1. (a) How would you verify this nucleosome map in the UAS of your target gene? How would your final gel look like? 2 + 1 \frac{1}{2}

(b) How would you assay SWI/SNF mediated nucleosome sliding? 2

(c) Give an example where nucleosomes are permissive for transcription. 1

Or

2. (a) How would you prove that abundance of H4Ac is highest in +/- 500 bp of TSS of your target gene? 3

(b) What is a 10 bp ladder? 2

(c) Compare Solenoid and Zigzag model of 30 nm fibre. 1 \frac{1}{2}

3. (a) What are histone variants? Name a histone variant involved in (i) DNA damage pathway; (ii) transcription regulation. Name the centromeric variant of histone H3 and explain how it regulates chromatin structure. 3 \frac{1}{2}

(b) You have subjected the following chromatin template to restriction endonuclease digestion with HpaII or Mspl or both. HpaII cannot cleave methylated DNA sequence; Mspl cleaves methylated DNA sequence. Number
of fragments expected upon each enzyme digestion or a combination of both the enzymes and the transcription status of each gene under normal condition will be:

(i) Hpall- 3  
    MspI- 3  
    Hpall+ MspI- 2  
    Gene X- Off; Gene Y- Off; Gene Z- Off

(ii) Hpall- 2  
     MspI- 2  
     Hpall+ MspI- 3  
     Gene X- Off; Gene Y- Off; Gene Z- Off

(iii) Hpall- 2  
     MspI- 2  
     Hpall+ MspI- 3  
     Gene X- On; Gene Y- On; Gene Z- Off

Or

4. (a) What are histone Chaperones? Apart from histone Chaperones what other factor is critical for a proper chromatin assembly? Name a replication dependent and independent histone chaperone. 1+1+1

(b) A wild type and two mutant histone chaperone proteins (X, Y, Z) are checked for their activity. A mutant show partially compromised activity, while the other show greater loss of function as compared to wild type. Can you suggest which one is wild type and the two mutants?
5. (a) Mention the name of major core and common subunit of eukaryotic RNA polymerase.
   (b) TBP helps RNA polymerase to recognize TATA box — how it acts when there is no TATA in a promoter?
   (c) What are the function of TF II H and TF II B?
   (d) Mention the name and role of one elongation factor is eukaryotic transcription. 1+1+2+1

Or

6. (a) Which factor stimulates proofreading of transcripts during eukaryotic transcription?
   (b) Describe the major features of class I and class II promoter element.
   (c) Describe the process of "repressor-directed histone deacetylation". 1+2+2

7. (a) Show diagrammatically the processing of pre-rRNA and ribosomal assembly in vertebrates. 2
   (b) Mention the role of RnaseP AND RnaseD in tRNA processing. 1
   (c) How 7-methylguanosine residue is formed at the 5' terminal of mRNA? 2

Or

8. (a) Protein diversity can be generated at the level of mRNA processing by:
   (i) Alternative splicing
   (ii) RNA interference
   (iii) Adding a cap at the 5' end and a poly (A) tail at the 3' end
   (iv) Splicing
   (v) RNA degradation.
   (b) Discuss in brief the different pathways by which mRNA can be degraded. 2
   (c) What is pseudoxons? How is it involved in diseases state? 2

For Neatness — 2