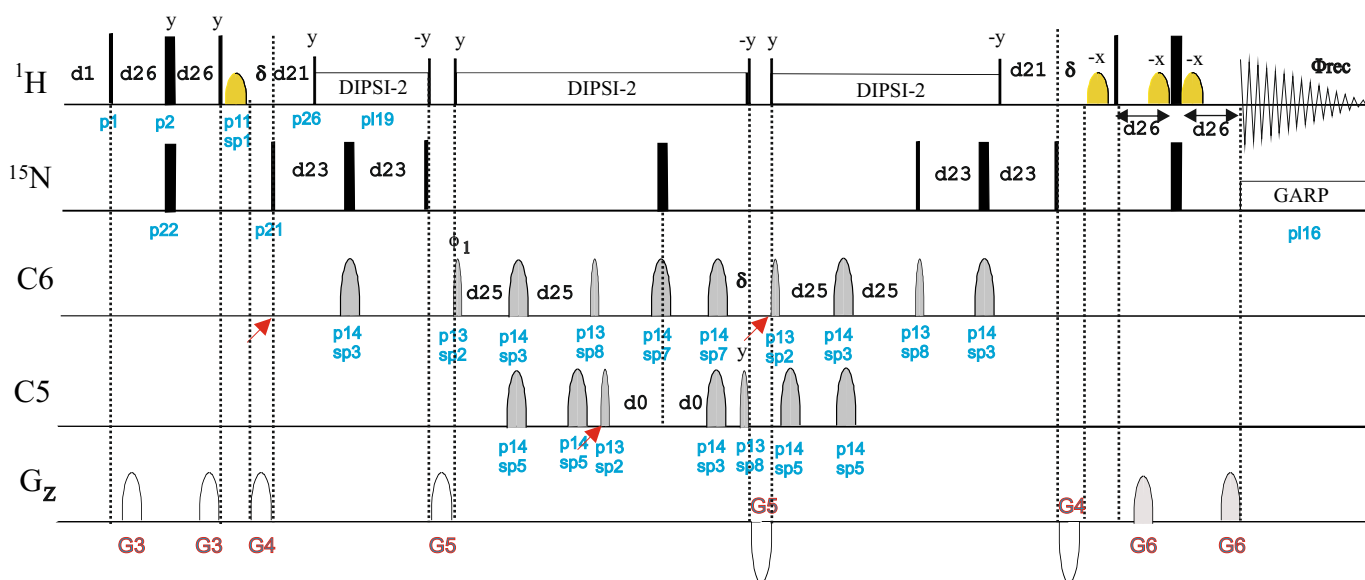


The chemical structure of 6-aminocaffeine is shown. It consists of a purine ring system with a carbonyl group at position 2, a methyl group at position 3, and an amino group at position 6. The structure is drawn with black lines for bonds, white circles for nitrogen atoms, red circles for oxygen atoms, and black text for labels. The amino group is represented as NH₂.

B. Fuertig, C. Richter, W. Bermel & H. Schwalbe,
J. Biomol. NMR 28, 69-79 (2004)



na_hnc6c5etgpsi



d1=1.5s
d26=1/4J(NH)=2.78ms
d23=1/4J(C6N)=25ms
d25=1/4J(C6C5)=2.8ms
d21=1/2J(NH)=5.56ms
p11=1s (spnam1=Squa100.1000)
p14=1ms (spnam3/5/7=Q3.1000)
p13=1ms (spnam2=Q5.1000 and spnam8=Q5tr.1000)
cnst25=C6(G) chemical shift=160ppm
cnst26=C5(G) chemical shift=119ppm
o2p=C5 chemical shift=165ppm
o3p=160ppm

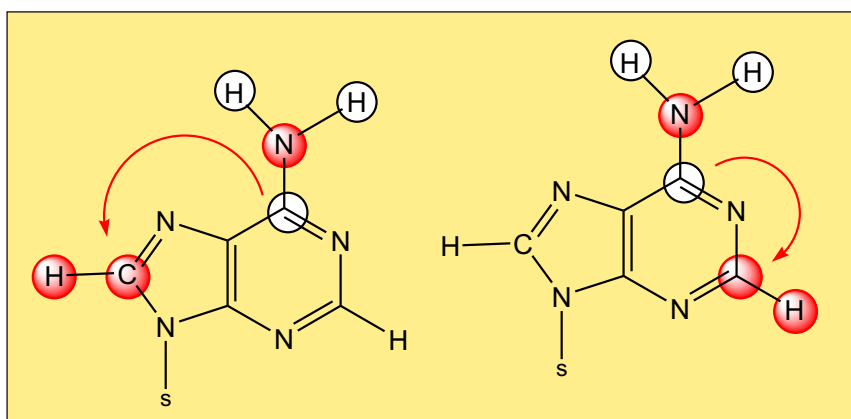
3D (H)N(C)CH Experiment

Experiment Description:

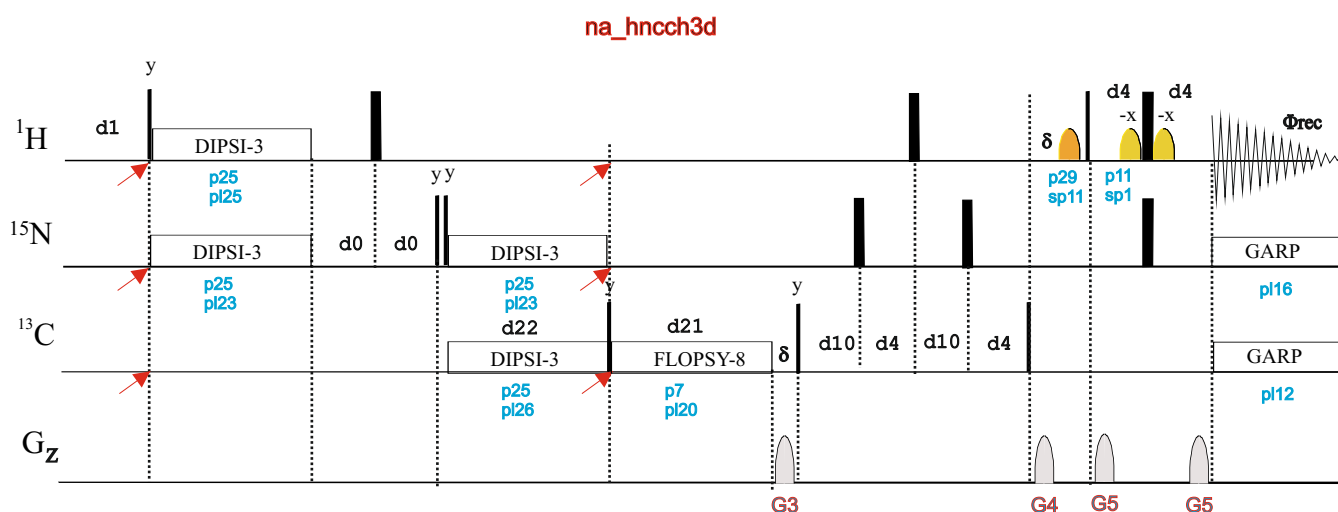
The 3D HNCCH experiment allows the correlation of the imino N nitrogen with the H2/C2 and H8/C8 spin systems in adenines.

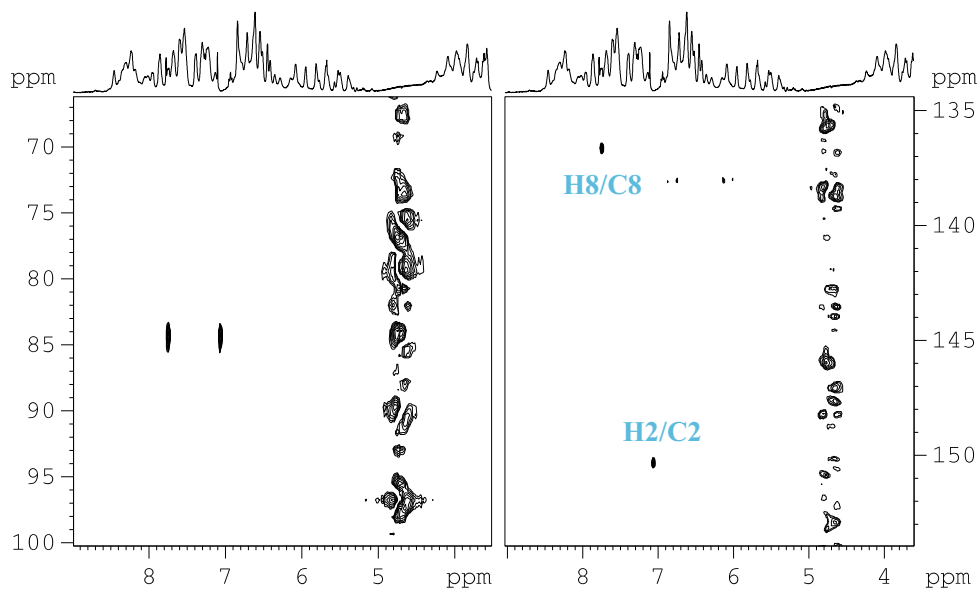
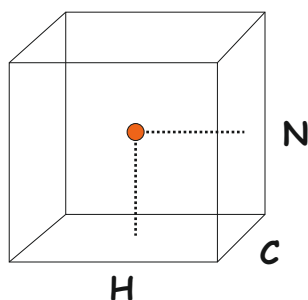
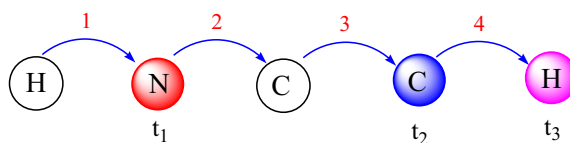
References:

J.-P. Simorre, G.R. Zimmermann, L. Mueller & A. Pardi, *J. Am. Chem. Soc.* 118, 5316-5317 (1996)



The experiment uses three different cross-polarization transfer schemes. First, a heteronuclear cross-polarization (HCP) transfer from ^1H to ^{15}N . Then, another HC transfer from N to C followed by a homonuclear TOCSY CC transfer





$d1=1.5s$
 $d4=1/4J(CH)=1.25ms$
 $p11=p29=1s$ (spsam1=Squa100.1000)
 $p25=226us$
 $d21=CC\ TOCSY=38ms$
 $d22=CN\ TOCSY=45ms$
 $o1p=cnst18=4.7ppm$
 $cnst19=NH\ chemical\ shift$
 $cnst25=C6\ chemical\ shift=160ppm$
 $o2p=cnst29=145\ ppm\ (Caro)$
 $o3p=cnst31=81ppm\ (NH2)$

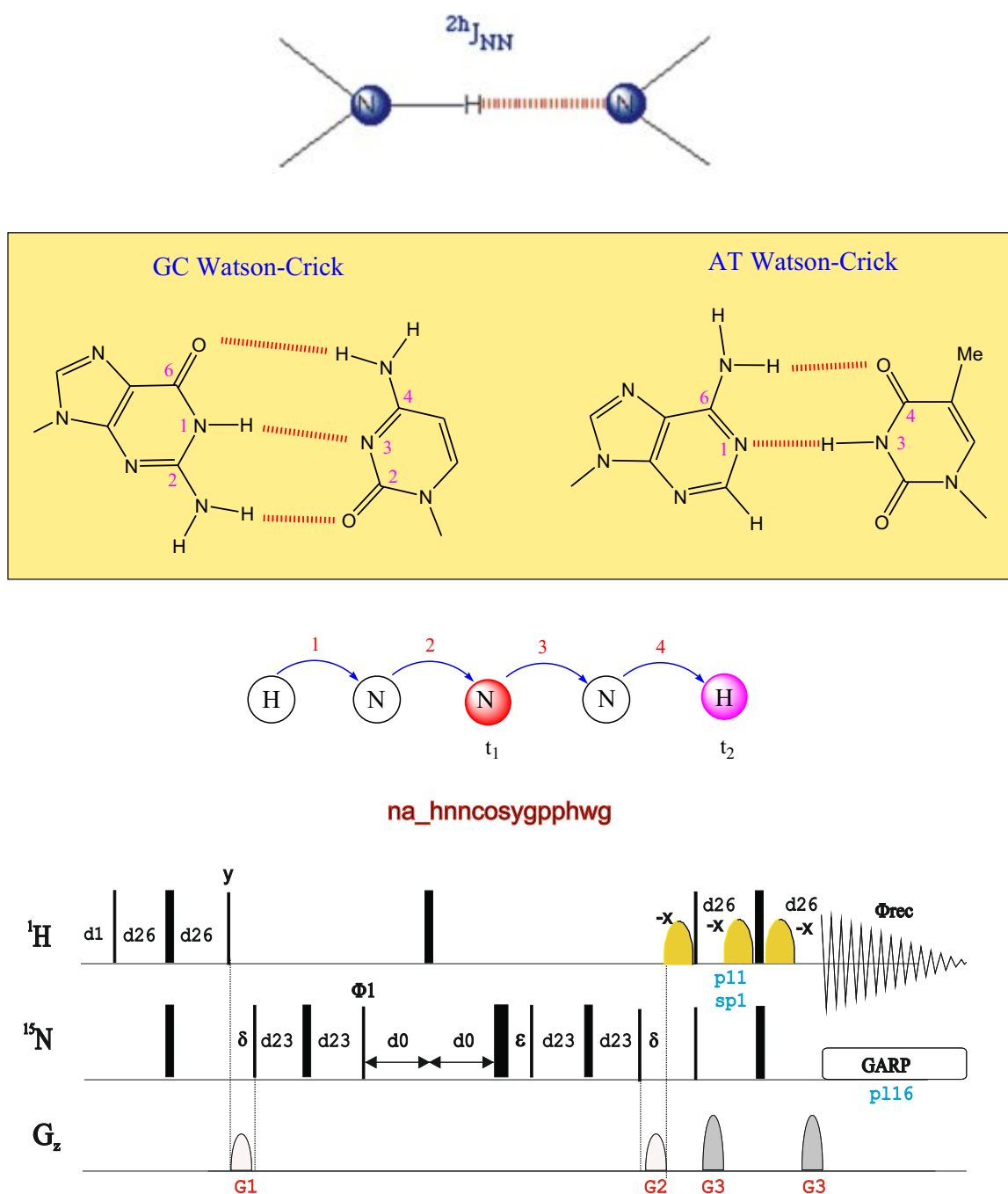
3D hydrogen-bond HNN Experiment

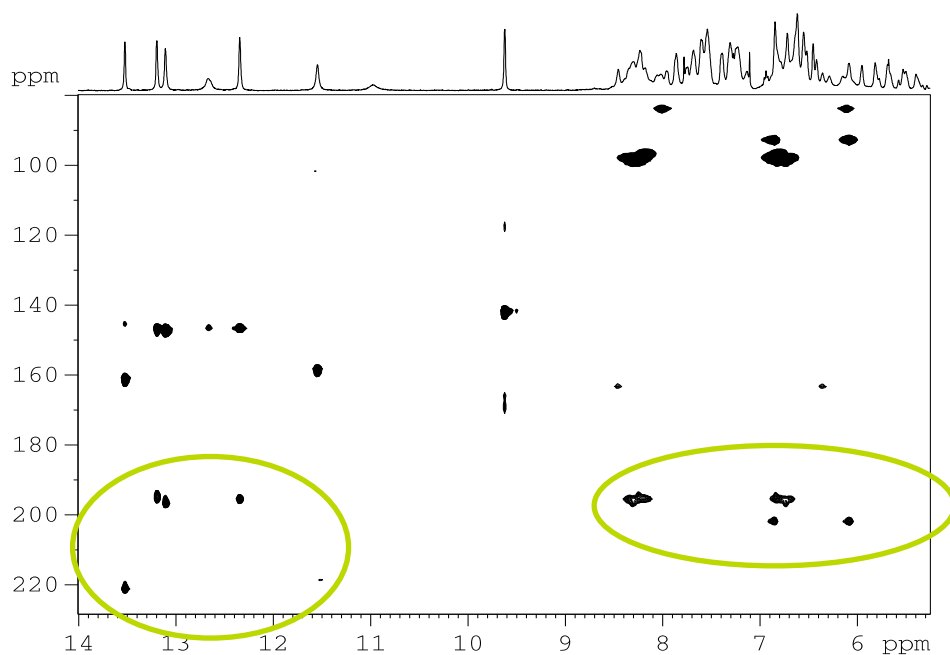
Experiment Description:

Experiment to detect hydrogen-bond NH-N connectivities (98jacs8293, 20NAR1585-28).

References:

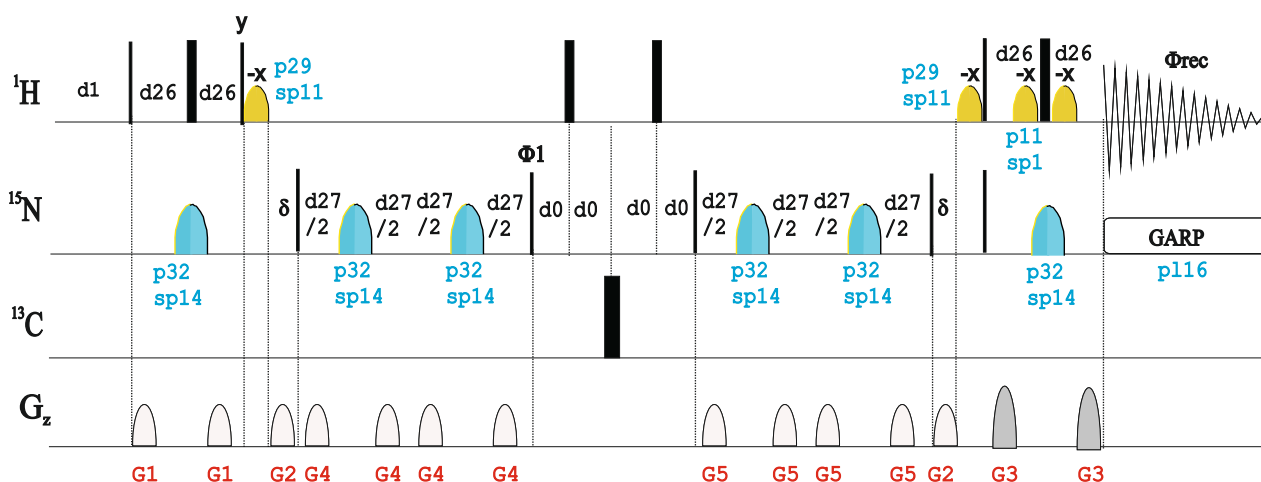
A.J. Dingley & S. Grzesiek, J. Am. Chem. Soc. 120, 8293 - 8297 (1998)



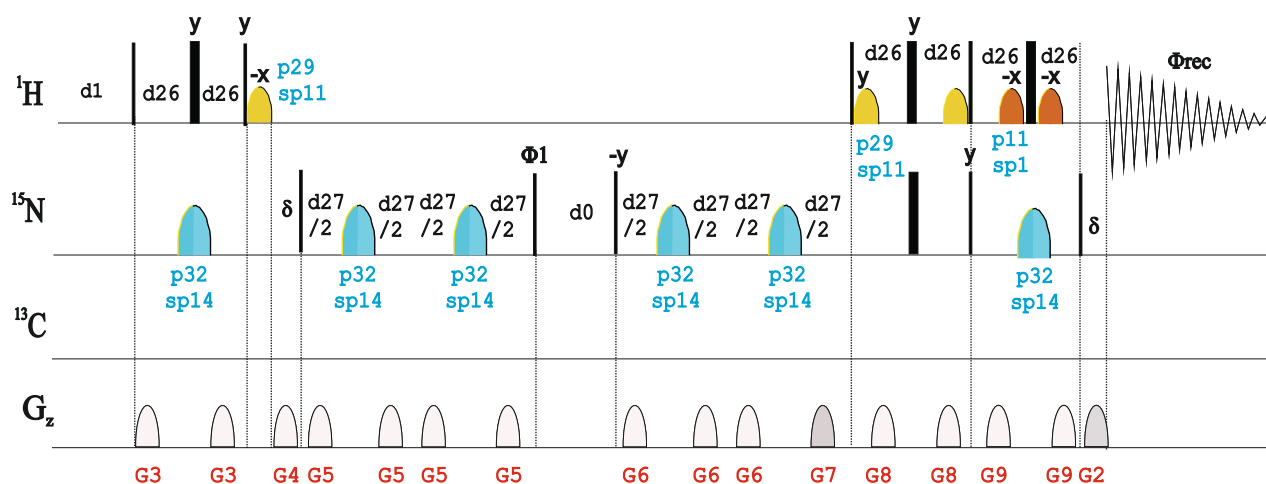


d1=1.5s
p11=90° water selective
=1ms (Squa100.1000)
d26=1/4J(NH)=2.25ms
d23=1/4J(NN)=15ms

na_hnncosygpphspwg



na_trhnncosygpphspwg



BRUKER PULSE PROGRAM CATALOGUE

NMRGuide

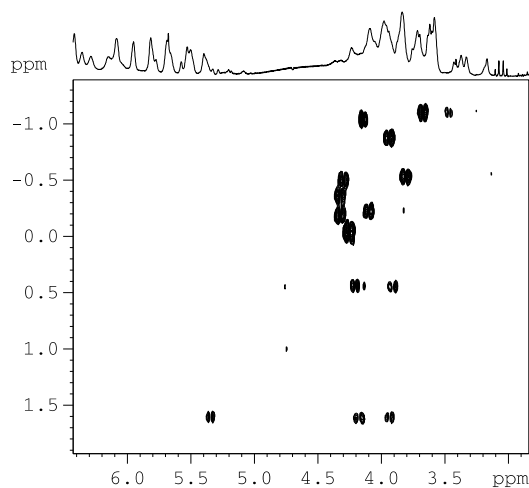
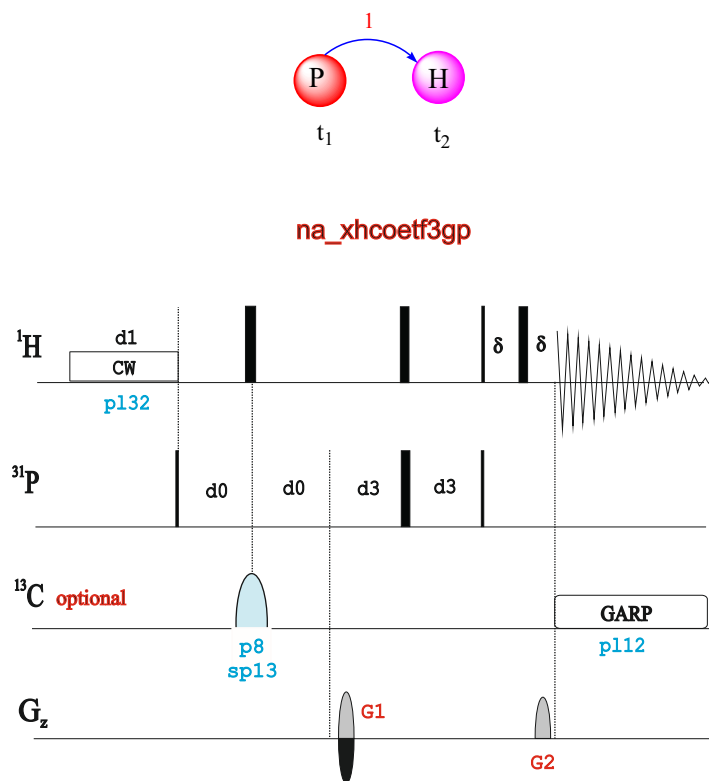
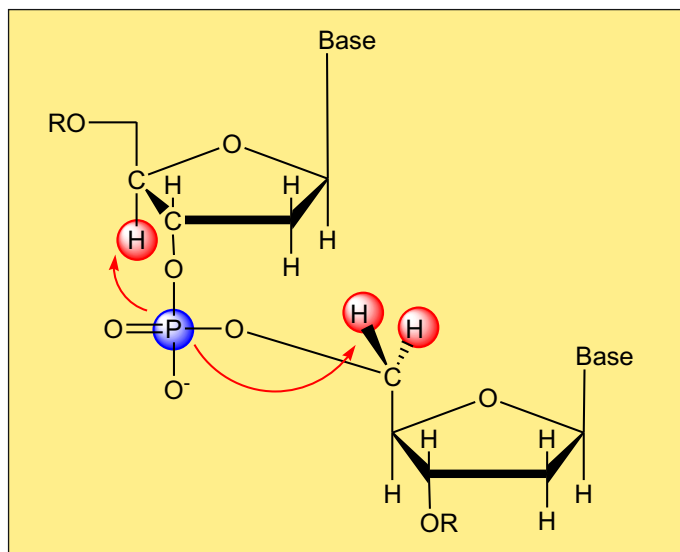
NUCLEIC-ACID NMR 2D & 3D HCP EXPERIMENTS

2D 31P-1H HETCOR or HP COSY Experiment

Experiment Description

Experiment to achieve sequential backbone assignment via through-bond $J(\text{H3}'(i)\text{P}(i))$ and $J(\text{H5}'/\text{H5}''(i+1)\text{P}(i))$ connectivities in unlabeled and ^{13}C -labeled NAs.

The pulse sequence uses a direct ^{31}P -to- ^1H INEPT-like transfer and can be also driven in a constant-time mode..

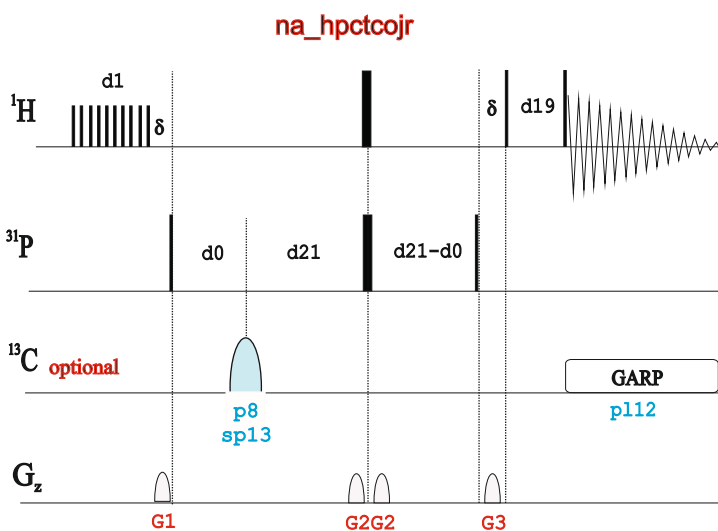
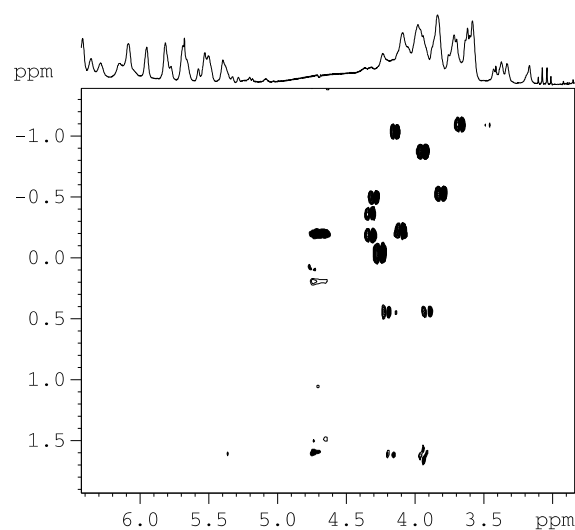
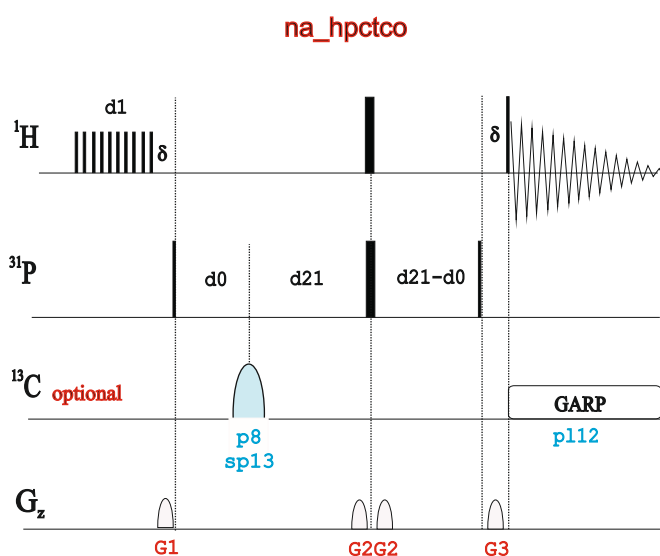
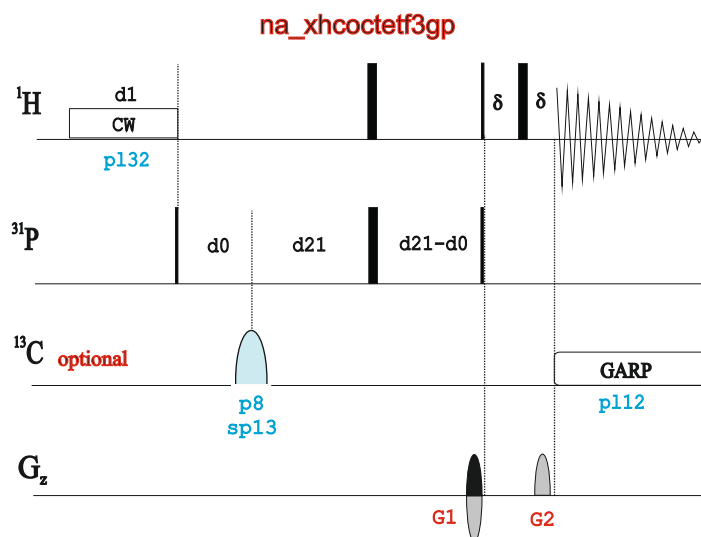
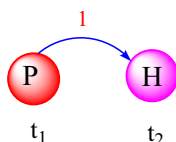


d1=1.5 s
d3=1/6J(PH)=16.6 ms
(optimized cnst2=10Hz with cnst11=6)
o3p=0 ppm
o2p=77 ppm

2D Constant-time HP COSY Experiment

Experiment Description:

Constant-time version of the ^1H - ^{31}P HETCOR or HP-COSY experiment



$d1=1.5$ s
 $d21=1/4J(\text{PH})=22$ ms
 (optimized $\text{cnst4}=11\text{Hz}$)
 $o3p=0$ ppm
 $o2p=77$ ppm

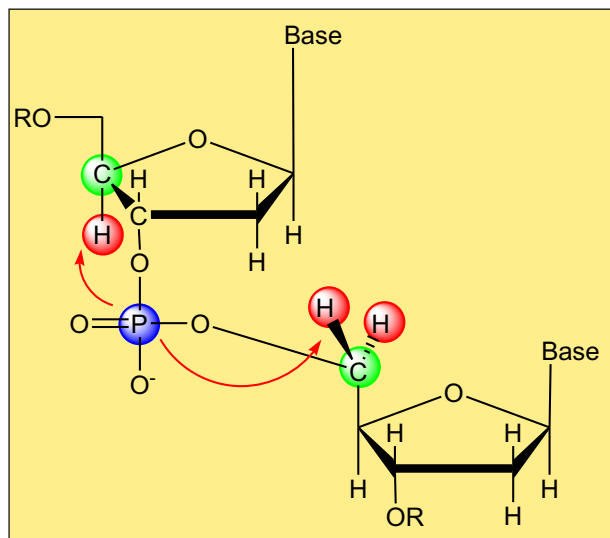
3D CT PHCH Experiment

Experiment Description

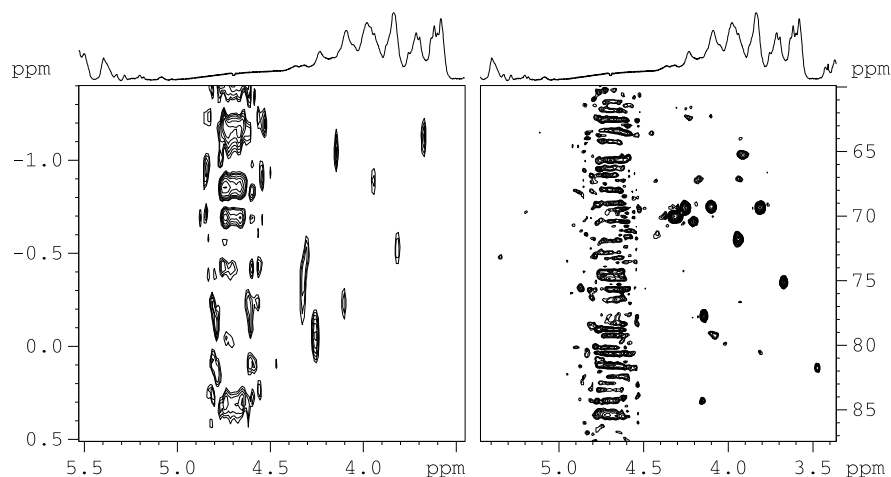
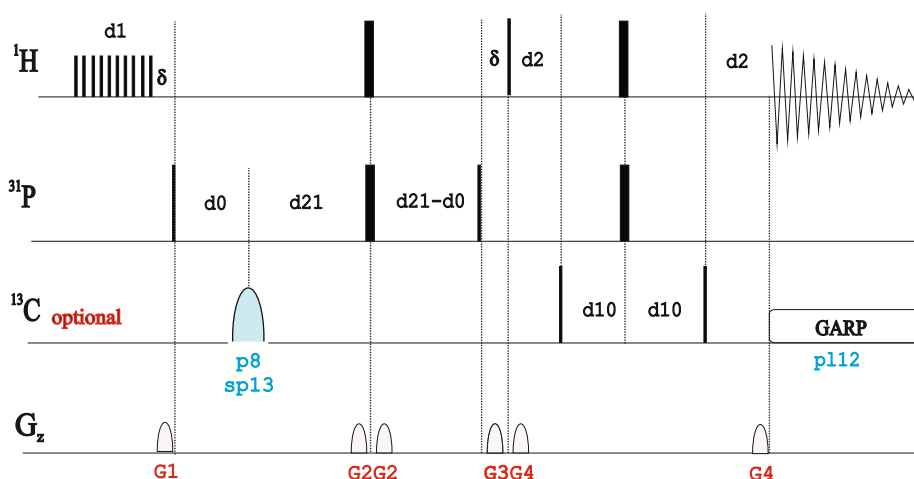
The 3D constant-time version of the P(H)CH experiment extends the backbone assignment of the HP experiment to C3'(i) and C5'(i+1) carbons by means a 1H-13C HMQC building block.

References:

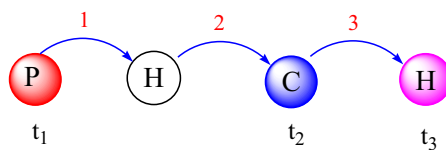
1. T. Carlomagno, M. Hennig & J.R. Williamson, J. Biomol. NMR 22, 65-81 (2002)
2. G. Varani, F. Aboul-ela, F. Allain & C.C. Gubser, J. Biomol. NMR 5 315-320 (1995)



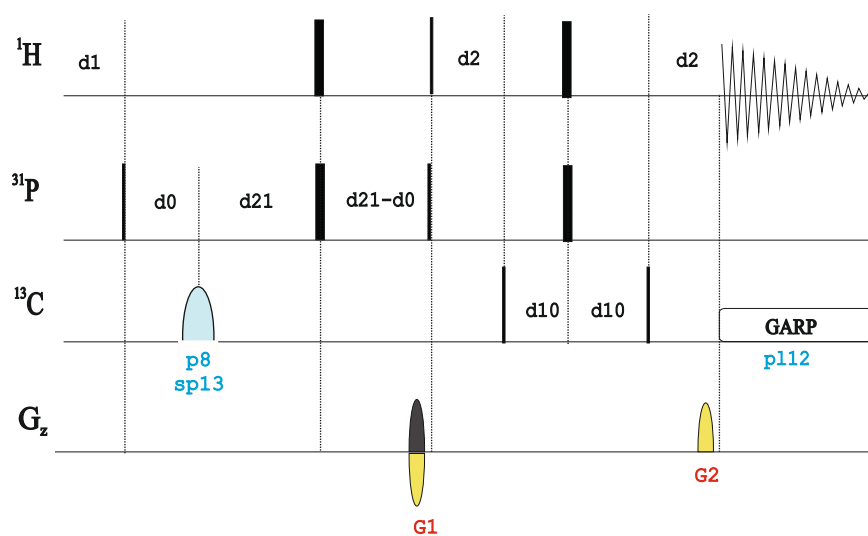
na_hpcctco3d



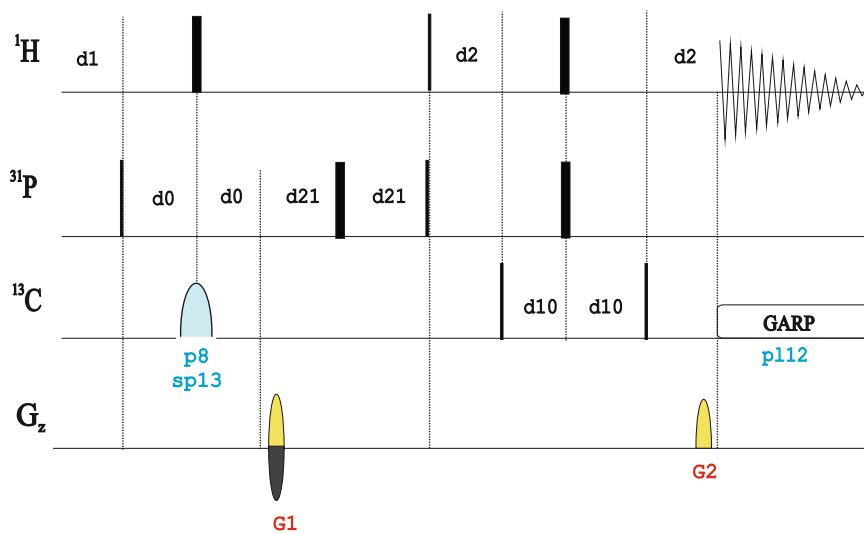
d1=1.5 s
d21=1/4J(PH)=22.7ms
(optimized cnst4=J(PH)=11Hz)
d2=1/2J(CH)=3.44ms
(optimized cnst2=J(CH)=145Hz)



na_hpcocetf3gp3d

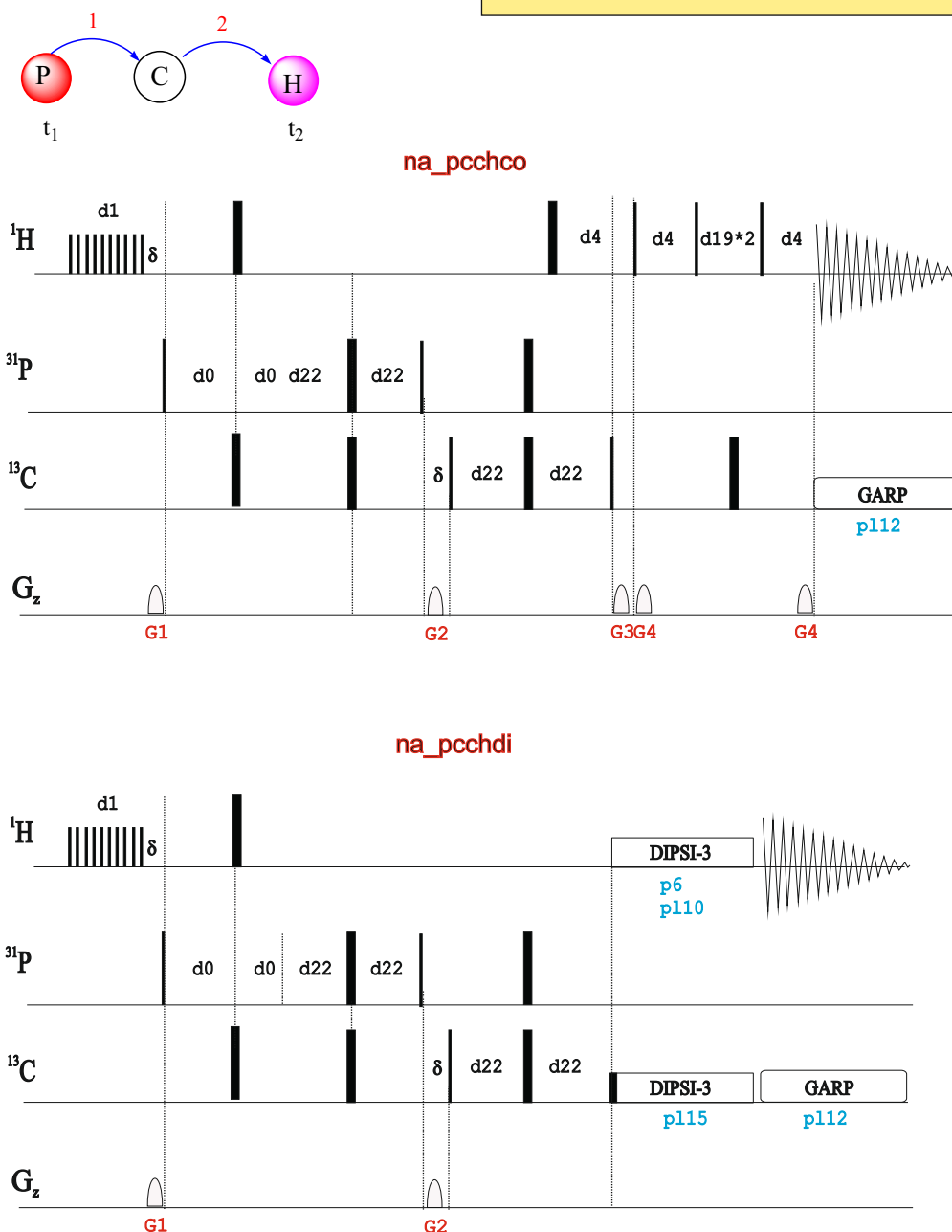


na_hpcocetf3gp3d



Experiment Description

References:



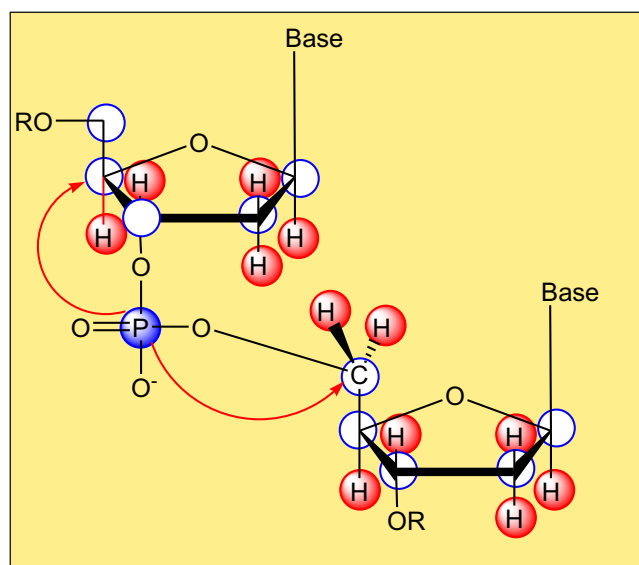
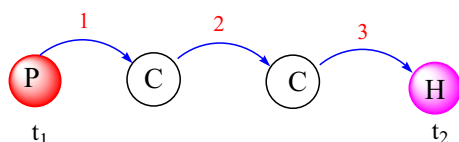
2D P(CC)H Experiment

Experiment Description

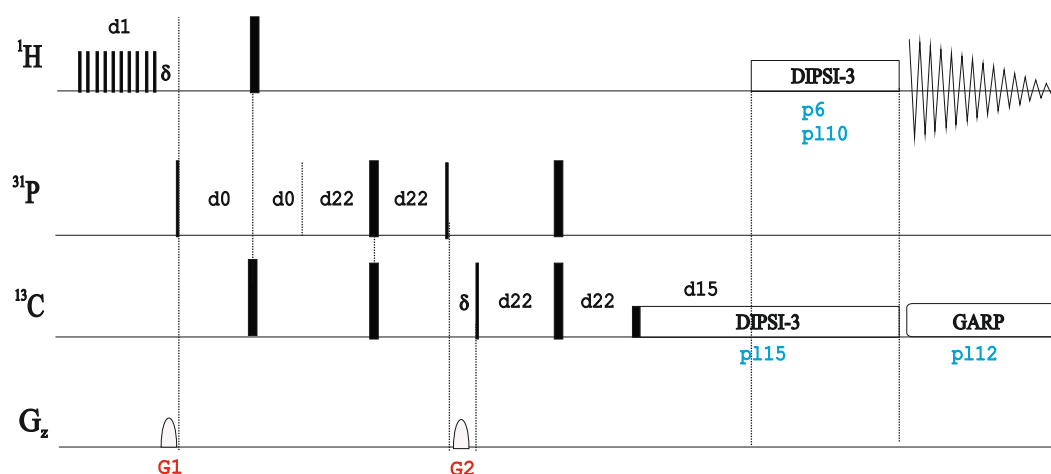
Extension of the P(C)H experiment in which after the P-to-C transfer, a C-C TOCSY transfer relays the information through all carbons of the ribose ring and, finally, a C-to-P cross-polarization scheme allows to detect all ribose protons

References:

S.S. Wijmenga, H.A. Heus, H.A.E. Leeuw, H. Hoppe, M. van der Graaf & C.W. Hilbers, J. Biomol. NMR 5, 82-86 (1995).



na_pcchdi2



d15: TOCSY mixing time (CC) [13 msec]
d22: 1/(4J(CP)) [12.5 msec]

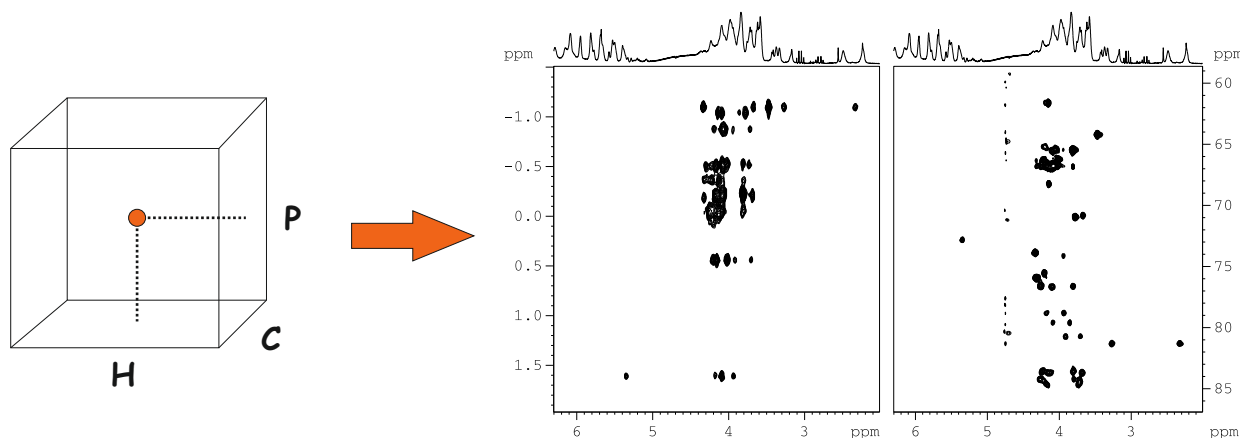
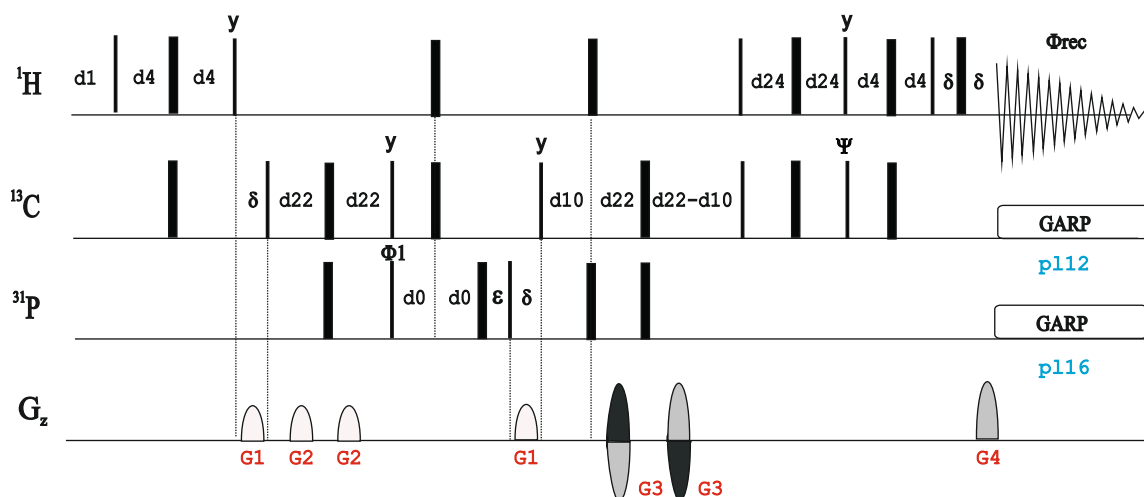
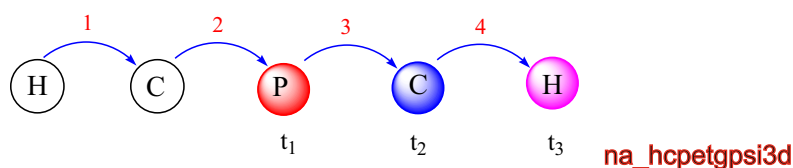
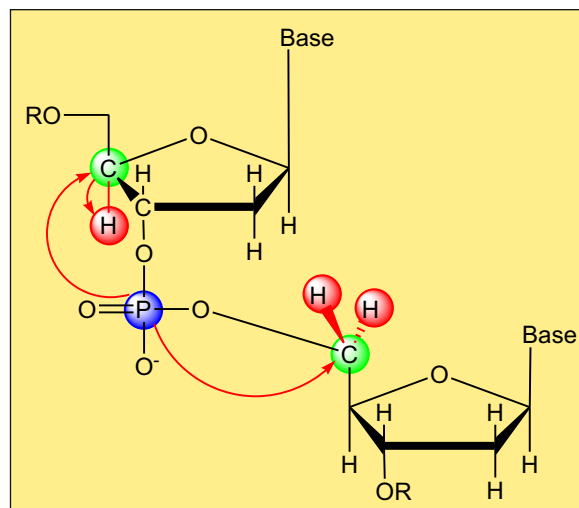
3D HCP Experiment

Experiment Description:

Out-and-back pulse scheme to correlate backbone P, C and H in a 3D experiment (94jacs6472).

References:

J.P. Marino, H. Schwalbe, C. Anklin, W. Bermel, D.M. Crothers & C. Griesinger, *J. Am. Chem. Soc.* 116, 6472 - 6473 (1994)

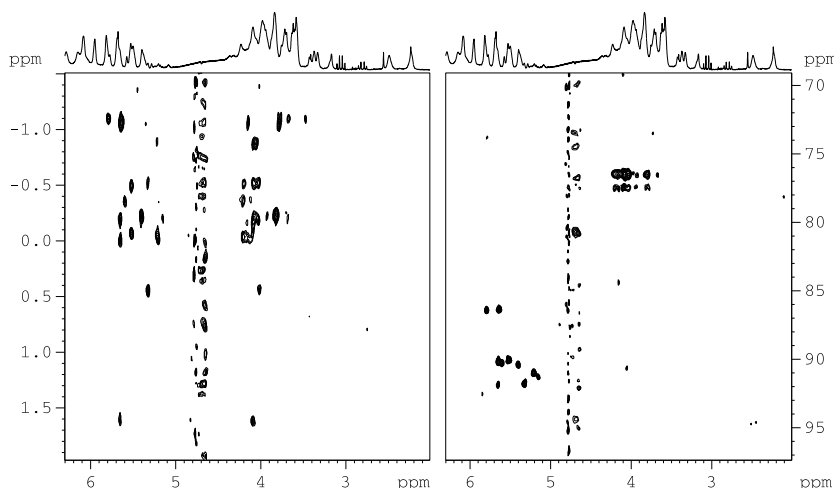
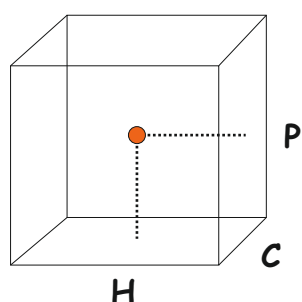


d1=1.5 s
d4=1/4J(CH)=1.6 ms (optimized cnst2=J(CH)=155Hz)
d22=1/8J(CP)=12.5ms (optimized cnst5=J(CP)=10Hz)
d24=0.8 ms (optimized cnst11=8)

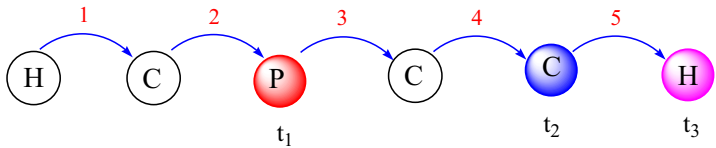
Experiment Description:

References:

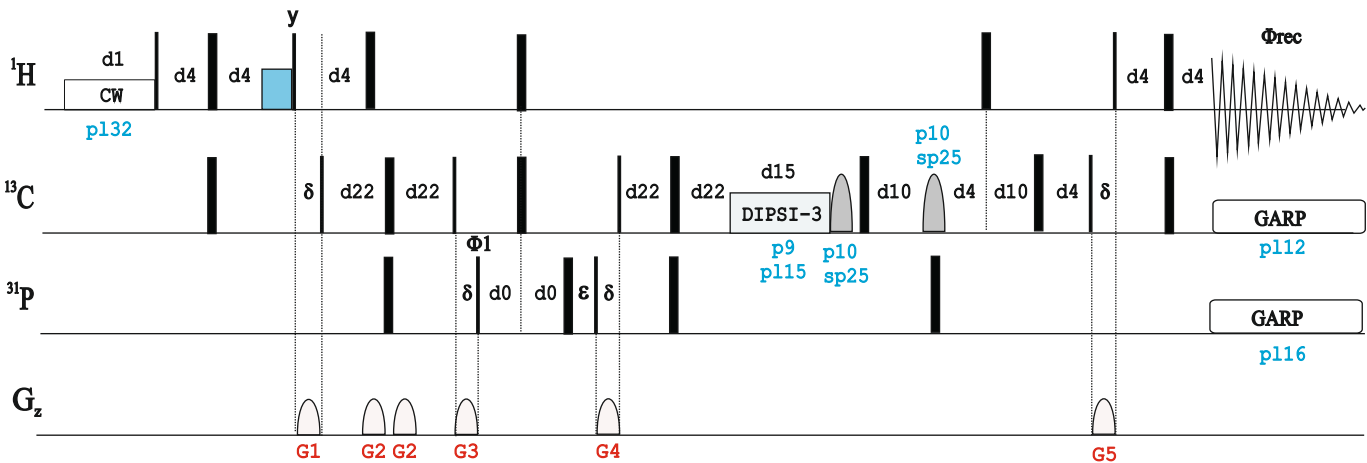
NMR Spectrum



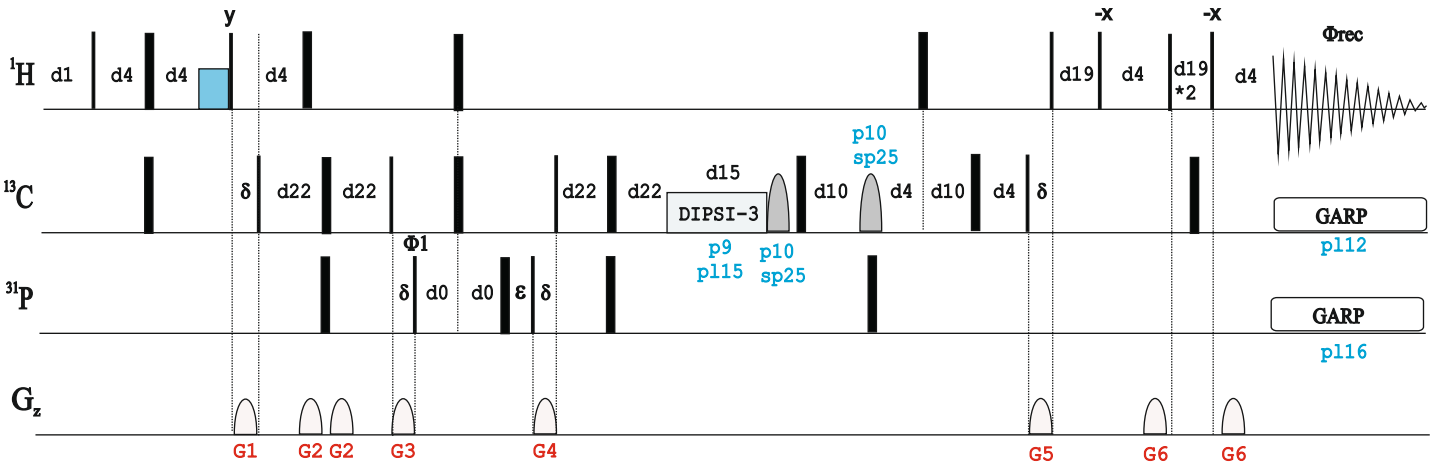
d1=1.5 s
d4=1/4J(CH)=1.6 ms
(optimized cnst2=J(CH)=155Hz)
d22=1/8J(CP)=12.5ms
(optimized cnst5=J(CP)=10Hz)
d15=CC TOCSY mixing=11 ms



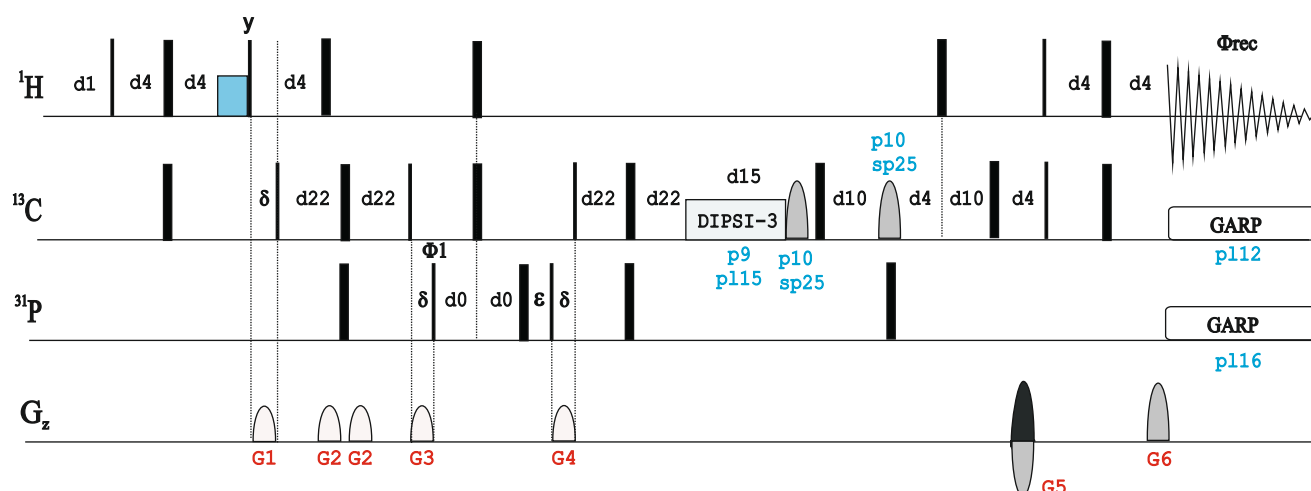
na_hcpdigp3d



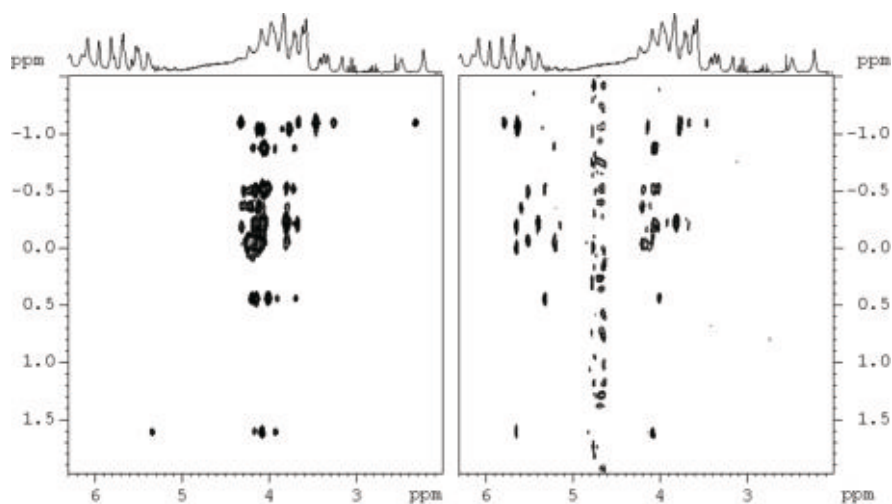
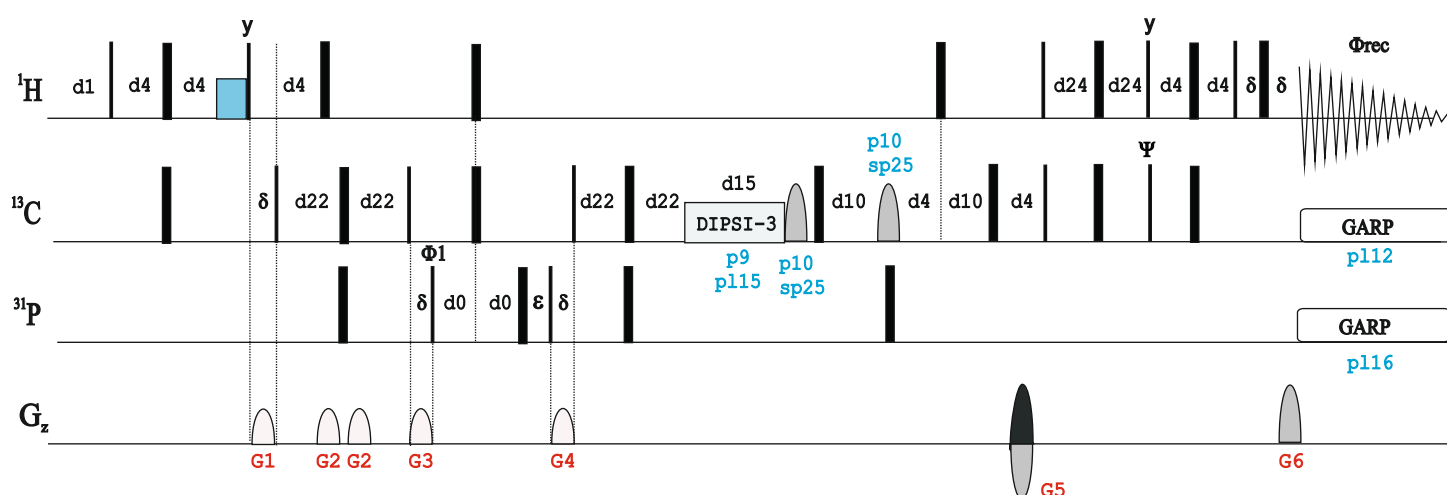
na_hcpdigpjr3d



na_hcpdietgp3d



na_hcpdietgpsi3d



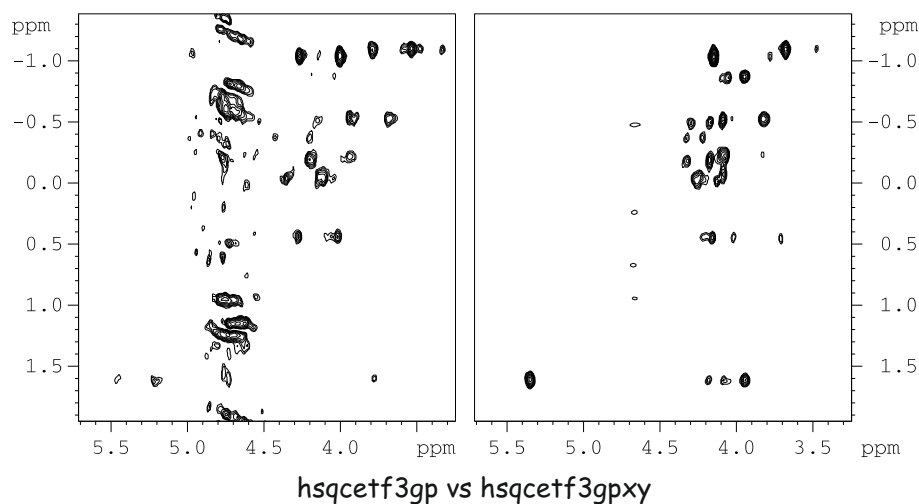
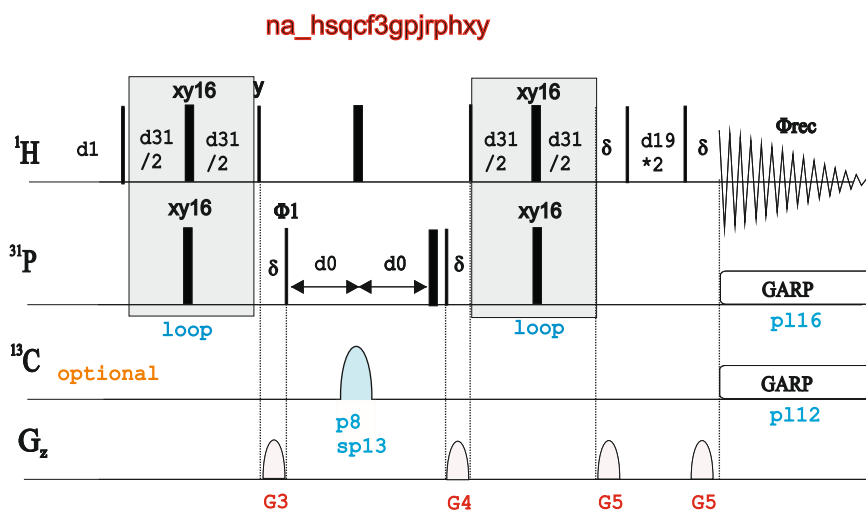
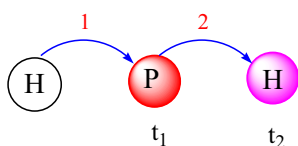
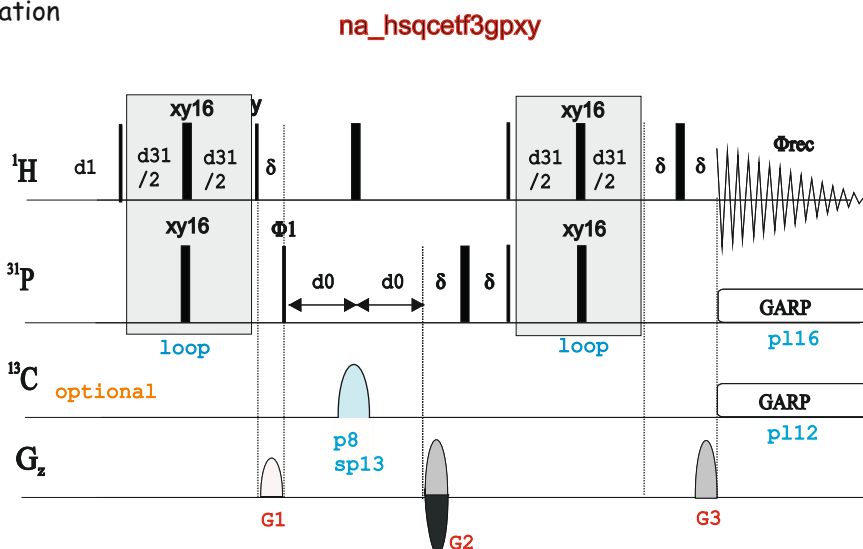
2D ^1H - ^{31}P HSQC using CPMG-XY16 Experiment

Experiment Description:

Modified version of the long-range optimized ^1H - ^{31}P HSQC experiment in which a CPMG-XY16 pulse train is included to avoid ^1H - ^1H modulation and exchange processes.

References:

B. Luy & J.P. Marino,
J. Am. Chem. Soc. 123,
11306-11307 (2001)



d1=1.5 s
d26=1/4J(PH)=12.5 ms
(optimized cnst4=J(PH)=J(20Hz)
d21=delay in CY16-CPMG=100us

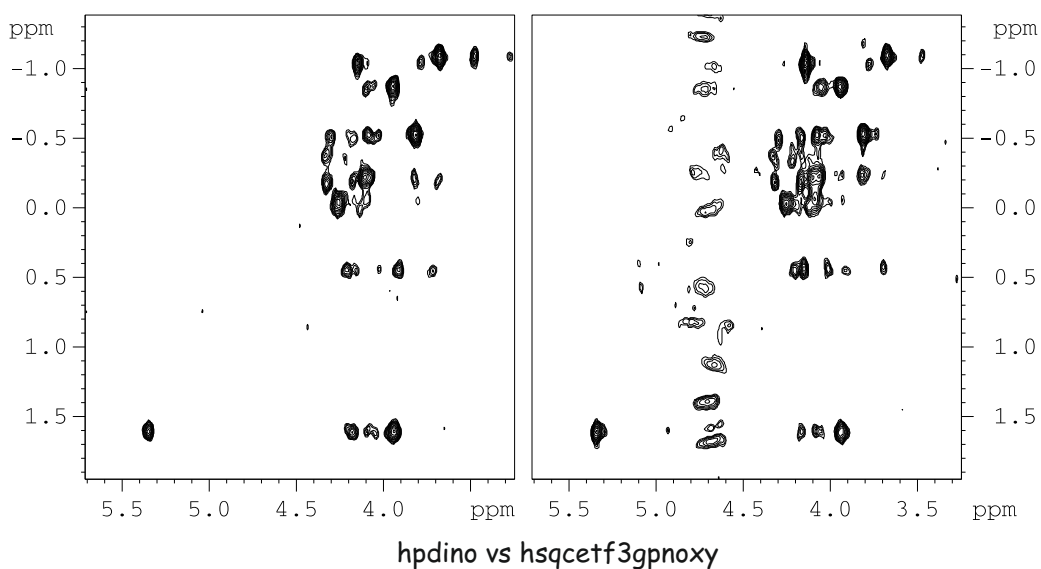
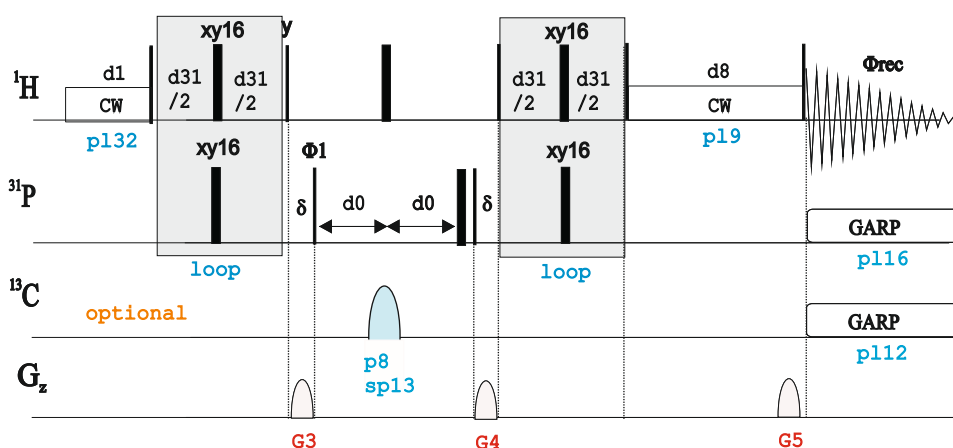
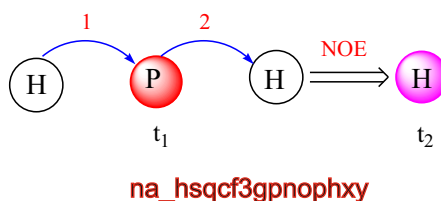
2D ^1H - ^{31}P HSQC-NOESY using CPMG-XY16 Experiment

Experiment Description:

Modified HSQC-NOESY pulse scheme involving CPMG-XY16 transfer during the INEPT periods.

References:

B. Luy & J.P. Marino,
J. Am. Chem. Soc. 123,
11306-11307 (2001)



d1=1.5 s
d26=1/4J(PH)=12.5ms
(optimized cnst4=J(PH)=20Hz)
d21=delay in CY16-CPMG=100us
d8=NOE mixing time

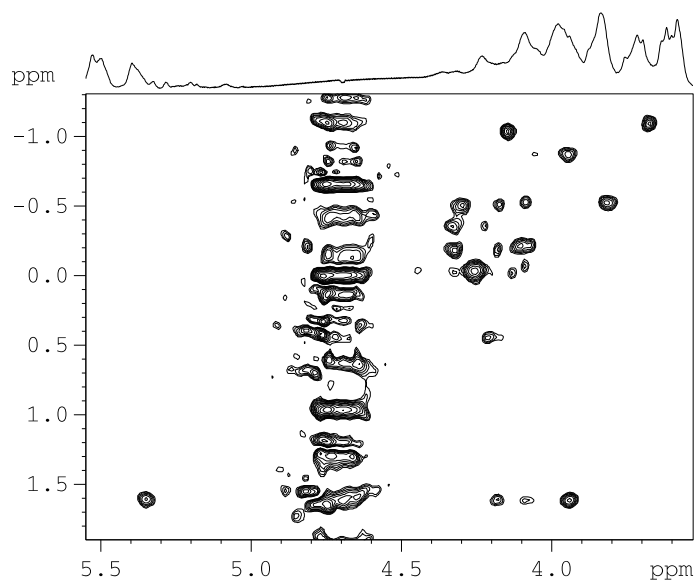
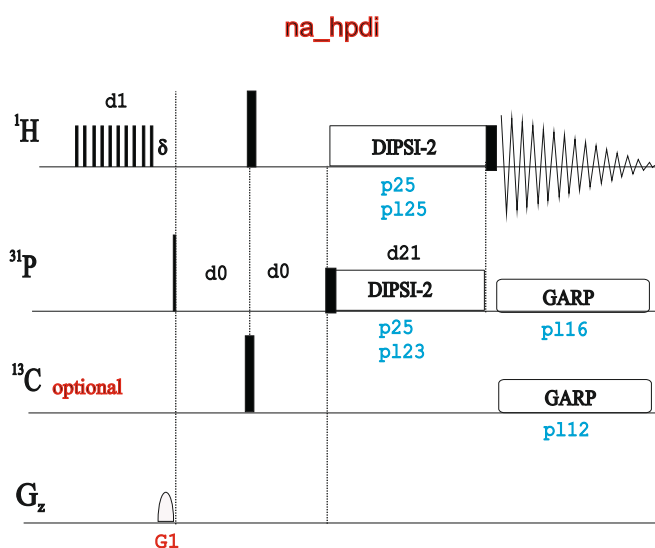
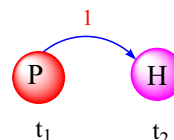
2D ^1H - ^{31}P HeteroTOCSY Experiment

Experiment Description:

Experiment to correlate ^{31}P and ^1H chemical shifts that uses Heteronuclear cross-polarization for magnetization transfer from ^{31}P to ^1H via $J(\text{PH})$.

References:

G.W. Kellogg, J. Magn. Reson. 98, 176-182 (1992)



d1=1.5 s
d21=1/6J(PH)=20 ms
(heteroTOCSY mixing)

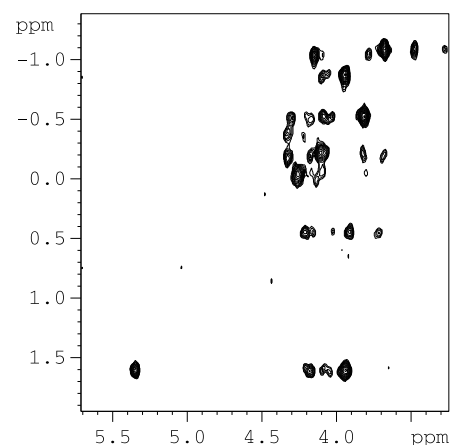
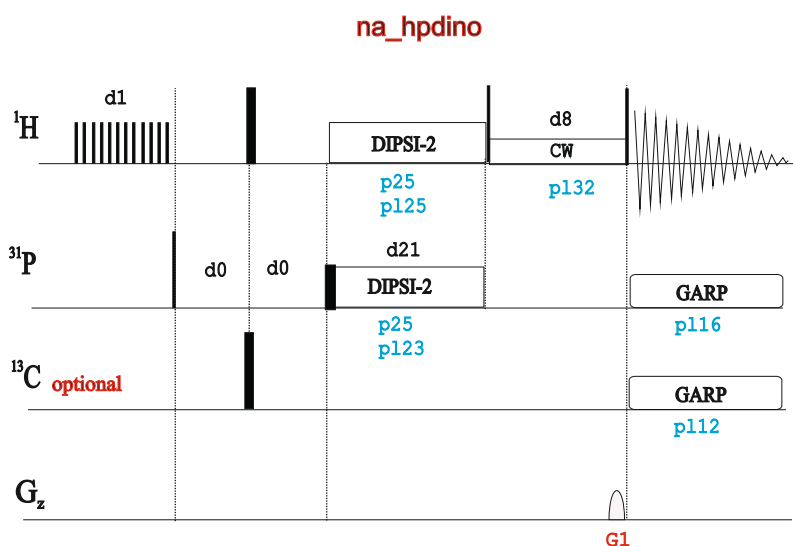
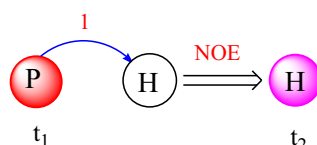
2D HeteroTOCSY-NOESY Experiment

Experiment Description

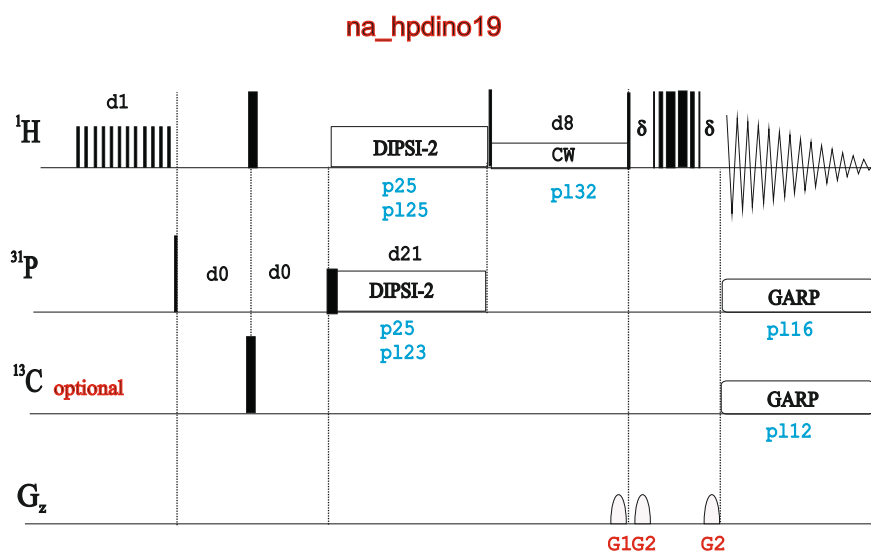
2D Cross-polarization version of a ^{31}P -edited NOESY experiment.

References:

G.W. Kellogg, A.A. Szewczak & P.B. Moore, J. Am. Chem. Soc. 114, 2727-2728 (1992)



d1=1.5 s
d21=1/6J(PH)=20 ms
(heteroTOCSY mixing)



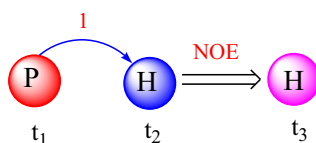
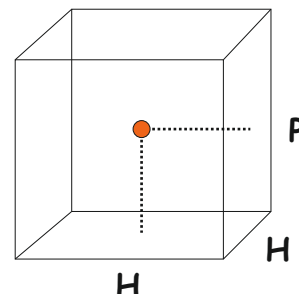
3D HeteroTOCSY-NOESY Experiment

Experiment Description

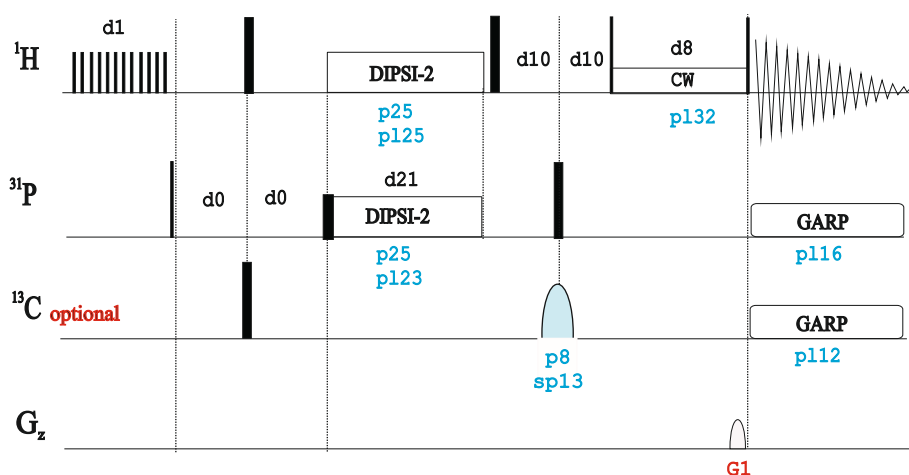
3D Cross-polarization version of a P-edited 1H-1H NOESY experiment that provides a 3D P,H,H map.

References:

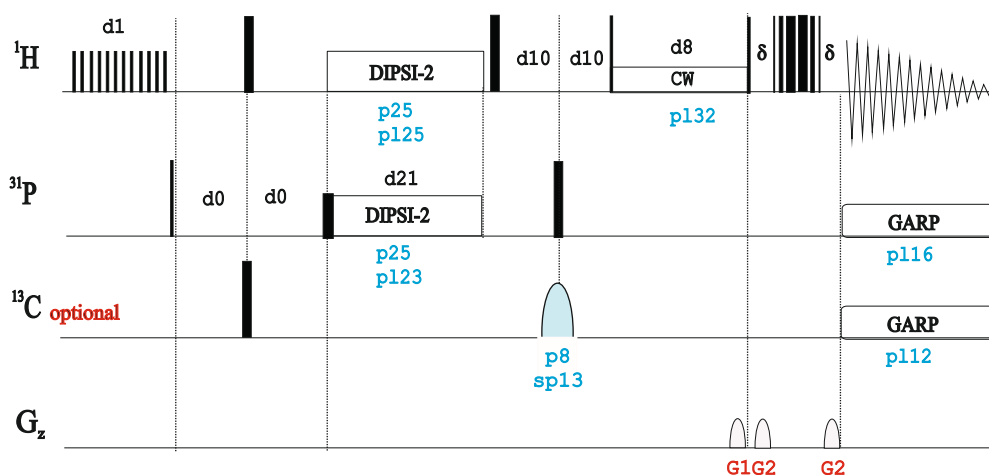
G.W. Kellogg & B.I. Schweitzer, J. Biomol. NMR 3, 577-595 (1993)



na_hpdino3d



na_hpdino193d



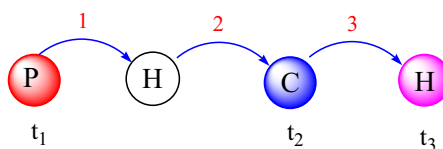
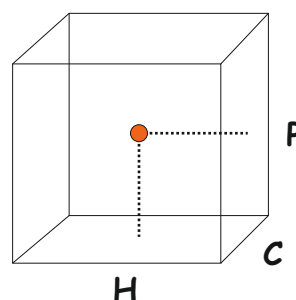
3D HeteroTOCSY-COSY Experiment

Experiment Description

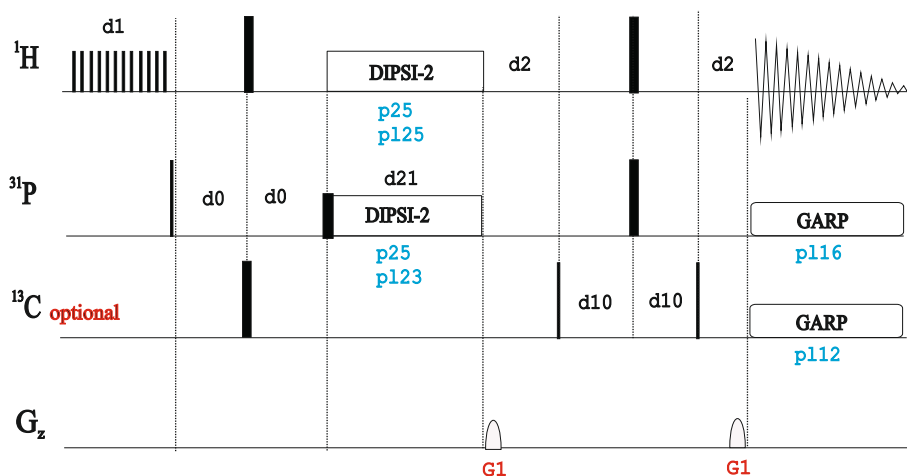
3D version of the PHCH experiment that uses cross-polarization for P-to-H transfer. The experiment provides a 3D correlation P;C;H map.

References:

G. Varani, F. Aboul-ela, F. Allain & C.C. Gubser,
J. Biomol. NMR 5 315-320 (1995)



na_hpdico3d

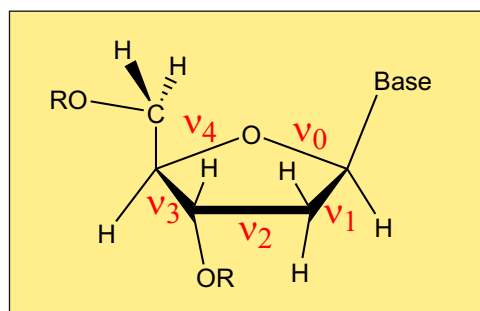
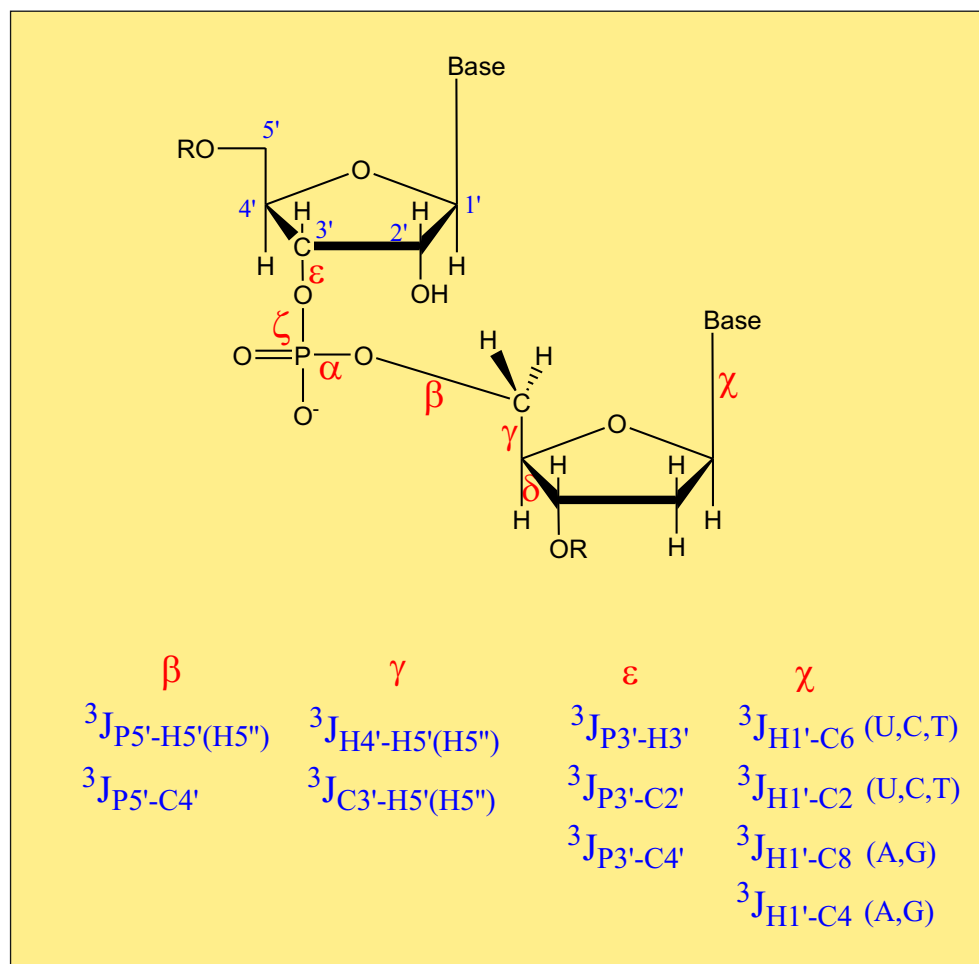


BRUKER PULSE PROGRAM CATALOGUE

NMRGuide

NUCLEIC-ACID NMR EXPERIMENTS TO MEASURE J

Important Dihedral angles in nucleic acids:



2D HSQC Experiment for measuring $J(\text{CH})$

Experiment Description

Modified sensitivity-improved HSQC pulse scheme for the stereospecific assignment of $\text{H5'}/\text{H5''}$ diastereotopic protons in NAs by measurement of homonuclear $J(\text{H4'}/\text{H5'})$ and heteronuclear $J(\text{C4'}/\text{H5'})$ coupling constants.

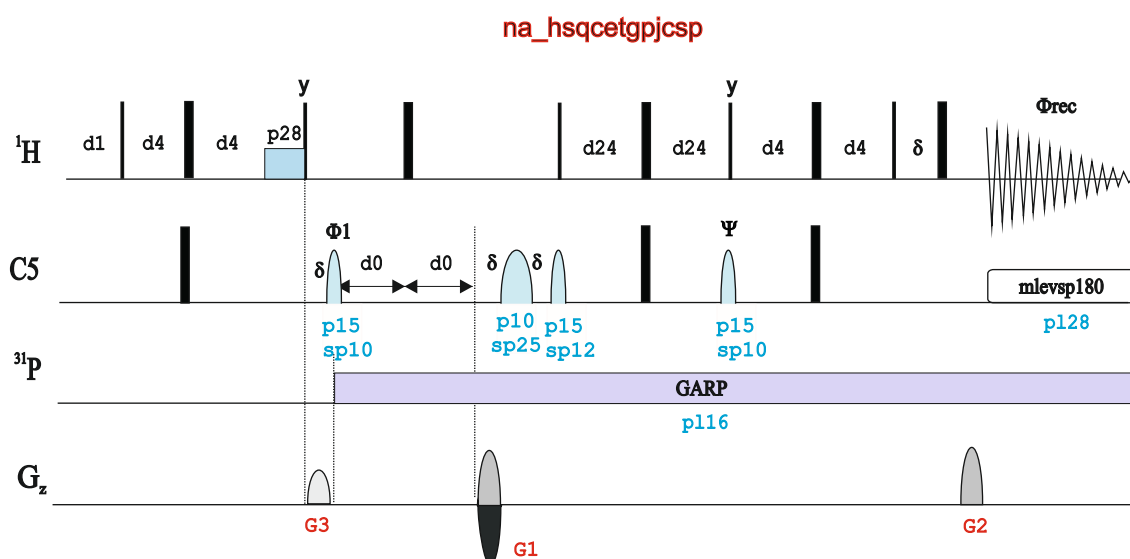
Also useful for measurement of $J(\text{C2'}/\text{H1'})$ via N in $^{13}\text{C}/^{15}\text{N}$ labeled NAs

References:

J.P. Marino, H. Schwalbe, S.J. Glaser, C. Griesinger, J. Am. Chem. Soc. 118, 4388 - 4395 (1996).

Related Experiments:

Also see the original 2D HSQC experiment.



p15=2 ms (Q5/Q5tr)
p10=2 ms (Q3)
p128= Selective C5 decoupling

3D H(C)CH-E.COSY Experiment

Experiment Description:

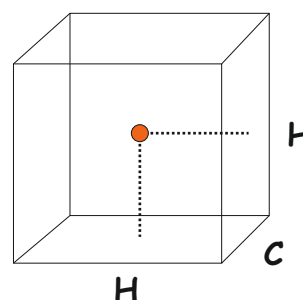
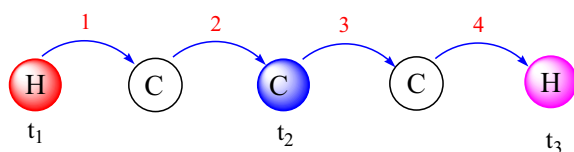
Modified HCCH-COSY pulse scheme to measure $J(\text{CH})$ in ribose rings.

References:

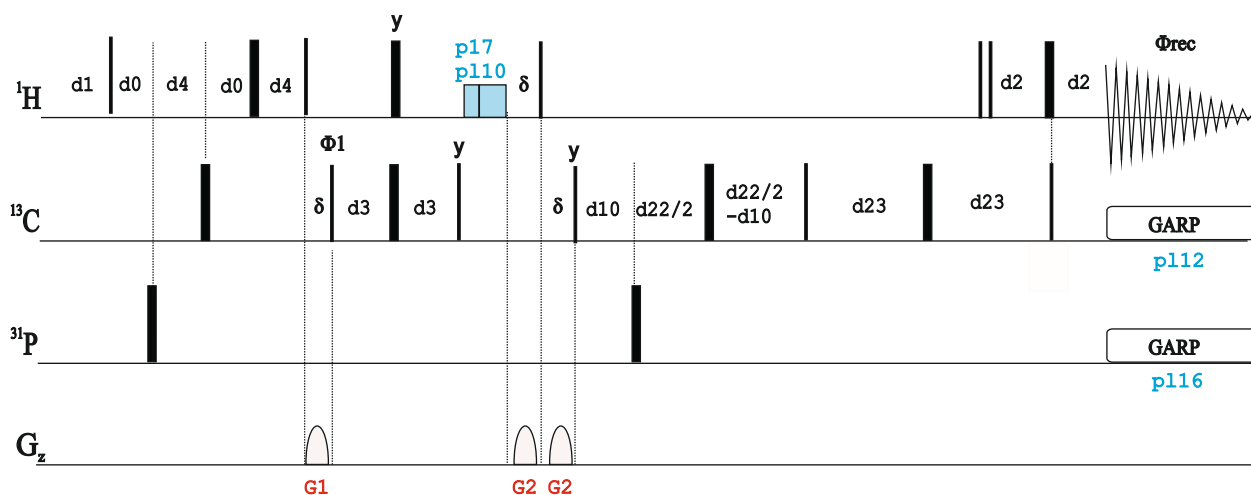
1. L.E. Kay, G.Y. Xu, A.U. Singer, D.R. Muhandiram & J. D. Forman-Kay J. Magn. Reson. B 101, 333 - 337 (1993)
2. H. Schwalbe, J.P. Marino, G.C. King, R. Wechselberger, W. Bermel & C. Griesinger, J. Biomol. NMR 4, 631 - 644 (1994)

Related Experiments:

Also see other HCCH-type experiments



na_hcchecgp3d



$d2 = 1/2J(\text{CH})$
 $d4 = 1/4J(\text{CH}) = 1.6\text{ms}$
 $d3 = 1/4J(\text{CH})$
 $d23 = 1/8J(\text{CC}) = 3.1\text{ms}$
 $d22 = \text{Constant-time C period.}$
 For all correlations $3/4J(\text{CC}) = 18.8\text{ms}$
 For C1' and C5' $1/2J(\text{CC}) = 12.5\text{ms}$

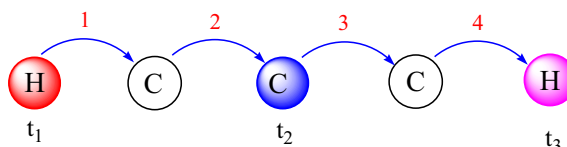
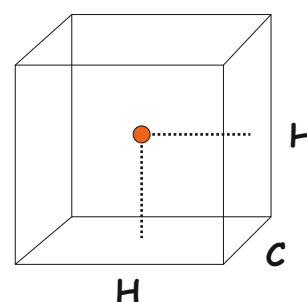
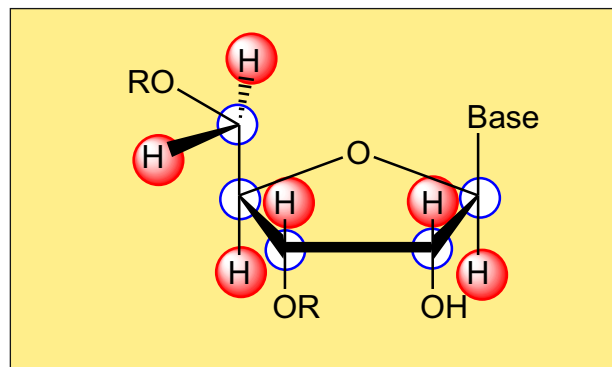
3D H(C)CH-TOCSY Experiment

Experiment Description

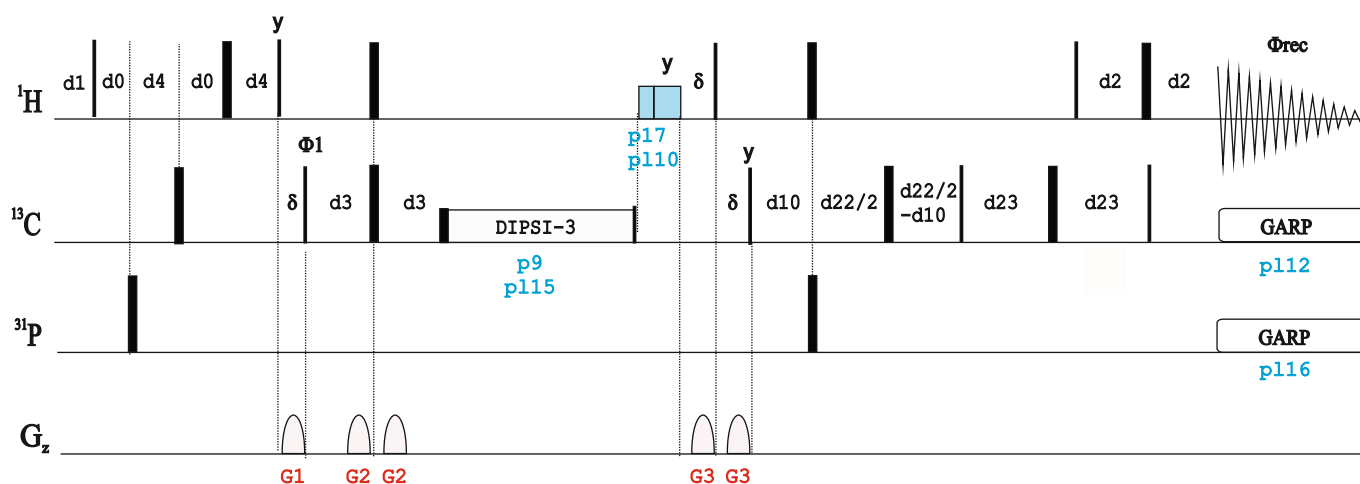
Specific HCCH-TOCSY experiment to identify all ^1H and ^{13}C nuclei belonging to the same sugar ring in ^{13}C -labeled NAs. Alternative to classical COSY and TOCSY experiment. Also see other HCCH-COSY and HCCH-TOCSY experiments.

References:

- L.E. Kay, G.Y. Xu, A.U. Singer, D.R. Muhandiram & J. D. Forman-Kay J. Magn. Reson. B 101, 333 - 337 (1993)
- H. Schwalbe, J.P. Marino, S.J. Glaser & C. Griesinger, J. Am. Chem. Soc. 117, 7251 - 7252 (1995)
- J.P. Marino, H. Schwalbe, S.J. Glaser & C. Griesinger, J. Am. Chem. Soc. 118, 4388 - 4395 (1996)
- S.J. Glaser, H. Schwalbe, J.P. Marino & C. Griesinger, J. Magn. Res. B 112, 160 - 180 (1996).



na_hochfwdigp3d



$d2 = 1/2J(\text{CH})$
 $d4 = 1/4J(\text{CH}) = 1.6\text{ms}$
 $d3 = 1/4J(\text{CH})$
 $d23 = 1/8J(\text{CC}) = 3.1\text{ms}$
 $d22 = \text{Constant-time C period.}$
 For all correlations $3/4J(\text{CC}) = 18.8\text{ms}$
 For C1' and C5' $1/2J(\text{CC}) = 12.5\text{ms}$

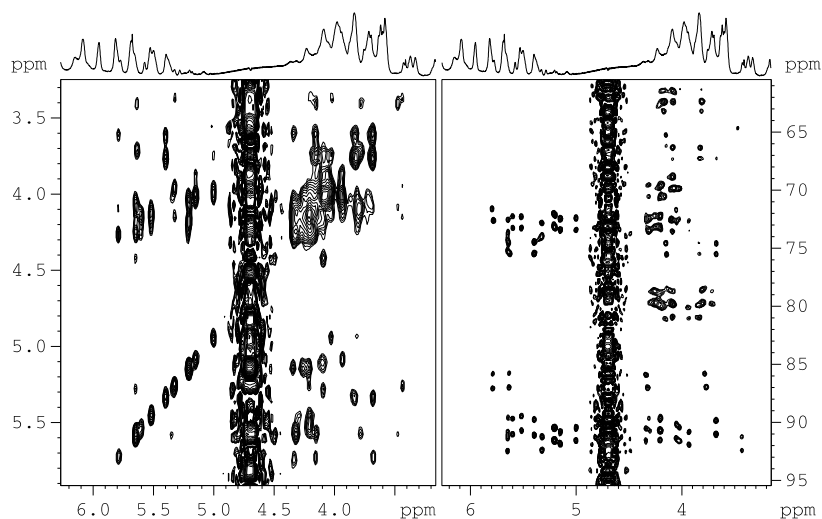
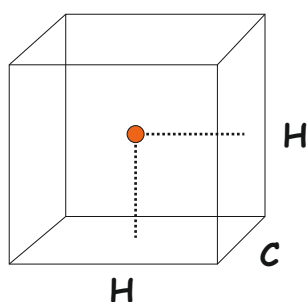
3D H(C)CH-TOCSY E.COSY Experiment

Experiment Description:

E.COSY version of the HCCH-TOCSY experiment to measure $J(H4'H5')$ coupling constants (96jacs4388)

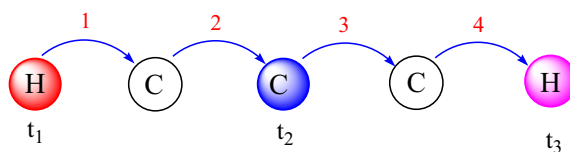
References:

L.E. Kay, G.Y. Xu, A.U. Singer, D.R. Muhandiram & J. D. Forman-Kay J. Magn. Reson. B 101, 333 - 337 (1993)
H. Schwalbe, J.P. Marino, S.J. Glaser & C.Griesinger, J. Am. Chem. Soc. 117, 7251 - 7252 (1995)
J.P. Marino, H. Schwalbe, S.J. Glaser & C.Griesinger, J. Am. Chem. Soc. 118, 4388 - 4395 (1996)
S.J. Glaser, H. Schwalbe, J.P. Marino & C. Griesinger, J. Magn. Res. B 112, 160 - 180 (1996)

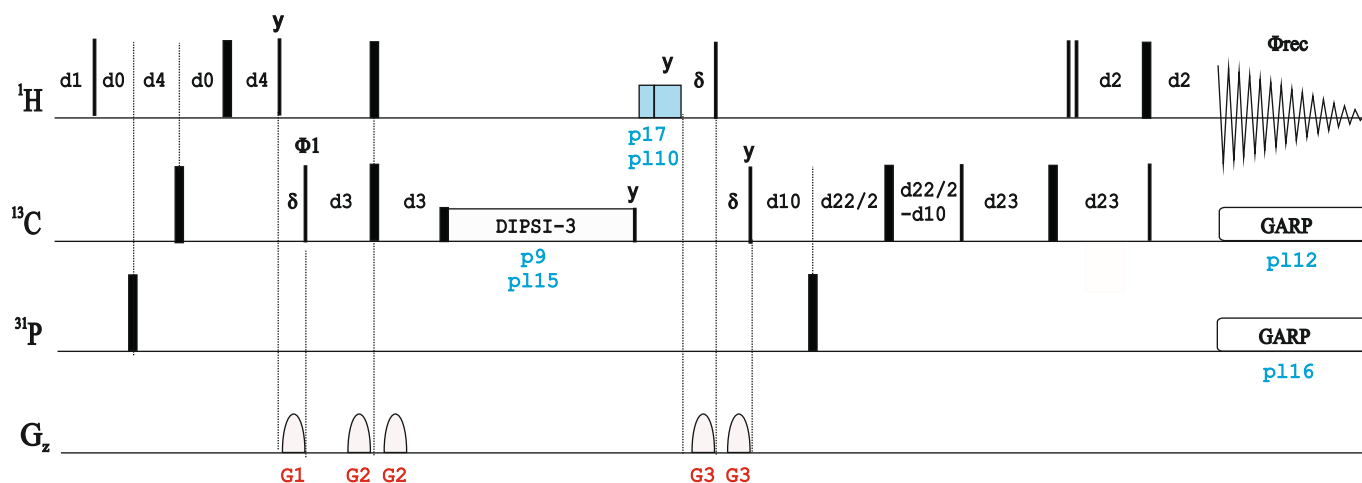


E.COSY pattern
in the C dimension
of the 2D HC plane

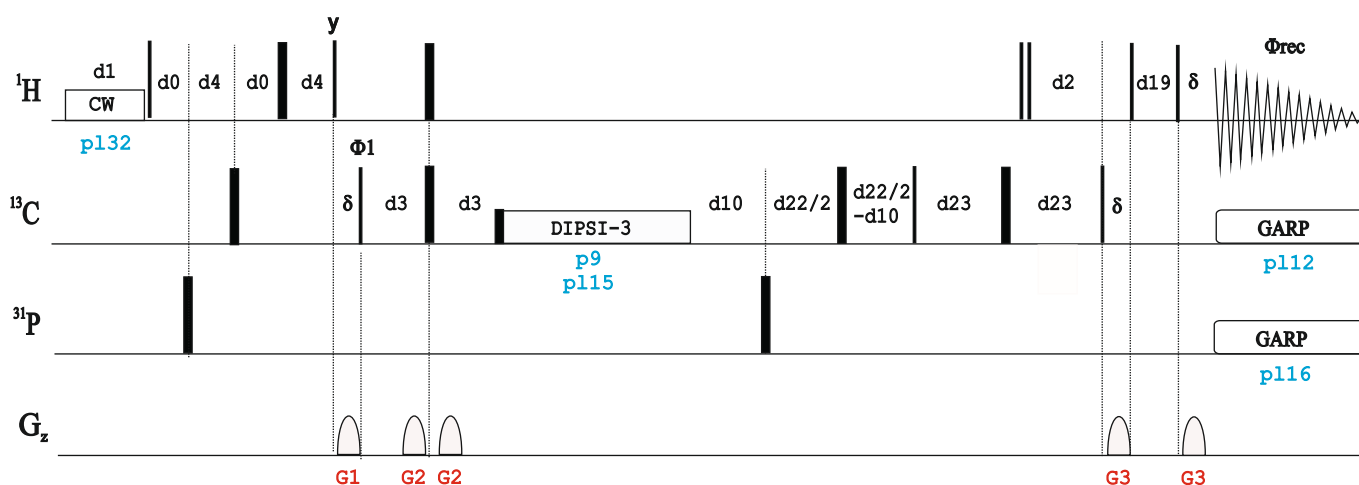
d1=1.5s
d3=1/4J(CH)=1.55ms
d4=1/4J(CH)=1.56ms
(optimized cnst2=160Hz)
d22=CT(C)=7.6ms
d23=1/8J(CC)=3.1ms
(optimized for cnst8=38Hz)
l1=2 for CC TOCSY=9.2ms using p9=26us



na_hcchfwdiecg3d



na_hcchfwdiecgpr3d



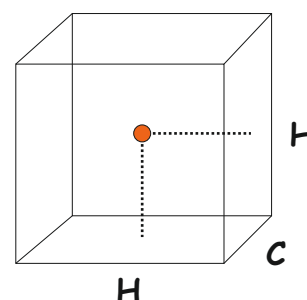
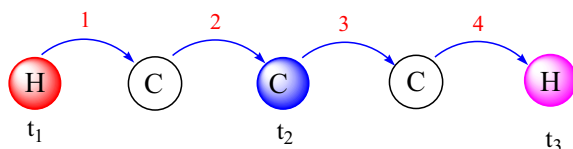
Forward-directed quantitative 3D H(C)CH-TOCSY Experiment

Experiment Description:

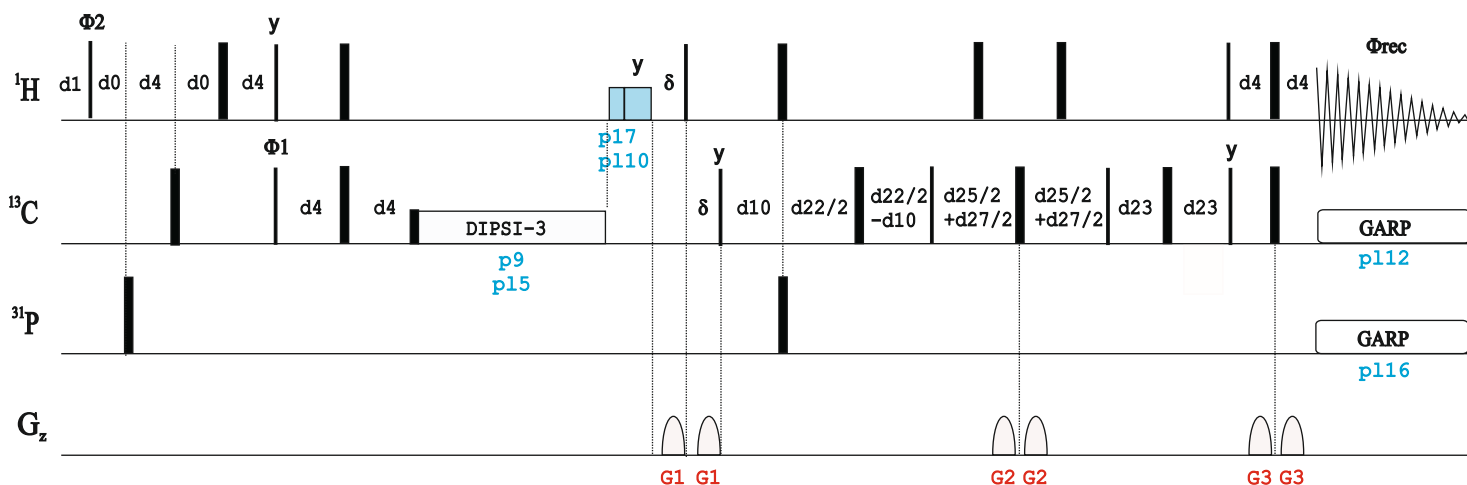
Modified HCCH-TOCSY version to measure $J(\text{HH})$ and $J(\text{CH})$ coupling constants

References:

1. I.C. Felli, C. Richter, C. Griesinger & H. Schwalbe, J. Am. Chem. Soc. 121, 1956 - 1957 (1999)
2. C. Richter, C. Griesinger, I.C. Felli, P.T. Cole, G. Varani & H. Schwalbe, J. Biomol. NMR 15, 241 - 250 (1999)



na_ghcchfwdigp3d



$d4 = 1/4J(\text{CH}) = 1.6\text{ms}$
 $d23 = 1/8J(\text{CC}) = 3.1\text{ms}$
 $d22 = \text{Constant-time C period.}$
 For all correlations $3/4J(\text{CC}) = 18.8\text{ms}$
 For C1' and C5' $1/2J(\text{CC}) = 12.5\text{ms}$
 $d25 = \text{development of cross-correlated relaxation} = 25\text{ms}$

 For reference experiment $d27 = 1/2J(\text{CH}) = 3.1\text{ms}$
 For cross-peak experiment $d27 = 0$

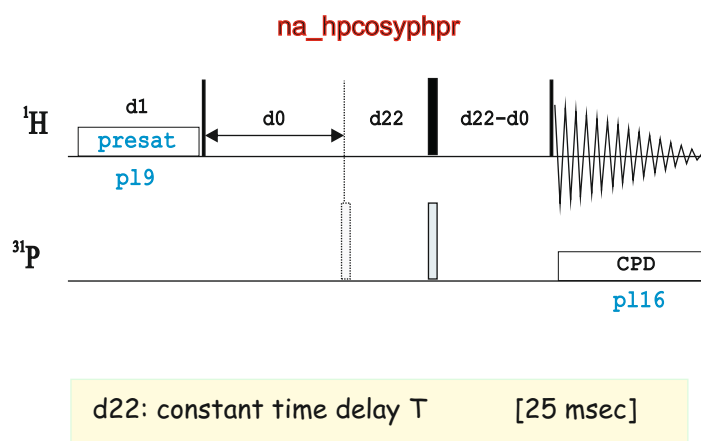
2D Constant-time HH-{31P} COSY Experiment

Experiment Description

Constant-time 1H-1H COSY experiment for the measurement of J(H3-P) coupling constants in NAs (98jmr164-134). Two experiments are recorded varying the position of the 180° 31P pulse.

References:

G.M. Clore, E.C. Murphy, A.M. Gronenborn & A.Bax, J. Magn. Res. 134, 164 - 167 (1998)

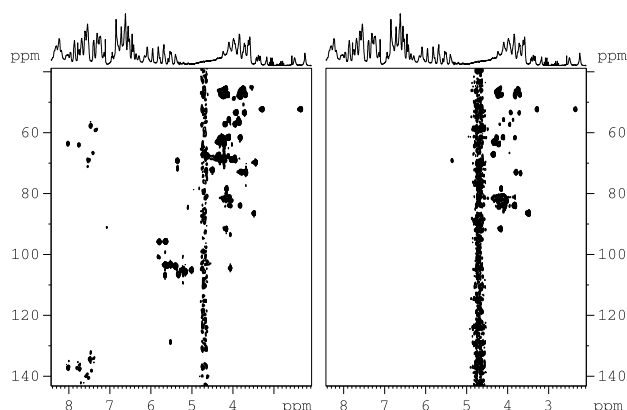
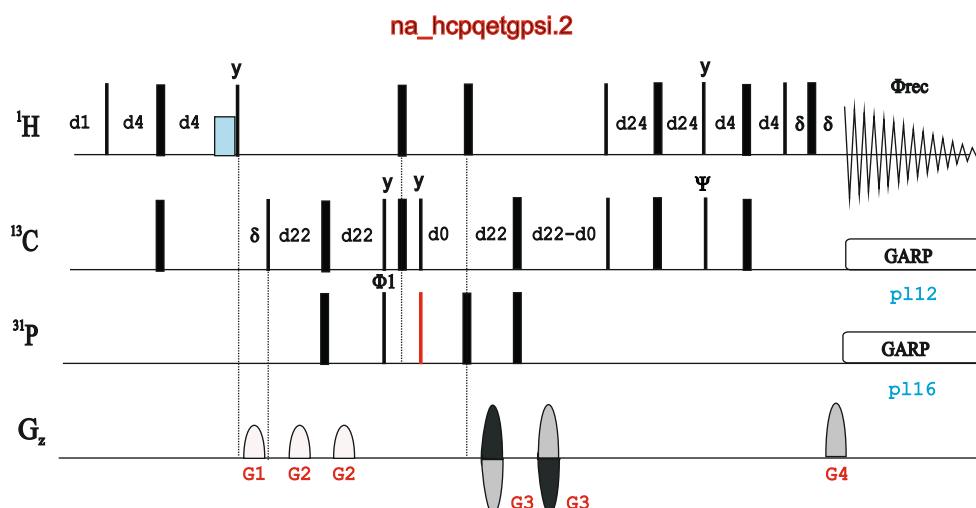
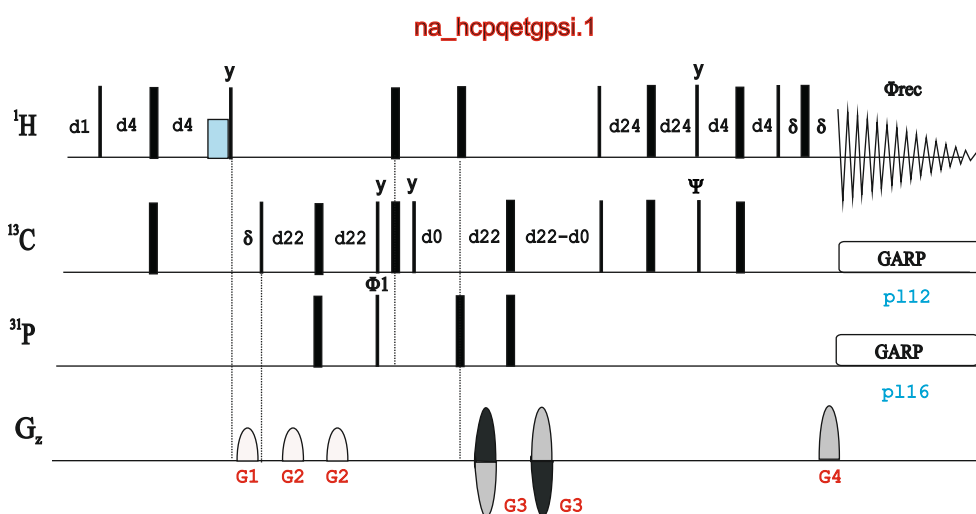
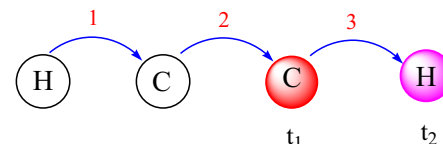


2D quantitative HC(P) Experiment

Experiment Description:

Modified 2D version of the put-and-back HCP experiment to measure $J(\text{CP})$ coupling constants. Independent reference-peak and a cross-peak experiment are separately recorded.

C. Richter, B. Reif, K. Woerner, S. Quant, J.P. Marino, J.W. Engels,
C.Griesinger & H.Schwalbe, J. Biomol. NMR 12, 223-230 (1998)



$d1=1.5s$
 $d4=1/4J(\text{CH})=1.6ms$
 $cnst2=J(\text{CH})$
 $cnst5=J(\text{CP})$

$d22=CT(1/J(\text{CC})$ for $J(\text{CC})=40\text{Hz}$ and
 $1/4J(\text{C4}'-\text{P})=12.5ms$
 $1/4J(\text{C5}'-\text{P})=25ms$

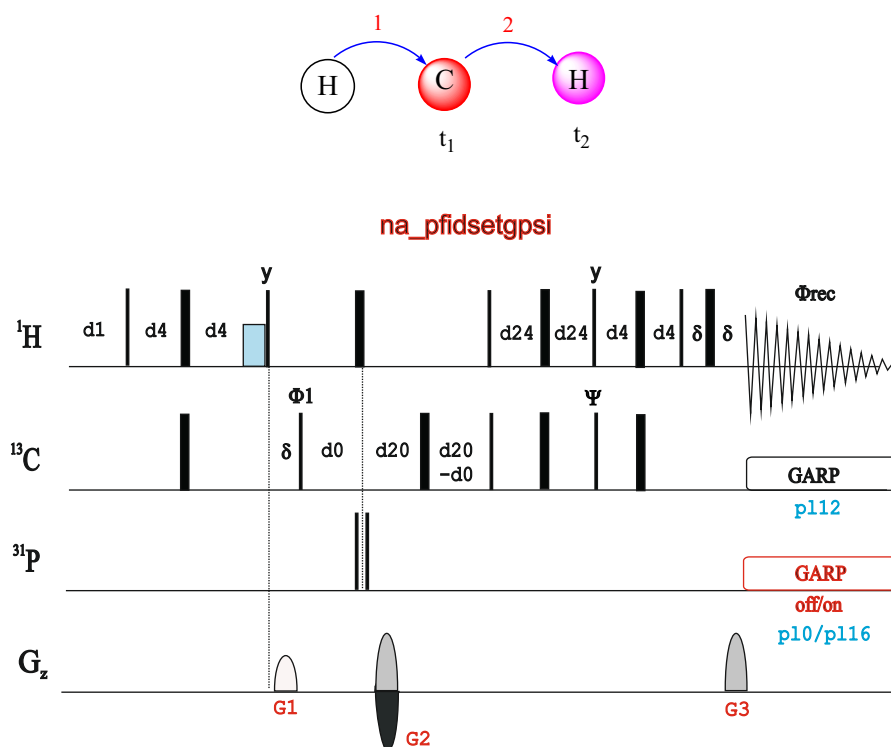
2D P-FIDS Experiment

Experiment Description:

Modified HSQC experiment to measure $J(\text{HP})$ and $J(\text{CP})$ in Nas.
Two experiments are recorded with optional ^{31}P decoupling during ^1H acquisition.

References:

1. H. Schwalbe, W. Samstag, J.W. Engels, W. Bermel & C. Griesinger, J. Biomol. NMR 3, 479 - 486 (1993)
2. H. Schwalbe, J.P. Marino, G.C. King, R. Wechselberger, W. Bermel & C. Griesinger, J. Biomol. NMR 4, 631 - 644 (1994)



$d4 = 1/4J(\text{CH})$
 $d24$ optimized as a function of CH_n multiplicity
 $d20 = 1/2J(\text{CC}) = 12.5\text{ms}$ or $3/2J(\text{CC}) = 37.5\text{ms}$

