

第一大題 選擇題(1-20)，考生應作答於試卷首頁「選擇題作答區」(每題2分)

Please select the **best** answer.

1) Protein helping in opening of DNA double helix in front of replication fork is:

(A) DNA ligase	(B) DNA helicase
(C) DNA polymerase	(D) DNA topoisomerase

2) Which of the following mechanism of DNA polymerase helps in preventing error during DNA replication

(A) rechecking	(B) proof checking
(C) proof reading	(D) double checking

3) A mechanism that can cause a gene to move from one linkage group to another is:

(A) Crossing over	(B) Duplication
(C) Inversion	(D) Translocation

4) Which of the following protein involved in mismatch repair?

(A) MutS	(B) UvrB
(C) UDG	(D) photolyase

5) The distortion in DNA helix due to pyrimidine dimer formation is called as:

(A) link	(B) kink
(C) nick	(D) sink

6) DNA replicates during

(A) G1 phase	(B) G2 phase
(C) S phase	(D) M phase

7) If the codon UAC on mRNA changes into UAG as a result of a base substitution in DNA, it will result in

(A) Silent mutation	(B) Mis-sense mutation
(C) Nonsense mutation	(D) Frameshift mutation

8) Substitution of an adenine base by guanine in DNA is known as what mutation?

(A) Transition	(B) Transversion
(C) Transposition	(D) Transformation

9) A silent mutation is most likely to result from

(A) Substitution of the first base of a codon	(B) Substitution of the third base of a codon
(C) Conversion of a nonsense codon into a sense codon	(D) Conversion of a sense codon into a nonsense codon

10) Restriction enzymes are used in genetic engineering because they

(A) Can join DNA fragments at specific sequence	(B) Cut DNA at specific sequence
(C) Cut RNA at specific sequence	(D) Cut protein at specific sequence

11) Which of the following statements is (are) **true**?

- (i) Both prokaryotic and eukaryotic mRNAs use start and stop codons to signal the start and end of translation.
  - (ii) Both prokaryotic and eukaryotic mRNAs include ribosome-binding sites (RBSs) to recruit the ribosome to the start codon.
  - (iii) Both prokaryotic and eukaryotic mRNAs are polycistronic.
  - (iv) Polyribosome happens on both prokaryotic and eukaryotic mRNAs.
- (A) (i) and (ii)                      (B) (ii) and (iii)                      (C) (i) and (iv)  
 (D) (i), (ii) and (iv)              (E) (i), (ii), (iii), and (iv)

12) The sequence 5'-CCA-3' at the 3' terminus of every tRNA is

- (A) to recognize the codon by base pairing with the mRNA.
- (B) to recognize ribosomal RNAs.
- (C) to stabilize the tRNA structure.
- (D) to couple to the cognate amino acid.
- (E) none of the above.

13) What is the role of tRNA in translation?

- (A) It brings together two subunits of a ribosome.
- (B) It couples an amino acid with aminoacyl-tRNA synthetase.
- (C) It helps fold up the finished polypeptide chain.
- (D) It catalyzes peptidyl transferase activity.
- (E) It binds to an mRNA codon and carries the corresponding amino acid.

14) Which of the following statements is (are) **false**?

- (i) Histone acetyl transferase functions in chromatin remodeling and removes acetyl groups from lysine amino acids on histone proteins.
  - (ii) Aminoacyl tRNA synthetase removes the amino acid from charged tRNA.
  - (iii) Ribosomal RNA catalyzes peptide-bond formation during translation.
  - (iv) Peptidyl transferase catalyzes peptide bond formation during translation.
- (A) (i) and (ii)                      (B) (i) and (iii)                      (C) (ii) and (iii)  
 (D) (i), (ii) and (iii)              (E) (i), (ii), and (iv)

15) How can a carrot plant express a bacterial gene?

- (A) Because the bacterial gene hijacks the carrot's cellular machinery.
- (B) Because the genetic code is the same in both organisms.
- (C) Because of the wobble phenomenon.
- (D) Because of the degeneracy of the genetic code.
- (E) A carrot cannot express a bacterial gene.

16) In the genetic code, both AAU and AAC code for asparagine. For this reason, the code is said to be

- (A) degenerate.                      (B) nonspecific.                      (C) universal.
- (D) ambiguous.                      (E) wobbly.

- 17) In a gene sequence, the DNA codon for tryptophan experiences a mutation at the first base position, changing it to T. What will the resulting amino acid be?  
 (A) Tryptophan (no change)      (B) Serine      (C) Arginine  
 (D) Threonine      (E) None (a stop codon will halt translation)
- 18) The energy of \_\_\_\_\_ is consumed during translation for one round of elongation after initiation is completed.  
 (A) 1 GTP      (B) 2 GTPs      (C) 1 ATP  
 (D) 1 GTP and 1 ATP      (E) 2 GTPs and 1 ATP
- 19) Which of the following statements about translation is **false**?  
 (A) eIFs recognize the 5' cap and then recruit the small subunit of the ribosome to the eukaryotic mRNA.  
 (B) The small subunit of the ribosome scans along the eukaryotic RNA until it encounters a start codon.  
 (C) The elongation factor EF-Ts structurally mimics that of a tRNA bound to a protein during elongation.  
 (D) The 16S rRNA located within the A-site of the small subunit helps select against incorrect codon-anticodon pairings in prokaryotes.  
 (E) None of the above.
- 20) A mutant strain of bacteria is isolated in which the amino acid glutamine is often erroneously substituted for glutamic acid during protein synthesis. What might explain this defect?  
 (i) A mutant tRNA synthetase could be erroneously charging tRNA<sup>Glu</sup> with glutamine (instead of glutamic acid), causing glutamine to be incorporated at glutamic acid-encoding codons.  
 (ii) The cell contains an enzyme that converts glutamic acid-tRNA<sup>Gln</sup> to glutamine-tRNA<sup>Gln</sup>, and that the mutation lies within this enzyme, causing it to erroneously convert glutamic acid substrates to glutamine that are correctly attached to tRNA<sup>Glu</sup>.  
 (iii) A mutation lies in a tRNA synthetase that charges all tRNA<sup>Asp</sup>, tRNA<sup>Asn</sup>, tRNA<sup>Gln</sup>, and tRNA<sup>Glu</sup>, causing glutamine to be incorporated at glutamic acid-encoding codons.  
 (A) Only (i) is possible      (B) Only (ii) is possible      (C) Only (iii) is possible  
 (D) Both (i) and (ii) are possible      (E) All of (i), (ii), and (iii) are possible

Codon table

Amino acid	Codons	Amino acid	Codons
Ala/A	GCU, GCC, GCA, GCG	Leu/L	UUA, UUG, CUU, CUC, CUA, CUG
Arg/R	CGU, CGC, CGA, CGG, AGA, AGG	Lys/K	AAA, AAG
Asn/N	AAU, AAC	Met/M	AUG
Asp/D	GAU, GAC	Phe/F	UUU, UUC
Cys/C	UGU, UGC	Pro/P	CCU, CCC, CCA, CCG
Gln/Q	CAA, CAG	Ser/S	UCU, UCC, UCA, UCG, AGU, AGC
Glu/E	GAA, GAG	Thr/T	ACU, ACC, ACA, ACG
Gly/G	GGU, GGC, GGA, GGG	Trp/W	UGG
His/H	CAU, CAC	Tyr/Y	UAU, UAC
Ile/I	AUU, AUC, AUA	Val/V	GUU, GUC, GUA, GUG
START	AUG	STOP	UAA, UGA, UAG

見背面

第二大題是非題 (21-25 題每題 1 分)

- 21) Two sequenced DNA fragments from different individuals, AAGCCTA to AAGCTTA, contain difference in a single nucleotide. In this case we say that there are two loci: C and T. True or False?
- 22) Single nucleotide polymorphisms (SNPs) may fall within coding sequences and non-coding regions of genes, or in the intergenic regions. SNPs that are not in protein-coding regions are silent polymorphisms and don't affect gene expression. True or False?
- 23) The variability of microsatellites is due to a higher rate of mutation that can be explained most frequently by slipped strand mispairing during DNA replication on a single DNA strand. True or False?
- 24) Pyrosequencing is a method of DNA sequencing based on the "sequencing by synthesis" principle. It differs from Sanger sequencing and relies on the detection of pyrophosphates released as nucleotide incorporation, rather than chain termination with dideoxynucleotides. True or False?
- 25) Loss of heterozygosity (LOH) can be identified in cancers by noting the presence of heterozygosity at a genetic locus in normal germline DNA, and the absence of heterozygosity at that locus in tumor DNA. All of the paired normal and tumor DNAs tested can provide informative data of LOH study. True or False?

第三大題簡答題 (配分列於各題後)

- 26) How many types of dinucleotide repeat? What are they? (6 分)
- 27) Why should we carry out melting curve analysis after SYBR Green-based quantitative PCR amplification? (3 分)

28) According to the allele frequencies in Taiwan (Table 1), please calculate the PI of three loci listed, CPI and PP below. (6 分)

Locus	Alleged Father	Child	Paternity index (PI)
D3S1358	12,15	15, 20	
D8S1179	14,14	14,15	
D18S51	13,23	13,15	
Combined paternity index (CPI)			
Probability of paternity (PP)			

Table 1 The allele frequencies in Taiwan

D3S1358 Allele frequency	D8S1179 Allele frequency	D18S51 Allele frequency
12 0.0010	10 0.1300	10 0.0050
13 0.0020	11 0.1300	11 0.0080
14 0.0400	11.2 0.0030	12 0.0620
15 0.2500	12 0.1300	13 0.2000
16 0.3200	13 0.2300	14 0.2200
17 0.2300	14 0.2000	15 0.2000
18 0.0560	15 0.1300	16 0.1100
19 0.0050	16 0.0560	17 0.0800
20 0.0006	17 0.0130	18 0.0400
21 0.0002	18 0.0027	19 0.0460
		20 0.0200
		21 0.0200
		22 0.0200
		23 0.0080
		24 0.0050

29) It is known that there is a disease caused by overexpressed mutant fusion protein due to chromosomal translocation. Please propose at least two molecular techniques for identification (diagnostics). (5 分)

見背面

30) If you just identify a coding sequence of a novel gene, how can you know that whether this gene is expressed in a specific tissue or organ? And even you proof that this gene is expressed in this tissue, how can you further know its expression pattern, region as well as cellular localization? (5 分)

31) Please briefly describe the principle of SYBR-green and TaqMan QPCR (Quantitative Polymerase Chain Reaction) techniques and its application. (5 分)

32) If we want to know whether A protein will physically interact with B protein in the cell, how can you design experiments to proof? (5 分)

第四大題問答題 (配分列於各題後)

33) By sequence alignment, you identify potential -10 and -35 elements in a bacteria promoter. Please design one straightforward experiment to demonstrate that RNA polymerase can bind at regions centered on the -10 and -35 elements. (10 分)

34) Please describe two proposed models for how transcription by eukaryotic RNA polymerase II terminates after transcribing a gene. If you want to know which one is favored for a specific gene, how can you design experiments to prove that? (10 分)

試題隨卷繳回