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Because of this, the C-N bond length is also shorter than normal C-N single bonds. The peptide unit which is made up of the CO-NH atoms is thus relatively rigid and planar, although free rotation can take place about the C_α-N and C_α-C bonds i.e, the bonds either side of the peptide bond, permitting adjacent peptide units to be different angles. The hydrogen of the amino group is nearly always on the opposite side (trans) of the double bond to the oxygen of the carboxyl group, rather than on the same side (cis).

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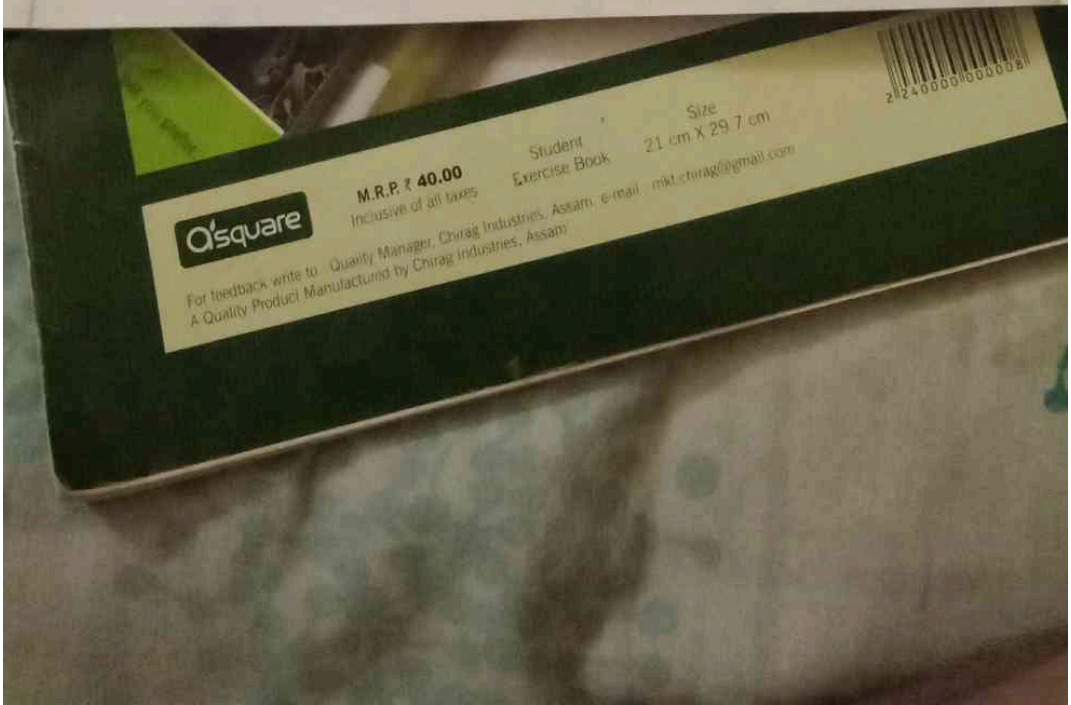
Classification of Proteins:—

Depending on solubility properties and on known chemical and physical differences, proteins are classified into two major groups — single proteins and conjugated proteins.

1. Simple proteins:— They are compounds that on hydrolysis, yield only amino acids. On the basis of solubility properties simple proteins can be further divided into six groups as below—



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i) Albumins :— They are soluble in water and in dilute salt solutions. They can be coagulated by exposure to heat.

eg :- β-amylase of Barley

ii) Globulins :— They are insoluble or sparingly soluble in water. They are soluble in dilute salt solutions. They also can be coagulated by exposure to heat. Eg :- Storage proteins of seeds.

iii) Glutelins :— They are insoluble in neutral solutions but are soluble in weak acid or basic solutions.

Eg :- Glutenin of wheat, oryzenin of rice.

iv) Prolamines :— They are insoluble in water and absolute ethanol but are soluble in 70 to 80 percent ethanol. On hydrolysis they yield relatively large quantities of proline and ammonia. Eg :- Zein of maize, gliadin of wheat and rye, hordein of barley.

v) Histones :- They are soluble in water and are rich in basic amino acids, such as arginine and lysine. They have been found in cell nuclei and may remain associated with nucleic acids.

vi) Protamines:— They are soluble in water and are rich in basic amino acids. They also are found in nuclei and probably remain associated with nucleic acids but this protein lack amino acids tyrosine and tryptophan and contain no sulphur.

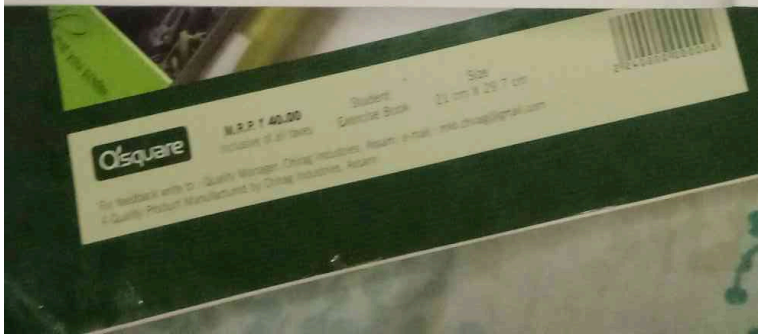
d. Conjugated proteins:— The conjugated proteins are associated with a nonamino acid component which is referred to as prosthetic group. A/c to the varied prosthetic groups, conjugated proteins are divided into following divisions—

i) Nucleoproteins:— On hydrolysis they yield a simple protein and a nucleic acid.

ii) Glycoproteins:— They are associated with carbohydrate as prosthetic groups. Eg. some proteins of cell membrane.

iii) Lipoproteins:— They are associated with lipids as prosthetic groups and are insoluble in water. Eg:- some membrane proteins.

iv) Chromoproteins:— They are associated with pigments as prosthetic groups. Eg: Flavo proteins, Rhodopsins, carotenoid pigments



haemoglobins etc

v) Metalloproteins:- They have metal molecules as their prosthetic groups E.g. some respiratory enzymes

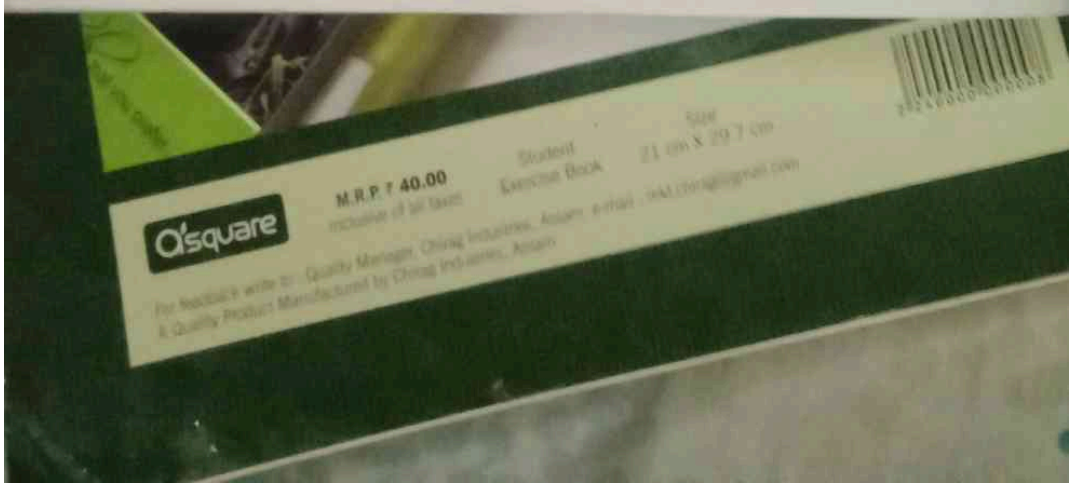
Biosynthesis of Proteins:-

The proteins are macromolecules consisting of a series of varying amounts/numbers of 20 different amino acids. The proteins molecules differ from each other in their length and definite sequence of amino acids. The protein molecules synthesis is directly under genetic control and the master molecule DNA dictates the exact sequence of amino acids in a synthesizing protein. There are two major steps in the mechanism of protein synthesis, which are as below —

1. Transcription:- Transcription is a synonyms for RNA synthesis, in molecular biology. The necessary information for specific sequence and the total number of amino acids, to be incorporated into the protein, are stored in the master molecules DNA in the form of sequence of bases. * DNA transfer the information to the protein synthesising apparatus through the

special messanger called messanger RNA or mRNA
The transfer of information from DNA to RNA is called transchiption. The process of transcription itself involve 2 steps :—

1) Polymerase binding and initiation :— First, the double stranded DNA gets uncoiled and the two strands are seperated from each other by breaking of hydrogen bonds between bases. Out of the two strands, one is coding strand and the other is template strand, later takes part in mRNA synthesis i.e. transchiption. RNA polymerase is the enzyme for RNA synthesis. There a only one type of RNA polymerase in prokaryotes, while there are are three different RNA polymerases in eukaryotes. RNA polymerase binds itself at a start signal or initial binding site on the template strand of the DNA, which is called as promoter site. The enzyme bears a sigma (σ) factor which recognises the promoter sequence without any copies mistakes.



ii) Elongation:— After the initial binding, the enzyme copies the base sequence of template DNA strand accurately and complementary ribonucleotides (i.e. ATP, GTP, UTP and CTP) are joined together by the enzyme at a rate of 30 nucleotides per second. Elongation of the RNA proceeds in the 5'-3' direction.

* The portion of DNA responsible for synthesis of mRNA leading to the production of one polypeptide chain is known as gene.

iii) Termination:— Termination of transcription takes place when the polymerase arrives at a stop signal on the DNA. A new termination factor called rho (ρ) factor, a protein with ATP ase activity causes the release of the completed RNA molecules. The terminal region of the RNA transcription ends in 4-8 consecutive U residues.

The region of DNA template (gene) coding for a single protein is also called a cistron. In prokaryotes there are gene clusters (polycistronic mRNA). Prokaryotic polycistronic mRNA contains several start (AUG) and stop (UAG, UAA, UGA) codons for several protein synthesis in the same mRNA. On the other hand in eukaryotes, the mRNA are always monocistronic and have

a single start (AUG) codon per mRNA molecule.

2. Translation:— Translation involves chiefly three cell components — mRNA, tRNA and ribosomes. Out of these RNA molecule is about 74-95 nucleotides long. About half of the nucleotides of a tRNA are base paired to form double helices and all tRNA molecules common clover leaf secondary structure. The 5' terminal residue form double helices and have common primary and secondary structure. The 5' terminal residue is usually phosphorylated guanine (pGi). The base sequence at the 3' end is CCA. During synthesis of the aminoacyl-tRNA, the amino acid is covalently bound to the residue of the CCA sequence at the 3' end. Each tRNA molecule carries only single amino acid. Each tRNA molecule carries only a single amino acid. Each t-RNA molecules also bears a triplet of bases called an 'anticodon' which is complementary to the codon of the mRNA, corresponding to a specific amino acid.

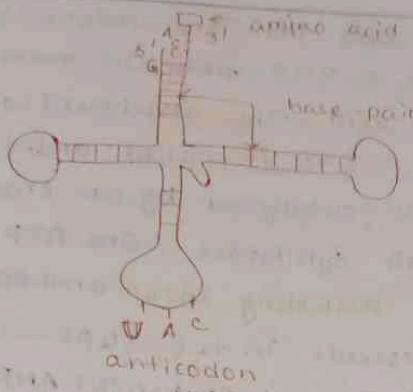


Fig :- Clover leaf secondary str. of a t-RNA

Ribosomes are the cytoplasmic organelles where protein synthesis takes place. Each ribosome is made up of two sub units - one smaller and other larger. In case of prokaryotes the two subunits are 30s and 50s while in eukaryotes, they are 40s and 60s. The two subunits are not bound together when they are not involved in protein synthesis. Each a specialised RNA called ribosomal RNA (rRNA)

The process of translation proceeds in three steps — Initiation, elongation and termination

i) Initiation :- The step are as below—

a) Amino acid activation :- There is at least one t-RNA for each amino acid, in the cell However, because of the redundancy of the genetic code,

(quality of super flous)

there may be more than one codons and hence more than one t-RNA molecules exist for the same amino acid. The attachment of an amino acid to a t-RNA is called amino acid activation and is catalysed by an enzyme called aminoacyl t-RNA synthetase. One ATP is involved in the reaction resulting into aminoacyl t-RNA.

The reaction proceeds in two steps —

- Amino acid + ATP ⟷ Aminoacyl AMP + PP;
- Aminoacyl AMP + t-RNA → Aminoacyl - tRNA + AMP

b) Initiation of protein synthesis is catalysed by 3 proteins called initiation factors (IF_1, IF_2, IF_3) in prokaryotes). Initiation begins with the binding of IF_1 and IF_3 to the small (30S) ribosomal subunit. The small subunit then binds to the mRNA via the shine Dalgarno sequence (AGGAGGU) and moves 3' along the mRNA until it locates the AUG initiation codon. In prokaryotes ~~the first~~ aminoacid initiation codon In prokaryotes the first aminoacid of a new protein is N-formyl methionine (f Met). The initiator t-RNA charged with N-formyl

methionine and in a complex with IF_2 and GTP (f Met-tRNA fMet/ IF_2 /GTP) now binds. IF_3 is released subsequently. The complex of mRNA, f Met-tRNA f Met, IF_1, IF_2 and the 30s subunit is called the 80s initiator complex. The large (50s) ribosomal subunit now binds, with the released of IF_1 and IF_2 and hydrolysis of GTP, to form a complete 70s initiation complex. Besides the binding site for mRNA, Each complete 70s ribosome has three binding sites for t-RNAs. They are- aminoacyl-t-RNA site or A site, peptidyl-t-RNA site or P-site and exit site or E-site. In initiation stage, the initiator amino acyl-t-RNA binds directly at the P site

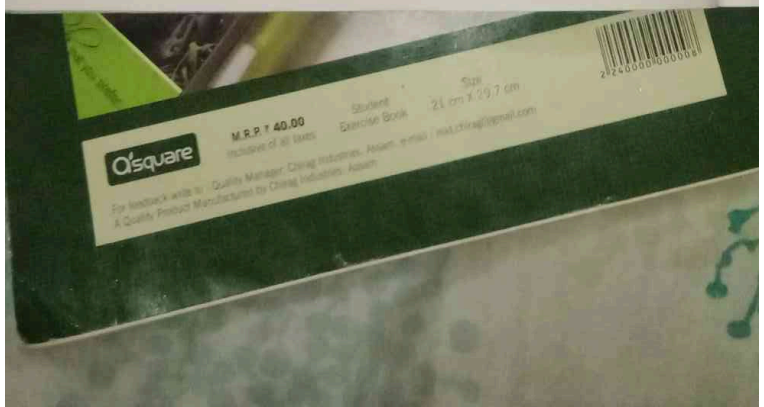
ii) Elongation :- Elongation of the polypeptide chain occurs in three steps namely aminoacyl-tRNA binding, peptide bond formation and translocation.

a) Aminoacyl-tRNA binding :- In this first step, the corresponding aminoacyl t-RNA for the second codon binds to the A-site via codon-anticodon interaction. This binding of the aminoacyl-tRNA requires elongation factor EF-TU and GTP, which bind as an

amino acyl-tRNA/EF-TU/GTP complex. Following binding the GTP molecule in the EF to release

b) Peptide bond formation:— The second step, i.e. the peptide bond formation is catalysed by peptidyl transferase, part of the large ribosomal subunit. In this step, the carboxyl end of the amino acid bound to the tRNA in the P-site is uncoupled from the t-RNA and becomes joined by a peptide bond to the amino group of the amino acid linked to the t RNA in the A-site.

c) Translocation:— In the third step, a complex of elongation factor EF-G (also called translocase) and GTP (i.e, EF G/GTP) binds to the ribosome. Three concerted movements now occur, collectively called diacylated t-RNA moves from the A-site moves to the P-site, and the ribosome moves along the m-RNA from 5' to 3' direction, by three nucleotides to place the next codon in the A-site. During translocation events GTP is hydrolysed to GDP and inorganic phosphate and EF-G is released.



After translocation, the A-site is empty and ready to receive the next aminoacyl-tRNA. The A-site and the E-site cannot be occupied simultaneously. Thus the deacylated t-RNA is released from the E-site before next amino acyl tRNA binds to the A-site to start a new round of elongation Elongation adding of amino acid to the C-terminal end of the growing polypeptide for each codon that is read by the ribosome.

iii) Termination:— UAG, UAA and UGA are said to be termination codons or stop codons, which unlike codons, do not contain aminoacyl t-RNAs. Complementary to them. So when one of these three termination codons are present third release factor RF_3 is also needed to assist RF_1 or RF_2. These release factors cause the peptidyl transferase to transfer the polypeptide to a water molecule instead of aminoacyl t-RNA. Thus the bond between the polypeptide and t-RNA in the P-site is cleaved effectively. The released polypeptide now leaves ribosome, followed by the mRNA and free t-RNA and the ribosome dissociates into 30S and 50S sub-units.