

NMR OF NUCLEIC ACIDS

Radovan Fiala

Literature

Books

Saenger, W., Principles of Nucleic Acid Structure, Springer 1984.

Bloomfield, V. A., Crothers, D. M., Tinoco, I., Nucleic Acids, Structures, Properties, and Functions, Univ. Sci. Books, 2000.

Wuthrich, K., NMR of Proteins and Nucleic Acids, Wiley, 1986.

Review articles

Can be downloaded from <https://web.ncbr.muni.cz/~fiala/>

Bowater, R. P., Waller, Z. AE., DNA Structure, In: eLS. John Wiley & Sons, Chichester, 2014.

Wijmenga, S. S., van Buuren, B. N. M., The use of NMR methods for conformational studies of nucleic acids, Progr. NMR Spect. 32, (1998), 287-387.

Furtig, B. et al., NMR of RNA, ChemBioChem 4 (2003), 936-962.

equipment, and to Dr. G. E. R. Deacon and the captain and officers of R.R.S. *Discovery II* for their part in making the observations.

¹ Young, F. B., Gerrard, H., and Jevons, W., *Phil. Mag.*, **40**, 149 (1920).

² Longuet-Higgins, M. S., *Mon. Not. Roy. Astro. Soc., Geophys. Supp.*, **5**, 285 (1949).

³ Von Arx, W. S., Woods Hole Papers in Phys. Oceanogr. Meteor., **11** (3) (1950).

⁴ Ekman, V. W., *Arkiv. Mat. Astron. Fysik. (Stockholm)*, **2** (11) (1905).

MOLECULAR STRUCTURE OF NUCLEIC ACIDS

A Structure for Deoxyribose Nucleic Acid

WE wish to suggest a structure for the salt of deoxyribose nucleic acid (D.N.A.). This structure has novel features which are of considerable biological interest.

A structure for nucleic acid has already been proposed by Pauling and Corey¹. They kindly made their manuscript available to us in advance of publication. Their model consists of three intertwined chains, with the phosphates near the fibre axis, and the bases on the outside. In our opinion, this structure is unsatisfactory for two reasons: (1) We believe that the material which gives the X-ray diagrams is the salt, not the free acid. Without the acidic hydrogen atoms it is not clear what forces would hold the structure together, especially as the negatively charged phosphates near the axis will repel each other. (2) Some of the van der Waals distances appear to be too small.

Another three-chain structure has also been suggested by Fraser (in the press). In his model the phosphates are on the outside and the bases on the inside, linked together by hydrogen bonds. This structure as described is rather ill-defined, and for this reason we shall not comment on it.

We wish to put forward a radically different structure for the salt of deoxyribose nucleic acid. This structure has two helical chains each coiled round the same axis (see diagram). We have made the usual chemical assumptions, namely, that each chain consists of phosphate di-ester groups joining β -D-deoxyribofuranose residues with 3',5' linkages. The two chains (but not their bases) are related by a dyad perpendicular to the fibre axis. Both chains follow right-handed helices, but owing to the dyad the sequences of the atoms in the two chains run in opposite directions. Each chain loosely resembles Furburg's² model No. 1; that is, the bases are on the inside of the helix and the phosphates on the outside. The configuration of the sugar and the atoms near it is close to Furburg's 'standard configuration', the sugar being roughly perpendicular to the attached base. There

This figure is purely diagrammatic. The two ribbons symbolize the two phosphate-sugar chains, and the horizontal rods the pairs of bases holding the chains together. The vertical line marks the fibre axis

is a residue on each chain every 3.4 Å. in the z-direction. We have assumed an angle of 36° between adjacent residues in the same chain, so that the structure repeats after 10 residues on each chain, that is, after 34 Å. The distance of a phosphorus atom from the fibre axis is 10 Å. As the phosphates are on the outside, cations have easy access to them.

The structure is an open one, and its water content is rather high. At lower water contents we would expect the bases to tilt so that the structure could become more compact.

The novel feature of the structure is the manner in which the two chains are held together by the purine and pyrimidine bases. The planes of the bases are perpendicular to the fibre axis. They are joined together in pairs, a single base from one chain being hydrogen-bonded to a single base from the other chain, so that the two lie side by side with identical z-co-ordinates. One of the pair must be a purine and the other a pyrimidine for bonding to occur. The hydrogen bonds are made as follows: purine position 1 to pyrimidine position 1; purine position 6 to pyrimidine position 6.

If it is assumed that the bases only occur in the structure in the most plausible tautomeric forms (that is, with the keto rather than the enol configurations) it is found that only specific pairs of bases can bond together. These pairs are: adenine (purine) with thymine (pyrimidine), and guanine (purine) with cytosine (pyrimidine).

In other words, if an adenine forms one member of a pair, on either chain, then on these assumptions the other member must be thymine; similarly for guanine and cytosine. The sequence of bases on a single chain does not appear to be restricted in any way. However, if only specific pairs of bases can be formed, it follows that if the sequence of bases on one chain is given, then the sequence on the other chain is automatically determined.

It has been found experimentally^{3,4} that the ratio of the amounts of adenine to thymine, and the ratio of guanine to cytosine, are always very close to unity for deoxyribose nucleic acid.

It is probably impossible to build this structure with a ribose sugar in place of the deoxyribose, as the extra oxygen atom would make too close a van der Waals contact.

The previously published X-ray data^{5,6} on deoxyribose nucleic acid are insufficient for a rigorous test of our structure. So far as we can tell, it is roughly compatible with the experimental data, but it must be regarded as unproved until it has been checked against more exact results. Some of these are given in the following communications. We were not aware of the details of the results presented there when we devised our structure, which rests mainly though not entirely on published experimental data and stereochemical arguments.

It has not escaped our notice that the specific pairing we have postulated immediately suggests a possible copying mechanism for the genetic material. Full details of the structure, including the conditions assumed in building it, together with a set of co-ordinates for the atoms, will be published elsewhere.

We are much indebted to Dr. Jerry Donohue for constant advice and criticism, especially on interatomic distances. We have also been stimulated by a knowledge of the general nature of the unpublished experimental results and ideas of Dr. M. H. F. Wilkins, Dr. R. E. Franklin and their co-workers at

King's College, London. One of us (J. D. W.) has been aided by a fellowship from the National Foundation for Infantile Paralysis.

J. D. WATSON
F. H. C. CRICK

Medical Research Council Unit for the Study of the Molecular Structure of Biological Systems, Cavendish Laboratory, Cambridge, April 2.

¹ Pauling, L., and Corey, R. B., *Nature*, **171**, 346 (1953); *Proc. U.S. Nat. Acad. Sci.*, **38**, 84 (1953).

² Furburg, S., *Acta Chem. Scand.*, **6**, 634 (1952).

³ Chargaff, E., for references see Zamenhof, S., Braverman, G., and Chargaff, E., *Biochim. et Biophys. Acta*, **9**, 402 (1953).

⁴ Wyatt, G. R., *J. Gen. Physiol.*, **36**, 201 (1952).

⁵ Astbury, W. T., *Symp. Soc. Exp. Biol.*, **1**, Nucleic Acid, 66 (Camb. Univ. Press, 1947).

⁶ Wilkins, M. H. F., and Randall, J. T., *Biochim. et Biophys. Acta*, **10**, 192 (1953).

Molecular Structure of Deoxypentose Nucleic Acids

WHILE the biological properties of deoxypentose nucleic acid suggest a molecular structure containing great complexity, X-ray diffraction studies described here (cf. Astbury¹) show the basic molecular configuration has great simplicity. The purpose of this communication is to describe, in a preliminary way, some of the experimental evidence for the polynucleotide chain configuration being helical, and existing in this form when in the natural state. A fuller account of the work will be published shortly.

The structure of deoxypentose nucleic acid is the same in all species (although the nitrogen base ratios alter considerably) in nucleoprotein, extracted or in cells, and in purified nucleate. The same linear group of polynucleotide chains may pack together parallel in different ways to give crystalline^{1,2}, semi-crystalline or paracrystalline material. In all cases the X-ray diffraction photograph consists of two regions, one determined largely by the regular spacing of nucleotides along the chain, and the other by the longer spacings of the chain configuration. The sequence of different nitrogen bases along the chain is not made visible.

Oriented paracrystalline deoxypentose nucleic acid ('structure B' in the following communication by Franklin and Gosling) gives a fibre diagram as shown in Fig. 1 (cf. ref. 4). Astbury suggested that the strong 3.4-Å. reflexion corresponded to the internucleotide repeat along the fibre axis. The ~34 Å. layer lines, however, are not due to a repeat of a polynucleotide composition, but to the chain configuration repeat, which causes strong diffraction as the nucleotide chains have higher density than the interstitial water. The absence of reflexions on or near the meridian immediately suggests a helical structure with axis parallel to fibre length.

Diffraction by Helices

It may be shown³ (also Stokes, unpublished) that the intensity distribution in the diffraction pattern of a series of points equally spaced along a helix is given by the squares of Bessel functions. A uniform continuous helix gives a series of layer lines of spacing corresponding to the helix pitch, the intensity distribution along the *n*th layer line being proportional to the square of J_n , the *n*th order Bessel function. A straight line may be drawn approximately through

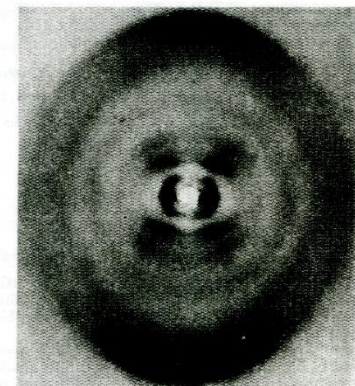


Fig. 1. Fibre diagram of deoxypentose nucleic acid from *E. coli*. Fibre axis vertical

the innermost maxima of each Bessel function and the origin. The angle this line makes with the equator is roughly equal to the angle between an element of the helix and the helix axis. If a unit repeats *n* times along the helix there will be a meridional reflexion (J_0^2) on the *n*th layer line. The helical configuration produces side-bands on this fundamental frequency, the effect³ being to reproduce the intensity distribution about the origin around the new origin, on the *n*th layer line, corresponding to *C* in Fig. 2.

We will now briefly analyse in physical terms some of the effects of the shape and size of the repeat unit or nucleotide on the diffraction pattern. First, if the nucleotide consists of a unit having circular symmetry about an axis parallel to the helix axis, the whole diffraction pattern is modified by the form factor of the nucleotide. Second, if the nucleotide consists of a series of points on a radius at right-angles to the helix axis, the phases of radiation scattered by the helices of different diameter passing through each point are the same. Summation of the corresponding Bessel functions gives reinforcement for the inner-

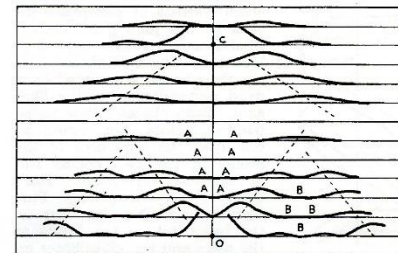
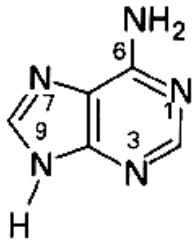
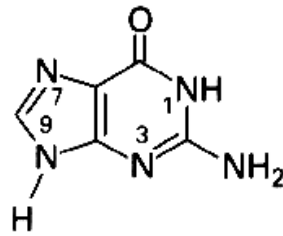


Fig. 2. Diffraction pattern of system of helices corresponding to structure of deoxypentose nucleic acid. The squares of Bessel functions are plotted about 0 on the equator and on the first, second, third and fifth layer lines for half of the nucleotide mass at 20 Å. diameter and remainder distributed along a radius, the mass at a given radius being proportional to the radius. About *C* on the tenth layer line similar functions are plotted for an outer diameter of 12 Å.

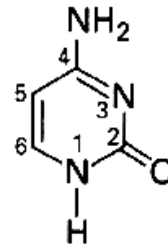
Base numbering



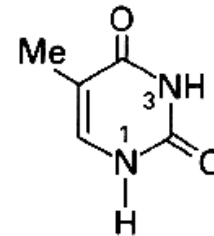
adenine



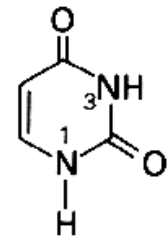
guanine



cytosine

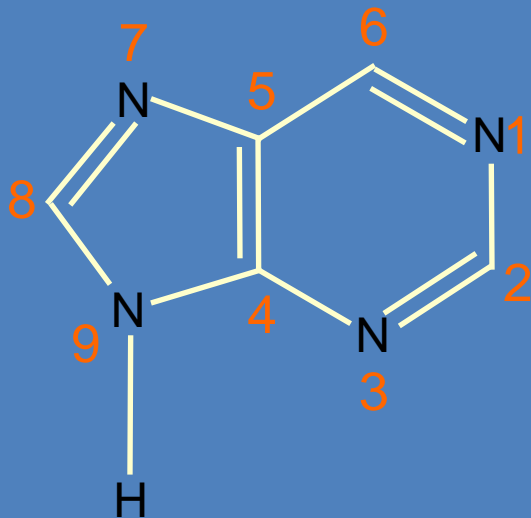


thymine

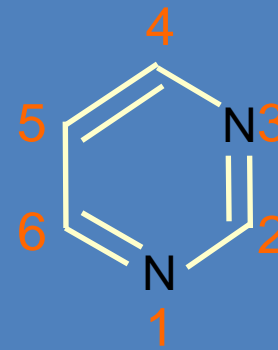


uracil

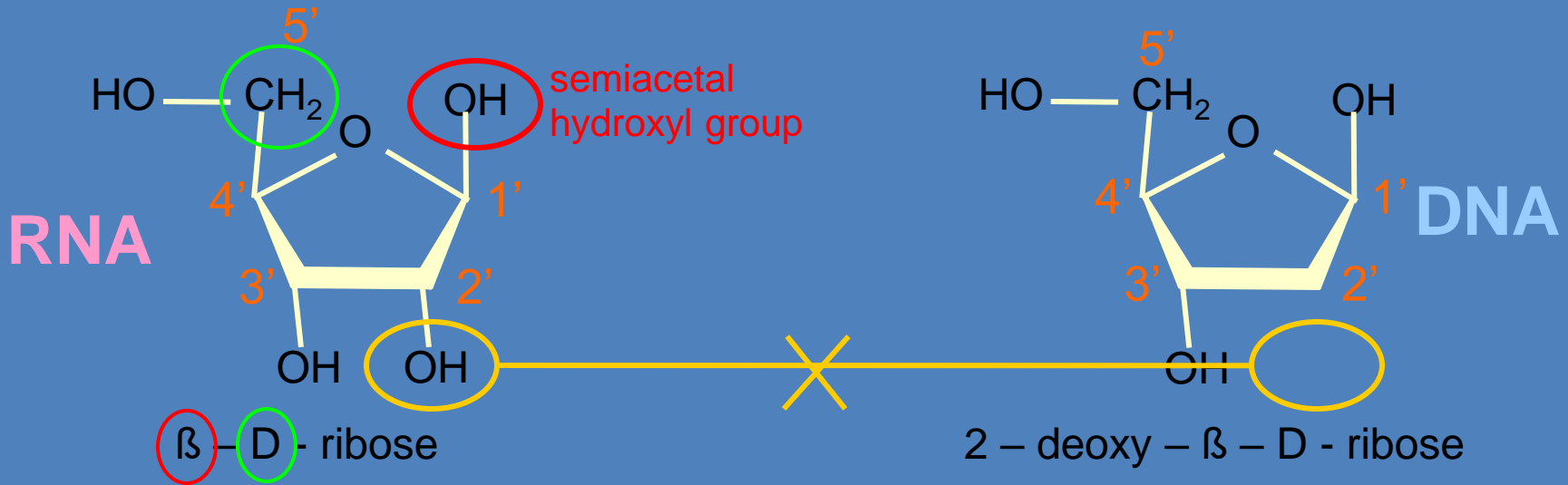
PURINES



PYRIMIDINES



Sugar - pentoses



Other aldopentoses: arabinose, xylose, lyxose

semiacetal hydroxyl group

+ base

N-glycosidic bond

nukleoside

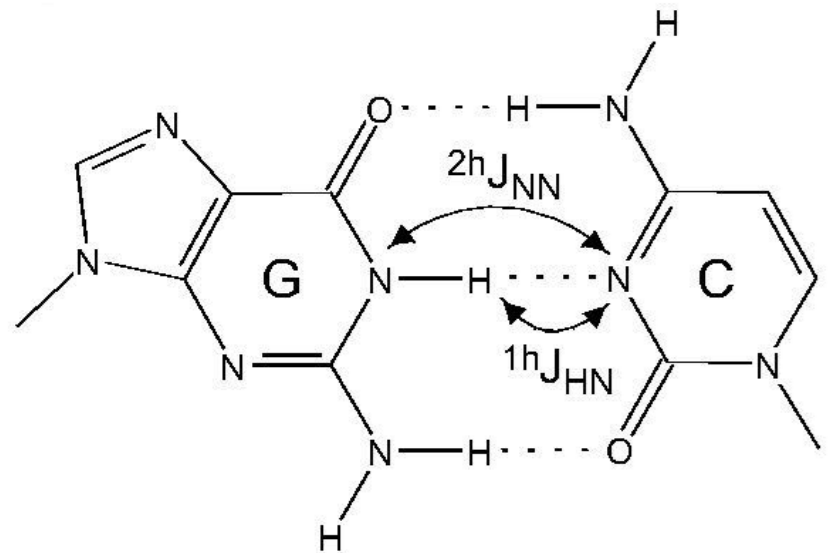
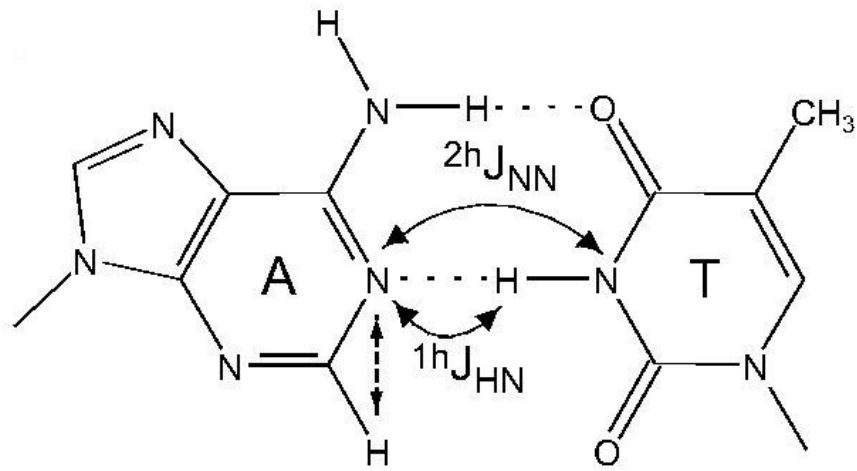
C1' - N1

pyrimidines

C1' - N9

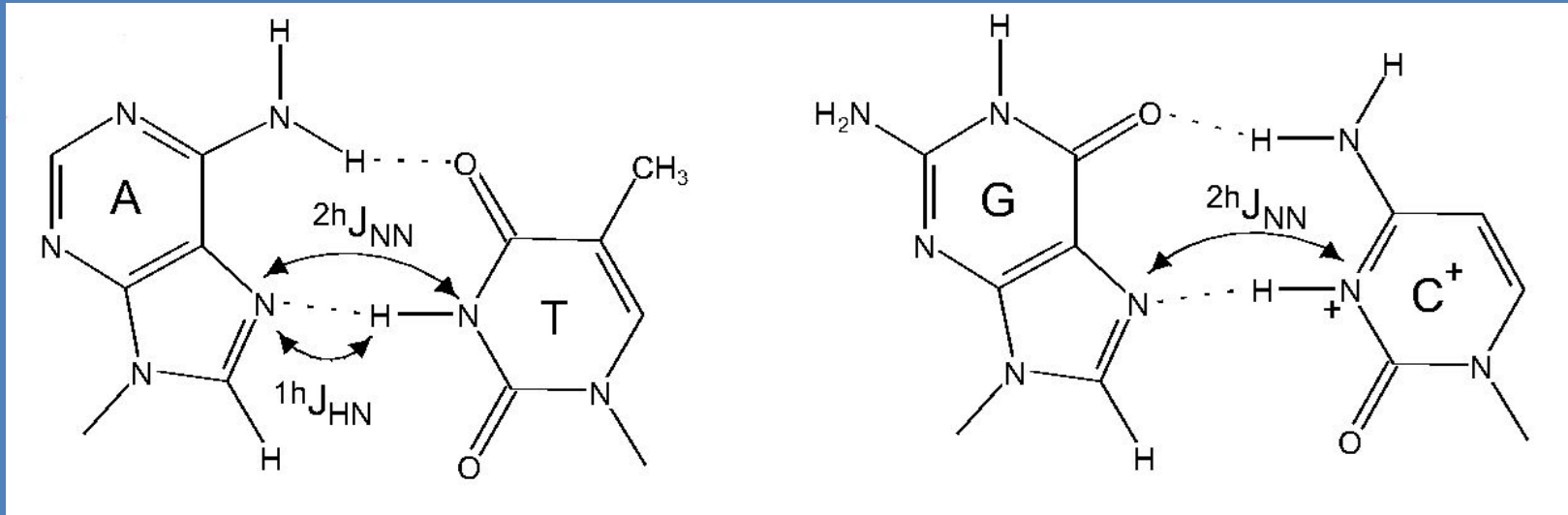
purines

Base pairing

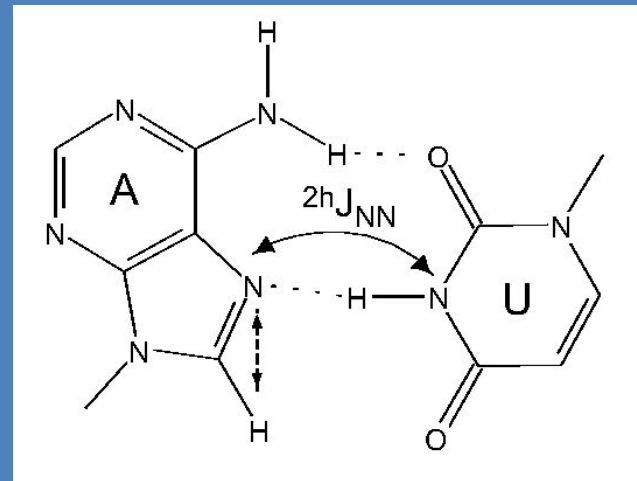


Watson-Crick pairs

Base pairing



Hoogsteen and
reverse Hoogsteen
pairs



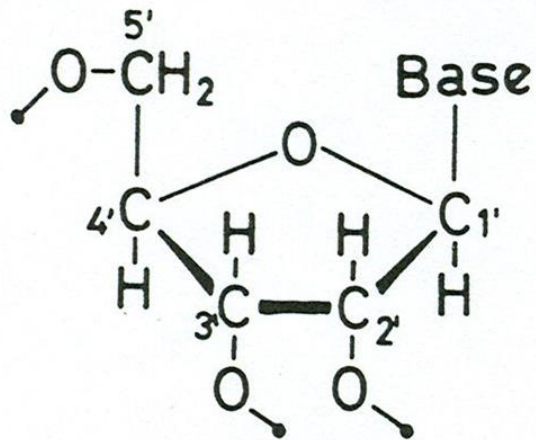
Nuclear properties of selected isotopes

Isotope ($I=1/2$)	$\gamma \times 10^{-7}$ (rad T ⁻¹ s ⁻¹)	ν at 11.74T (MHz)	Natural Abundance (%)	Sensitivity	
				Rel. ^a	Abs. ^b
¹ H	26.75	500.0	99.98	1.00	1.00
¹³ C	6.73	125.7	1.11	1.6×10^{-2}	1.8×10^{-4}
¹⁵ N	-2.71	50.7	0.37	1.0×10^{-3}	3.8×10^{-6}
³¹ P	10.83	202.4	100	6.6×10^{-2}	6.6×10^{-2}

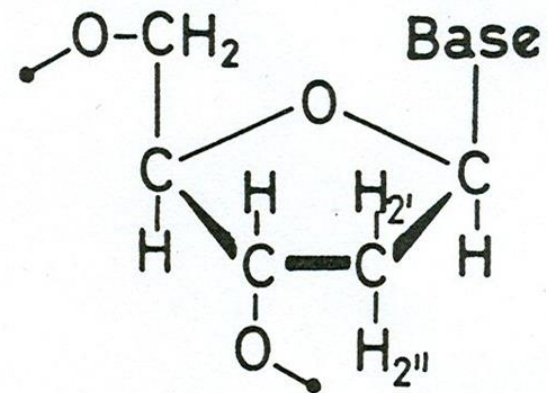
^a Relative sensitivity at constant field for equal number of nuclei.

^b Product of relative sensitivity and natural abundance.

Spin systems in ribose and deoxyribose

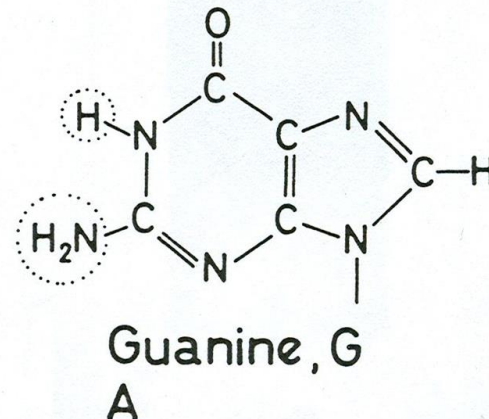
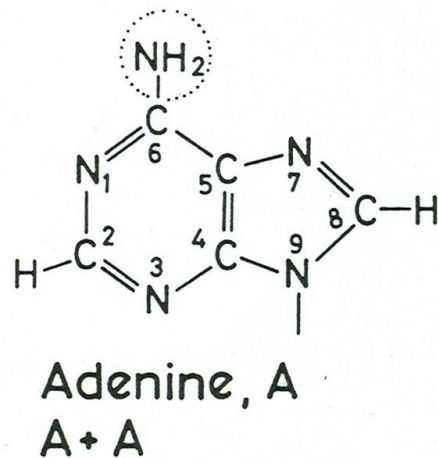
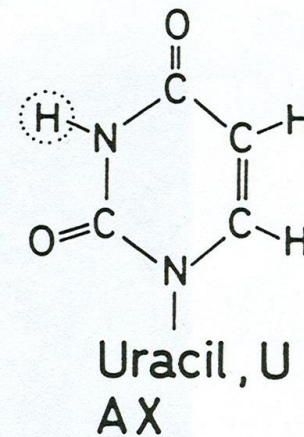
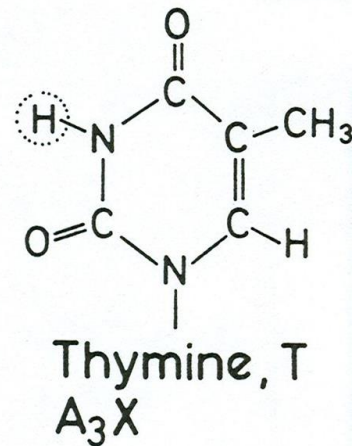
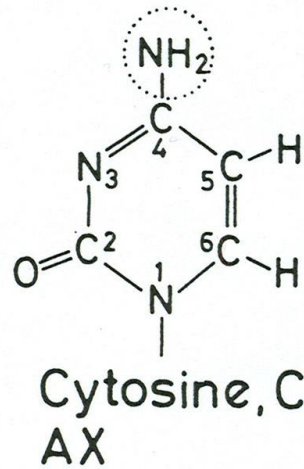


β -D-Ribose
XWTPMA

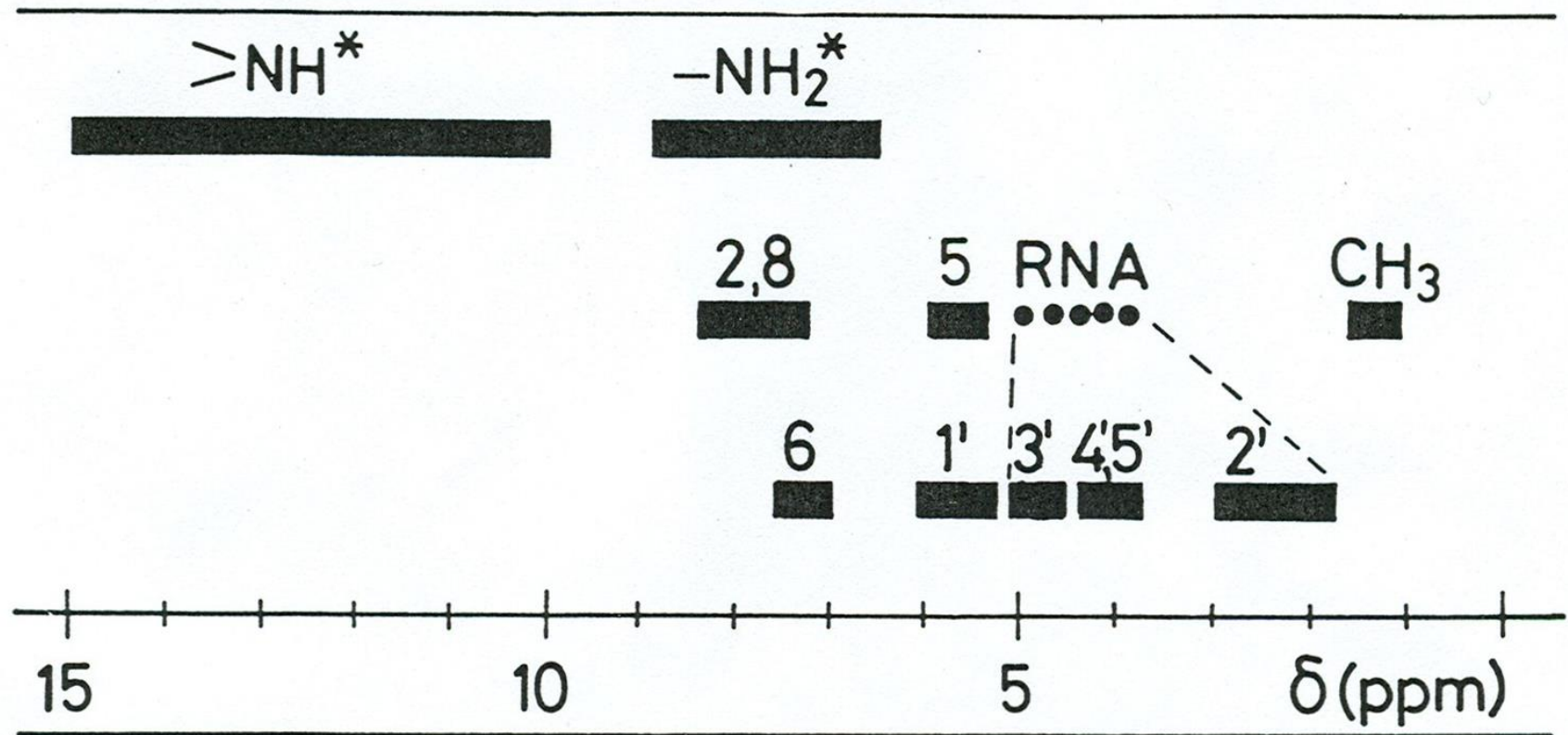


2'-Deoxy- β -D-Ribose
XAMWTNP

Spin systems in nucleic acid bases



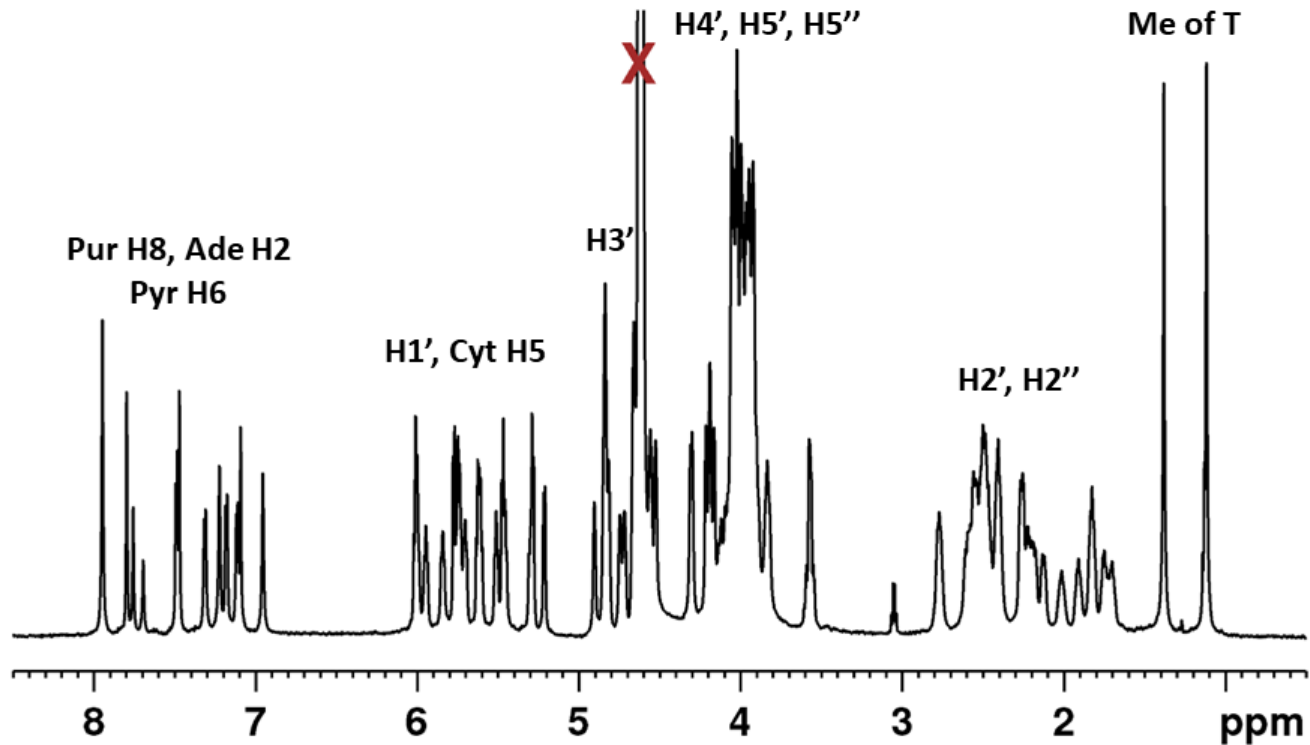
^1H chemical shift ranges in DNA and RNA



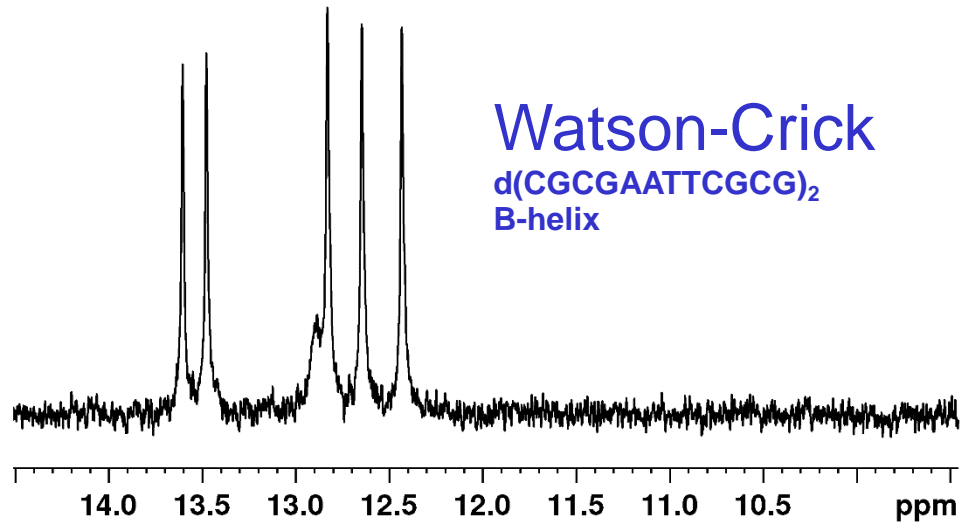
^1H chemical shift ranges in DNA and RNA

Code	δ (ppm)	Comments
2'	1.8-3.0	2'H, 2''H in DNA
4',5'	3.7-4.5	4'H, 5'H, 5''H in DNA
3'	4.4-5.2	3'H in DNA
•••••	3.7-5.2	2'H, 3'H, 4'H, 5'H, 5''H in RNA
1'	5.3-6.3	1'H
CH_3	1.2-1.6	CH_3 of T
5	5.3-6.0	5H of C and U
6	7.1-7.6	6H of C, T and U
2,8	7.3-8.4	8H of A and G, 2H of A
$-\text{NH}_2^*$	6.6-9.0	NH_2 of A, C and G
$>\text{NH}^*$	10 - 15	Ring NH of G, T and U

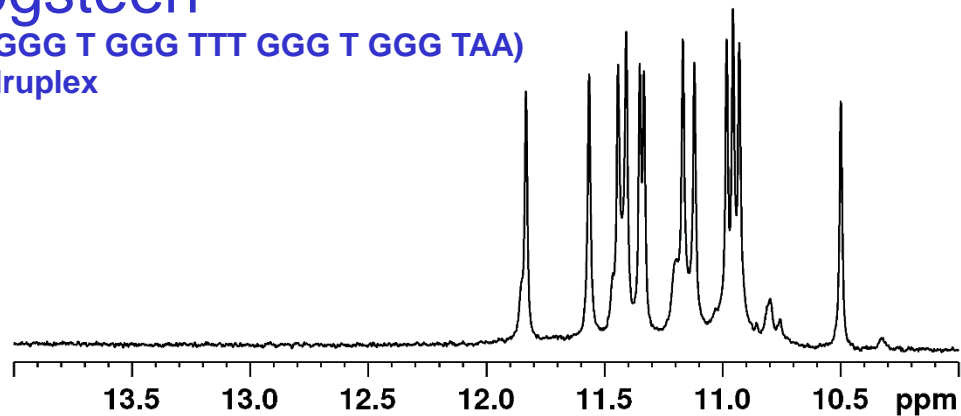
^1H NMR spectrum of d(CGCGAATTCGCG)



^1H NMR spectra in H_2O

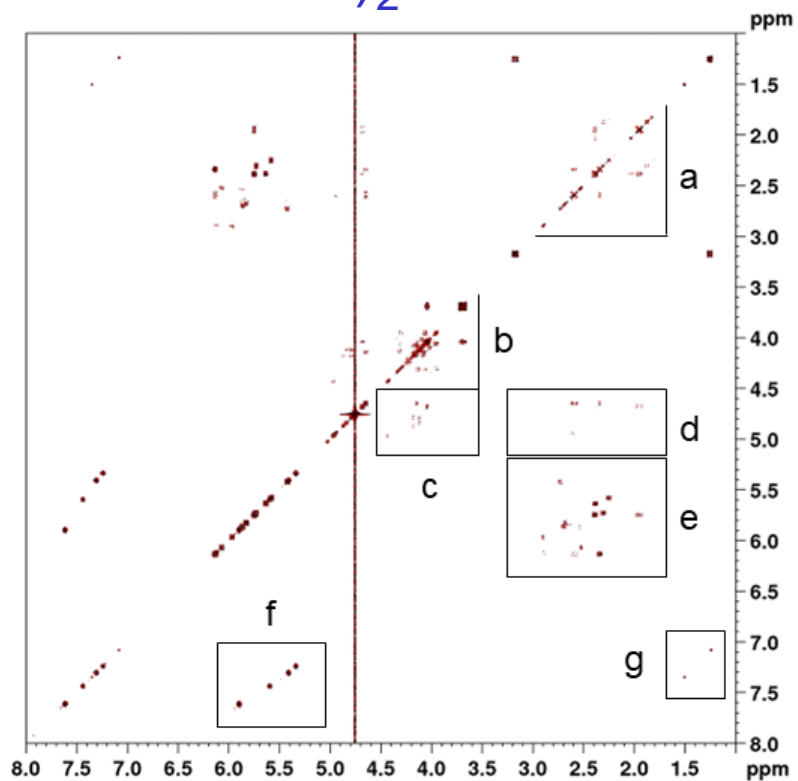


Hoogsteen
 $\text{d}(\text{AAT GGG T GGG TTT GGG T GGG TAA})$
G-quadruplex



^1H COSY spectrum of DNA

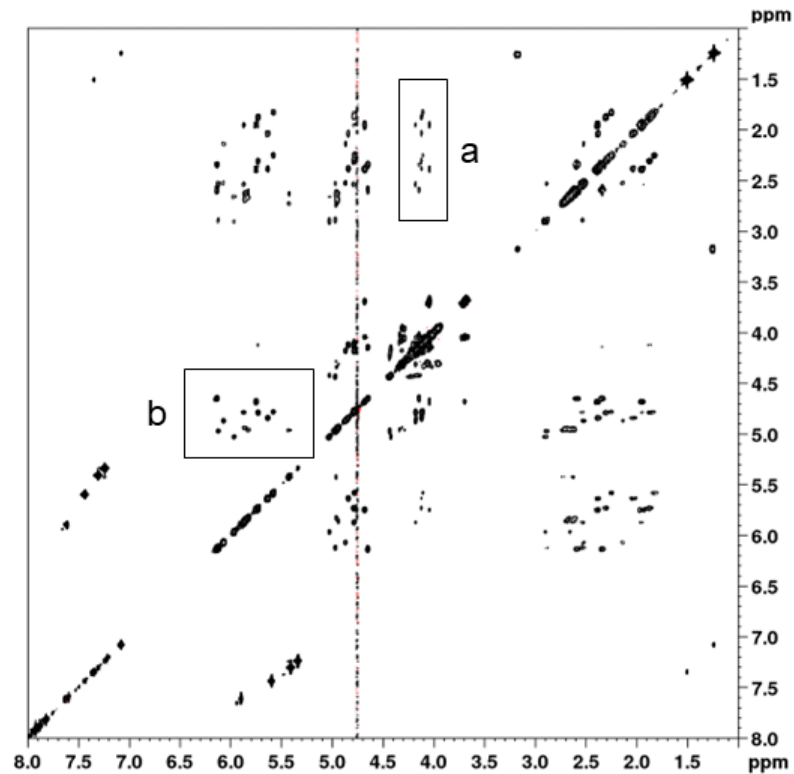
d(CGCGAATTCGCG)₂



- a H2'-H2''
- b H4'-H5',5''
H5'-H5''
- c H3'-H4'
- d H2',2''-H3'
- e H1'-H2',2''
- f H5-H6 (Cyt)
- g CH₃-H6 (Thy)

^1H TOCSY spectrum of DNA

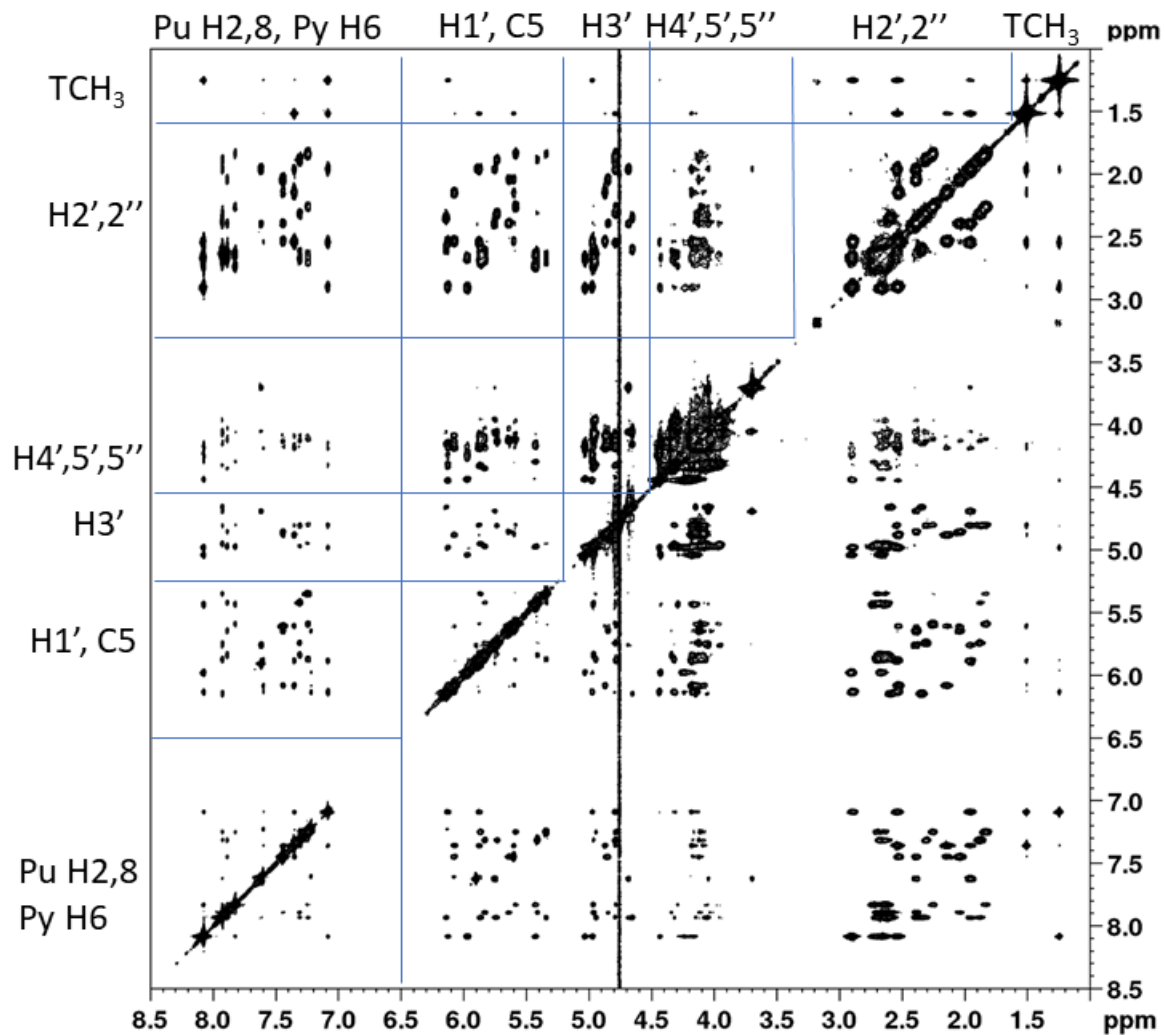
$\text{d}(\text{CGCGAATTCGCG})_2$



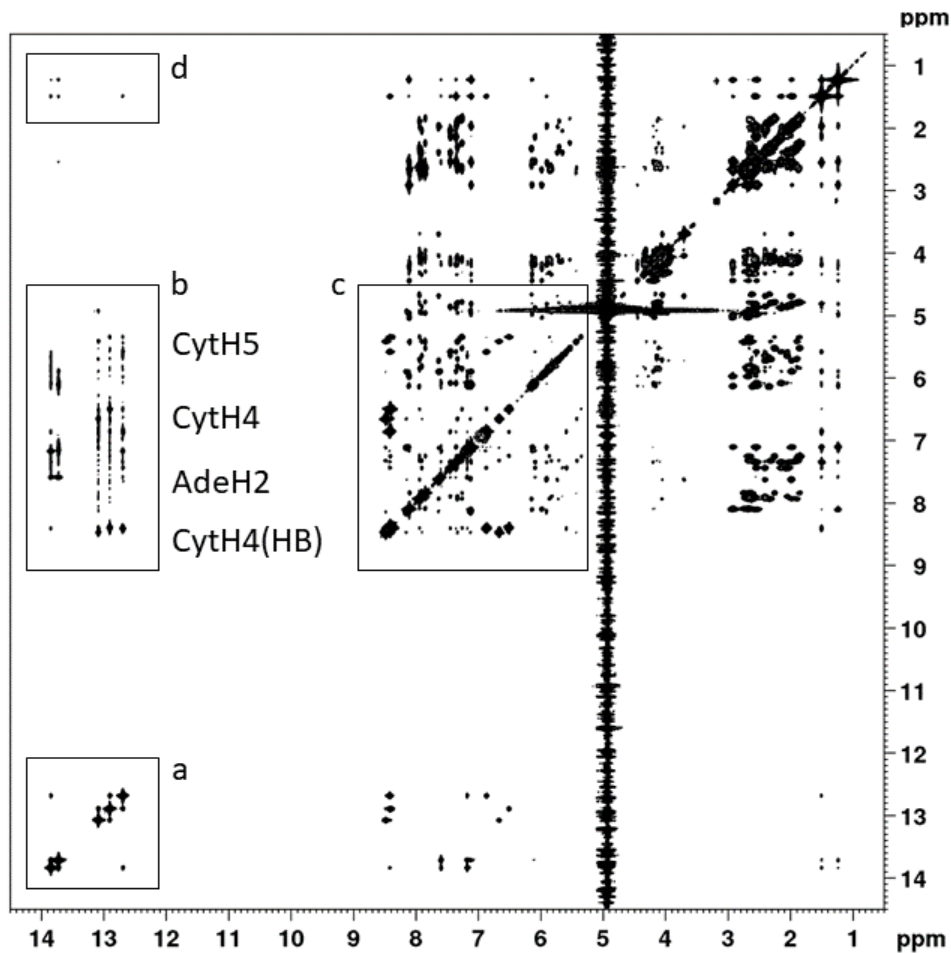
- a $\text{H4}'\text{-H2}',\text{2}''$
- b $\text{H1}'\text{-H3}'$

^1H NOESY spectrum of DNA in D_2O

d(CGCGAATTCGCG)₂



^1H NOESY spectrum of DNA in H_2O



$d(\text{CGCGAATTCGCG})_2$

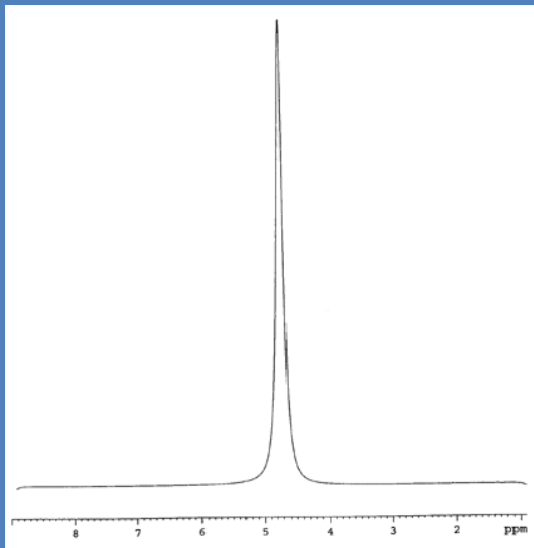
- a H imino - H imino
- b H imino - H amino
H imino - AdeH2, CytH5
- c H amino - H amino
H amino - AdeH2, CytH5, H6
- d H imino - TCH_3

Water suppression

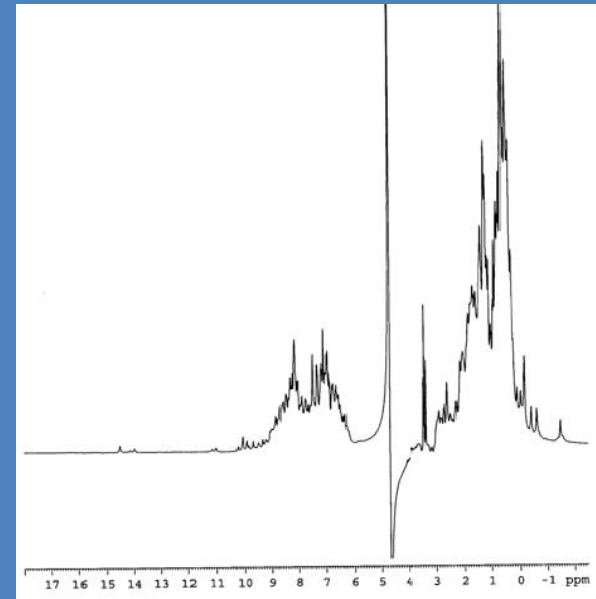
$[\text{H}_2\text{O}] = 55,000 \text{ mM}$

$[\text{Protein}] < 5 \text{ mM}$

$[\text{H}_2\text{O}]/[\text{Protein}] > 11,000$

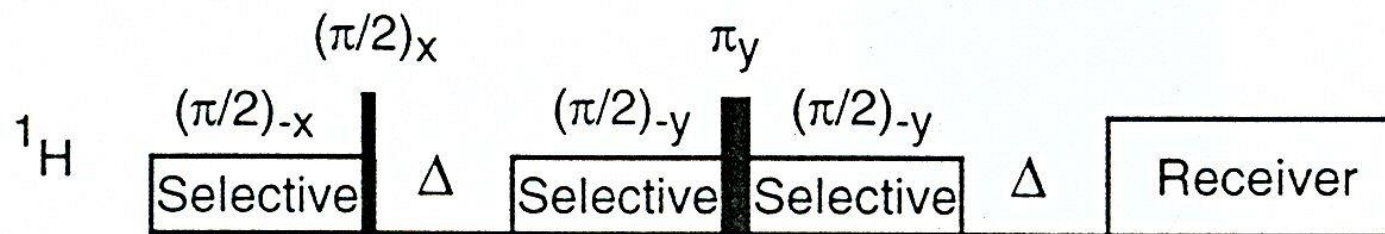
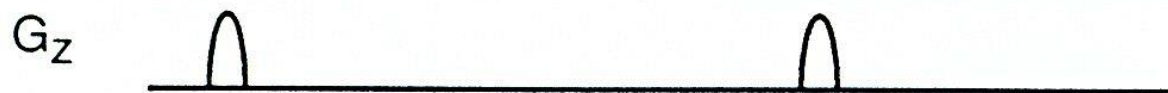
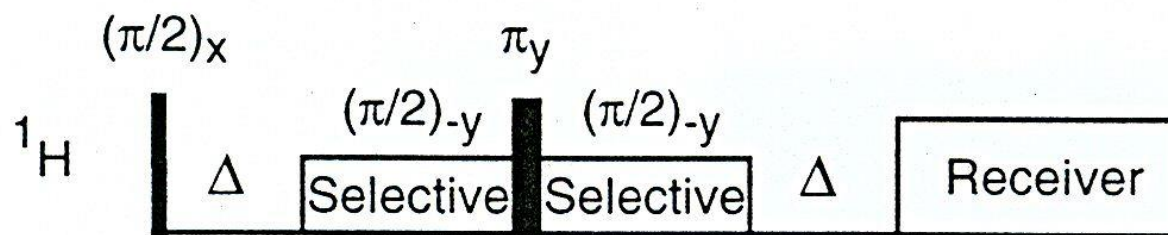


Water suppression



Sample : 1 mM TEP-I in 90% H₂O/10%D₂O, pH 6.0, 290 K.

WATERGATE



Structure Determination Procedure

Structure Determination:

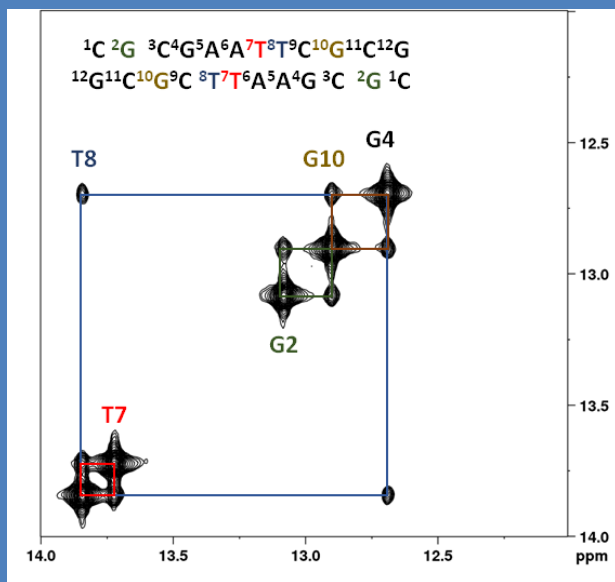
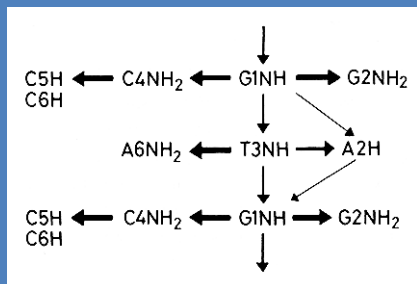
- | | | |
|------|----------------------------|---------------------------------|
| I) | Assignment | NOESY, COSY, HSQC
TOCSY..... |
| II) | Local Analysis | |
| | •glycosidic torsion angle | (NOE, <u>COSY</u>) |
| | •sugar puckering | (COSY, NOE) |
| | •backbone conformation | (COSY) |
| | •base pairing | (NOE, <u>COSY</u>) |
| III) | Global Analysis | |
| | •sequential | (NOE, COSY) |
| | •inter strand/cross strand | (NOE, <u>COSY</u>) |
| | •dipolar coupling | (HSQC, <u>HSQC</u>) |

Resonance Assignment

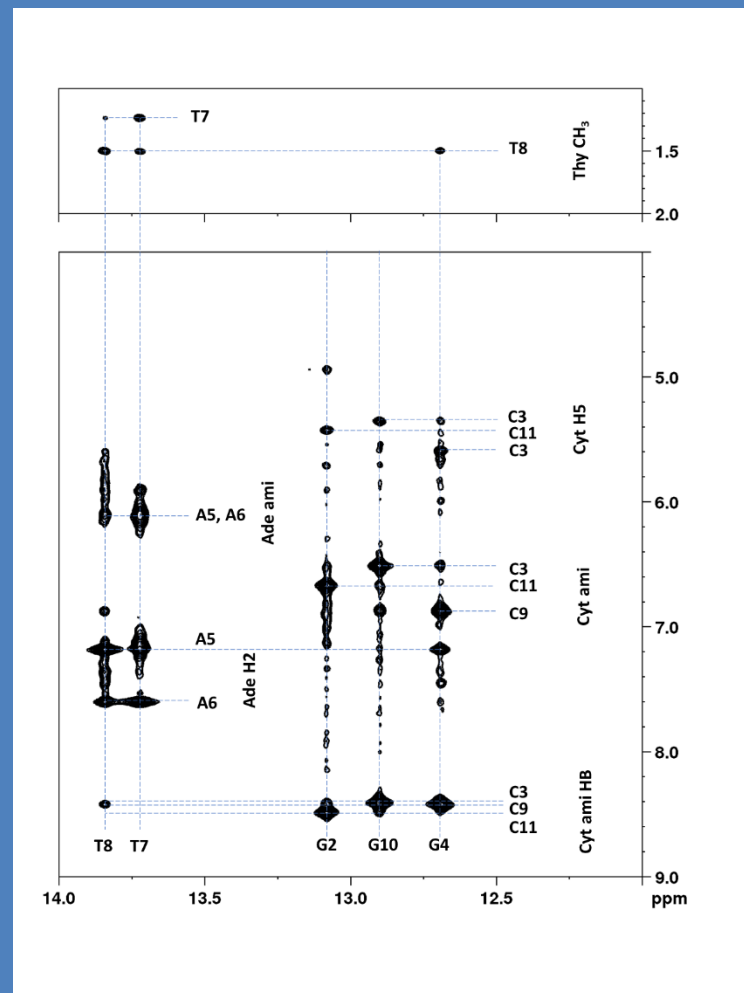
A) Exchangeable protons:	1D ^1H , 2D NOESY
B) Non-exchangeable protons	
• Aromatic Spin Systems:	2D DQF-COSY (H5-H6), 2D NOESY
• Sugar Spin Systems:	2D DQF-COSY 2D TOCSY
• Sequential Assignment:	2D NOESY 2D (^{31}P , ^1H) HETCOR
C) Correlation of exchangeable and non-exchangeable protons:	2D NOESY

Sequential connectivities with exchangeable protons

Dickerson's dodecamer
d(CGCGAATTCGCG)₂

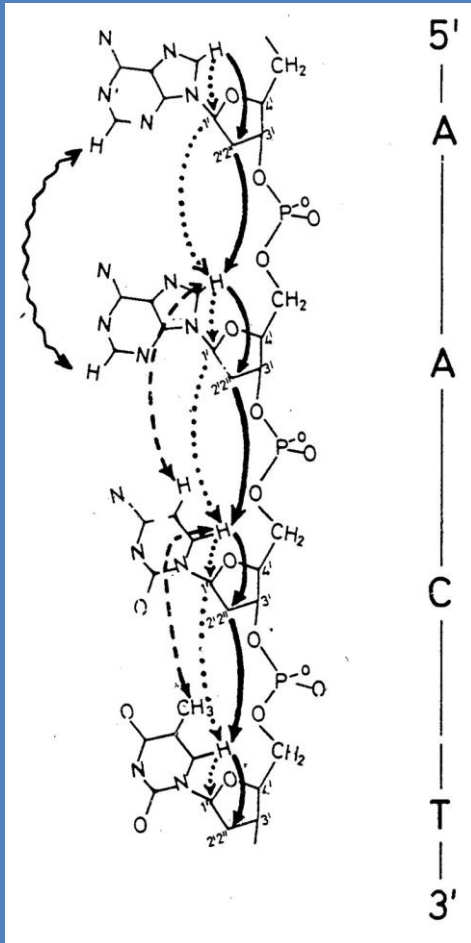


imino-imino

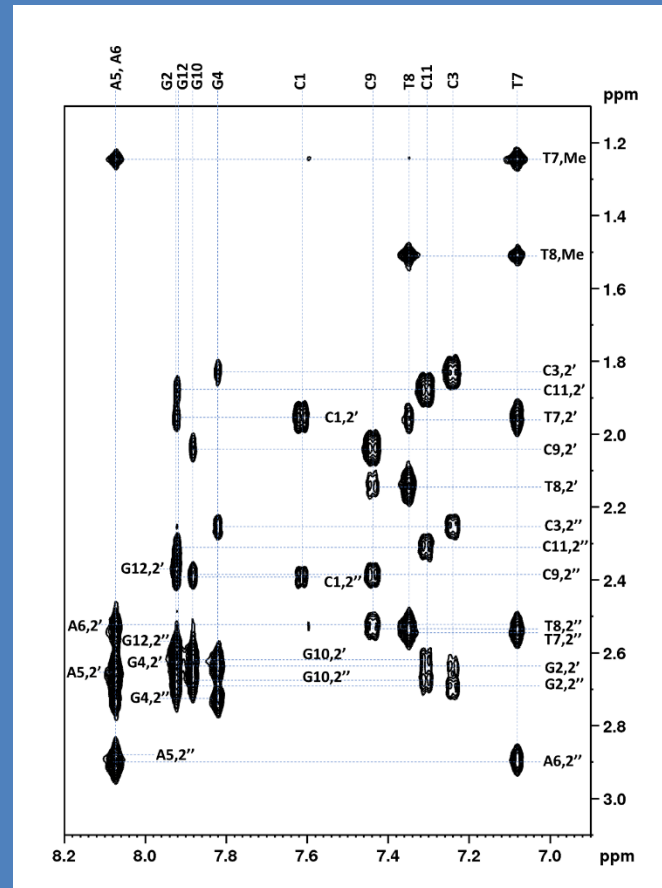


imino-amino

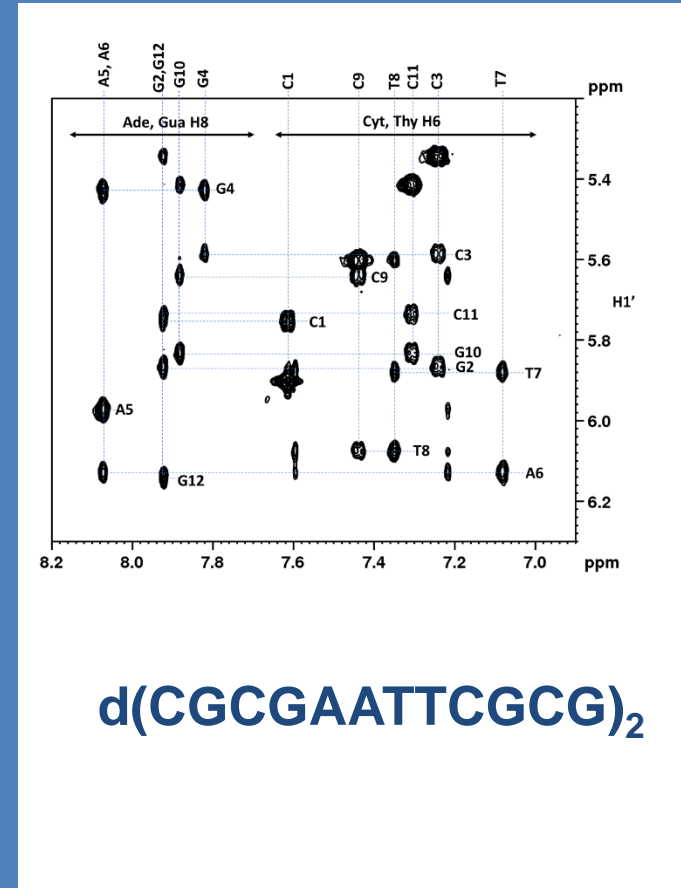
Sequential resonance assignments



H6/8-H2',2''/Me



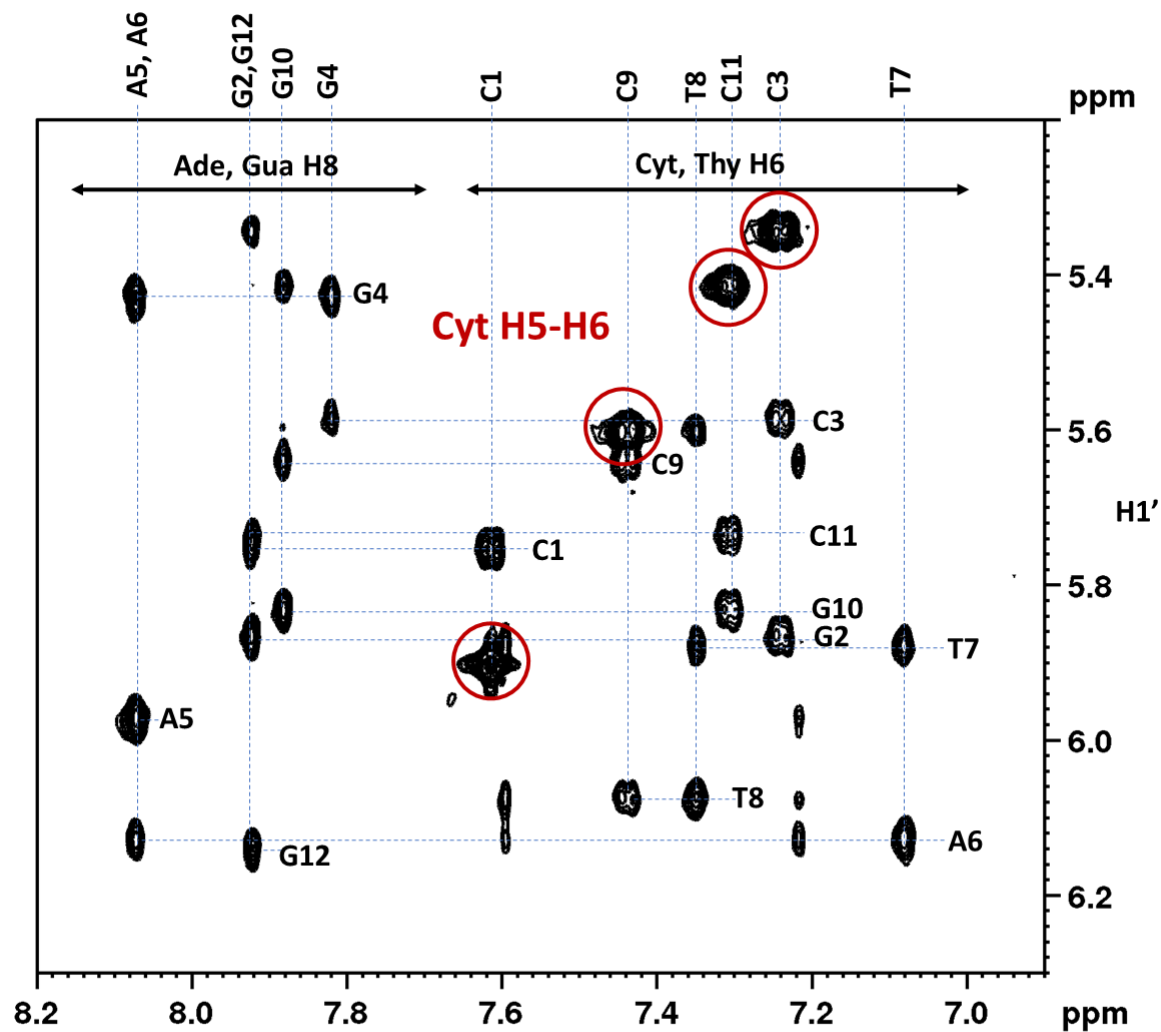
H6/8-H1'



d(CGCGAATTCGCG)₂

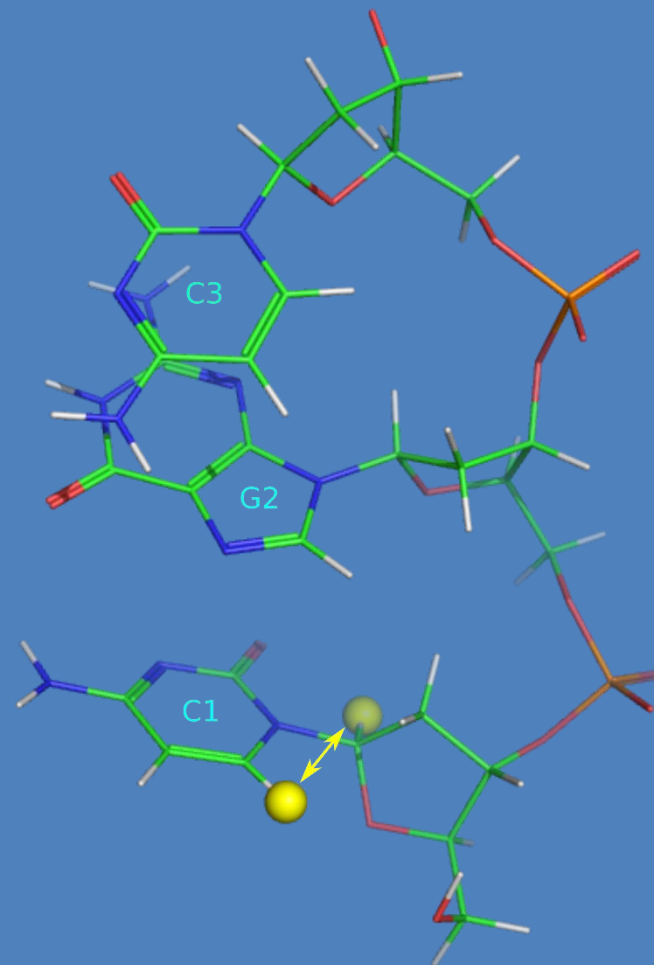
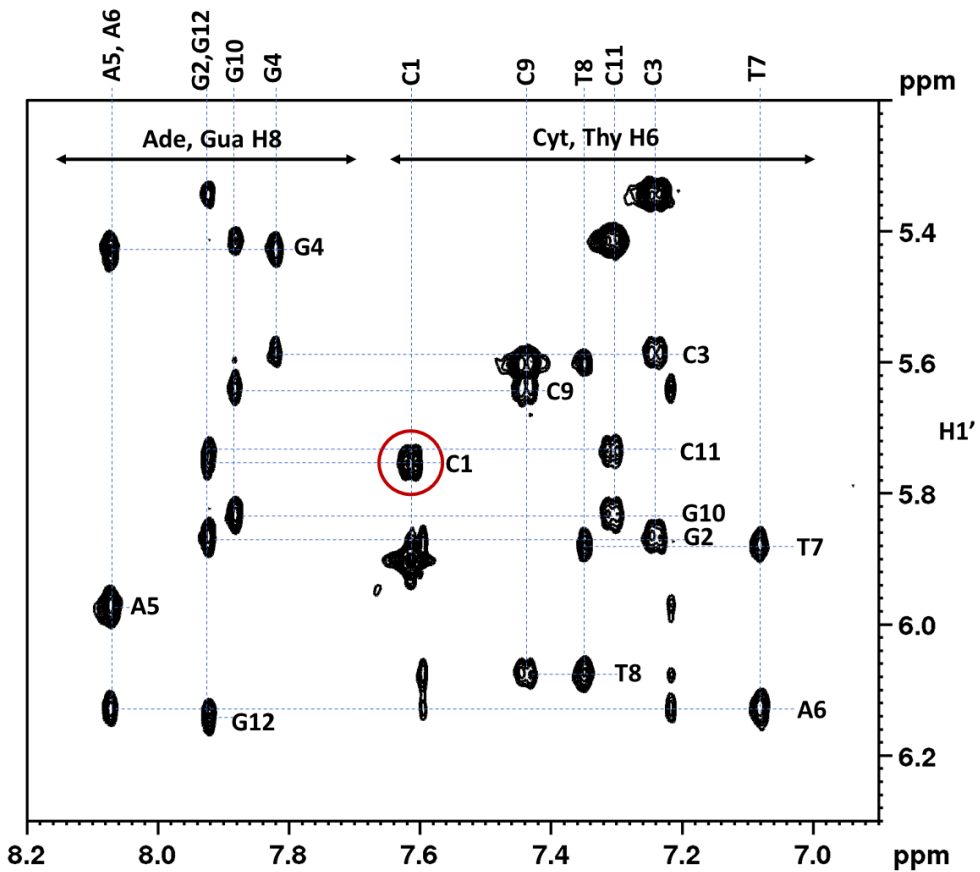
Assignment based on H6/8-H1' connectivities

d(CGCGAATTCGCG)₂



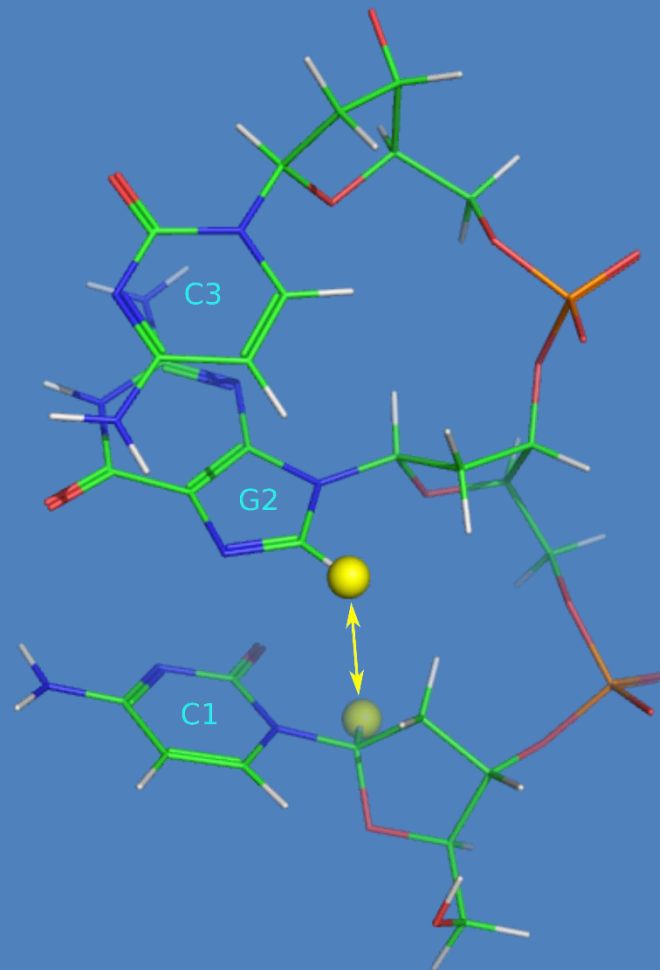
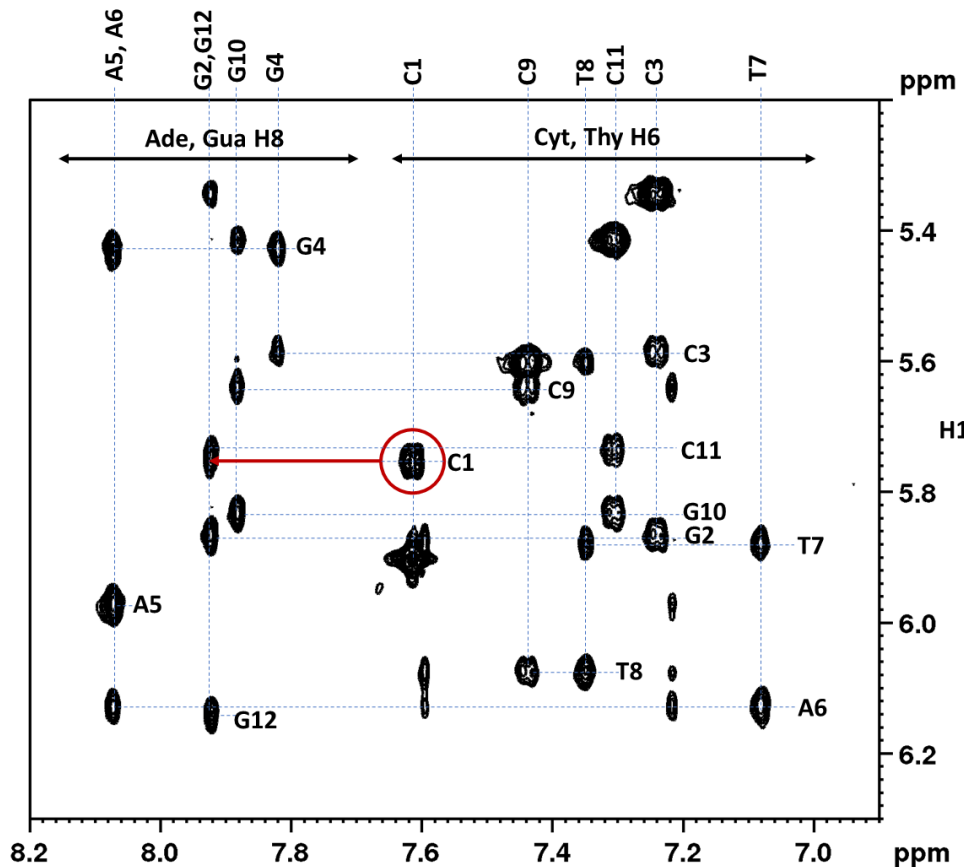
Assignment based on H6/8-H1' connectivities

d(CGCGAATTCGCG)₂



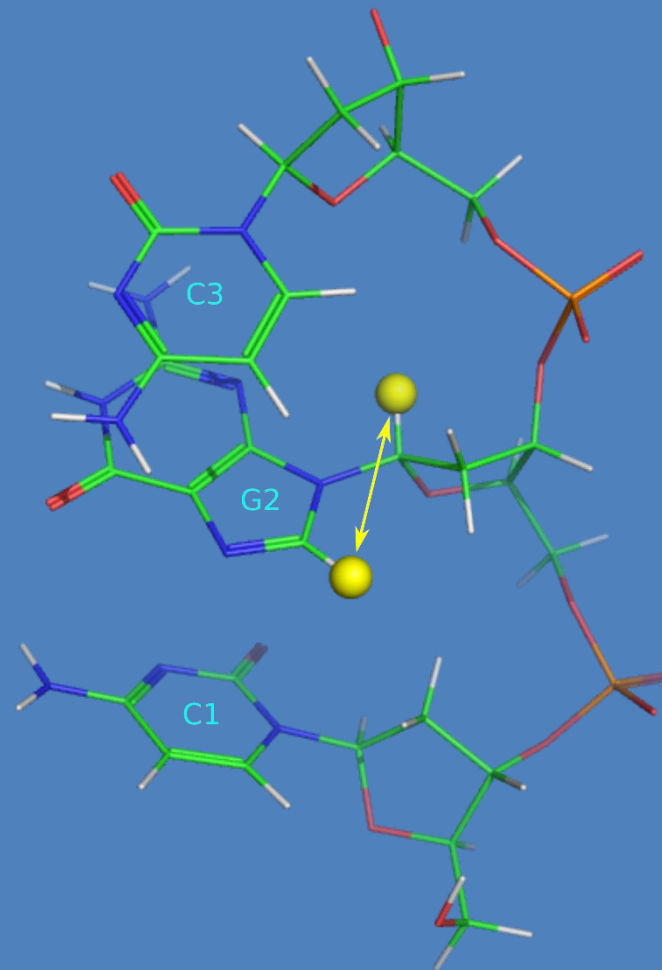
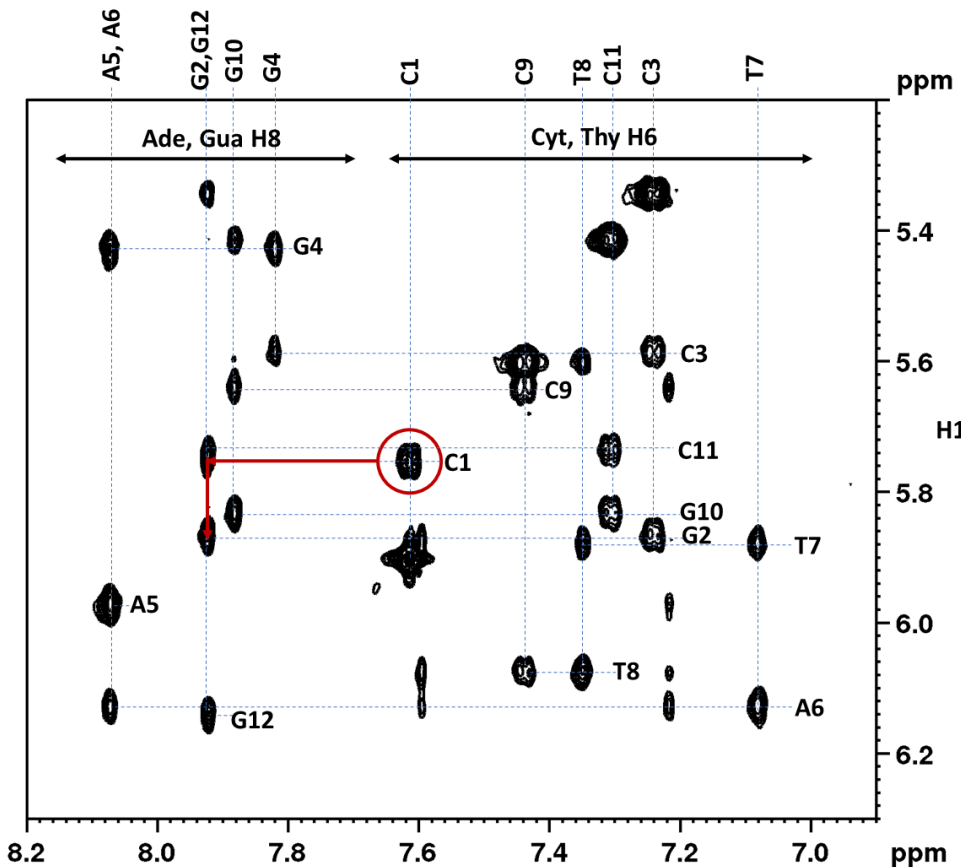
Assignment based on H6/8-H1' connectivities

d(CGCGAATTCGG)₂



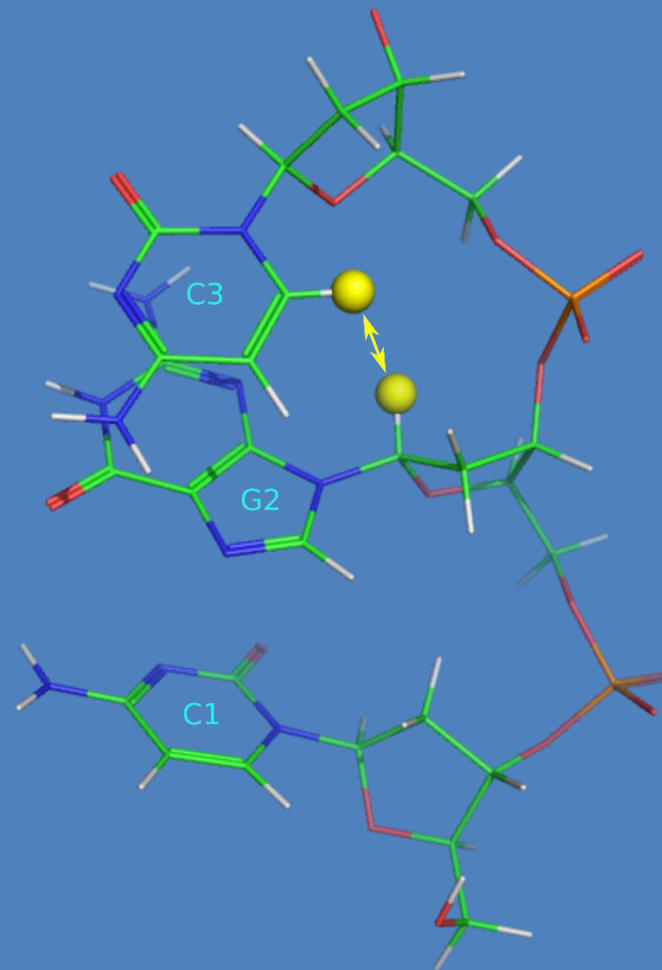
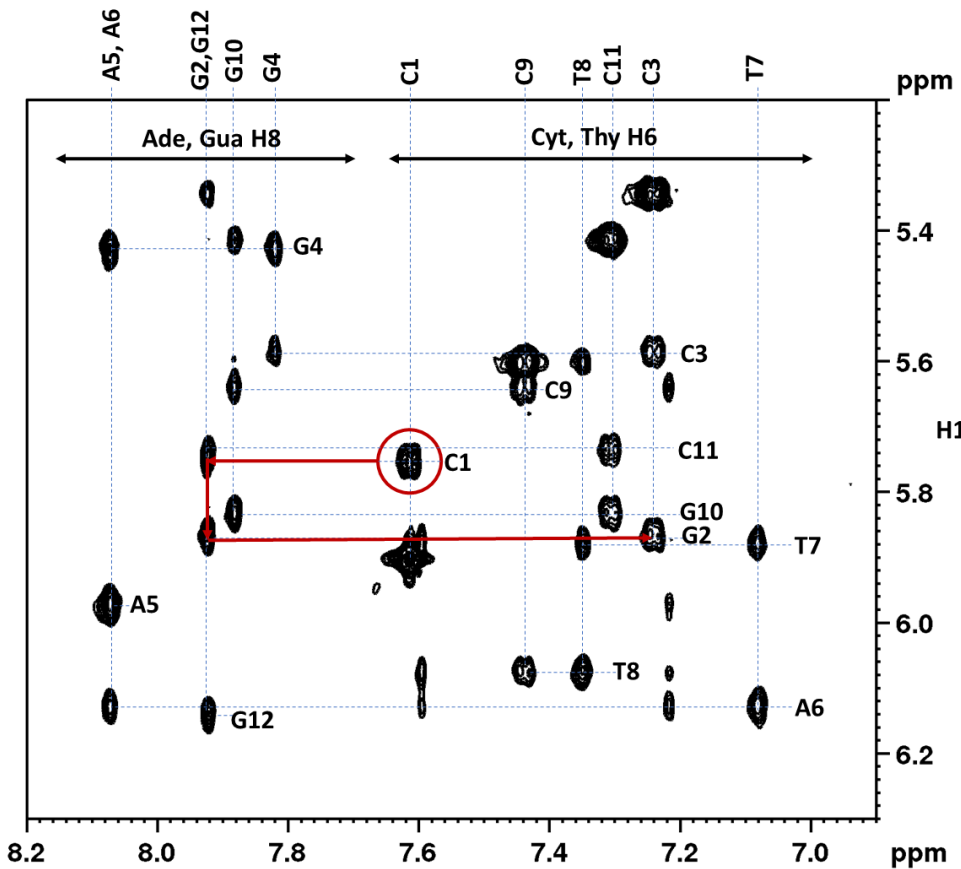
Assignment based on H6/8-H1' connectivities

d(CGCGAATTCGCG)₂



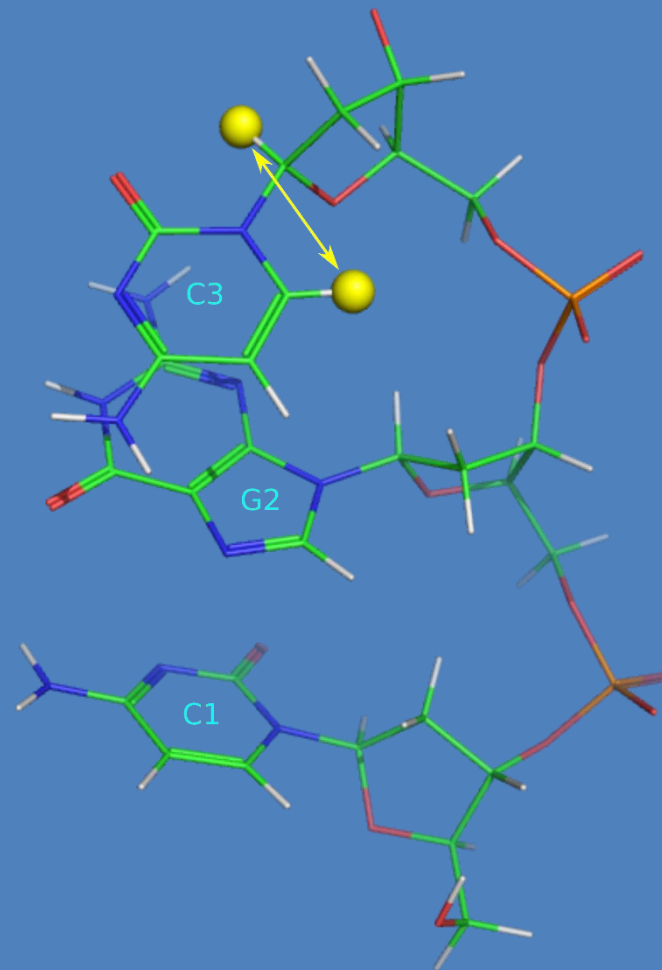
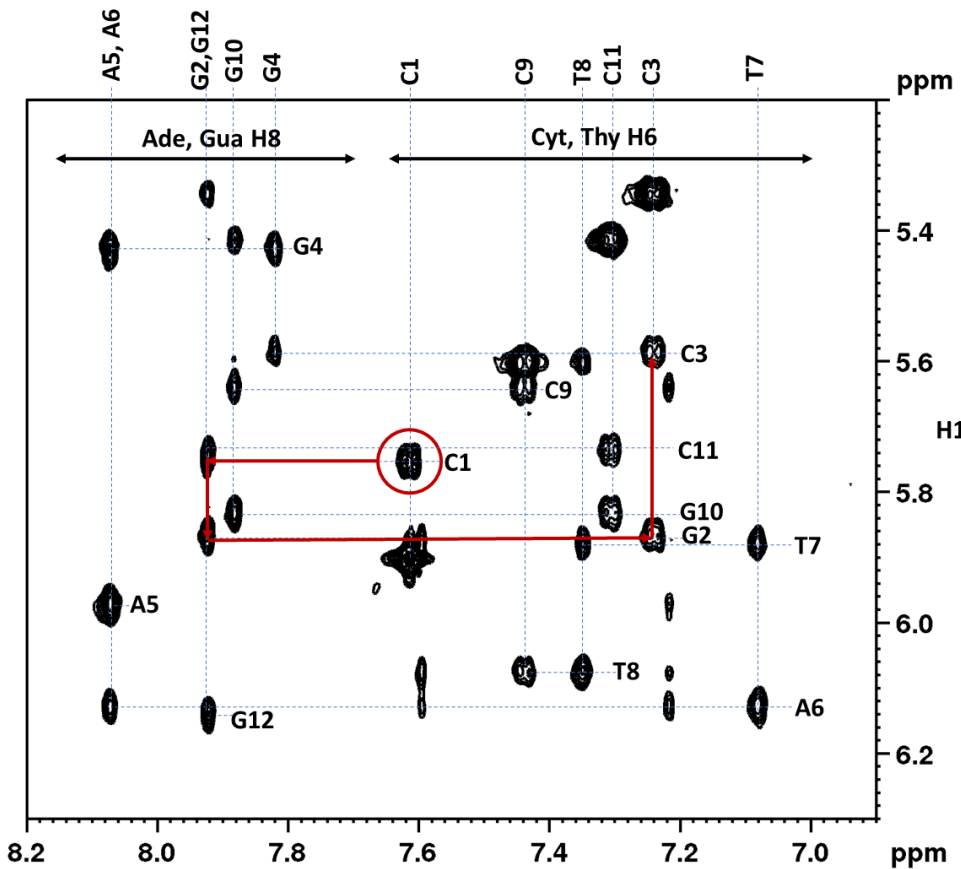
Assignment based on H6/8-H1' connectivities

d(CGCGAATTCGG)₂



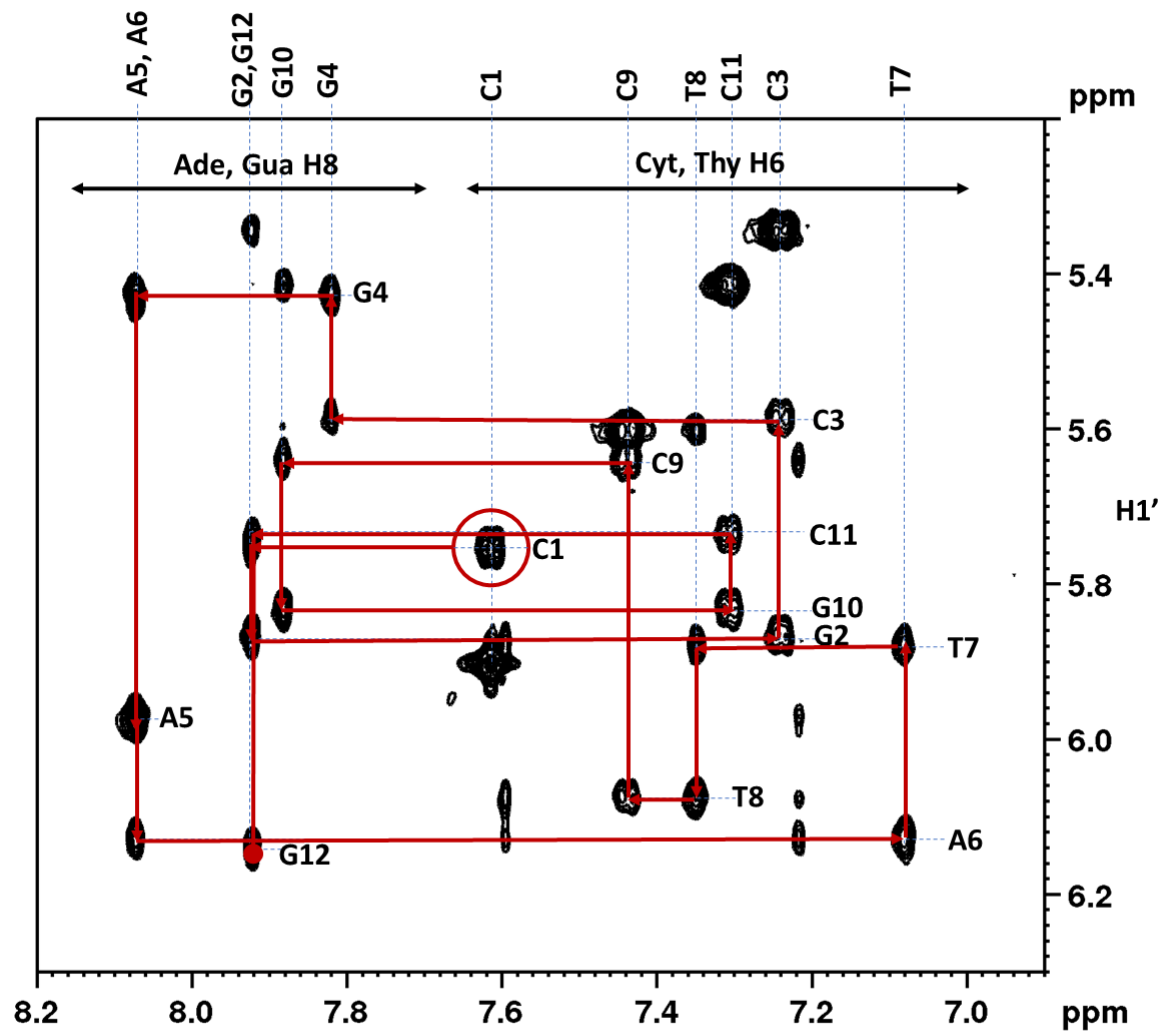
Assignment based on H6/8-H1' connectivities

d(CGCGAATTCGCG)₂



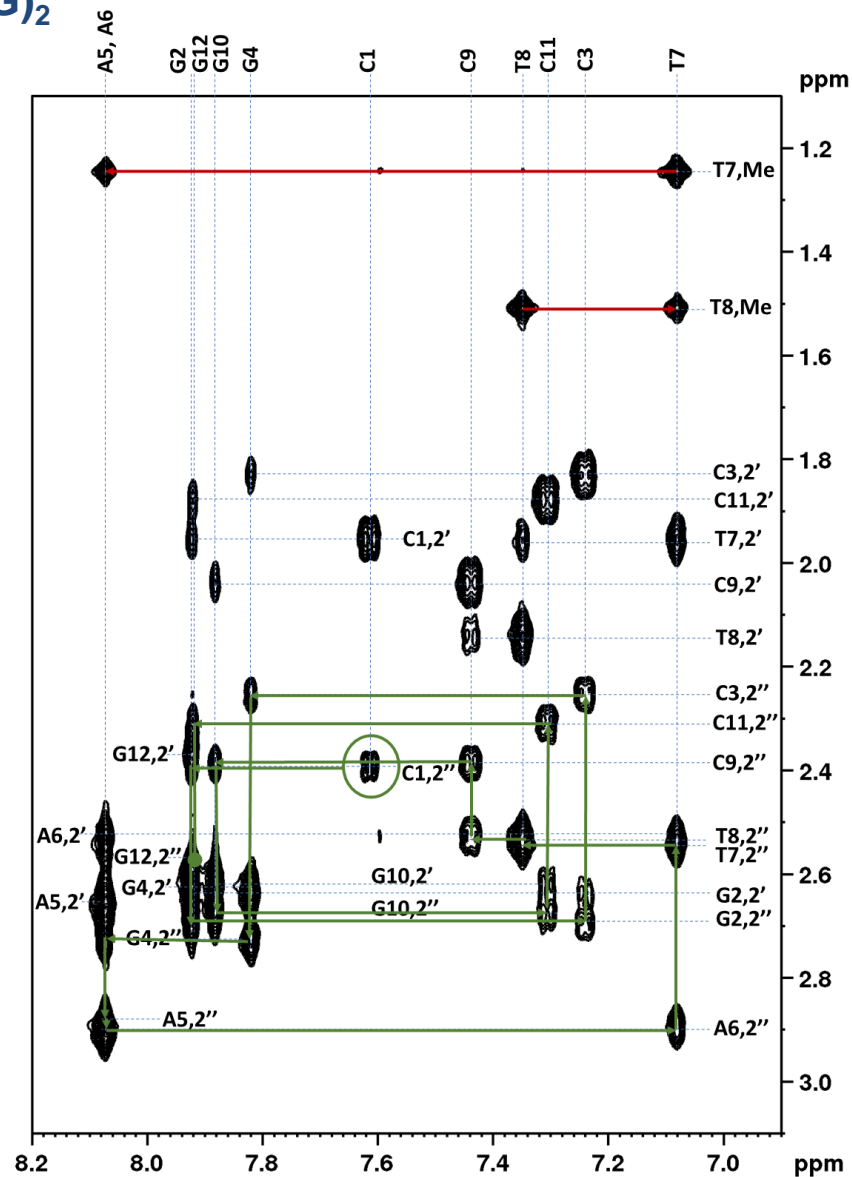
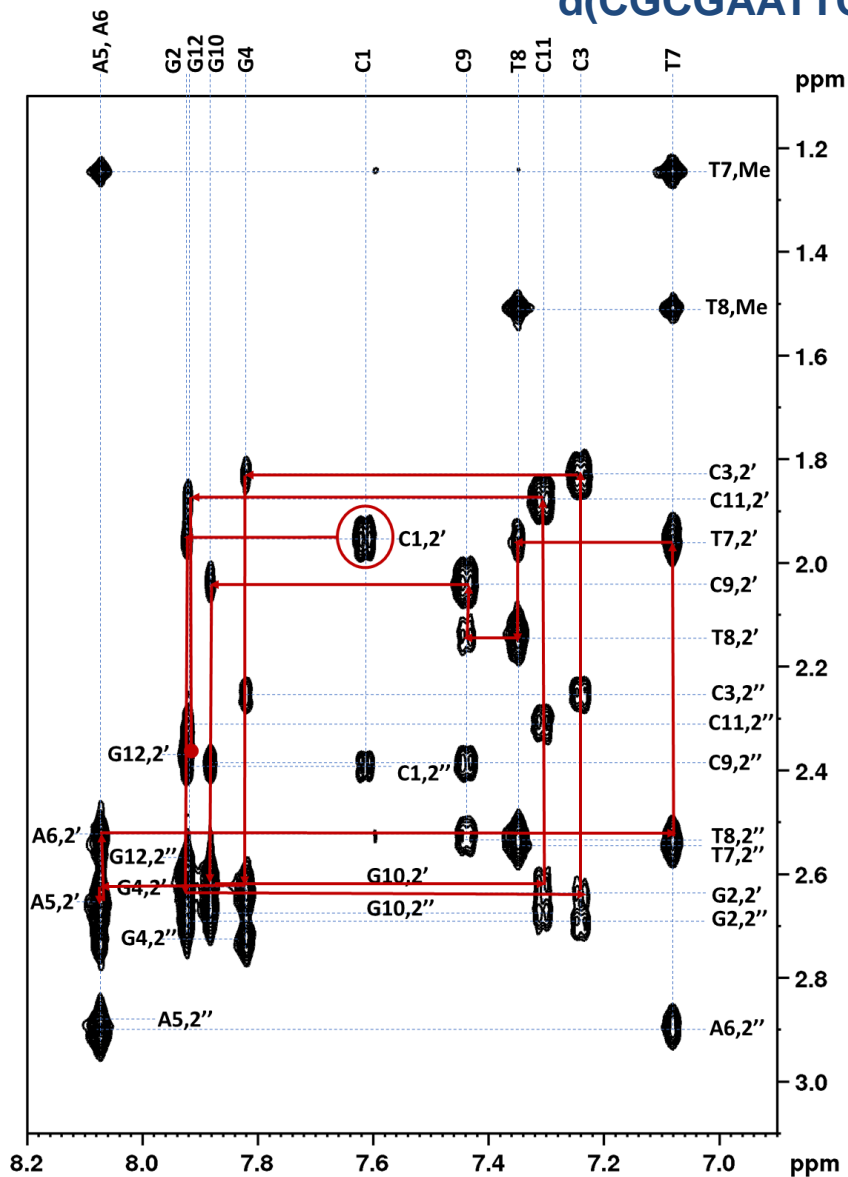
Assignment based on H6/8-H1' connectivities

d(CGCGAATTCGCG)₂

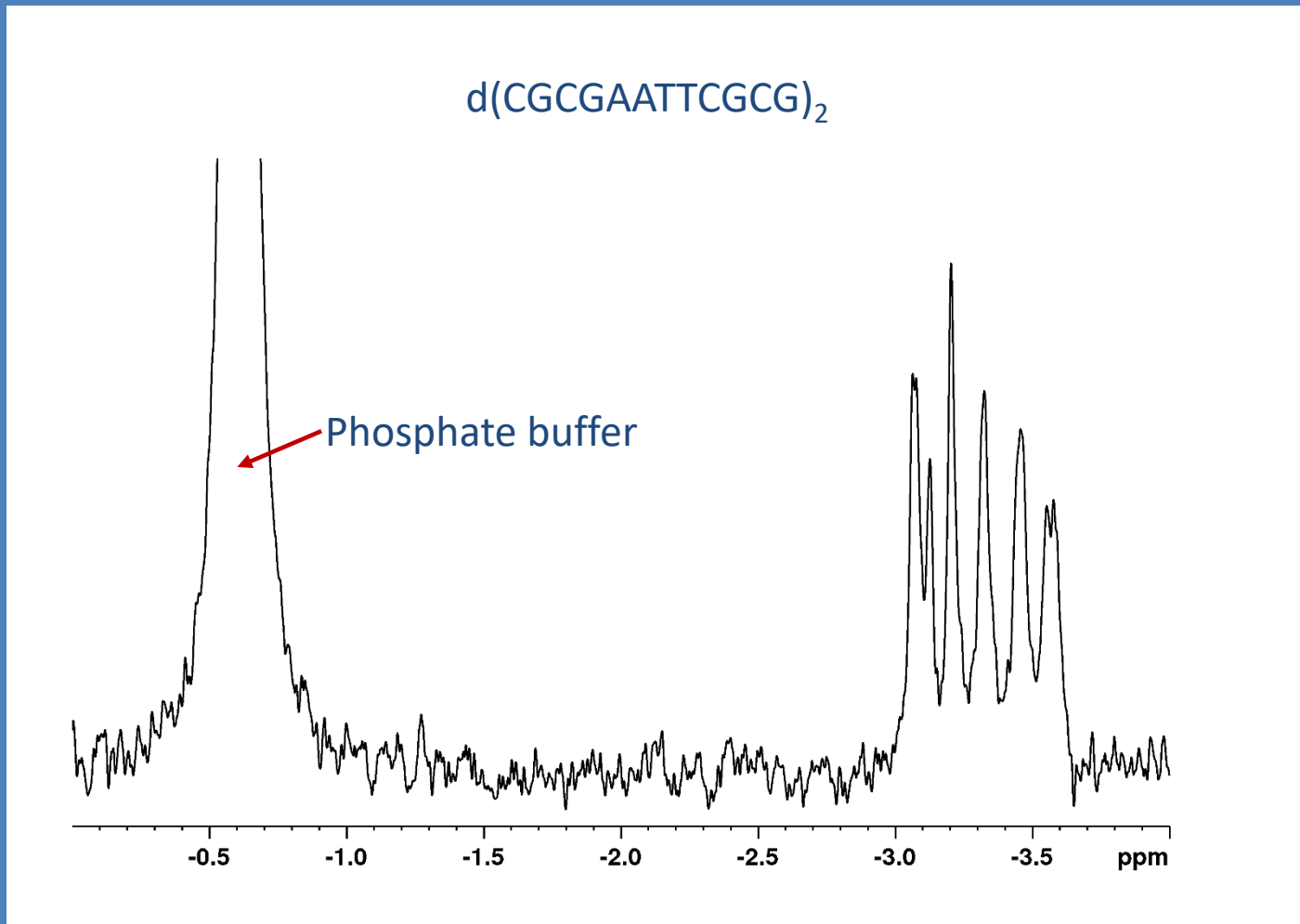


Assignment based on H6/8-H2'2'' connectivities

$d(\text{CGCGAATTCGCG})_2$



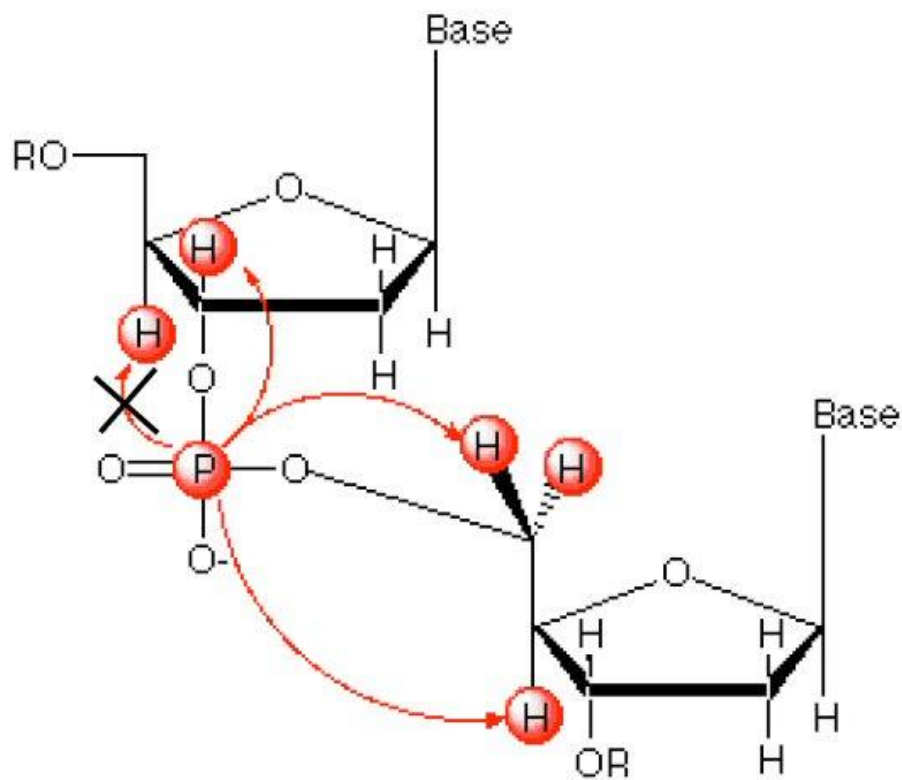
^{31}P spectrum of DNA



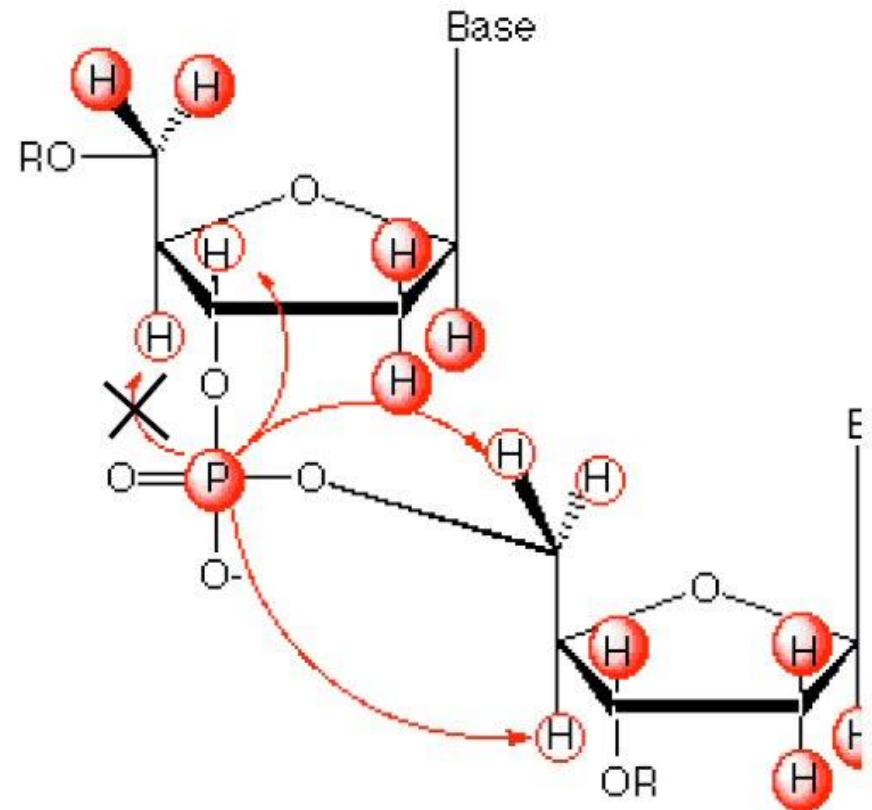
Assignment of Sugar-Phosphate Backbone

^{31}P NMR

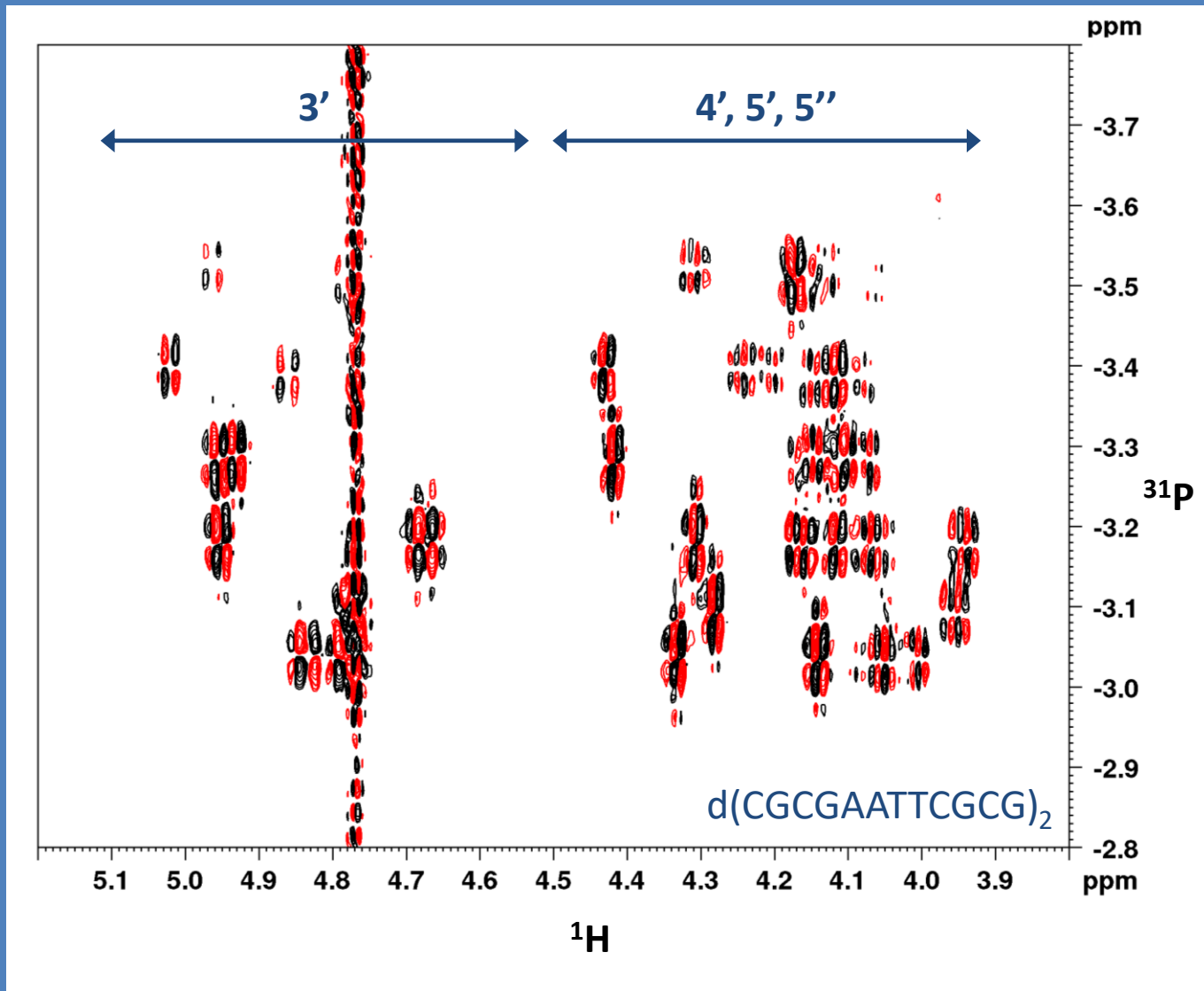
HP-COSY



HP-TOCSY



^1H - ^{31}P correlation spectrum



Sugar pucker

The five membered furanose ring is not planar. It can be puckered in an envelope form (E) with 4 atoms in a plane or it can be in a twist form. The geometry is defined by two parameters: **the pseudorotation phase angle (P)** and the **pucker amplitude (Φ)**.

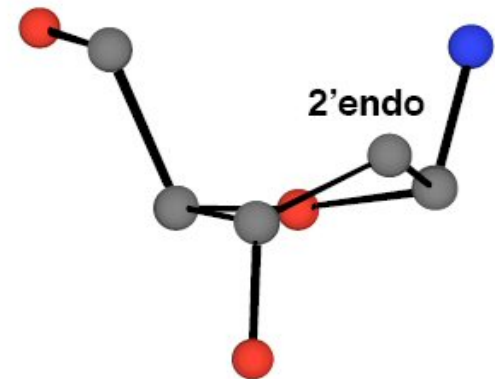
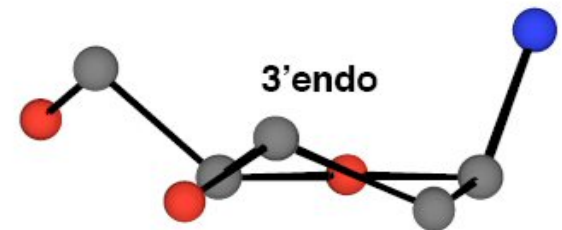
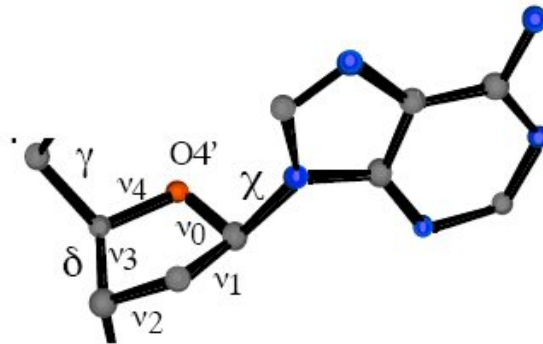
In general:

RNA (A type double helix) C3' endo.

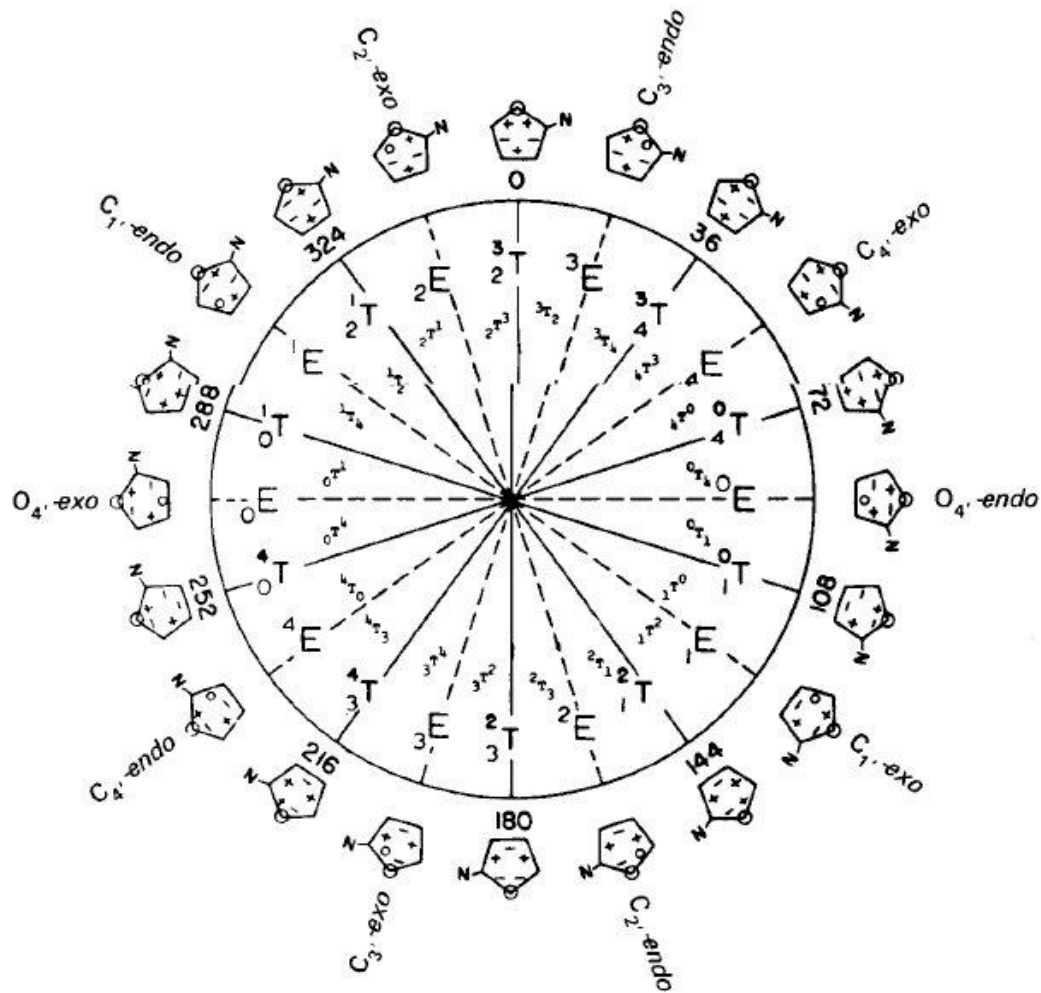
DNA (B type double helix) C2' endo.

$$\nu_i = \Phi_m \cos (P + 144 (j-2))$$

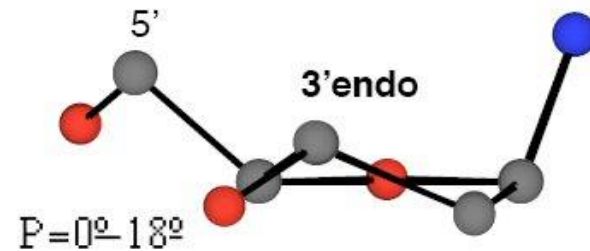
$$\delta = \nu_3 + 125^\circ$$



N (Northern)

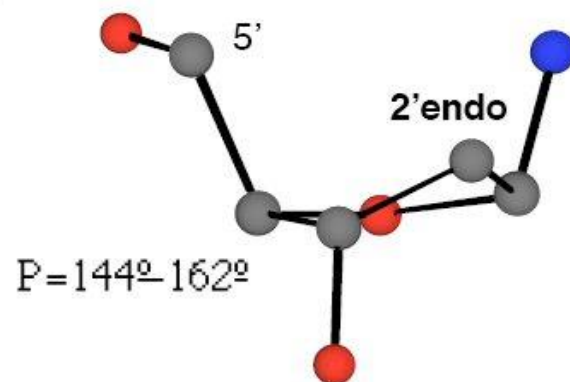


(Southern)



Ribose: $^3J_{H1'-H2'} \approx 1 \text{ Hz}$

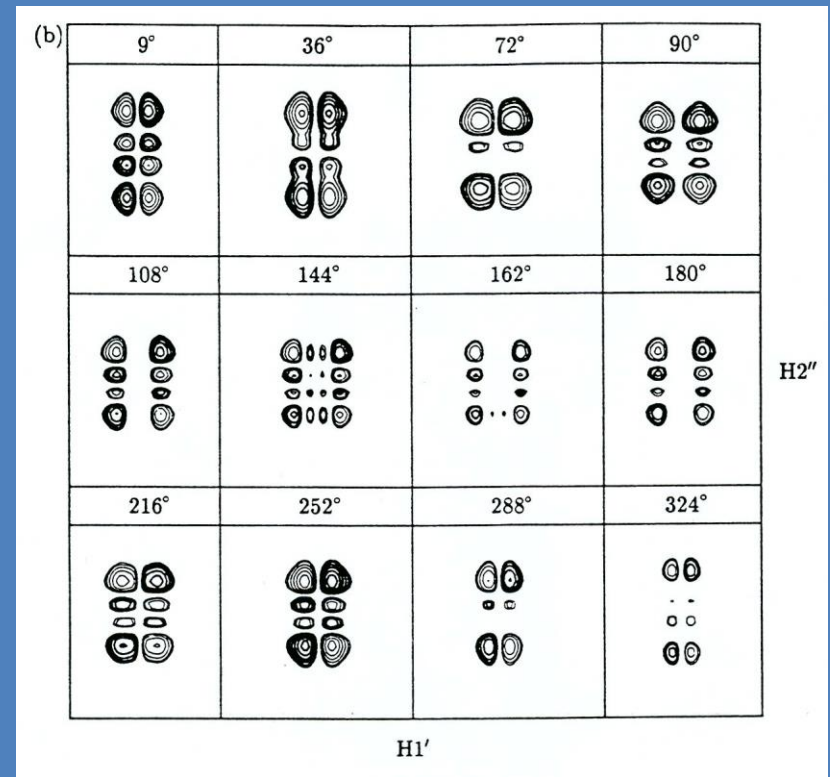
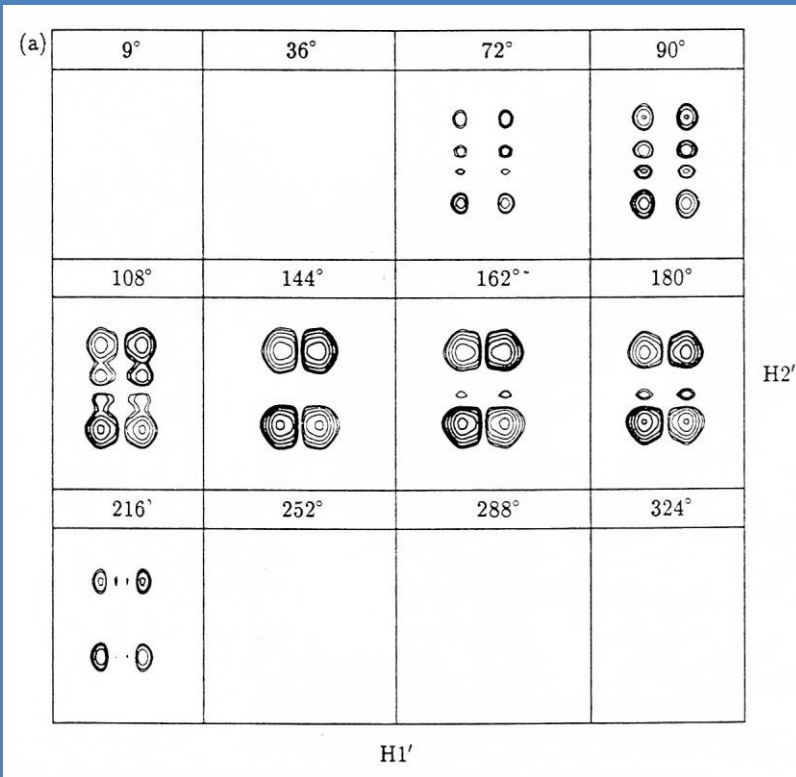
Deoxyribose: $^3J_{H1'-H2'} \approx 1.8 \text{ Hz}$



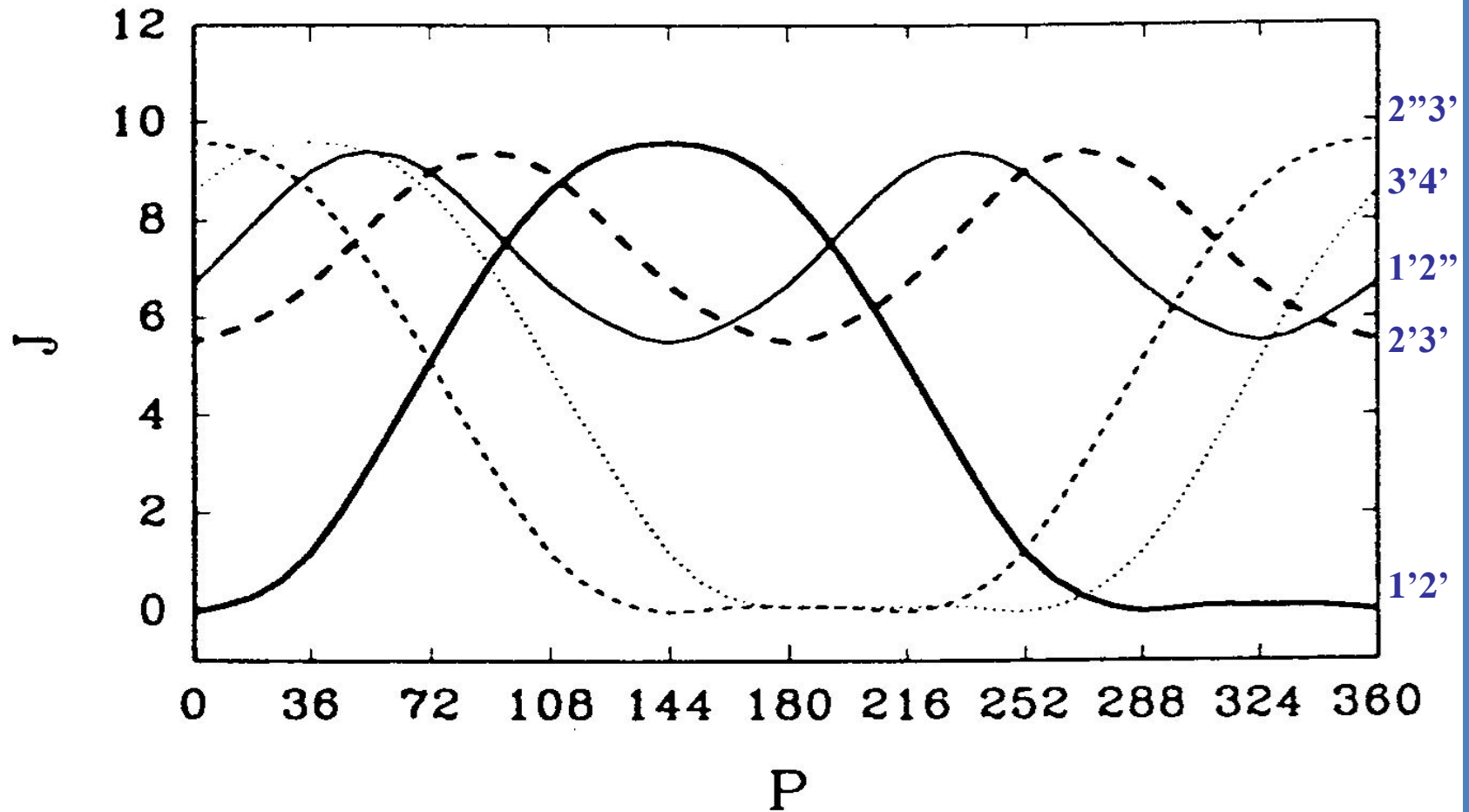
Ribose: $^3J_{H1'-H2'} \approx 7.9 \text{ Hz}$

Deoxyribose: $^3J_{H1'-H2'} \approx 10 \text{ Hz}$

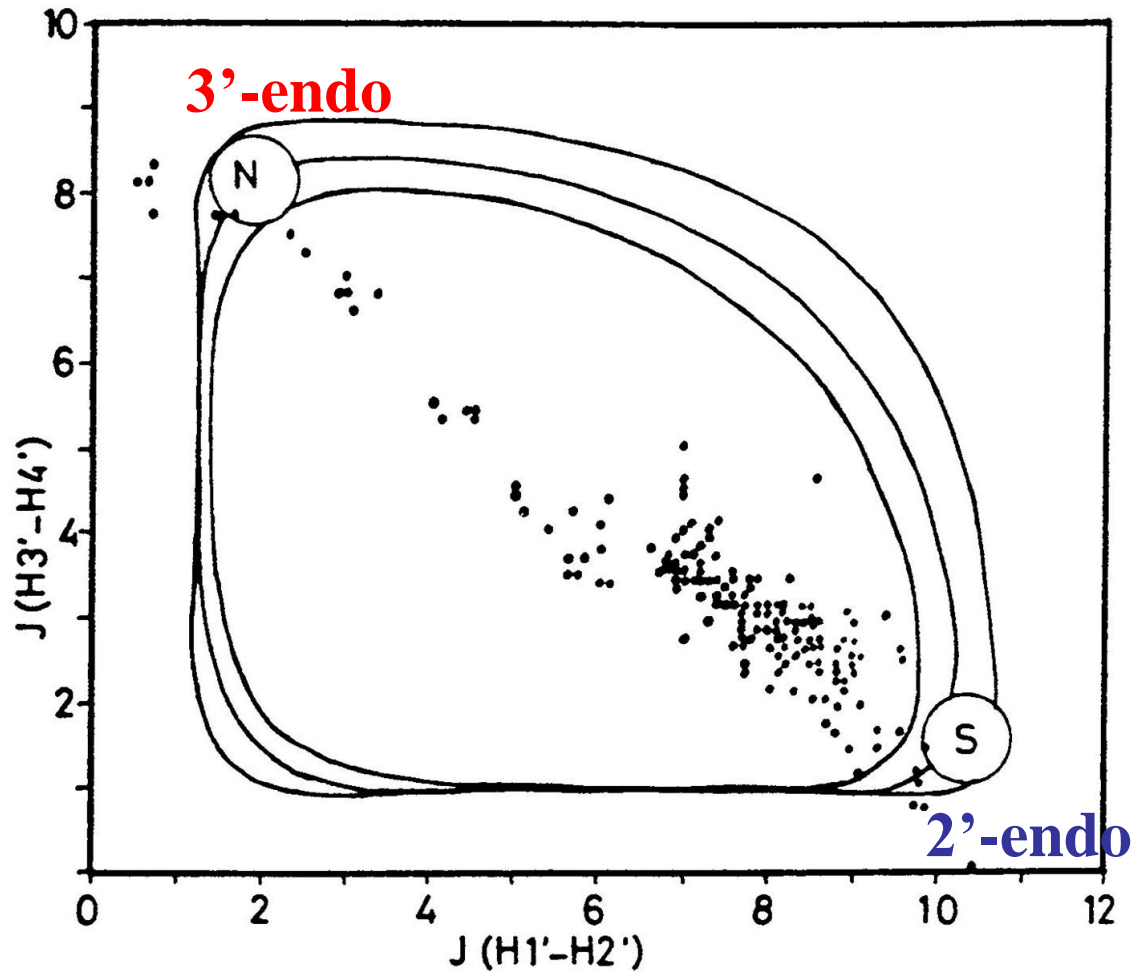
J-couplings from COSY spectra



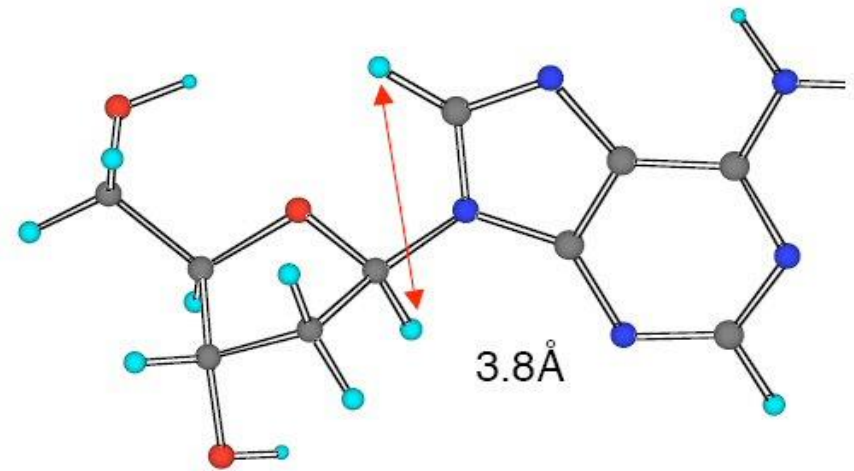
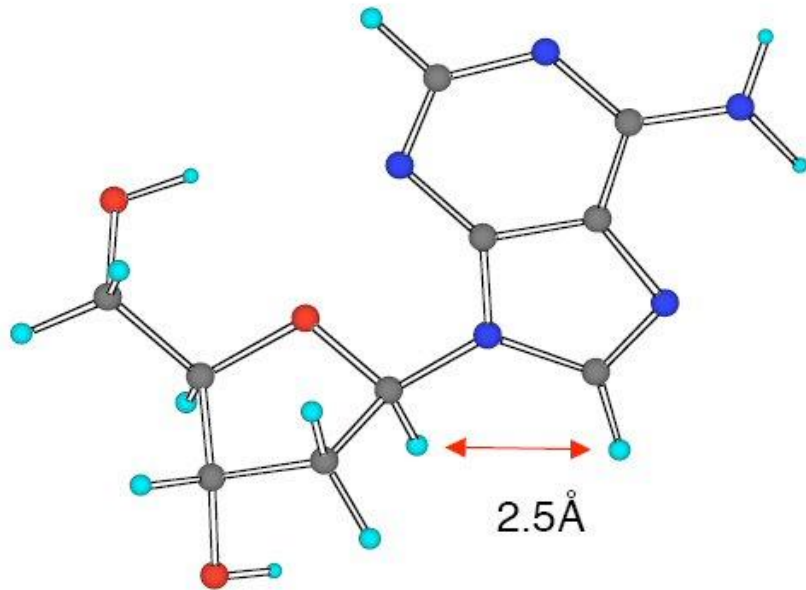
P determination from J-couplings



Equilibrium of N and S conformations



Distance information determines the glycosidic torsion angle



- How do we get distance information?
 - Nuclear Overhauser effect ($< 6\text{\AA}$)

Heteronuclear NMR of Nucleic Acids

In most cases, requires samples isotopically enriched by ^{13}C and ^{15}N (except for HSQC, HMQC)

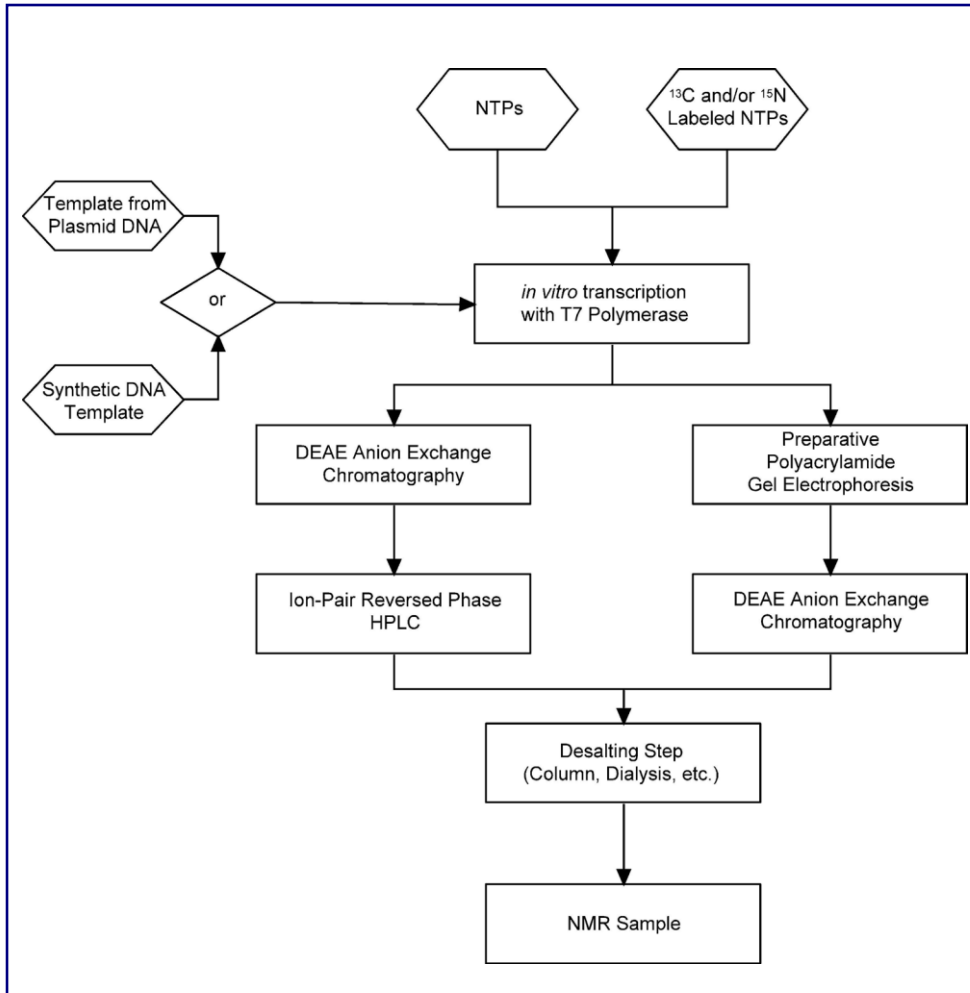
Assignment uses NOE or through-bond experiments

Traditional constraints (NOEs, J-couplings)

Novel constraints (RDCs, residual CSA)

Studies of intramolecular dynamics

RNA preparation



Labeled NTPs

Available commercially

Can be grown in cells

E. Coli

¹³C-glucose, ¹⁵N-ammonium

M. Methylotropus

¹³C-methanol, ¹⁵N-ammonia

Assignment procedure for labeled NA NOE based (I)

I. (H₂O)

Correlation of exchangeable protons with ¹⁵N

2D ¹H-¹⁵N HSQC NH imino optimized (Gua and Ura)

2D ¹H-¹⁵N HSQC NH₂ amino optimized (Cyt, Gua, Ade)

Sequential assignment of exchangeable protons

3D NOESY-HSQC (¹H-¹H-¹⁵N, imino ¹⁵N edited NOESY)

imino-imino and imino-amino interactions

3D NOESY-HSQC (¹H-¹H-¹⁵N, amino ¹⁵N edited NOESY)

amino-imino interactions



II. (H₂O)

Assignment of non-exchangeable protons with NOE connectivities to imino and amino protons

3D NOESY-HSQC (¹H-¹H-¹⁵N, imino/amino ¹⁵N edited NOESY)

interactions of aromatic protons with imino and amino groups



Assignment procedure for labeled NA

NOE based (II)

III. ($^2\text{H}_2\text{O}$) **Identification of hydrogen and carbon atoms in sugars**

2D ^1H - ^{13}C CT-HSQC identification of H-C pairs

3D HCCH-COSY identification of neighboring C-H groups

3D HCCH-RELAY H1'-C2'/C3' correlation

3D HCCH-TOCSY H1'-C2'/C3'/C4'/C5' correlation

Identification of hydrogen and carbon atoms in bases

2D ^1H - ^{13}C CT-HSQC identification of H-C pairs

2D/3D HCCH-COSY H5-H6 and C5-C6 correlations in pyrimidines

Sequential assignment

3D NOESY-HSQC (^1H - ^1H - ^{13}C), H6/8-H1', H6/8-H2' correlations

IV. ($^2\text{H}_2\text{O}$) **Assignment of ^{31}P resonances**

^1H - ^{31}P HETCOR/heteroTOCSY

Assignment procedure for labeled NA

Through bond correlations (I)

I. (H₂O) **Correlation of exchangeable protons with ¹⁵N**
2D ¹H-¹⁵N HSQC **NH imino optimized (Gua and Ura)**
2D ¹H-¹⁵N HSQC **NH₂ amino optimized (Cyt, Gua, Ade)**

II. (H₂O) **Correlation of imino and amino protons with non-exchangeable base protons**
HCCNH-TOCSY / HNCCH-TOCSY

Assignment procedure for labeled NA

Through bond correlations (II)

III. ($^2\text{H}_2\text{O}$)

Correlation of non-exchangeable protons with ^{13}C

2D ^1H - ^{13}C CT-HSQC identification of H-C pairs
3D HCCH-COSY identification of neighboring C-H groups
3D HCCH-TOCSY H1'-C2'/C3'/C4'/C5' correlation

Identification of hydrogen and carbon atoms in bases

2D ^1H - ^{13}C CT-HSQC identification of H-C pairs
2D/3D HCCH-COSY H5-H6 and C5-C6 correlations in pyrimidines
HCCH-TOCSY / ^1H - ^{13}C HMBC H2-H8 correlations in Ade

Sugar-base correlations

$\text{H}_s\text{C}_s\text{N}$ and $\text{H}_b\text{C}_b\text{N}$
 $\text{H}_s\text{C}_s\text{NC}_b\text{H}_b$ / $\text{H}_s\text{C}_s\text{NH}_b$

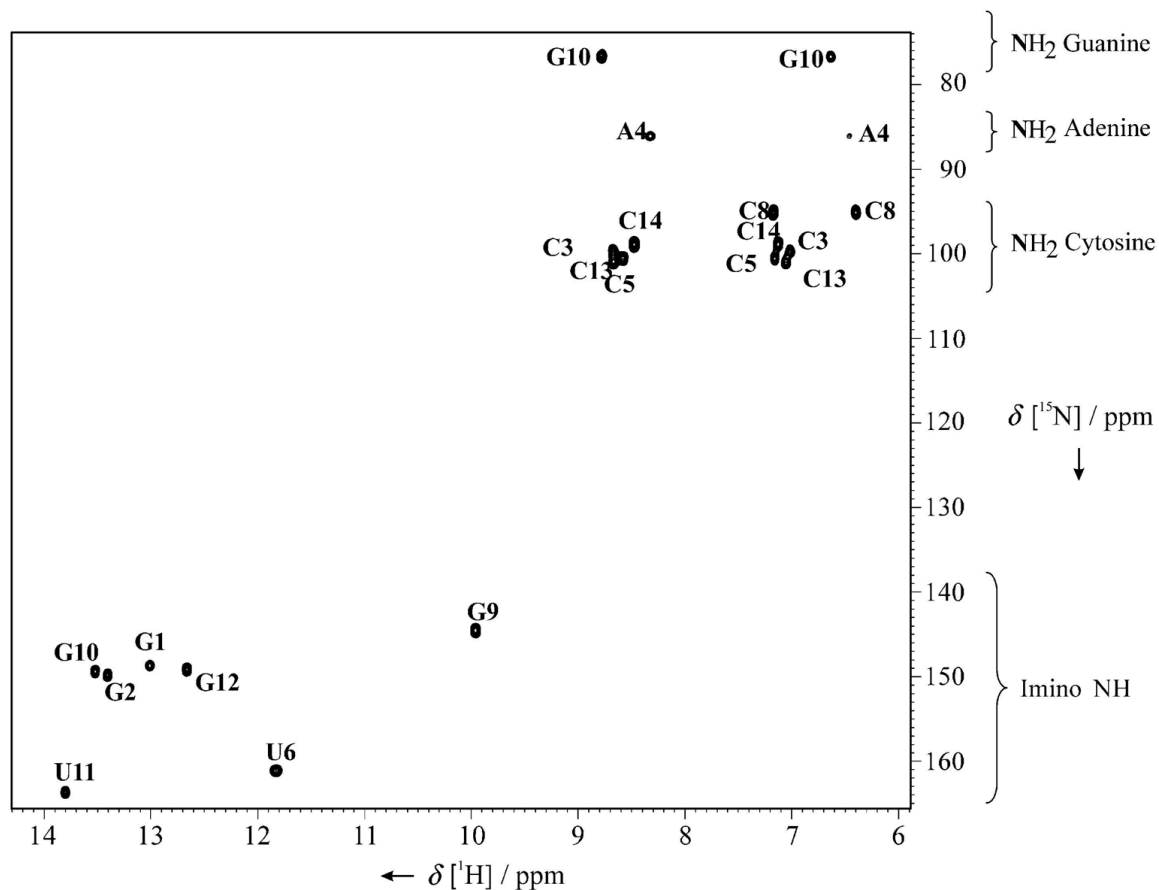
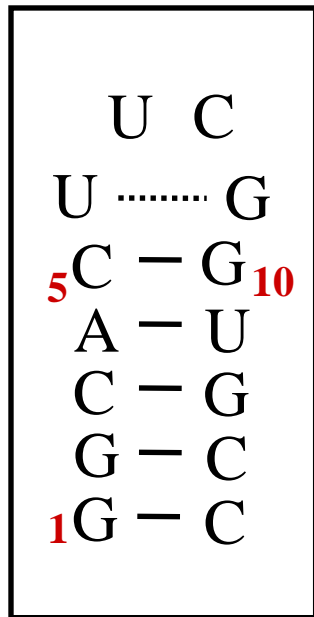


IV. ($^2\text{H}_2\text{O}$)

Sequential assignment of ^{31}P resonances across the sugar-phosphate backbone

HCP / PCH / PCCH-TOCSY / HPHCH

Correlation of exchangeable protons with ^{15}N

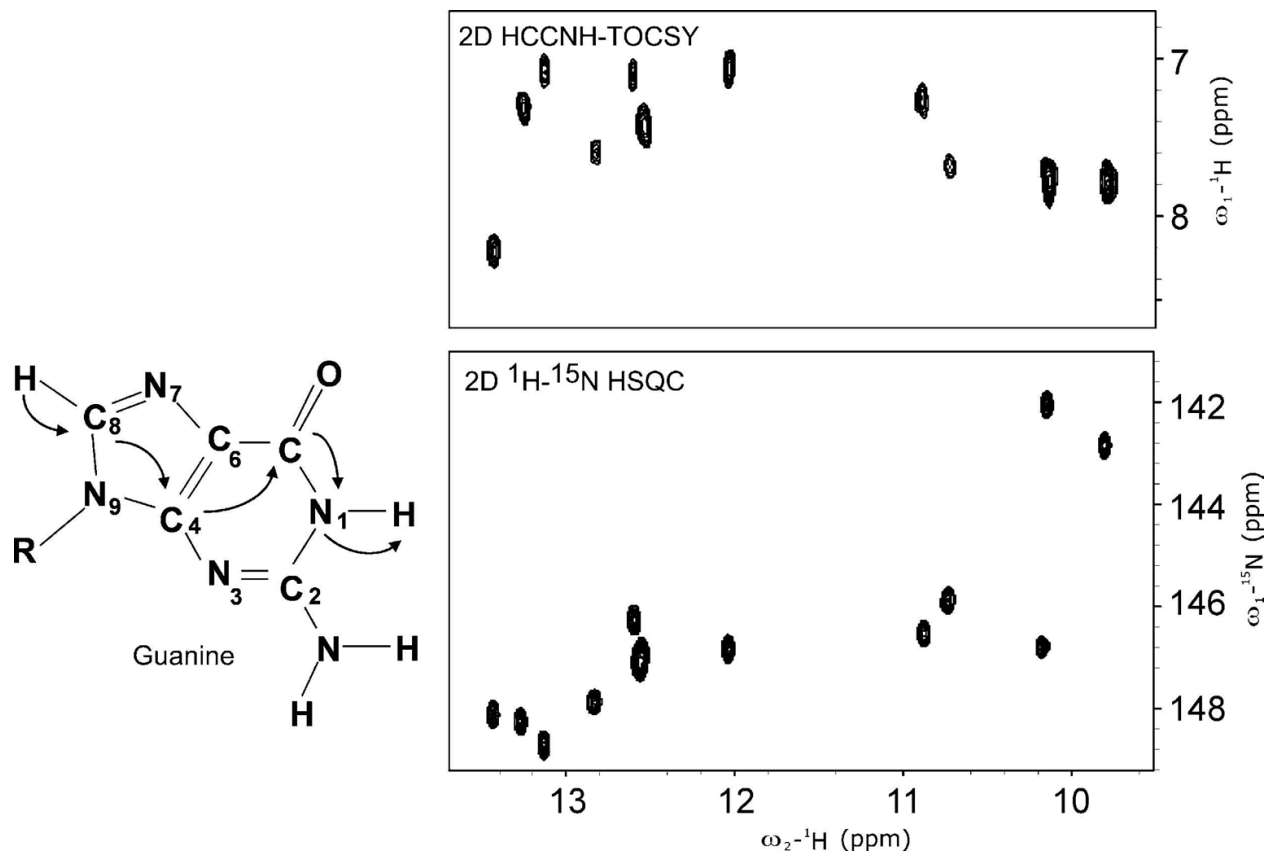


Gradient sensitivity-enhanced HSQC
 Kay, Keifer, Saarinen, JACS 1992.

Assignment of imino protons in loops

Correlation of exchangeable and non-exchangeable protons

Labeled samples – HCCNH-TOCSY

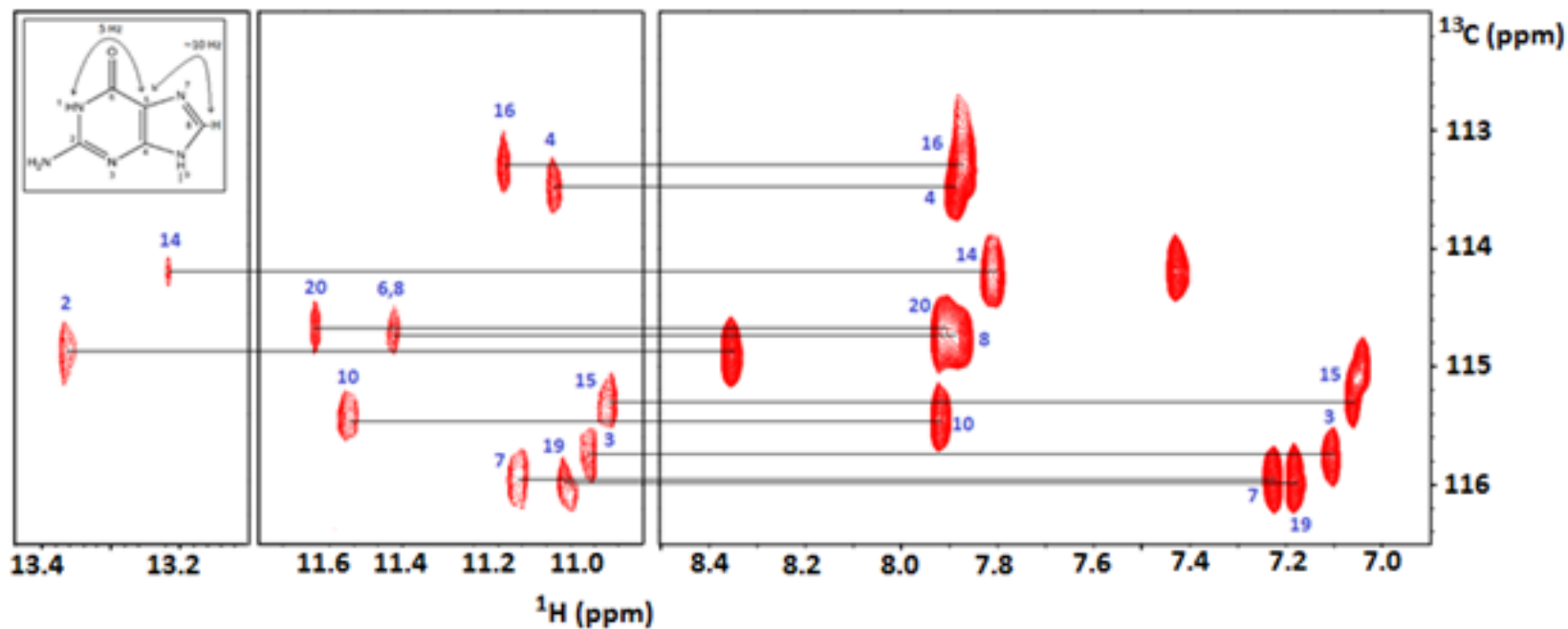


Fiala et al. JACS 1996, Sklenar et al. J. Biomol. NMR 1996.

Assignment of imino protons in loops

Correlation of exchangeable and non-exchangeable protons

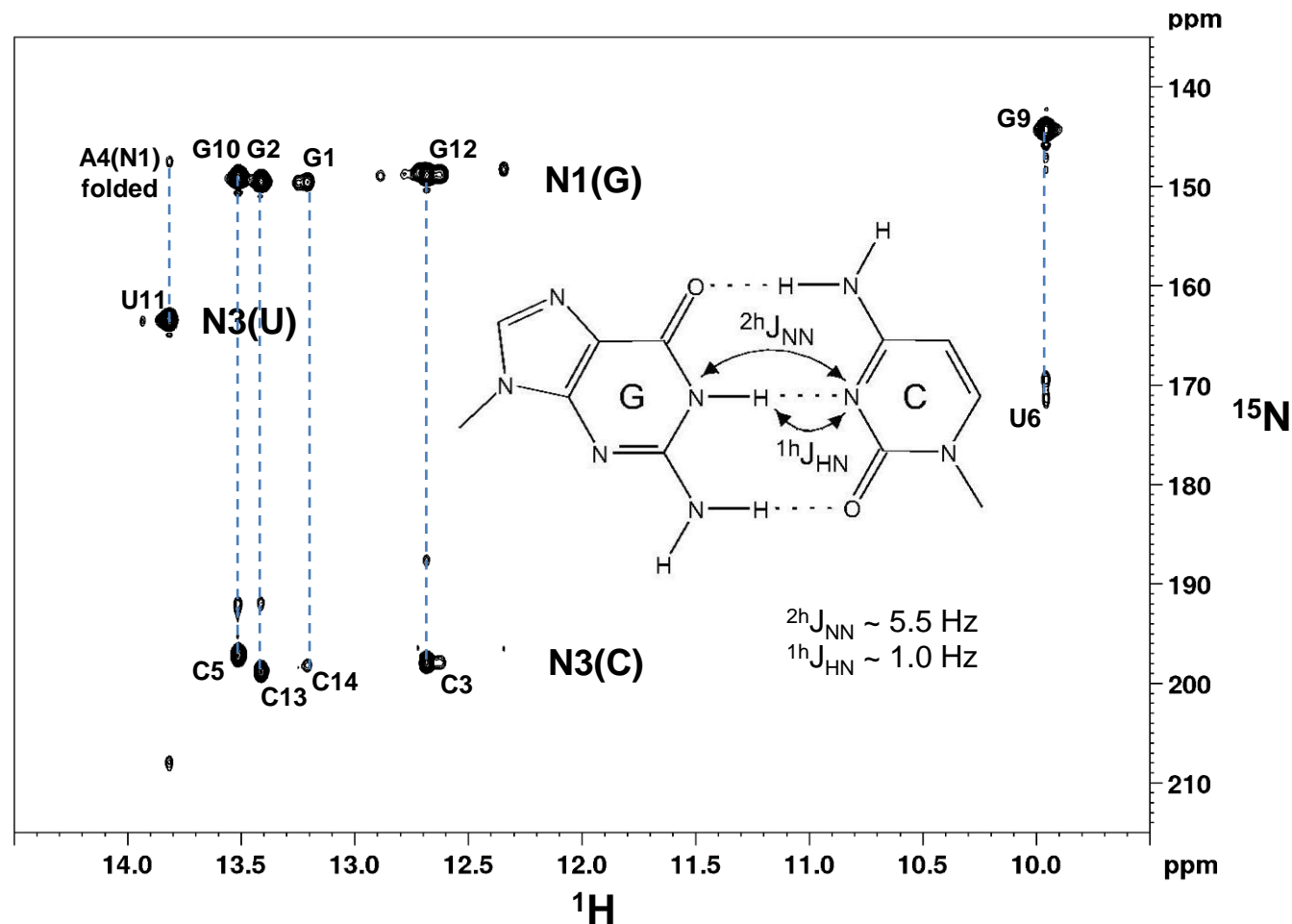
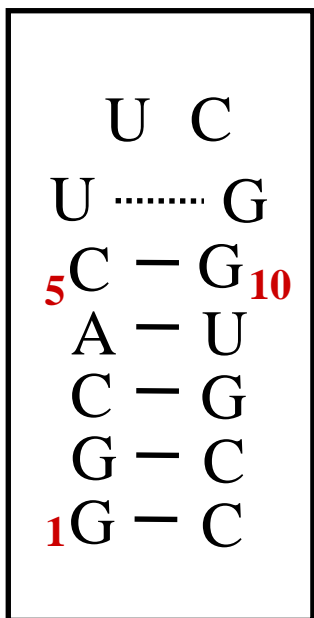
Unlabeled samples – JRHMBC



“Green Monkey” 5'-CGGGCGGGCGCGAGGGAGGGC-3' (21 nt)

Phan, Journal of Biomolecular NMR, 16: 175–178, 2000.

Correlation across the hydrogen bond HNN-COSY experiment

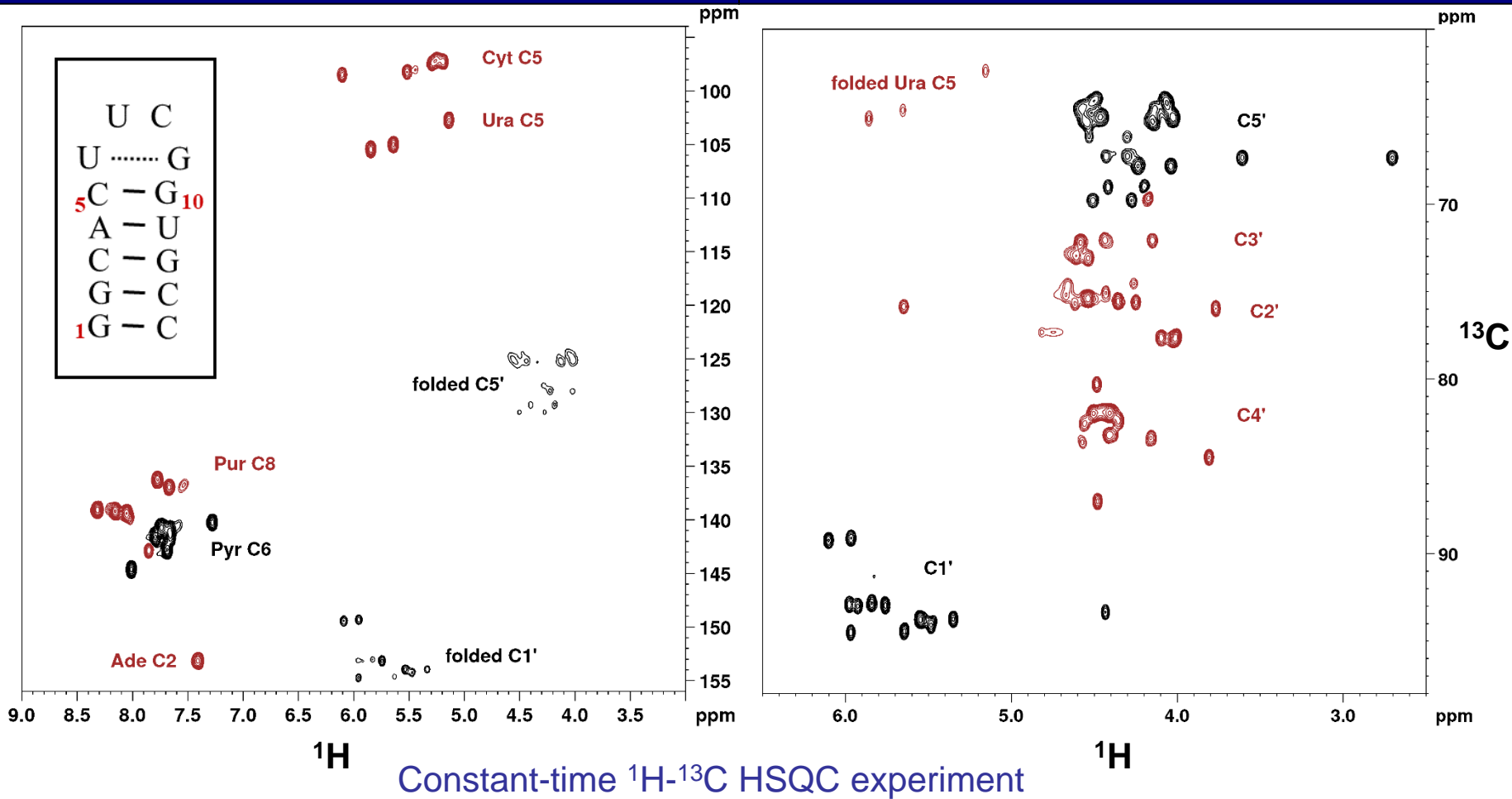


Dingley and Grzesiek, JACS 1998

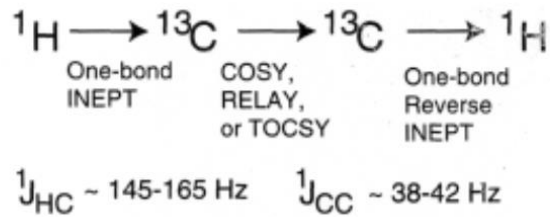
Identification of hydrogen and carbon atoms in bases and sugars

base

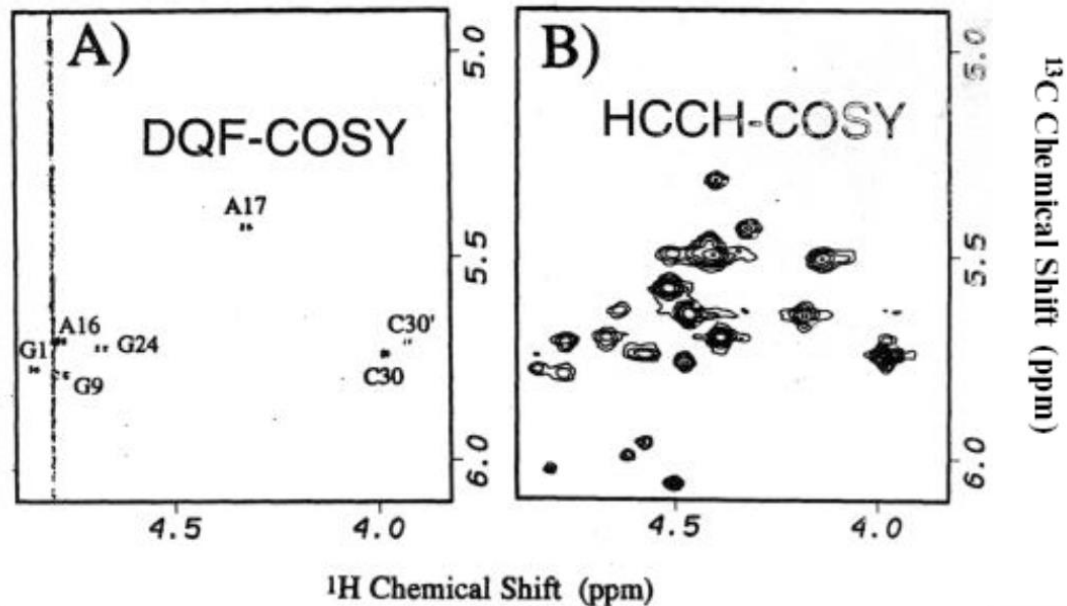
sugar



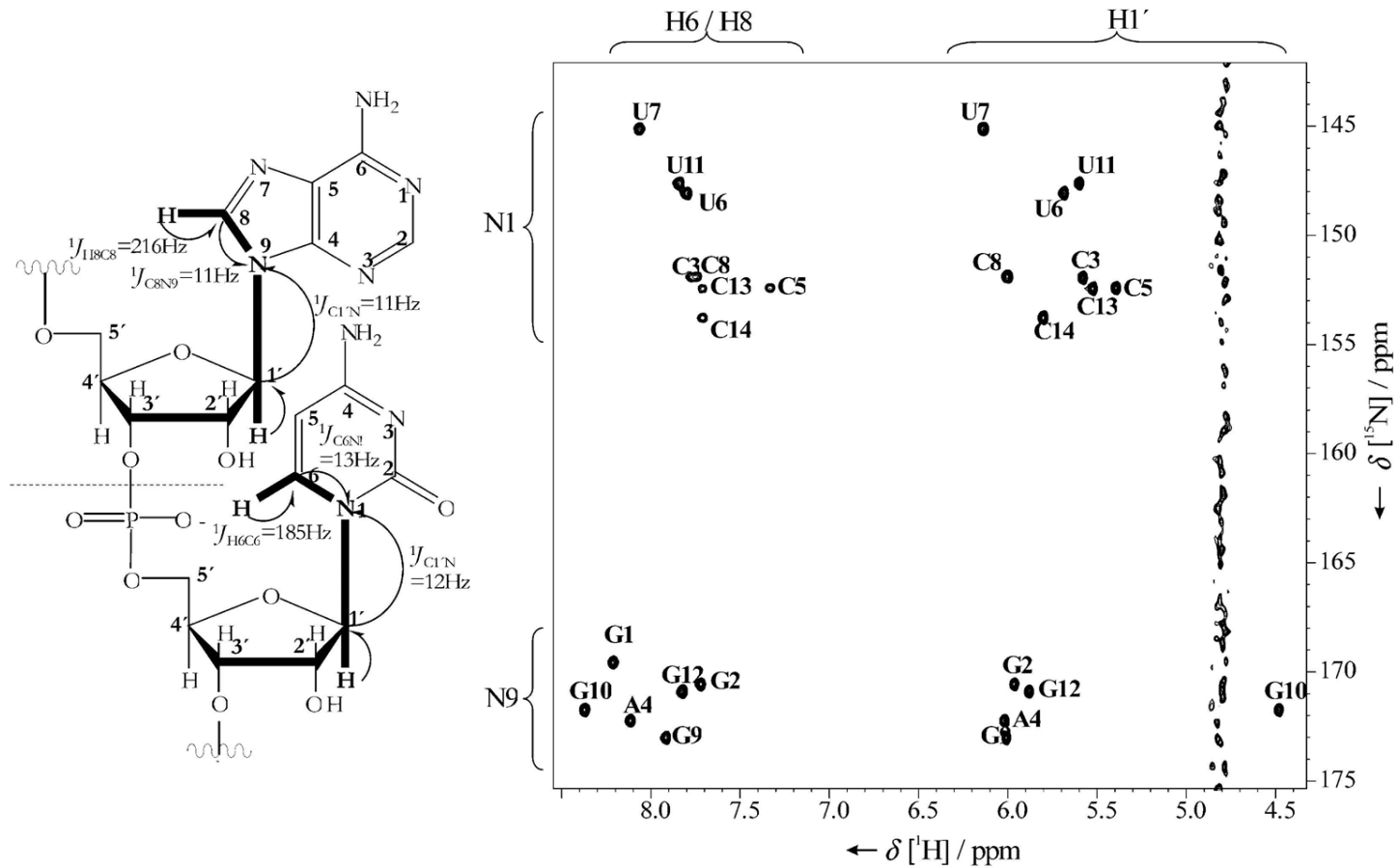
Assignment of non-exchangeable protons: HCCH-type experiments



Allows for unambiguous assignments of
 ${}^1\text{H}$ and ${}^{13}\text{C}$ ribose as well as
 $\text{H}_5\text{C}_5\text{C}_6\text{H}_6$ in pyrimidines

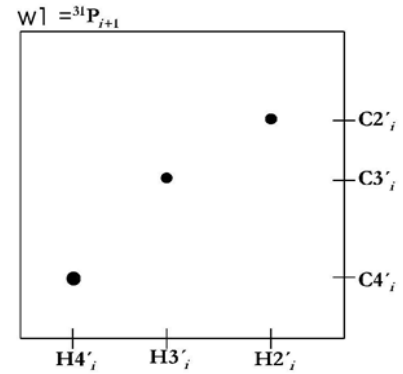
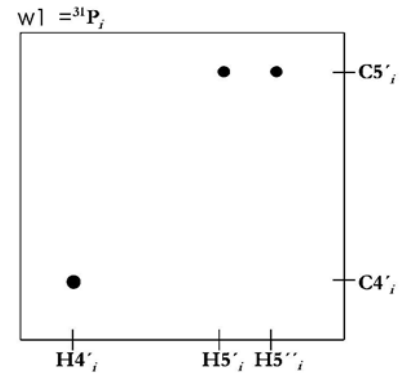
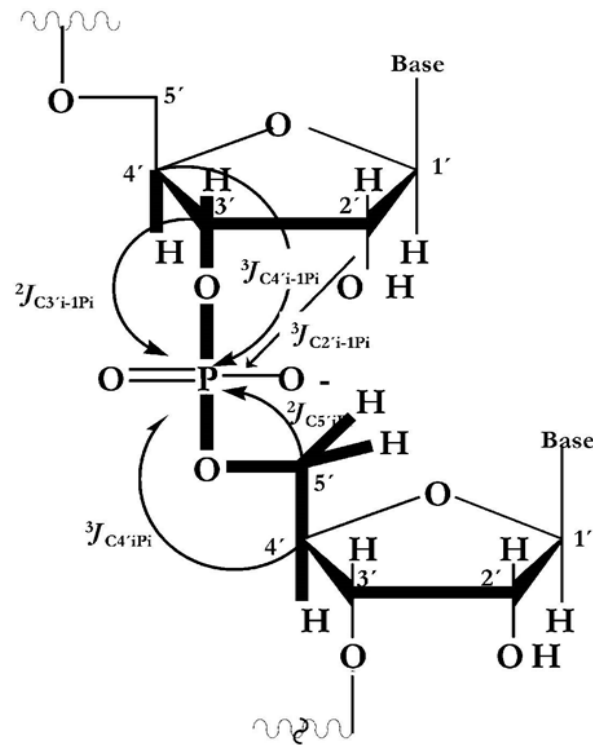


Sugar to base correlation – the HCN experiment



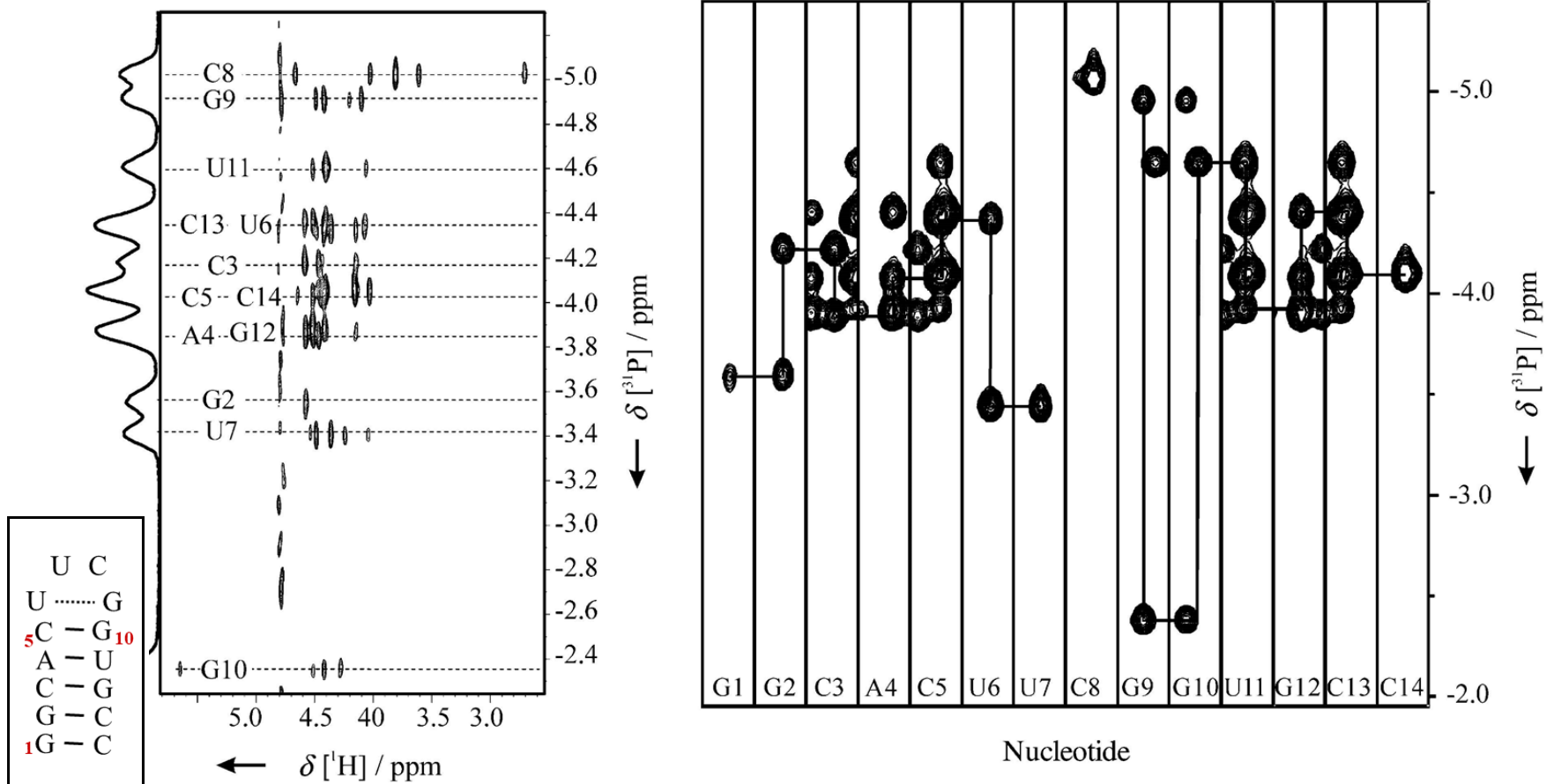
Sklenar et al., J. Biomol. NMR 1993, 1994, Fiala et al., J. Biomol. NMR 1998, 2000.

Sugar to phosphate correlation – the HCP experiment

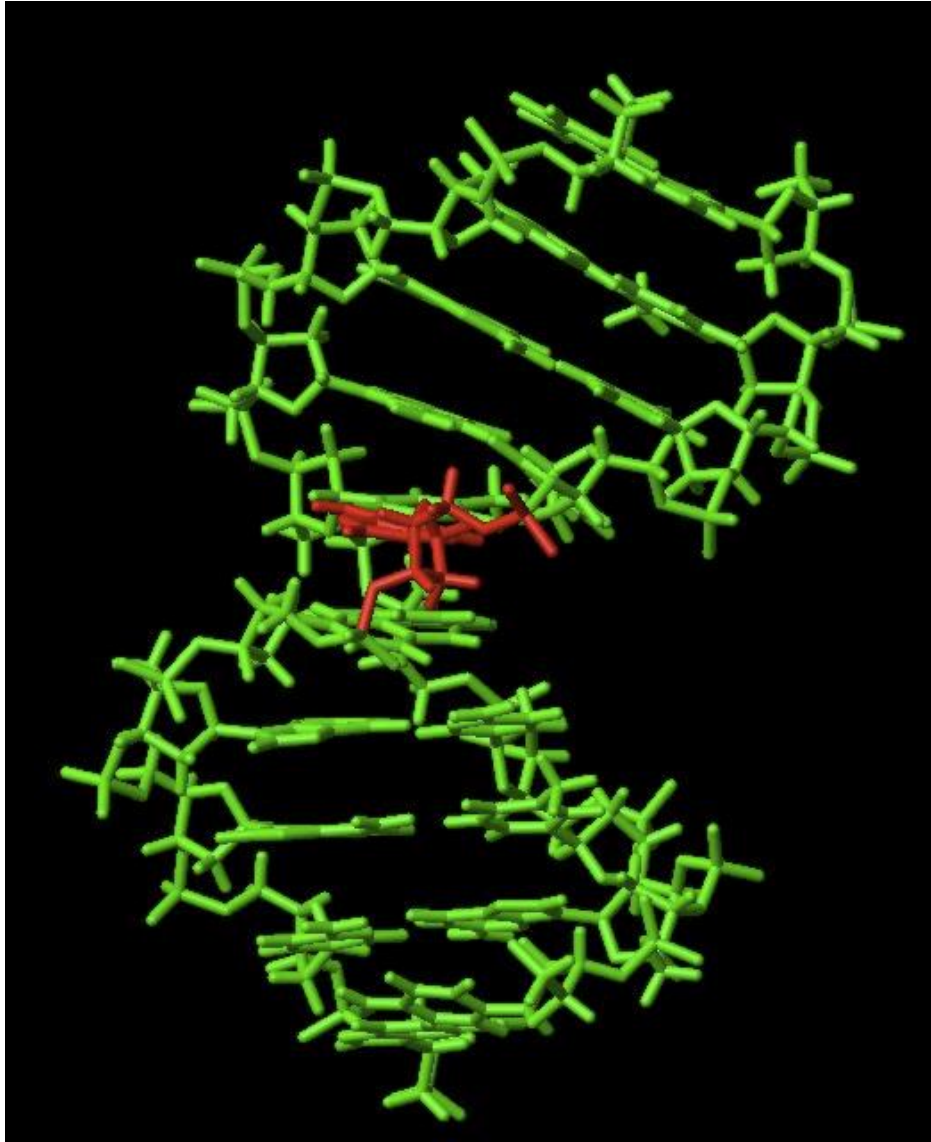


Sugar to phosphate correlation – the HCP experiment

real spectra – nt-14 RNA with UUCG loop



Dipolar couplings



Dipolar couplings add to J couplings

They show up as a field or alignment media dependence of the coupling

If the overall orientation of the molecule is known the orientation of the vectors can be determined

