

第一大題，選擇題 ※ 注意：請於試卷內之「選擇題作答區」依序作答。

1. 在原核生物的 RNA 轉錄作用中，所謂的“holoenzyme”係指下列何者？(2 分)
 - (A) $\alpha 2\beta 2\omega + \sigma$
 - (B) $\alpha 2\beta 2\sigma + \omega$
 - (C) $\alpha 2\beta\beta' + \sigma$
 - (D) $\alpha 2\beta\beta'\sigma + \omega$
2. 真核細胞 RNA polymerase CTD tail 的磷酸化修飾，與 RNA 轉錄及 RNA processing 因子的徵募(recruitment)有關。下列配對何者正確？(2 分)
 - (A) elongation 時，Ser2 需被磷酸化
 - (B) promoter escape 需要 Ser2 磷酸化
 - (C) polyadenylation 時，Ser5 需被磷酸化
 - (D) preinitiation complex 的 Ser5 會被磷酸化
3. 在真核生物 RNA 轉錄結束(termination)時，哪一個 model 需要其它蛋白質參與？(2 分)
 - (A) Allosteric model
 - (B) Rho-dependent model
 - (C) Scrunching model
 - (D) Torpedo model
4. 下列何者會辨認 5' splice site? (2 分)
 - (A) BBP (branchpoint-binding protein)
 - (B) U1 snRNP
 - (C) U2AF 65 subunit
 - (D) U2AF 35 subunit
5. 下列有關 RNA editing 的敘述，何者正確？(2 分)
 - (A) 可經由 pyrophosphorolytic editing 進行
 - (B) APOBEC1 可透過 guide RNA 修飾 RNA 的序列
 - (C) 不會造成 RNA 序列的插入(insertion)或缺失(deletion)
 - (D) apolipoprotein B 主要透過 cytidine deaminase 修飾 RNA 的序列

第二大題，簡答題

6. 請畫出原核生物 promoter 上的基本構造及相關位置 (5 分)。
7. 請敘述原核生物的 RNA polymerase 從 closed complex 轉換到 open complex 過程中所產生的構造改變 (5 分)。
8. 何謂 Spliceosome (5 分)。
9. 請任意列舉 5 種人類或大腸桿菌中的 DNA polymerase 並說明其生理功能。(5 分)

第三大題，簡答：抽取細胞 DNA 以吸光度 A260/280 可進行純度分析，一般為 1.6-1.8 之間，

10. 若 DNA 測得 A260/280 = 1.5 則可能受到細胞中那種物質污染，可以用什麼方法再純化？(4 分)
11. 若 DNA 測得 A260/280 = 1.9 則可能受到細胞中那種物質污染，可以用什麼方法再純化？(4 分)

見背面

第四大題，簡答：人類基因體中超過六成以上為基因間序列(intragenic sequences),

12. 試問這些基因間序列的起源為何? (4分)

13. 上述基因間序列可能有那些生物功能? (4分)

14. 列舉特定的 intragenic sequences 可以應用在檢驗及司法鑑定的用途。(4分)

第五大題，情境題

Scientists recently found the association of genetic mutations with a specific type of early onset muscular dystrophy. Several different mutations have been found in *mus-1*, a gene that is specifically expressed in skeletal muscles. Although both men and women could be affected, in several families with *mus-1* mutation, men bearing *mus-1* mutation usually show symptoms at earlier ages and with higher severity than women. The research team found that, when *mus-1* homolog is deleted in mice, embryogenesis failed.

15. Based on the description, the mutations associated with the disease are most likely be: (2分)

(A) Deletion

(B) Nonsense mutation

(C) Missense mutation

(D) Transverse mutation

(E) Chromosome rearrangement

16. Which of the following would best describe the familiar muscular dystrophy described above? (3分)

(A) autosomal recessive

(B) autosomal dominant

(C) sex-linked recessive

(D) sex-linked dominant

17. The research team examined muscle samples from affected individuals in this particular family, and found unknown aggregates around the muscle fibers. The scientists proposed the aggregates are formed by the mutated Mus-1 protein. Please describe one experiment that would test this hypothesis. (問答 5分)

18. In another family affected by this disease, the researchers found a shorter Mus-1 protein. After further investigation, they found the protein lack of a small portion at its C-terminus. Suppose this family is affected by a single nucleotide change of the *mus-1* gene, please speculate how a point mutation would lead to shorter protein. (問答 5分)

第六大題問答題

19. Many virus hijack the translation machinery after entering the host cell. Please give an example of such, and contrast the translation machinery with and without viral infection. (5分)

20. What is nonsense-mediated mRNA decay? How is this pathway important for the quality control of gene expression? (5分)

第七大題，分子生物學技術簡答題

21. Next-generation sequencing (NGS) technology is a powerful tool to achieve precision medicine. Please describe TWO principles of NGS technology and the application of NGS in the medical research. (5分)

接次頁

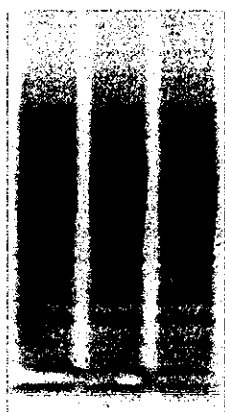
22. If we want to know the possibility of whether A protein can physically interact with B protein in the cell, what kind of experiments in vitro and in vivo you can perform to proof? (5 分)

23. You just identified a novel mutation in a gene and it may be a potential cancer driver mutation. How can you proof its driver mutation role by serial experiments and propose its application in clinical therapy? (5 分)

24. Real-time quantitative polymerase chain reaction (RT-QPCR) is a technique widely used for nucleic acid quantification. Please compare SYBR-green and TaqMan QPCR in principle, advantage, disadvantage, and application issues. (5 分)

25. Western blot is a widely used technique for protein expression analysis. However, results with stability, reliability, and reproducibility require a well-trained skill. Please try to analyze the possible cause of each Western blot result in below. (M, marker) (5 分)

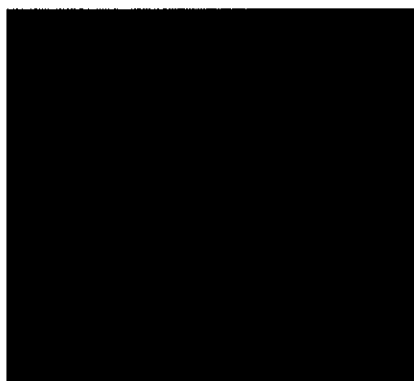
A.



← Protein interested

B.

M



C.

M

