1 Mark Questions

1. Nucleolus is involved in the synthesis of
(a) *r*RNA (b) *t*RNA
(c) DNA (d) *m*RNA

2. In tryptophan operon, tryptophan acts as
(a) repressor (b) activator
(c) co-repressor (d) co-activator

3. Positive selection of T-cells ensures
(a) MHC restriction
(b) self tolerance
(c) TCR engagements
(d) activation by co-stimulatory signal

4. A DNA-binding motif is
(a) helix-loop-helix (b) helix-turn-helix
(c) helical wheel (d) loop-helix-wheel

5. Amino acids responsible for N-linked and O-linked glycosylation of proteins are
(a) asparagine and aspartic acid
(b) glutamine and serine
(c) glutamic acid and serine
(d) asparagine and threonine

6. One of the following compounds is not a neurotransmitter
(a) dopamine (b) glutamic acid
(c) histidine (d) glycine

7. Approximate molecular weight (kDa) the product after translation of a 390 bases *m*RNA will be
(a) 48 (b) 26
(c) 39 (d) 14

8. Lineweaver-Burk plot is a plot of
(a) $\frac{1}{v^0}$ *vs* $\frac{1}{[S]}$ (b) v_0 *vs* $[S]$
(c) v_0 *vs* $\frac{1}{[S]}$ (d) $\frac{1}{v_0}$ *vs* $[S]$

9. A mixture of proteins (W, X, Y, Z) elute from Sephadex G-200 column in the order W, X, Y, Z. The protein with maximum electrophoretic mobility on SDS-PAGE will be
(a) W (b) X
(c) Y (d) Z

10. Specific precursor for all prostaglandins is
(a) Oleic acid (b) Arachidonic acid
(c) Palmitic acid (d) α-Linolenic acid

2 Marks Questions

11. Chymotrypsin and lysozyme are involved respectively in
A. Removal of successive carboxyl terminal residues
B. Hydrolytic eleavage of peptide bond
C. Cleavage of glycosidic C—O bond
D. Oxygen transport in blood
(a) A and B (b) B and C
(c) B and D (d) C and D

12. Match the items in group I with those in group II.

Group I	Group II
A. Isotype switching	1. V_H domain
B. Clonal energy	2. Non-responsive to self antigen
C. Class II MHC	3. Non-responsive T_H cells
D. Self tolerance	4. β_2-microglobulin

	A	B	C	D
(a)	1	4	3	2
(b)	2	4	1	3
(c)	1	3	4	2
(d)	2	1	3	4

13. Multiple RNA plymerase transcribes a DNA template, unwinding about 1.5 turns of DNA template per transcription bubble. From the structural information of classical B-DNA, how many transcription bubbles are possible for a 180 base pair DNA molecule?
(a) 12 (b) 27
(c) 6 (d) 270

14. Match the items in group I with the most appropriate separation techniques in group II.

Group I	Group II
A. Mixture of glycine and albumin	1. Gas chromatography
B. Mixture of 20 and 60 kDa proteins	2. Dialysis
C. Histones from nuclear extract	3. Affinity chromatography
D. Lectins	4. Size exclusion chromatography
	5. Thin layer chromatography
	6. Cation exchange chromatography

	A	B	C	D
(a)	1	4	3	5
(c)	2	4	6	3

	A	B	C	D
(b)	5	3	6	1
(d)	6	5	2	4

15. In the two half reactions

$$\text{Acetaldehyde} + 2H^+ 2e^- \longrightarrow \text{Ethanol}$$

$$\Delta E^0 = -0.16\ V$$

$$NADH + H \rightarrow NAD + 2H^+ + 2e^-$$

$$\Delta E^0 = 0.32\ V$$

$$F = 23{,}063\ cal/V)$$

The ΔG° for coupled reaction will be

(a) + 7,400 cal (b) − 7,400 cal
(c) − 22,200 cal (d) + 22,200 cal

16. Match the parameters in group I with the correct options in group II.

Group I	Group II
A. K_m	1. Catalytic efficiency of the enzyme
B. K/K_m	2. Affinity of enzyme to the inhibitor
C. pk_a	3. Affinity of enzyme to the substrate
D. k_i	4. Maximum buffering capacity

	A	B	C	D
(a)	3	1	2	4
(c)	1	2	4	3

	A	B	C	D
(b)	3	1	4	2
(d)	1	4	2	3

17. The rise per residue of α-helix is about 1.5 A. A protein spans 4 nm bilayer 7 times through its transmembrane α-helical domain. Approximately, how many amino acid residues constitute the transmembrane domain of the protein?

(a) 105 (b) 450
(c) 30 (d) 190

18. Match the proteins in group I with their correct functions in group II.

Group I	Group II
A. Shaker protein	1. Inner membrane receptor
B. Bacteriorhodopsin	2. Active transport
C. Porin	3. Voltage gated K^+ channel
D. ABC transporter	4. Light driven H^+ pump
	5. Membrane fusion
	6. β-barrel simple diffusion channel

	A	B	C	D
(a)	4	2	3	5
(c)	6	1	5	4

	A	B	C	D
(b)	5	3	4	6
(d)	3	4	6	2

19. The metabolic disorders, alkaptonuria and phenylketonuria are caused by defects in the enzymes'

A. Glucose 6- phosphatase
B. Phenylalanine hydroxylase
C. Homogentisate 1, 2-dioxygenase
D. Tyrosinase

(a) B and C (b) A and C
(c) A and B (d) B and D

20. Match the metabolic pathways in group I with the corresponding enzymes in group II.

Group I	Group II
A. β-oxidation	1. Ribulose bisphosphate carboxylase
B. Glycolysis	2. Phosphofractokinase 1
C. Gluconeogenesis	3. Phosphenol pyruvate carboxykinase
D. Calvin cycle	4. Thiolase
	5. Phosphofructokinase 2

	A	B	C	D
(a)	4	2	3	5
(c)	3	1	5	2

	A	B	C	D
(b)	3	2	4	1
(d)	4	2	3	1