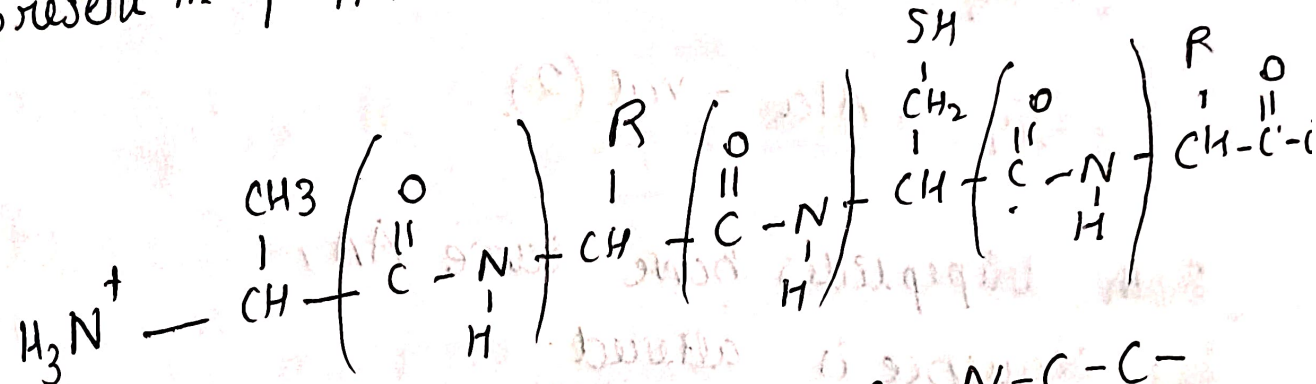
Primary Structure. (8 marks)

- It refers to number and sequence of aminoacid present in polypeptide chain.



- This forms a N-C-C-N-CC-N-C-C- primary structure is read from NH_2-- terminal to the -COOH terminal.

(1) The primary structure is read from NH_2-- terminal to the -COOH terminal.

(2) Each amino acid is identified by it's specific R-group.

(3) The primary structure is held together by covalent bonds such as peptide bonds.

(4) There are 20 different amino acids in living things.

(5) It is therefore possible to have an ∞ no. of primary structures.

Sequence & numbering of amino acids.

- Gly - val - Ala (1)
- Gly - Ala - val (2).

Both bipeptides have same AA, but sequence is altered.

- when the sequence changes, peptide differs.
- each protein has a unique sequence of amino acids, decided by genes.

N- terminal & C - terminal ends.

- The two ends of polypeptide chains are referred to as.
- The carboxyl terminal (C-terminal) end where free alpha carboxyl group is seen.

The Amino terminal (N-terminal) end.

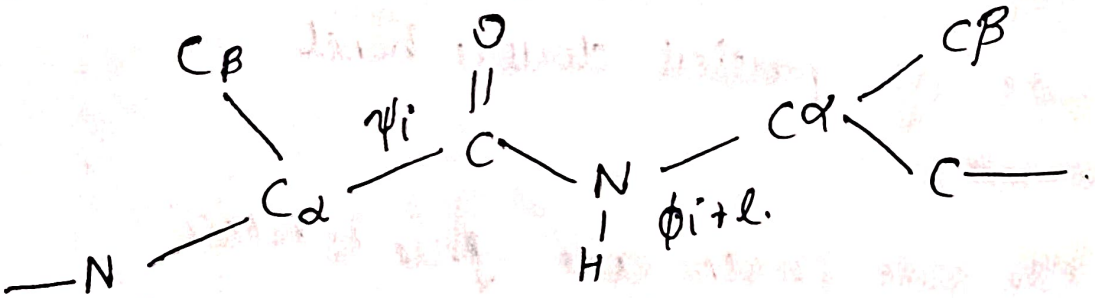
- End where free alpha amino group is seen.

V.Impt - write 5 → full marks

Characteristics of peptide Bond.

1. Peptide Bond is planer.

- all six atoms → α-C (of first aminoacid), C=O, NH, α-C (of second aminoacid) lie in the same plane.



2. Partial Double Bond.

1.49
1.32 1.27

- Normal Bond length between C-N single bond is 1.49 A°.
- Normal Bond length between C=N double bond is 1.27 A°.

Bond length of a peptide bond (C-N distance) is between these 2 values; 1.32 A°, giving it a partial double bond character.

3. No. Freedom of Rotation

- peptide bond has no freedom of rotation because of partial double bond character.
- The side chains are free to rotate on either side of the peptide bond.

4. C-N. bond is trans in nature

The two α-C's are on opposite side of the double bond.

5. Ramachandran angles

- The angle of rotation is called Ramachandran angles.

→ The angle of rotation in required to the bond between the nitrogen & the αC is referred to as phi.

- while the ∠ of rotation btwn αC & (carbonyl carbon is referred to as psi.

Branched & Circular proteins

- Mostly, polypeptide chains are linear.
- Branched proteins are formed by Interchain disulphide bridges.

Interchain disulphide bridges.

- Covalent disulphide bonds between different polypeptide chains in the same protein.

Ibrachain disulphide bridges

- covalent disulphide bonds btwn some portions of the same polypeptide chain

Rarely, proteins may be in Circular form
eg: Gramicidin.

Pseudopeptide.

Instead of alpha carboxyl group, gamma carboxyl group may enter into bond formation.

eg: glutathione.

(gamma glutamyl cysteinyl glycine).

Primary structure of Insulin.

- Insulin is composed of two polypeptide chains - A chain {glycine chain}
  B chain {phenylalanine chain}.

- A & B chains are linked together by two disulphide Bonds, and an additional disulfide is formed within the A chain.

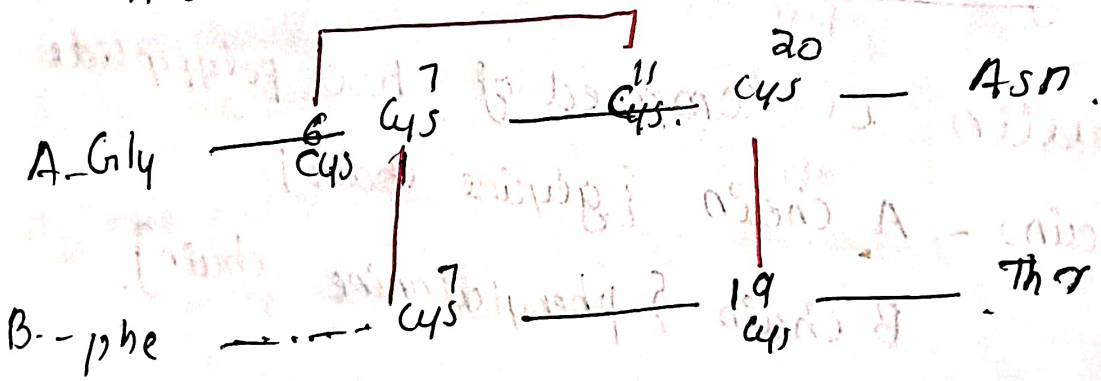
- The A chain consists of 21 amino acids and B chain of 30 amino acids.

Two Interchain disulphide Bonds.

- between A 7th cys and B 7th cys.
- b/w A 20th cys & B 19th cys.

Connect A & B chains.

- One Interchain disulphide Bond is present between 6th & 11th residues of A chain.



A chain → glycine chain.

B chain → phenylalanine chain.

Biologically active Insulin.

- Insulin is first synthesised as a single polypeptide ~~chain~~ called preproinsulin.
- It is then cleaved forming proinsulin. 86 AA.

- proinsulin undergoes maturation into active insulin (51 AAs) by the removal of central fragment called the C-peptide, and leaving 2 peptide chains, the B- & A- chains, linked by 2 disulfide bonds.
- C peptide is released into circulation.

→ primary structure of proteins — 8 marks