國立高雄大學九十七學年度研究所碩士班招生考試試題

科目：分子生物學
考試時間：100 分鐘

系所：
生物科技研究所碩士班甲組　　是否使用計算機：是
本科原始成績：100 分

I、單選題(每題 2 分，答題時請註明題號依序寫在答案卷上，以大寫字母 ABCDE 回答)

1. The phosphodiester bonds that link adjacent nucleotides in both RNA and DNA:
   A) are uncharged at neutral pH.
   B) link A with T and G with C.
   C) form between the planar rings of adjacent bases.
   D) are susceptible to alkaline hydrolysis.
   E) link the 3′ hydroxyl of one nucleotide to the 5′ hydroxyl of the next.
2. Some restriction enzymes produce sticky (cohesive) ends. This means that they:
   A) digest both DNA strands at the same base pair.
   B) cut in regions of high GC content, leaving ends that can form more hydrogen bonds than ends of high AT content.
   C) make ends that can anneal to cohesive ends generated by any other restriction enzyme.
   D) stick tightly to the ends of the DNA they have cut.
   E) make a staggered double-strand cut, leaving ends with a few nucleotides of single-stranded DNA protruding.
3. In DNA sequencing by the Sanger　dideoxy method:
   A) radioactive dideoxy ATP is included in each of four reaction mixtures before enzymatic synthesis of complementary strands.
   B) specific enzymes are used to cut the newly synthesized DNA into small pieces, which are then separated by electrophoresis.
   C) the dideoxynucleotides must be present at high levels to obtain long stretches of DNA sequence.
   D) the role of the dideoxy CTP is to occasionally terminate enzymatic synthesis of DNA where Gs occur in the template strands.
   E) the template DNA strand is radioactive.
4. Which of the following statements about the genomes or proteomes is **False**?:
   A) Current estimates indicate that humans have about 25,000 genes.
   B) The genome of *Mycoplasma genitalium* is the known smallest genome of the self-replication organisms.
   C) DNA microarray, 2D-gel electrophoresis, MALDI-TOF, and protein chip are powerful tools for genomics or proteomics analysis.
   D) The *E. coli* is the first bacterium which genome was sequenced completely.
   E) Functional genomics focuses on the dynamic aspects such as gene transcription, translation, and protein-protein interactions.

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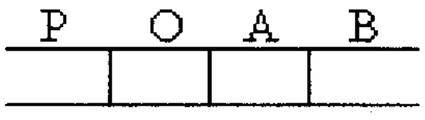
5. The diagram below represents a hypothetical operon in *E. coli.* It consists of two structural genes (A and B), which code for the enzymes A-ase and B-ase, respectively, and also includes P (promoter) and O (operator) regions as shown.



When a certain compound (X) is added to the growth medium of *E. coli,* the separate enzymes A-ase and B-ase are both synthesized at a 50-fold higher rate than in the absence of X. (X has a molecular weight of about 200.) Which of the following statements is **True** of such an operon ?

A) All operon (P, O, A, and B) will be transcribed into an mRNA that will then be translated into four different proteins.
B) The repressor for this operon binds just to the right of A.
C) Adding X to the growth medium causes a repressor protein to be released from the O region.
D) Synthesis of the mRNA from this operon is not changed by the addition of compound X.
E) Two mRNA molecules are made from this operon, one from gene A the other from gene B.

6. A transcription unit that is 1800 nucleotides long may use 1,200 nucleotides to make a protein consisting of 400 amino acids. This is best explained by the fact that

A) there is redundancy and ambiguity in the genetic code.
B) many nucleotides are needed to code for each amino acid.
C) many noncoding nucleotides are present.
D) nucleotides break off and are lost during the transcription process.
E) there are termination exons near the beginning of mRNA.

7. Which of the following statements about the core enzyme of *E. coli* RNA polymerase is **False**?

A) In the absence of the σ subunit, core polymerase has little specificity for where initiation begins.
B) The core enzyme has no polymerizing activity until the σ subunit is bound.
C) It is required for the synthesis of mRNA, rRNA, and tRNA in *E. coli.*
D) It can start new chains de novo or elongate old ones.
E) The RNA product is complementary to the DNA template.

8. If proteins were composed of only 12 different kinds of amino acids, what would be the smallest possible codon size in a genetic system with four different nucleotides?

A) 1
B) 2
C) 3
D) 4
E) 12

9. Which of the following statements about the synthesis of rRNA and tRNA in *E. coli* is **True**?
   A) Both rRNA and some tRNAs are part of the same primary transcript.
   B) The tRNA sequences all lie at the 3 nd of the rRNA transcripts
   C) Primary tRNA transcripts undergo methylation, but rRNA sequences are not methylated.
   D) Each rRNA sequence (16S, 23S, 5S) is transcribed into a separate primary transcript.
   E) There is a single copy of the rRNA genes.
10. Which one of the following statements about the elongation phase of protein synthesis is **True**?
   A) Peptidyl transferase is a ribozyme.
   B) At least five high-energy phosphoryl groups are expended for each peptide bond formed.
   C) Peptidyl transferase catalyzes the attack of the carboxyl group of the incoming amino acid on an ester linkage in the nascent polypeptide.
   D) Elongation factor EF-Tu facilitates translocation.
   E) During elongation, incoming aminoacylated tRNAs are first bound in the P site.
11. In contrast to bacteria, eukaryotic chromosomes need multiple DNA replication origins because:
   A) their replication rate is much slower, and it would take too long with only a single origin per chromosome.
   B) eukaryotic chromosomes cannot usually replicate bidirectionally.
   C) eukaryotic genomes are not usually circular, like the bacterial chromosome is.
   D) the processivity of the eukaryotic DNA polymerase is much less than the bacterial enzyme.
   E) they have a variety of DNA polymerases for different purposes, and need a corresponding variety of replication origins.
12. *E. coli* DNA polymerase III :
   A) is efficient at nick translation.
   B) is the principal DNA polymerase in chromosomal DNA replication.
   C) contains a $5' \rightarrow 3'$ proofreading activity to improve the fidelity of replication.
   D) synthesizes only the leading strand; DNA polymerase I synthesizes the lagging strand.
   E) can initiate replication without a primer.
13. A certain bacterial mRNA is known to represent only one gene and to contain about 800 nucleotides. If you assume that the average amino acid residue contributes 110 to the peptide molecular weight, the largest polypeptide that this mRNA could code for would have a molecular weight of about:
   A) 800.
   B) 5,000.
   C) 30,000.
   D) 80,000.

E) An upper limit cannot be determined from the data given.

14. In a mammalian cell, DNA repair systems:
    A) are generally absent, except in egg and sperm cells.
    B) can repair deletions, but not mismatches.
    C) are extraordinarily efficient energetically.
    D) normally repair more than 99% of the DNA lesions that occur.
    E) can repair most types of lesions except those caused by UV light.
15. Which of the following is **True** for both prokaryotic and eukaryotic gene expression?
    A) After transcription, a 3' poly(A) tail and a 5' cap are added to mRNA.
    B) Translation of mRNA can begin before transcription is complete.
    C) mRNA is synthesized in the 3' → 5' direction.
    D) The mRNA transcript is the exact complement of the gene from which it was copied.
    E) RNA polymerase may recognize a promoter region and begin transcription.

II、請寫出題意所代表的分子生物學專有名詞英文全名(每題 2 分，寫出全名但字彙拼錯者，該題以得 1 分計算；以中文作答不計分，請謹慎作答。)

1. Transferring DNA fragments separated by gel electrophoresis to a suitable support medium such as nitrocellulose, in preparation for hybridization to a labeled probe.
2. Control of gene expression by specific mRNA degradation caused by insertion of a double-stranded RNA into a cell.
3. The enzyme that links a tRNA to its cognate amino acid.
4. The branched DNA structure formed by the first strand exchange during recombination.
5. A transcript carrying the information that, during translation, specifies the amino acid
6. Small DNA fragment, 1000-2000 bases long, created by discontinuous synthesis of the lagging strand.
7. A 300-nt RNA that resembles a tRNA and can rescue a stalled ribosome on a non-stop mRNA.
8. A high-capacity cloning vector consisting of yeast left and right telomeres and a centromere. It can replicate in yeast cells.
9. A set of three contiguous nucleotides in a tRNA molecule that are complementary to a set of three contiguous nucleotides in an mRNA.
10. An enzyme that recognizes a specific duplex DNA sequence and cleaves phosphodiester bonds on both strands at or near the recognition site.

11. A segment of a gene that is transcribed but is then excised from the primary transcript during processing to a functional RNA molecule.

12. A technique to change one or more specific nucleotides in a cloned gene in order to create an altered form of a protein with a specific amino acid change(s).

13. A single nucleotide difference between two or more individuals at a particular genetic locus.

14. A laboratory technique which is used to amplify and simultaneously quantify a targeted DNA molecule. It enables both detection and quantification (as absolute number of copies or relative amount when normalized to DNA input or additional normalizing genes) of a specific sequence in a DNA sample.

15. A sequence to which a ribosome can bind and begin translating in the middle of a transcript, without having to scan from 5? end.

III. 問答題

1. If you want to label the 3? end of DNA with large fragment DNA polymerase I by end-filling method, what kind of the isotope, [α-^{32}P]dNTP, [β-^{32}P]dNTP or [γ-^{32}P]dNTP, should be used for the labeling, why? When you want to label an isotope on the 5? end of DNA fragment with polynucleotide kinase, what kind of the isotope, [α-^{32}P]ATP, [β-^{32}P]ATP or [γ-^{32}P]ATP, should be used for the labeling, why? **(5 分)**

2. Describe the activities of following enzymes that are used for recombinant DNA technology: (1) alkaline phosphatase (2) *E. coli* exonuclease III (3) Klenow fragment (4) RNase H (5) S1 nuclease. **(5 分)**

3. Identify the following consensus sequences (what process or system they are used in and their basic function...you don't need to list names of factors that bind unless you want to). **(10 分)**
   (1) AAUAAA
   (2) TATAAA
   (3) AGGAGGNNNNNNNAUG (Note: N represents any base)
   (4) GUaagt.....(N).....UACUAAC.....(N).....cAG (capital letters are absolutely conserved, small letters are frequently but not absolutely conserved)
   (5) Tyr Ser Pro Thr Ser Pro Ser

4. A double-stranded DNA with (91.5 kb). Please answer following questions: **(10 分)**
   (a) How many full double-helical turns does this DNA contain?
   (b) How long is the DNA in microns (1 micron = 10^4 Å)?

(c) What is the molecular mass of this DNA?

(d) How many genes of average size (encoding proteins of about 22,000 molecular weight) can this DNA contain?

(e) How many phosphorus atoms does the DNA contain?

(Hint: The spacing between base pairs is about 3.4 x 10^{-4} μm (=3.4Å). One double-helical turn encompasses 10.5 bp. One base pair has a molecular mass of about 660 daltons. The average molecular mass of an amino acid is about 110 daltons.)

5. Please answer following questions base on a portion of a bacterial gene sequence showed below. The template strand is on the bottom. **(10 分)**

5?GTATCGTATGCATGCATCGTGAC-3
3?CATAGCATACGTACGTAGCACTG-5

(a) Assuming that transcription starts with the first T in the template strand, and continue to the end, what would be the sequence of the mRNA derived from this fragment?

(b) Find the initiation codon in this mRNA. (indicate with underline)

(c) Would there be an effect on translation of changing the first G in the template strand to a C? If so, what effect?

(d) Would there be an effect on translation of changing the second T in the template strand to a G? If so, what effect?

(e) Would there be an effect on translation of changing the last T in the template strand to a C? If so, what effect?

(Hint: You do not need to know the genetic code to answer these questions; you just need to know the nature of initiation and termination codons.)