

This examination paper consists of 4 pages.

Appendices: none

Permitted materials: none

The number of answers for each question must match the number shown in brackets to the right.

1. RNA synthesis

- proceeds in 3'→5' direction
 - is catalyzed by an RNA polymerase
 - can be initiated at any site on the DNA strand
 - requires dATP, dTTP, dGTP, and dCTP
 - is facilitated by DNA supercoiling
- (2)

2. RNA can be processed by

- chemical modification
 - addition of a 5' cap
 - addition of sugar molecules
 - splitting off the 3' untranslated region
 - joining the 5' and 3' ends by RNA ligase
 - cutting into pieces
- (3)

3. Bacterial genomes

- do not contain transposable elements (transposons)
 - are always circular
 - are compacted by supercoiling
 - frequently contain operons
 - are normally diploid
- (2)

4. Linkage analysis

- is used in physical mapping
 - is based on Mendel's laws
 - can only be used with prokaryotes
 - is based on recombination frequencies
 - requires unlinked genes
- (2)

5. Base stacking

- occurs in DNA
 - does not occur in RNA
 - occurs in DNA-binding proteins
 - destabilizes molecules
 - involves hydrophobic interactions
- (2)

6. Retrotransposition

- requires a reverse transcriptase
 - can be replicative or conservative
 - involves a DNA copy of the transposon
 - is only found in eukaryotes
 - involves a transposase enzyme
- (3)

7. Histones

- are proteins
 - contain nucleic acids
 - are synthesized in nuclei
 - are parts of nucleosomes
 - are bound to membranes
- (2)

8. Possible functions of genes

- can be assigned by homology searching
 - can be probed by directed mutagenesis
 - can be deduced from their location in genomes
 - can be found by exon trapping
 - are known for most genes in sequenced genomes
- (2)

9. Telomers are located

- at the ends of ribosomal RNA
 - in centromers
 - in the middle of chromosomes
 - at the ends of chromosomes
 - in nuclear DNA
 - in mitochondrial DNA
 - in prokaryotes
 - in eukaryotes
- (3)

10. Interspersed repetitive DNA

- can be microsatellites
 - can be minisatellites
 - can be retrotransposons
 - can be DNA transposons
 - can be pseudogenes
- (2)

11. Members of a multigene family

- have largely identical sequences
 - are always clustered on the same chromosome
 - are often not expressed at the same time
 - cannot be pseudogenes
- (2)

12. **PCR is used for**

- reverse transcribing RNA into DNA
 - digesting proteins
 - digesting DNA
 - copying plasmids
 - amplifying DNA
 - amplifying proteins
- (1)

13. **Partial linkage**

- is found for genes on different chromosomes
 - is the basis for genetic mapping
 - can be demonstrated by cross-breeding experiments
 - was discovered by Gregor Mendel
 - might occur during mitosis
- (2)

14. **DNA sequencing by the chain termination method results in sequences of maximum**

- 100-200 bp
 - 400-500 bp
 - 600-800 bp
 - 900-1100 bp
 - 1200-1400 bp
- (1)

15. **Genetic maps**

- are usually less accurate than physical maps
 - are based on polymorphic sequences
 - use a clone library as mapping reagent
 - are deduced from linkage analyses
 - use only genes or tandem repeats as markers
- (3)

16. **Operons**

- are characteristic for eukaryotic genomes
 - contain more than one gene
 - contain more than one promoter
 - contain always similar genes
 - contain almost no intergenic sequences
- (2)

17. **All restriction enzymes**

- are isolated from bacteria
 - cut only in the DNA motif that they bind to
 - cut only in sequences containing Gs and Cs
 - create either cohesive ("sticky") or blunt ends
 - digest DNA from one end of the molecule
 - are proteins
- (3)

18. Transformation

- converts DNA into RNA
- converts RNA into proteins
- joins two DNA fragments
- cuts DNA into fragments
- introduces DNA into cells
- removes genomes from cells
- is used in cloning of DNA

(2)

19. Most R-groups of the 20 amino acids in proteins are

- non-polar
- polar
- negatively charged
- positively charged

(1)

20. Microsatellites

- are interspersed genome-wide repeats
- are usually shorter than 150 bp
- are not in the same position of the genome in different individuals
- are often found in retroviruses
- can easily be amplified by PCR

(2)