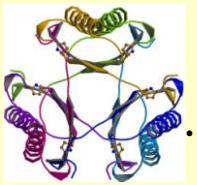
Image Formation

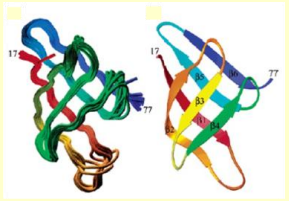
• Light Photography

λ ~ 400 - 700 nm

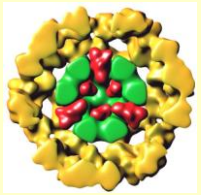


• X-Ray

λ ~ 0.1 nm



• NMR



• Electron Microscopy

λ ~ 0.001 - 0.1 nm

Structure Determination by Multidimensional NMR

1. **NMR Basics**
   - **Spin states / Energy of transitions / Boltzmann Distribution**
   - **What defines a "500 MHz" NMR?**
   - **Chemical shifts / splitting - How to interpret basic NMR spectra?**
2. **Many types of NMR experiments**
   - **COSY / NOESY**
3. **What is multidimensional NMR? Requirements and limitations of the method?**
4. **What is the "Assignment Problem"?**
5. **How are "Assignments" made?**
6. **From peaks to secondary structure to a 3D model.**
   - **How is the protein "model" obtained?**
7. **Comparison of structure determination by X-ray vs. NMR.**

History of NMR

- First described by Isidor Rabi in 1938 when he was experimenting on lithium using molecular beams
- Felix Bloch and Edward Purcell expanded on Rabi's techniques in 1946, concentrating on NMR in liquids and solids

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What is NMR?

- An analytical chemistry technique used to determine content and purity of a sample, as well as the molecular structure
- Used to study known and unknown compounds
- Provides information about the number and types of atoms in a molecule

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What is a Tesla? How strong is a magnetic field of 1 T?

1 T (tesla) = 10^4 gauss

1 gauss = 10^{-4} kg C^{-1} s^{-1}

- **10^{-9}–10^{-8} gauss**: human brain magnetic field
- **0.31–0.58 gauss**: the Earth's magnetic field ~ 5 x 10^{-5} T
- **50 gauss**: a typical refrigerator magnet
- **100 gauss**: a small iron magnet
- **2000 gauss**: a small neodymium-iron-boron (NIB) magnet
- **15,000-30,000 gauss**: a medical magnetic resonance imaging electromagnet
- **10^{12}–10^{13} gauss**: the surface of a neutron star[3]

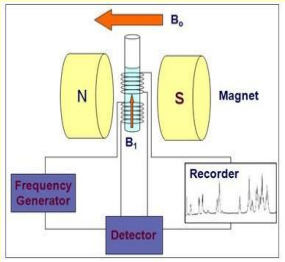
H NMR - Physical Methods

Generation of peaks:

Fluctuation in magnetic field when a hydrogen atom relaxes

Different positions relative to TMS:

Nuclei are shielded or deshielded due to circulating sigma, π, and lone pair electrons.



$$\Delta E = \frac{\gamma h B_o}{2\pi} = h\nu$$

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H NMR - Physical Methods

Larmor equation:

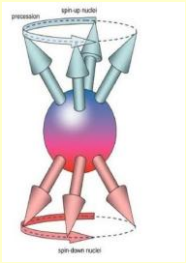
$$\nu = \frac{\gamma B_o}{2\pi}$$

where:

ν is the linear precessional frequency

B_o is the magnetic field strength of the magnet

γ is the gyromagnetic ratio

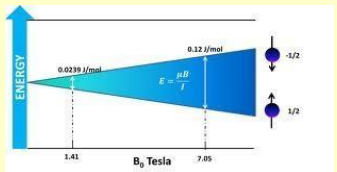


Energy absorbed during the resonance phenomena:

$$\Delta E = \frac{\gamma h B_o}{2\pi} = h\nu$$

where:

h is Planck's constant



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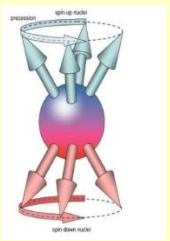
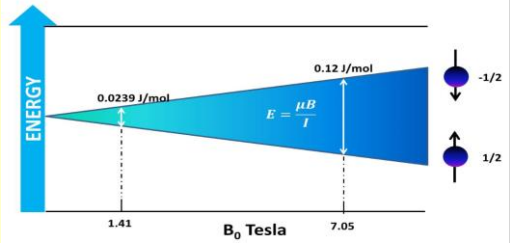




When a group of spins is placed in a magnetic field, each spin aligns in one of the two possible orientations either positive or negative. In sample, which contains a specific NMR-active nucleus, the nuclei will be distributed throughout the various spin states. The energy separation between these states is relatively small and the energy from thermal collisions is sufficient to place many nuclei into higher energy spin states. The number of nuclei in each spin state can be described by the Boltzmann distribution. The Boltzmann equation expresses the relationship between temperature and the related energy as shown below.

$$\frac{N_{upper}}{N_{lower}} = e^{\frac{-\Delta E}{kT}} = e^{\frac{-h\nu}{kT}}$$

Where N_{upper} and N_{lower} represent the population of nuclei in upper and lowe energy states, E is the energy difference between the spin states, k is the Boltzmann constant (1.3805x10-23 J/Kelvin) and T is the temperature in K. At room temperature, the number of spins in the lower energy level, N_{lower}, slightly outnumbers the number in the upper level, N_{upper}.

http://chemwiki.ucdavis.edu/Physical_Chemistry/Spectroscopy/Magnetic_Resonance_Spectroscopies/Nuclear_Magnetic_Resonance/NMR%3A_Theory#Distribution_of_Particles_Between_Magnetic_Quantum_States

NMR Methods

Nuclear spin (nuclear spin Quantum Number *I*)

No spin: #neutrons and #protons both even - 12C, 16O
Half-integer spin (1/2, 3/2, 5/2): #neutrons + #protons odd - 1H, 13C, 15N
Integer spin (1, 2, 3): #neutrons and #protons both odd - 2H, 14N

Spin Quantum Numbers of Common Nuclei

Element	^{1}H	^{2}H	^{12}C	^{13}C	^{14}N	^{16}O	^{17}O	^{19}F
Nuclear Spin Quantum No (I)	1/2	1	0	1/2	1	0	5/2	1/2
No. of Spin States	2	3	0	2	3	0	6	2

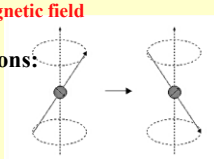
Elements with odd mass or odd atomic number have nuclear "spin".

http://www.chem.umd.edu/courses/chem243davis/

NMR Methods

Nuclear spin and the **splitting of energy levels** in a **magnetic field**

Nuclear spin quantum # "*I*" ; $2I + 1$ orientations:



Magnetic quantum # "m; (m = $-I$ to $+I$)
e.g. $I = ½$; $m = -1/2$, $+1/2$

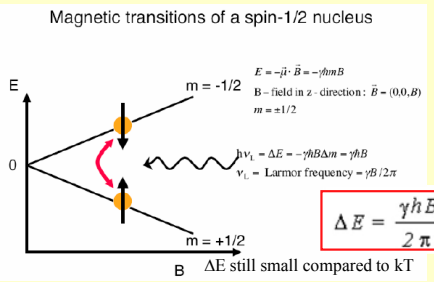
Nuclear magnetic moment

$$\mu = \frac{\gamma I h}{2\pi}$$

Energy of level "*m*"

$$E = -\frac{\gamma h}{2\pi} m B$$

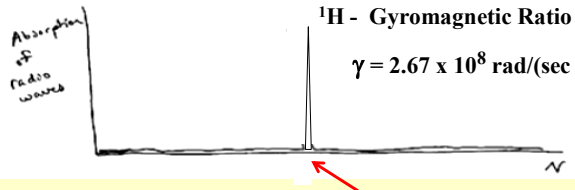
Magnetic transitions of a spin-1/2 nucleus



$$\Delta E = \frac{\gamma h B}{2\pi}$$

ΔE still small compared to kT

NMR Spectrum of Water (H_2O) in a magnetic field of 11.7 Tesla – one peak since both protons are equivalent.



^{1}H - Gyromagnetic Ratio

$\gamma = 2.67 \times 10^{8}$ rad/(sec Tesla)

$\Delta E = \gamma\, h\, B/2\pi = h\,\nu$ or $\nu = \gamma\, B/2\pi$

$\nu = [(2.67 \times 10^{8}$ rad/(sec Tesla) (11.7 Tesla)$]\ /2\pi$

$\nu = 4.97 \times 10^{8}$ /sec = 497 MHz

ΔE still small compared to kT

$$\Delta E = \frac{\gamma h B}{2\pi} = h\,\nu$$

ΔE = h ν with ν ~ 500 MHz
= 6.63×10^{-34} J-s (5.0×10^{8} /s)
= 3.31×10^{-25} J

Boltzmann constant: k = R/T
$PV = nRT = NkT$

kT = (1.38 x 10^{-23} J/K)(298 K)
= 4.11×10^{-21} J

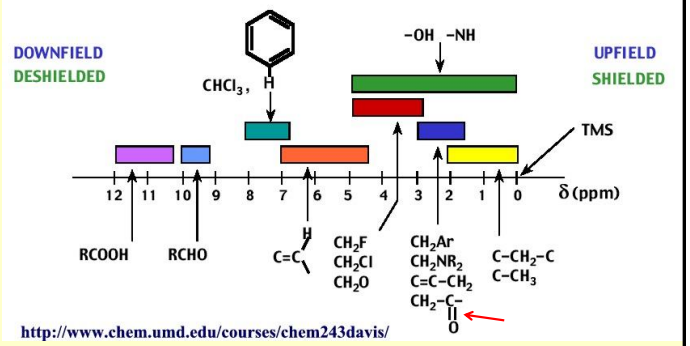
Boltzmann distribution: the probability of a system being in a state with energy E is proportional to $e^{-\Delta E / kT}$

$$\frac{n+}{n-} = e^{-\Delta E / kT}$$

= exp(- 3.31x 10^{-25} J/ 4.11 x 10^{-21} J
= exp(-0.00008) = 0.99992

for 100,992 nuclei ⇒ $\frac{n+}{n-} = \frac{99{,}992}{100{,}000}$

NMR Chemical Shift Chart



Chemical Shift - Makes measurements independent of magnetic field strength – measure frequency of sample vs. frequency of reference compound.

Information from a basic proton NMR spectrum :

1) *Number of signals → number of types of equivalent protons*
2) *Position of signals (chemical shift) → types of protons ("shielded" / "deshielded")*
3) *Relative Intensity of signals (integration) → rel. # protons*
4) *Signal splitting (spin-spin coupling) → n + 1 rule*
   - *one neighboring proton ↑ or ↓ (doublet)*
   - *two neighboring protons ↑↑ or ↑↓ or ↓↑ or ↓↓ (triplet – 1:2:1)*
   - *three neighboring protons ↑↑↑ or ↑↑↓ or ↑↓↑ or ↓↑↑ or ↓↓↑ or ↓↑↓ or ↑↓↓ or ↓↓↓ (quartet) 1:3:3:1*

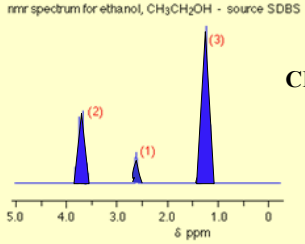
High vs. Low Resolution NMR Spectra

What a low resolution NMR spectrum tells you

Number of peaks -- number of different environments

Ratio of the areas under the peaks -- ratio of the numbers of hydrogen atoms

Chemical shifts -- environment the hydrogens



CH_3-CH_2-OH

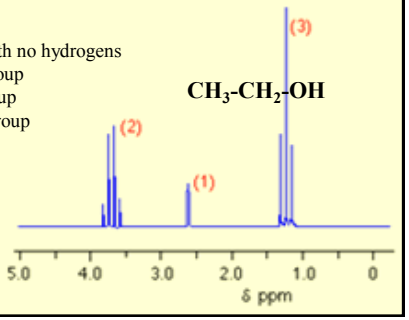
High vs. Low Resolution NMR Spectra

What a high resolution NMR spectrum tells you

In a high resolution spectrum, single peaks in the low resolution spectrum are split into clusters of peaks due to spin-spin coupling. Amount of splitting (**n+1 rule**) tells you about the number of hydrogens attached to the carbon atom ***next door.***

Singlet - next door to carbon with no hydrogens
Doublet - next door to a CH group
Triplet - next door to a CH_2 group
Quartet - next door to a CH_3 group

CH_3-CH_2-OH

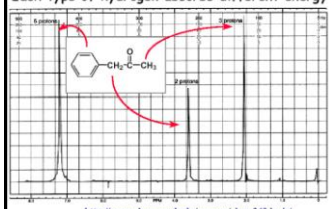


NMR Methods Proteins

Small molecule NMR

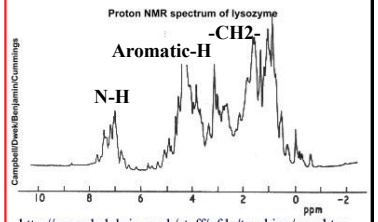
^{1}H NMR Spectrum of Phenylacetone

Each type of hydrogen absorbs different energy



http://www.chem.umd.edu/courses/chem243davis/

"Big" molecule NMR



http://www.bch.bris.ac.uk/staff/pfdg/teaching/nmr.htm

Sample requirements

- ~ 0.25 ml 0.5 mM protein
  (= 2.5 mg for 20 kDa protein)
- ^{15}N, ^{13}C, (^{2}H) labelled (*E. coli*)
- MWT < ~ 60 kDa for 3D structure
- MWT < ~100 (800) kDa for secondary structure, functional tests, etc.

http://www.ti.inf.ethz.ch/ew/Lehre/GCMB07/material/lecture13/NMR.pdf

Limitations for Structure Determination by Multidimensional NMR Methods

1. **Protein must be "smallish" (< 300-500 amino acid residues)**
2. **Protein must be soluble and well behaved in solution.**
   (1-2 mM or 30 mg/mL for a 20kDa protein)
3. **Must be able to solve the "Assignment" Problem**

   Gly43 CA-H vs. Gly87 N-H, etc.

4 **Must have sufficient number of distance restraints**

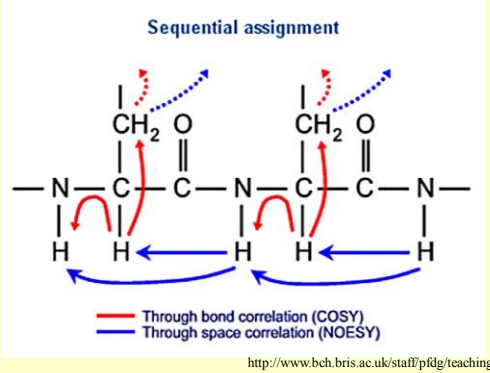
   Gly43 CA-H / Gly87 N-H 3.0 – 4.5 A, etc.

Structure Determination of Proteins in Solution

- Resonance assignment (COSY)
- Distance assignment (NOESY)
- Structure calculation

NMR Methods – COSY vs. NOESY

Two-dimensional **COSY** (**CO**rrelation **S**pectroscop**Y**) experiments allow you to **determine the connectivity** of a molecule by determining which protons are spin-spin coupled. One could accomplish the same task by a detailed analysis of spin-spin splittings, given high enough resolution.



http://www.bch.bris.ac.uk/staff/pfdg/teaching/nmr.htm

Resonance assignment by COSY

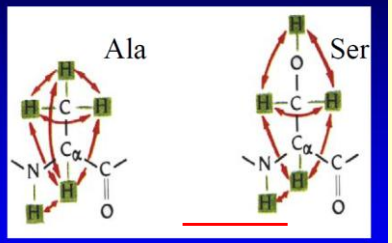
- COSY spectra show frequency correlations between nuclei that are connected by chemical bonds
- Since the different amino acids have a different chemical structure they give rise to different patterns in COSY spectra
- This information can be used to determine the frequencies of all nuclei in the molecule. This process is called resonance assignment
- Modern assignment techniques also use information from COSY experiments with ^{13}C and ^{15}N nuclei

http://www.ti.inf.ethz.ch/ew/Lehre/GCMB07/material/lecture13/NMR.pdf

COSY (Correlation Spectroscopy)

Two-dimensional COSY NMR experiments give correlation signals that correspond to pairs of hydrogen atoms which are connected through chemical bonds.

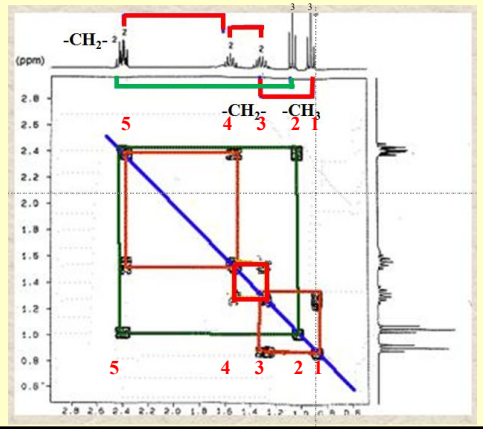
Typical COSY correlations are observable for "distances" of up to three chemical bonds.



COSY correlations between covalently bonded hydrogen atoms

NMR Methods – COSY (thru bonds)

Small molecule "2D" NMR - empirical formula $C_7H_{14}O$



NOESY is a acronym for Nuclear Overhauser Effect Spectroscopy. NOE is the perturbation of the magnetization of one spin due to dipolar coupling with another spin. Since this interaction is detected through space the NOESY experiment provides important information on inter-nuclear distances.

NOE = the change in the intensity of the NMR signal of one nucleus when the sample is irradiated with radiowaves at the NMR absorption frequency of another nearby nucleus.

The NOE depends on the distance between nuclei.

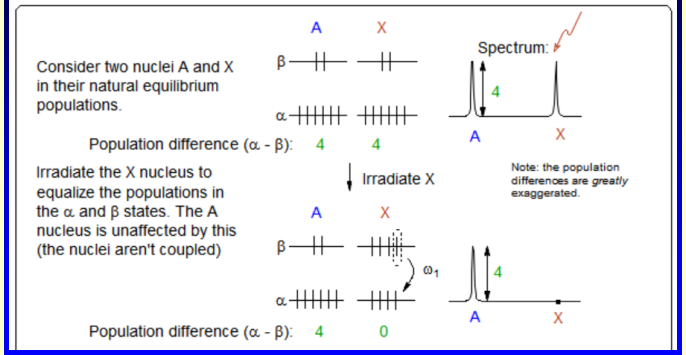
In general,

^{1}H to ^{1}H distance = 3 Å there is a large NOE

^{1}H to ^{1}H distance = 4 Å there is a medium NOE

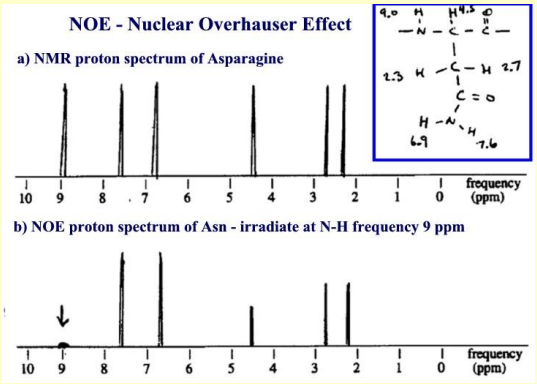
^{1}H to ^{1}H distance = 6 Å there is a small NOE

Distances from NOESY spectra:



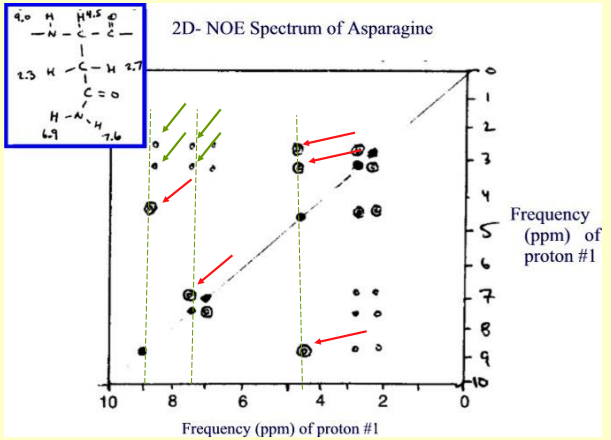
http://www.chem.wisc.edu/areas/reich/nmr/08-tech-02-noe.htm

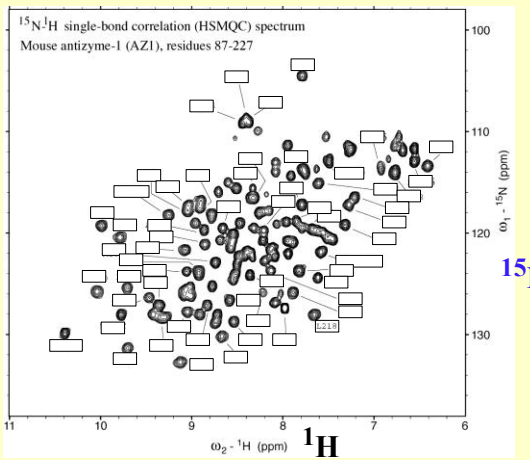
Nuclear Overhauser Effect (NOE) - 1 Dimension



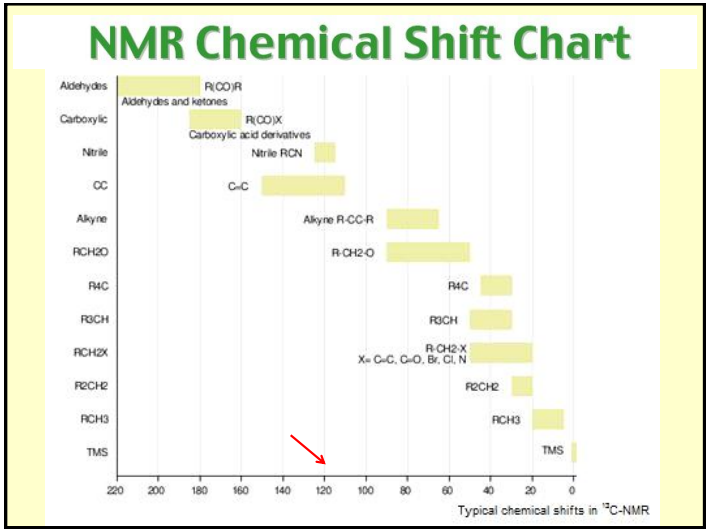
Amide –N-H (9.0) vanishes since populations have been equalized. Proton at 4.5 ppm has biggest change since it is closest.

Nuclear Overhauser Effect (NOE) – 2 Dimensions





The ^{15}N-^{1}H correlated HSQC spectrum of AZ-1Δ86. The relatively disperse resonances are typical of a protein that is folded and suitable for structural study by NMR methods. Some of the assigned resonances are labeled.



Proton Chemical Shifts

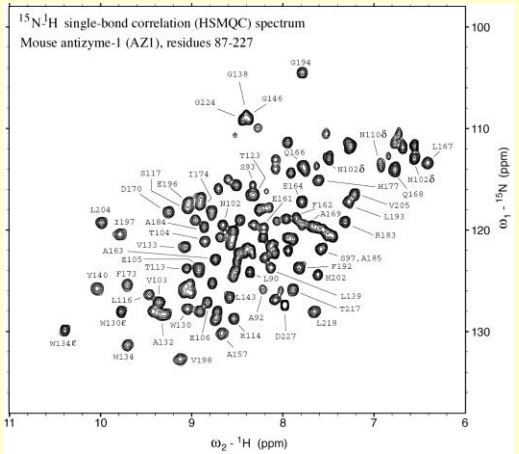
Residue	NH	αH	βH	Others
Gly	8.40	3.97		
Ala	8.25	4.35	1.39	
Val	8.44	4.18	2.13	0.97,0.94(CH3)
Ile	8.20	4.23	1.90	21.48,1.10 (CH2), 0.95 (γ CH3), 0.89 (δ CH3)
Leu	8.42	4.38	1.65,1.65	1.65 (γ CH), 0.94,0.90(δ CH3)
Pro	-	4.44	2.28,2.02	2.03 (γ CH2), 3.68,3.65 (δ CH2)
Ser	8.38	4.50	3.88	
Thr	8.24	4.35	4.22	1.23 (γ CH3)
Asp	8.41	4.76	2.84,2.75	
Glu	8.37	4.29	2.09,1.97	2.31,2.28 (γ CH2)
Lys	8.41	4.36	1.85,1.76	1.45 (γ CH2), 1.70 (δ CH2), 3.02 (ε CH2), 7.53 (γ NH3)
Arg	8.27	4.38	1.89,1.79	1.70 (γ CH2), 3.32 (δ CH2), 7.17,6.62 (NH)
Asn	8.75	4.75	2.83,2.75	7.59,6.91 (δ NH2)
Gln	8.41	4.73	2.13,2.01	2.38 (γ CH2), 6.87,7.59 (γ NH2)
Met	8.42	4.52	2.15,2.01	2.64 (γ CH2), 2.13 (ε CH3)
Cys	8.31	4.69	3.28,2.96	
Trp	8.09	4.70	3.32,3.19	7.1-7.5 (aromatic), 10.22 (NH)
Phe	8.23	4.66	3.22,2.99	7.3-7.4 (aromatic)
Tyr	8.18	4.60	3.13,2.92	6.85-7.15 (aromatic)
His	8.41	4.63	3.26,3.20	7.14-8.12 (aromatic)

Carbon Chemical Shifts

Residue	αC	βC	Others of Distinction
Gly	45	-	
Ala	53	18	
Val	60	33	20 (CH3)
Ile	58	38	18 (γ CH3), 14 (δ CH3)
Leu	53	40	25 (δ CH3)
Pro	60	30	50 (δ CH2)
Ser	58	65	
Thr	62	70	18 (γ CH3)
Asp	55	35	
Glu	55	28	
Lys	53	32	40 (ε CH2)
Arg	55	30	42 (δ CH2)
Asn	55	35	
Gln	55	32	
Met	55	35	16 (ε CH3)
Cys	55	35(ox)/25(red)	
Trp	55	28	90-110 (aromatic)
Phe	55	35	115-125 (aromatic)
Tyr	55	35	95 (ε C), 125 (δ C)
His	55	28	100 (δ 2), 130 (ε 1)

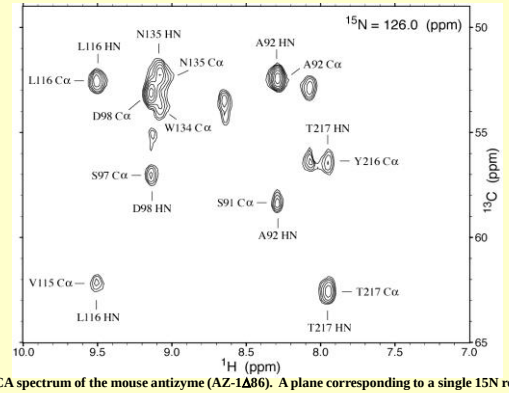
az1_80_136.xls

	A	B	C	D	E	F	G	H	I	J	K	L	M
1	no	type	HN	N	CA	CA-1	CB	CB-1	CO	CO-1	HA	HB	HG
2	87	D											
3	88	H											
4	89	S			58.6		63.7		173.9		4.42		
5	90	L	8.42	124.2	55.2	58.8	42.3	63.6	176.7	174.1	4.44	1.67	1.82,1.57
6	91	S	8.24	116.1	58.1	55.1	63.8	42.0	173.3	176.7	4.48	3.92	
7	92	A	8.27	125.6	52.4	58.2	19.4	63.8	176.6	173.3	4.48	1.45	
8	93	S	8.39	115.2	57.8	52.3	64.2	19.4	172.8	176.7	4.60	3.94	
9	94	I	8.62	124.3	61.1	57.8	37.6	64.1	175.0	173.0	4.22		
10	95	L	8.70	130.2	55.9	61.1	43.9	37.6	175.9	175.0	4.55	1.62	
11	96	Y	7.82	119.1	58.1	55.9	42.5	43.9	171.9	175.9	4.62		
12	97	S	7.62	121.6	57.0	58.0	65.3	42.4	171.4	171.9	4.99	3.77,3.66	
13	98	D	9.14	126.0	53.1	57.0	40.8	65.2	174.8	171.3	4.48		
14	99	E	8.76	115.8	59.1	53.3	29.0	40.8	176.3	174.8	4.14	2.33,2.06	
15	100	R	8.82	118.1	56.8	59.0	32.4	29.0	174.8	176.3	4.66		
16	101	L	8.60	121.5	53.9	56.4	46.7	32.6	174.3	174.8	5.32	1.66,1.60	1.26
17	102	N	8.70	119.6	53.7	53.9	42.0	46.5	173.5	174.2	5.20	2.75	
18	103	Y	9.41	127.0	61.3	53.8	33.4	42.0	174.2	173.5	5.11	2.05	
19	104	T	8.89	121.1	60.0	61.3	71.4	33.4	172.0	174.2	5.13		1.17
20	105	E	8.96	123.7	55.0	60.0	31.9	71.6	175.2	172.2	5.21		
21	106	E	8.87	127.1	54.0	55.0	29.7	32.0		175.4	4.78	1.85	
22	107	P	no		56.8		32.3						
23	108	T	7.94	114.4	61.4	56.8	71.0	32.5	172.3	176.0	4.66	4.04	1.12
24	109	S	8.59	123.8	55.0	61.6		70.9		172.5	4.31		
25	110	N			53.1		39.3						
26	111	D	8.47	119.8	55.1	53.0		39.3		173.9	4.51	2.76	
27	112	K			56.9		28.6		173.5		5.19		
28	113	T	9.09	123.6	62.9	56.9	69.1	28.6	173.3	173.5	4.35	4.14	1.16
29	114	R	8.58	128.8	55.1	62.9		69.1		173.3	4.56	1.68, 1.80	
30	115	Y	9.05	125.2	62.3	54.8	33.2	32.6	174.0	174.0	4.79	2.05	1.03,0.98
31	116	L	9.50	126.4	52.7	62.3	44.9	33.2	175.3	173.9	5.45	1.8	
32	117	S	9.08	117.8	57.1		63.1		173.6	175.4	5.07	3.85, 3.72	
33	118	I	9.38	128.0	61.0	57.1	39.3	63.1		173.7	4.41	2.12	
34	119	Q	8.95	127.9	54.8	61.1	30.9	39.3		172.7	5.01	1.95, 2.12	



The ^{15}N-^{1}H correlated HSQC spectrum of AZ-1Δ86. The relatively disperse resonances are typical of a protein that is folded and suitable for structural study by NMR methods. Some of the assigned resonances are labeled.

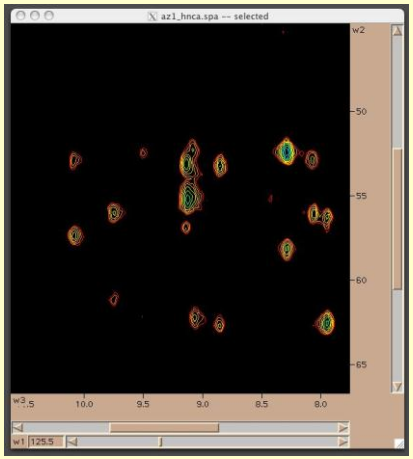
3-dimensional "triple-resonance" NMR
is used for solving the **assignment problem**.



3-D HNCA spectrum of the mouse antizyme (AZ-1Δ86). A plane corresponding to a single 15N resonance frequency is shown, obtained using our 500 MHz cryo-probe equipped instrument. Resonance peaks correlate the backbone amide ^{1}H and ^{15}N nuclei with the alpha 13C of within the same and preceeding amino acid.

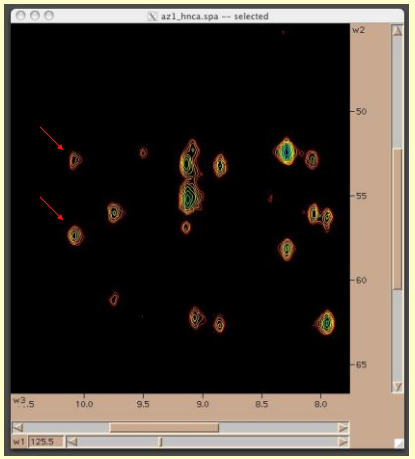
Assignments: AZ-1

"HNCA" spectrum.



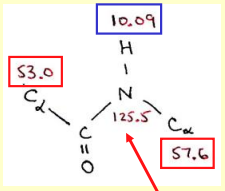
Assignments: AZ-1

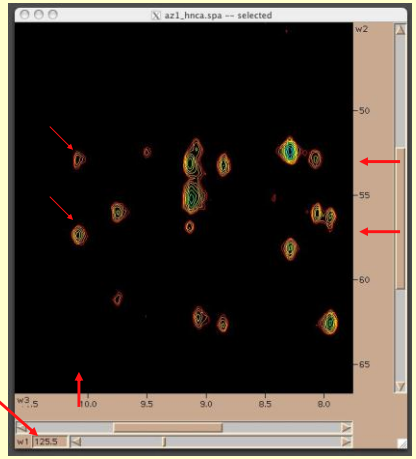
"HNCA" spectrum.



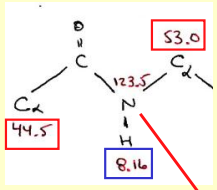
Assignments: AZ-1

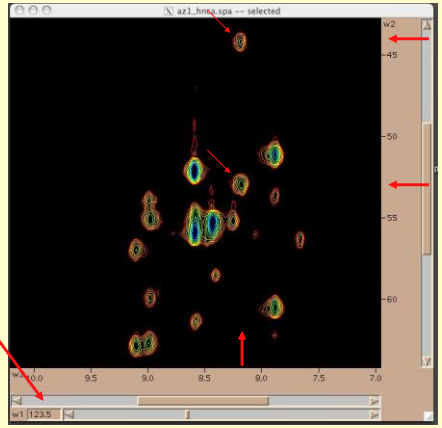
"HNCA" spectrum.



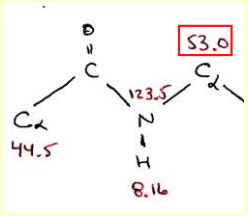


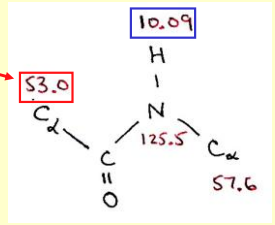
Assignments: AZ-1

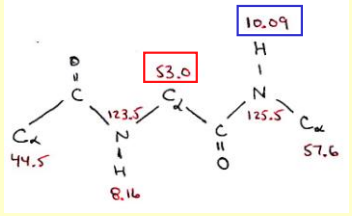




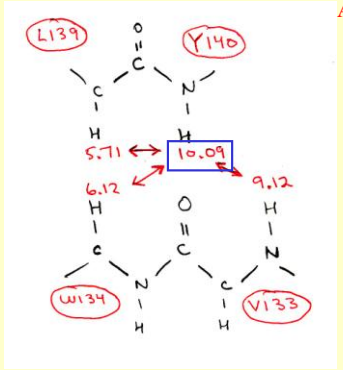
Assignments: AZ-1





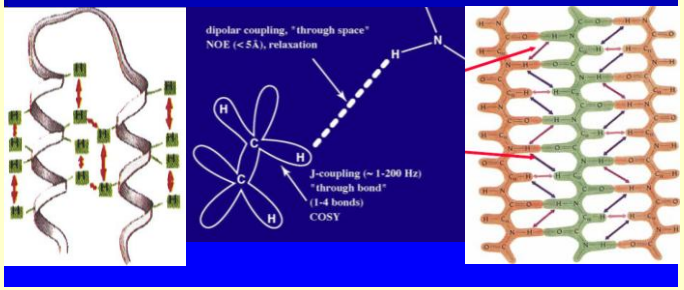


Distance Restraints: AZ-1



Distances from NOESY spectra:

- secondary structure elements
- calculation of three-dimensional structure



http://www.ti.inf.ethz.ch/ew/Lehre/GCMB07/material/lecture13/NMR.pdf

Types of restraints available from NMR experiments

1. NOEs give rough distances between assigned atoms - given as upper and lower bounds.
2. COSY spectra and J-couplings give dihedral angle restraints

Also have constraints from what you know about the protein:

1. Connectivity due to known aa geometry & sequence
2. Standard bond lengths and angles

Energy Refinement

$$E_{TOTAL} = E_{EMPIRICAL} + E_{EFFECTIVE}$$

$$E_{EFFECTIVE} = E_{XREF} + E_{NOE} + E_{HARM} + E_{CDIH} + E_{NCS} + E_{DG} + E_{RELA} + E_{PLAN}$$

$$E_{EMPIRICAL} = \Sigma^{N}_{p=1} [w^{p}_{BOND}E_{BOND} + w^{p}_{ANGL}E_{ANGL} + w^{p}_{DIHE}E_{DIHE} + w^{p}_{IMPR}E_{IMPR} + w^{p}_{VDW}E_{VDW} + w^{p}_{ELEC}E_{ELEC} + w^{p}_{PVDW}E_{PVDW} + w^{p}_{PELE}E_{PELE} + w^{p}_{HBON}E_{HBON}].$$

Bonded Energy Terms

$$E_{BOND} = \sum_{bonds} k_b(\tau - \tau_o)^2$$

$$E_{ANGL} = \sum_{angles} (k_\theta (\theta - \theta_0)^2 + k_{ub}(r_1 3 - r_{ub})^2)$$

$$E_{DIHE} = \sum_{dihedrals\ i=1,m} k_{\varphi i} (1 + \cos(n\varphi_i + \delta_i)) \text{ if } n_i > 0$$

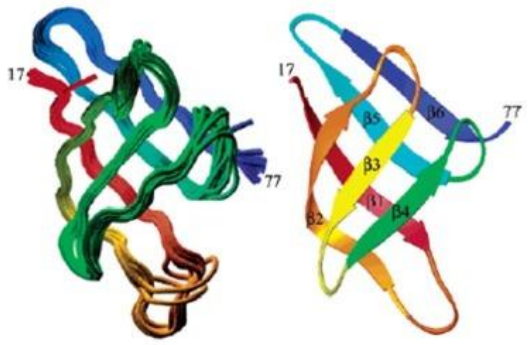
$$\sum_{dihedrals\ i=1,m} k_{\varphi i} (\varphi_i - \delta_i)^2 \text{ if } n_i = 0$$

$$E_{IMPR} = \sum_{impropers\ i=1,m} k_{\varphi i} (1 + \cos(n\varphi_i + \delta_i)) \text{ if } n_i > 0$$

$$\sum_{impropers\ i=1,m} k_{\varphi i} (\varphi_i - \delta_i)^2 \text{ if } n_i = 0$$

Table 1: Summary of Refinement and Structural Statistics for the *A. fulgidus* aRpp29 Protein (Residues 17−77)[a]

intraresidue NOEs	215
sequential NOEs (residue *i* to *i* + 1)	178
medium-range NOEs (residue *i* to *i* + 2, 3, 4)	18
long-range NOEs	143
dihederal angle restraints	70
hydrogen bond restraints	27
total structural restraints	651
no. of unique starting structures for simulated annealing	10
no. of simulated annealing runs, differing in initial trajectories	200
rmsd for backbone atoms (residues 17−77)	0.87 Å
rmsd for side chain atoms (residues 17−77)	1.78 Å
av no. of NOE violations >0.2 Å (per structure)	3.2 ± 1.0
av no. of NOE violations >0.5 Å (per structure)	0
residues in most favored regions of the Ramachandran plot	71.2 ± 2.6%
residues in additionally allowed regions of the Ramachandran plot	21.2 ± 4.6%
residues in generously allowed regions of the Ramachandran plot	5.8 ± 2.7%
residues in disallowed regions of the Ramachandran plot	1.9 ± 0.9%
rmsd for covalent bonds	0.0034 ± 0.0001
rmsd for covalent angles	0.511 ± 0.015
rmsd for improper angles	0.581 ± 0.016



Biochemistry **2003,** *42,* 13541−13550

NMR Structure of an Archaeal Homologue of Ribonuclease P Protein Rpp29

David J. Sidote and David W. Hoffman*

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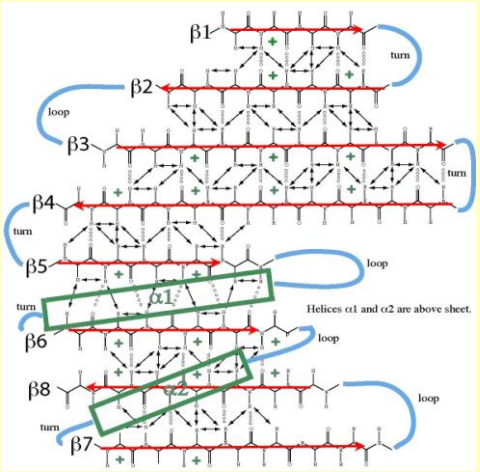
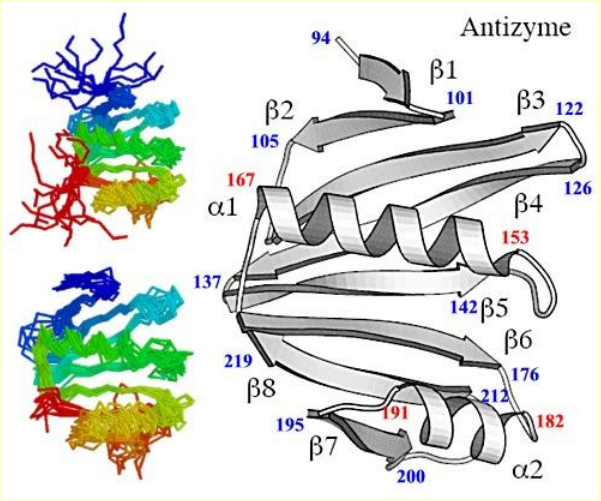
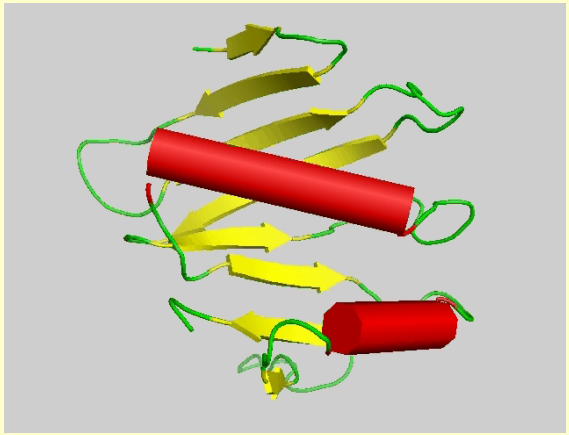
Secondary Structure of Antizyme Fragment

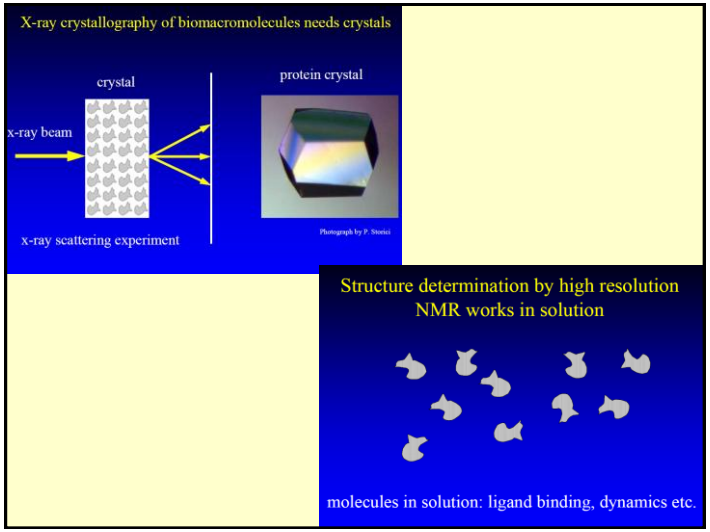






Summary: How are NMR structures solved?

1. **Solution phase technique** - protein at mM concentration in a buffer. Currently limited to proteins ≤ 30-50 kDa.
2. **Measure resonant frequencies** of ^{1}H, ^{13}C, ^{15}N atoms in a magnetic field.
   1D, 2D, 3D NMR
3. **Assign peaks** observed in the spectrum to individual amino acids.
   COSY
4. **Measure distances** between different residues < 6Å apart to get restraints. Need many restraints per residue.
   NOESY
5. **Build structures** consistent with the experimental distance restraints and principles of sterochemistry.
   Simulated Annealing
6. Yields a **set of structures** consistent with the data.
   Blur-o-gram



Comparison of X-ray vs. NMR Structure Determination

a) Limitations.

X-ray: Need crystals
NMR: MW limit (over about 40 kDa spectra are too complex to interpret)

b) Ease of structure determination.

c) Quality of structural information obtained.

X-ray: Usually has the advantage, especially with high-resolution structures, due to direct visualization of the molecule.

NMR: Very good quality structures are also obtained, though usually not as detailed as the best x-ray structures. Quality of the NMR structure depends on the # of distance and angle constraints obtainable from the data.

d) NMR has some advantages over x-ray crystallography:

Information may be obtained on the dynamics of structures. Such as hydrogen bond opening frequencies, & rotational times of bond vectors.