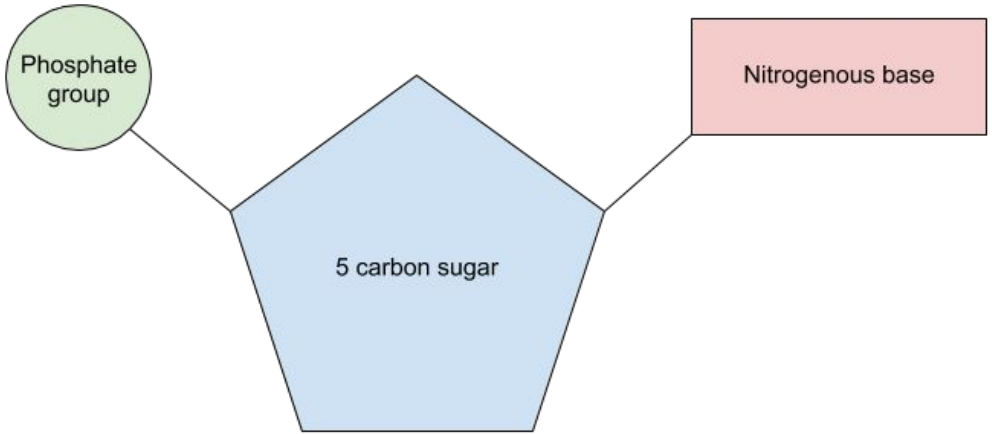
# OCR (B) Biology A-level

## 2.1.4 - Nucleic acids

Flashcards

# Draw the structure of a nucleotide.

# Draw the structure of a nucleotide.



# Name the pentose sugars in DNA & RNA.

Name the pentose sugars in DNA & RNA.

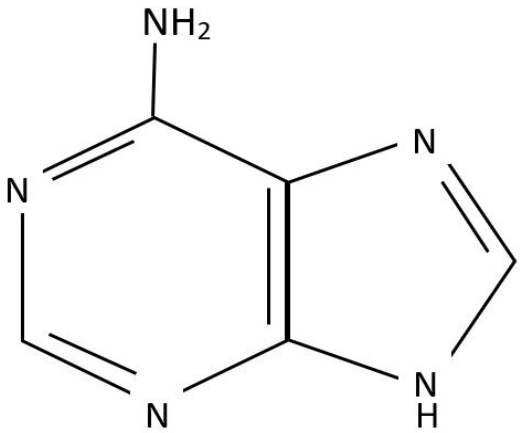
DNA: deoxyribose

RNA: ribose

Name the purine bases and describe their structure.

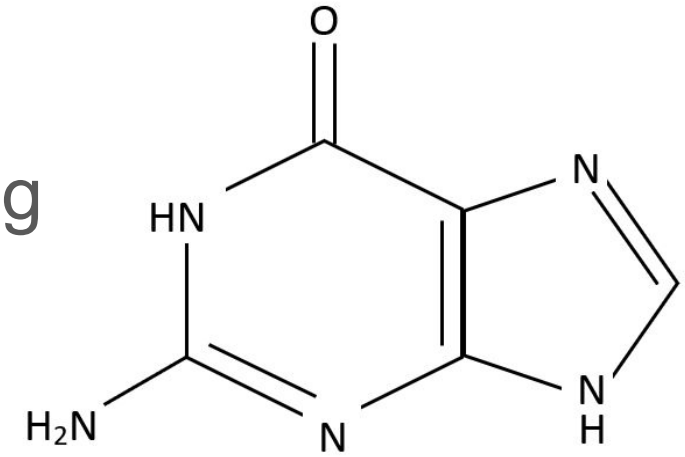
# Name the purine bases and describe their structure.

adenine $C_5H_5N_5$




**Double** ring structure

guanine $C_5H_5N_5O$

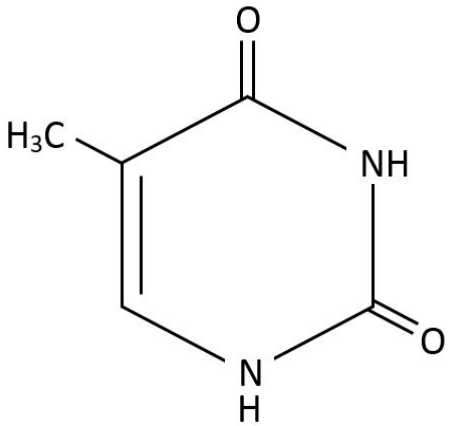


# Name the pyrimidine bases and describe their structure.

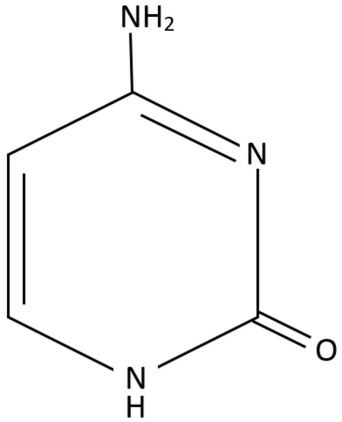
# Name the pyrimidine bases and describe their structure.

**Single** ring structure

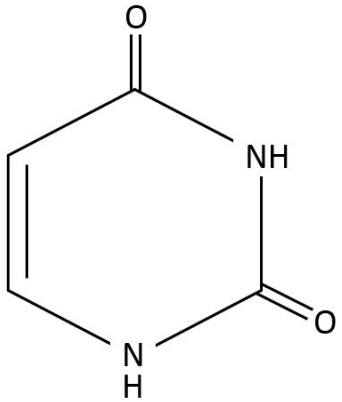
thymine $C_5H_6N_2O_2$




cytosine




uracil $C_4H_4N_2O_2$



# Describe how polynucleotide strands form.

Describe how polynucleotide strands form.

Enzymes catalyse condensation reactions between adjacent nucleotides to form strong phosphodiester bonds (‘sugar-phosphate backbone’).

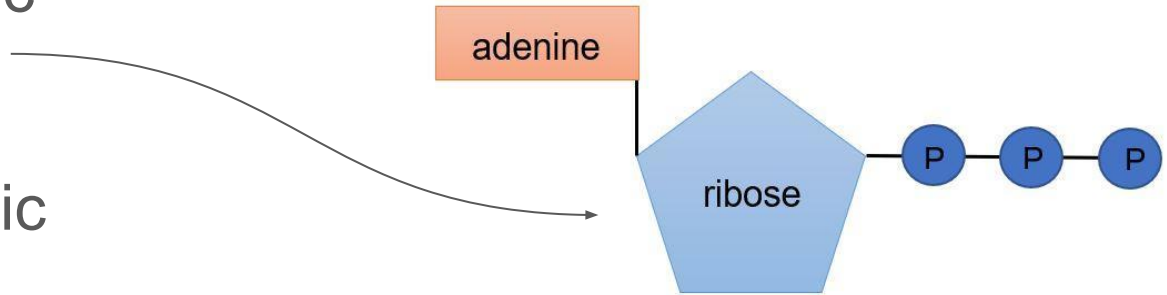
# Describe the structure of adenosine triphosphate (ATP) and adenosine diphosphate (ADP).

# Describe the structure of adenosine triphosphate (ATP) and adenosine diphosphate (ADP).

Phosphorylated nucleotide derivative of adenine

ATP has 3 inorganic phosphate groups

ADP has 2 inorganic phosphate groups



# Describe how DNA can be purified by precipitation.

# Describe how DNA can be purified by precipitation.

Add ethanol & a salt to aqueous solution.

Nucleic acids precipitate out of solution.

Centrifuge to obtain pellet of nucleic acid.

Wash pellet with ethanol & centrifuge again.

# Describe the structure of DNA.

# Describe the structure of DNA.

Double-stranded polymer of nucleotides twists to form a **double helix**.

**H-bonds** form between **complementary base pairs** (AT & GC) on strands that run antiparallel

# Name the complementary base pairs in DNA and RNA.

# Name the complementary base pairs in DNA and RNA.

| DNA: 2 H-bonds between adenine (**A**) + thymine (**T**) | RNA: 2 H-bonds between adenine (**A**) + uracil (**U**) |
|---|---|

Both have 3 H-bonds between guanine (**G**) + cytosine (**C**)

# What are Chargaff's rules?

# What are Chargaff's rules?

Evidence for complementary base pairing in DNA. A & T / G & C occur in a 1:1 ratio. Sequencing one DNA strand therefore allows scientists to deduce the sequence of the complementary strand.

Composition of DNA varies between species.

# Why is DNA replication described as semi-conservative?

# Why is DNA replication described as semi-conservative?

Strands from original DNA molecule act as templates.

New DNA molecule contains 1 old strand & 1 new strand (specific base pairing enables genetic material to be conserved accurately).

# Explain the role of DNA helicase in semi-conservative replication.

Explain the role of DNA helicase in semi-conservative replication.

Breaks H-bonds between base pairs to form 2 single strands, each of which can act as a template.

# How is a new strand formed during semi-conservative replication?

# How is a new strand formed during semi-conservative replication?

1. Free activated DNA nucleotides attach to exposed bases by complementary base pairing.
2. **DNA polymerase** joins adjacent nucleotides on new strand in a 5' → 3' direction via condensation reactions to form phosphodiester bonds.
3. H-bonds reform.

# Outline the features of the genetic code.

# Outline the features of the genetic code.

- **non-overlapping**: each triplet is only read once
- **degenerate**: more than one triplet codes for the same amino acid (64 possible triplets for 20 amino acids)
- **universal**: same bases and sequences used by all species

# What is a mutation?

# What is a mutation?

A random alteration to the DNA base sequence. Mutations often arise spontaneously during DNA replication.

# How do genes determine the structure of proteins?

# How do genes determine the structure of proteins?

DNA base triplets code for amino acids. Triplet sequence determines amino acid sequence.

Protein primary structure determines where bonds form when folding into tertiary structure e.g. to determine shape of enzyme active site.

# Name the 3 main types of RNA in cells.

Name the 3 main types of RNA in cells.

- messenger RNA (mRNA)
- transfer RNA (tRNA)
- ribosomal RNA (rRNA)

# Describe the structure of mRNA.

# Describe the structure of mRNA.

- 2000 nucleotides (shorter than DNA)
- contains uracil instead of thymine
- single helix
- unstable

# Describe the structure of tRNA.

# Describe the structure of tRNA.

- single strand of about 80 nucleotides
- folded into clover shape (some paired bases)
- anticodon on one end, amino acid binding site on the other

a) anticodon binds to complementary mRNA codon

b) amino acid corresponds to anticodon

# What do transcription and translation produce and where do they occur?

# What do transcription and translation produce and where do they occur?

**Transcription** produces mRNA, occurs in nucleus

**Translation** produces proteins, occurs in the cytoplasm on ribosomes (made of protein + rRNA)

# Outline the process of transcription.

# Outline the process of transcription.

1. RNA polymerase binds to promoter region on a gene.
2. Section of DNA uncoils into 2 strands with exposed bases. Antisense strand acts as template.
3. Free nucleotides are attracted to their complementary bases.
4. RNA polymerase joins adjacent nucleotides to form phosphodiester bonds.

# What happens after a strand of mRNA is transcribed?

# What happens after a strand of mRNA is transcribed?

- RNA polymerase detaches at terminator region
- H-bonds reform & DNA rewinds
- splicing removes introns from pre-mRNA in eukaryotic cells
- mRNA moves out of nucleus via nuclear pore & attaches to ribosome

# Outline the process of translation.

# Outline the process of translation.

1. Ribosome moves along mRNA until ‘start’ codon reached.
2. tRNA anticodon attaches to complementary bases on mRNA via hydrogen bonding.
3. Condensation reactions between amino acids on tRNA form peptide bonds. Requires energy from ATP hydrolysis.
4. Process continues to form polypeptide chain until ‘stop’ codon is reached.