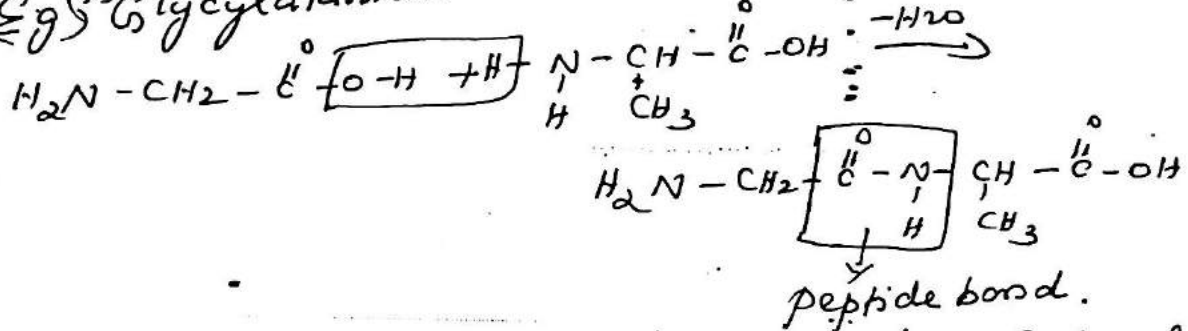
(25)

UNIT III

PEPTIDES:-

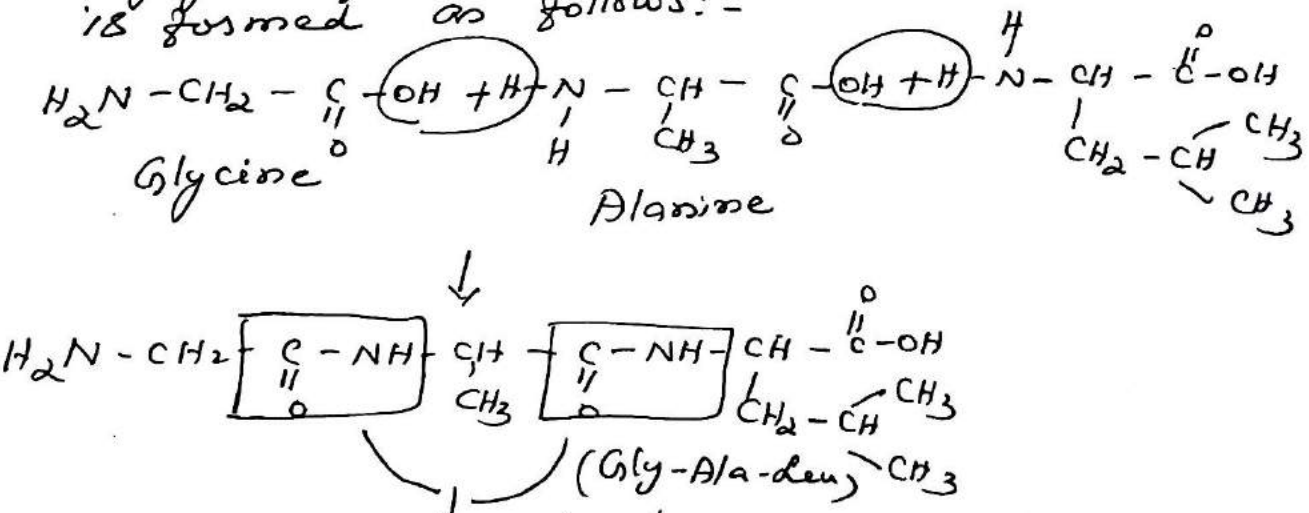
Peptide is a substance derived from two or more same or different aminoacids and connected through peptide bonds. α-aminoacids are the monomers from which the polymeric peptides are derived. There is interaction between amino group and carboxyl group of amino acids resulting in the formation of peptides involving amide (-NHCO-) linkages known as peptide linkages.

Eg:- Glycylalanine is formed as follows.



Glycylalanine (Gly-ala)

(ii) Glycylalanyl leucine is formed as follows:-



(A tripeptide → two peptide bonds).

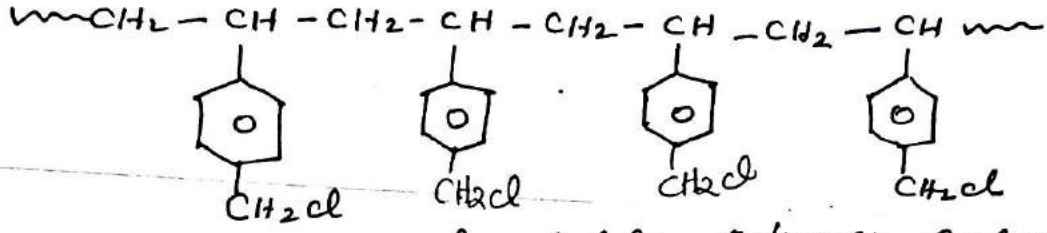
Depending upon the no of amino acid units per molecule, peptides are classified into dipeptides, tripeptides and polypeptides and finally protein. A peptide of molecular weight upto 10,000 is known as polypeptide and above that is a protein.

(22) (23)

TRIPEPTIDE SYNTHESIS:-

SOLID PHASE / MERRIFIELD METHOD:-

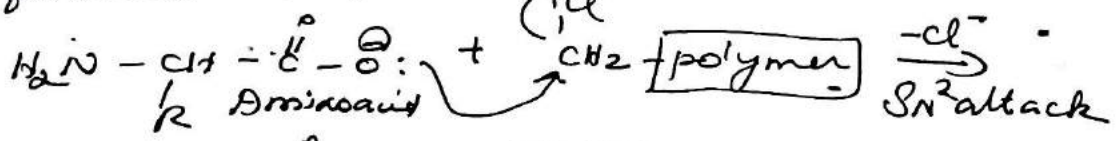
In this method, an aminoacid or a peptide is bound chemically to an insoluble synthetic polymer (Cl-CH_2-polymer) and then chain is build up with one aminoacid residue at a time at the free end.

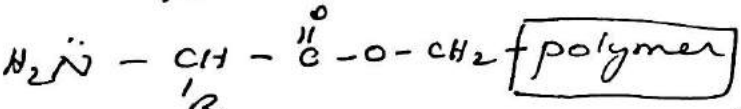


Insoluble polymer (ClCH$_2$-polymer).

(1) A basic solution of the aminoacid in ethylacetate is shaken with the insoluble polymer.

(2) Carboxylate ion of the aminoacid through SN^2 attack polymer bound aminoacid derivative is formed, as follows.

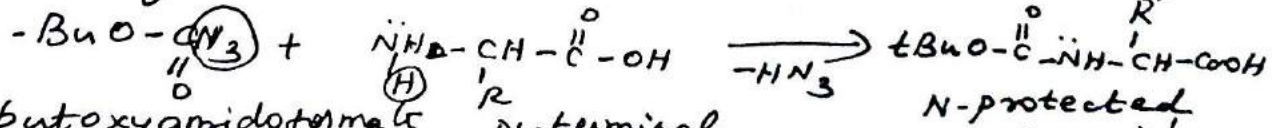




polymer bound aminoacid derivative.

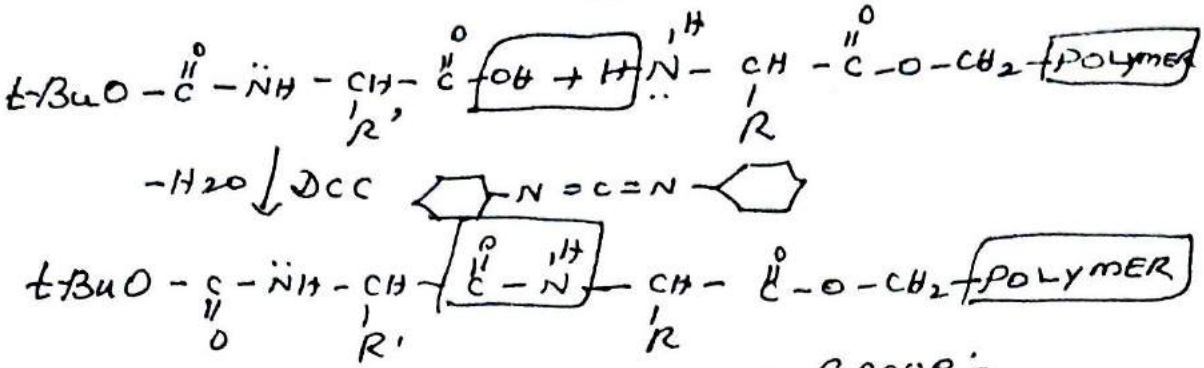
(3) PROTECTION OF NH_2 end of N-terminal aminoacid:-

The amino group of N-terminal aminoacid is protected by reaction with t-butoxyazidoformate.



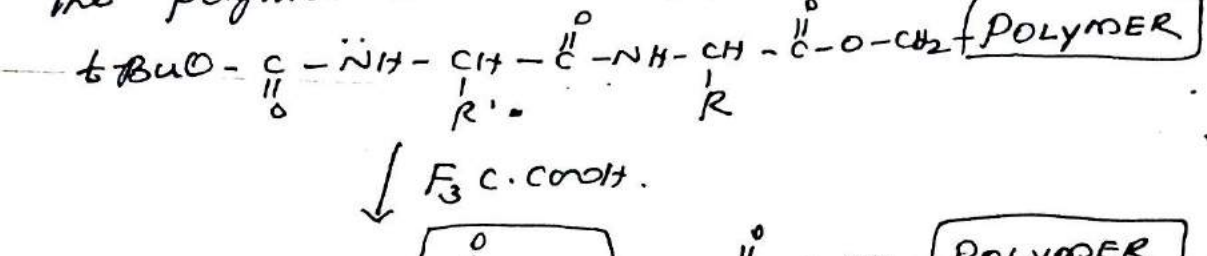
(4) CONDENSATION WITH polymer-bound aminoacid derivative:-

N-protected aminoacid is then condensed with the polymer-bound aminoacid derivative in the presence of dicyclohexylcarbodiimide (DCC)



⑤ REMOVAL OF THE PROTECTING GROUP:-

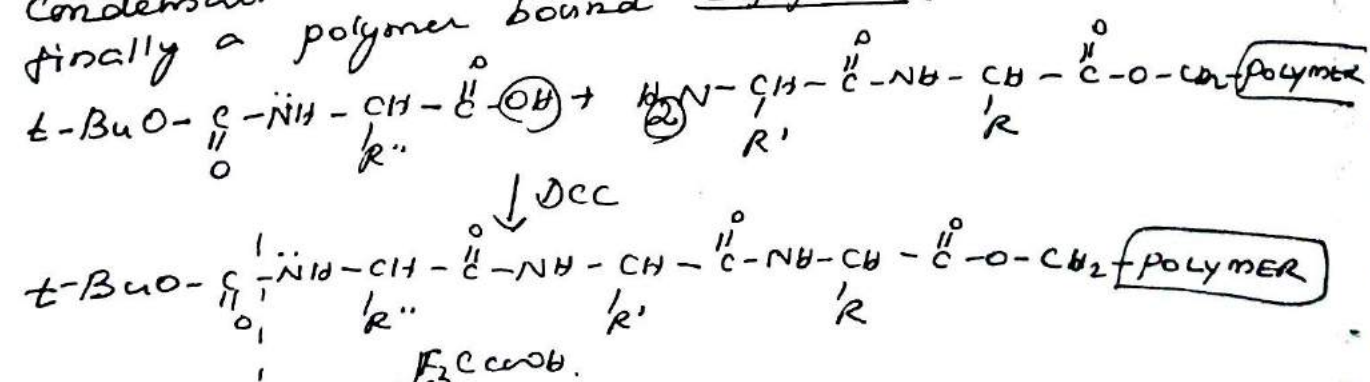
The condensation product so obtained is treated with trifluoroacetic acid (CF_3COOH) to remove the protecting group and to get the polymer bound dipeptide.



POLYMER BOUNDED DIPEPTIDE.

⑥ FORMATION OF TRIPEPTIDE:-

The polymer bounded dipeptide is treated with another N-protected amino acid followed by condensation in the presence of DCC to give finally a polymer bound tripeptide.

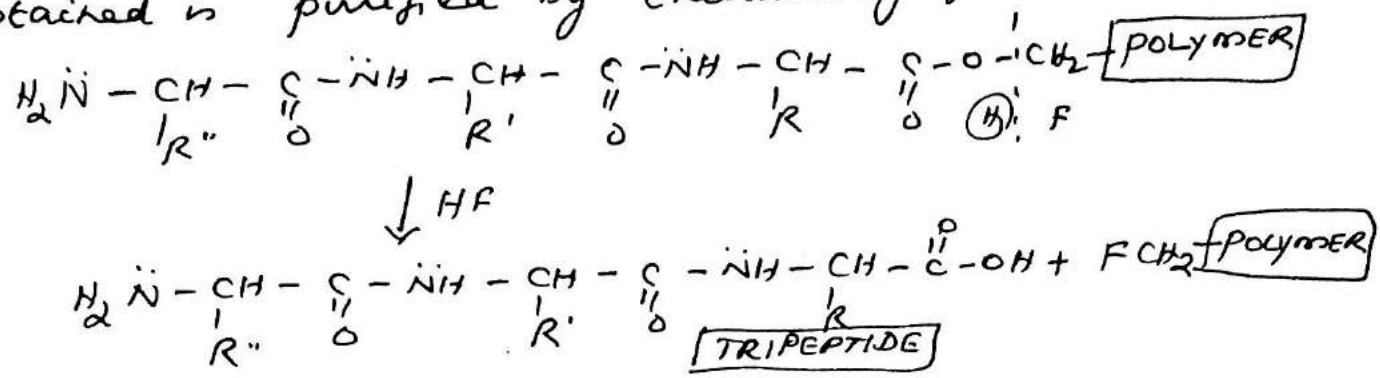


The same procedure is repeated again & again to get polypeptide of desired length.

⑦ Removal of polymer resin to get tripeptide:-

The desired polypeptide, in this case

tripeptide is then removed from the polymer resin by adding anhydrous HF. The peptide bonds remain unaffected. The crude tripeptide thus obtained is purified by chromatographic method.



TERTIARY STRUCTURE OF PROTEINS:-

(1) According to secondary structure of proteins, there are adequate inter chain hydrogen bonds to maintain the α-helical configuration of protein in the crystalline state.

(2) But they are not strong enough to stabilise α-helical conformation in aqueous solution since water molecules can compete for hydrogen bonding sites on the α-helical backbone.

(3) This may result in the disruption of the internal bonds and protein would assume a random configuration, simultaneous with disruption.

(4) But experimental facts have shown that α-helical configuration of protein is not destroyed when dissolved in water.

(5) This observation leads to the conclusion that there must be some other forces involved in compressing the long spiral chains into the definite geometrical structures.

(6) The resulting three dimensional shape formed by precise folding and bending of polypeptide chain in the helical coil is referred to as the tertiary structure of protein

(1) The linkages responsible for this compact structure are believed to be due to the nature of amino acid side chains within the molecule.

(8) Mostly proteins are extremely compact and spherical in shape.

(9) Their non-polar side-chains are directed towards the interior of the molecule (i.e)- hydrophobic and their polar side chains are projected outwards from the surface of the molecule (i.e) towards aqueous region.

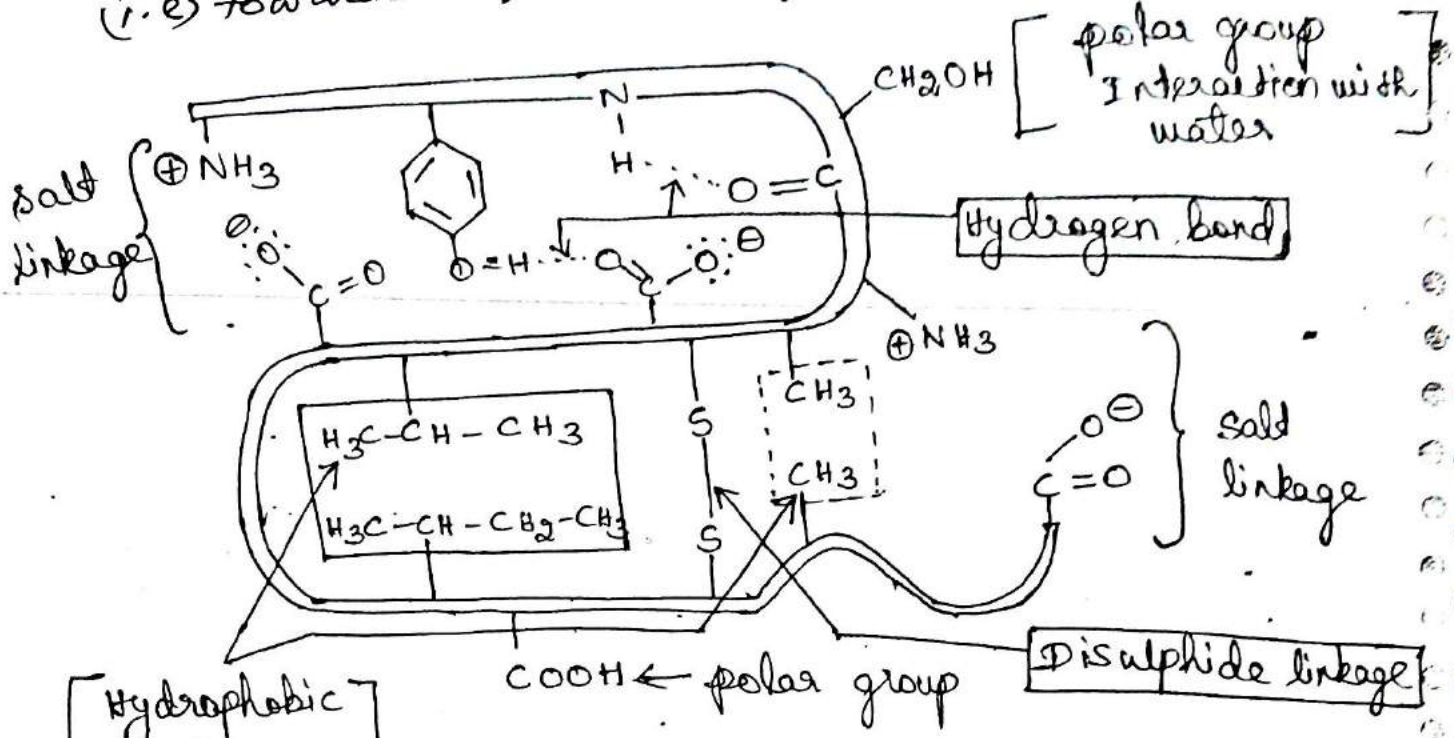


Fig. Various bonds that stabilizes the tertiary structure of proteins.

PROTEIN SYNTHESIS:-

Protein synthesis consists of 3 steps.
(i) Transcription (ii) Translation (iii) Termination.

TRANSCRIPTION:-

The formation of m-RNA on one of two strands of DNA double helix is known as transcription.

(1) A small part of the DNA double helix unwinds and one of the two strands serves as a template for complimentary ribonucleotide to line up.
(2) Sugar-phosphate bond formation occurs in 5→3 sense.
(3) This process is catalysed by enzymes called RNA polymerases.

④ Therefore, complete synthesis of m-RNA requires four major ribonucleoside triphosphates, as template and RNA polymerase (enzyme)

n_1 ATP, n_2 GTP, n_3 CTP, n_4 UTP —(DNA template, RNA polymerase)→ RNA — AMP, GMP, CMP, UMP + $(n_1 + n_2 + n_3 + n_4)$ pyrophosphate.

(Ribonucleoside monophosphate)

⑤ The completed mRNA molecule does not remain in double helix with DNA but separates and migrates from the nucleus. The DNA then returns to its stable double helix structure.

TRANSCATION:-

① The segment of a DNA molecule that codes for the biosynthesis of one complete polypeptide chain is called a gene.

② The mechanism of protein biosynthesis is directed by messenger RNA (mRNA) and take place on ribosomes.

③ On the ribosome, mRNA serves as a template to pass on the genetic information that it has transcribed or collected from DNA.

④ m-RNA carries information in a three letter code. Since, this code is derived from a gene segment of DNA, therefore called genetic code.

⑤ The ribonucleotide sequence in mRNA forms a code that determines the order in which different amino acid residues are to be arranged.

⑥ $4^3 = 64$ possible triads of the four bases in RNA, 61 code for specific aminoacids while remaining 3 of the 64 codons are known to code for chain termination.

⑦ The following table gives the meaning of each codon.

Table 1. Codon assignments of base triads.

First base (5 end)	Second base	Third Base (3 end) P. 935			
		U	C	A	G
U	U	Phe	Phe	Leu	Leu
	C	Ser	Ser	Ser	Ser
	A	Tyr	Tyr	termination	termination
	G	Cys	Cys	termination	Trp
C	U	Leu	Leu	Leu	Leu
	C	Pro	Pro	Pro	Pro
	A	His	His	Gln	Gln
	G	Arg	Arg	Arg	Arg
A	U	Ile	Ile	Ile	Met
	C	Thr	Thr	Thr	Thr
	A	Asn	Asn	Asn	Lys
	G	Ser	Ser	Arg	Arg
G	U	Val	Val	Val	Val
	C	Ala	Ala	Ala	Ala
	A	Asp	Asp	Glu	Glu
	G	Gly	Gly	Gly	Gly

(8) The code collected in mRNA is read by transfer RNA (tRNA) in a process called translation. There are atleast 60 different transfer RNAs: one for each of the codons.

(9) Each specific tRNA acts as a carrier to bring a specific aminoacid into place so that it may be transferred to the growing protein chain.

(10) Transfer RNA (consists of about 70 to 100 ribonucleotides) is bound to a specific amino acid by an ester linkage through the free 3'-hydroxyl on ribose at the 3 end of the tRNA.

(11) Each t-RNA also contains in its structure a segment called anticodon, a sequence of three ribonucleotides complementary to the codon sequence.

(12) The codon sequence C-U-G on mRNA for example would be read by leucine bearing t-RNA having the complementary ~~to the~~ anti codon base sequence GAC.

(13) In this way, codon mRNA is read by different tRNAs to put correct aminoacid into its proper place for enzyme mediated transfer to the growing peptide.

(14) When the synthesis of the proper protein is completed a termination codon signals the end and the protein is released from the ribosome.

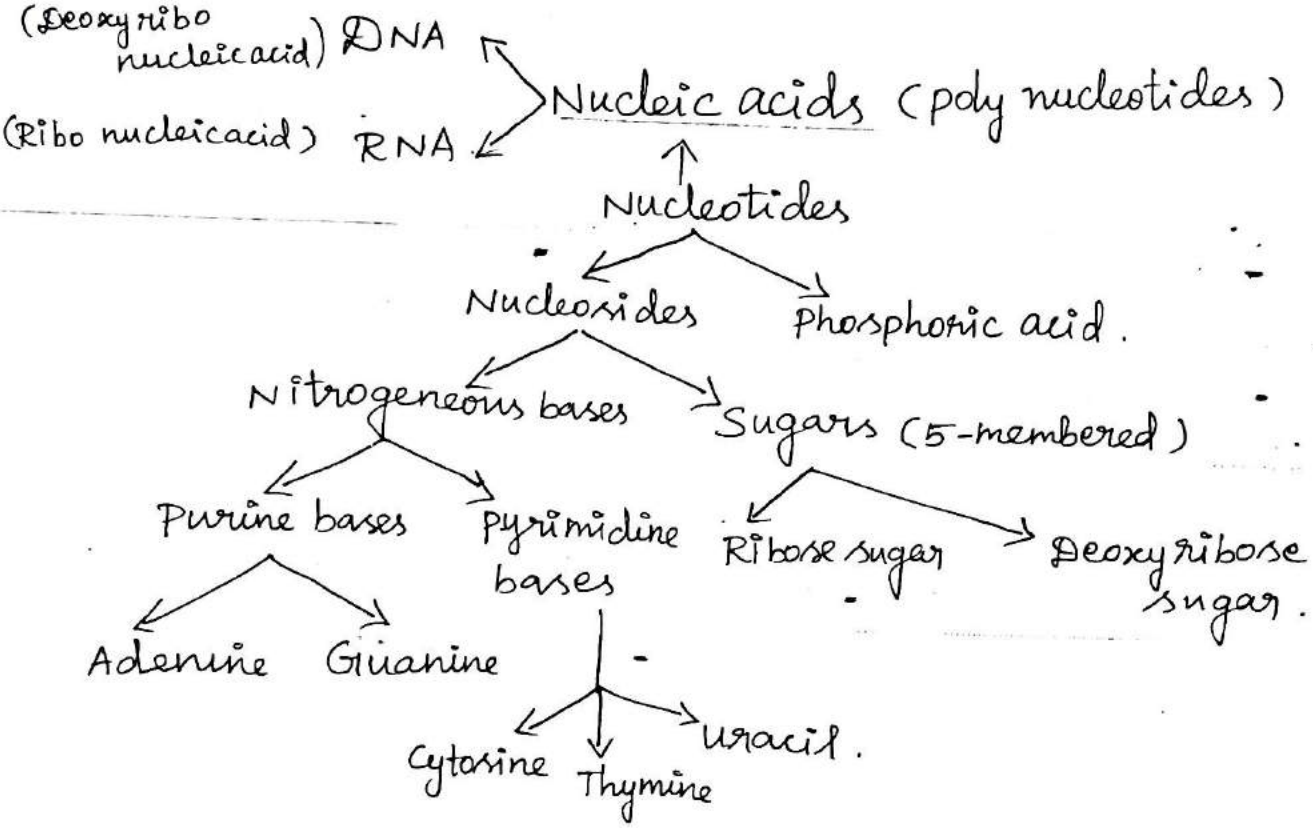
Major
Histone → protein + Minor protein

2. Million

23 pairs ~ F ~ M

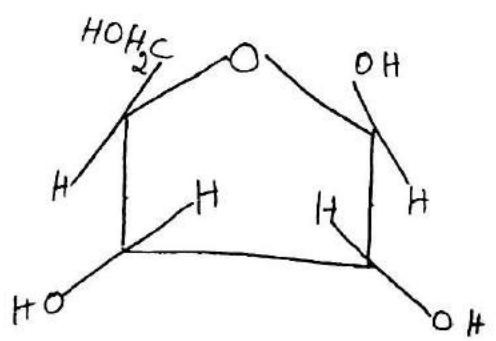
NUCLEIC ACIDS

* Genes are called nucleoproteins since they contain nucleic acid proteins. 46 chromosomes which carry genes, which are responsible for heridity. Nucleic acids are polymeric compounds of high molecular weight The monomers are nucleotides.

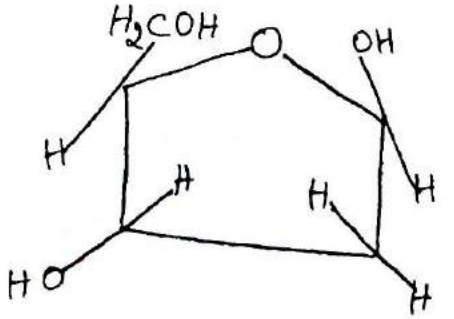


Nucleoside :

A nucleoside is composed of a purine / apyrimidine base and a ribose / a deoxyribose sugar.



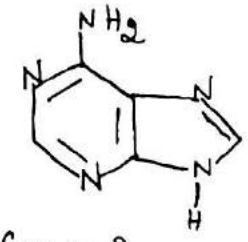
Ribose sugar



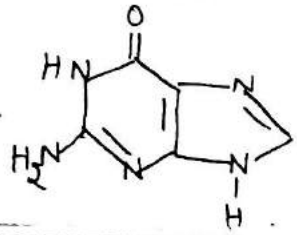
2-deoxyribose sugar

PURINE BASES

① Adenine

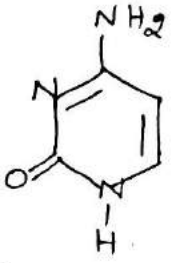


② Guanine

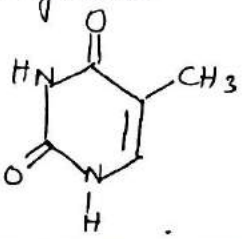


PYRIMIDINE BASES.

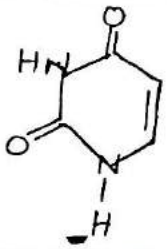
① Cytosine



② Thymine

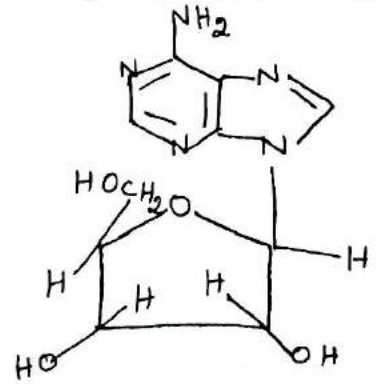


③ Uracil



NAME OF THE NUCLEOSIDE	BASE	SUGAR.
Containing purine bases)		
① ADENOSINE	① Adenine	① D - Ribose.
② DEOXYADENOSINE	② ,,	② 2 -deoxy ribose.
③ GUANOSINE	③ Guanine	③ D - Ribose.
④ DEOXYGUANOSINE	④ ,,	④ 2 - deoxy ribose.
Containing pyrimidine bases.		
⑤ CYTIDINE	⑤ Cytosine	⑤ D - Ribose.
⑥ DEOXYCYTIDINE	⑥ ,,	⑥ 2 - Deoxyribose.
⑦ THYMIDINE	⑦ Thymine	⑦ D - Ribose
⑧ DEOXYTHYMIDINE	⑧ ,,	⑧ 2 - deoxy ribose.
⑨ URIDINE	⑨ Uracil	⑨ D - Ribose.
⑩ DEOXYURIDINE	⑩ ,,	⑩ 2 - deoxy ribose.

Structure of adenosine :-



Krebs cycle
Glycolysis → break
Oxidative ~~phosphorylation~~ decarboxylation

e⁻ transport / in the presence of oxygen → 32 molecules of ATP

BIOLOGICAL IMPORTANCE OF NUCLEOTIDES :-

① Nucleotides are important intracellular molecules.

② They play an important role in carbohydrate, fat and protein metabolism.

③ Purine and pyrimidine nucleotides are precursors of RNA & DNA.

④ Purine and pyrimidine nucleotides act as high energy sources (E.g)

(i) Adenosine triphosphate (ATP)
(ii) Cytidine triphosphate (TP)

⑤ They act as coenzymes (E.g) Flavin adenine dinucleotide (FAD).

⑥ Certain nucleotides function as Vitamin B
(E.g) (i) Nicotinamide adenine dinucleotide (NAD)
(ii) Flavin adenine dinucleotide (FAD)

⑦ Adenosine triphosphate (ATP) is involved in oxidative phosphorylation.

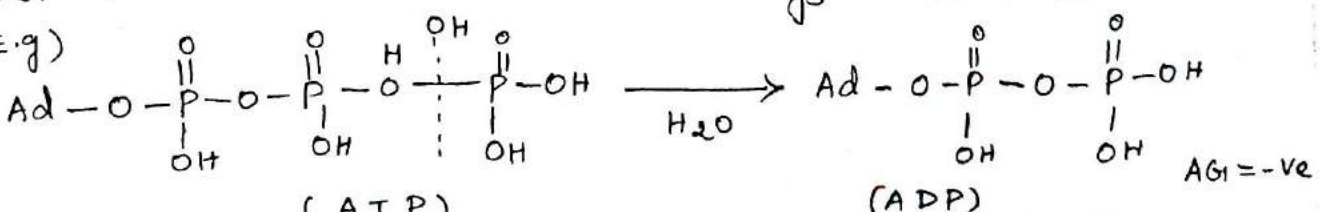
⑧ They act as carriers of heridity functions.

Energy carriers :-

① The –P–O–P– bonds present in nucleotides are high energy phosphate bonds and on account of these bonds, some nucleotides act as energy carriers.
(E.g) Adenosine diphosphate (ADP), Adenosine triphosphate (ATP)

② When a new bond is formed energy is absorbed and when a bond broken energy is released.

(E.g)



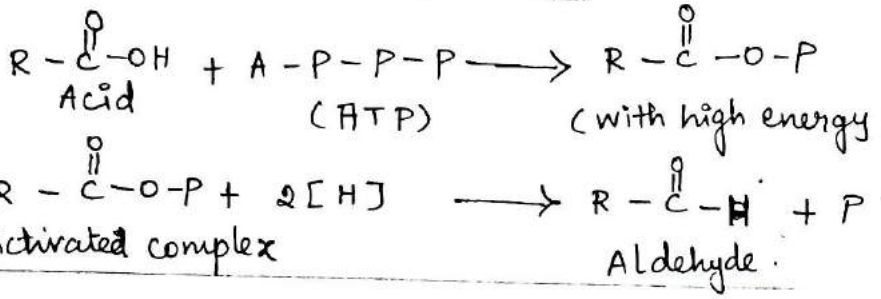
(ATP) (ADP) + H_3PO_4

③ During synthesis of ADP and ATP in the cell, energy is absorbed. Required energy is derived from oxidation of carbohydrates and fats.

④ Primary function of respiration is to produced ATP from ADP

⑤ whenever energy is required for any body function. ATP changes into ADP liberating the required energy.

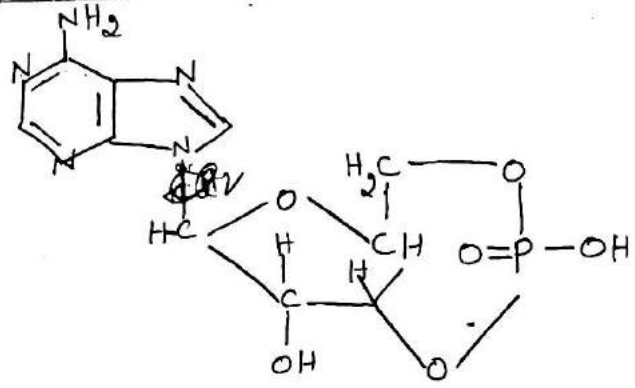
⑥ Some reactions which are thermodynamically unfavourable (e.g) [reduction of RCOOH to RCHO] in the lab can be accomplished in the living systems at room temperature and that too at pHa = 7



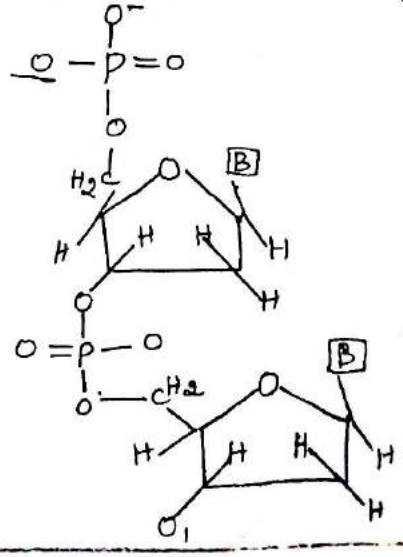
Nucleotide :-

"Nucleotides are the nucleosides phosphorylated on one or more of the hydroxyl groups of the sugar. so they are phosphoric esters of nucleosides".

Structures of adenosine monophosphate :-



Representation of a portion of DNA molecule :



BIOLOGICAL IMPORTANCE OF NUCLEIC ACIDS :-

(1) DNA is called as master molecule since it controls the function of cell.

(2) Due to its self-replication, it is responsible for maintaining heridity from generation to generation.

(3) It gives instruction and information to the cell for protein synthesis.

(4) r-RNA and m-RNA are also involved in protein synthesis.

(5) Nucleic acids can undergo mutation.

(6) DNA produces t-RNA which helps in placing amino acids in the code for protein synthesis.

(7) Nucleotides such as NAD, FAD can act as hydrogen acceptors which are involved in the transport of hydrogen atoms or e^-s during biological oxidation-reduction.

STRUCTURE OF DNA :- DOUBLE HELIX STRUCTURE :-

Based on the X-ray diffraction data of Wilkins and Franklin, Watson and Crick proposed a model for DNA structure.

(1) It is made up of two polynucleotide chains with a number of nucleotide chains.

(2) The two strands are coiled about one another to form a double stranded helix. The helix has two external helical grooves.

(3) The diameter of the double helix is 20 Å

(4) The double helix is a right handed helix.

(5) The two polynucleotide strands of the DNA double helix are antiparalled.

(6) Base pairing - in DNA molecule, purines are linked with pyrimidines. The base pairs are joined through hydrogen bonding. Adenine is linked with thymine

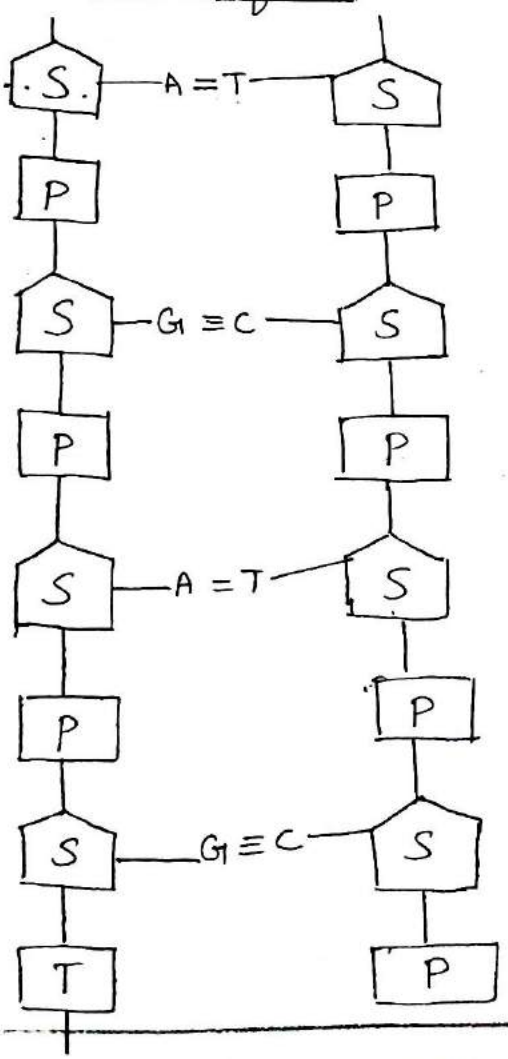
(A = T) through two hydrogen bonds and guanine is linked with ~~cytosine~~ cytosine (G ≡ C) through three hydrogen bonds.

⑦. The distance between the two bases is about 3.4Å. A complete turn of the two strands of the DNA is made up of 10 such intervals i.e 34Å. There are 10 base pairs per twist of the helix.

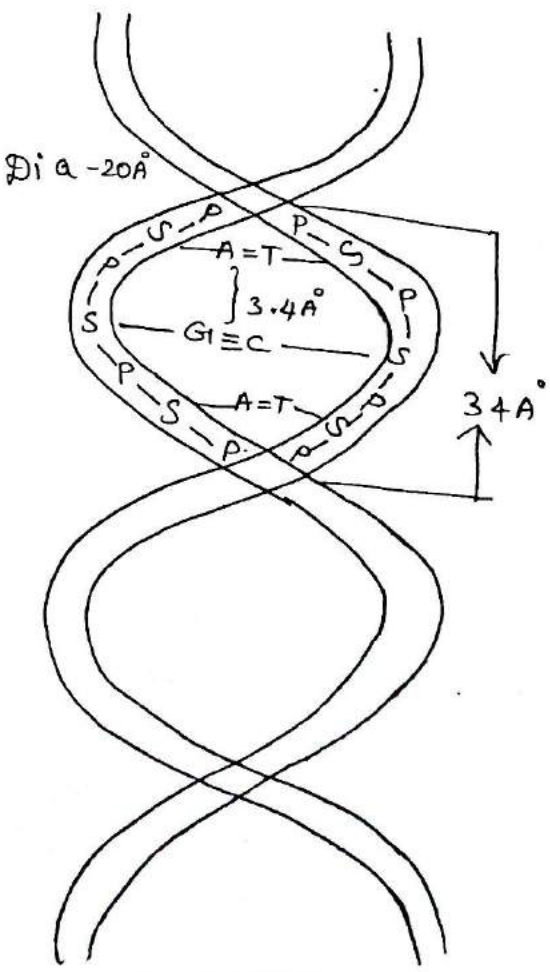
⑧. The two chains of DNA are complementory to each other. If the sequence of bases in one chain is A, G, A, T, G, C then the sequence of bases in the second chain is T, C, T, A, C, G.

⑨ A DNA molecule looks like a ladder. The sugars and phosphate form the back bones and base-pairs form the horizontal rungs.

Ladder form



Double helix structure



(33)

DIFFERENCES BETWEEN DNA AND RNA

S.No	PROPERTIES	DNA	RNA
1	(Location) Presence	Nucleus, Mitochontria, chloroplasts,	Cytoplasm, Nucleus (small quantities)
2.	Pyrimidine bases	cytosine, Thymine	cytosine, Uracil.
3.	pentose sugar	De-oxyribose	Ribose.
4.	Structure	Double stranded (or) single stranded.	single stranded.
5.	Hydrolysing enzyme	Deoxyribose nuclease	Ribonuclease.
6.	Role in cell	Genetic information	protein synthesis.
7.	A:T, G:C	Should be 1:1	Need not to be 1:1
8.	Molecular weight	2-6 million	25,000 - 2 million.
9.	Variation of quantity.	constant in each cell of the species	Varies in different cell.
10.	Types	linear intracellular, circular extracellular	mRNA, tRNA, rRNA Each has many types.
11.	Replication	Can replicate itself	Can't replicate formed by DNA.
12.	Bases	Doesn't contain unusual bases.	may contain unusual bases in addition to normal ones.
13	Component of	chromosome.	Ribosome.
14.	Genetic material	in all organisms.	in certain Viruses.
15.	primer.	Needed for replication	NO primer is needed for replication.

REPLICATION OF DNA

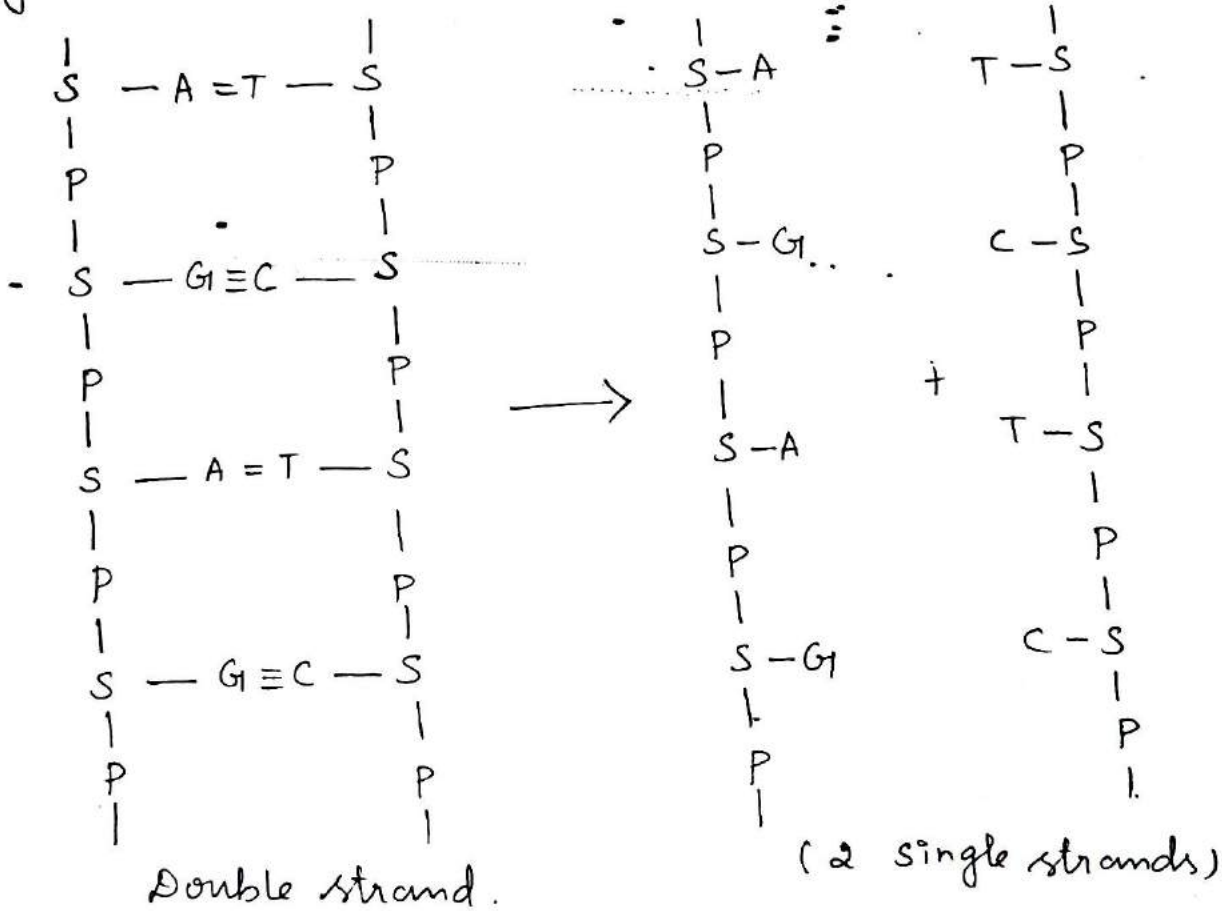
1) DNA molecule has a unique property of replication. (building up another identical molecule).

2) Double strand is separated into two single strands.

3) Each single strand is capable of synthesising its complementary strand which is separated from it.

4) The synthesised single strand is the carbon copy of the separated one.

5) In this way, two double strands of DNA molecules are produced which are exactly replicate of the original DNA molecule.



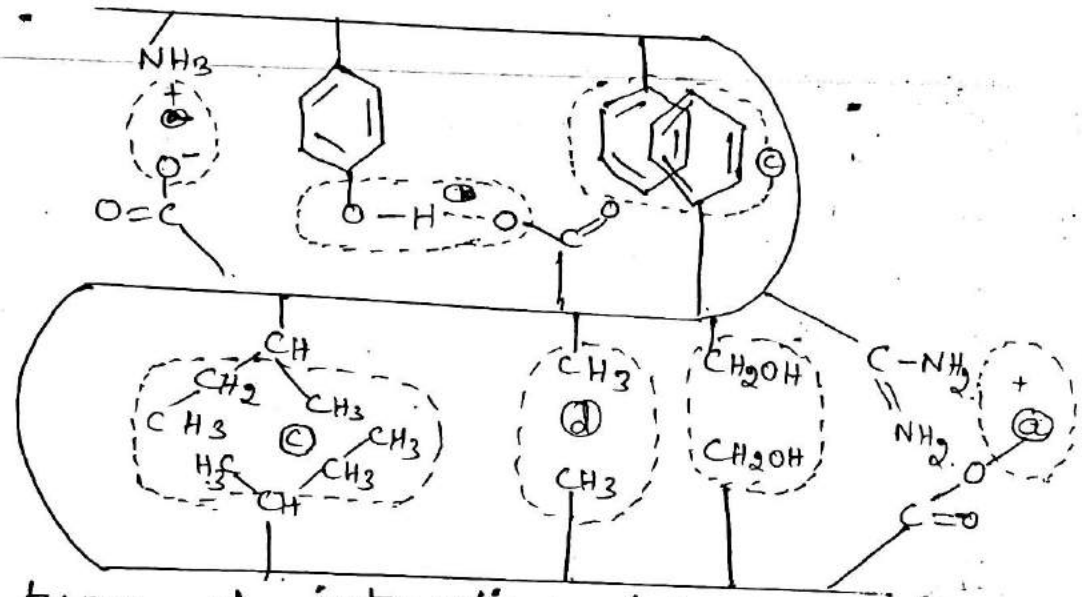
Double strand. (2 single strands)

6. For this complicated process, two enzymes known as DNA polymerase and DNA ligase are used.

Types of Bonds in Tertiary Structure of Proteins: (33)

Hydrogen bonding is importance in the stabilisation of secondary structure, i.e, the α-helix and pleated sheets of proteins.

The tertiary structure involves hydrogen bonding, ionic, chemical and hydrophobic bonds. From this following figure.



Several types of interactions between side chain substituents which stabilise protein structure a) Salt linkages between ionic groups. b) Hydrogen bonding between polar groups c) Hydrophobic interactions between non-polar groups. d) Vandar Waal's interactions between non-polar groups.

Disulphide bond also maintains the tertiary structure But it is of covalent nature. Therefore it is generally included in primary structure. These forces maintain coiling and folding in a definite manner, thus giving rise to a highly specific internal structure of the protein.

Hydrogen bonds :- In tertiary structures of proteins are expected to form between two amino acids, one of which contains a hydrogen group like -OH as in tyrosine while the other contains a hydrogen acceptor group like a —COOH as in Glutamic acid.

Ionic bonds :- In tertiary structures of Proteins are expected to form between aminoacid side groups which are capable of ionising to form electrically charged species. In these bonds, R- groups with unlike charges like NH_3^+ of lysine and COO^- of Glutamic acid would be attracted to each other whereas groups having similar charges would repel each other.

Hydrophobic (non-polar) bonds :- It is formed between the hydrocarbon-like side chains (e.g. between two methyl or phenyl groups) that tend to prefer to be present in the interior of the protein molecule where less water is present.

The distinction between Vander Waals types of linkages and hydrophobic linkages is not well defined.

In addition to the above mentioned linkages, there also occurs

Polar group interaction with water on the surface, However, it is to be noted that these are of much less importance than the Hydrophobic forces.

Techniques :

The various techniques used for studying tertiary structures of Proteins are X-ray analysis. Viscocity measurements, diffusion, Light-scattering, ultracentifugal method, electron microscopy.

Progress has been made on the X-ray diffraction analysis of a number of proteins that differ in biological function, size and in the number of poly peptide chain per molecule.

a) A typical globular protein is compact with extensive folding of the polypeptide chain to give a spherical shape. The compact nature of the molecule places the side chains of amino acid residues on the surface of the molecule and most hydrophobic side chains inside the molecule. Examples of globular protein are mycoglobin and haemoglobin.

b) A fibrous protein has a large helical content and is a rigid molecule

of rod shape. For example, α-keeralin consits of three α helicals which are wound round each other like Strands in a rope. On the other hand, silk fiberoin, also fiberous Protein, Consists of pleated sheets in which the polypeptide chains are antiparallel.

(23)

(25)

BIOSYNTHESIS OF CHOLESTEROL:-

All carbon atoms of cholesterol are derived from acetyl CoA. The major sites of synthesis of cholesterol are liver, adrenal cortex, testes, ovaries and intestine. All nucleated cells can synthesize cholesterol.

STEP I:- CONDENSATION:-

Two molecules of acetyl CoA condense to form acetoacetyl CoA catalysed by cytoplasmic acetoacetyl CoA synthase.

STEP II:- PRODUCTION OF HMG CoA:-

A third molecule of acetyl CoA condenses with acetoacetyl CoA to form beta-hydroxy beta-methyl glutaryl CoA (HMG CoA). The enzyme used is HMG CoA synthase. HMG CoA present in cytosol is utilised for cholesterol synthesis

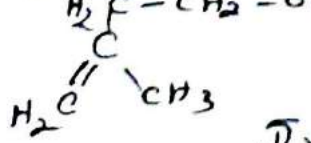
STEP III:- THE COMMITTED STEP:-

It is the rate-limiting step in which HMG CoA is converted to mevalonate which is catalysed by HMG CoA reductase enzyme takes place. It is a microsomal enzyme.

STEP IV:- PRODUCTION OF 5-Carbon Unit:-

(i) Mevalonate is successively phosphorylated to phosphomevalonate, to pyrophosphomevalonate, then to 3-phospho-5-pyrophosphomevalonate (I)

(ii) This then undergoes decarboxylation to give isopentenyl pyrophosphate (II) a five carbon unit by the enzyme decarboxylase



(II)

For the formation of (I), there are three small steps in which one molecule of ATP is added in each step. These 3 small steps along with the

decarboxylation step are known as first phase of cholesterol synthesis.

STEP I:- CONDENSATION OF 5-CARBON UNITS:-

II is converted into dimethyl allyl pyrophosphate (III) by the enzyme isomerase

III dimerises by Transferase enzyme into Geranyl pyrophosphate, (IV) which is a ten carbon unit.

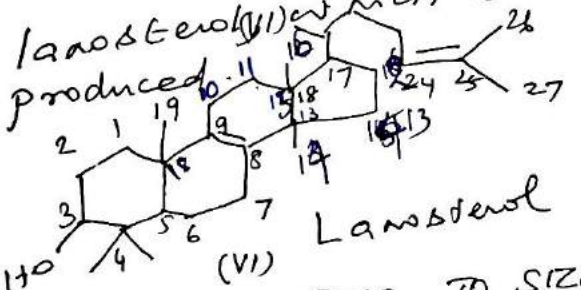
IV again condenses with II and the enzyme Transferase, which is a 15 C unit; Farnesyl pyrophosphate (V) is formed by

V is converted into squalene, a 30 C unit by ~~condensing~~ dimerization with the help of the enzyme squalene synthase.

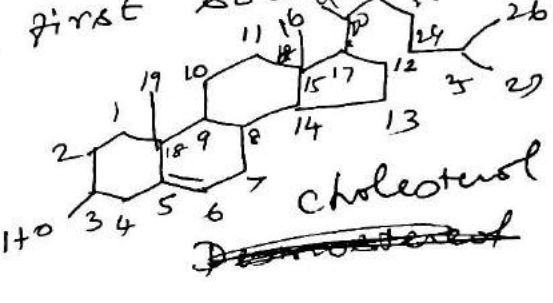
STEP VI CYCLISATION:-

Squalene now undergoes oxidation by epoxidase using molecular oxygen and NADPH to form squalene epoxide.

D cyclase converts it to 30C compound lanosterol (VI) which is a first steroid produced.



Lanosterol (VI)



Cholesterol

~~Desmosterol~~

STEP VII CUTTING TO SIZE:-

Next, the 3 additional methyl groups on carbon atoms 4 & 14 are removed to produce zymosterol.

Then the double bond migrates from 8-9 position to 5-6 position, when desmosterol is formed. Desmosterol is present in fetal brain. It is absent in adult brain and reappears in gliomas (brain tumor)

Finally the double bond in the side chain (between carbon 24-25) is reduced by NADPH when Cholesterol is formed

VII

STRUCTURE OF RNA :-

(1) Ribonucleic acid is a long unbranched macromolecule consisting of nucleotides joined by 3'→5' phosphodiester bonds.
(2) pentose ribose sugar has a free hydroxyl group in position 2'.
(3) It does not exist in a regular conformation like a double-chain DNA although some viruses have double-stranded RNA.
(4) The single RNA strand is folded upon itself, either entirely or in certain regions. like a hairpin loops
(5) In the folded region, a majority of the bases are complementary and are joined by hydrogen bonds. This helps in the stability of the molecule.
(6) In the unfolded region, the bases have no complements
(7) Due to this, RNA is not having the purine-pyrimidine equality that is found in DNA. On a single chain of RNA, the molar proportions of purines and pyrimidines can vary considerably.
(8) In RNA, adenine pairs with uracil and guanine with cytosine. This base pairing is of importance when RNA is being synthesised by DNA and when RNA is involved in protein synthesis.
(9) In ribose moieties, the polynucleotides linked together by phosphate diester bonds between 3' and 5' position of ribose moieties.
(10) There is internal hydrogen bonding within the chain to keep it in a coiled position.
(11) There are 3 types of RNA, t-RNA, m-RNA and r-RNA.
(12) t-RNA has clover-leaf structure. The clover-leaf structure provides a maximum amount of base-pairing by means of hydrogen bonding. In the loop region, there is no hydrogen

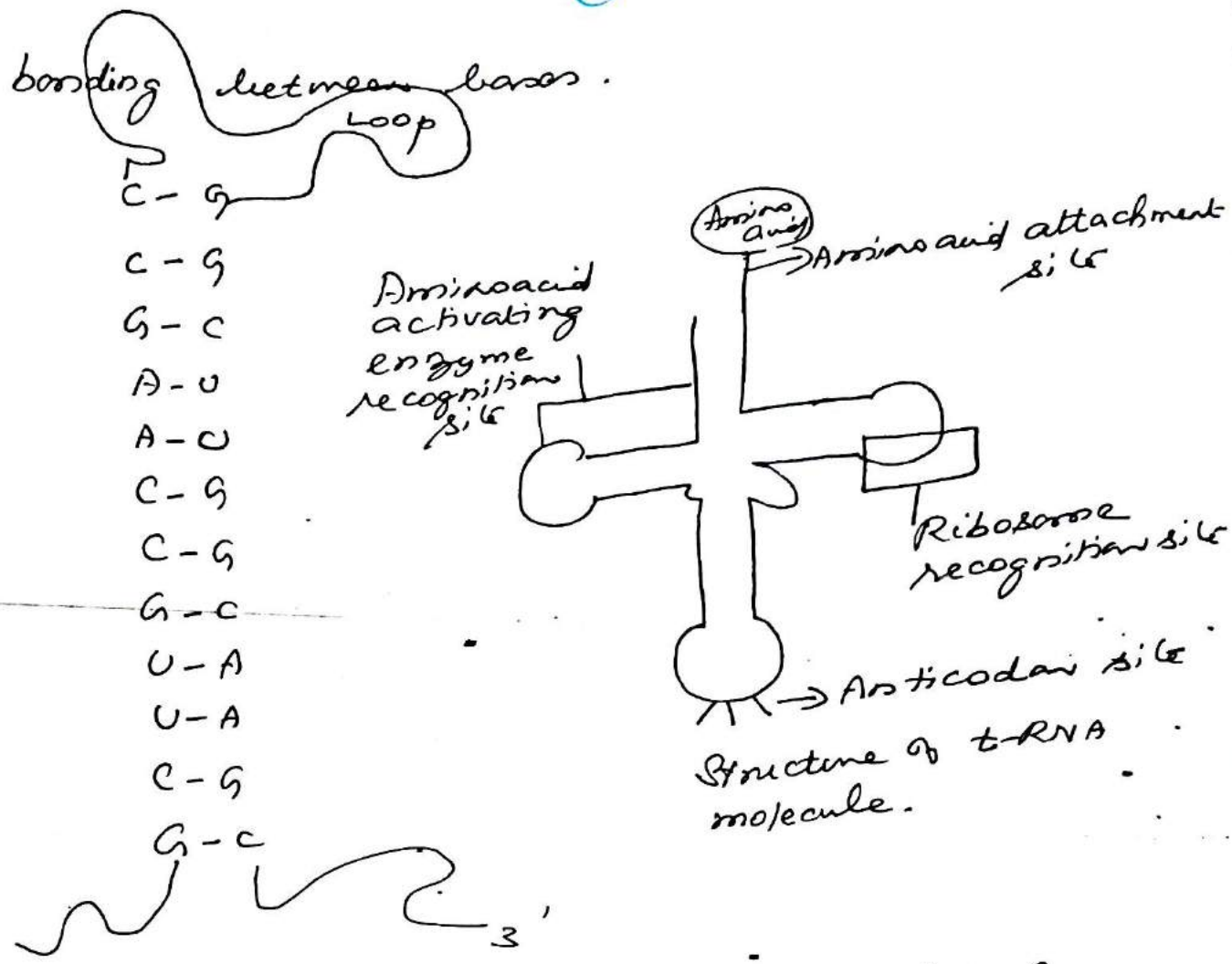


Diagram showing secondary structure of single-stranded RNA molecule.

(13) Messenger RNA is always single stranded. It contains mostly the bases adenine, guanine, cytosine & uracil. The sequence of bases in m-RNA is complementary to the bases constitute the genetic code.

(14) Ribosomal RNA may be a short compact rod, a compact coil or an extended strand.

what are the biological function of nucleic acids. Explain them.

① Replication
② Protein Syntheiis

COMPONENTS OF NUCLEIC ACIDS :-

Nucleic acids hydrolyse to yield different degradation products depending upon the conditions of the hydrolysis. For example,

a) When nucleic acids are treated with aqueous ammonia at 115°C or $Ba(OH)_2$, they get hydrolysed to yield nucleotides.

Nucleic acids $\xrightarrow{Aq.NH_3 \text{ at } 115°C \text{ or } Ba(OH)_2}$ Nucleotides

b) When nucleotides are treated with aqueous ammonia at 175°C, they yield nucleosides and phosphoric acid.

Nucleotides $\xrightarrow{Aq.NH_3 \text{ at } 175°C}$ Nucleosides $+ H_3PO_4$

c) When nucleosides are treated with dil. HCl, they yield purines, pyrimidines and Sugar.

Nucleosides $\xrightarrow{\text{Inorganic acid}}$ Sugar + Purines + pyrimidine

d) Enzymatic hydrolysis of nucleic acids with nucleinase yields nucleotides.

Nucleic acids $\xrightarrow{\text{Nucleinase}}$ Nucleotides

e) When nucleic acids are heated with 12N perchloric acid or formic acid, they are Completely degraded to purines and pyrimidines, Sugar and phosphoric acid.

Nucleic acids $\xrightarrow{HClO_4 \text{ or } HCOOH}$ Purines + pyrimidines + Sugar + phosphoric acid

The above hydrolysis experiments of nucleic acids are Sumarised below.

f) When nucleic acids are heated with MgO in Solution, they yield nucleorides and phorphoric acid.

Nucleic acids $\xrightarrow{MgO \text{ in Solution: heat}}$ Nucleosides + phosphoric acid.

The above hydrolysis components of nucleic acids are Summarised as follows.

Nucleic acids

12 N perchloric acid or Formic acid → Sugar + purines + pyrimidines + phosphoric acid.

MgO in solution / heat → Nucleosides + H_3PO_4

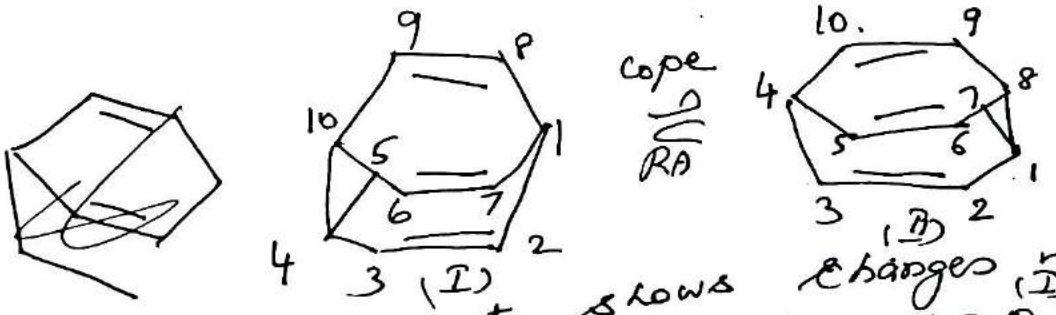
Aq. NH_3 at 115°C or $Ba(OH)_2$ → Nucleotides

Enzyme (nuclease) Aq. NH_3 at 175°C → Nucleosides + H_3PO_4

Inorganic acid → Sugar + purines + pyrimidines

Structure of BULLVALENE - FLUXIONAL STRUCTURE:-

(1) Bullvalene has the following structure.



(2) Cope rearrangement shows changes in the position of cyclopropane ring from 4, 5, 10 (I) to 1, 7, 8 (II)

(3) Any of these two structures then undergo several Cope rearrangements. In all, there are $10!/3$ or more than 1.2 million tautomeric forms and cyclopropane ring can be at any 3 carbons that are adjacent.

④ This is called as valence tautomerism and is different from resonance even though only electron shift occurs in the two.

⑤ The difference between these two phenomena is only in valence tautomerism, there is change in the position of nuclei.

⑥ At and above 100°C, structure I, bullvalene undergoes valence tautomerism and are said to have fluxional structure.

⑦ Since each of these tautomers (1.2 million forms) is equivalent to all the others, this is called as infinitely degenerate Cope rearrangements.

⑧ Bullvalene at -25°C, shows two peaks with an area ratio of 6:4 in NMR spectrum. This is in accordance with a single nontautomeric structure The six are for six vinylic protons (2, 3, 6, 7, 8 & 9) and the four are for allylic protons (1, 4, 5, 10)

⑨ But at 100°C, the compound shows only one nmr peak. ^{13}C nmr of bullvalene also shows only one peak at 100°C as above 100°C.

⑩ This clearly indicates that at 100°C, the compound rapidly interchanges its structure among 1.2 million equivalent forms.

GENETIC CODE:

A triplet sequence of nucleotides on the mRNA is the codon for each amino acid. Since there are four different bases, they can generate 64 (4^3) different codons or code words by permutations and combinations. For example, the codon for phenyl alanine is UUU. Nirenberg was awarded the Nobel prize in 1968 for deciphering the genetic code. There are 61 tRNA species, carrying 20 amino acids, which translate 61 codons. Important features of genetic code.

Salient Features of the Genetic Code:-

i) TRIPLET CODONS

The codes are on the mRNA. Each codon is a consecutive sequence of three bases on the mRNA. e.g. UUU code for phenylalanine.

ii) NONOVERLAPPING:

The codes are consecutive. Therefore the starting point is extremely important. The codes are read one after another in a continuous manner, e.g. AUG, CAU, GAU, GCA, etc.,

iii) NON PUNCTUATED

There is no punctuation between the codons. It is consecutive or continuous.

iv) DEGENERATE:

The Table 41.3 shows that 61 codes stand for the 20 amino acids. So one amino acid has more than one codon. For examples serine has 6 codons; while glycine has

4 codons. This is called degeneracy of the code. Generally speaking, if the amino acid has more than one codon, the first two bases in the codon will be the same, only the third one is different. This reduces the effect of mutations

V. UNAMBIGUOUS:.

Though the codons are degenerate, they are unambiguous; or without any doubtful meaning. That is one codon stands only for one amino acid.

VI) UNIVERSAL

The codons are the same for the same amino acid in all species; the same for "Elephant and E. Coli". The genetic code has been highly preserved during evolution.

vii) Wobbling Phenomenon:.

The reduced stringency between the third base of the codon and the complementary nucleotide in the anticodon is called wobbling. The pairing of codon and anticodon can wobble at the third letter. For example, GGU, GGC and GGA are the codes for glycine; all three will pair with the anticodon CCI (I = Inosinic acid) of glycine tRNA. The degeneracy of genetic code and wobbling phenomenon together will reduce the effect of mutations

viii) TERMINATOR CODONS:-

There are three codons which do not code for any particular amino acids. They are "nonsense codons". more correctly termed as punctuator codons or terminator codons. They put "full stop" to the protein synthesis. There three codons are UAA, UAG and UGA. UGA is a stop codon; but in special circumstances, it stands for Seleno-cysteine (the "21st" amino acid)

ix) Initiator codon :

In most of the cases, AUG acts as the initiator codon. AUG also acts as the codon for Methionine. In a few proteins, GUG may be the initiator codon.