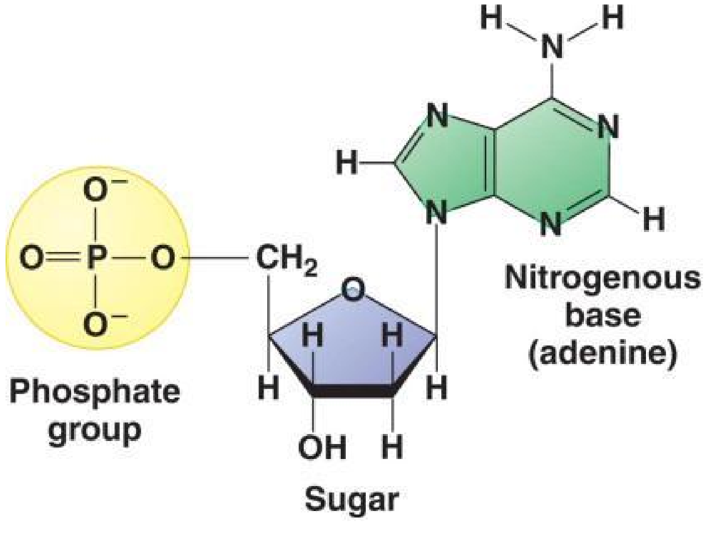
Year 12 HL

IB BIOLOGY

A1.2 DNA and RNA



Name:

Teacher: Mr Trent

A1.2.1—DNA as the genetic material of all living organisms

A1.2.2—Components of a nucleotide

A1.2.3—Sugar–phosphate bonding and the sugar–phosphate “backbone” of DNA and RNA

A1.2.4—Bases in each nucleic acid that form the basis of a code

A1.2.5—RNA as a polymer formed by condensation of nucleotide monomers

A1.2.6—DNA as a double helix made of two antiparallel strands of nucleotides with two strands linked by hydrogen bonding between complementary base pairs

A1.2.7—Differences between DNA and RNA

A1.2.8—Role of complementary base pairing in allowing genetic information to be replicated and expressed

A1.2.9—Diversity of possible DNA base sequences and the limitless capacity of DNA for storing information

A1.2.10—Conservation of the genetic code across all life forms as evidence of universal common ancestry

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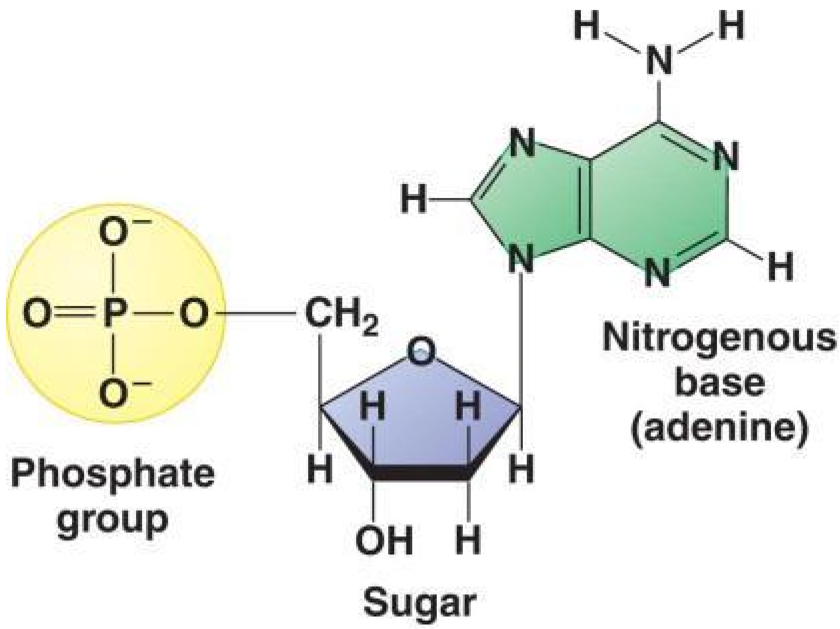
A1.2.11—Directionality of RNA and DNA

A1.2.12—Purine-to-pyrimidine bonding as a component of DNA helix stability

A1.2.13—Structure of a nucleosome

A1.2.14—Evidence from the Hershey–Chase experiment for DNA as the genetic material

A1.2.15—Chargaff’s data on the relative amounts of pyrimidine and purine bases across diverse life forms



Pre-test

1.DNA stands for?

2. DNA is a polymer made up of what type of monomers?
a. monosaccharides
b. fatty acids
c. amino acids
d. nucleotides

3. The information on a DNA molecule is in the form of a 4 letter code. Which letters make up the code?
a. A,B,C,D
b. A,T,G,U
c. A,T,C,G
d. A,T,C,U

4. A section of DNA that codes for a characteristic, such as eye colour, is called what?
a. chromosome
b. gene
c. nucleotide
d. genome

5. How many strands make up a DNA molecule?

6. What shape is the DNA molecule?

7. The backbone of a DNA molecule is made up of
a. Sugar and a phosphate group
b. Nitrogenous bases and phosphate groups
c. Sugar and nitrogenous bases
d. Sugar, a phosphate group and nitrogenous base

8. A length of DNA sequence that contains information that is capable of being translated into a polypeptide product is called a …
a. Genome
b. Chromosome
c. Gene
d. Nucleotide

9. A change in the sequence of the DNA is called what?
a. mutation
b. variation
c. alteration
d. modification

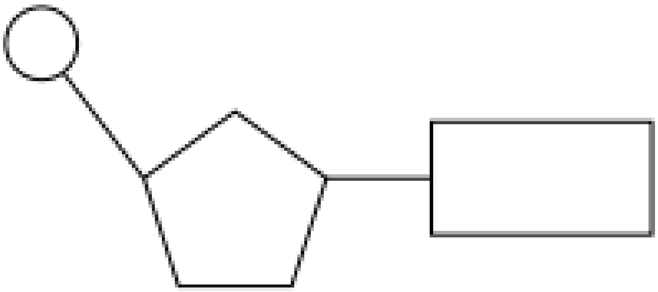
10. The total amount of hereditary material in a cell is called what?
a. genetic makeup
b. chromosome number
c. genome
d. diploid number

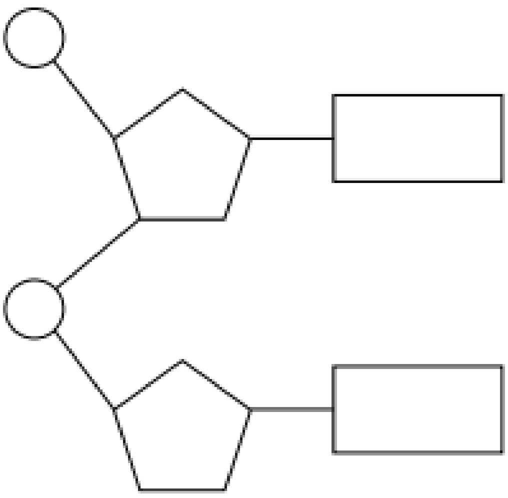
A1.2.2—Components of a nucleotide

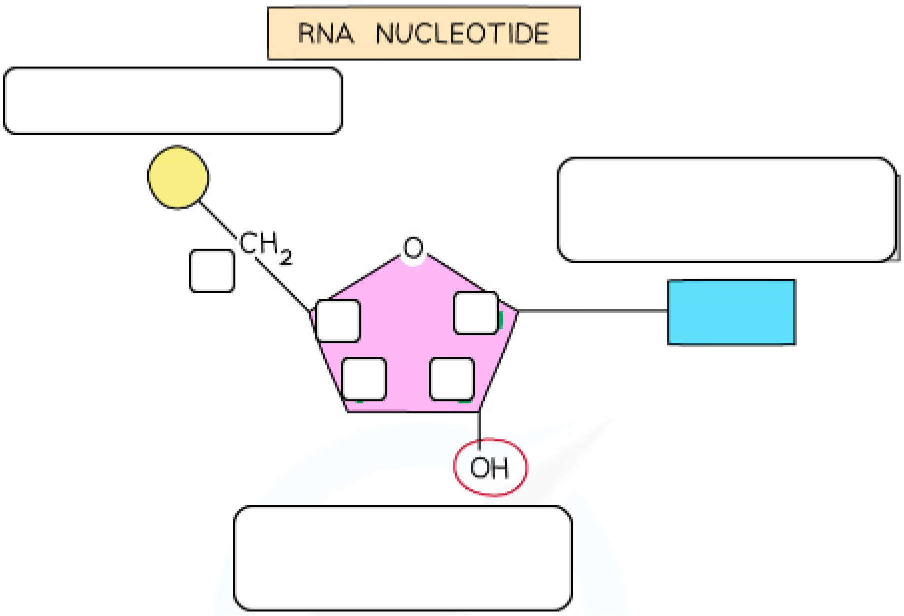
A1.2.3—Sugar–phosphate bonding and the sugar–phosphate “backbone” of DNA and RNA

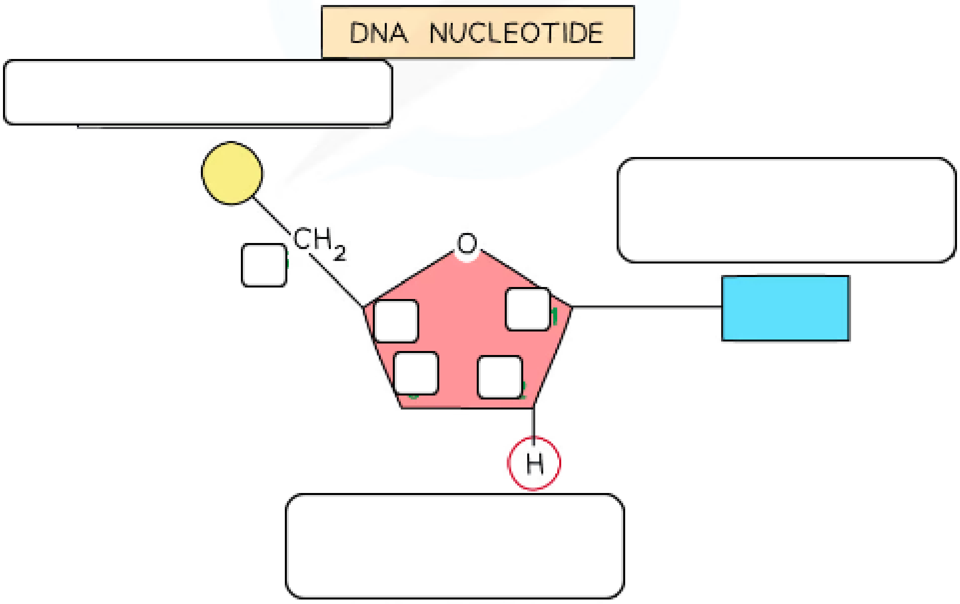
A1.2.5—RNA as a polymer formed by condensation of nucleotide monomers

- State the two types of nucleic acid.
- Outline the parts of a nucleotide.
- Identify and label carbons by number (for example, C1, C2, C3) on a nucleotide drawing.
- Explain how nucleotides can connect to form a nucleic acid polymer.









- State the names of the nitrogenous bases found in DNA and RNA.

- State the complementary base pairing rules.

Checkpoint:

1. Outline how the DNA nucleotides are linked together (you may choose to use a simplified diagram to respond).

2. Outline the rules involved with the pairing of the nitrogenous bases (how does complementary base pairing work?). What is Chargaff's ratio?

3. What sort of bonds is used to join the **nitrogenous bases** together?

A1.2.7—Differences between DNA and RNA

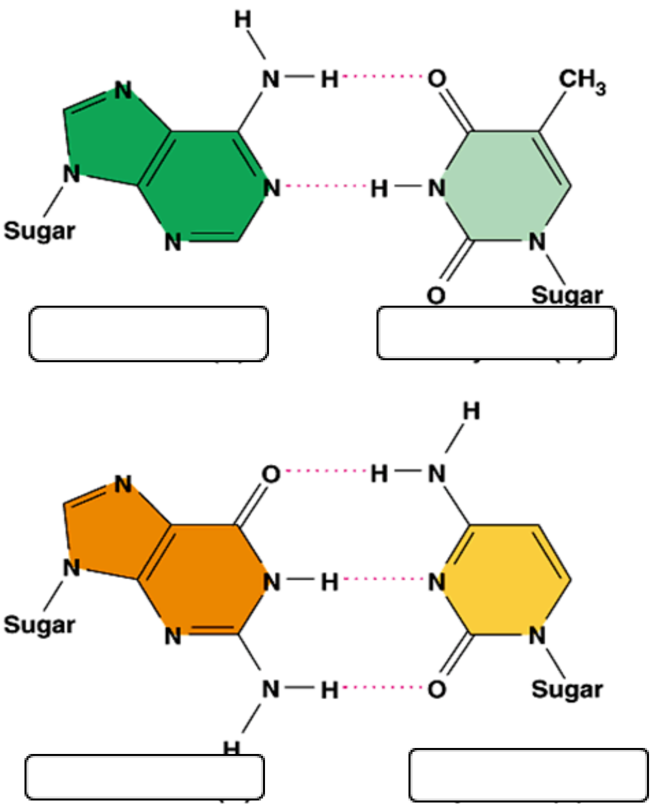
DNA and RNA

Complete the table comparing the structure of DNA and RNA:

DNA	**RNA**

A1.2.6—DNA as a double helix made of two antiparallel strands of nucleotides with two strands linked by hydrogen bonding between complementary base pairs
A1.2.8—Role of complementary base pairing in allowing genetic information to be replicated and expressed
A1.2.15—Chargaff's data on the relative amounts of pyrimidine and purine bases across diverse life forms

- Define antiparallel in relation to DNA structure.
- Outline the formation of a DNA double helix by hydrogen bonding between nitrogenous bases.
- Identify the four bases of DNA based on the numbers of rings (purines or pyrimidines) and the number of hydrogen bonds it can form.
- State the number of nitrogenous bases per complete turn of the DNA double helix.



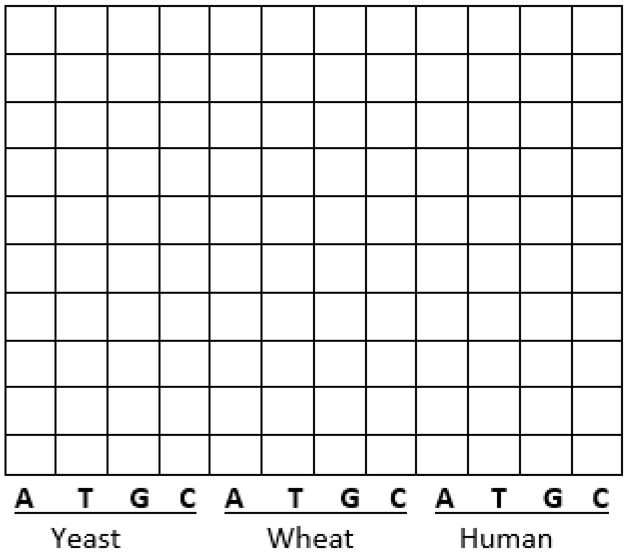
What is antiparallel and draw this below?

A1.2.15—Chargaff's data on the relative amounts of pyrimidine and purine bases across diverse life forms

Table 1. Nitrogen Base Make-Up of Different Organisms' DNA (in Percentages)				
Organism	**A**	**T**	**G**	**C**
Mycobacterium tuberculosis	15.1	14.6	34.9	35.4
Yeast	31.3	32.9	18.7	17.1
Wheat	27.3	27.1	22.7	22.8
Sea Urchin	32.8	32.1	17.7	17.3
Marine crab	47.3	47.3	2.7	2.7
Turtle	29.7	27.9	22.0	21.3
Rat	28.6	28.4	21.4	21.5
Human	30.9	29.4	19.9	19.8

Data Analysis – Refer to Table 1 to answer the questions.

1. Create a graph to show the nitrogen base make-up for yeast, wheat and humans.



2. What observations can you make about the data in Table 1? What patterns do you notice?

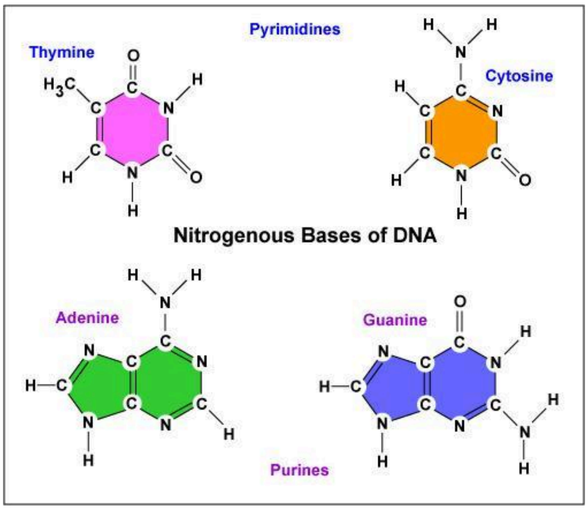
3. What does the data in Table 1 show about the make-up of DNA for different species?

4. How does this support the idea that DNA could be the genetic material? Explain.

<u>Purines & Pyrimidines</u> – As shown below, <u>adenine</u> and <u>guanine</u> are similarly shaped nitrogenous bases called ***purines***. <u>Thymine</u> and <u>cytosine</u> are similar in shape and they are classified as ***pyrimidines***.

1. For <u>five different organisms</u> in Table 1 (on the front), calculate the ratio of purines to pyrimidines.

Organism	**% Purines (A+G)**	**% Pyrimidines (T + C)**	**Ratio**

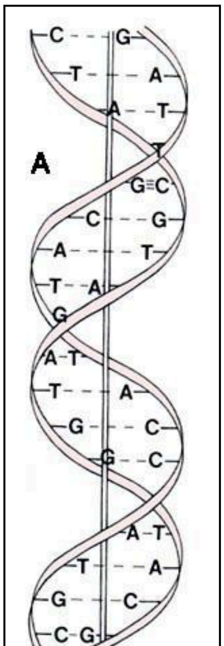


2. What can you conclude about the <u>Purine : Pyrimidine</u> ratio of DNA for all organisms?

<u>Piecing it Together</u> - Chargaff's data was a central piece of evidence used by James Watson and Francis Crick in 1953 to successfully describe the structure of DNA. **Look at the drawing of DNA below**.

1. What do you notice about the arrangement of the nitrogen bases? Record as many
observations as you can.

2. How did <u>Chargaff's data</u> help Watson & Crick predict that DNA looks like this?



A1.2.4—Bases in each nucleic acid that form the basis of a code
A1.2.9 Diversity of possible DNA base sequences and the limitless capacity of DNA for storing information
A1.2.10—Conservation of the genetic code across all life forms as evidence of universal common ancestry

The specific order of these bases carries the genetic information and codes for the **synthesis of proteins** and the functioning of living organisms.

Diversity of DNA base sequences: DNA is composed of four different nucleotide bases: adenine (A), cytosine (C), guanine (G), and thymine (T). These bases can be arranged in any sequence along the DNA molecule. The diversity of DNA base sequences arises from the countless possible combinations of these four bases. For example, a short DNA sequence of only 10 bases can have 4^10 (or 1,048,576) possible combinations. With longer DNA sequences, the number of possible combinations increases exponentially, resulting in an incredibly diverse range of genetic information.

Limitless capacity for storing information: The structure of DNA, with its double helix and complementary base pairing, allows for the storage of vast amounts of genetic information. Each base along the DNA molecule acts as a unit of information. By arranging these bases in specific sequences, DNA can encode and store an immense amount of genetic information. This information includes instructions for the development, functioning, and reproduction of all living organisms.

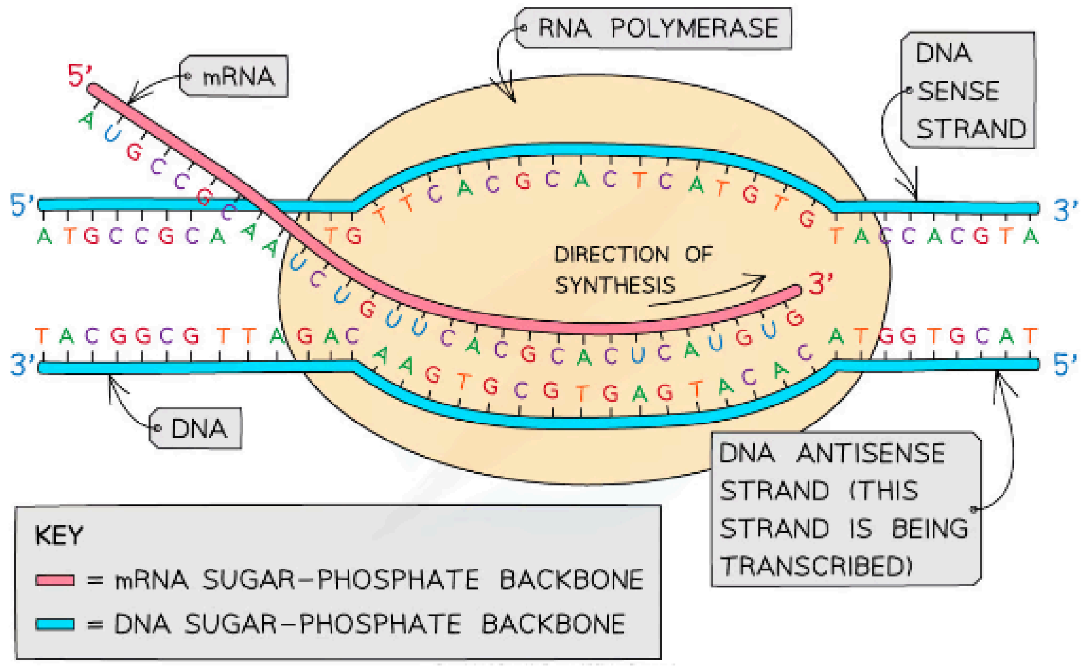
The genetic code refers to the specific correspondence between the sequence of nucleotide bases in DNA or RNA and the sequence of amino acids in proteins. This code acts as a language that translates the information stored in DNA into the production of proteins, which are essential molecules for the structure and function of living organisms. One of the most remarkable observations is that the genetic code is virtually universal. With a few minor exceptions, all living organisms on Earth, from bacteria to plants to humans, use the same genetic code. This means that the same set of codons (three-nucleotide sequences) specifies the same amino acids across all organisms. For example, the codon AUG universally codes for the amino acid methionine, and the codon GGG codes for the amino acid glycine in all organisms.

The conservation of the genetic code across diverse life forms suggests a common origin or ancestry. If different life forms evolved independently without a common ancestor, one would expect to see different genetic codes with no consistent pattern. However, the fact that the genetic code is shared across such a wide range of organisms strongly implies a shared evolutionary history.

This universal genetic code suggests that all life forms on Earth share a common ancestry, with a common origin of the genetic code early in the history of life. It indicates that the genetic code has been conserved and passed down from an ancient common ancestor to all subsequent generations of organisms.

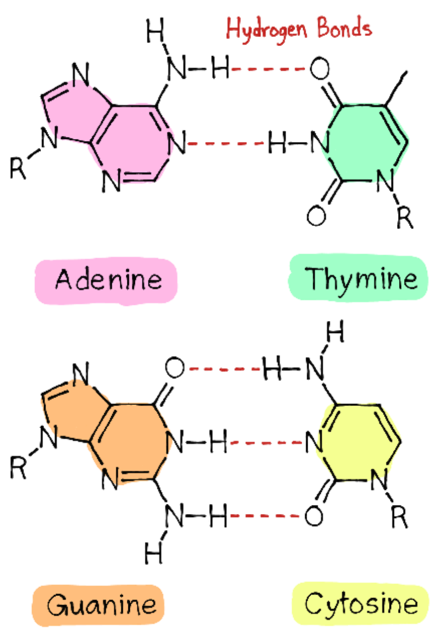
The conservation of the genetic code is consistent with the concept of universal common ancestry proposed by the theory of evolution. It provides strong evidence that all organisms, regardless of their diversity and complexity, are interconnected through a common evolutionary history and share a common origin of life on Earth.

A1.2.11—Directionality of RNA and DNA



Explain why directionality of RNA and DNA is important

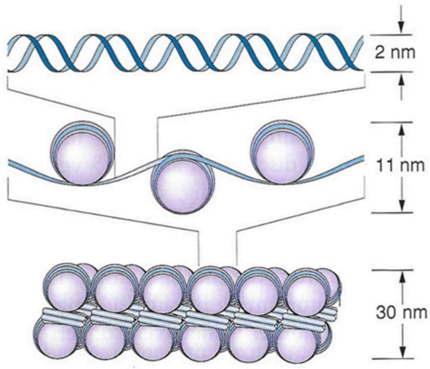
A1.2.12—Purine-to-pyrimidine bonding as a component of DNA helix stability



Base Pair Geometry: The specific geometry of the purine-to-pyrimidine base pairs optimizes the fit between the bases and facilitates proper stacking of the DNA molecule. The complementary base pairs fit together snugly, allowing the DNA strands to align and form a stable double helix structure.

A1.2.13—Structure of a nucleosome
A1.2.14—Evidence from the Hershey–Chase experiment for DNA as the genetic material

Define **supercoiling:**



List some reasons why supercoiling needs to occur:

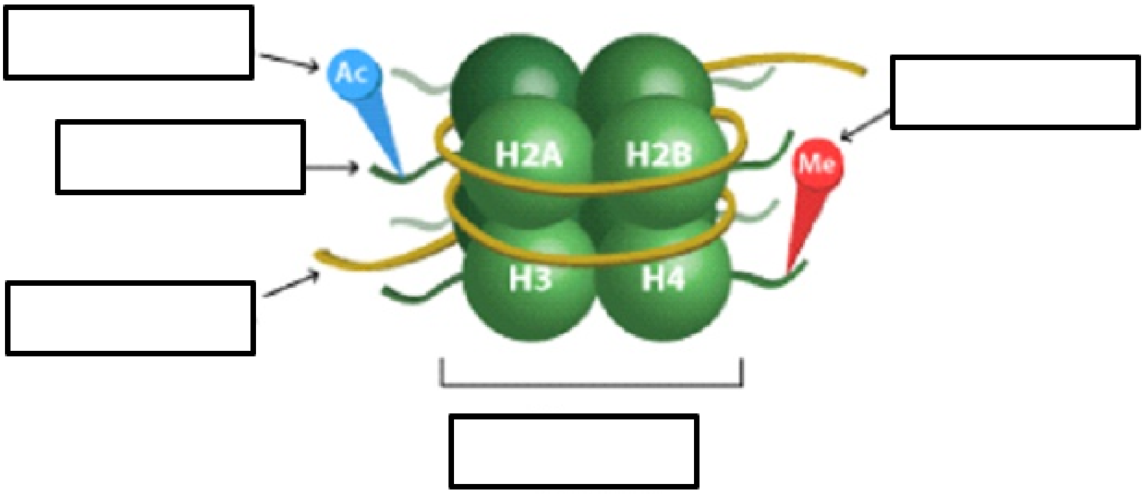
Watch the video here:
https://www.dnalc.org/resources/3d/08-how-dna-is-packaged-advanced.html

Answer these questions:

How many histone proteins make up the core of the nucleosome?

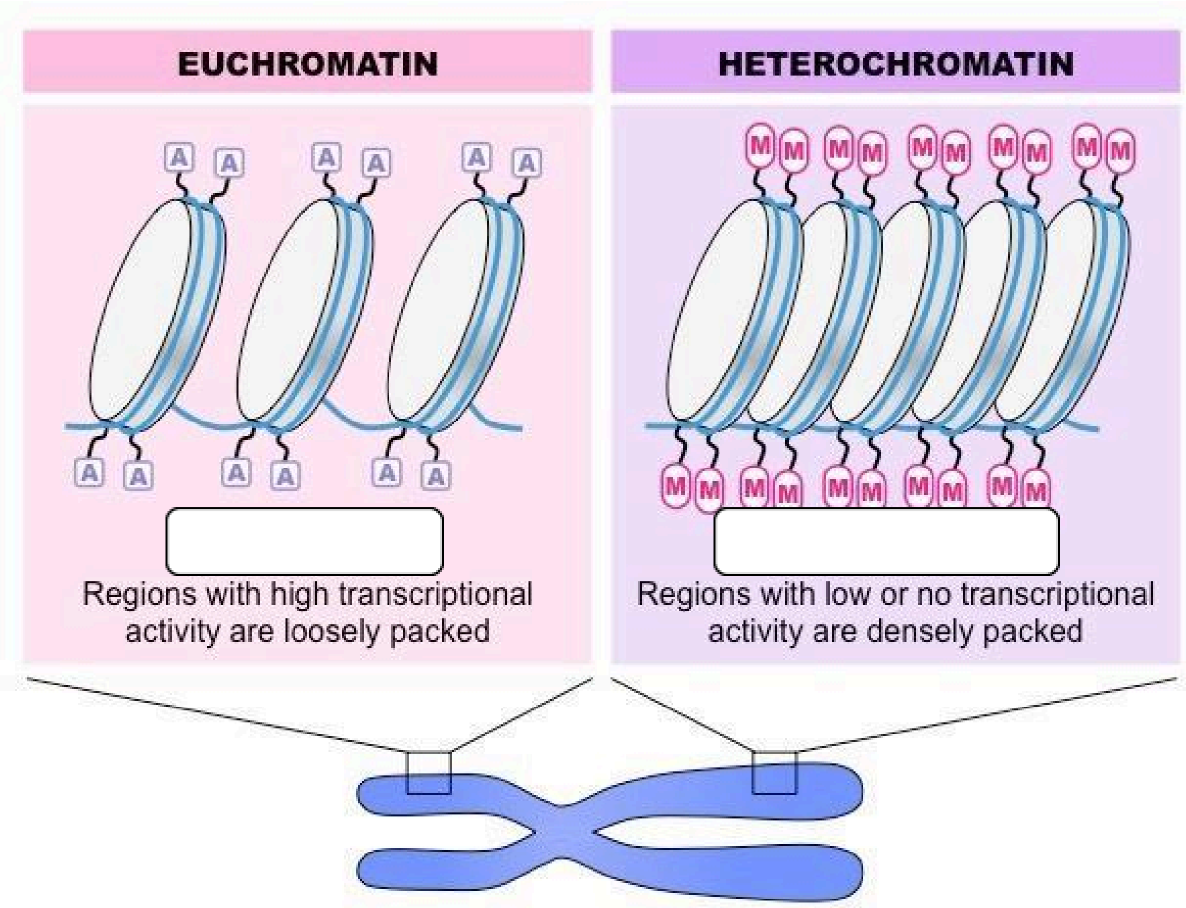
How many different types of histone proteins make up the core?

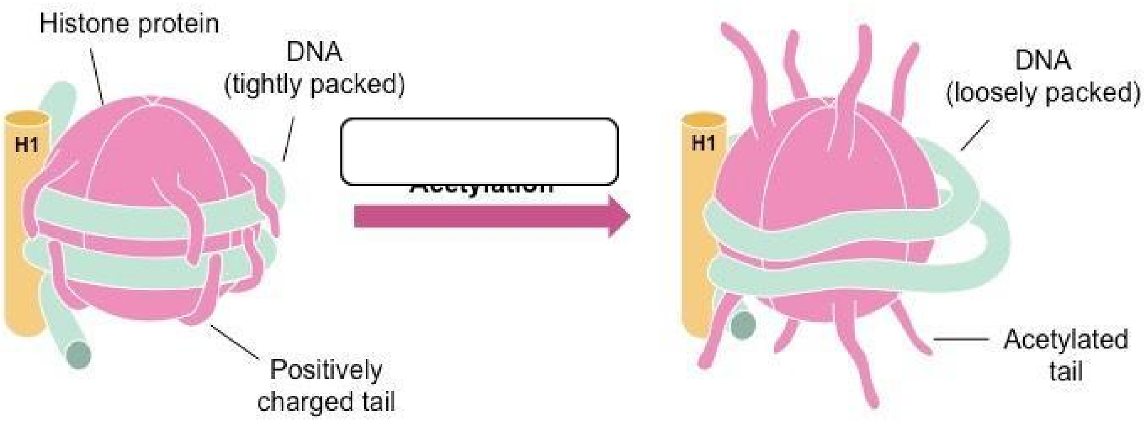
How many nucleotide bases are found in the DNA which wraps around the histone protein core?
150 base pairs
What is the role of the ninth histone protein?



Label the structure of a nucleosome, including the H1 protein, the octamer core proteins, linker DNA and two wraps of DNA.

In the space below, draw and label a nucleosome:





Alfred ____________ and **Martha** ____________ wanted to solve this problem by finding out if protein or DNA was the genetic material of viruses.

Hershey and Chase chose to study the ________________________, which infects the ***E. Coli*** bacterium (image of both above), because of its very simple structure consisting of just:

- _______________ (capsid)
- _______________ inside the coat

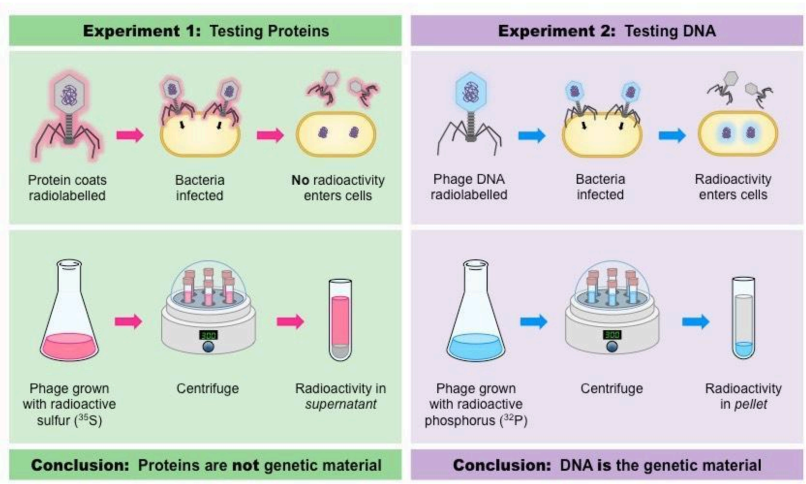
- Viruses **inject** their ___________________ into cells.
- The non-genetic part of the virus remains_____________ the cell.

Amino acids containing _______________ **isotopes** were used to **label** the virus:

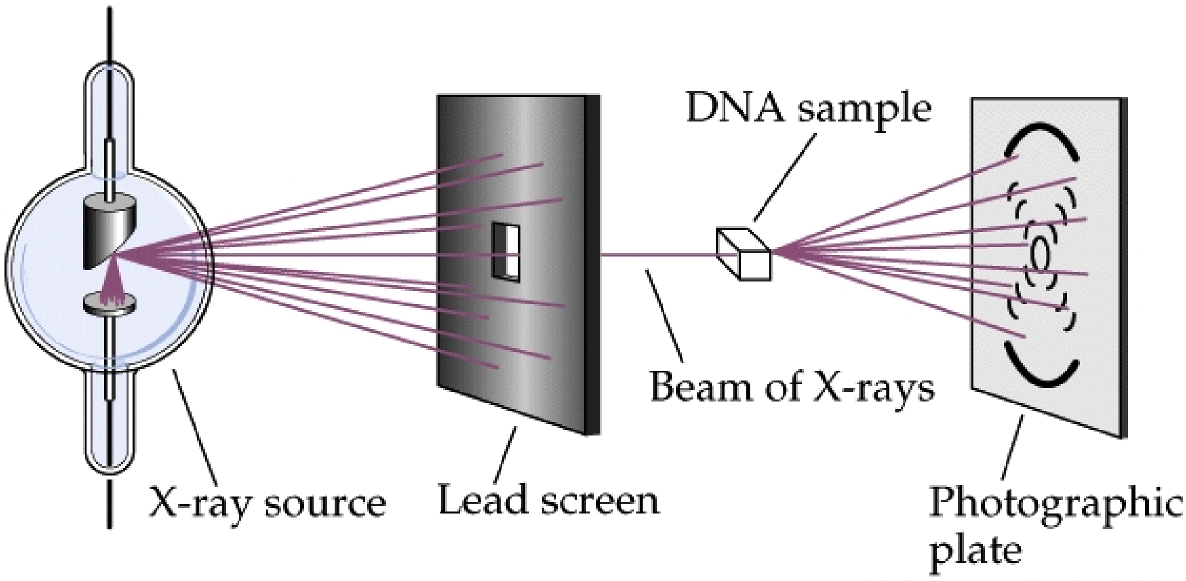
- S_____________ **(^{35}S)** for the **Protein** coat (capsid) □ Disulphide bridges
- P_______________**(^{32}P)** for the **DNA** □ Phosphate group

- At the end of the experiment a **centrifuge** was used to separate them:
- the smaller **virus** remained in the **supernatant** (liquid)
- the _______________ formed a **pellet**

- **Sulfur (^{35}S)**_____________ remained in **supernatant**
- **Phosphorus (^{32}P)**______________ was found in the **pellet**
- Hershey and Chase **deduced** that **DNA** therefore was the _______________ used by viruses because **DNA** (labelled by ^{32}P) was being _________________ into the **bacteria**.



What is x-ray diffraction and crystallography?



Rosalind Franklin concluded:

- DNA exists as a long, thin molecule of _______________
- The structure is highly _____________
- DNA is _____________

Outline the role of Chargaff, Watson, Crick, Franklin and Wilkins in the discovery of DNA structure.
Explain how Watson and Crick used model building to determine the structure of DNA.

1. Which of the following are connected by hydrogen bonds?

A. Hydrogen to oxygen within a molecule of water

B. Phosphate to sugar in a DNA molecule

C. Base to sugar in a DNA molecule

D. Hydrogen to oxygen between two different molecules of water

(Total 1 mark)

2. The percentage of thymine in the DNA of an organism is approximately 30%. What is the percentage of guanine?

A. 70%

B. 30%

C. 40%

D. 20%

(Total 1 mark)

3. Which molecule is found in both DNA and RNA?

A. Ribose

B. Uracil

C. Phosphate

D. Amino acid

(Total 1 mark)

4. What are pyrimidines in DNA?

A. Types of nucleotides

B. Types of base pairs

C. Types of sugars

D. Types of bases

(Total 1 mark)

5. Draw a labelled diagram to show **four** DNA nucleotides, each with a different base, linked together in **two** strands.

(5)

1. D

2. D

3. C

4. D

5. Award [1] for each of these structures clearly drawn and labelled.four nucleotides shown in diagram with one nucleotide clearly labelled;
base, phosphate and deoxyribose (shown as pentagon) connected between the correct carbons and labelled at least once;
backbone labelled as covalent bond between nucleotides correctly shown as 3′ to 5′ bond;
two base pairs linked by hydrogen bonds drawn as dotted lines and labelled;
two H bonds between A and T and three H bonds between C and G;
adenine to thymine and cytosine to guanine; do not accept initials of bases antiparallel orientation shown; [5]