

國立成功大學

111學年度碩士班招生考試試題

編 號： 298

系 所： 分子醫學研究所

科 目： 分子生物學

日 期： 0220

節 次： 第 3 節

備 註： 不可使用計算機

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※ 考生請注意：本試題不可使用計算機。請於答案卷(卡)作答，於本試題紙上作答者，不予計分。

第一部分(共 30 分)

A. 單選題 Single-choice questions (10 分，每題 1 分)

1. If the doubling time of a bacterial culture is 30 min, by what factor does the cell density increase in 3 hr?
(A) 8
(B) 16
(C) 32
(D) 64
(E) 128
2. If the recombination frequencies occur between the indicated markers a, b, c, and d are: a x d=3%; b x c=7%; a x c=10%; b x d=14%; c x d=6%, what is the gene order?
(A) a-b-d-c
(B) a-c-d-b
(C) a-d-c-b
(D) b-d-a-c
(E) c-b-a-d
3. A protein has a molecular weight of 8800 Da. How many amino acids residues the protein may have?
(A) 40
(B) 50
(C) 60
(D) 70
(E) 80
4. A double strand DNA has a molecular weight of 231000 Da. How long is the DNA molecule in basepairs?
(A) 250
(B) 350
(C) 450
(D) 550
(E) 650
5. Analysis of a DNA sample indicates that 16% of the bases are Adenine. What is the percentage of Cytosine?
(A) 9%
(B) 16%
(C) 24%
(D) 34%
(E) 68%

6. Which statement is incorrect regarding transposons
- (A) The simplest transposons are called insertion sequences
 - (B) Transposons have direct terminal repeats and generate inverted terminal repeats of flanking DNA at the target site
 - (C) Transposons can carry other genes in addition to those coding for transposition
 - (D) Transposition occurs by both replicative and non-replicative mechanisms
 - (E) Transposition is mostly initiated by nicking the transposon ends and target site and joining the nicked ends into a strand transfer complex
7. Which statement is incorrect regarding RNA splicing and catalytic RNA
- (A) Group I intron may undertake self-splicing by transesterification.
 - (B) Some group I introns code for endonucleases that sponsor mobility.
 - (C) Some group II introns code for reverse transcriptases.
 - (D) RNA editing can be directed by guide RNAs.
 - (E) RNA editing is not occurred at individual bases.
8. When mature mRNA produced by the insulin gene is hybridized with denatured chromosomal DNA, which of the following will most likely be observed?
- (A) No hybridization would occur under any conditions.
 - (B) Hybridization of mRNA would occur with random sections of chromosomal DNA.
 - (C) Hybridization of mRNA with DNA would occur in a continuous stretch that is equal to the length of the mRNA.
 - (D) Hybridization of mRNA with DNA would occur but with many single-stranded loops of DNA.
 - (E) Hybridization of mRNA with DNA would occur but with many single-stranded loops of mRNA.
9. Which statement is incorrect regarding mRNA processing?
- (A) The 5' end of the nascent RNA is capped with 5-methylguanylate
 - (B) Termination occurs at any one of multiple termination sites downstream from the poly A site.
 - (C) After the primary transcript is cleaved at the poly A site, a string of adenosine is added.
 - (D) For short primary transcripts with few introns, splicing usually follows cleavage and polyadenylation.
 - (E) For large genes with multiple introns, introns often are spliced out before transcription is complete.
10. Which statement is incorrect regarding the eukaryotic promoter?
- (A) The eukaryotic promoter region is a segment of DNA located upstream of a gene. However, some core promoter elements can be found downstream of the transcription start site.
 - (B) It contains an RNA polymerase binding site, a transcription start site, and several cis-regulatory sequences.
 - (C) The TATA box is a motif located 25-30 base pairs upstream from the translation start site.
 - (D) The core promoter is the binding site for RNA polymerase and is usually located between -35 and +35 nucleotides from the transcription start site.
 - (E) The Initiator element, composed of the degenerate sequence YYANWYY*, contains the transcription

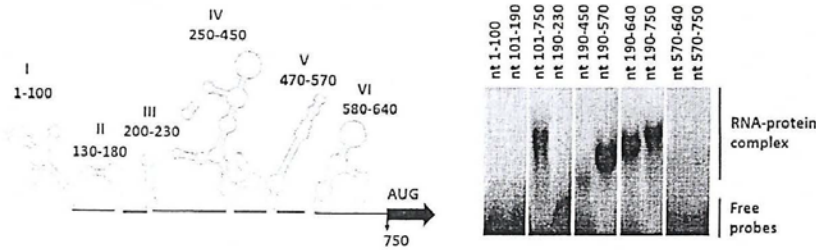
start site.

B. 簡答題 Define the following terms (10 分，每題 2 分)

1. None-sense mediated mRNA decay
2. Cis-acting element
3. Z-DNA
4. Polycistronic mRNA
5. Plaque assay

C. 問答題 Assay question (10 分)

A scientist found that a cellular protein X can interact with the 5'UTR of an RNA virus. He wants to identify the possible binding sites of the 5'UTR to the protein X. The possible interacting secondary structures of the 5'UTR are predicted by him using the Mfold software, which show 6 highly structured stem loops (I-VI). The first and the last nucleotides in each secondary structure are numbered as indicated below. By using the so called EMSA technique, he was able to use different nucleotide probes to identify the binding sites of the 5'UTR to protein X. A figure depicting the result is shown below. Please answer the following four questions.



1. What is EMSA?
2. How many methods you know to generate the nucleotide probes? please describe two of them in details.
3. What is his finding?
4. If the interaction region is in the so called IRES region, what is IRES and what will be the functional relevance of X protein?

第二部分 簡答題與問答題(共 30 分)

1. 1) Please define the CRISPR (Clustered Regularly Interspaced Short Palindromic Repeat) system (6 分).
2) The engineered CRISPR/Cas 9 system has been applied to perform gene editing in mammalian cells and the system often results in a double-strand break (DSB) within the target DNA. Please name the two main repair pathways for DSB and compare the outcomes of these two repair pathways in mammalian cells (8 分).
2. Define the TATA box and the CpG island of eukaryotic genes (6 分).
3. Define the bacterial operon regarding general function and general structure, and use Lac operon to

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describe its regulation (10 分).

第三部分 簡答題與問答題 (共 40 分)

1. RNA sequencing (RNA-seq) is a genome-wide approach for the detection and quantitative analysis of mRNA molecules in a biological sample and is useful for studying cellular responses to stimuli. What is the name for one central molecular biology technique used in this approach? Please list the key ingredients required for using this technique (10 分).
2. Since the discovery that as much as 98% of human genomes do not code for proteins, several classes of non-coding RNA molecules have been reported to regulate the expression of their targets. Please 1) name two different classes of such molecules and 2) specifically list the known mechanism(s) for each class to modulate gene expression (10 分).
3. Please use a table to 1) list the difference (s) between genetic and epigenetic changes, and 2) specifically list their effects on the DNA, RNA and protein after a genetic or epigenetic change on a eukaryotic gene (10 分).
4. RNA-editing processes show great molecular diversity, and some appear to be evolutionarily recent acquisitions that arose independently.
 - 1) Please briefly define RNA editing and its effect on the product of edited gene (5 分)
 - 2) Which of the following statement(s) about RNA editing is correct? (There could be more than 1 answers) (5 分).
 - A) The editosome can edit in 5' to 3' direction along the primary RNA transcript.
 - B) Edited mRNAs could have the amino acid sequence of the encoded protein differs from that predicted by the genomic DNA sequence.
 - C) RNA editing can occur in mRNA, tRNA, rRNA, miRNA and cRNA.
 - D) The diversity of RNA editing phenomenon includes deamination, methylation, and phosphorylation.
 - E) RNA editing can occur in the cell nucleus and cytosol but not mitochondria and plastids.