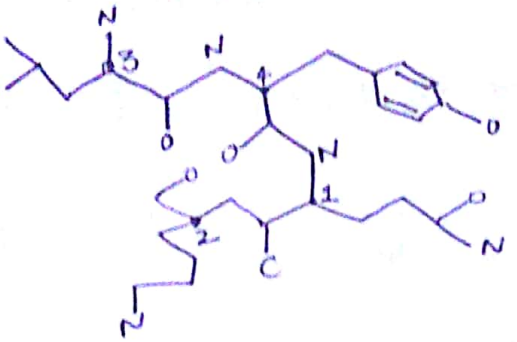
ABA - Assignment 12. 20161172 Pratik Mandlecha.

Q1

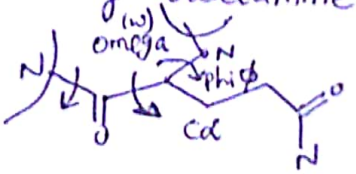
→



a) There are 4 residue in the polypeptide.

b)
i) Glutamine GLN Q → polar, uncharged
ii) Lysine LYS K → positively charged.
iii) Leucine LEU L → Hydrophobic
iv) Tyrosine TYR Y → polar, uncharged.

c) considering Glutamine.



Q2

→ SAVE ME I AM TRAPPED IN A GENE.

S A V E M E I A M T R A P P E
Ser - Ala - Val - Glu - Met - Glu - Ile - Ala - Met - Thr - Arg - Ala - Pro - Pro - Glu -
D I N A G E N E
Asp - Ile - Asn - Ala - Gly - Glu - Asn - Glu.

PN - HS - HM - PM - HM - PM - HM - HS - HM - PN - PP - HS - HM -
- HM - PM - PM - HM - PN - HS - HS - PM - PN - PM.

Q3.

→ The helical parameters are

i) n → number of residues per turn.
ii) P ⇒ rise in angstroms per turn.
iii) d ⇒ P/n ⇒ rise in angstroms per residue.

For example

2 * 2$_7$ (strand) means no. of residues per turn $n = 2.2$.

S_{10} (helix) → number of residue per turn = 3. and rise per turn = 6.

$\therefore d = P/n = 2A^\circ$.

for S_{10} (helix) $\phi = -49^\circ$ and $\psi = -26^\circ$.

3.6_{13} (α-helix) → the number of residues per turn $n = 3.6$.

and rise per turn $P = 5.4\ A^\circ$.

$\therefore d = P/n = \frac{5.4}{3.6} = \underline{1.5\ A^\circ}$.

for 3.6_{13} (α-helix) ⇒ $\phi = -54^\circ$ & $\psi = -47^\circ$.

(γ-helix) ⇒ Number of residues per turn $n = 4.4$

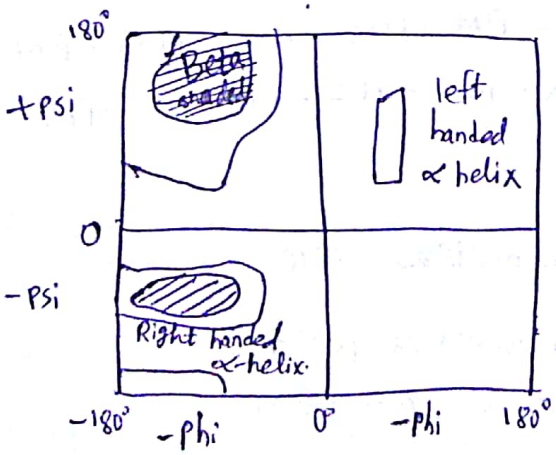
rise per turn $P = 5.2A^\circ$.

$\therefore d = \frac{P}{n} = 1.18\ A^\circ$.

for 4.4_{16} (γ-helix) $\phi = -57^\circ$ & $\psi = -70^\circ$.

For an α-helix, rise per residues $d = 1.5\ A^\circ$ So length of a 20 residue long polypeptide chain if it were in an alpha-helical formation = $20(1.5) = \boxed{30A^\circ}$.

(b)



No. of residue per turn in α-helix = 3.6.

There are 18 residue in the wheel diagram so number of turns in wheel diagram = $\frac{18}{3.6} = 5$.

(ii) No. of residue per turn in α-helix = 3.6.

$3.6 \longrightarrow 360^\circ$

$1 \longrightarrow 100^\circ$. $\therefore$ Angle between 1 residues = 100°.

There are 18 spokes in wheel diagram.

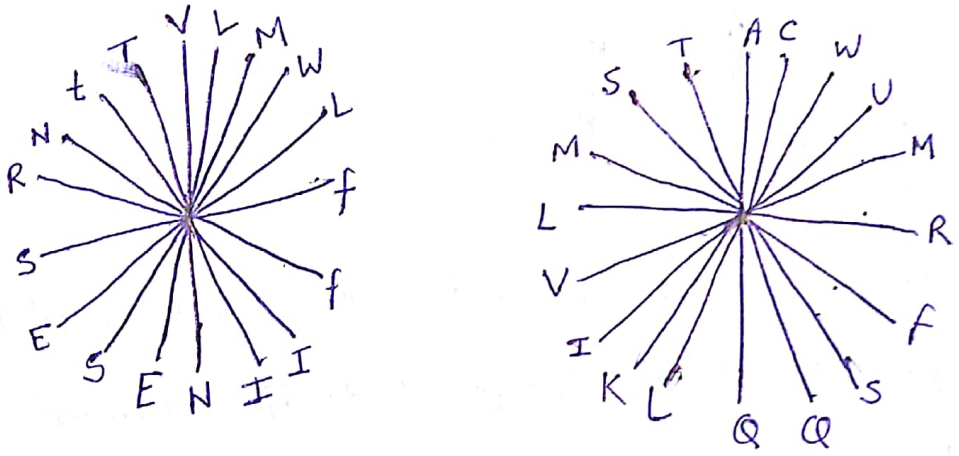
$18 \longrightarrow 360^\circ$

$1 \longrightarrow 20^\circ$.

$\therefore$ Angle b/w spokes $= 20^\circ$.

So, For every residue its next residue occur at $\frac{100}{20} = 5^{th}$ position.

(iii)

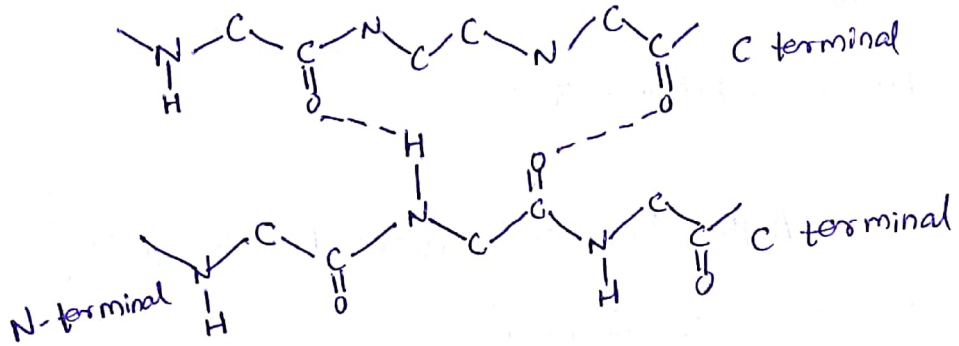


In ① all the polar residues lie on the left side and hydrophobic residues lie on the right side. So the helix is Aliphatic.

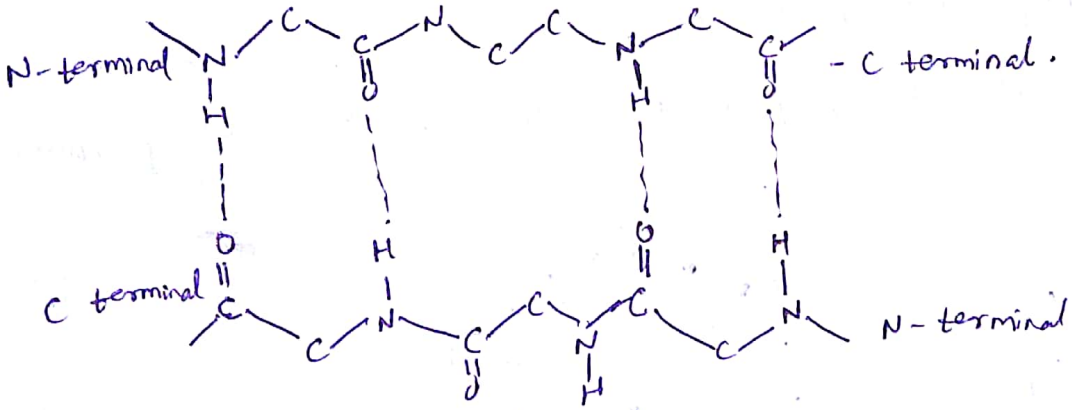
In ② hydrophilic and hydrophobic residues lie on both sides, so the helix is not Aliphatic.

Ans 4(a) (i) Cis (ii) Trans (iii) Trans (iv) Trans (v) Trans.

(b) In parallel sheets, amino acids chains are in same direction.



In anti-parallel sheets amino acid chains are in opposite direction.



Anti-parallel arrangement produces the strongest inter-strand stability because it allows the inter-strand hydrogen bonds b/w carbonyl & Amines to be planar which is their preferred orientation. Inter-strand hydrogen bonding is less stable in parallel arrangement because it introduces non-planarity on the inter strand hydrogen bonding pattern.

In aqueous environments proteins fold in such a way that the polar residues are in contact with the solvent and hydrophobic parts are burried (away from solvents). so, polar residues typically form surface amino acids and hydrophobic residues typically form buried amino acids.

If the environment is non-polar as in case of membrane proteins in hydrophobic membrane, hydrophobic residues are exposed to the lipid bilayer.

(b) Proteins contains a hydrophobic group but it is a surface amino acid. This is because the closed ring in proline limits its flexibility. It does not follow the general principles discussed above in (a) and can't occur as helix or sheet but it occurs as a surface.

ABA Assignment 13. 20161172. Pratik Mandlecha.

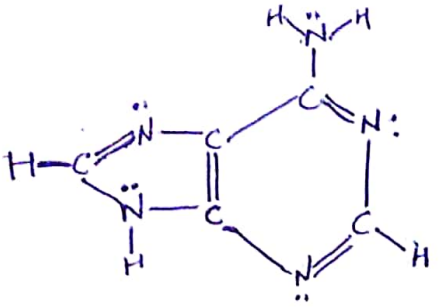
1

→ Structures of A, T, U, G, C.

(A) Diagrams with labels and lone pairs.

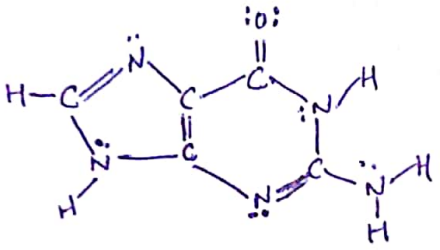
A → Adenine
T → ~~Pirimidine~~ Thymine.
U → Uracil (U)
G → Glycine
C → Cysteine

i)



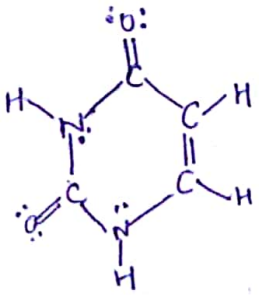
Adenine (A). → in DNA & RNA.

ii)



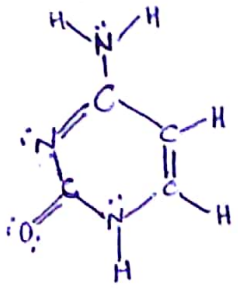
Guanine (G). → in DNA and RNA

(iii)



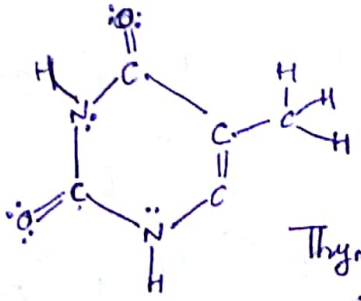
Uracil (U) → in RNA only

(iv)



Cytosine (C)
↓
in DNA & RNA.

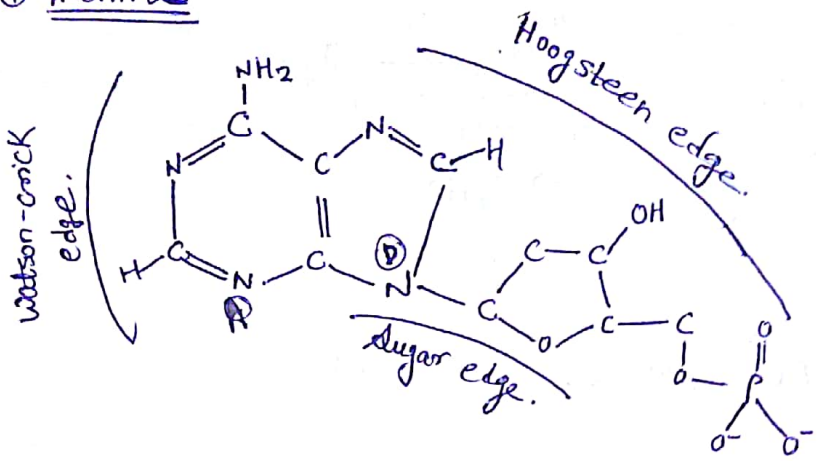
(v)



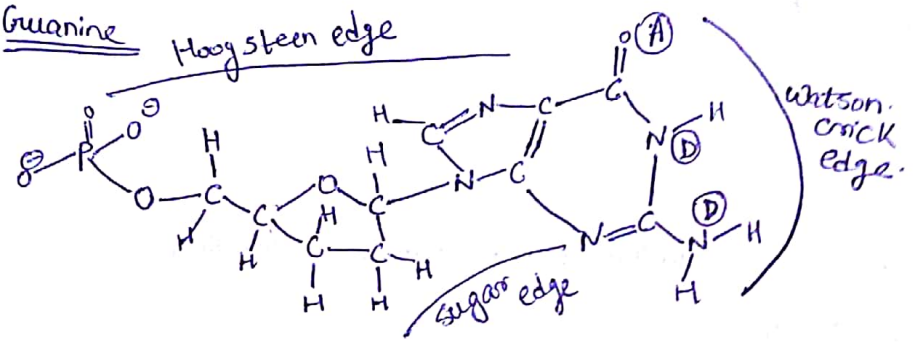
Thymine (T)
↓
in DNA only

(B) EDGES in ATUGC and hydrogen bond — Donor (D) / Acceptor (A) — in ATUGC.

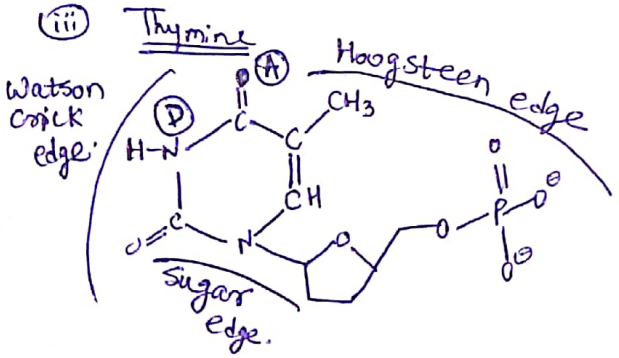
(i) Adenine



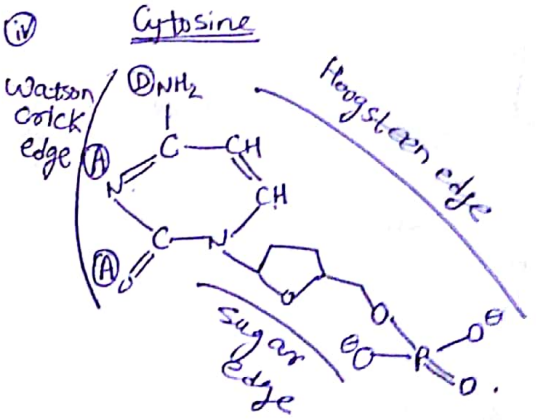
(ii) Guanine



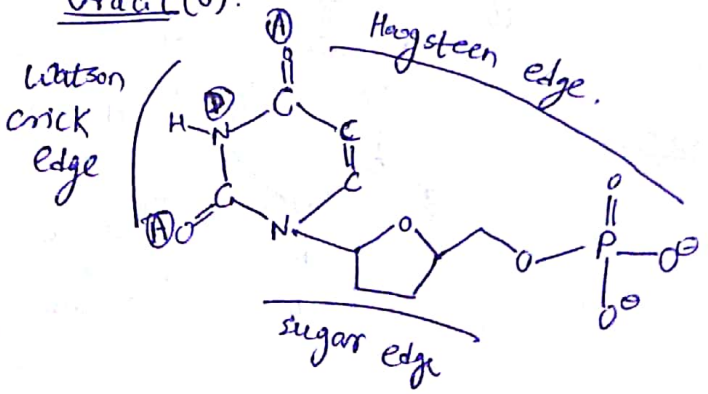
(iii) Thymine



(iv) Cytosine



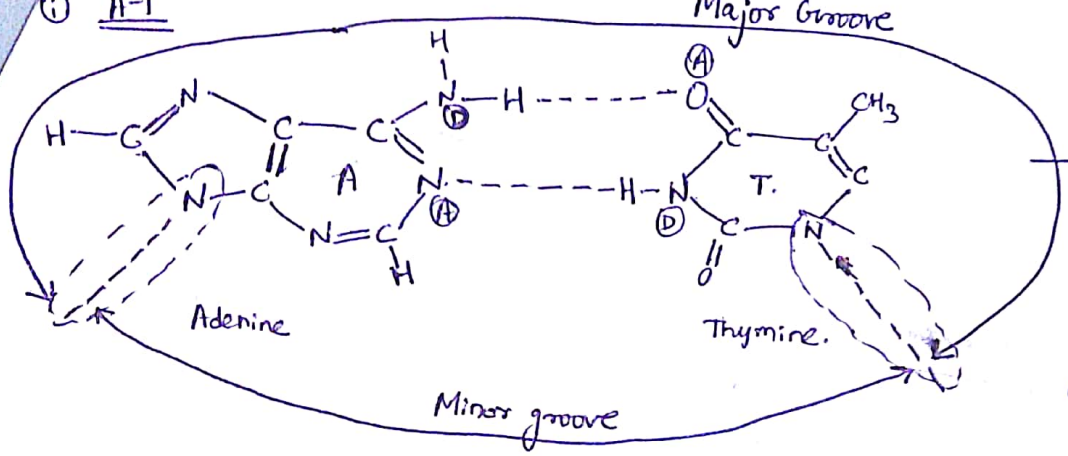
(v) Uracil (U).



-T ; G-C base pairs

D: Donor
A: Acceptor.

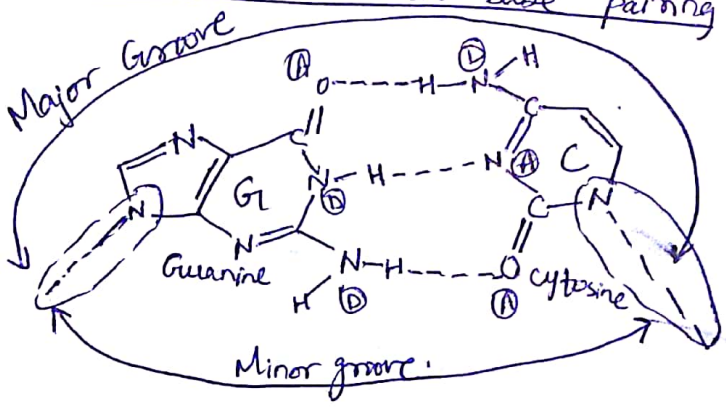
(i) A-T



Watson crick cis base pairing of A and T.

Circles indicate sugar attachment.

(ii) G-C Watson-crick cis base pairing..



4