國立彰化師範大學 99 學年度碩士班招生考試試題

系所：生物技術研究所　　科目：分子生物學

☆☆請在答案紙上作答☆☆　　

Section 1: Multiple choices. Please choose **the best answer** for each question. (3% each)

1. DNA polymerase III is a complex containing _____.

(a) catalytic subunits
(b) proofreading subunits
(c) "sliding clamp" subunits
(d) all of the above
(e) none of the above

2. The first nucleotides cannot be linked in a newly synthesized strand in DNA replication, _____ is required.

(a) a DNA primer
(b) an RNA primer
(c) DNA polymerase
(d) ligase
(e) helicase

3. Okazaki fragments are used to elongate _____.

(a) the leading strand toward the replication fork
(b) the lagging strand toward the replication fork
(c) both strands in both directions
(d) the leading strand away from the replication fork
(e) the lagging strand away from the replication fork

4. DNA replication *in vivo* is discontinuous due to _____.

(a) polymerase slippage
(b) sister-chromatid crossing over
(c) DNA are replicated in the 5' to 3' direction
(d) numerous number of replication origins
(e) DNA polymerase III is involved in replicating the leading strand but not the lagging strand

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5. The “sticky ends” of DNA refers to:

(a) single-stranded overhangs resulting from restriction digestion
(b) any restriction enzyme site
(c) selection for plasmids lacking antibiotic resistance gene
(d) DNA with palindromic feature
(e) the process of putting both ends of DNA together

6. Which of the following techniques would show the amount and size of a gene product?

(a) Southern blot
(b) Western blot
(c) PCR
(d) DNA sequencing
(e) Northern blot

7. What is a Klenow fragment?

(a) is important only for DNA repair
(b) is a fragment of DNA polymerase I that requires 3’→5’exonuclease activity
(c) is a topoisomerase for unwinding DNA
(d) is a fragment of DNA polymerase I that lacks 5’→3’exonuclease activity
(e) involves aminoacyl-tRNA synthetase

For questions 8~10, choose the best answer from the following:

(a) Western blot
(b) Northern blot
(c) PCR
(d) STR
(e) RFLP

8. This assay requires two DNA primers.
9. This assay would be used to determine the size of a protein.
10. This assay characterizes alleles based on the presence or absence of restriction sites.

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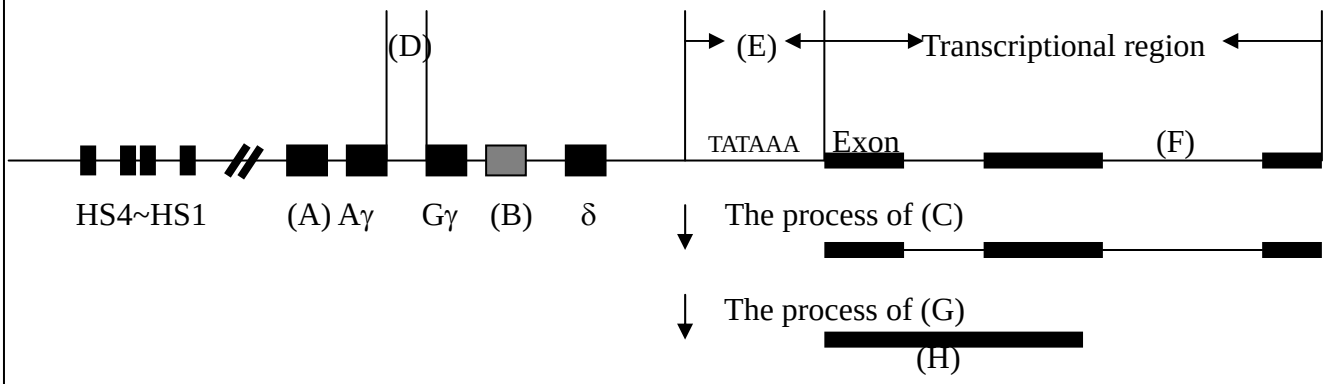
Section 2 : Filling the blanks. (2% each)

1. The family of human globin genes



Fill in the proper answer in each blank (**A~H**)

A._____

B. _____

C. _____

D. _____

E. _____

F. _____

G. _____

H._____

2. Glucocorticoid receptor (ER) is known as a transcription factor, which binding site is called _____, which is also a _____ (1. promoter; 2 enhancer; 3 silencer). In normal condition, it is localized in _____, and its activation requires binding of _____. The amino acid sequence of its DNA binding domain is **$X_nCX_2CX_{13}CX_2CX_{14\text{-}15}CX_5CX_9CX_2CX_n$,** which is known as **_____.**

3. Filling the blanks regarding the action of mi-RNA.

a) The dsRNA-specific ribonuclease _____ digests the pri-miRNA in the nuclease to release hairpin pre-miRNA,

b) _____, a member of the RNase III superfamily of bidentate nucleases, cleaves pre-miRNA,

c) The full name of RISC is _____

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Section 3 : Short Answer

1. Please describe and calculate how to make a 500 mL solution that is 50 mM NaCl, 20% SDS (v/v if the stock solution of SDS is 50% w/v), 0.01 M Tris-HCl, pH 7.5. (FW= formula weight; FW NaCl = 58.44; FW Tris = 121; FW SDS = 288.4) (4%)
2. Discuss the basic method and materials that are needed to carry out PCR. (4%)
3. Please describe the mechanism of prokaryotic transcription. (5%)
4. Please describe how the eukaryotic polymerase I promoter region and its transcription factors work. (5%)
5. How many kinds of RNA molecules in eukaryotic cell? Please describe these RNA functions. (5%)
6. Please describe the mechanism of nuclear pre-mRNA splicing. (5%)
7. Fig 1. showed the full coding cDNA sequence of X gene, please answer the following questions:
   Please design a pair of primers that can be used to clone the coding region of X gene by PCR. (1%)
   What is the full-length cDNA? (1%)
   How to get the full-length cDNA sequence of X gene? (5%)
   How to find the transcriptional start site in X gene? (3%)

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1   atgggatatg ttcggaggtg cgctgcaacc ttcaaccccc tgttaggtgc tgtgacctcc
61  agacagaagc acgctctccc tgacctcaca tatgactatg gtgcacttga gcctcacatc
121 tgtgctgaga ttatgcagct tcatcacagc aagcaccatg caacatatgt caacaacctc
181 aatgtcacag aggagaaata tcaagaggct ctggccaagg gtgatgtgac aacccaagtc
241 tcccttcagc ctgcattgaa atttaatgga ggtggtcata ttaatcatac catattctgg
301 acaaatctgt cacccaatgg cggtggagaa ccacagggtg agctgttgga ggccataaag
361 cgtgactttg gctcatttca gaagatgaaa gagaagatat cagctgccac cgtggctgtt
421 cagggctcag gctggggctg gctgggcttt gaaaaagaga gcggaagatt gaggattgca
481 gcgtgtgcta accaagaccc tttgcaaggg accacaggtc tcatcccact gcttgggata
541 gatgtctggg aacatgcgta ctatctccag tacaagaacg ttagaccgga ctatgttaag
601 gccatctgga atgttgtaaa ctgggagaat gtcggcgagc gtttccaagc tgccaagtaa
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Fig 1. The full coding sequence of X gene. Underline denotes the start and stop codon.