

1. List three major differences between DNA and RNA structures. (6%)
2. Explain why life may have evolved from an RNA world. (4%)
3. Define the following terms:
 - (1) nucleoid (3%)
 - (2) nucleosome (3%)
 - (3) telomere (3%)
 - (4) Okazaki fragment (3%)
4. Describe two ways how DNA polymerases control the fidelity of replication. (4%)
5. What is the role of base flipping in DNA repair? What does the repair machinery accomplish by relying on this phenomenon? (4%)
6. miRNAs and siRNAs are small RNAs that play an important role in eukaryotic gene silencing.
 - (1) What do siRNA and miRNA stand for? (2%)
 - (2) What are their differences in terms of origins? (4%)
 - (3) Both RNAs employ similar mechanisms to silence expression. Briefly describe their mechanism in gene silencing. (4%)
7. Answer the following questions about DNA sequencing:
 - (1) The Sanger method has stood as the gold standard DNA sequencing technique over the last three decades. Please describe the key principle of Sanger sequencing. (3%)
 - (2) Sanger method is considered as the 'first-generation' technology, and the newer approaches for high throughput DNA sequencing introduced recently have been regarded as next-generation sequencing (NGS) technologies. One of the most widely-used NGS techniques is pyrosequencing. Please explain the key principle of pyrosequencing. (4%)
 - (3) What is the major advantage of pyrosequencing in comparison to Sanger sequencing? (3%)
8. Please define the following terms: (24%)
 - (1) UP element of the bacterial promoter
 - (2) The carboxy-terminal domain (CTD) of RNA polymerase II
 - (3) Allolactose
 - (4) Serine/Arginine-rich (SR) protein
 - (5) Heterochromatin protein 1 (HP1)
 - (6) Transposon
 - (7) Internal ribosome entry site (IRES)-mediated translation
 - (8) Shine-Dalgarno sequence
9. Gcn4 is a transcription factor that directs amino acid biosynthesis in yeast. Please explain how short upstream ORFs control Gcn4 translation? (6%)
10. Spinal muscular atrophy (SMA) is a kind of motor neuron disease. Please explain the defect in pre-mRNA splicing of SMA that causes deficiency in the full-length SMN protein. (6%)
11. Histone codes play a crucial role in transcriptional regulation in eukaryotes. Posttranslational modifications of Lys-9 (K9) and Ser-10 (S10) on the tail of histone H3 are well known. Please describe how chromatin modifications of K9 and S10 influence each other. (6%)
12. How does transcriptional termination regulate lytic development of bacteriophage lambda? (8%)