系所:<u>生物技術研究所</u> 科目:<u>分子生物學</u>

☆☆請在答案紙上作答☆☆

共5頁,第1頁

- 一、單選擇題,選出最好的答案(每題2分共60分)
- 1. Which of the following is an important difference between eukaryotic and prokaryotic DNA replication?
 - (A) eukaryotic DNA polymerases are faster
 - (B) more DNA polymerases are found in eukaryotes
 - (C) multiple origins of replication in eukaryotes
 - (D) RNA primers are not required in eukaryotes
- 2. Meselson and Stahl demonstrated the mode of DNA replication is semi-conservative by separating DNA from different generations using:
 - (A) density gradient centrifugation
- (B) gel electrophoresis
- (C) an electron microscope
- (D) ³⁵S radioisotope labeling
- 3. In homologous genetic recombination, RecA protein is involved in:
 - (A) formation of Holliday intermediates and branch migration
 - (B) introduction of negative supercoils into the recombination products
 - (C) nicking the two duplex DNA molecules to initiate the reaction
 - (D) resolution of the Holliday intermediate.
- 4. What is the target site for transposase?
 - (A) promoter of its own gene
 - (B) the inverted repeats and the target sequence
 - (C) the target sequence and the internal resolution site
 - (D) the telomeres and the long terminal repeats
- 5. Which of the following statements is *FALSE* regarding DNA replication?
 - (A) DNA Polymerase I possesses $5' \rightarrow 3'$ polymerase activity
 - (B) DNA Polymerase I possesses $5' \rightarrow 3'$ exonuclease activity
 - (C) PriA removes the Single Stranded Binding (SSB) proteins
 - (D) Primase seals the nicks between nucleotides on the lagging strand
- 6. Which one of the following is **NOT** directly involved with mobile genetic elements?
 - (A) a specific short DNA sequence
 - (B) rolling of the Holliday junction
 - (C) the functioning of a sequence-specific DNA recombinase
 - (D) insertion of circular DNA into chromosomal DNA
- 7. During replication of linear chromosomal DNA, one end of one strand of each replicated chromosome is missing some DNA sequence. What is the cause for this incomplete replication?
 - (A) highly compacted chromatin in the telomere region

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共5頁,第2頁

(B) inability to syn	thesize a primer for	the continuously	made leading s	trand to be	able to f	fully
replicate its ten	nplate DNA					

- (C) inability to synthesize a primer for the last Okazaki fragment made so that it can fully replicate its template DNA
- (D) inability to ligate the last Okazaki fragment to the one immediately preceding it
- 8. The spontaneous loss of a purine (guanine or adenine) from cellular DNA is repaired by
 - (A) base excision repair

(B) transcription coupled repair

(C) post-replication repair

- (D) photolyase
- 9. Why are DNA damaging agents effective for anticancer therapy?
 - (A) they are activated to reactive forms only in cancer cells
 - (B) they are deactivated to inactive forms in normal (non-cancerous) cells before they encounter DNA and damage the DNA
 - (C) the damage they cause to DNA is not repaired before cancer cells begin DNA replication
 - (D) cancer cells generally lack all ability to repair DNA
- 10. What is occurred to the nascent polypeptide during the elongation phase of translation?
 - (A) it moves back and forth between the tRNAs at the P and A sites during elongation.
 - (B) it starts at the A site then moves to the P site, then exits at the E site.
 - (C) it is always at the A site
 - (D) it is always at the P site
- 11. What is proteomics?
 - (A) is another term for genomics in humans
 - (B) is the study of the collection of proteins produced in a particular cell
 - (C) is the study of proteins produced by a particular gene.
 - (D) proves that a single gene codes for only one protein.
- 12. The proofreading of newly synthesized DNA, to excise incorrect nucleotides which have been inserted, is done by:
 - (A) a restriction endonucleases

(B) DNA polymerase III

(C) DNA gyrase

- (D) DNA ligase
- 13. Two copies each of histone H2A, H2B, H3, and H4 is a
 - (A) core nucleosome (B) chromatin (C) nucleoi (D) nucleosome
- 14. Which one of the following is not associated with translation?
 - (A) rRNA (B) tRNA (C) anticodon (D) snRNA.
- 15. What are miRNAs?
 - (A) encode small regulatory proteins
 - (B) are small RNAs that regulate the stability or translatability of mRNAs

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共5頁,第3頁

- (C) are translated to produce basic DNA binding proteins
- (D) A and C are correct
- 16. If you want to make a genomic library with DNA fragments averaging about 45 kb in length, which vector will be most appropriate to use?
 - (A) plasmid. (B) lamda phage (C) cosmid (D) bacteria artificial chromosome (BAC)
- 17. Which of the following is true about snRNPs?
 - (A) They are made up of both DNA and proteins.
 - (B) They bind to splice sites at each end of the exon.
 - (C) They joint together to form the spliceosome.
 - (D) They act only in the cytosol.
- 18. Which of the following can *not* bind DNA?
 - (A) Greek key β -barrel domain.
- (B) Leucine zippers (bZIP) motif.

(C) Homeodomains.

- (D) Zinc fingers.
- 19. Which of the following belongs to prokaryotic core promoter elements?
 - a. Pribnow box; b. TATA box; c. -10 box; d. CAAT box; e. -35 box.
 - (A) bd. (B) ce. (C) abe. (D) abce.
- 20. Which condition can induce the largest gene expression of the *lac* operon?
 - (A) high concentration of glucose and lactose.
 - (B) high concentration of glucose and low concentration of lactose.
 - (C) low concentration of glucose and high concentration of lactose.
 - (D) low concentration of glucose and lactose.
- 21. A particular triplet of bases in the template strand of DNA is 5' AGT 3'. The corresponding codon for the mRNA transcribed is
 - (A) 3' UCA 5'. (B) 3' UGA 5'. (C) 5' TCA 3'. (D) 3'ACU 5'.
- 22. 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) RNA polymerase binds to the promoter region to begin transcription.
 - (D) The mRNA transcript is the exact complement of the gene from which it was copied.
- 23. Which of the following is the function of a poly (A) signal sequence?
 - (A) It adds the poly (A) tail to the 3' end of the mRNA.
 - (B) It codes for a sequence in eukaryotic transcripts that signals enzymatic cleavage ~10-35 nucleotides away.
 - (C) It allows the 3' end of the mRNA to attach to the ribosome.
 - (D) It is a sequence that codes for the hydrolysis of the RNA polymerase.

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共5頁,第4頁

- 24. In eukaryotic cells, transcription cannot begin until?
 - (A) the two DNA strands have completely separated and exposed the promoter.
 - (B) the DNA introns are removed from the template.
 - (C) the 5' caps are removed from the mRNA.
 - (D) several transcription factors have bound to the promoter.
- 25. Which of the following is *not* true of mRNA processing after transcription in eukaryotic cells?
 - (A) Exons are cut out before mRNA leaves the nucleus.
 - (B) Nucleotides may be added at both ends of the RNA.
 - (C) Ribozymes may function in RNA splicing.
 - (D) RNA splicing can be catalyzed by spliceosomes.
- 26. Genomic imprinting, DNA methylation, and histone acetylation are all examples of
 - (A) genetic mutation.

- (B) epigenetic phenomena.
- (C) single nucleotide polymorphism (SNP).
- (D) cancer properties.
- 27. Which of the following best describes siRNA?
 - (A) a short double-stranded RNA, one of whose strands can complement and inactivate a target sequence of mRNA.
 - (B) a single-stranded RNA that can, where it has internal complementary base pairs, fold into cloverleaf patterns.
 - (C) a double-stranded RNA that is formed by cleavage of hairpin loops in a larger precursor.
 - (D) a double-stranded RNA that is formed the spliceosomes.
- 28. What is the most logical sequence of steps for adding foreign DNA into a plasmid and inserting the plasmid into a bacterium?
 - a. Transform bacteria with recombinant DNA molecule;
 - b. Cut the plasmid DNA using restriction enzymes;
 - c. Extract plasmid DNA from bacterial cells;
 - d. Hydrogen-bond the plasmid DNA to nonplasmid DNA fragments;
 - e. Use ligase to seal plasmid DNA to nonplasmid DNA.
 - (A) acbde. (B) bceda. (C) cbdea. (D) dcbea.
- 29. Which of the following tools of recombinant DNA technology is *incorrectly* paired with its use?
 - (A) restriction enzyme–production of RFLPs.
 - (B) DNA ligase–enzyme that cuts DNA, creating the sticky ends of restriction fragments.
 - (C) DNA polymerase–used in a polymerase chain reaction to amplify sections of DNA.
 - (D) reverse transcriptase–production of cDNA from mRNA.
- 30. DNA microarrays have made a huge impact on genomic studies because they
 - (A) can be used to eliminate the function of any gene in the genome.

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共5頁,第5頁

- (B) can be used to introduce entire genomes into bacterial cells.
- (C) allow the expression of many or even all of the genes in the genome to be compared at once.
- (D) allow physical maps of the genome to be assembled in a very short time.

二、問答題:(共40%)

- 1. Please describe and calculate how to make a 500 mL solution that is 20mM NaCl, 2% SDS (v/v; if the stock solution of SDS is 50% w/v), 10 mM Tris-HCl, pH 7.5. (FW= formula weight; FW NaCl = 58.44; FW Tris = 121; FW SDS = 288.4). (10%)
- 2. Contrast the functions of three main types of RNA. (10%)
- 3. Describe the transcription initiation process in eukaryotes. (5%)
- 4. Describe the mechanism of splicing of nuclear mRNA precursors by snRNPs. (5%)
- 5. Figure 1 is the SOD1 cDNA sequence of zebrafish, please design a pair of primer sequence to clone the full-coding region of zebrafish SOD1 cDNA(4%). How to express and purify the recombinant zebrafish SOD1 from *E. coli* (6%). Please describe detail

2864 J. Agric. Food Chem., Vol. 46, No. 7, 1998 Ken et al. TCGAGCGGCCGCCCGGGCAGGTGTCAGC ATG GTG AAC AAG GCC GTT TGT GTG CTT AAA GGC ACC GGT GAA GTG ACC GGC V С V G L K ACC GTC TAT TTC AAT CAA GAG GGT GAA AAG AAG CCA GTG AAG GTG ACT GGT E E 131 GAA ATT ACT GGC CTT ACT CCA GGA AAA CAT GGT TTC CAC GTC CAT GCC TTT P G 182 GGT GAC AAC ACA AAC GGC TGC ATC AGT GCA GGT CCG CAC TTC AAC CCT CAT G C Ι S A 233 GAC AAA ACT CAT GGT GGG CCA ACC GAT AGT GTT AGA CAC GTC GGA GAC CTG G P D 284 GGT AAT GTG ACC GCT GAT GCC AGT GGT GTT GCA AAA ATT GAA ATC GAG GAT G 335 GCA ATG CTG ACT CTG TCA GGC CAA CAT TCT ATT ATT GGG AGG ACC ATG GTG G Η 386 ATT CAT GAG AAG GAG GAT GAC TTG GGG AAG GGT GGC AAT GAG GAA AGT CTA D G K 437 AAA ACT GGC AAC GCT GGT GGT CTG GCT TGT GGA GTG ATC GGC ATC ACT 488 CAG TGAATCTGCTCTAATGGAAGAGCCGGTTGAAATATTGGTGACCAATGTGGATGCCTCTGAAGCA

Figure 1