編號： 330 國立成功大學 107 學年度碩士班招生考試試題

系　　所：醫學檢驗生物技術學系

考試科目：分生與細胞生物　　考試日期：0206，節次：1

※ 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。

簡答題 (共 100 分)

1. Describe the regulatory mechanism of trp operon （6 分） and its regulation by attenuation （4 分）

2. What is CRISPR and how it works? （10 分）

3. Describe the sequential steps of protein translation （5 分）

4. If you are given a piece of fresh mouse liver tissue and all the required reagents for gene cloning, please briefly describe how you can clone a liver gene-X into vector Y step-by-step and how you can make sure you have the correct gene sequence. （15 分）

5. 請寫出三種主要的 Cell Junction 種類，並解釋他們的功能為何? (6 分)

6. Please compare the difference between Sanger DNA sequencing and next generation sequencing (NGS). （4 分）

7. 請詳細說明 lagging strand DNA replication 的複製過程？（10 分）

8. List the enzymes and proteins involved in DNA replication and their functions. （15 分）

Please read the abstract and answer the following questions:

9. Methods for the targeted disruption of protein function have revolutionized science and greatly expedited the systematic characterization of genes. Two main approaches are currently used to disrupt protein function: DNA knockout and RNA interference, which act at the genome and mRNA level, respectively. A method that directly alters endogenous protein levels is currently not available. Here, we present Trim-Away, a technique to degrade endogenous proteins acutely in mammalian cells without prior modification of the genome or mRNA. Trim-Away harnesses the cellular protein degradation machinery to remove unmodified native proteins within minutes of application. This rapidity minimizes the risk that phenotypes are compensated and that secondary, non-specific defects accumulate over time. Because Trim-Away utilizes antibodies, it can be applied to a wide range of target proteins using off-the-shelf reagents. Trim-Away allows the study of protein function in diverse cell types, including non-dividing primary cells where genome- and RNA-targeting methods are limited. (Cell 171:1692-1706, 2017.)
   a. Give a title for this abstract (in English). （2 分）
   b. Describe the main proteolytic pathways in eukaryotes. （5 分）
   c. Give examples of genome- and RNA-targeting methods for interfering with protein expression. （8 分）

10. "YAP is a mechanosensitive transcriptional activator with a critical role in cancer, regeneration, and organ size control. Here, we show that force applied to the nucleus directly drives YAP nuclear translocation by decreasing the mechanical restriction of nuclear pores to molecular transport. Exposure to a stiff environment leads cells to establish a mechanical connection between the nucleus and the cytoskeleton, allowing forces exerted through focal adhesions to reach the nucleus. Force transmission then leads to nuclear flattening, which stretches nuclear pores, reduces their mechanical resistance to molecular transport, and increases YAP nuclear import. The restriction to transport is further regulated by the mechanical stability of the transported protein, which determines both active nuclear transport of YAP and passive transport of small proteins. Our results unveil a mechanosensing mechanism mediated directly by nuclear pores, demonstrated for YAP but with potential general applicability in transcriptional regulation." (Cell 171: 1397-1410, 2017.)

a. Give a title for this abstract (in English). （2 分）
b. Describe three types of cytoskeletons and their functional roles in cell biology. （8 分）