CAIE Biology A-level

Topic 6: Nucleic Acids and Protein Synthesis

Flashcards

Draw the structure of a nucleotide.

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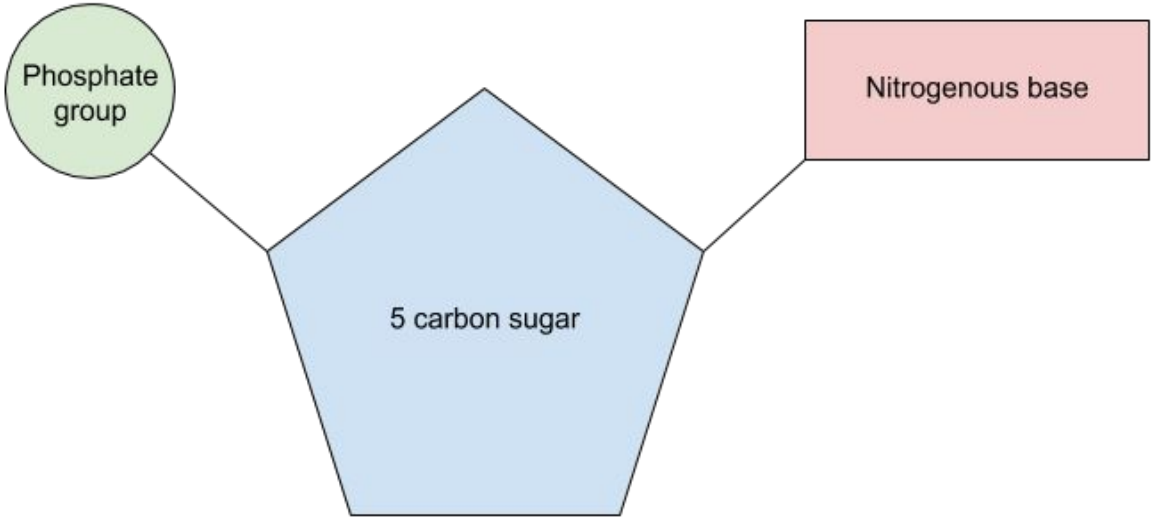

Name the pentose sugars in DNA and RNA.

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- **Deoxyribose** in DNA
- **Ribose** in RNA

Describe the structure of DNA.

Describe the structure of DNA.

- **Double-stranded** polymer of nucleotides twisted to form a double helix
- Nucleotides joined by **phosphodiester** bonds
- Hydrogen bonds form between **complementary base pairs**, A and T, C and G
- **Antiparallel** strands

Name the purine bases and describe their structure.

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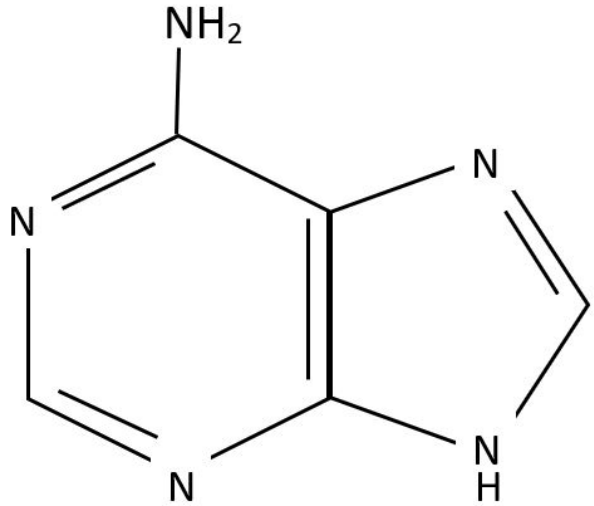
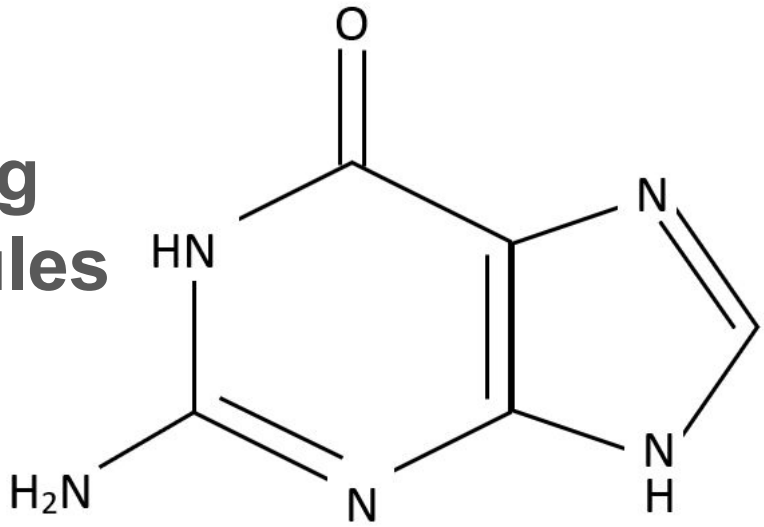
Adenine $C_5H_5N_5$



two-ring molecules

Guanine $C_5H_5N_5O$

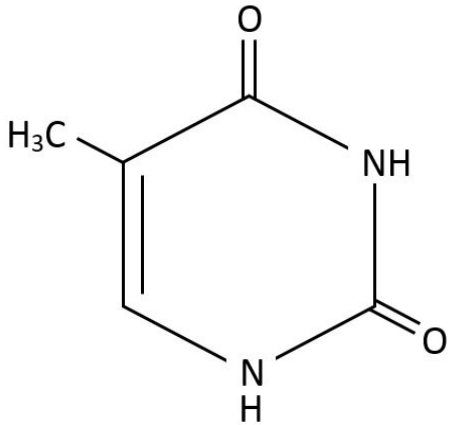


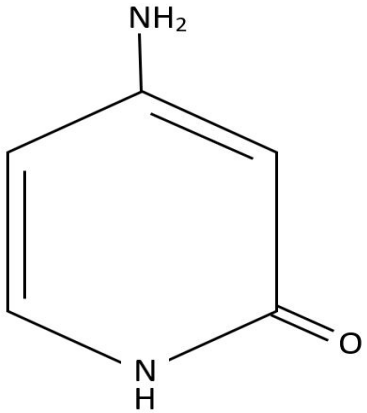
Name the pyrimidine bases and describe their structure.

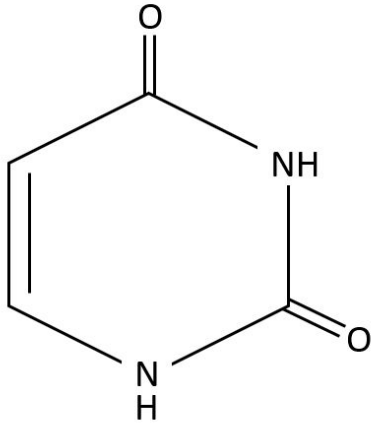
Name the pyrimidine bases and describe their structure.

one-ring molecules

Thymine $C_5H_6N_2O_2$ Cytosine $C_4H_5N_3O$ Uracil $C_4H_4N_2O_2$







What is complementary base pairing?

What is complementary base pairing?

- Describes how hydrogen bonds form between complementary purine and pyrimidine bases
- **Two bonds** form between **A** and **T** (or **U**)
- **Three bonds** form between **G** and **C**

Why is DNA replication described as semiconservative?

Why is DNA replication described as semiconservative?

- Strands from original DNA molecule act as templates
- New DNA molecule contains **1 old strand** and **1 new strand** (**specific base pairing** enables genetic material to be **conserved** accurately)

How is a new strand formed during semiconservative replication?

How is a new strand formed during semiconservative replication?

1. Free nucleotides from nuclear sap attach to exposed bases via 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. Hydrogen bonds form between complementary base pairs

Outline the role of DNA ligase in DNA replication.

Outline the role of DNA ligase in DNA replication.

As DNA replicates in an antiparallel fashion, the leading strand (5’ 3’) is replicated continuously whereas the lagging end (3’ 5’) is replicated discontinuously.

Short nucleotide sequences (**Okazaki fragments**) are formed. DNA ligase catalyses the formation of **phosphodiester bonds** between Okazaki fragments.

Describe the structure of RNA.

Describe the structure of RNA.

- **Single-stranded** polymer of nucleotides
- Nucleotides joined by **phosphodiester** bonds
- Hydrogen bonds form between **complementary base pairs**, A and U, C and G

What is the function of mRNA?

What is the function of mRNA?

Carries genetic information from the nucleus to the ribosomes for protein synthesis.

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
- Sequence of amino acids determines protein's primary structure
- Protein primary structure determines where bonds form when folding into tertiary structure, e.g. determines shape of enzyme active site

What is a mutation?

What is a mutation?

A random alteration to the DNA base sequence, altering the order of coded amino acids. This may result in a change in protein structure. Mutations often arise spontaneously during DNA replication.

State the three types of gene mutation.

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- Substitution
- Insertion
- Deletion

What are the consequences of substitution mutations?

What are the consequences of substitution mutations?

- **Silent** mutation (no consequence) as DNA is degenerate
- Mutation may alter the amino acid coded for. This can alter the structure of the polypeptide causing it to no longer function - **missense** mutation
- Mutation may lead to the production of a stop codon. The length of the polypeptide chain is shorter - **nonsense** mutation

What are the consequences of insertion/ deletion mutations?

What are the consequences of insertion/ deletion mutations?

Produce a frameshift, altering each subsequent codon and rendering the protein non-functional.

Describe the structure of tRNA.

Describe the structure of tRNA.

- Single strand of 80 nucleotides
- Folded into clover shape (some paired bases)
- Anticodon on one end, amino acid binding site on the other
  - Anticodon binds to complementary mRNA codon
  - 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 in ribosomes (made of protein and rRNA).

Outline the process of transcription.

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1. **DNA helicase** unwinds section of DNA, breaking hydrogen bonds between the DNA strands. **Antisense** strand acts as a **template**.
2. **RNA polymerase** binds to promoter region on a gene
3. **Free RNA nucleotides** align next to their complementary bases
4. RNA polymerase joins adjacent RNA nucleotides, forming **phosphodiester bonds**
5. RNA polymerase reaches stop codon and detaches. mRNA complete.

Define the term exon.

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Regions of DNA or RNA that code for amino acid sequences.

Define the term intron.

Define the term intron.

Non-coding sequences of DNA found between exons.

What happens after a strand of mRNA is transcribed?

What happens after a strand of mRNA is transcribed?

- RNA polymerase detaches at terminator region
- Hydrogen bonds reform and DNA rewinds
- Splicing removes introns from pre-mRNA (primary transcript) in eukaryotic cells, leaving only exons
- mRNA moves out of nucleus via nuclear pore and attaches to ribosome

Outline the process of translation.

Outline the process of translation.

1. mRNA attaches to groove between subunits of ribosome
2. Ribosome moves along mRNA until ‘start’ codon reached
3. Amino acid-tRNA complex anticodon attaches to **complementary** mRNA codon via **hydrogen bonding**. Another complex binds
4. **Peptide bond** forms between adjacent amino acids in the complexes
5. Ribosome moves along one codon and release empty tRNA. Process continues to form polypeptide chain until ‘stop’ codon is reached.