

# SMART EXAM RESOURCES

## TOPIC QUESTIONS: NUCLEIC ACID AND PROTEIN SYNTHESIS

### SUB-TOPIC: COMPLEMENTARY BASE PAIRING SET-1-QP-MS

1

- (a) Table 2.1 shows two messenger RNA (mRNA) codons. Fill in the complementary transfer RNA (tRNA) anticodons in the spaces provided.

Table 2.1

mRNA codons	GCG	ACA
complementary tRNA anticodons		

[2]

- (b) Calculate the minimum number of DNA nucleotides necessary to code for a polypeptide with 238 amino acids.

Show your working.

answer ..... nucleotides [2]

**MARK SCHEME:**

- (a)** (GCG) CGC ;  
(ACA) UGU ; [2]
- (b)** 714 ;; **A** 717 / 720  
*if, no / incorrect, answer given, award one mark for correct working* [2]

2 As a result of transcription and translation, a polypeptide chain is produced. Proteins with quaternary structure contain two or more polypeptide chains.

An antibody molecule and a haemoglobin molecule both show quaternary structure.

(a) Table 6.1 shows some features of an antibody molecule and a haemoglobin molecule.

Complete Table 6.1 to produce a summary of the features of the two molecules.

**Table 6.1**

feature	antibody	haemoglobin
fibrous or globular		
number and names of polypeptide chains	two heavy and two light chains	
type of bond holding polypeptide chains together		ionic






[3]

(b) The base sequence shown in Fig. 6.1 is a short section of a longer length of DNA that is transcribed to produce mRNA. When translated, this short section produces the amino acid sequence threonine (Thr), proline (Pro), cysteine (Cys).

Fill in the two **unshaded** boxes in Fig. 6.1 to show:

- the mRNA codon for Cys
- the tRNA anticodon for Thr.

You do **not** need to give the codon and anticodon sequences in the shaded boxes.

DNA strand transcribed	TGT	GGC	ACA
mRNA strand produced			
tRNA anticodon sequence		GGC	
amino acid sequence	Thr	Pro	Cys

**Fig. 6.1**

[2]

[Total: 5]

## MARK SCHEME:

(a)	row 1 globular + globular ; row 2 2, alpha / $\alpha$ , globin, and 2, beta / $\beta$ , globin (chains); A 2 alpha and 2 beta chains row 3 disulfide (bridges / bonds) ; covalent is neutral	3
(b)	mRNA strand produced UGU ; tRNA anticodon sequence UGU ;	2
	<b>Total:</b>	<b>5</b>

### 3

Table 5.1 shows the triplets of bases on the template polynucleotide of DNA for some amino acids.

**Table 5.1**

amino acid		DNA triplets
glutamic acid	(glu)	CTT CTC
histidine	(his)	GTA GTG
leucine	(leu)	GAA GAG GAT GAC
proline	(pro)	GGA GGG GGT GGC
threonine	(thr)	TGA TGG TGT TGC
valine	(val)	CAA CAG CAT CAC

Fig. 5.1 shows the base sequences in DNA and mRNA for the first seven amino acids of the  $\beta$  chain of haemoglobin.

DNA	CAC	.....	GAC	TGA	GGA	CTC	CTC
mRNA	GUG	CAC	CUG	.....	CCU	GAG	GAG
$\beta$ chain	val	his	.....	thr	pro	glu	glu

**Fig. 5.1**

(a) (i) Use Table 5.1 to complete Fig. 5.1. [3]

(ii) State the term used to describe the sequence of amino acids in a polypeptide.

.....[1]

**MARK SCHEME:**

**(a) (i)** GTG ;

ACU ;

leu ;

[3]

**(ii)** primary structure ;

[1]

**4** Lysozyme is an enzyme found in many places within the human body. It consists of a single polypeptide folded into a complex shape.

Fig. 3.1 shows a ribbon model of lysozyme.



**Fig. 3.1**

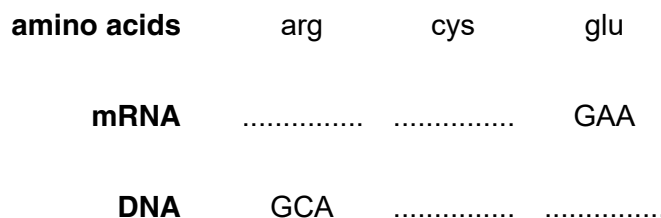
Table 3.1 shows some mRNA codons and the amino acids for which they code.

**Table 3.1**

amino acid	abbreviation	mRNA codons					
glutamic acid	glu	GAA	GAG	–	–	–	–
phenylalanine	phe	UUU	UUC	–	–	–	–
lysine	lys	AAA	AAG	–	–	–	–
proline	pro	CCA	CCC	CCG	CCU	–	–
threonine	thr	ACA	ACC	ACG	ACU	–	–
valine	val	GUA	GUC	GUG	GUU	–	–
cysteine	cys	UGC	UGU	–	–	–	–
arginine	arg	CGC	CGA	CGU	CGG	AGA	AGG

Fig. 3.2 shows,

- the sequence of three amino acids in the human lysozyme polypeptide
- part of a possible sequence of nucleotide bases for the mRNA that codes for these amino acids
- one of the corresponding nucleotide bases in the DNA.



**Fig. 3.2**

- (i) Use the information in Table 3.1 to complete the nucleotide sequences for the mRNA and the DNA shown in Fig. 3.2. Write your answer on Fig. 3.2. [3]
- (ii) Explain why the human gene for lysozyme may have a different nucleotide sequence from the answer you have given in (c)(i).

.....

.....

.....

..... [2]



**MARK SCHEME:**

(i) mRNA CGU ; UGC / UGU GAA  
DNA GCA ACG / ACA CTT ; [3]

(ii) many / several / more than one, triplet for each amino acid ; **A** codon  
an e.g. from Table 3.1 ;  
degenerate code / description e.g. 64 possible triplets for 20 amino acids ; **A** codons  
AVP ; e.g. may be an intron in this region, different nucleotides at the beginning  
(signal sequence) [2 max]

5

Table 5.1 shows the triplets of bases on the template polynucleotide of DNA for some amino acids.

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amino acid		DNA triplets
glutamic acid	(glu)	CTT CTC
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leucine	(leu)	GAA GAG GAT GAC
proline	(pro)	GGA GGG GGT GGC
threonine	(thr)	TGA TGG TGT TGC
valine	(val)	CAA CAG CAT CAC

Fig. 5.1 shows the base sequences in DNA and mRNA for the first seven amino acids of the  $\beta$  chain of haemoglobin.

DNA	CAC	.....	GAC	TGA	GGA	CTC	CTC
mRNA	GUG	CAC	CUG	.....	CCU	GAG	GAG
$\beta$ chain	val	his	.....	thr	pro	glu	glu

**Fig. 5.1**

(a) (i) Use Table 5.1 to complete Fig. 5.1. [3]

(ii) State the term used to describe the sequence of amino acids in a polypeptide.

.....[1]

**MARK SCHEME:**

**(a) (i)** GTG ;

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