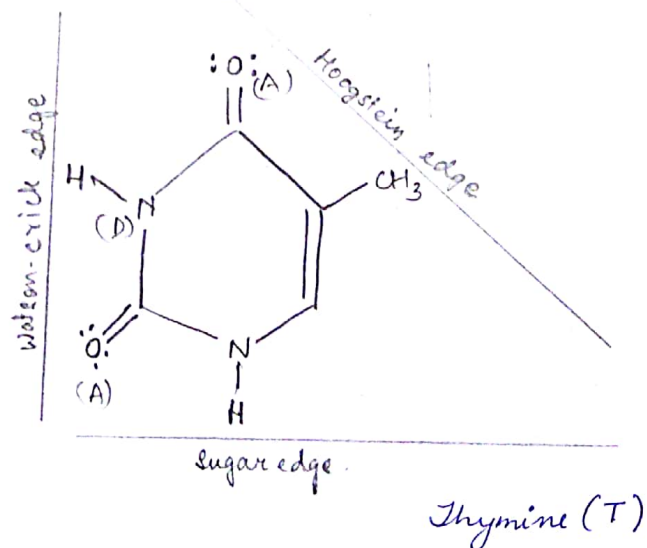
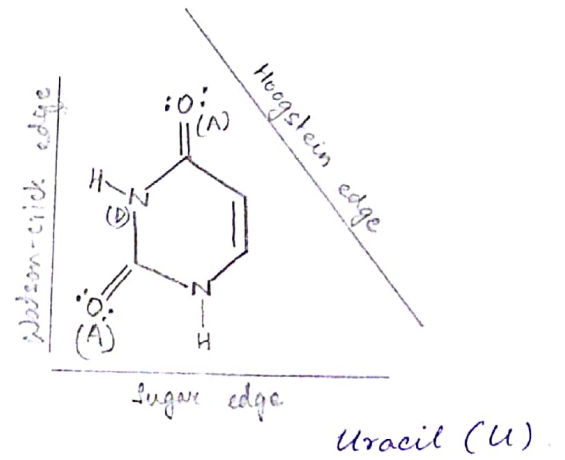
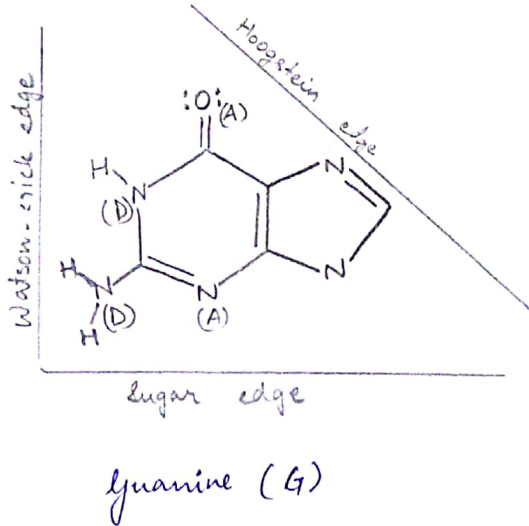
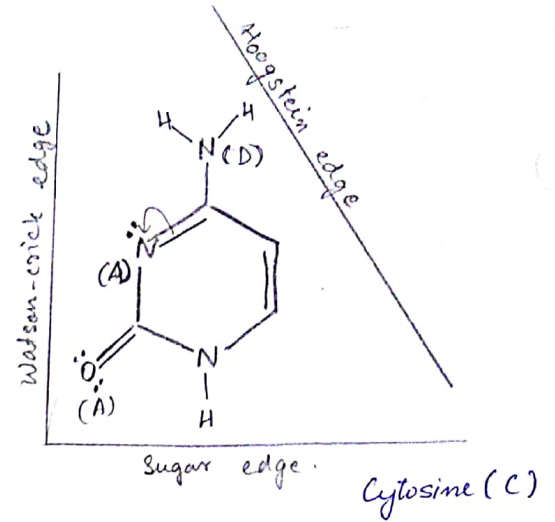
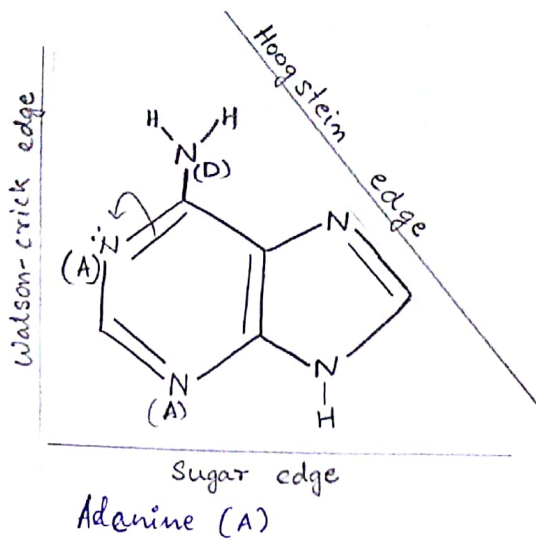
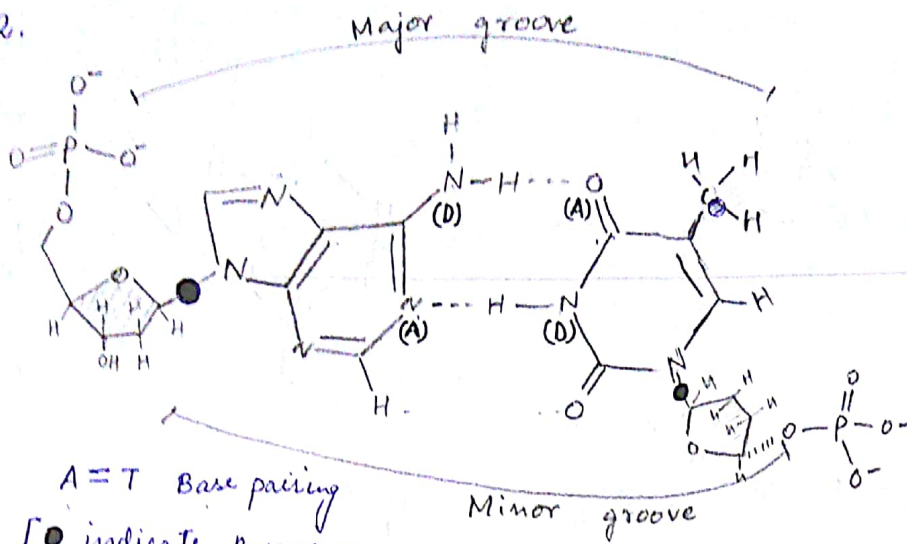


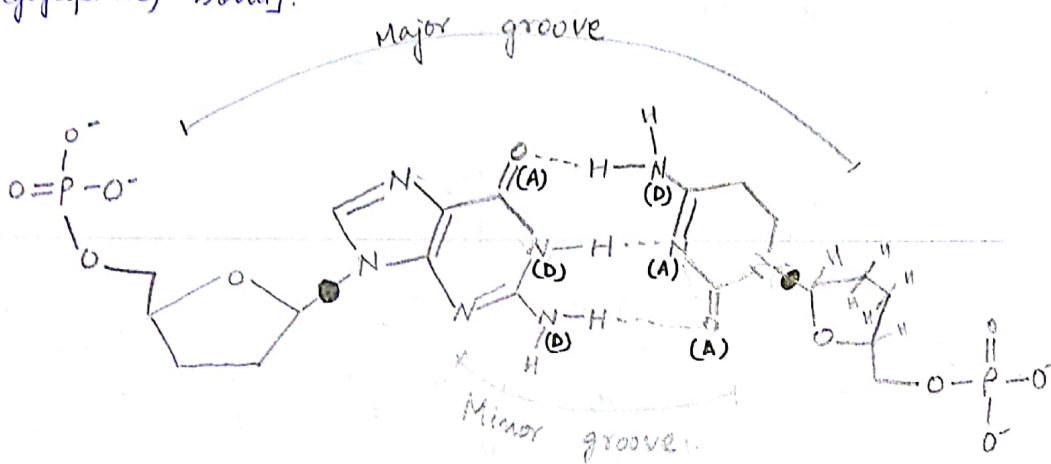
1.



2.

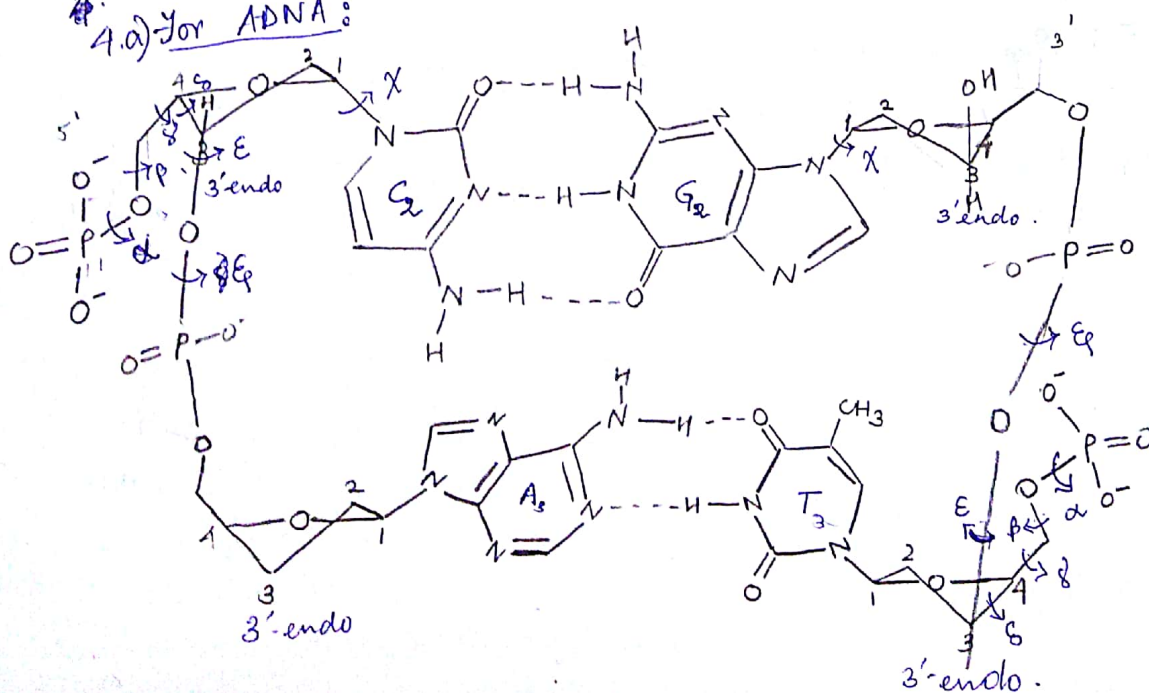


Cis - base pairing
of A=T.



Cis - base
pairing
of G≡C

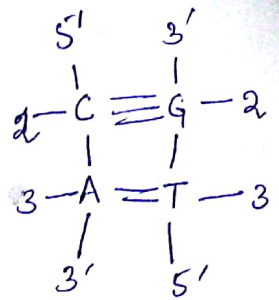
4. a) For ADNA:



A-DNA:

Base	α	β	γ	δ	ϵ	ζ	χ
5' end C ₂ ↓ same strand 3' end A ₃	P ₂ -O ₂	O ₂ -C5' ₂	C5' ₂ -C4' ₂	C4' ₂ -C3' ₂	C3' ₂ -O ₂	O ₂ -P ₃	N ₂ -C1' ₂
	P ₃ -O ₃	O ₃ -C5' ₃	C5' ₃ -C4' ₃	C4' ₃ -C3' ₃	C3' ₃ -O ₃	O ₃ -P ₄	N ₃ -C1' ₃
	P ₂ -O ₂	O ₂ -C5' ₂	C5' ₂ -C4' ₂	C4' ₂ -C3' ₂	C3' ₂ -O ₂	O ₂ -P ₁	N ₂ -C1' ₂
3' end G ₂ ↓ same strand 5' end T ₃	P ₃ -O ₃	O ₃ -C5' ₃	C5' ₃ -C4' ₃	C4' ₃ -C3' ₃	C3' ₃ -O ₃	O ₃ -P ₂	N ₃ -C1' ₃

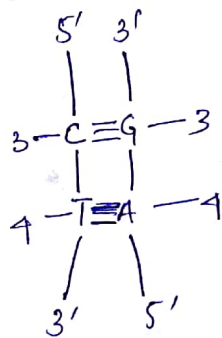
Numbering



B-DNA:

	α	β	γ	δ	ϵ	ζ	χ
5' end C ₃ ↓ same strand 3' end T ₄	P ₃ -O ₃	O ₃ -C5' ₃	C5' ₃ -C4' ₃	C4' ₃ -C3' ₃	C3' ₃ -O ₃ *	O ₃ -P ₄	N ₃ -C1' ₃
	P ₄ -O ₄	O ₄ -C5' ₄	C5' ₄ -C4' ₄	C4' ₄ -C3' ₄	C3' ₄ -O ₄	O ₄ -P ₅	N ₄ -C1' ₄
3' end G ₃ ↓ same strand 5' end A ₄	P ₃ -O ₃	O ₃ -C5' ₃	C5' ₃ -C4' ₃	C4' ₃ -C3' ₃	C3' ₃ -O ₃	O ₃ -P ₂	N ₃ -C1' ₃
	P ₄ -O ₄	O ₄ -C5' ₄	C5' ₄ -C4' ₄	C4' ₄ -C3' ₄	C3' ₄ -O ₄	O ₄ -P ₃	N ₄ -C1' ₄

Numbering



For A-DNA:

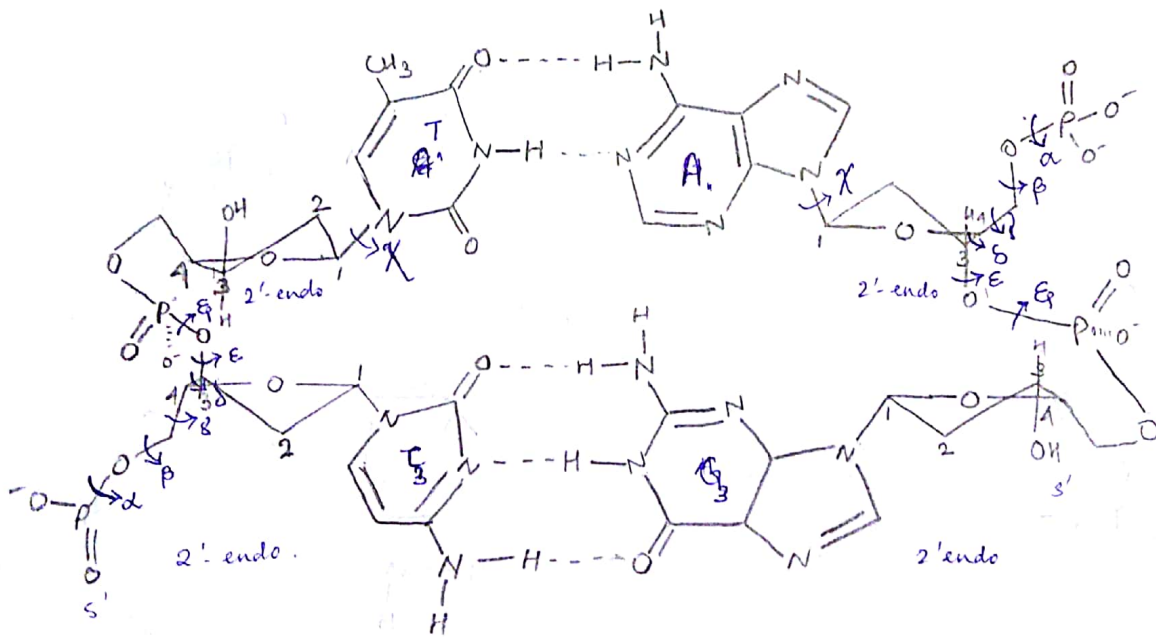
A = T			G \equiv C		
Sugar pucker	A	T	Sugar pucker	G	C
3' endo	3 rd base from one 5' end.	3 rd base from one 3' end.	3' endo	2 nd base from one 3' end.	2 nd base from one 5' end.

The torsion angles have been marked in the figure.

The G and T are the 1st and 3rd base of the same strand starting from 3' end. Respectively.

The A and C are the 1st and 3rd base of the same strand starting from 5' end respectively.

For B-DNA:



A = T			G \equiv C		
Sugar pucker	A	T	Sugar pucker	G	C
2' endo	4 th base from one 3' end.	4 th base from one 5' end.	2' endo	3 rd base from one 3' end.	3 rd base from one 5' end.

The torsion angles have been marked in the figure.

b) Z-DNA:

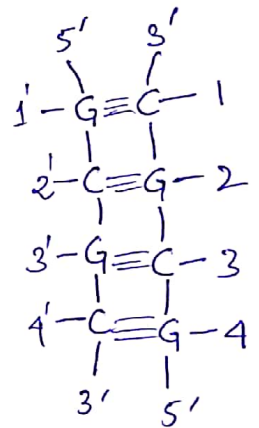
Position	Nucleotides	Sugar pucker
1'	G	3'-endo
1	C	2'-endo-3'-exo
2'	C	2'-endo-3'-exo
2	G	3'-endo
3'	G	3'-endo
3	C	2'-endo-3'-exo
4'	C	2'-endo-3'-exo
4	G	3'-endo

1', 2', 3', 4' are bases on the same strand

1, 2, 3, 4 are the bases on complementary strand respectively for 1', 2', 3', 4'.

	α	β	γ	δ	ϵ	ζ	χ
5'-end. G ₁ '	P ₁ -O ₁	O ₁ -CS' ₁	CS' ₁ -CA' ₁	CA' ₁ -C3' ₁	C3' ₁ -O ₁	O ₁ -P ₂	N ₁ -C1' ₁
C ₂ '	P ₂ -O ₂	O ₂ -CS' ₂	CS' ₂ -CA' ₂	CA' ₂ -C3' ₂	C3' ₂ -O ₂	O ₂ -P ₃	N ₂ -C1' ₂
G ₃ '	P ₃ -O ₃	O ₃ -CS' ₃	CS' ₃ -CA' ₃	CA' ₃ -C3' ₃	C3' ₃ -O ₃	O ₃ -P ₄	N ₃ -C1' ₃
C ₄ '	P ₄ -O ₄	O ₄ -CS' ₄	CS' ₄ -CA' ₄	CA' ₄ -C3' ₄	C3' ₄ -O ₄	O ₄ -P ₅	N ₄ -C1' ₄
3'-end. C ₁	P ₁ -O ₁	O ₁ -CS' ₁	CS' ₁ -CA' ₁	CA' ₁ -C3' ₁	C3' ₁ -O ₁	O ₁ -P _(n-1)	N ₁ -C1' ₁
G ₂	P ₂ -O ₂	O ₂ -CS' ₂	CS' ₂ -CA' ₂	CA' ₂ -C3' ₂	C3' ₂ -O ₂	O ₂ -P ₁	N ₂ -C1' ₂
C ₃	P ₃ -O ₃	O ₃ -CS' ₃	CS' ₃ -CA' ₃	CA' ₃ -C3' ₃	C3' ₃ -O ₃	O ₃ -P ₂	N ₃ -C1' ₃
G ₄	P ₄ -O ₄	O ₄ -CS' ₄	CS' ₄ -CA' ₄	CA' ₄ -C3' ₄	C3' ₄ -O ₄	O ₄ -P ₃	N ₄ -C1' ₄

Numbering



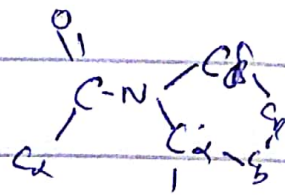
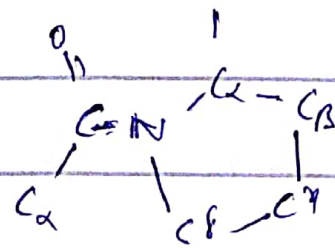
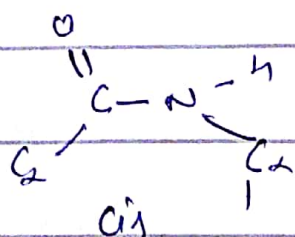
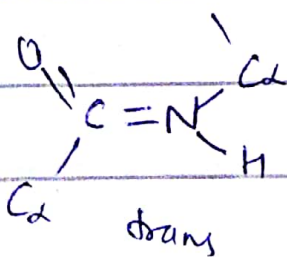
Tutorial - 2

Protein structure | PDB

helix, sheet (parallel/antiparallel), turn,
loop.

1Kh8 (cis proline at P114)

- 1) Cis-trans proline identification
- 2) draw the structure of ~~pep~~ polypeptide chain of your name.
- 3) Protein having α helix, sheet
 α/β both, β hair pin
- 4) structure from PDB (molecule of the month).



Tutorial - 3

b) Nucleic Acid

Assignment -

- 1) str of Nitrogen Base (A, T, G, C, U)
- 2) Identify RNA / DNA in given str
- 3) 5' or 3' end of strand
- 4) Canonical / Non Canonical basepair

Vec & Vec base

aligning
sheet

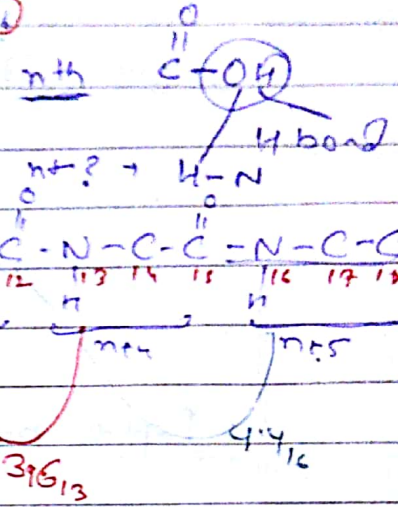
classmate

Date
Page

residue no. of atom of that particular is

helix -
n - 1

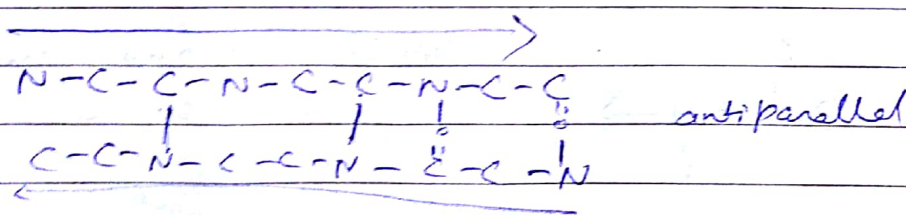
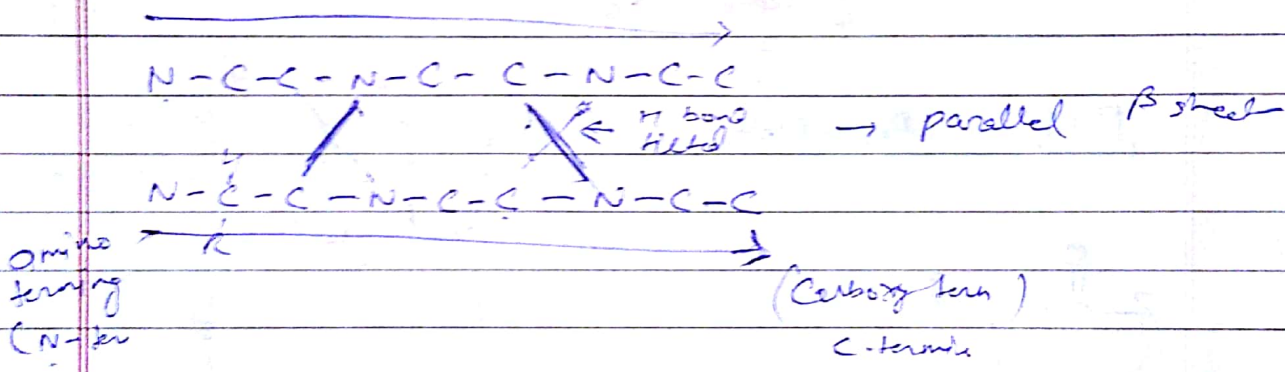
2-27, 3-10, 3-613, 4-416



① draw
N-C-C backbone
n=6

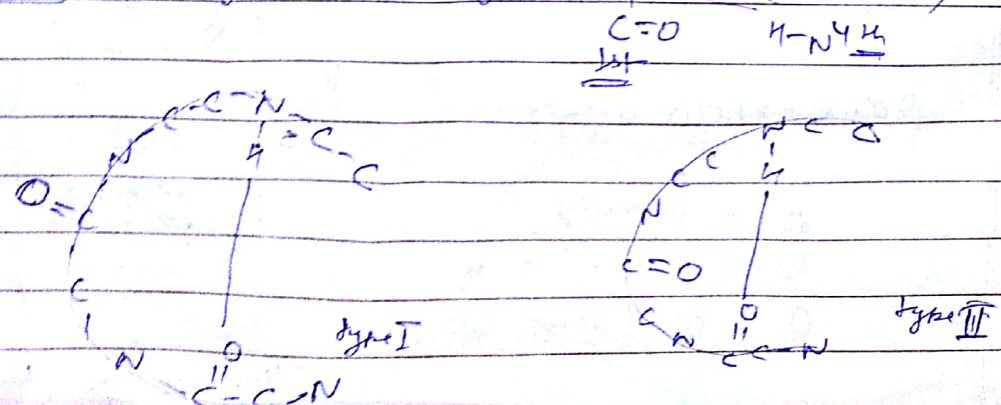
② not all
atom

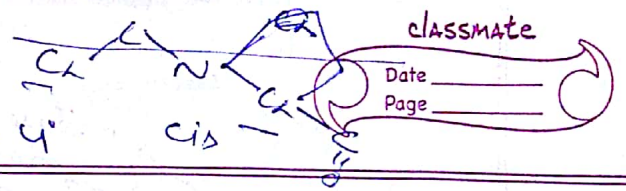
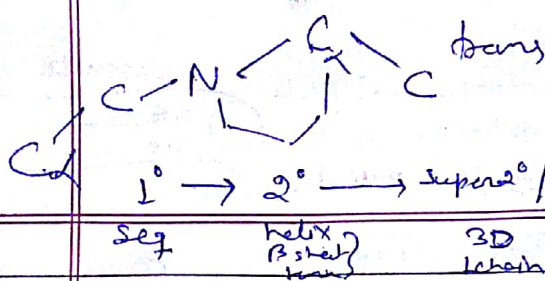
sheet → two strand



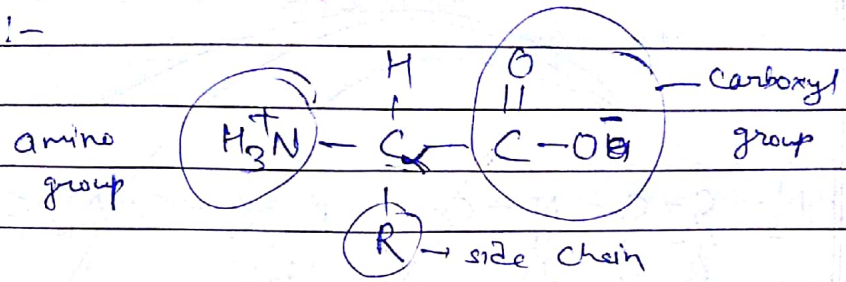
turn → type I & type II (4 AA)

coil

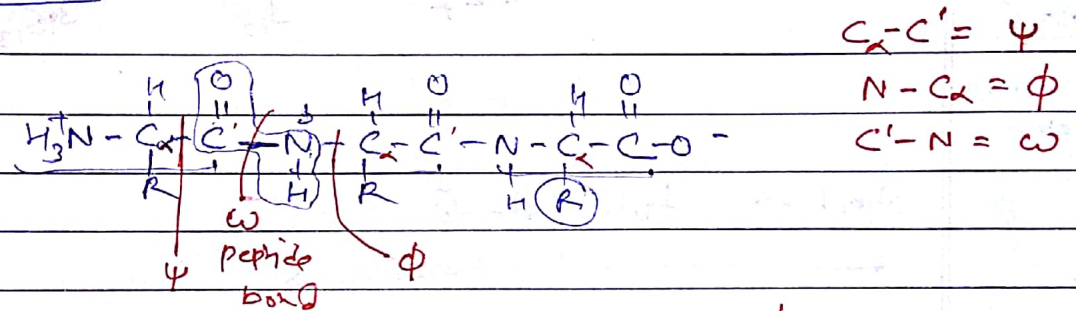




Amino Acids :-

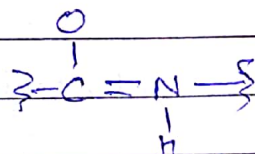
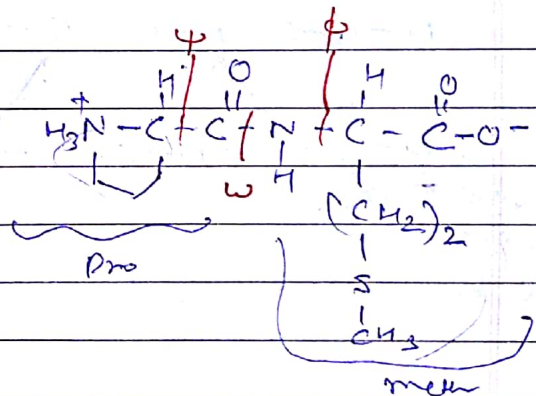
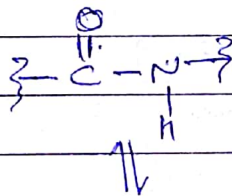


Peptide bond -



PM

Pro-Met



Ramachandran Plot

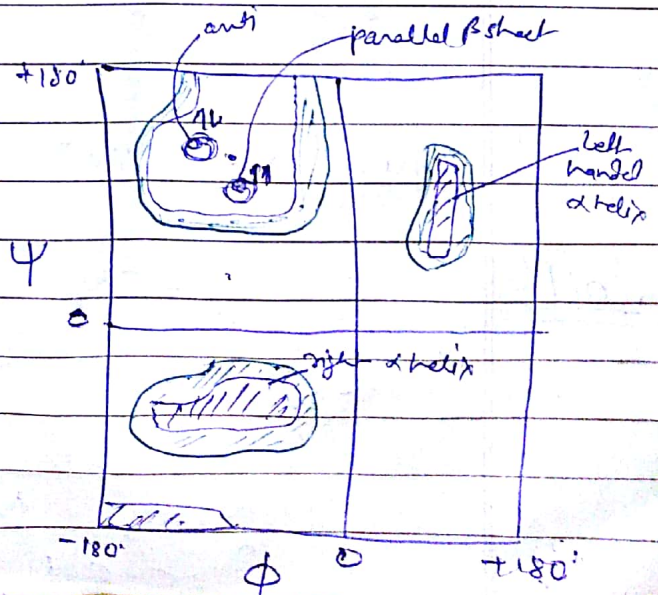
plot ϕ v/s ψ

Proline \rightarrow helix breaker.

\square \rightarrow generally

\square \rightarrow allowed region

\square \rightarrow disallowed region



Cis-trans proline

Nucleic acid

(Nitrogen base, sugar + Phosphate group)
NB
charge

Pos

DNA

RNA

NB

Purine → A, G

A, G

Pyrimidine → T, C

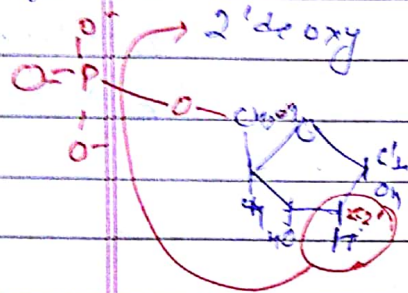
U, C

5th methyl

Sugar

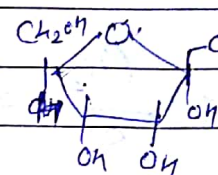
ribose

ribose

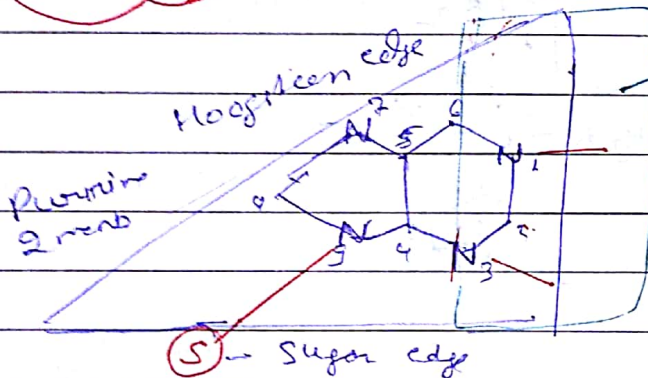


C' → numbering
of sugar

C1, C2, C3, ...



Sugar



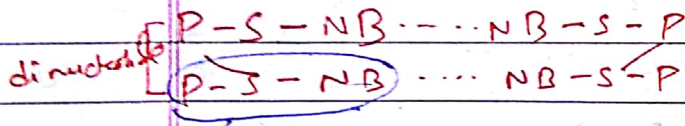
Watson & Crick edge
A = T, G = C

Base pair with H bond

N + 1, 3, 7, 9 (A/G)

[G]

G → =O, 2 - NH₂
G → -NH₂



dinucleotide

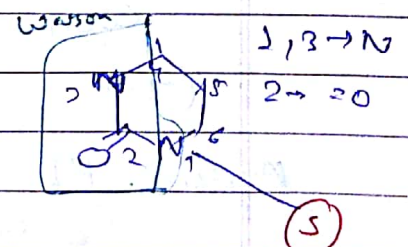
Pur → A & G → Ng → Sugar C1'

Pys → T, U & C → H bond
N1 → Sugar C1'

nucleotide = P + S + NB

nucleoside = NB + S

Pyrimidine
1 member ring



(A = T) Major → A D A
Minor → A D A



Neutral AA

Acidic AA

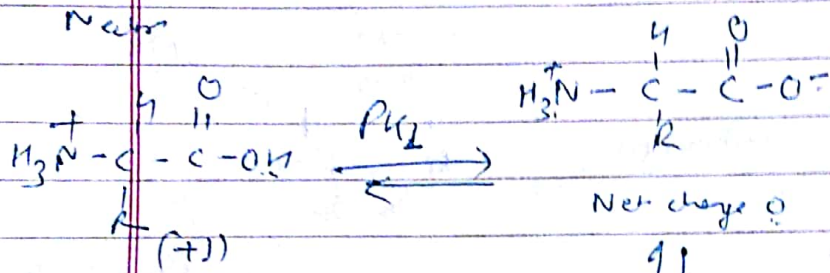
Basic AA

(hydrophilic) Polar → VIPMALGTW

(hydrophobic) Nonpolar → YCTSN

Charged +ve → basic → HRRK

-ve → acidic → ED

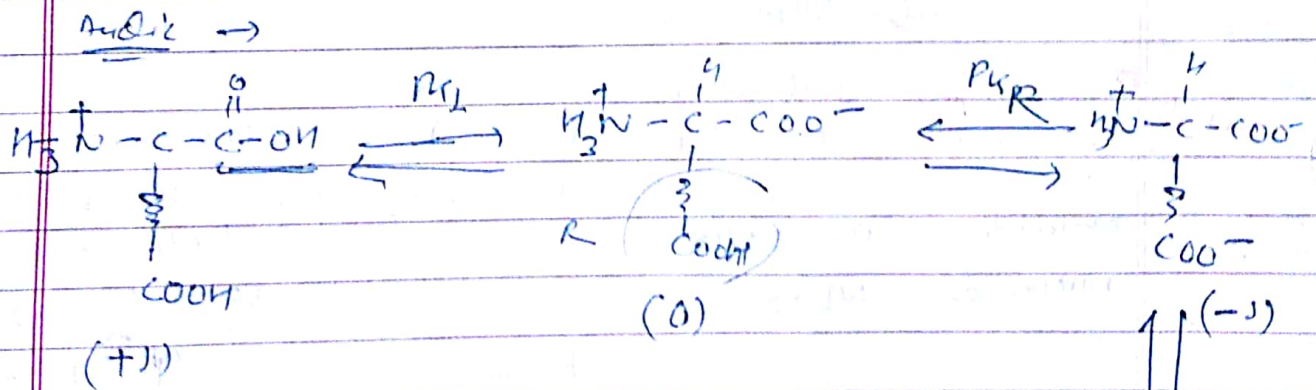
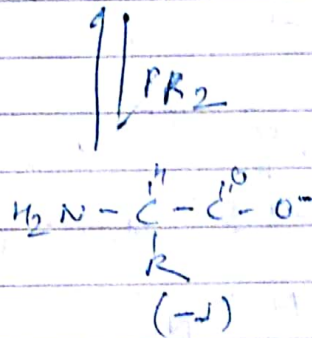


PK₁ → COOH

PK₂ → NH₃

PK_R → A/R

$$\text{PI} = \frac{\text{PK}_1 + \text{PK}_2}{2}$$



$$\text{Acidic PI} = \frac{\text{PK}_1 + \text{PK}_R}{2}$$

