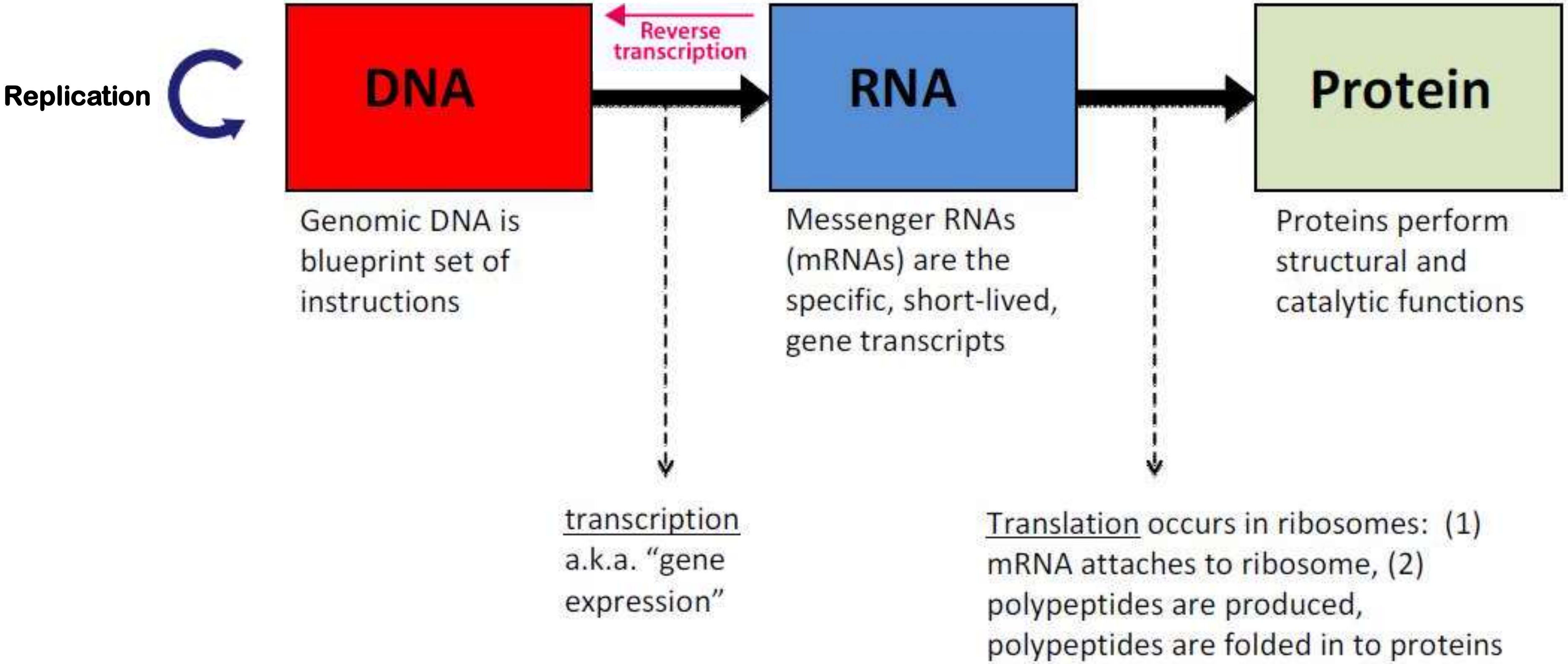
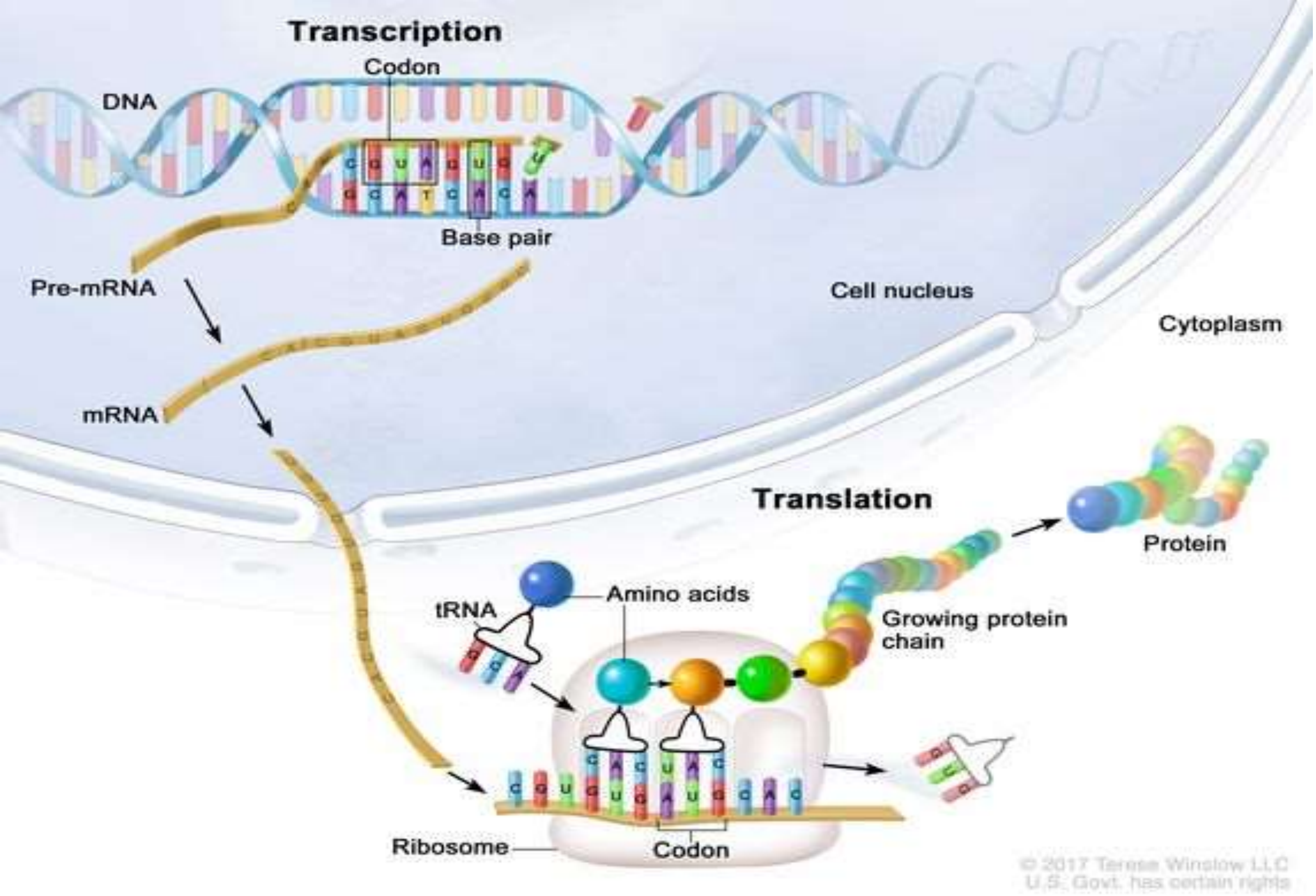
CENTRAL DOGMA

The central dogma is a framework for understanding the flow of genetic information in biological systems. It states that DNA makes RNA, and RNA makes protein.





Transcription
Codon
DNA
Base pair
Pre-mRNA
mRNA
Cell nucleus
Cytoplasm
Translation
Protein
Amino acids
tRNA
Growing protein chain
Ribosome
Codon
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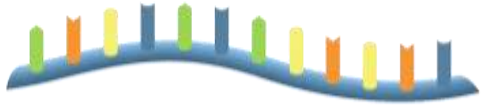
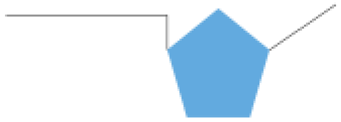
NUCLEIC ACIDS

- Large biomolecules essential for life
- Store genetic information (DNA)

- Help in protein synthesis (RNA)

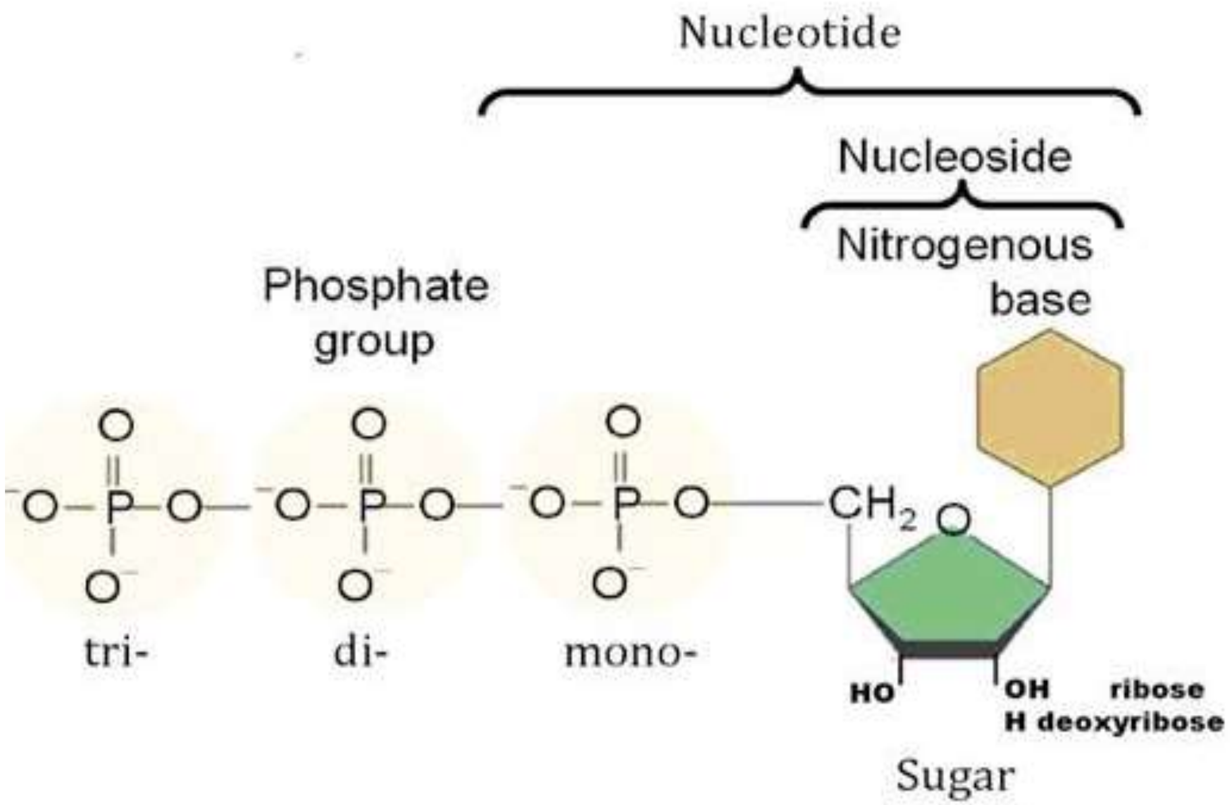


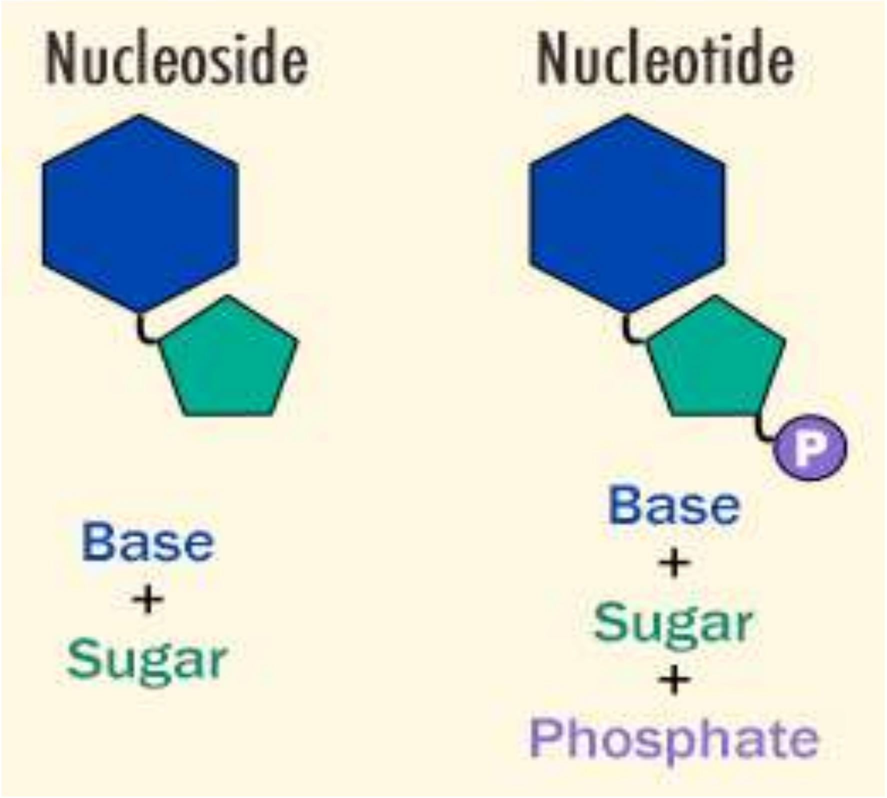
- Helps in energy storage and transfer (ATP & NADPH)



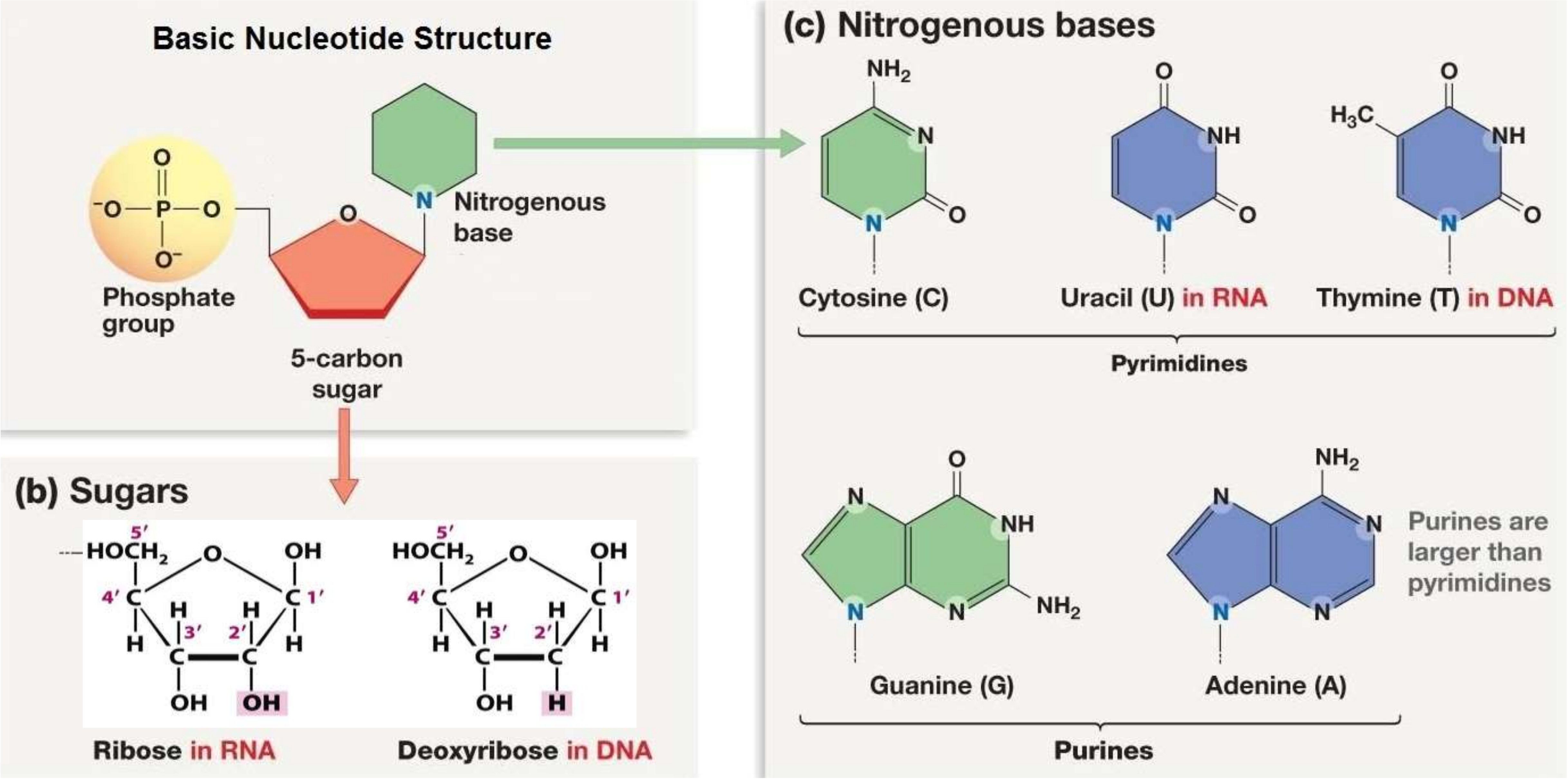
COMPOSITION OF NUCLEIC ACIDS

Nucleic acids are polymers made up of a linear array of monomers called **nucleotides**.



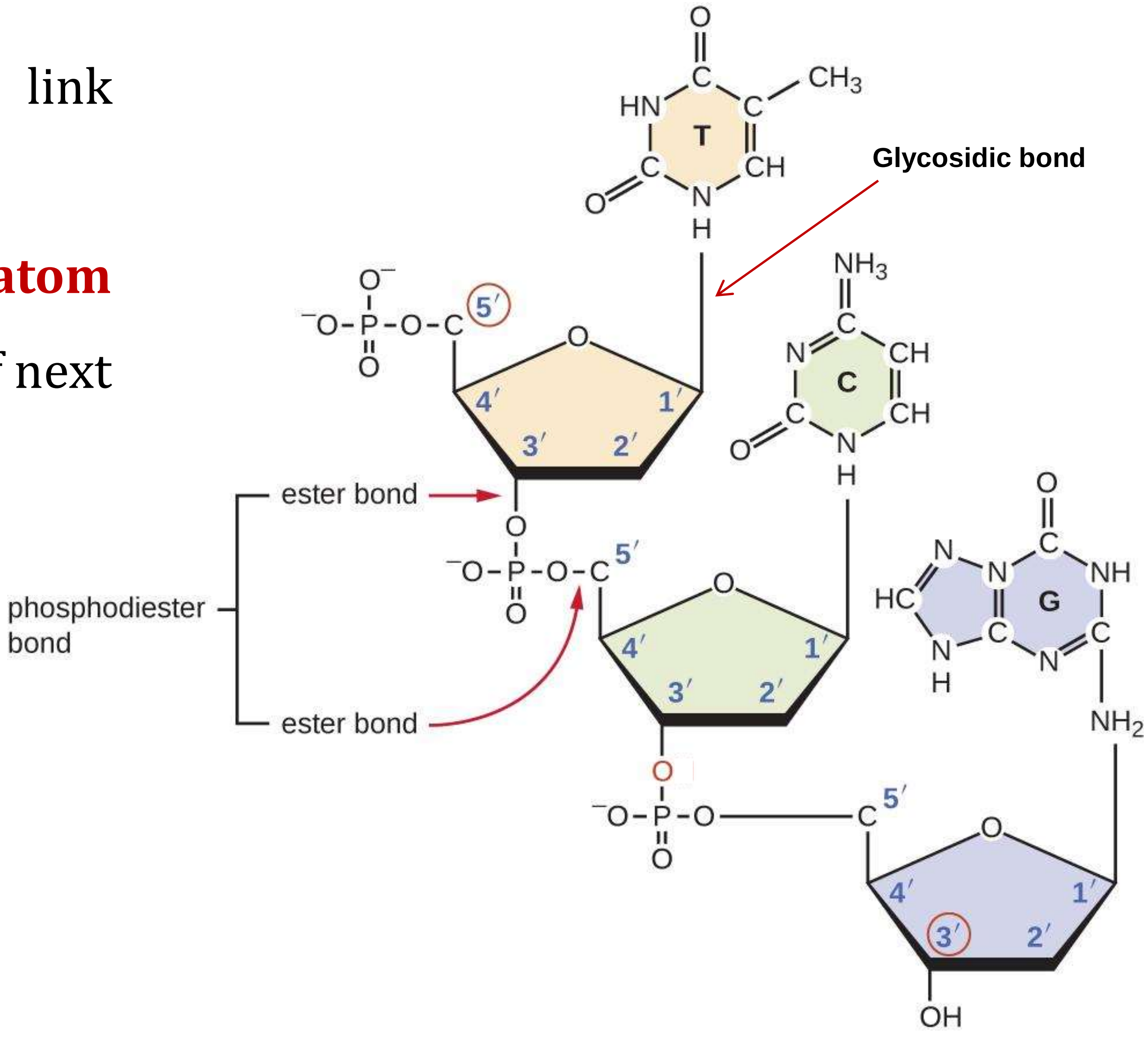


COMPOSITION OF NUCLEIC ACIDS



Phosphodiester linkage

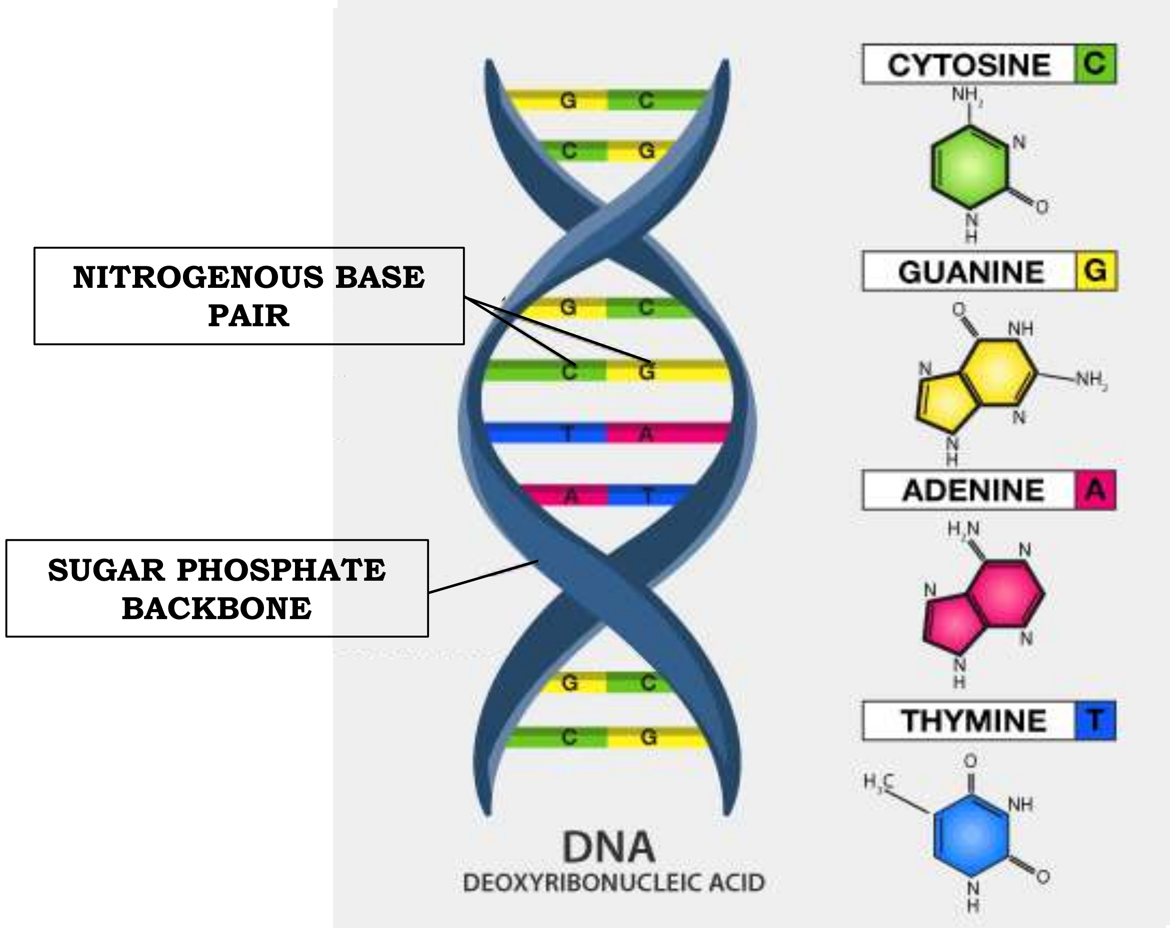
- Phosphodiester bonds (covalent bond) link successive nucleotides in nucleic acids
- The linkage is between the **3' carbon atom** of one nucleotide and **5' carbon atom** of next nucleotide via a phosphate group.



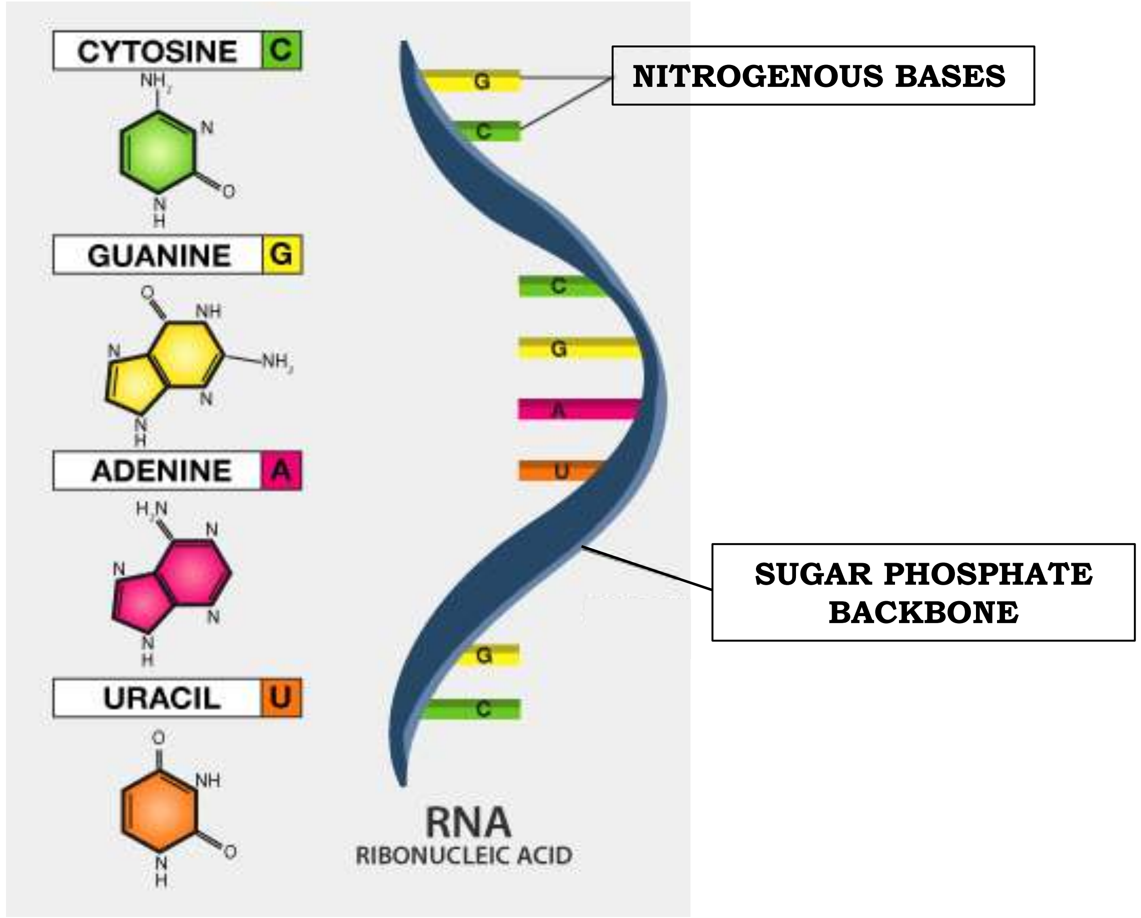
- **3' –end is one with a free 3'-hydroxyl.**
- **5' –end is one with a free or phosphorilated 5'-hydroxyl.**

TYPES OF NUCLEIC ACIDS

DEOXYRIBONUCLEIC ACID (DNA)



RIBONUCLEIC ACID (RNA)



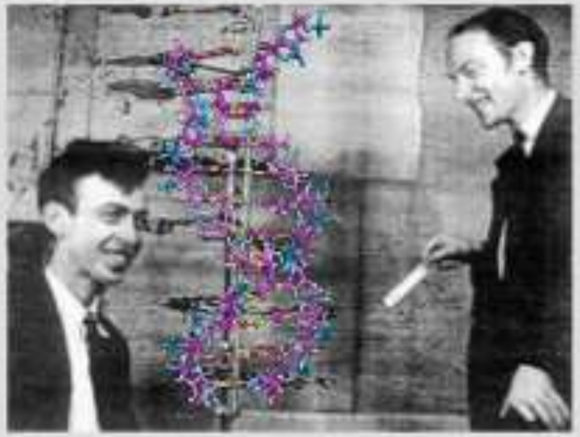
DNA

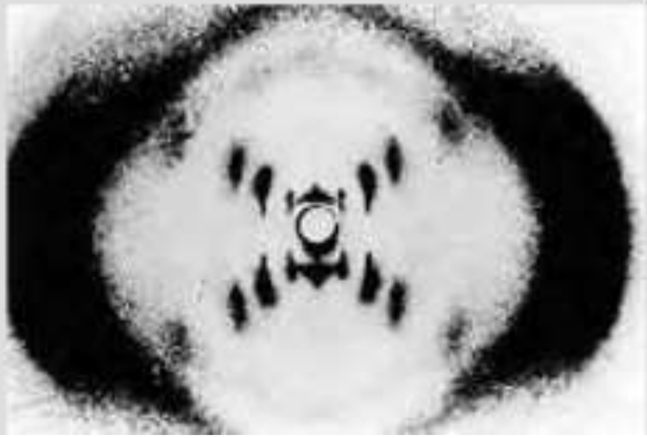
Discovery of the DNA double helix

- **Frederick Griffith** -(1928) Discovers that a factor in diseased bacteria can transform harmless bacteria into deadly bacteria.

- **Maurice Wilkines** - worked on the structure of DNA.

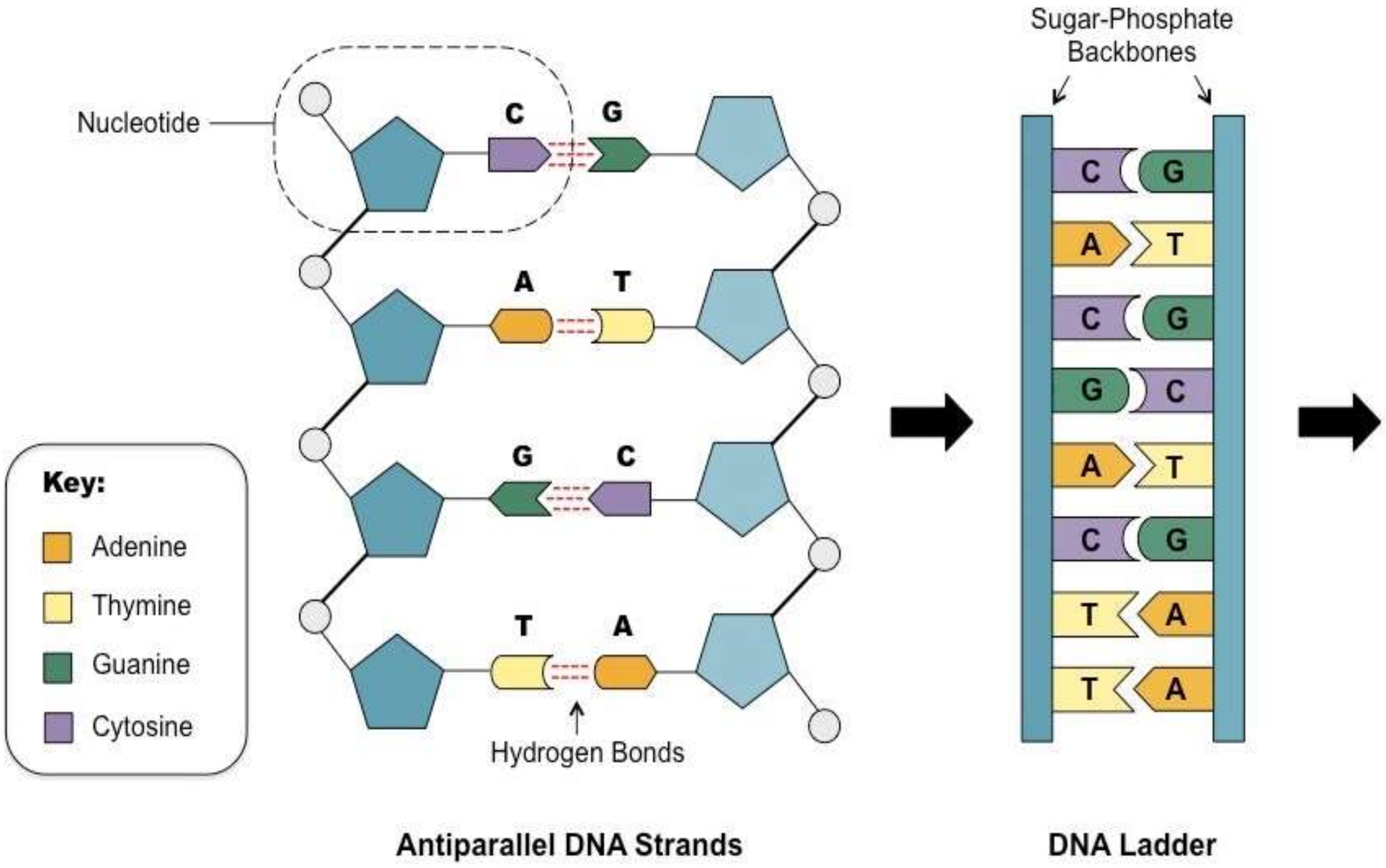
- **Rosalind Franklin** -(1952) - Worked out helical structure of DNA by X-ray photo of DNA.
- **Watson and Crick** - (1953) described the DNA molecule from Franklin's X-ray.

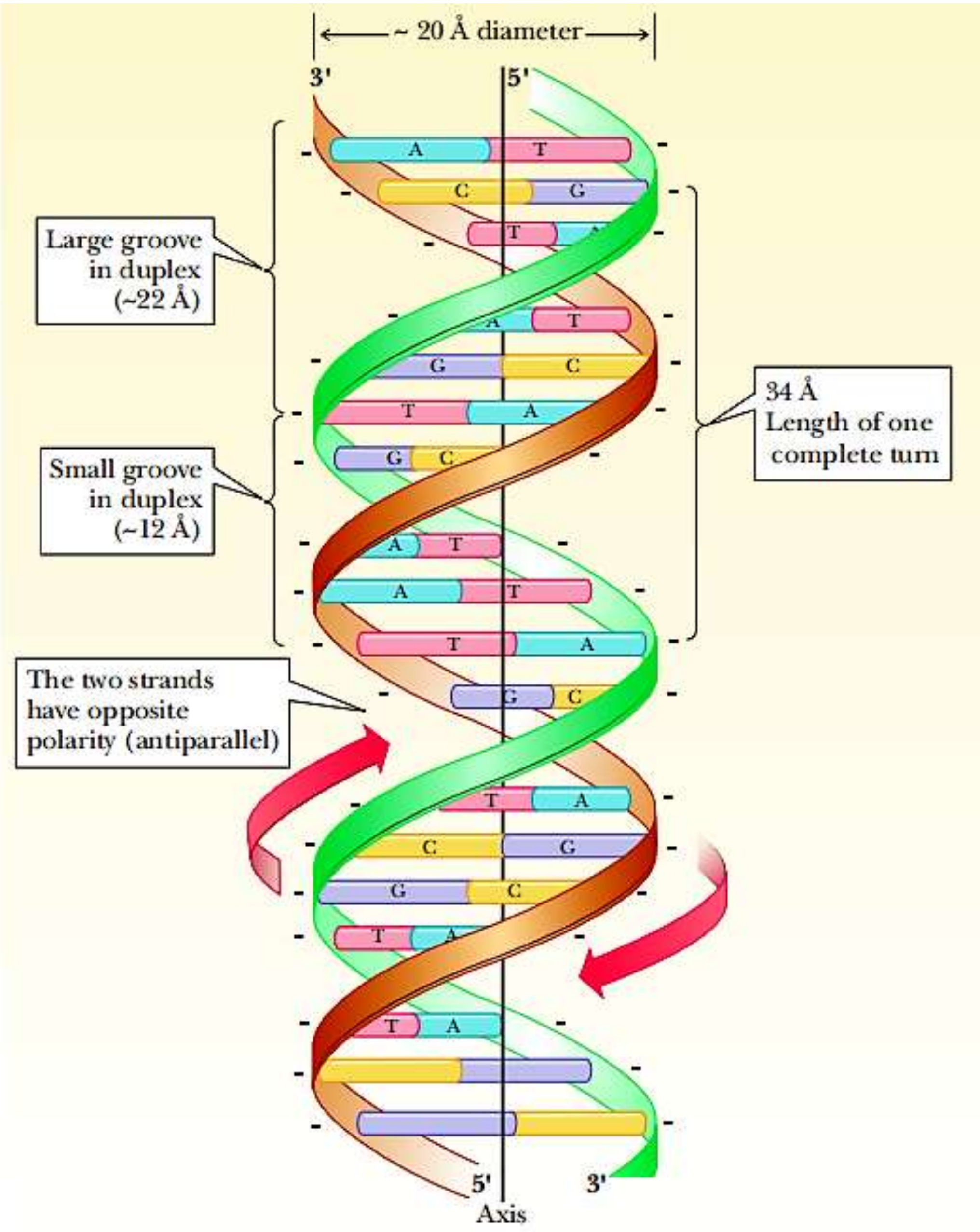




Double helical structure of DNA

The double helical structure of DNA was proposed by **James Watson and Francis Crick** in **1953** (Nobel Prize, 1962).





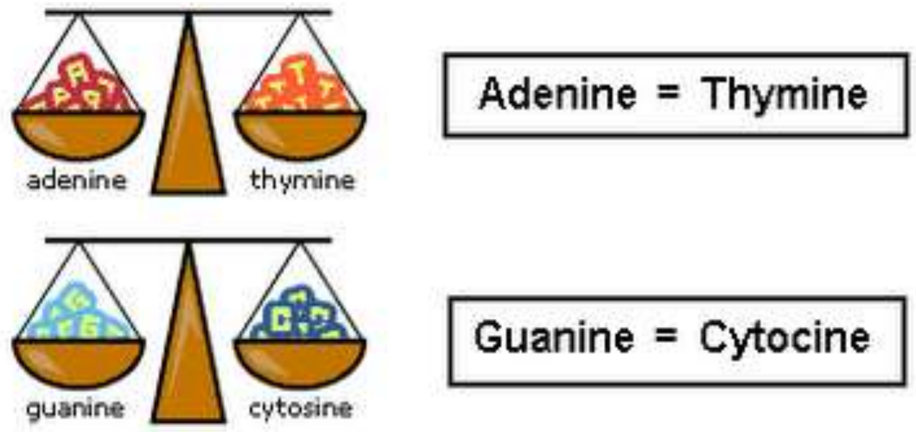
Salient features of Watson-Crick model of DNA

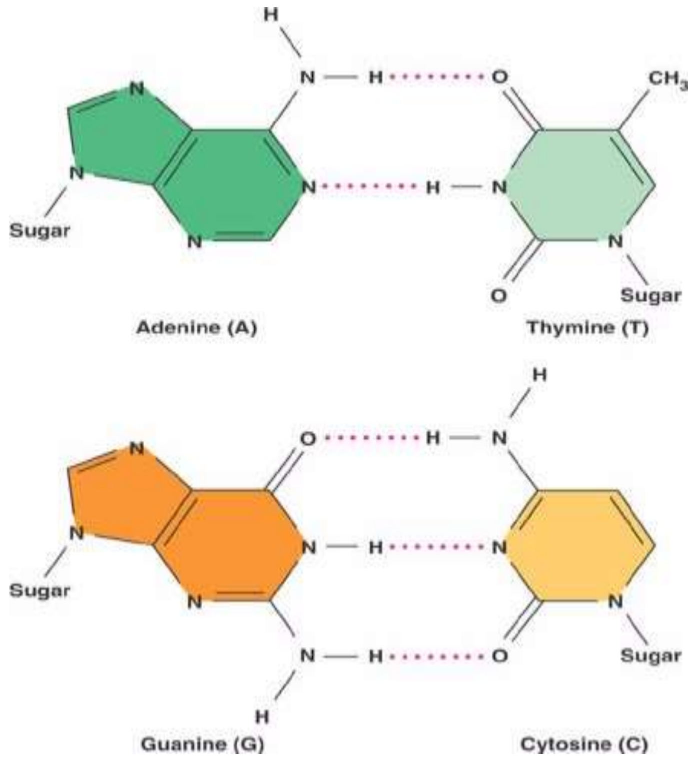
1) The DNA is a right handed double helix. It consists of two polydeoxyribonucleotide chains (strands) twisted around each other on a common axis.
2) The two strands are **antiparallel**, i.e., one strand runs in the 5´ to 3´ direction while the other in 3´to 5´direction.
3) The width (or diameter) of a double helix is **20 A° (2 nm)**.
4) Each turn (pitch) of the helix is **34 A° (3.4 nm)** with **10 pairs** of nucleotides, each pair placed at a distance of about **3.4 A°**.
5) Each strand of DNA has a hydrophilic deoxyribose phosphate backbone (3´- 5' phosphodiester bonds) on the outside (periphery) of the molecule while the hydrophobic bases are stacked inside (core).
6) The two polynucleotide chains are not identical but **complementary** to each other due to base pairing.
7) The two strands are held together by **hydrogen bonds** formed by complementary basepairs. The A-T pair has 2 hydrogen bonds while G-C pair has 3 hydrogen bonds. The G - C is stronger by about 50% than A = T.
8) The hydrogen bonds are formed between a purine and a pyrimidine only. If two purines face each other, they would not fit into the allowable space. And two pyrimidines would be too far to form hydrogen bonds. The only base arrangement possible in DNA structure, from spatial considerations is A-T, T-A, G-C and C-G.
9) The complementary base pairing in DNA helix **proves Chargaff's rule**. The content of adenine equals to that of thymine (A = T) and guanine equals to that of cytosine (G = C).
10) The genetic information resides on one of the two strands known as **template strand or antisense strand**. The opposite strand is **sense strand**.
11) The double helix has (wide) **major grooves** and (narrow) **minor grooves** along the phosphodiester backbone. Proteins interact with DNA at these grooves, without disrupting the base pairs and double helix.

CHARGAFF'S RULE

- This rule states that there is a 1:1 ratio of purines (A,G) to pyrimidines (T,C)
- This is true because A binds with T and G binds with C
- Mismatches of this pairing leads to improper folding and alignment which must be repaired.

(%A + %T) + (%G + %C) = 100%

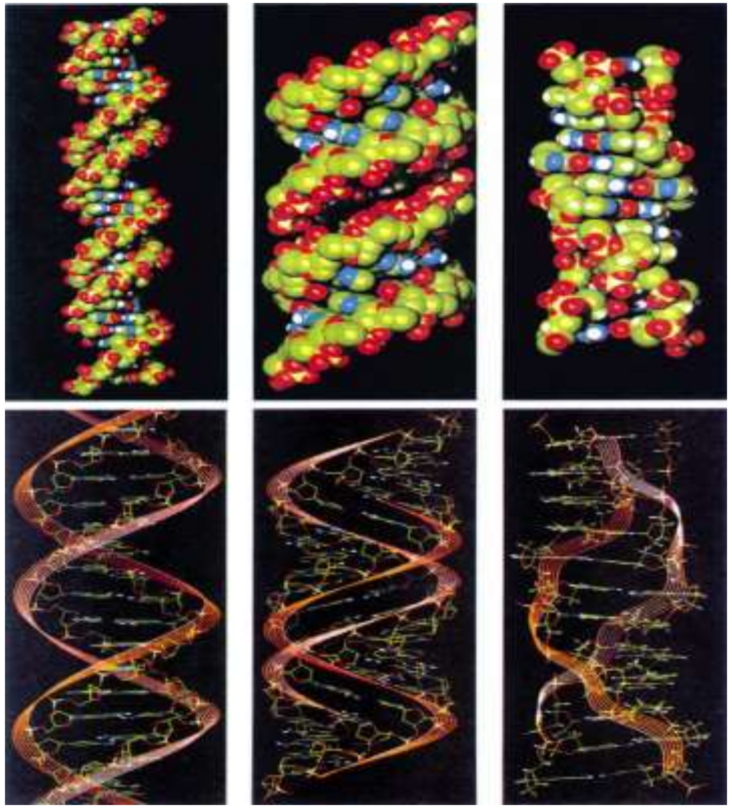




CONFORMATIONS OF DNA DOUBLE HELIX

Variation in the conformation of the nucleotides of DNA is associated with conformational variants of DNA.

The B-form of DNA double helix, described by Watson and Crick, is the most predominant form under physiological conditions.



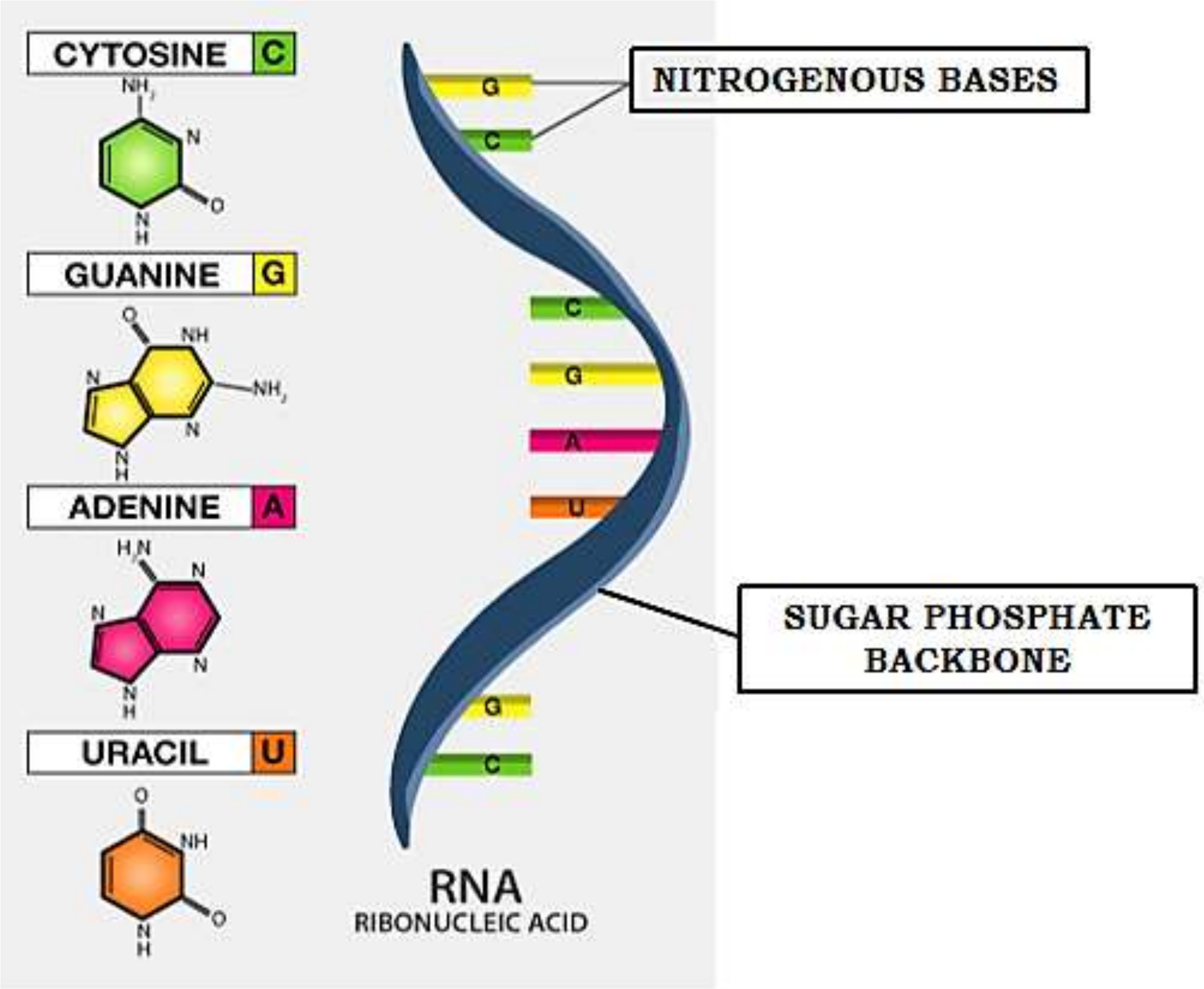
Computer-generated images of B-DNA (left), A-DNA (center) and Z-DNA (right)

Feature	*B-DNA*	*A-DNA*	*Z-DNA*
Helix type	Right-handed	Right-handed	Left-handed
Helical diameter (nm)	2.37	2.55	1.84
Distance per each complete turn (nm)	3.4	3.2	4.5
Rise per base pair (nm)	0.34	0.29	0.37
Number of base pairs per complete turn	10	11	12
Base pair tilt	+19°	−1.2° (variable)	−9°
Helix axis rotation	Major groove	Through base pairs (variable)	Minor groove

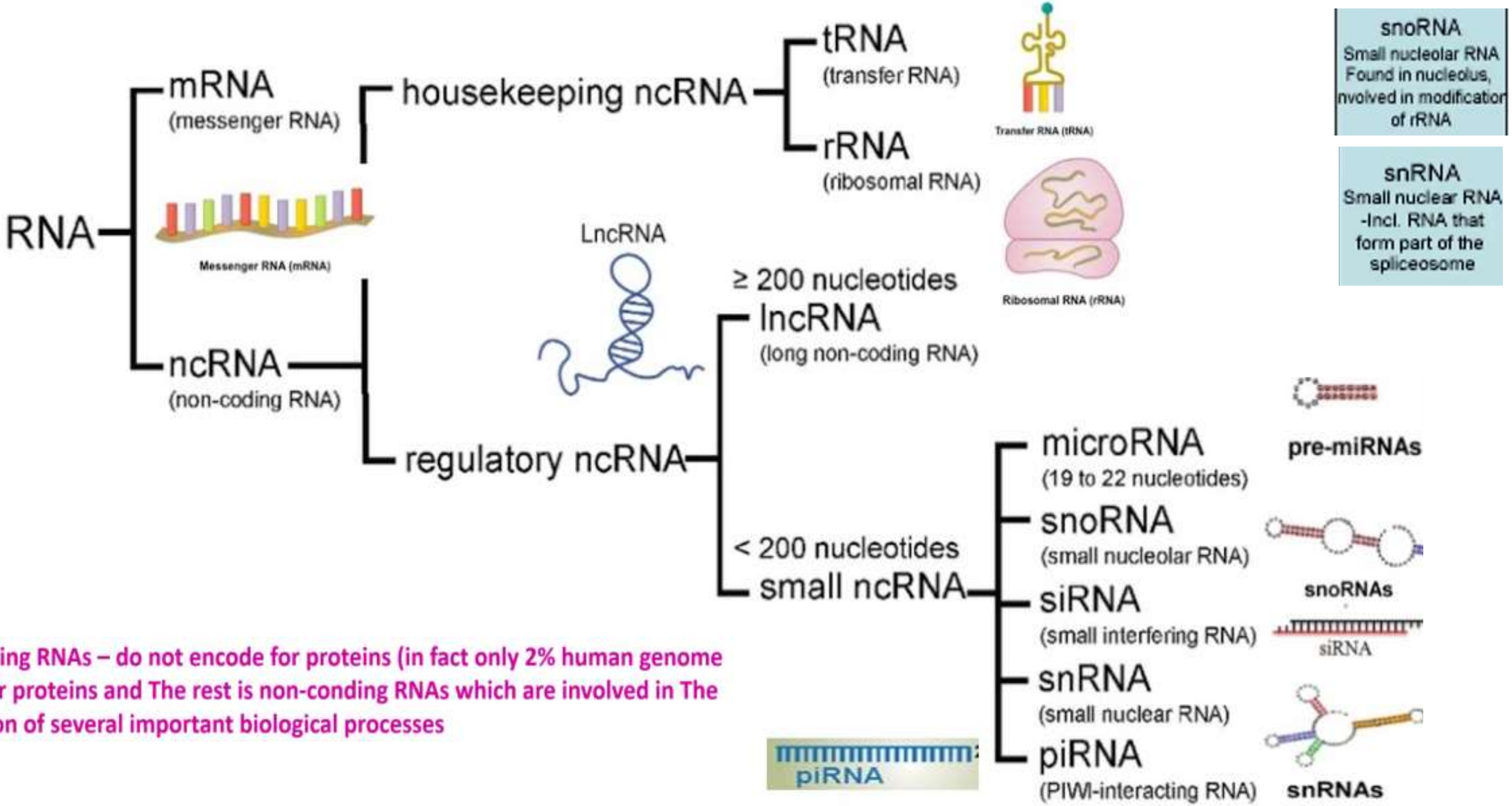
RIBONUCLEIC ACID (RNA)

(Similar to DNA with several key differences)

- Made up of a repeating strand of nucleotides, contains all 3 parts similar to DNA (sugar, phosphate, nitrogen base)
- The sugar in RNA is called Ribose
- Contains the nitrogen base Uracil instead of Thymine. Uracil will bind to Adenine (like thymine did)
- RNA is single strand
- **Chargaff's rule—not obeyed**



TYPES OF RNA



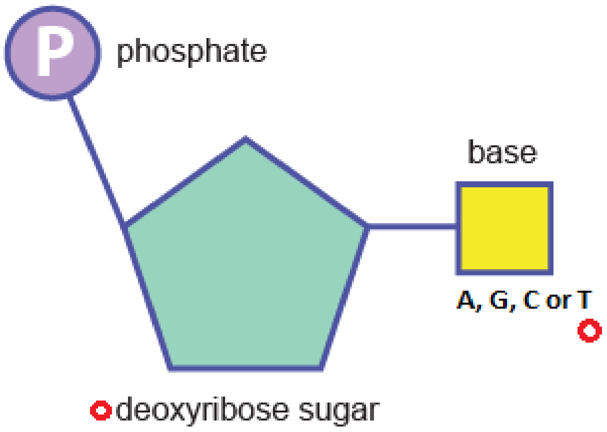
Non-coding RNAs – do not encode for proteins (in fact only 2% human genome codes for proteins and The rest is non-conding RNAs which are involved in The regulation of several important biological processes

The Roles of Different Kinds of RNA

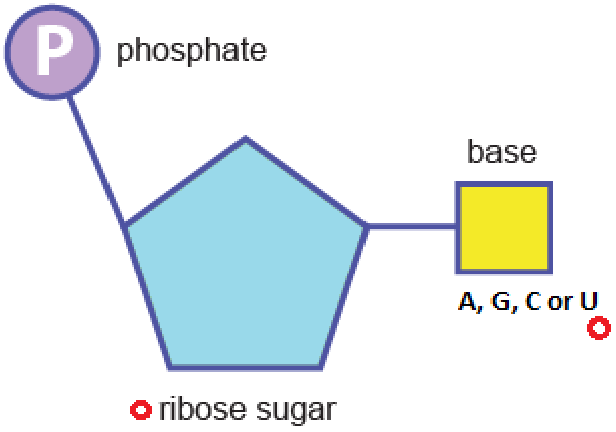
RNA Type	Size	Function
Transfer RNA	Small	Transports amino acids to site of protein synthesis
Ribosomal RNA	Several kinds—variable in size	Combines with proteins to form ribosomes, the site of protein synthesis
Messenger RNA	Variable	Directs amino acid sequence of proteins
Small nuclear RNA	Small	Processes initial mRNA to its mature form in eukaryotes
Small interfering RNA	Small	Affects gene expression; used by scientists to knock out a gene being studied
Micro RNA	Small	Affects gene expression; important in growth and development
Long noncoding RNA	Variable (long)	Still under debate, but appears to affect development and be related to certain disease states.

Difference between DNA and RNA are:

DNA	RNA
It is double stranded nucleic acid.	It is single stranded nucleic acid.
It contains deoxyribise sugar.	It contains ribose sugar.
It contains Thymine (T) as a nitrogenous base.	It contains Uracil (U) instead of Thymine.
It is the genetic and hereditary material of the cells.	It is involved in synthesis of proteins.
Follows Chargaff's rule	Doesn't follow Chargaff's rule



DNA



RNA

SAMPLE QUESTIONS

1) In DNA if the percentage of C is 13%, what will be the percentages of A, T and G?

Ans: If C = 13% according to Chargaff's rule **G = 13%**.

So, A + T = 100 - (C + G)

= 100 - 26

= 74

Therefore, **A or T** will be **37% each**

2) How many phosphodiester bonds are present in a DNA molecule of 50 bp?

Ans: If the no. of base pairs in DNA is 'n'

No. of phosphodiester bonds in a DNA molecule = 2n-2

Here, no. of base pairs (n) = 50

Therefore, no. of phosphodiester bonds in a DNA molecule = (2 x 50) - 2

= 100 - 2 = **98**

SAMPLE QUESTIONS

3) In a DNA molecule of 100 base pairs, the content of T was found to be 20%. Calculate the total no. of H-bonds present in the molecule?

Ans: 100 base pairs = 200 bases.

20% of 200 is 40.

If T is 40, A will be 40, G and C will be 200 - 80 = 120 i.e., 60 each.

A-T base pair have 2 H bonds between them.

So, 40 A-T pairs will have 40 x 2 = **80 H Bonds**

G-C pair has 3 H bonds between them.

So, 60 G-C pairs will have 60 x 3 = **180 H Bonds**

Hence, **total H bonds** will be 80 + 180 = **260**

SAMPLE QUESTIONS

4) How many nucleotides are there in a B-DNA of length 68 nm?

Ans: Length of DNA **=** 68 nm or 680 Ångström

Average distance between a base pair in a B-DNA is 3.4 Ångström

Hence, 680/ 3.4 = 200 base pairs

2 complementary bases from both strands form a base pair or we can say 2 nucleotides from each strand form 1 base pair

Hence, 200 x 2 = **400 nucleotides** are present

SAMPLE QUESTIONS

5) A double helical B-DNA molecule of 680 Å length has 20% thymine. Calculate the total no. of H-bonds present in the molecule?

Ans: Length of DNA = 680 Å

In B-DNA, distance between 2 base pairs is 3.4 Å

Hence, total number of **base pairs** in the molecule is 680/3.4 = **200**

So, total number of bases is 200 x 2 = **400**

Out of 400 bases, 20% is thymine

So, **T** = 20/100 x 400 = **80**

If T is 80, A will be 80, G and C will be 400 - 160 = 240 i.e., 120 each.

A-T base pair have 2 H bonds between them.

So, 80 A-T pairs will have 80 x 2 = **160 H Bonds**

G-C pair has 3 H bonds between them.

So, 120 G-C pairs will have 120 x 3 = **360 H Bonds**

Hence, **total H bonds** will be 160+ 360 = **520**

SAMPLE QUESTIONS

6) A double helical B-DNA molecule has 248 phosphodiester bonds and 90 thymine residues in total. Find out the total number of bases, percentage of each base, total number of hydrogen bonds and the length of the DNA molecule in Å.

Ans: No. of phosphodiester bonds in B-DNA molecule = 2n-2

So, 2n-2 =248, i.e., n is (248+2)/2 = 125 base pairs or **250 bases in total**.

Out of 250 bases, 90 is thymine

(i) So, **T** = **90, A** = **90,** G + C = 250 - 180 = 70, so **G** = **35** and **C** = **35**

(ii) % of T = (90/250)*100 = 36, % A = 36, % of G = 50 - %A = 14, % C = 14

(iii) A-T base pair have 2 H bonds between them, so 90 A-T pairs have 90 x 2 = 180 H bonds

G-C base pair have 3 H bonds between them, so 35 G-C pairs have 35 x 3 = 105 H bonds

Hence, **total H bonds** will be 180+ 105 = **285**

(iv) Average distance between a base pair in a B-DNA is 3.4 Ångström

Hence, 125 x 3.4 = **425 Å** is the length of the DNA molecule

SAMPLE QUESTIONS

7) A double-stranded DNA of length 102 nm has 300 H-bonds formed by G-C pairs only. What can be the concentration of Adenine?

Ans: Length of DNA molecule = 102 nm or 1020 Å

In DNA, distance between 2 base pairs is 3.4 Å

Hence, total number of **base pairs** in the molecule is 1020/3.4 = 300

= 300 x 2 = 600 bases

G-C pair has 3 H bonds between them.

Hence, 300 H bonds are present in between 100 G-C pairs

So, number of A-T pairs is 300 - 100 = 200

% A = (200/600) x 100 = **33.33**

SAMPLE QUESTIONS

8) How many hydrogen bonds are present in three turns of ds B-DNA molecule if 20% nucleotides are thymine?

Ans: 1 turn of DNA helix has 10 bps

3 turns of ds B-DNA will have 3 x 10 = 30 bps or 30 x 2 = 60 bases/nucleotides

Out of 60 bases, 20% is thymine

So, **T** = 20/100 x 60 = **12**

If T = 12 then A = 12

A-T base pair have 2 H bonds between them, so 12 A-T pairs have 12 x 2 = **24 H bonds**

G + C = 60 - 24 = 36, so G = 18 and C = 18

G-C base pair have 3 H bonds between them, so 18 G-C pairs have 18 x 3 = **54 H bonds**

Hence, **total H bonds** will be 24 + 54 = **78**

SAMPLE QUESTIONS

9) A double helical A-DNA molecule of 580 Å length has 20% thymine? Calculate the total no. of H-bonds present in the molecule?

Ans: Length of DNA = 580 Å

In A-DNA, distance between 2 base pairs is 2.9 Å

Hence, total number of **base pairs** in the molecule is 580/2.9 = **200**

So, total number of bases is 200 x 2 = **400**

Out of 400 bases, 20% is thymine

So, **T** = 20/100 x 400 = **80**

If T is 80, A will be 80, G and C will be 400 - 160 = 240 i.e., 120 each.

A-T base pair have 2 H bonds between them.

So, 80 A-T pairs will have 80 x 2 = **160 H Bonds**

G-C pair has 3 H bonds between them.

So, 120 G-C pairs will have 120 x 3 = **360 H Bonds**

Hence, **total H bonds** will be 160+ 360 = **520**

SAMPLE QUESTIONS

10) Calculate the total number of hydrogen bonds present in the stretch of a double helical DNA with the sequence 5' ATGCCTAA 3' ?

Ans: DNA sequence is 5' ATGCCTAA 3'

In a double helical DNA molecule A always base pairs with T by two hydrogen bonds and G bonds with C by three hydrogen bonds.

So, total A+T = 5, hence 5 x 2 = **10 H bonds**

G+C = 3, hence 3 x 3 = **9 H bonds**

Hence, the total number of hydrogen bonds present in the sequence of a stretch of a double helical DNA 5' ATGCCTAA 3' is 10 + 9 = **19**.

SAMPLE QUESTIONS

11) During the process of transcription, the DNA-RNA hybrid formed has 10% A in DNA, 12% A in RNA and 1998 phosphodiester bonds in total. From the given data, calculate the total number of riboses, percentage of each base, the total number of N-glycosidic bonds and hydrogen bonds formed and length of the hybrid in Å.

Ans: No. of phosphodiester bonds in a DNA molecule = 2n-2

Therefore, 2n-2 = 1998, n = **1000 base pairs** or 2000 bases in total.

Since, 1 strand is DNA and another is RNA so, **total number of riboses = 1000**

In DNA there is 10% A i.e., out of 1000 bases **A = 100** . These 100 A base pair with **100 U** of RNA

Similarly, in RNA there is 12% A i.e., out of 1000 bases **A = 120** which base pair with **120 T** of the DNA strand.

Therefore, in the DNA strand A + T = 100 + 120 = 220 , so the remaining bases i.e., **1000 - 220 = 780 is G + C**

Similarly, in the RNA strand U + A = 100 + 120 = 220, hence **G + C = 1000 - 220 = 780**

Hence, in the hybrid, the total % of A = (220/2000) x 100 = 11, % of T = (120/2000) x 100 = 6, % of U = (100/2000) x 100 = 5

Total G + C = 780 + 780 = 1560, therefore % of G = (780/2000) x 100 = 39 and % of C = 39

Since, there are 2000 bases in total and each base is attached to the sugar in the nucleotide by 1 N-glycosidic bond so **the total number of N-glycosidic bonds = 2000**

A-U base pair have 2 H bonds between them, so 100 A-U pairs have 100 x 2 = **200 H bonds**

A-T base pair have 2 H bonds between them, so 120 A-T pairs have 120 x 2 = **240 H bonds**

G-C pair has 3 H bonds between them. So, 780 G-C pairs will have 780 x 3 = **2340 H Bonds**

Hence total number of H bonds = 200 + 240 + 2340 = 2780

In DNA, distance between 2 base pairs is 3.4 Å.

Since the RNA strand is being formed from the DNA strand, the **distance between 2 bps in the hybrid will be also 3.4 Å**

Therefore, if 1 bp = 3.4 Å, 1000 bps = 1000 x 3.4 = **3400 Å**