

Week 17

A-Level Biology

Homework bundle for this week

本周作业合集

exercises.lol

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6. Nucleic acids and protein synthesis

Starter Quiz · 课前小测

A-Level Biology

Name: _____ Score: _____

- A single nucleotide is made of:
 - ☐ a phosphate, a 5-carbon sugar and a base
 - ☐ two sugars and a base
 - ☐ an amino acid and a phosphate
 - ☐ three bases
- DNA replication is "semi-conservative" because each new molecule has:
 - ☐ one original (old) strand and one newly made strand
 - ☐ two brand-new strands
 - ☐ two original strands
 - ☐ no original strands
- A gene is a sequence of DNA that codes for:
 - ☐ one polypeptide
 - ☐ one nucleotide
 - ☐ one sugar
 - ☐ the whole organism at once
- A gene mutation is:
 - ☐ a change in the base sequence of DNA
 - ☐ a change in the number of cells
 - ☐ a change in the cell membrane
 - ☐ a loss of all the DNA
- ATP releases energy for the cell when:
 - ☐ its last phosphate group is broken off
 - ☐ a base is added
 - ☐ it joins with DNA
 - ☐ its sugar changes to deoxyribose
- In semi-conservative replication, each new DNA molecule keeps one of the original strands.
 - ☐ True ☐ False

7. Free nucleotides line up against the exposed template bases by _____ base pairing.

8. A group of three mRNA bases that codes for one amino acid is called a _____.

9. A substitution can sometimes leave the amino acid unchanged.

☐ True ☐ False

10. In DNA, A always pairs with T, and C always pairs with _____.

6. Nucleic acids and protein synthesis

Answers · 答案

A-Level Biology

1. a phosphate, a 5-carbon sugar and a base

Every nucleotide has three parts: a phosphate group, a pentose sugar, and a nitrogen-containing base.

2. one original (old) strand and one newly made strand

Each daughter molecule conserves one parental strand and pairs it with one new strand.

3. one polypeptide

A gene is a length of DNA that codes for a single polypeptide.

4. a change in the base sequence of DNA

A gene mutation is a change to the sequence of bases in a DNA molecule.

5. its last phosphate group is broken off

ATP has three phosphates; breaking off the terminal phosphate releases energy.

6. True

That is exactly what "semi-conservative" means — one old strand is conserved in each copy.

7. complementary

Each template base attracts its complement (A–T, C–G), so the new strand is an exact partner.

8. codon

Three bases = one codon (triplet); the matching three bases on a tRNA are its anticodon.

9. True

Because the code is degenerate, the new triplet may still code for the same amino acid — no change.

10. G

Complementary base pairing: A–T (2 hydrogen bonds) and C–G (3 hydrogen bonds).

6.1 Structure of nucleic acids and replication of DNA

Name: _____ Class: _____ Date: _____ **Total: 27 marks****KEY WORDS** base 碱基 • strand 链 • nucleotide 核苷酸 • adenine 腺嘌呤 • replication 复制

Objective

Build the skills to answer exam questions on the **structure of nucleic acids** and **replication of DNA** — **nucleotides** 核苷酸, **complementary base pairing** 碱基互补配对, and **semi-conservative replication** 半保留复制.

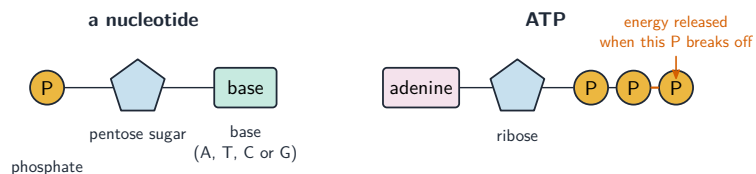
You must be able to:

- describe a nucleotide (including ATP) and classify bases as **purines** 嘌呤 or **pyrimidines** 嘧啶
- describe the DNA double helix (base pairing, hydrogen bonds, antiparallel strands, phosphodiester bonds)
- use base-pairing ratios in calculations and describe semi-conservative replication

1 Worked examples

■ Nucleotides and bases

A **nucleotide** is a **phosphate** 磷酸 + a 5-carbon sugar + a nitrogen **base** 碱基. **ATP** is a nucleotide with adenine, ribose and **three** phosphates.

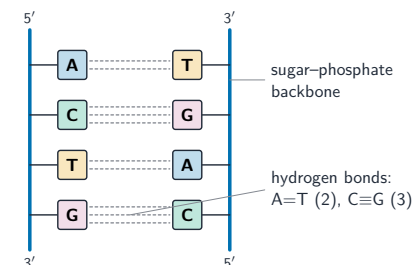


A nucleotide; ATP has three phosphates

Bases come in two groups: **purines** (double ring) = adenine, guanine; **pyrimidines** (single ring) = cytosine, thymine, uracil.

■ DNA structure and base pairing

Two **antiparallel** 反平行 strands (one 5'→3', one 3'→5') twist into a **double helix** 双螺旋. Backbones are sugar-phosphate joined by **phosphodiester bonds** 磷酸二酯键. The strands are held by base pairs: **A=T** (2 hydrogen bonds), **C≡G** (3 hydrogen bonds).



the two strands run in opposite directions (antiparallel)

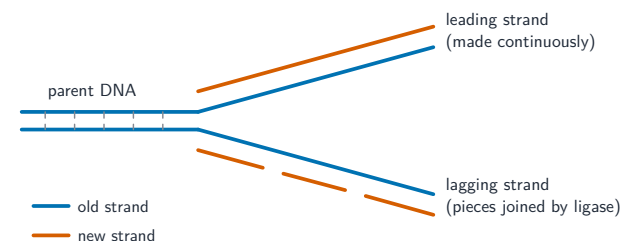
A pairs with T (2 H-bonds), C with G (3); the strands are antiparallel

■ Base-ratio calculations

Because A pairs with T and C pairs with G, **%A = %T** and **%C = %G**, and all four add to 100%. So if 28% of bases are adenine: **%T = 28**, so **%A + %T = 56**, leaving **%C + %G = 44**, so **%G = 22%**.

■ Semi-conservative replication

In the S phase the helix unwinds; each old strand is a template; **DNA polymerase** 聚合酶 adds nucleotides only 5'→3'. So the **leading strand** is made continuously and the **lagging strand** in pieces joined by **DNA ligase** 连接酶. Each new molecule keeps one old and one new strand.



each new molecule = one old strand + one new strand (semi-conservative)

Semi-conservative: each new molecule keeps one old strand and one new strand

2 Practice

2.1 State the three parts of a nucleotide. [3]

2.2 State the number of hydrogen bonds between (a) A and T, and (b) C and G. [2]

3 Exam-style questions

3.1 Which statement about the two strands of a DNA molecule is correct? [1]

- A they are identical in base sequence
- B they run in the same direction
- C they are antiparallel and complementary
- D they are joined by phosphodiester bonds between bases

3.2 In a sample of DNA, 20% of the bases are cytosine. What percentage are adenine? [1]

- A 20%
- B 30%
- C 40%
- D 60%

3.3 DNA replication is described as semi-conservative.

(a) Explain what “semi-conservative” means. [2]

(b) Explain why one new strand (the lagging strand) is made in short pieces. [2]

3.4 A DNA molecule contains 1200 bases, of which 360 are guanine. Calculate the number of adenine bases. Show your working. [3]

3.5 A short length of one DNA strand has the base sequence **T A C G G A T C A A T**.

(a) Write the sequence of the complementary strand, and state the rule you used. [2]

(b) Describe the structure of a DNA nucleotide, and explain how nucleotides are joined into a strand. [4]

(c) Explain what is meant by *semi-conservative* replication, and describe the roles of DNA helicase and DNA polymerase. [4]

(d) In one organism 22% of the bases in its DNA are adenine. Calculate the percentage that is guanine, and explain your reasoning. [3]

Solutions

2.1 a phosphate group; a (5-carbon/pentose) sugar; a nitrogen-containing base.

2.2 (a) 2; (b) 3.

3.1 C. The strands are antiparallel and complementary; bases pair by hydrogen bonds, and phosphodiester bonds are within each backbone.

3.2 B. $\%C = \%G = 20$, so $C+G = 40$; $A+T = 60$, so $\%A = 30$.

3.3 (a) each new DNA molecule contains one original (old) strand and one newly made strand.

(b) DNA polymerase can only add nucleotides in the $5' \rightarrow 3'$ direction, so on the strand running the “wrong” way it must work in short pieces away from the fork, later joined by ligase.

3.4 guanine = 360, so cytosine = 360; $C+G = 720$, so $A+T = 1200 - 720 = 480$; adenine = $480/2 = 240$.

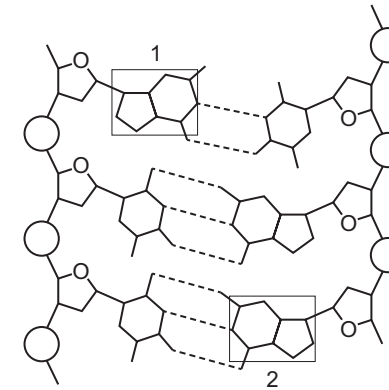
3.5 (a) **A T G C C T A G T T A**; complementary base pairing — adenine always pairs with thymine and cytosine with guanine.

(b) A nucleotide is a deoxyribose sugar, a phosphate group and one of four nitrogenous bases. Nucleotides join by **condensation** between the phosphate on carbon 5 of one sugar and the hydroxyl on carbon 3 of the next, giving a sugar–phosphate backbone linked by phosphodiester bonds.

(c) Each new double helix contains **one** original strand and one newly made strand. DNA helicase unwinds the helix and breaks the hydrogen bonds between the base pairs, separating the two strands; free nucleotides then pair with the exposed bases; DNA polymerase joins those nucleotides together by forming the phosphodiester bonds of the new backbone.

(d) Adenine pairs only with thymine, so thymine is also 22%; $A + T = 44\%$, leaving 56% for $C + G$; C and G are equal, so guanine is 28%.

23 The diagram shows a section of DNA. Two of the bases in this section are labelled 1 and 2.



Which row correctly identifies the bases 1 and 2?

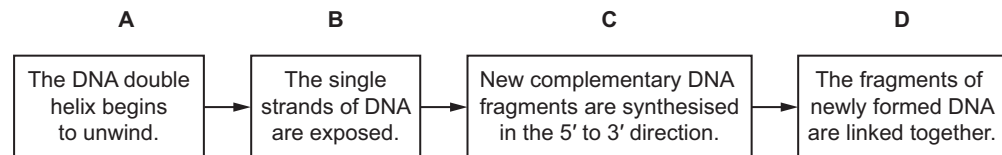
	base 1	base 2
A	purine	adenine
B	purine	guanine
C	pyrimidine	adenine
D	pyrimidine	guanine

24 Which row describes the role of the enzymes DNA polymerase and DNA ligase?

	DNA polymerase	DNA ligase
A	adds nucleotides in a $5'$ to $3'$ direction	joins sections of DNA together on the lagging strand
B	adds nucleotides in a $3'$ to $5'$ direction	joins sections of DNA together on the leading strand
C	adds nucleotides in a $3'$ to $5'$ direction	joins sections of DNA together on the lagging strand
D	adds nucleotides in a $5'$ to $3'$ direction	joins sections of DNA together on the leading strand

24 The flow diagram shows some of the stages in the replication of a lagging strand of DNA.

Which stage of DNA replication uses the enzyme DNA ligase?



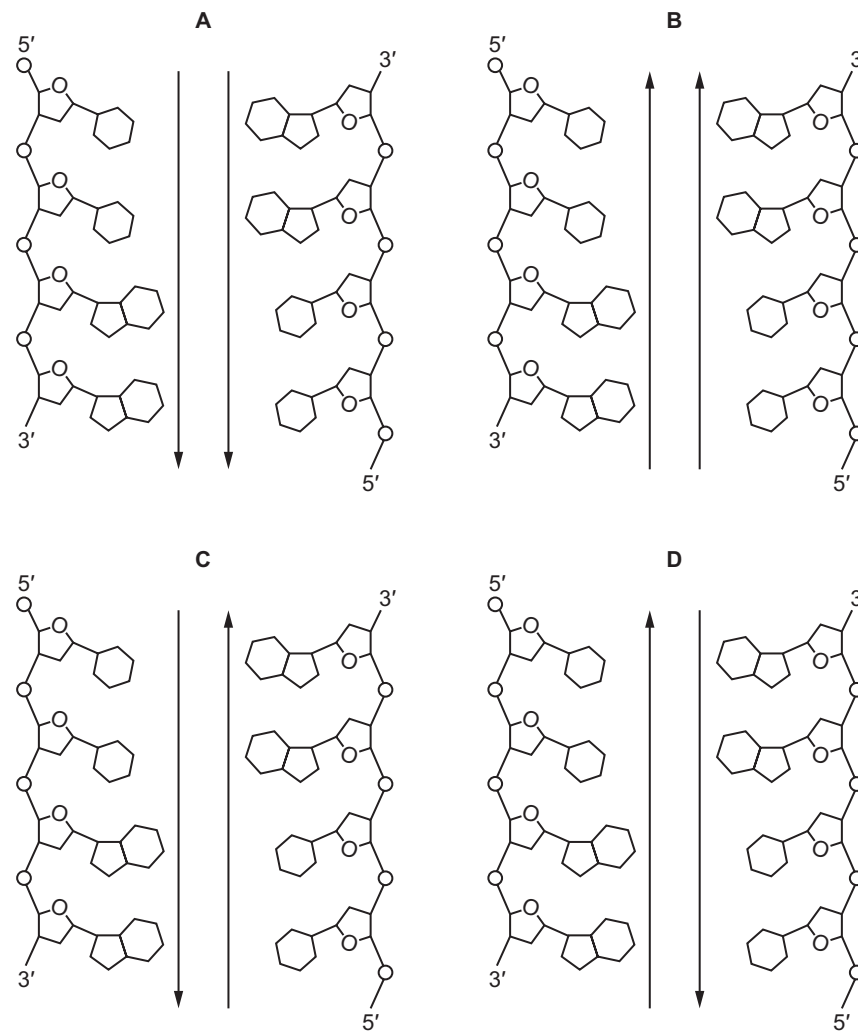
25 Which statements about complementary base pairing are correct?

- 1 It occurs during translation.
- 2 Purines and pyrimidines are the same size.
- 3 The base pairs are of equal length.
- 4 Uracil forms three hydrogen bonds with adenine.

A 1 and 2 **B** 1 and 3 **C** 2 and 3 **D** 3 and 4

22 During DNA replication, the two original strands of a DNA molecule separate.

Which diagram shows the direction in which DNA polymerase moves along each of the original strands during DNA replication?



- 4 (a) Fig. 4.1 shows a phosphorylated nucleotide which is one of the monomers that is used to synthesise DNA during replication.

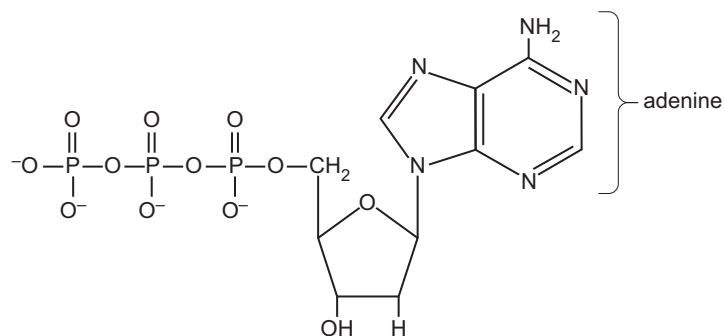


Fig. 4.1

- (i) State the meaning of monomers of DNA.
..... [1]
- (ii) State how ATP differs in structure from the phosphorylated nucleotide shown in Fig. 4.1.
.....
.....
..... [1]
- (iii) State the process occurring in all cells that results in the production of ATP.
..... [1]

- (b) Fig. 4.2 shows a short length of a DNA molecule. One of the strands of the DNA molecule is labelled Y.

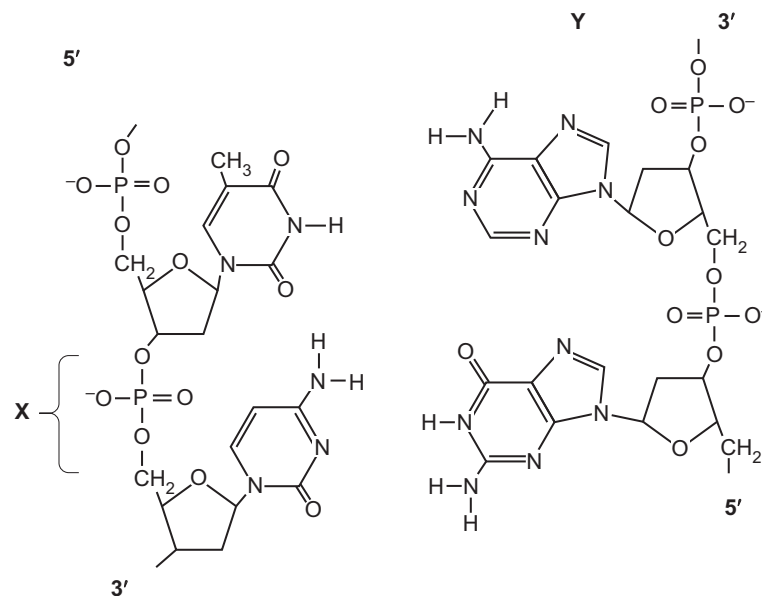


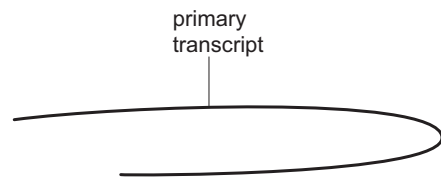
Fig. 4.2

- (i) Complete Fig. 4.2 by drawing dotted lines to represent all the hydrogen bonds between the two strands of the DNA molecule.
..... [2]
- (ii) State the name of the bond X.
..... [1]

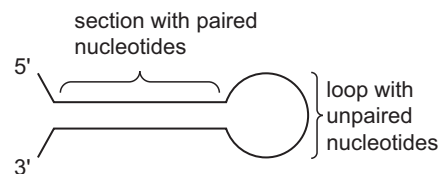
[Total: 6]

- 3 Small interfering RNA (siRNA) is a short length of double-stranded RNA (dsRNA), approximately 21 to 25 nucleotides long. siRNA helps to regulate protein synthesis in cells.
- (a) Fig. 3.1 is an outline summary of one way in which a primary transcript can be processed to produce a molecule of siRNA. The transcript does **not** code for a sequence of amino acids.

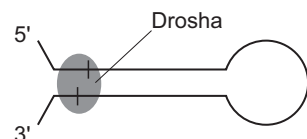
step 1: a primary transcript is synthesised from one strand of DNA



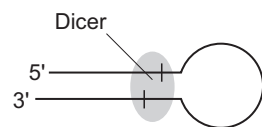
step 2: the primary transcript loops and a section of the RNA becomes double stranded



step 3: the enzyme Drosha attaches and cleaves (cuts) the RNA to produce a shorter length



step 4: in the cytoplasm, the enzyme Dicer attaches and cleaves the RNA



step 5: siRNA, which is double stranded and has 2 unpaired nucleotides at each 3' end, is produced

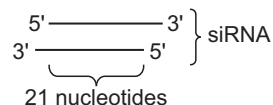


Fig. 3.1

- (i) In **step 2** in Fig. 3.1, the single-stranded primary transcript loops and forms a section where dsRNA is present.

Explain how it is possible for the double-stranded section of RNA to be held together in **step 2** and maintained this way in **steps 3, 4 and 5**.

.....

.....

.....

.....

..... [2]

- (ii) After **step 3**, the shorter dsRNA produced by the action of Drosha is transported to the cytoplasm, where it is cleaved further by Dicer to produce ds siRNA.

Suggest why two different enzymes, Drosha and Dicer, are needed to cut dsRNA into shorter lengths.

.....

.....

.....

.....

..... [2]

- (b) From 2018, siRNA has been used as a therapeutic drug to treat a number of diseases.

The presence of molecules of siRNA in the cytoplasm can result in the cleavage of messenger RNA (mRNA) molecules coding for a protein involved in the disease. This prevents the synthesis of the protein.

Describe the differences between a molecule of mRNA and a molecule of siRNA, such as the siRNA shown in **step 5** in Fig. 3.1.

.....

.....

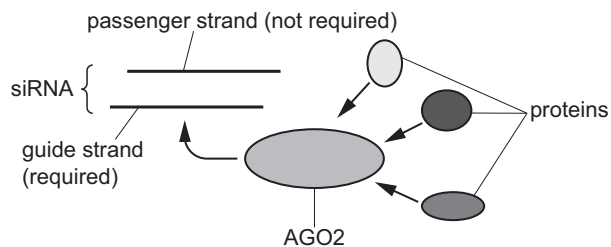
.....

.....

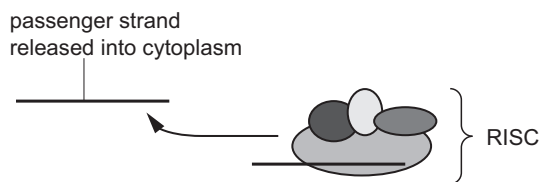
..... [2]

(c) Fig. 3.2 summarises how mRNA coding for a protein involved in disease can be targeted and cleaved by siRNA.

presence of siRNA activates a protein, AGO2, which binds siRNA and other proteins to form a complex known as RISC



passenger strand is separated from RISC



RISC uses guide strand to target and bind mRNA for cleavage

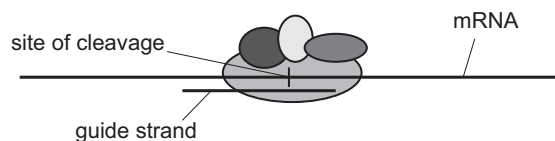


Fig. 3.2

(i) With reference to Fig. 3.2, state why the passenger strand needs to be separated and released from the RISC.

.....

 [1]

(ii) The aim of siRNA therapy is to prevent or decrease the synthesis of a protein involved in the disease being treated.

A target mRNA molecule can be cleaved in a different location by a RISC with a different siRNA.

Suggest how cleaving mRNA in different locations will have different effects on protein synthesis **and** explain how these different effects can result in a lack of functioning protein.

.....

 [3]

[Total: 10]

6.2 Protein synthesis

Name: _____ Class: _____ Date: _____

Total: 17 marks

KEY WORDS gene 基因 • triplet 三联体 • mutation 突变 • intron 内含子 • translation 翻译

Objective

Build the skills to answer exam questions on **protein synthesis** — the **genetic code** 遗传密码, **transcription** 转录 and **translation** 翻译, splicing, and **gene mutations** 基因突变.

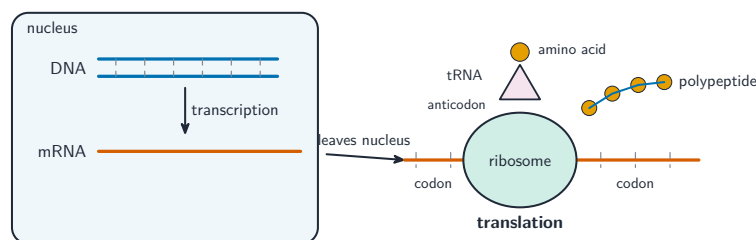
You must be able to:

- describe the universal triplet code and the roles of RNA polymerase, mRNA, codons, tRNA, anticodons and ribosomes
- work out an mRNA sequence and amino acids from a DNA template
- explain splicing (introns/exons) and the effects of substitution, deletion and insertion mutations

1 Worked examples

■ The genetic code and protein synthesis

A **gene** 基因 is a DNA sequence coding for one **polypeptide** 多肽. The code is read in **triplets** 三联体 (three bases): each codes one amino acid or a start/stop signal. It is **universal**.



Transcription (nucleus) → mRNA → translation (ribosome) → polypeptide

- transcription** — RNA polymerase copies the DNA **template strand** 模板链 into mRNA (uracil pairs with adenine).
- translation** — at the **ribosome** 核糖体, mRNA is read in **codons** 密码子;

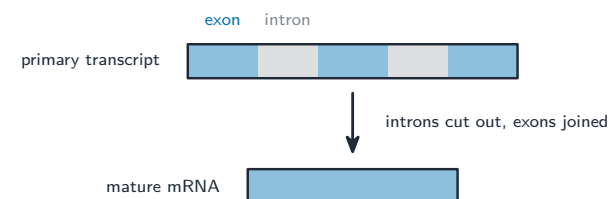
tRNA 转运 RNA brings amino acids whose **anticodon** 反密码子 pairs with the codon; amino acids join by peptide bonds.

■ Reading the code from a DNA template

To find the amino acids, copy the template into mRNA (A→U, T→A, C→G, G→C), then read the mRNA codons. Example: DNA template TAC → mRNA codon AUG (the start codon, methionine); the tRNA anticodon is UAC.

■ Splicing

In eukaryotes the **primary transcript** 初级转录本 has coding **exons** 外显子 and non-coding **introns** 内含子. The introns are removed and exons joined to make the finished mRNA.



Splicing removes introns and joins exons

■ Mutations

original	A	T	G	C	A	T	T	A	C
substitution	A	A	G	C	A	T	T	A	C
deletion	A	T	G	A	T	T	A	C	
insertion	A	T	G	G	C	A	T	T	A

red = changed base; shaded = shifted by a frameshift (deletion or insertion)

A substitution changes one triplet; a deletion or insertion shifts every later triplet (a frameshift)

- substitution** 替换 — one base swapped; changes at most one amino acid (sometimes none).
- deletion** 缺失 / **insertion** 插入 — shifts how every later triplet is read (a **frameshift**), usually changing many amino acids.

2 Practice

2.1 Name the molecule that (a) carries the code from the nucleus to the ribosome, and (b) brings amino acids to the ribosome. [2]

2.2 Complete the table for this DNA template strand. [3]

DNA template	mRNA codon	tRNA anticodon
T A C		
C G A		

3 Exam-style questions

3.1 What is a codon? [1]

- **A** a triplet of DNA bases on the template strand
- **B** a triplet of mRNA bases coding for one amino acid
- **C** a tRNA molecule
- **D** an enzyme that builds mRNA

3.2 Which type of mutation is most likely to change **every** amino acid after the point of mutation? [1]

- **A** a substitution
- **B** a deletion of one base
- **C** no mutation changes later amino acids
- **D** a substitution at the start codon

3.3 (a) Describe what happens during transcription. [3]

(b) Explain the roles of tRNA and the ribosome during translation. [3]

3.4 (a) Explain why a substitution mutation sometimes has no effect on the polypeptide. [2]

(b) Explain why removing introns is necessary before translation. [2]

Solutions

2.1 (a) messenger RNA (mRNA); (b) transfer RNA (tRNA).

2.2 TAC → mRNA AUG → anticodon UAC; CGA → mRNA GCU → anticodon CGA.

3.1 B. A codon is a triplet of mRNA bases coding for one amino acid (or stop).

3.2 B. A deletion causes a frameshift, changing every later triplet.

3.3 (a) RNA polymerase binds and the DNA unwinds at the gene; free RNA nucleotides pair with the template strand (A with U); they are joined into mRNA, which leaves the nucleus.

(b) each tRNA brings a specific amino acid and its anticodon pairs with the matching mRNA codon; the ribosome moves along the mRNA and joins the amino acids by peptide bonds in order.

3.4 (a) most amino acids are coded by more than one triplet, so the changed triplet may still code for the same amino acid.

(b) introns are non-coding; if left in they would be translated into wrong/extra amino acids, giving a faulty polypeptide.

22 The gene that codes for protein R is 130 kb long.

Protein R is 220 kDa in mass.

The typical mass of an amino acid is 110 Da.

(1000 base pairs = 1 kb, 1000 Da = 1 kDa)

Which row is correct?

	approximate length of introns in this gene / base pairs	approximate length of mRNA for this gene / base pairs
A	6000	6000
B	6000	130 000
C	124 000	6000
D	124 000	130 000

25 The table shows some of the DNA triplet codes for some amino acids.

amino acid	DNA triplet code	amino acid	DNA triplet code
arginine	GCA	glycine	CCA
arginine	GCC	glycine	CCG
arginine	GCG	glycine	CCT
asparagine	TTA	lysine	TTC
asparagine	TTG	lysine	TTT
cysteine	ACA	proline	GGA
cysteine	ACG	proline	GGC
STOP	ATC	valine	CAC

The base sequence on the template DNA strand coding for part of a polypeptide is shown.

CCA TTC ACG GCG TTA GCA

Two mutations occur in this sequence during DNA replication.

Which mutated DNA would result in two different amino acids?

A CCA ATC ACG GCG TTG GCA

B CCA TTC ACA GCA TTA GCA

C CCA TTC ACG CCG TTA GCC

D CCA TTC ACG GCG TTC GGA

25 In a gene, the 20 common amino acids are each coded for by three bases in adjacent nucleotides.

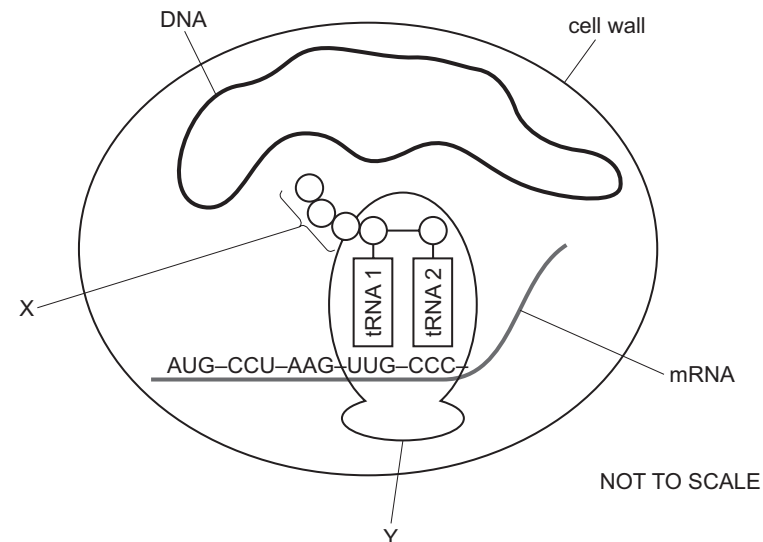
Why is there a difference between the number of amino acids and the number of possible triplet codes?

- A** 44 triplets have **no** functions.
- B** Some amino acids are coded for by more than one triplet.
- C** Some triplets have unknown functions.
- D** There are 44 'start' and 'stop' triplets.

26 How is a primary transcript modified to form mRNA?

- A** It becomes longer as exons are joined together.
- B** It becomes shorter as exons are removed.
- C** It becomes longer as introns are joined together.
- D** It becomes shorter as introns are removed.

27 The diagram shows protein synthesis in a prokaryote.



Which row is correct for molecule X, structure Y and the anticodon of tRNA 1?

	molecule X	structure Y	anticodon of tRNA 1
A	amino acid	80S ribosome	AAC
B	polypeptide	80S ribosome	UUG
C	polypeptide	70S ribosome	AAC
D	protein	70S ribosome	UUG

26 Which statement is correct for protein synthesis?

- A** During translation, the strand of DNA used is the template strand.
- B** mRNA is formed when introns are removed from the primary transcript.
- C** The DNA primary transcript is modified by removing exons.
- D** tRNA has codons which attach to anticodons on the mRNA.

27 A mutation occurred in this original DNA nucleotide sequence.

CTAG AATCCTCTCCC

After the mutation occurred, the new DNA nucleotide sequence coded for the amino acids Asp, Leu, Gly and Glu.

The table shows the amino acids that are coded for by each DNA triplet.

		2nd base							
		A		G		T		C	
1st base	A	AAA	Phe	AGA	Ser	ATA	Tyr	ACA	Cys
		AAG	Phe	AGG	Ser	ATG	Tyr	ACG	Cys
		AAT	Leu	AGT	Ser	ATT	Stop	ACT	Stop
		AAC	Leu	AGC	Ser	ATC	Stop	ACC	Trp
	G	GAA	Leu	GGA	Pro	GTA	His	GCA	Arg
		GAG	Leu	GGG	Pro	GTG	His	GCG	Arg
		GAT	Leu	GGT	Pro	GTT	Gln	GCT	Arg
		GAC	Leu	GGC	Pro	GTC	Gln	GCC	Arg
	T	TAA	Ile	TGA	Thr	TTA	Asn	TCA	Ser
		TAG	Ile	TGG	Thr	TTG	Asn	TCG	Ser
		TAT	Ile	TGT	Thr	TTT	Lys	TCT	Arg
		TAC	Met	TGC	Thr	TTC	Lys	TCC	Arg
	C	CAA	Val	CGA	Ala	CTA	Asp	CCA	Gly
		CAG	Val	CGG	Ala	CTG	Asp	CCG	Gly
		CAT	Val	CGT	Ala	CTT	Glu	CCT	Gly
		CAC	Val	CGC	Ala	CTC	Glu	CCC	Gly

Which type of gene mutation occurred in the DNA nucleotide sequence?

- A deletion of one nucleotide
- B insertion of one nucleotide
- C insertion of two nucleotides
- D substitution of one nucleotide

23 Which statements about anticodons are correct?

- 1 The base sequence of an anticodon will always be the same as that of the corresponding triplet on the transcribed DNA strand.
- 2 There are 20 naturally occurring amino acids, so therefore there are only 20 anticodons as each anticodon is specific for only one amino acid.
- 3 The formation of hydrogen bonds between the bases of the anticodon with those of the complementary mRNA codon must occur before the new peptide bond can form.

- A 1, 2 and 3
- B 1 and 2 only
- C 3 only
- D 3 only

24 Part of a DNA molecule is transcribed to form an RNA molecule that is then modified.

Which row describes the RNA molecule before and after modification?

	before modification	after modification
A	contains exons and introns	contains exons only
B	contains exons and introns	contains introns only
C	contains exons only	contains introns only
D	contains introns only	contains exons only

- 3 The gene *LCT* codes for the enzyme lactase. In babies, lactase synthesis is necessary for digesting lactose, the sugar found in milk.

Another gene, *MCM6*, has introns that have a regulatory role in the expression of gene *LCT*. Gene *MCM6* codes for a protein that has **no** involvement in lactase synthesis.

As children get older, the *MCM6* introns are responsible for a decrease in lactase synthesis. This decrease in lactase synthesis is known as lactase non-persistence.

- (a) *LCT* and *MCM6* are located on the same chromosome in humans.

Suggest differences between gene *LCT* and gene *MCM6*, **other than** their locations in different positions on the same chromosome.

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..... [3]

- (b) With reference to the process of lactase synthesis, explain the relationship between:

- a transcribed strand and a primary transcript
- a primary transcript and messenger RNA (mRNA).

.....

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.....

.....

..... [2]

- (c) A mutation in a regulatory intron of *MCM6* allows lactase synthesis to continue. This is known as lactase persistence. In this mutation, the number of nucleotides in the intron remains the same, but one of the nucleotides is different to the original nucleotide.

State the type of mutation that is the cause of lactase persistence.

.....

..... [1]

- (d) Fig. 3.1 summarises the reaction catalysed by lactase.

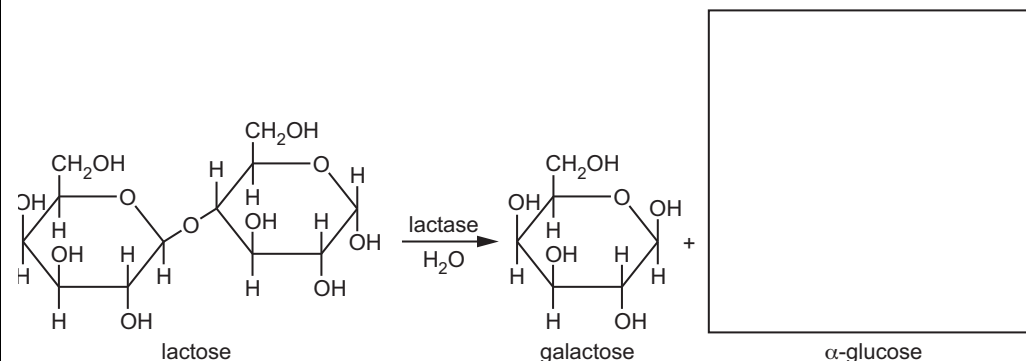


Fig. 3.1

Draw the ring structure of α -glucose in the box provided to complete Fig. 3.1. [1]

- (e) Some people with lactase non-persistence may be lactose intolerant. They may have symptoms, such as abdominal pain, if their diet contains lactose.

- (i) Lactase supplements (tablets) can be taken before milk or milk-based products are consumed to avoid symptoms of lactose intolerance.

A student compared the activity of two different concentrations of a lactase supplement using an artificial substrate, ONPG, instead of lactose.

A solution of ONPG is colourless, but the hydrolysis of ONPG by lactase releases a coloured product.

The student planned to follow the progress of the reaction for each concentration of lactase using a colorimeter.

Explain why the student chose to use a colorimeter to follow the progress of the reaction for each concentration of lactase.

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..... [2]

- Scientists carried out an investigation to compare the activity of lactase immobilised in very small magnetic beads (magnetic microspheres) with free lactase, at different temperatures and at different pH values.

Fig. 3.3 shows the activity of immobilised lactase and the activity of free lactase at 8 different pH values.



With reference to Fig. 3.2 and Fig. 3.3, explain why the results indicate that there are **other** advantages in using immobilised lactase instead of free lactase to produce lactose-free products.

..... [4]

[Total: 13]