

系所組別： 生物化學暨分子生物學研究所甲、乙組

考試科目： 分子生物學

考試日期： 0308 · 節次： 2

※ 考生請注意：本試題 可 不可 使用計算機

一、選擇題：(60 分，單選，每題 3 分，答錯每題倒扣 0.75 分)

1. “Housekeeping genes” in bacteria are commonly expressed constitutively, but not all of these genes are expressed at the same level (the same number of molecules per cell). The primary mechanism responsible for variations in the level of constitutive enzymes from different genes is that:
 - (a) all constitutive enzymes are synthesized at the same rate, but are not degraded equally.
 - (b) their promoters have different affinities for RNA polymerase holoenzyme.
 - (c) some constitutively expressed genes are more inducible than others.
 - (d) some constitutively expressed genes are more repressible than others.
 - (e) the same number of mRNA copies are made from each gene, but are translated at different rates.

2. Protein amino acid side chains can hydrogen bond in the major groove of DNA, and discriminate between each of the four possible base pairs. In which one of the following groups of amino acids can all three members potentially be used in such DNA-protein recognition?
 - (a) Ala, Asn, Glu
 - (b) Arg, Gln, Leu
 - (c) Asn, Gln, Trp
 - (d) Asn, Glu, Lys
 - (e) Glu, Lys, Pro

3. Which of the following are features of the wobble hypothesis?
 - (a) A naturally occurring tRNA exists in yeast that can read both arginine and lysine codons.
 - (b) A tRNA can recognize only one codon.
 - (c) Some tRNAs can recognize codons that specify two different amino acids, if both are nonpolar.
 - (d) The “wobble” occurs only in the first base of the anticodon.
 - (e) The third base in a codon always forms a normal Watson-Crick base pair.

4. Formation of the ribosomal initiation complex for bacterial protein synthesis does not require:
 - (a) EF-Tu.
 - (b) formylmethionyl tRNA^{Met}.
 - (c) GTP.
 - (d) initiation factor 2 (IF-2).
 - (e) mRNA.

(背面仍有題目,請繼續作答)

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5. It is possible to convert the Cys that is a part of Cys-tRNA^{Cys} to Ala by a catalytic reduction. If the resulting Ala-tRNA^{Cys} were added to a mixture of (1) ribosomes, (2) all the other tRNAs and amino acids, (3) all of the cofactors and enzymes needed to make protein in vitro, and (4) mRNA for hemoglobin, where in the newly synthesized hemoglobin would the Ala from Ala-tRNA^{Cys} be incorporated?
- (a) Nowhere; this is the equivalent of a nonsense mutation
 - (b) Wherever Ala normally occurs
 - (c) Wherever Cys normally occurs
 - (d) Wherever either Ala or Cys normally occurs
 - (e) Wherever the dipeptide Ala-Cys normally occurs
6. Which of the following is true about the sorting pathway for proteins destined for incorporation into lysosomes or the plasma membrane of eukaryotic cells?
- (a) Binding of SRP to the signal peptide and the ribosome temporarily accelerates protein synthesis.
 - (b) The newly synthesized polypeptides include a signal peptide at their carboxyl termini.
 - (c) The signal peptide is cleaved off inside the mitochondria by signal peptidase.
 - (d) The signal recognition particle (SRP) binds to the signal peptide soon after it appears outside the ribosome.
 - (e) The signal sequence is added to the polypeptide in a posttranslational modification reaction.
7. Glycosylation of proteins inside the endoplasmic reticulum does *not* involve:
- (a) a His residue on the protein.
 - (b) an Asn residue on the protein.
 - (c) dolichol phosphate.
 - (d) glucose.
 - (e) *N*-acetylglucosamine.
8. Which of the following is *not* known to be involved in initiation by eukaryotic RNA polymerase II?
- (a) DNA helicase activity
 - (b) DNA polymerase activity
 - (c) Formation of an open complex
 - (d) Protein binding to specific DNA sequences
 - (e) Protein phosphorylation

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9. During RNA processing, a branched (“lariat”) structure is formed during:
- attachment of a 5' cap to mRNA.
 - attachment of poly(A) tails to mRNA.
 - processing of preribosomal RNA.
 - splicing of all classes of introns.
 - splicing of group II introns.
10. Which of the following statements about the synthesis of rRNA and tRNA in *E. coli* is true?
- Both rRNA and some tRNAs are part of the same primary transcript.
 - Each rRNA sequence (16S, 23S, 5S) is transcribed into a separate primary transcript.
 - Primary tRNA transcripts undergo methylation, but rRNA sequences are not methylated.
 - The tRNA sequences all lie at the 3' end of the rRNA transcripts
 - There is a single copy of the rRNA genes.
11. Which one of the following statements about the reverse transcriptases of retroviruses and the RNA replicases of other single-stranded RNA viruses, such as R17 and influenza virus, is correct?
- Both enzymes can synthesize either RNA or DNA from an RNA template strand.
 - Both enzymes can utilize DNA in addition to RNA as a template strand.
 - Both enzymes carry the specificity for the RNA of their own virus.
 - Both enzymes have error rates similar to those of cellular RNA polymerases.
 - Both enzymes require host-encoded subunits for their replication function.
12. The Meselson-Stahl experiment established that:
- DNA polymerase has a crucial role in DNA synthesis.
 - DNA synthesis in *E. coli* proceeds by a conservative mechanism.
 - DNA synthesis in *E. coli* proceeds by a semiconservative mechanism.
 - DNA synthesis requires dATP, dCTP, dGTP, and dTTP.
 - newly synthesized DNA in *E. coli* has a different base composition than the preexisting DNA.
13. The bacteriophage λ can lysogenize after infecting a bacterium, i.e. integrate into the host bacterial chromosome by site-specific recombination, and may reside there for many generations before an excision event regenerates the viral genome in an infective form. Which one of the following is *not* a component of these events?
- Excision requires two host proteins and two virally-encoded proteins.
 - Integration requires a viral-specific protein, called integrase.

(背面仍有題目,請繼續作答)

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- (c) RecA protein is required to catalyze the insertional recombination event.
(d) The excision event relies on different sequences than the integration event.
(e) The virus and the host DNAs share a 15 bp "core" region of perfect homology.
14. The linking number (Lk) of a closed-circular, double-stranded DNA molecule is changed by:
- (a) breaking a strand, then rejoining it.
(b) breaking a strand, unwinding or rewinding the DNA, then rejoining it.
(c) breaking all hydrogen bonds in the DNA.
(d) supercoiling without the breaking of any phosphodiester bonds.
(e) underwinding without the breaking of any phosphodiester bonds.
15. Which of the following contributes to the structure of nucleosomes?
- (a) Plectonemic supercoiled DNA
(b) Relaxed closed-circular DNA
(c) Solenoidal supercoiled DNA
(d) Spacer DNA
(e) Z (left-handed) DNA
16. The double helix of DNA in the B-form is stabilized by:
- (a) covalent bonds between the 3' end of one strand and the 5' end of the other.
(b) hydrogen bonding between the phosphate groups of two side-by-side strands.
(c) hydrogen bonds between the riboses of each strand.
(d) nonspecific base-stacking interaction between two adjacent bases in the same strand.
(e) ribose interactions with the planar base pairs.
17. The size of the DNA region specifically recognized by type II restriction enzymes is typically:
- (a) 4 to 6 base pairs.
(b) 10 to 15 base pairs.
(c) 50 to 60 base pairs.
(d) 200 to 300 base pairs.
(e) about the size of an average gene.

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18. Which one of the following analytical techniques does *not* help illuminate a gene's cellular function?
- (a) DNA microarray analysis
 - (b) Protein chip analysis
 - (c) Southern blotting
 - (d) Two-dimensional gel electrophoresis
 - (e) Two-hybrid analysis
19. What are the energy needs for protein synthesis?
- (a) two phosphoanhydride bonds cleaved per amino acid residue
 - (b) four phosphoanhydride bonds cleaved per amino acid residue
 - (c) six phosphoanhydride bonds cleaved per amino acid residue
 - (d) two phosphoanhydride bonds to set up, then one per amino acid residue
 - (e) none of the above
20. Epistasis is the interaction between genes. Epistasis takes place when the action of one gene is modified by one or several other genes, which are sometimes called modifier genes. The gene whose phenotype is expressed is said to be _____, while the phenotype altered or suppressed is said to be _____.
- (a) dominant positive; dominant negative
 - (b) epistatic; dominant negative
 - (c) epistatic; hypostatic
 - (d) co-expressed; hypostatic
 - (e) complement; dominant negative

二、問答題：(40分，每題10分)

21. Please compare the main differences between prokaryotic and eukaryotic genomes, as well as the major differences between prokaryotic and eukaryotic DNA replications. (10%)
22. Please design and describe an inducible protein expression system in bacterium *Escherichia coli*, as well as design and set up a procedure or protocol for isolation and purification of the expressed protein. (10%)

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23. Please design and describe the techniques or approaches that can be used to identify and dissect the hypoxia-inducible factor HIF-1alpha binding sites in 5' regulatory region of a hypoxia responsive gene. (10%)
24. Please briefly describe the cellular proteolytic systems in the degradation of various classes of eukaryotic cell proteins; and explain the action mechanism and biological functions of the ubiquitin-proteasome induced protein degradation in eukaryotic cells. (10%)