注意：請於答案卷上依序作答，並應註明作答之題號

(一) 配合題：

Match each of the numbered words with the following *E. coli* DNA replication, recombination, and repair enzymes. Each enzyme may be used once, more than once, or not at all. (1 point/question)

___A___ catalyzes the decatenation of two circular replication products

___B___ bound to hemimethylated DNA inhibits reinitiation from recently replicated daughter origin.

___C___ can increase the processivity of assocated DNA polymerases.

___D___ is a specialized RNA polymerase to making short RNA primers on a single-stranded DNA template.

___E___ unwinds the DNA at the replication fork creating a single-stranded DNA template.

___F___ is the primary enzyme involved in the replication of *E. coli* chromosome.

___G___ and ___H___ can remove RNA primer.

Mutiple ___J___ proteins bind to the repeat sequence within *oriC* during the initiation of DNA replication.

___K___ cleaves specific DNA strands at the Holliday junction to complete recombination.

___L___ specifically recognizes Holliday junctions and promote branch migration.

___M___ assembles on single-stranded DNA and promotes strand invasion to initiate recombination.

___N___ possesses multiple enzymatic activities of helicase and nuclease which processes broken DNA molecules to generate regions of ssDNA for recombination.

___O___ and ___P___ are capable of translesion DNA synthesis that synthesize DNA directly across the site of the damage.

In nucleotide excision repair, a complex of ___Q___ and ___R___ scans the DNA to detecting damages.

In base excision repair, ___S___ recognizes and removes the damaged base resulting an abasic sugar.

___T___ directly reverses the formation of pyrimidine dimmers that result from ultraviolet irradiation damage.

Mismatches arise from replication errors are detected by a dimer of the mismatch repair protein ___U___.

1. β-proteins (sliding DNA clamp)
2. Dam methyltransferase
3. DNA glycosylase
4. DNA helicase
5. DNA ligase
6. DNA photolyase
7. DNA polymerase I
8. DNA polymerase II
9. DNA polymerase III
10. DNA polymerase IV (Din B)
11. DNA Polymerase V (UmuC)
12. DNA topoisomerase I
13. DNA topoisomerase II
14. DnaA
15. DnaB
16. DnaC
17. MutH
18. MutL
19. MutS
20. MutT
21. Primase
22. RecA
23. RecBCD
24. RNase H
25. RuvAB
26. RuvC
27. SeqA
28. Single-stranded binding protein
29. UvrA
30. UvrB
31. UvrC
32. UvrD

見背面

問答題

(二) Please describe the functions of σ factor in bacteria (15 points).

(三) Please describe the mechanisms proposed to ensure the occurrence of mutually exclusive splicing (15 points).

請簡述題(四-六)所列方法之原理及應用

(四) Electrophoretic mobility-shift assay (5 points)

(五) Chromatin immunoprecipitation assay (5 points)

(六) 請舉一例簡述 Shotgun sequencing 之作法 (10 points)

Short-Answer questions (七-十): Please be concise.

(七) What is one possible reason why nonstandard base pairing (wobble) is allowed during protein synthesis? (4 points)

(八) 5'-CAU-3' is a codon in mRNA that specifies the amino acid histidine in the position 59 of human protein A. (6 points)

(a) What is the corresponding anticodon in tRNA?

(b) What is the corresponding triplet in the coding DNA strand?

(c) What is the corresponding triplet in the template DNA strand?

(九) Describe how siRNA functions in regulation of expression and how this can be used as a tool in genetic research. (5 points)

(十) Several common protein structural motifs are now known to be involved in DNA recognition and binding in eukaryotic transcription factors. What are these, and how would researchers use genomic data to help figure out if new candidate genes encode such DNA-binding proteins? (5 points)

(十一) True-False questions: Please indicate whether each statement is true (O) or false (X). If false, <u>the points will only be credited when the statement is corrected</u> (2 points each).

1. During the termination of protein biosynthesis, hydrolysis of the bound ATP is accompanied by cleavage of peptide chain from tRNA in the P site and release of the tRNAs and the two ribosomal subunits.

2. Polysomes and rapid ribosome recycling increase the efficiency of translation.

3. A mutation causes a G to be inserted after the first base of the codon for tryptophan. Therefore, there will be a single amino acid substitution in the growing polypeptide chain.

4. Ribozymes in the small ribosomal subunit catalyze peptidyl transferase activity during translation elongation.

5. DNA acetylation plays an important role in genetic imprinting.

試題隨卷繳回