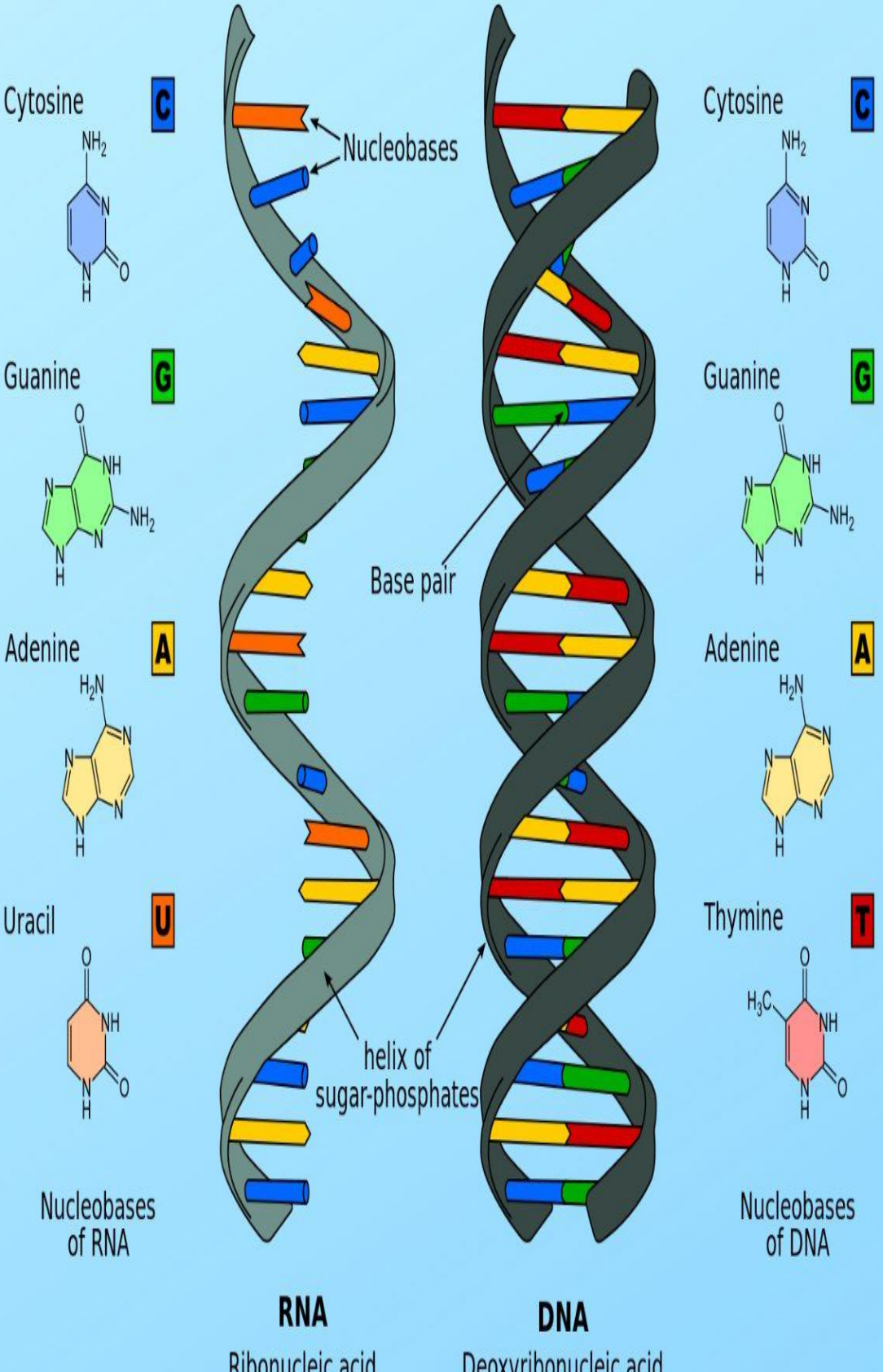
RNA vs DNA


Cytosine
C
Guanine
G
Adenine
A
Uracil
U
Nucleobases of RNA
Nucleobases
Base pair
helix of sugar-phosphates
Cytosine
C
Guanine
G
Adenine
A
Thymine
T
Nucleobases of DNA
RNA
Ribonucleic acid
DNA
Deoxyribonucleic acid

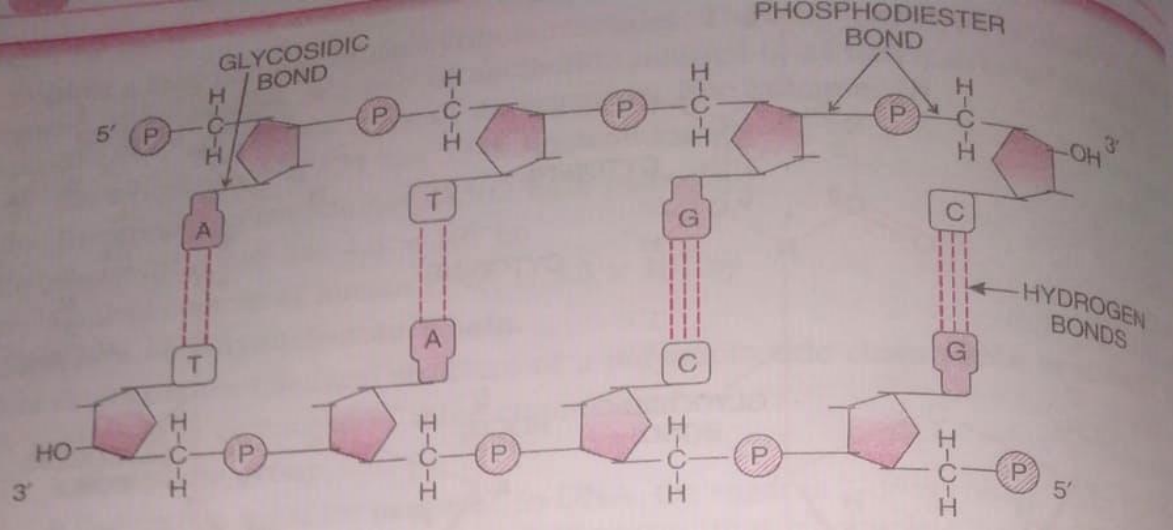


Fig. 6.4. A double sranded polynucleotide chain.

Polarity of Polynucleotide Chain

The polynucleotide chain shows polarity (direction). A polymer thus formed has at one end a free phosphate moiety (a part of a large molecule or structure) at 5′ end of sugar which is referred to as 5′ end of polynucleotide chain. Similarly, at the other end of the polymer the sugar has a free 3′–OH group which is referred to as 3′–end of the pol, nucleotide chain. The backbone in a polynucleotide chain is formed due to sugar and phosphates. The nitrogenous bases linked to sugar moiety project from the backbone.

In RNA, every nucleotide residue has an additional –OH group present at 2′–position in the ribose. Also, in RNA the uracil is present at the place of thymine (5-methyl uracil).

Structure of DNA

From 1950 to 1953 significant knowledge about structure of nucleic acid molecules was gained from the researches of **Erwin Chargaff, Maurice Wilkins, Rosalind Franklin, James Watson, Francis Crick** and others.

The correct structure of DNA was first worked out by James Watson and Francis Crick in 1953. Their **double-helix** model of DNA structure was based on two major investigations. Chargaff's rules for base pairing and the study of X-ray diffraction pattern of DNA which helped Watson and Crick to design the 3-dimensional structure of DNA.

Chargaff's Rules. Erwin Chargaff (1950) formulated important generalizations about DNA structure. These generalizations are called **Chargaff's rules.** These rules are summarized below.

(i) The purines and pyrimidines are always in equal amounts, *i.e.*, A + G = T + C.

(ii) The amount of adenine is always equal to that of thymine and the amount of guanine is always equal to that of cytosine, *i.e.*, A = T and G = C.

(iii) The base ratio A + T is constant for a species but may vary from one species to another. This ratio can be used to identify the species.

X-ray diffraction pattern of DNA. A technique for determining the three-dimensional structure of a large molecule is called **X-ray crystallography.** The pattern obtained after the

diffraction of X-ray through a crystal is termed as **X-ray diffraction pattern.**

In 1953, Maurice Wilkins and Rosalind Franklin took X-ray diffraction pictures of crystalline DNA. They concluded that DNA is a long molecule consisting of two similar strands running in parallel and helical manner where successive nucleotides occur at intervals of 0.34 nm (3.4 Å). They found DNA to have a diameter of 2 nm (20Å), major and minor grooves, a regular helix with 3.4 nm (34Å) distance and 10 pairs of nucleotides in each turn of spiral.

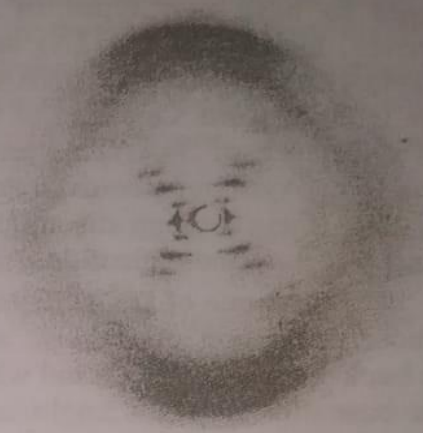


Fig. 6.5. An X-ray diffraction photograph of DNA that led to the double helix model of DNA structure. The heavy dark patterns (top and bottom) indicate that the bases are stacked perpendicular to the axis of the molecule with a periodicity of 3.4 Å.

Watson and Crick Model of DNA. The above investigations helped Watson and Crick to design a model of DNA molecule in 1953.

Watson and Crick along with Wilkins received Nobel Prize (Medicine or Physiology) in 1962 for double helical model of DNA and significance for information transfer in living material.

Watson and Crick model of DNA has the following important features.

1. **Two Polynucleotide Chains or Strands.** A DNA molecule is formed of two long polynucleoid chains formed of **deoxyribonucleotides.** Each deoxyribonucleotide of DNA is formed by cross-linking of three chemicals — phosphoric acid (H_3PO_4), deoxyribose sugar ($C_5H_{10}O_4$) and a nitrogenous base. Four types of nitrogenous bases occur in DNA. They belong to two groups, **purines** (9-membered double rings with nitrogen at 1, 3, 7 and 9 positions) and **pyrimidines** (six membered rings with nitrogen at 1 and 3 positions). DNA has two types of purines (**adenine** or A and **guanine** or G) and two types of pyrimidines (**cytosine** or C and **thymine** or T). Depending upon the type of nitrogen base, DNA has four kinds of deoxyribonucleotides — deoxyadenosine 5-monophosphate (d AMP), deoxy guaninosine 5-monophosphate (d GMP), deoxy thymidine 5-monophosphate (d TMP) and deoxy cytidine 5-monophosphate (d CMP).

2. **Glycosidic and Phosphodiester Bonds.** Nitrogen bases are attached to carbon 1′ of deoxyribose sugar through a **glycosidic bond** by either their N-1 (in case of primidine, cytosine or thymine) or N-9 (in case of purine, adenine or guanine) regions. The bond between two adjacent nucleotides of two adjacent sugar molecules at 3′ and 5′ positions with phosphate group is called **phosphodiester bond** (two ester formations by same phosphate radical).

Both types of bonds are formed by condensation reactions that involve elimination of water.

3. **DNA duplex.** As mentioned above a DNA molecule has two polynucleoid chains or strands. They are spirally coiled. The two spiral strands of DNA are collectively called **DNA duplex** (Fig. 6.6). DNA duplex has a diameter of 20Å. The two strands are not coiled upon each other but the whole double strand (DNA duplex) is coiled upon itself around a common axis in a right handed maner just as a rope stair is twisted to form a spiral. Thus, the coiling becomes **plectonemic,** *i.e.*, the two strands cannot be separated without completely unwinding them.

Due to spiral twisting, the DNA duplex comes to have two types of alternate grooves, major (length 22Å) and minor (length 12Å). The type of DNA described here is the B form. One turn of the spiral has a distance of 34Å. This length contains 10 deoxyribonucleoids in each chain so that the average distance between adjacent deoxyribonucleotide is 3.4 Å.

4. **Backbone of DNA Strand.** Deoxyribose sugar and phosphoric acid form the **back-bone of DNA** strand while nitrogen base lies at right angle to it. The back-bone is formed of alternate deoxyribose sugar and phosphoric acid groups. The nitrogen bases project at right angles to this back-bone from the region of sugar residues.

5. **Polarity.** The polynucleotide chains show polarity (direction). One end of each DNA strand has a free phosphate moiety (a part of a large molecule or structure) at 5 end of sugar which is called **5′ end** of DNA strand. The other end of the strand, the sugar has a free 3′–OH group which is termed **3′-end**. The nitrogenous bases linked to sugar moiety project from the backbone.

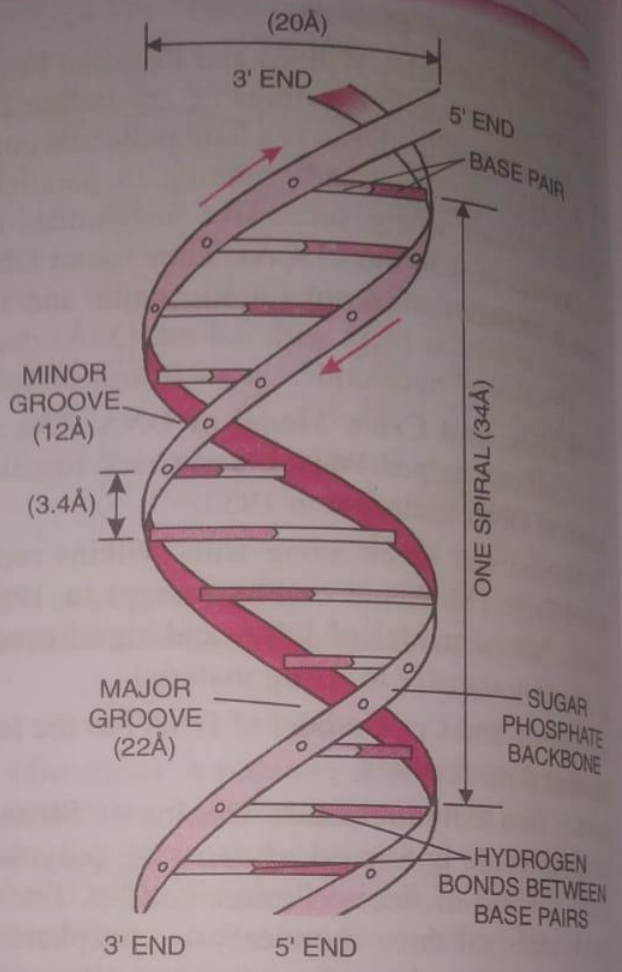


Fig. 6.6. Double helix structure of DNA as proposed by Watson and Crick (1953).

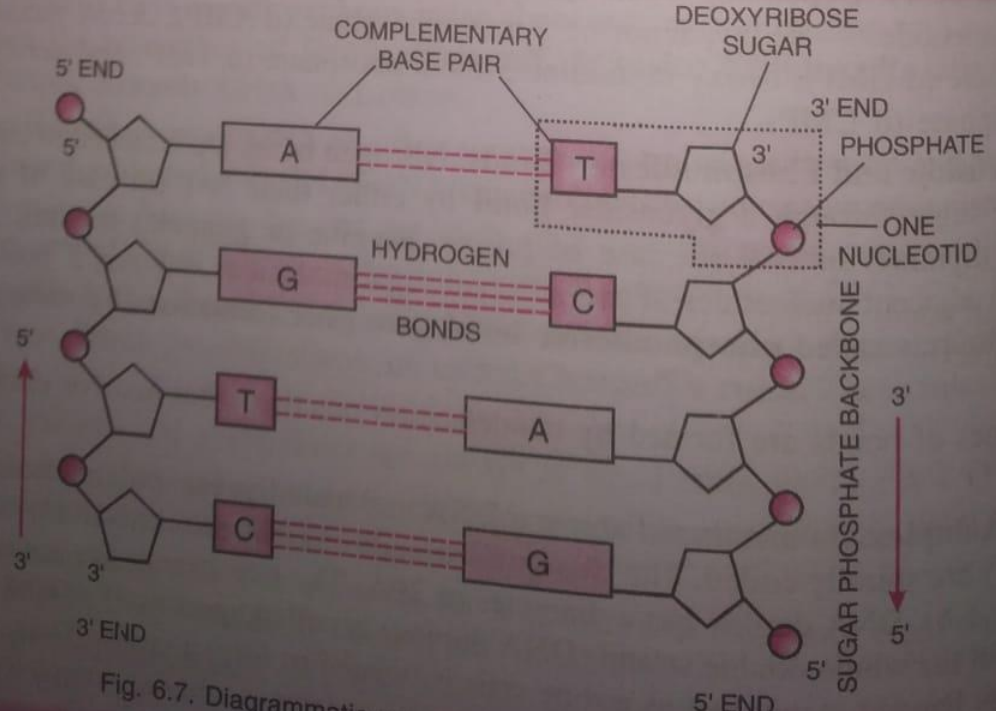


Fig. 6.7. Diagrammatic repres

6. **Complementary Base Pairing.** Base pairing is the pairing formed in DNA double helix between purine of one strand and pyrimidine of the second strand. Purines found in DNA are adenine (A) and guanine (G). Pyrimidines of DNA are thymine (T) and cytosine (C). Adenine of one strand always pairs with thymine of the other pair, *i.e.*, A + T and guanine of one strand always pairs with cytosine, *i.e.*, G + C. The amount of adenine is always equal to that thymine and amount of guanine is always equal to that of cytosine, *i.e.*, A = T and G ≡ C. This finding confirmed Chargaff's rule.

As was proved by the specific purine-pyrimidine (A + T and G + C) base pairing the two strands are always **complementary** (not identical) to each other.

The way in which the bases form pairs between the two DNA strands is known as **complementary base pairing.**

7. **Hydrogen Bonds.** The two strands of DNA are held together by hydrogen bonds between their bases. Two hydrogen bonds occur between adenine and thymine [A = T). There are three hydrogen bonds between guanine and cytosine (G ≡ C). G ≡ C bonds are stronger than A = T bonds.

8. **Antiparallel strands.** The two strands of DNA duplex are parallel but are oriented in opposite directions. Such strands are called **antiparallel.** The antiparallel strands form a right-handed helix. The 5′ end of one strand lies opposite 3′ end of the other. One strand is oriented in the 5′ → 3′ direction and the other strand in the 3′ → 5′ direction. This arrangement is useful in complementary base pairing and replication of DNA.

Salient Features of the Double-helix Structure of DNA

1. DNA has two polynucleotide chains.

2. The two chains of DNA have *antiparallel polarity*, 5′ → 3′ in one and 3′ → 5′ in other.

3. Backbone of each polynucleotide chain is made of alternate sugar–phosphate groups. The nitrogen bases project inwardly.

4. Nitrogen bases of two polynucleotide chains form complementary pairs, A opposite T and G opposite C.

5. A large sized purine always comes opposite a small sized pyrimidine. This generates uniform distance between two strands of helix.

6. Adenine (A) of one polynucleotide chain is held to thymine (T) of opposite chain by two hydrogen bonds. Guanine (G) of one chain is similarly held to cytosine (C) of the other chain by three hydrogen bonds.

7. The double chain is coiled in a helical fashion. The coiling is right handed. This coiling produces minor and major grooves alternately.

8. The pitch of helix is 3.4 nm (34 Å) with roughly 10 base pairs in each turn. The average distance between two adjacent base pairs comes to about 0.34 nm (0.34×10^{-9} m or 3.4 Å).

9. Planes of adjacent base pairs are stacked over one another. Alongwith hydrogen bonding, the stacking confers stability to the helical structure.

turn.

Z-DNA. Left handed helix, with zigzag and 12 base like **sugar-phosphate** back
nd 12 base pairs per turn of helix.

Differences in different forms of DNA

	B	Z	A	C	D
1. Handedness of helix	Right handed	Left handed	Right handed	Right handed	Right
2. Pitch of helix per turn	34 Å	46 Å	25 Å	30 Å	24 Å
3. Diameter of helix	20 Å	18 Å (thinnest)	26 Å (widest)	19Å	—
4. Stability	Stable and physiologically active form	Unstable	Unstable	Unstable	Unstable
5. Base pairs per turn of helix	10	12 (6 dimers)	11	9.33	8
6. Distance (vertical rise per base pair) between 2 base pairs	3.4 Å	3.8 Å	2.5 Å	3.3 Å	3.03 Å
7. Repeating unit	Mononucleotide	Dinucleotide	Mononucleotide	Mononucleotide	Mononucleotide

5. **Coding and Noncoding DNA.** Depending on the ability to form functional
functional products. DNA

DNA Packaging in Prokaryotes. In prokaryotes, such as *E. coli* though they do not have a defined nucleus, the DNA is not scattered throughout the cell. DNA (being negatively charged) is held with some **nucleoid–associated proteins (NAPs,** that have positive charges) in a region termed as **'nucleoid'.** The DNA in nucleoid is organised in large loops held by proteins.

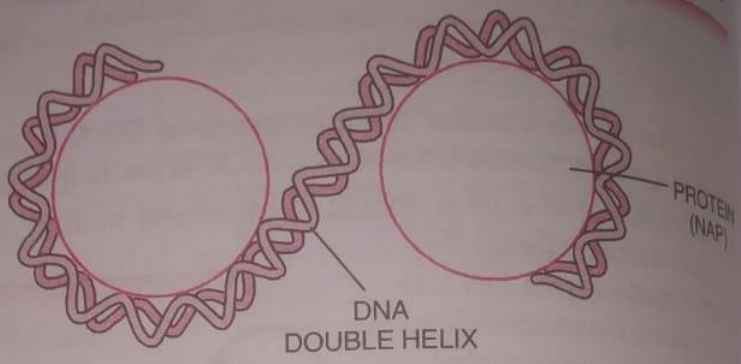


Fig. 6.11. DNA packaging in *E. coli.*

DNA Packaging in Eukaryotes. In eukaryotes, DNA packaging is carried out with the help of positively charged basic proteins called **histones.** Histones are rich in basic amino acid residues, **lysines** and **arginines**. Both the amino acid residues carry positive charges on their side chains. Histones and DNA are organised to form **nucleosome.** Small segment of DNA connecting two adjacent nucleosomes is called interbead or **linker DNA.** Nucleosome and linker DNA together constitute **chromatosome.** Nucleosome chain gives a **beads on string** appearance under electron microscope.

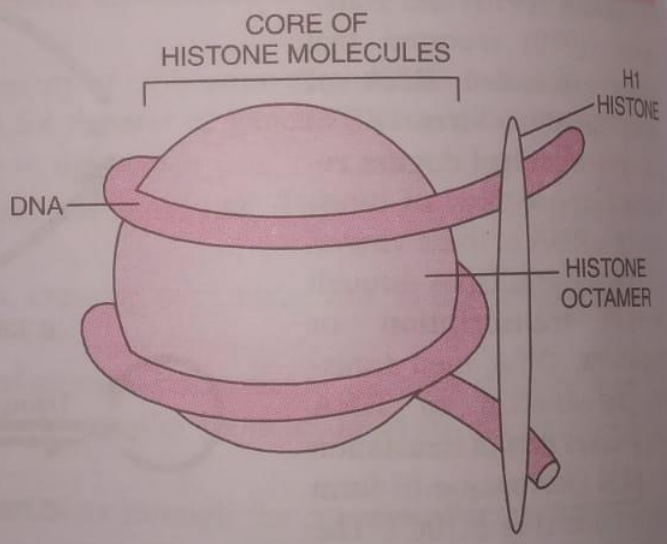


Fig. 6.12. Nucleosome.

Types of histones. There are five types of histone proteins — H_1, H_2A, H_2B, H_3 and H_4. Four of them (H_2A, H_2B, H_3 and H_4) occur in pairs to produce **histone octamer**, called **nu body** or core of nucleosome. DNA of about 200 bp makes 1.75 left handed turns over the histone octamer to form a nucleosome. A fifth type of histone called H_1 is attached over the linker DNA.

Histone-DNA Interactions. Histone contains a large proportion of the positively charged (basic) amino acids, lysine and arginine in their structure. DNA is negatively charged due to the phosphate groups on its backbone. The result of these opposite charges is strong attraction and therefore, high binding affinity between histones and DNA. Hydrogen bonding involving hydroxyl amino acids in the histone peptide and the phosphodiester backbone of DNA are also important in further stabilizing the structure.

Solenoid Model of Folding. The beaded string is coiled to form cylindrical coil or **solenoid** having 6 nucleosomes per turn. Actually the nucleosomal organisation has approximately **10 nm** thickness, which gets further condensed and coiled to produce a solenoid of a **30 nm** diameter. This solenoid structure undergoes further coiling to produce a chromatin fibre of **300 nm** diameter and then a chromatid of **700 nm** diameter and ultimately metaphase chromosome of **1400 nm** diameter.

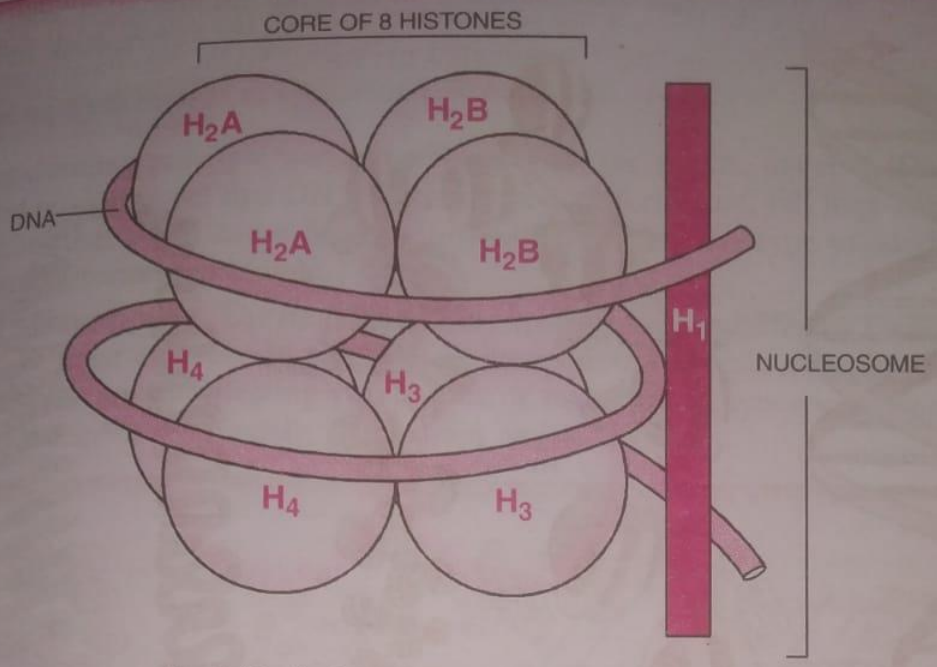


Fig. 6.13. Nucleosome showing different histones.

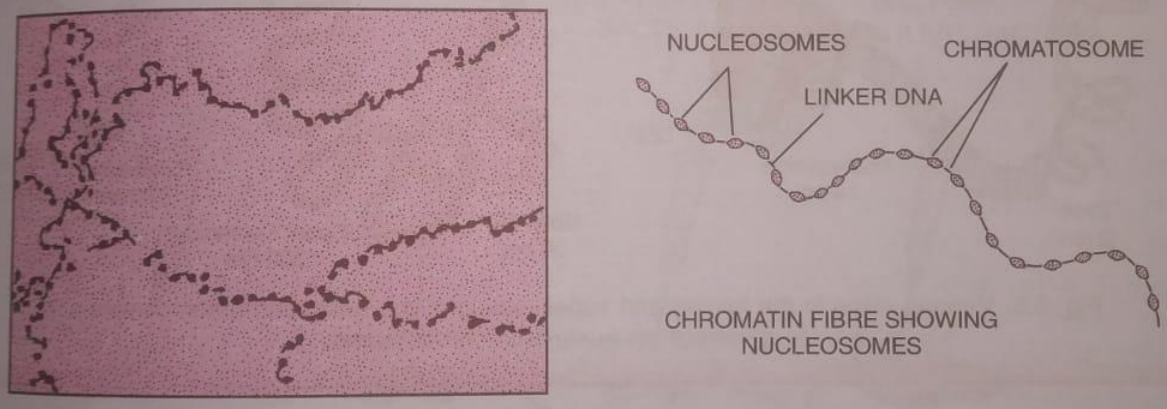


Fig. 6.14. EM picture - 'Beads-on-String'

Non-histone Chromosomal (NHC) Proteins. The packaging of chromatin at higher level requires additional set of proteins that collectively are referred to as **non-histone chromosomal (NHC) proteins.** On the basis of staining behaviour in a typical nucleus, chromatin is of two types : euchromatin and heterochromatin.

Differences between Euchromatin and Heterochromatin

Euchromatin	*Heterochromatin*
1. It stains lightly. 2. This chromatin is loosely packed. 3. It is transcriptionally active. 4. Replication takes place at early S-phase as it takes less time to unwind.	1. It stains darkly. 2. This chromatin is more densely packed. 3. It is transcriptionally inactive. 4. Replication takes place at late S-phase as it takes longer time to unwind.

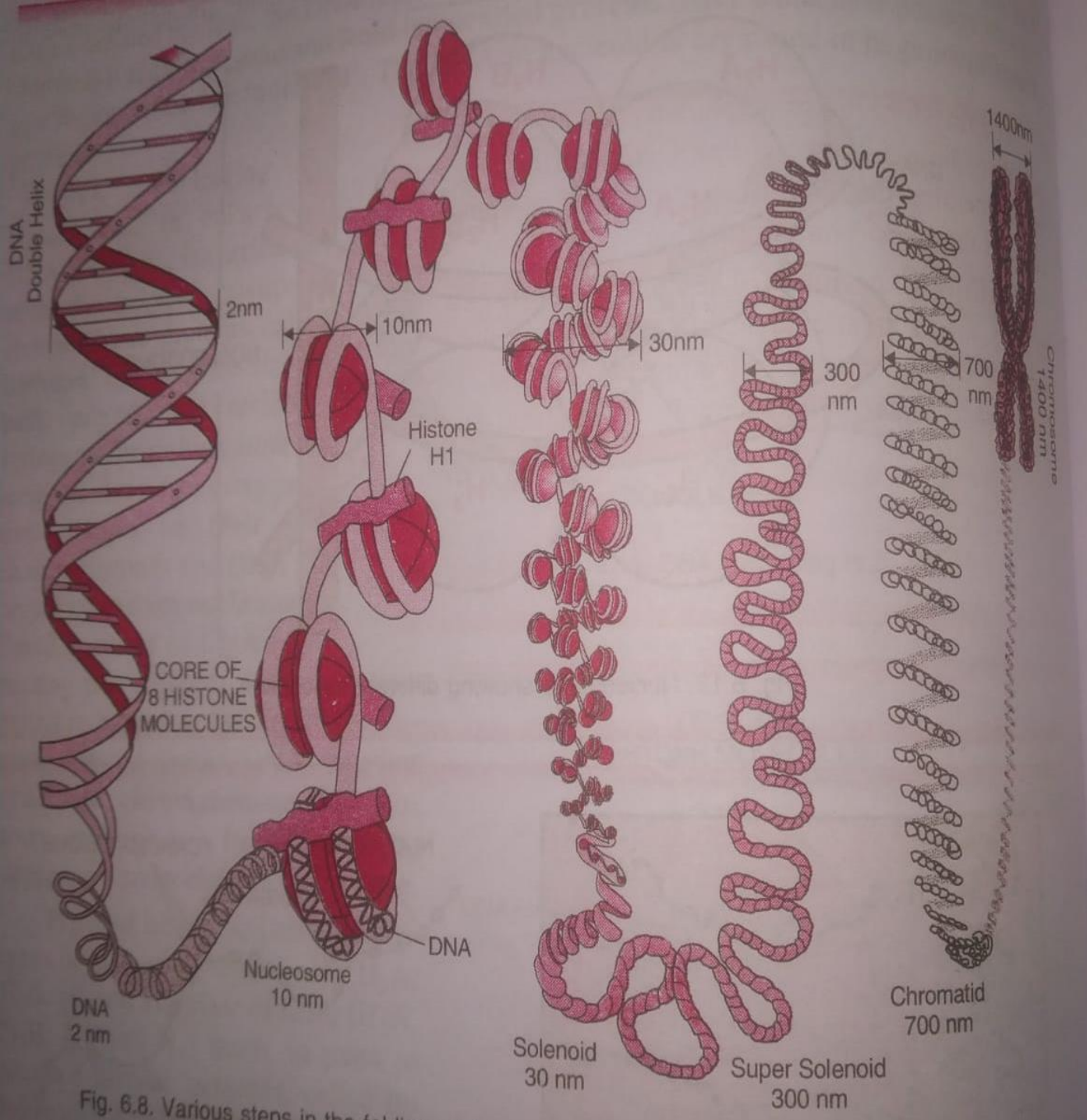
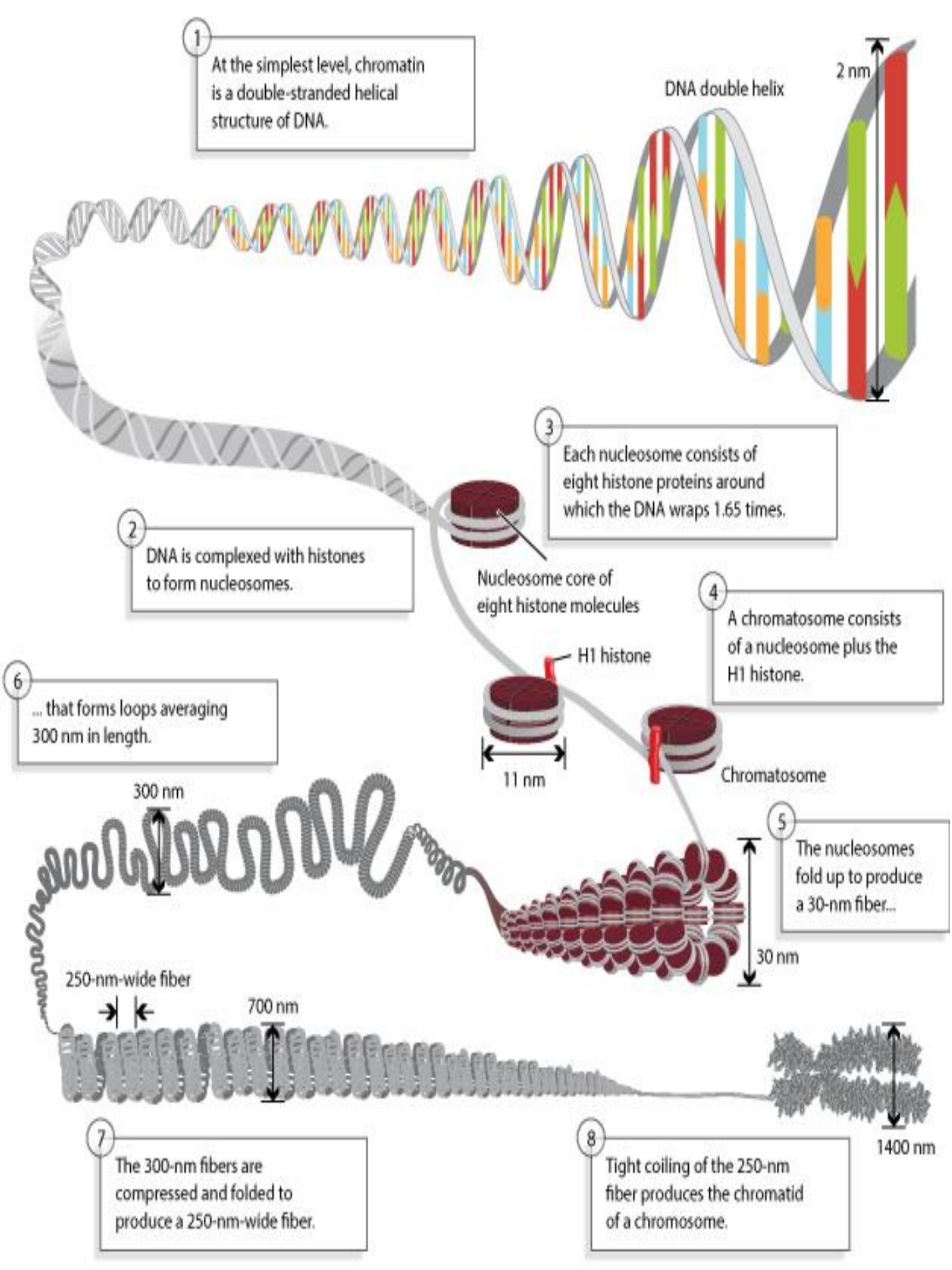


Fig. 6.8. Various steps in the folding and super folding of the basic chromatin components to generate an eukaryotic chromosome.

Theoretically how many such beads (nucleosomes) do you imagine are present in a human cell ?

200 bp are present in = 1 bead (typically)

$6.6. \times 10^9$ bp are present in = $\frac{1}{200} \times 6.6 \times 10^9$


1
At the simplest level, chromatin is a double-stranded helical structure of DNA.
DNA double helix
2 nm
3
Each nucleosome consists of eight histone proteins around which the DNA wraps 1.65 times.
2
DNA is complexed with histones to form nucleosomes.
Nucleosome core of eight histone molecules
4
A chromatosome consists of a nucleosome plus the H1 histone.
H1 histone
11 nm
Chromatosome
6
... that forms loops averaging 300 nm in length.
300 nm
5
The nucleosomes fold up to produce a 30-nm fiber...
30 nm
250-nm-wide fiber
700 nm
1400 nm
7
The 300-nm fibers are compressed and folded to produce a 250-nm-wide fiber.
8
Tight coiling of the 250-nm fiber produces the chromatid of a chromosome.

Differences Between DNA and RNA

DNA	*RNA*
1. It usually occurs inside nucleus and some cell organelles.	1. Very little RNA occurs inside nucleus. Most of it is found in the cytoplasm.
2. DNA is the genetic material.	2. RNA is not the genetic material except in certain viruses, *e.g.*, *Reovirus*.
3. It is double stranded with the exception of some viruses (*e.g.*, $\phi \times 174$).	3. RNA is single stranded with the exception of some viruses (*e.g.*, double stranded in *Reovirus*).
4. DNA contains over a million nucleotides.	4. Depending upon the type, RNA contains 70-12000 nucleotides.
5. Molecular weight ranges from 3-4 million in *Escherichia coli* to 263 million in chromosome 1 of human beings.	5. Molecular weight ranges from 25000-2,000,000.
6. It is Fuelgen positive.	6. RNA is Fuelgen negative.
7. DNA is of only two types; intra-nuclear and extra-nuclear.	7. There are at least three types of RNAs — mRNA, rRNA and tRNA.
8. It contains deoxyribose sugar.	8. It contains ribose sugar.
9. Nitrogen base thymine occurs in DNA alongwith three others — adenine, cytosine and guanine.	9. Thymine is replaced by uracil in RNA. The other three are similar — adenine, cytosine and guanine.
10. Unusual bases are very few or absent.	10. Many unusual or modified bases are often present.
11. Renaturation after melting is slow.	11. It is quite fast.
12. Hydrogen bonds are formed between complementary nitrogen bases of the opposite strands of DNA (A – T, C – G).	12. Base pairing through hydrogen bonds occurs only in the coiled parts.
13. DNA is spirally twisted to produce a regular helix.	13. The strand may get folded at places to produce a secondary helix or pseudohelix.
14. It replicates to form new DNA molecules.	14. It cannot normally replicate itself.
15. DNA replication requires a primer.	15. No primer is needed during the formation of RNA.
16. DNA transcribes genetic information to RNA.	16. RNA translates the transcribed message for forming polypeptides.
17. Its quantity is fixed for cell.	17. The quantity of RNA of a cell is variable.
18. DNA controls metabolism and genetics including variations.	18. It only controls metabolism under instructions from DNA.
19. Purine and pyrimidine bases are in equal number.	19. There is no proportionality between number of purines and pyrmidine bases.
20. It occurs in the form of prochromosome, chromatin or chromosomes.	20. It occurs in ribosomes or forms association with ribosomes.
21. ^{3}H precursor is ^{3}H-thymidine.	21. ^{3}H precursor is ^{3}H-uridine.
22. It is long lived.	22. Some RNAs are very short lived while others have somewhat longer life.
23. It can be hydrolysed by DNA-ase.	23. It is hydrolysed by RNA-ase.

GENETIC CODE

Though DNA

10. Splicing is not required.	11. It produces working copies for forming cellular structure and its functioning.
11. It multiplies and conserves the genome.	12. A lot of processing and modifications occur after transcription.
12. Only telomeric ends are synthesised separately.	13. Products usually degrade after their functioning is over.
13. Products do not degrade.	14. It occurs during G_1 and G_2 phases of cell cycle.
14. It occurs during S-phase of cell cycle.	

RNA or Ribonucleic Acid (Fig. 6.27)

RNA or ribonucleic acid is a single chain polyribonucleotide which functions as carrier of coded genetic or hereditary information from DNA to cytoplasm for taking part in protein and enzyme synthesis. At places RNA may appear partially double stranded due to folding or coiling of the single strand (Fig 6.28). It contains 70-12000 ribonucleotides joined end to end. The axis or back bone is formed of alternate residues of phosphate and ribose sugar. Phosphate combines with carbon 5′ of its sugar and carbon 3′ of next sugar similar to the arrangement found in DNA strand. Nitrogen bases are attached to sugars at carbon 1′ of the latter. There are four types of nitrogen bases—adenine (A), guanine (G, both purines), cytosine (C) and uracil (U, both pyrimidines). Nitrogen bases can be arranged in any sequence but the same is complementary to their sequence on DNA template. For example, a sequence of ATACTG of DNA template shall appear as UAUGAC over RNA. There are six types of RNAs—ribosomal, transfer, messenger, genomic (genetic), small nuclear and small cytoplasmic. Out of these the first three (rRNA, mRNA and tRNA) are major classes of RNAs that are involved in gene expression. RNA is **genomic** (genetic) in some viruses like TMV, HIV influenza virus etc. It is **double stranded** in reoviruses, wound tumor virus, Rice Dwarf virus and Mycophages.

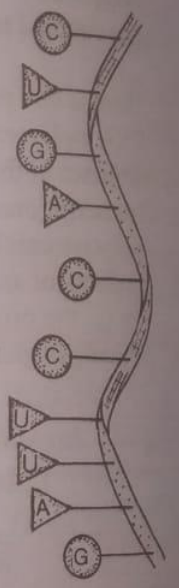


Fig. 6.27. Diagrammatic structure of RNA.

1. **Ribosomal RNA** (rRNA). It is the most abundant RNA (70-80% of total) which has 3-4 types. Some of its types (23S, 28S) are the longest of all RNAs. As the name indicates, rRNA is a constituent of ribosomes. Here it lies coiled in between and over the protein molecules. Depending upon their sedimentation coefficient, rRNAs of eucaryotes are of four types — 28S, 18S, 5.8S and 5S. Procaryotic ribosomes have three types of rRNAs — 23S, 16S and 5S. 28S, 5.8S and 5S (23S and 5S in procaryotes) occur in larger subunit of ribosome while 18S (16 S in procaryotes) is found in smaller subunit of ribosome. rRNA is transcribed in the form of a longer chain of 45S in eucaryotes and 30S in procaryotes. In eucaryotic transcript the arrangement in 5′ → 3′ direction is 18S — 5.8S — 28S. Several methylations occur prior to removal of spacer RNA. Removal of spacer RNA breaks the transcript into 2-3 parts. 5S is often transcribed separately.

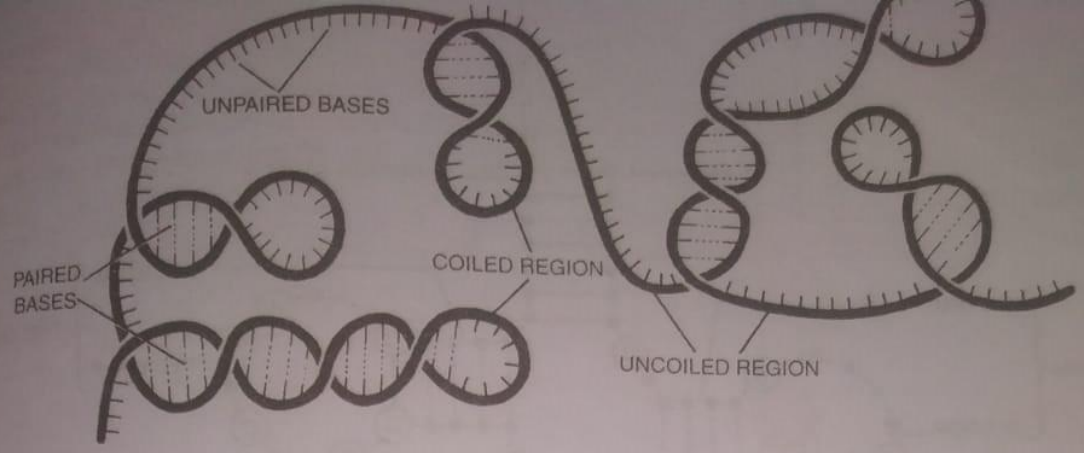


Fig. 6.28. Structure of rRNA (Schematic).

Functions. (i) rRNAs bind protein molecules and give rise to ribosomes. (ii) 3′ end of 18S rRNA (16S in procaryotes) has nucleotides complementary to those of cap region of mRNA. (iii) 5S rRNA and surrounding protein complex provide binding site for tRNA. (iv) rRNAs get associated with specific proteins to form ribosome subunits. 50S subunit of prokaryotic ribosome contains 23S rRNA, 5S rRNA and some 32 protein molecules. 30S subunit of prokaryotic ribosome has 16S rRNA and about 21 protein molecules. 60S subunit of eukaryotic ribosome contains 28S rRNA, 5S rRNA, 5.8S rRNA and about 50 protein molecules. 40S subunit of eukaryotic ribosome consists of 18S rRNA and some 33 protein molecules (Fig. 6.29).

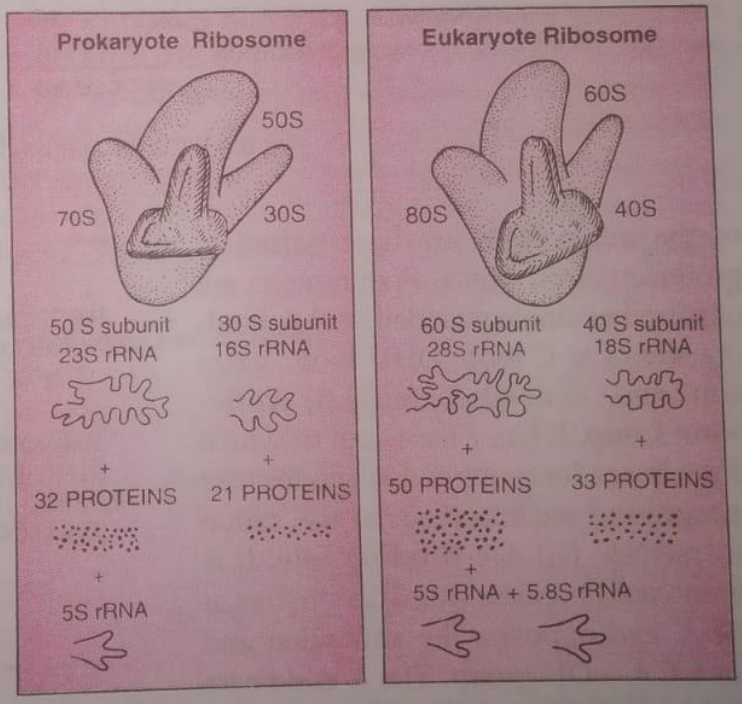


Fig. 6.29. Generalized structure of ribosome in prokaryotes and eukaryotes.

2. **Transfer RNA** (tRNA) — **The Adaptive Molecule.** It is also called **soluble** or **sRNA** in which form it was known before the discovery of genetic code. There are over 100 types of tRNAs. Transfer RNA constitutes about 15% of the total RNA. tRNA is the smallest RNA with 73-93 nucleotides and sedimentation coefficient of 4S. The nitrogen bases of several of its nucleotides get modified, *e.g.*, pseudouridine (ψ), dihydrouridine (DHU), inosine (I) ribo-thymidine (rT). This causes coiling of the otherwise single-stranded tRNA into L-shaped form (three dimensional, Klug, 1974) or clover-like form (two dimensional, Holley, 1965). About half

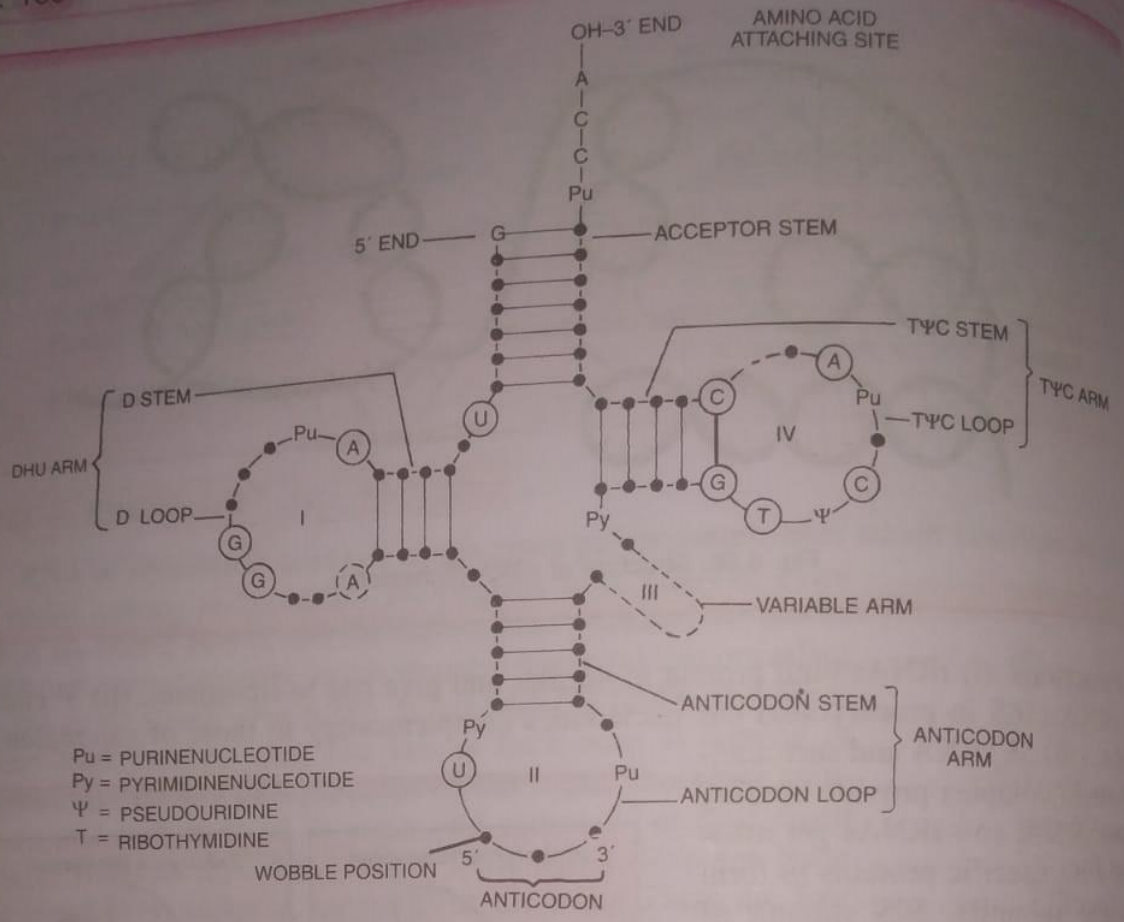


Fig. 6.30. Clover leaf model of tRNA.

of the nucleotides are base paired to produce paired stems. Five regions are unpaired or single stranded — AA-binding site, T ψ C loop, DHU loop, extra arm and anticodon loop. (i) **Anticodor Loop**. It has 7 bases out of which three bases form anticodon (nodoc) for recognising and attaching to the codon of mRNA. (ii) **AA-Binding Site.** It is amino acid binding site. The site lies at the 3′ end opposite the anticodon and has CCA—OH group. The 5′ end bears G. Amino acid or AA-binding site and anticodon are the two **recognition sites** of tRNA. (iii) **T ψ C Loop**. It has 7 bases out of which Ψ (pseudouridine) and rT (ribothymidine) are unusual bases. The loop is the site for attaching to ribosome. (iv) **DHU Loop.** The loop contains 8–12 bases. It is largest loop and has dihydrouridine. It is binding site for aminoacyl synthetase enzyme. (v) **Extra Arm**. It is a variable side arm or loop which lies between T ψ C loop and anticodon. It is not present in all tRNAs. The exact role of extra arm is not known.

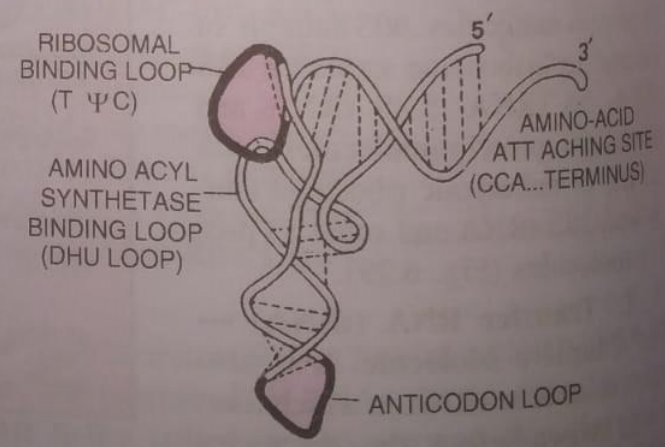


Fig. 6.31. L-form model of tRNA.

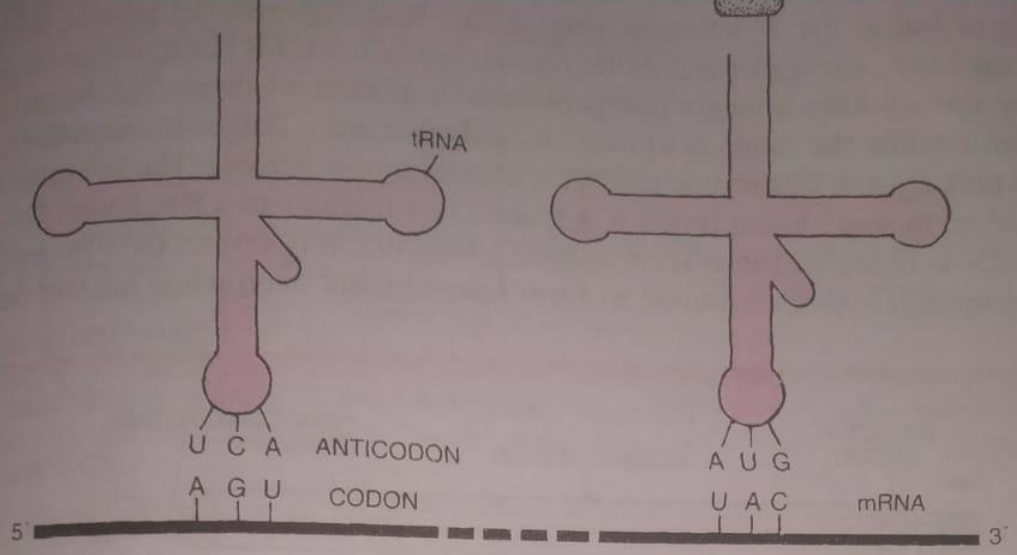


Fig. 6.32. tRNA — the adapter molecule.

Functions. (i) As first postulated by Crick, tRNA is **adapter molecule** which is meant for transferring amino acids to ribosomes for synthesis of polypeptides. There are different tRNAs for different amino acids. Some amino acids can be picked up by 2—6 tRNAs. tRNAs place specific amino acids at particular points during polypeptide synthesis as per codons of mRNA. Codons are recognised by anticodons of tRNAs. Specific amino acids are recognised by particular activating or aminoacyl synthetase enzymes. (ii) They hold peptidyl chains over the mRNAs. (iii) The initiator tRNA has the dual function of initiation of protein synthesis as well as bringing in of the first amino acid. There is, however, no tRNA for stop signals.

Differences between Codon and Anticodon

Codon	*Anticodon*
1. It is found in DNA and mRNA.	1. It occurs in tRNA.
2. Codon is complementary to a triplet of template strand.	2. It is complementary to a codon.
3. It determines the position of an amino acid in a polypeptide.	3. It helps in bringing a particular amino acid at its proper position during translation.

3. **Messenger RNA** (mRNA). It is a long RNA which constitutes 2—5% of the total RNA content of the cell. It brings instructions from the DNA for the formation of particular type of polypeptide. mRNA is, therefore, also called **informational** or **genetic RNA**. The instructions are present in the base sequence of its nucleotides. It is called **genetic code**. Three adjacent nitrogen bases specify a particular amino acid. Formation of polypeptide occurs over the ribosome. mRNA gets attached to ribosome. tRNAs are induced to bring amino acids in a particular sequence according to the sequence of codons present over mRNA. In eukaryotes mRNA has methylated (7-MeG) region at the 5′ terminus. It functions as a **cap** for attachment with ribosome. A Shine-Delgarno sequence is, instead, present in

prokaryotes. Cap is followed by an **initiation codon** (AUG) either immediately or after a small noncoding leader region. Then there is coding region followed by **termination codon** (UAA, UAG or UGA). After termination codon there is a small noncoding trailer region and poly A area or **tail** at the 3′ terminus (Fig. 6.33). Both cap and tail protect mRNA from enzymic breakdown. The leader and trailer regions are called **UTR** (Untranslated regions). An mRNA may specify only a single polypeptide or a number of them. The former is called **monocistronic** while the latter is known as **polycistronic**. Polycistronic mRNA is more common in prokaryotes. Eukaryotic mRNA is usually monocistronic. The life time of mRNA is also variable. In some lower forms it is from a few minutes to a few hours. On the other hand the mRNAs of higher forms seem to have a long life. It is several days in case of young red blood corpuscles which continue to form haemoglobin even when nucleus has degenerated.

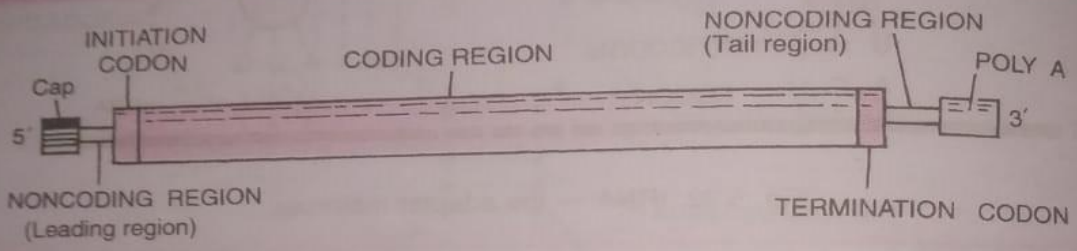


Fig. 6.33. Parts of an mRNA strand.

Functions. (i) mRNA carries coded information for translation into polypeptide formation. (ii) Through reverse transcription it can form compact genes which are used in genetic engineering. The phenomenon also occurs in nature and has added certain genes in the genomes. (iii) It has a cap region for attachment to ribosome. (iv) Cap protects the mRNA from degradation from enzymes. (v) mRNA has a tail region for protection from cellular enzymes and detachment from ribosome.

Differences between Initiation Codons and Termination Codons

Initiation Codons	*Termination Codons*
1. These codons are found at 5′ end of mRNA.	1. These are found at 3′ end of mRNA.
2. Mostly AUG (occasionally, GUG, UUG or CUG) is the initiation codon.	2. UAA, UAG and UGA are three terminal codons and only one is present at 3′ end.
3. It starts the initiation of protein synthesis.	3. It stops the process of protein synthesis.

Comparison between messenger, ribosomal and transfer RNAs

mRNA	rRNA	tRNA
1. It accounts for about 5% of total RNA in the cell.	It accounts for about 80% of total RNA in the cell.	It accounts for about 15% of total RNA in the cell.
2. It consists of 75-6000 bases.	It consists of 100–5000 bases.	It consists of 73–93 bases.
3. Its mol. wt. 25000-2000000 daltons.	It mol. wt. 35000–1800000 daltons.	Its mol. wt. is about 25000 daltons.
4. Its sedimentation coefficient is 6–30 S.	Its sedimentation coefficient is 5S, 5.8S, 28S and 18S in eukaryotes; 5S, 16S and 23S in prokaryotes.	Its sedimentation coefficient is 4S.

5.	It is moderate to large sized with moderate to maximum mol. weight but is least abundant.	It is smaller; moderate to large sized which is most abundant and highly coiled.	It is smallest and coiled like a clover leaf.
6.	It carries a coding message for many amino acids.	It carries no coding message.	It carries coding message for only one amino acid.
7.	It is linear and never coiled.	It is linear and coiled.	It is folded.
8.	It is synthesized by RNA polymerase II in nucleus.	Its synthesis occurs in nucleolus by RNA polymerase I.	It is synthesized by RNA polymerase III in nucleus.
9.	It has no modification of bases in coding region.	Modification of bases is very less.	About 5% bases are modified.
10.	It is of various types depending upon number of genes.	It is of 3 or 4 types.	It is of about 100 types.
11.	It is short lived (3 seconds to few days) and commonly degrades after protein synthesis.	It is most stable, used again and again and does not degrade.	It is quite stable, used again and again, degrades very slowly.
12.	It is called template/ nuclear/ messenger or informational RNA as it carries genetic information provided by DNA.	It is called insoluble RNA and forms ribosomes.	It is called soluble or adapter RNA and carries amino acids to mRNA during protein synthesis.

4. **Genomic RNA** (Genetic RNA). It is found in some viruses called riboviruses. Genomic RNA may be single stranded (*e.g.*, Tobacco Mosaic Virus or TMV) or double stranded (*e.g.*, Reovirus). It is fragmented in influenza virus. Genomic RNA acts as a hereditary material. It may replicate directly, or form DNA in the host cell to produce RNA of its own type.

5. **Catalytic RNAs.** Cech *et al* (1981) found catalytic activity (cleavage and covalent bond formation) in RNA precursor of ciliated protozoan called *Tetrahymena thermophila*. It was called **ribozyme**. In 1983, Altman *et al* discovered that ribonuclease - P that takes part in processing tRNA from its precursor is a biocatalyst made of RNA and protein. Noller *et al* (1992) found peptidyl transferase to be RNA enzyme.

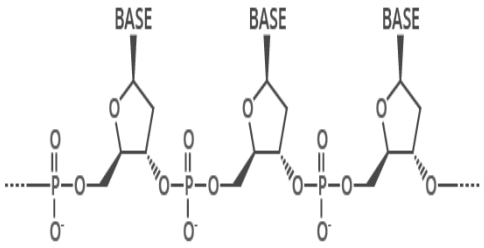
6. **Small Nuclear RNA** (snRNA). It is a small sized RNA present in the nucleus. Each RNA is combined with 7—8 molecules of proteins to form small nuclear ribonucleoprotein or snRNP. SnRNA takes part in splicing (U1 and U2), rRNA processing (U3) and mRNA processing (U7).

7. **Small Cytoplasmic RNA** (scRNA). It is small sized RNA occurring free in the cytoplasm. One such small cytoplasmic RNA is 7S and combines with 6 protein molecules to produce **signal recognition particle** or SRP. The latter helps in taking and binding a ribosome to endoplasmic reticulum for producing secretory proteins.

8. **RNA Interference (RNA*i*).** It is involved in regulating gene expression. **Micro RNAs** (*mi*RNAs) are 21-22 bp long RNAs which attach to complementary parts of *m*RNAs and bring about their degeneration. **Short interfering RNAs** (*si*RNAs) are double stranded 19-23 bp long RNAs which also do the same job. They become single stranded and form RISC (RNA induced silencing complex) after combining with proteins.

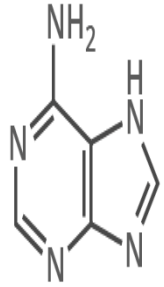
THE CHEMICAL STRUCTURE OF DNA

THE SUGAR PHOSPHATE 'BACKBONE'

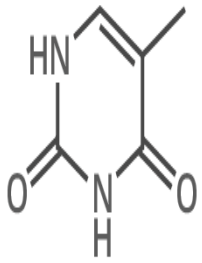


DNA is a polymer made up of units called nucleotides. The nucleotides are made of three different components: a sugar group, a phosphate group, and a base. There are four different bases: adenine, thymine, guanine and cytosine.

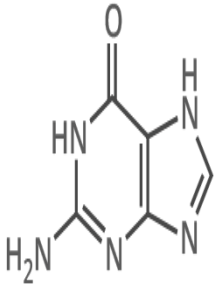
A ADENINE



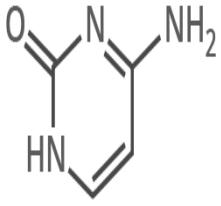
T THYMINE



G GUANINE

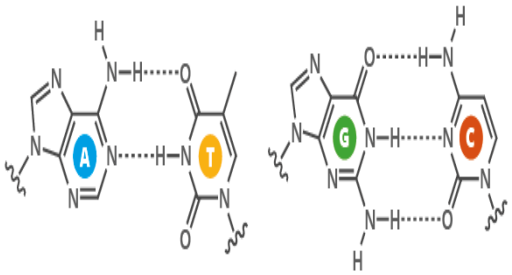


C CYTOSINE



WHAT HOLDS DNA STRANDS TOGETHER?

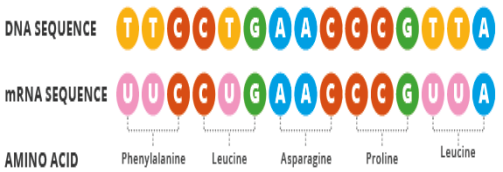
DNA strands are held together by hydrogen bonds between bases on adjacent strands. Adenine (A) always pairs with thymine (T), while guanine (G) always pairs with cytosine (C). Adenine pairs with uracil (U) in RNA.



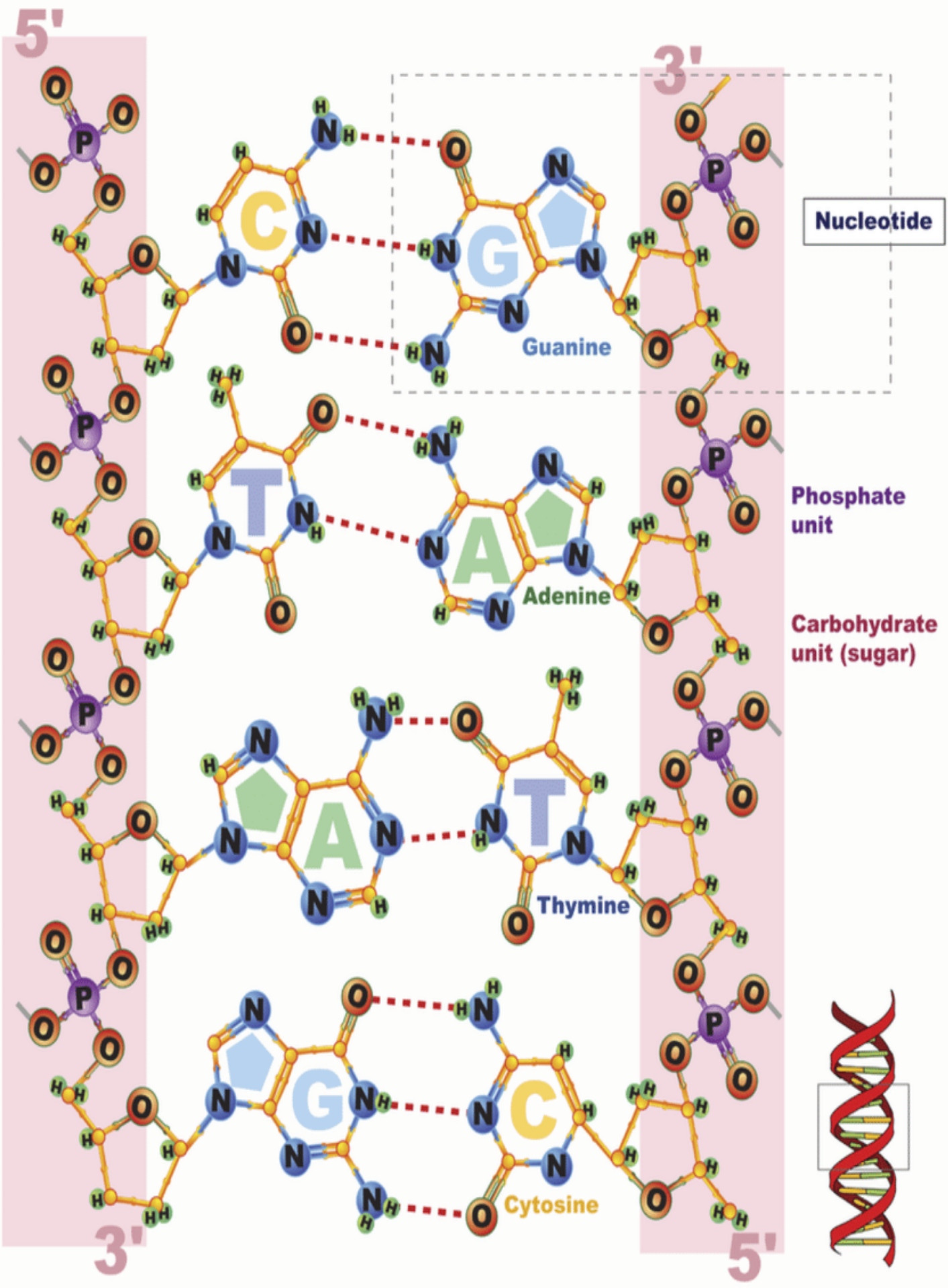
FROM DNA TO PROTEINS

The bases on a single strand of DNA act as a code. The letters form three letter codons, which code for amino acids - the building blocks of proteins.

An enzyme, RNA polymerase, transcribes DNA into mRNA (messenger ribonucleic acid). It splits apart the two strands that form the double helix, then reads a strand and copies the sequence of nucleotides. The only difference between the RNA and the original DNA is that in the place of thymine (T), another base with a similar structure is used: uracil (U).



In multicellular organisms, the mRNA carries genetic code out of the cell nucleus, to the cytoplasm. Here, protein synthesis takes place. 'Translation' is the process of turning the mRNA's 'code' into proteins. Molecules called ribosomes carry out this process, building up proteins from the amino acids coded for.


5'
3'
Nucleotide
Guanine
Phosphate unit
Adenine
Carbohydrate unit (sugar)
Thymine
Cytosine
3'
5'

Types of RNA Produced in Cells

mRNA

Encodes proteins

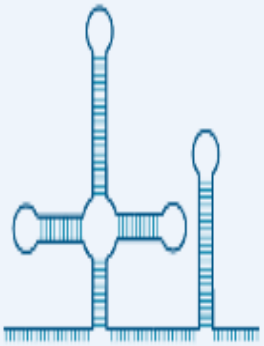
tRNA

Acts as adaptor between mRNA and amino acids

rRNA

Forms the ribosome

snRNA



Functions in various nuclear processes (e.g. splicing)

snoRNA

Facilitates chemical modification of RNAs

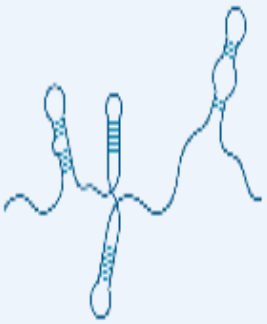
miRNA

Regulates gene expression

siRNA

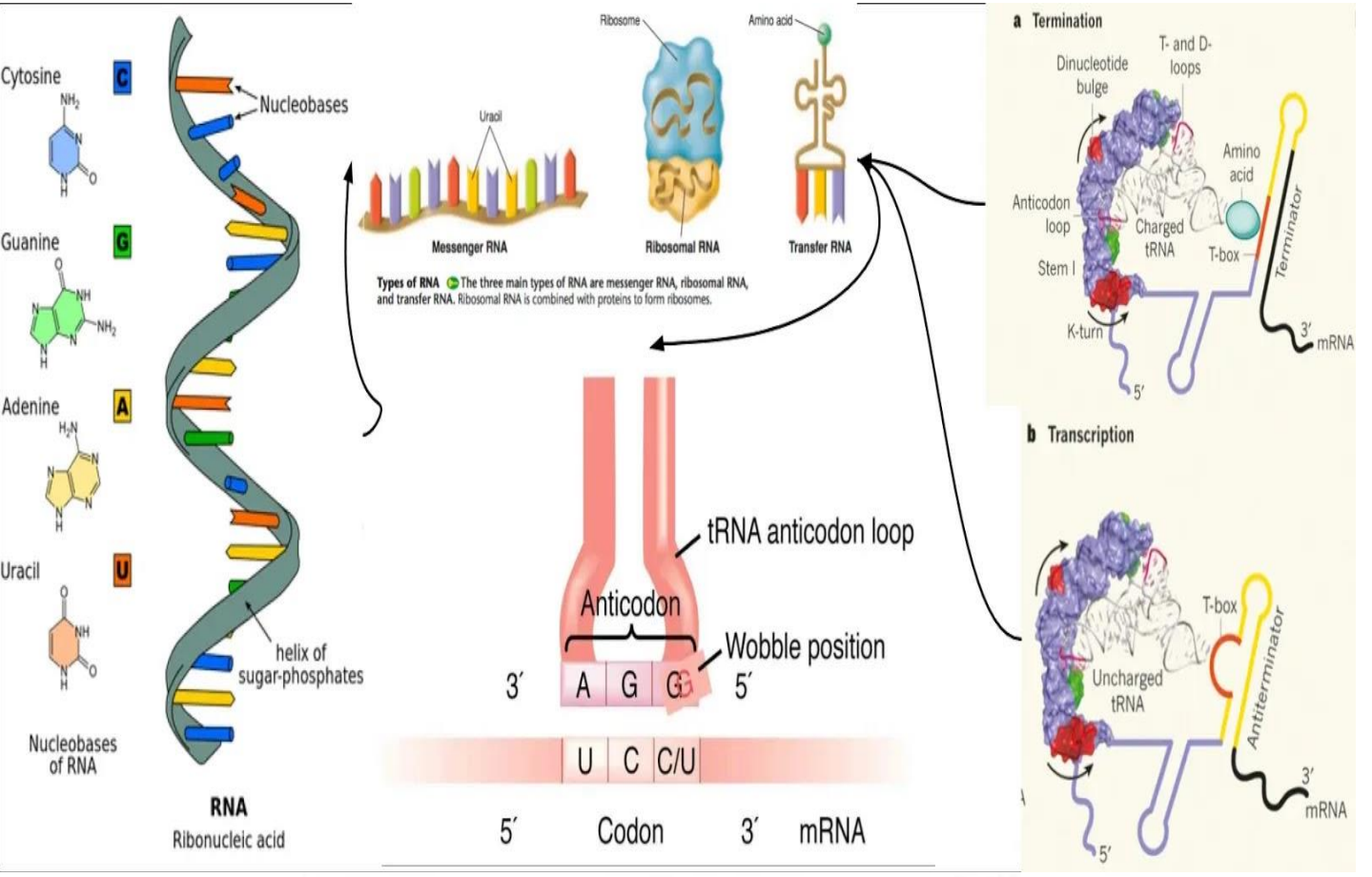
Silences gene expression

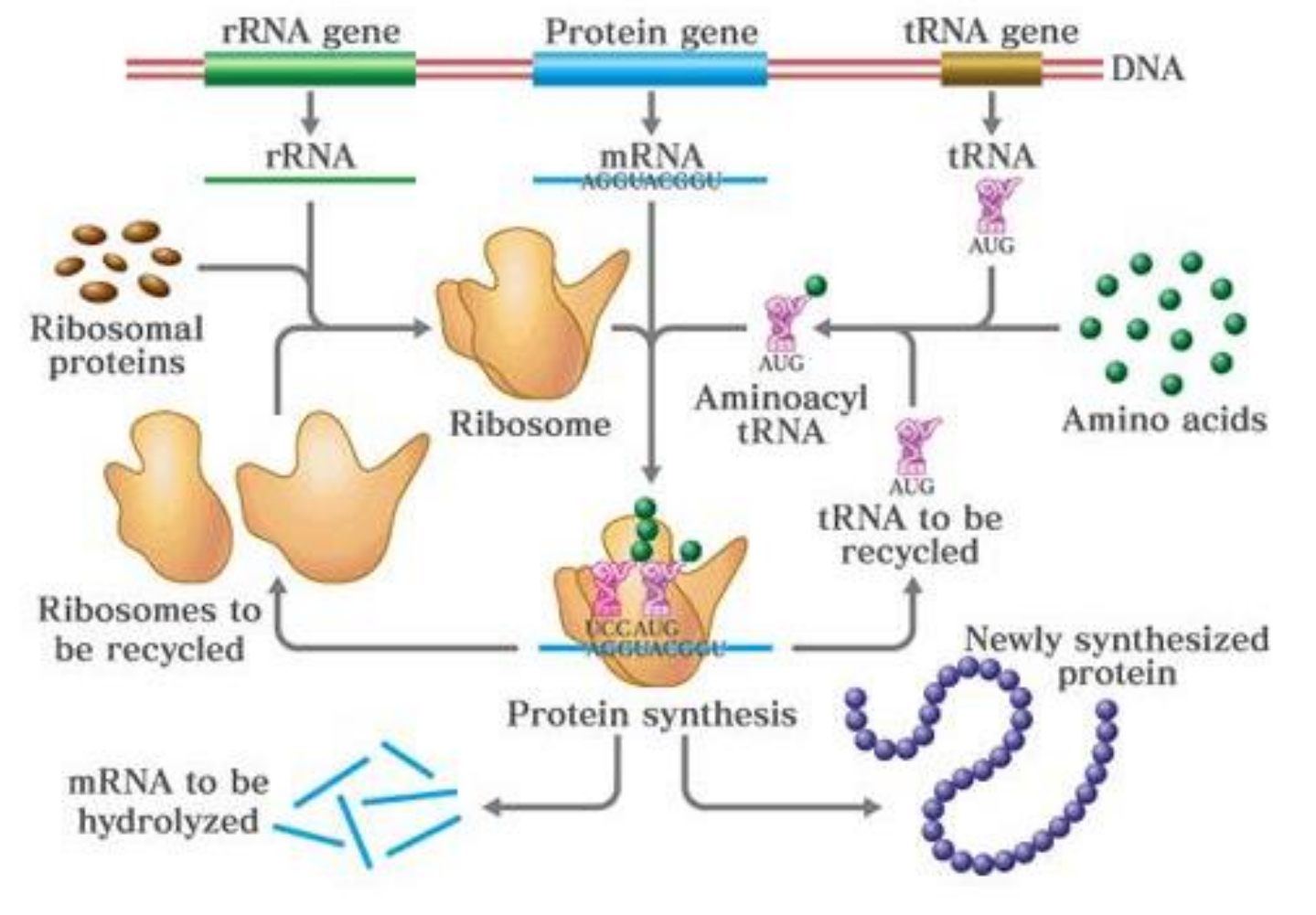
lncRNA



Regulates gene expression

Type	Abbreviation	Function(s)
Messenger RNA	mRNA	Transfers genetic information from genes to ribosomes to synthesize proteins.
Heterogeneous nuclear RNA	hnRNA	Serves as precursor for mRNA and other RNAs
Transfer RNA	tRNA	Transfers amino acid to mRNA for protein synthesis.
Ribosomal RNA	rRNA	Provides structural framework for ribosomes
Small nuclear RNA	snRNA	Involved in mRNA processing
Small nucleolar RNA	snoRNA	Plays a key role in processing of rRNA molecules
Small cytoplasmic RNA	scRNA	Involved in selection of proteins for export.
Transfer messenger RNA	tmRNA	Mostly present in Bacteria. Adds short peptide tags to proteins to facilitate the degradation of incorrectly synthesized proteins.


Cytosine
C
Nucleobases
Guanine
G
Adenine
A
Uracil
U
helix of sugar-phosphates
Nucleobases of RNA
RNA
Ribonucleic acid
Uracil
Messenger RNA
Ribosome
Ribosomal RNA
Amino acid
Transfer RNA
Types of RNA The three main types of RNA are messenger RNA, ribosomal RNA, and transfer RNA. Ribosomal RNA is combined with proteins to form ribosomes.
tRNA anticodon loop
Anticodon
Wobble position
3′ A G G 5′
U C C/U
5′ Codon 3′ mRNA
a Termination
Dinucleotide bulge
T- and D-loops
Amino acid
Anticodon loop
Charged tRNA
T-box
Terminator
Stem I
K-turn
3′ mRNA
5′
b Transcription
T-box
Uncharged tRNA
Antiterminator
3′ mRNA
5′


rRNA gene
Protein gene
tRNA gene
DNA
rRNA
mRNA
AGGUACGGU
tRNA
AUG
Ribosomal proteins
Ribosome
AUG
Aminoacyl tRNA
Amino acids
AUG
tRNA to be recycled
Ribosomes to be recycled
UCC AUG
AGGUACGGU
Newly synthesized protein
Protein synthesis
mRNA to be hydrolyzed

Secondary Structure of t-RNA