GATE Biotechnology

Sample Paper – 9

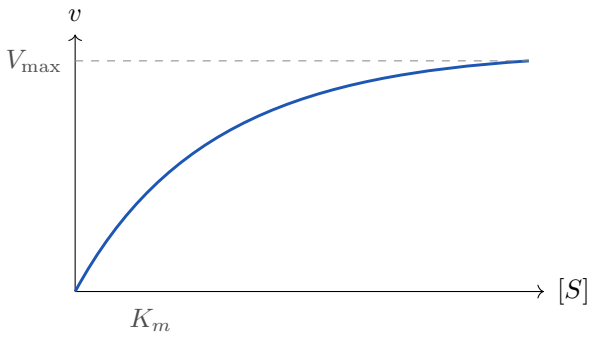
Duration: 128 Minutes **Maximum Marks: 72**

Instructions

- This paper contains **46 questions** covering the core **Biotechnology** subject of the GATE paper conducted by the IITs and IISc (General Aptitude and Engineering Mathematics are provided as separate papers).
- **Q1–Q20 carry 1 mark each** and **Q21–Q46 carry 2 marks each**, for a total of **72 marks**.
- Each question carries **negative marking of one-third of its allotted marks**: a wrong 1-mark question costs **0.33** and a wrong 2-mark question costs **0.67**. Unattempted questions carry no penalty.
- Every question here is a single-correct **MCQ**. The real GATE paper also has Multiple Select (MSQ) and Numerical Answer Type (NAT) questions, and **those carry no negative marking**.
- Attempt this paper in one timed sitting of about **128 minutes**, the share this core subject earns at GATE's overall pace of 180 minutes for 65 questions. Use $R = 8.314$ J mol^{-1}K^{-1}, take $\ln 2 = 0.693$ and $\ln 10 = 2.303$ where required, unless stated otherwise.

Biochemistry

Q1. An enzyme obeying Michaelis–Menten kinetics has a maximum velocity $V_{\max} = 120$ μmol min^{-1} and a Michaelis constant $K_m = 2$ mM, as sketched below. The initial reaction velocity when the substrate concentration $[S] = 6$ mM is: [1 mark]



(A) 90 μmol min^{-1}

(B) 60 μmol min^{-1}

(C) 120 μmol min^{-1}

(D) 30 μmol min^{-1}

Q2. According to Anfinsen's classic refolding experiments on ribonuclease, the information needed for a protein to fold into its correct native three-dimensional structure is contained entirely in its: **[1 mark]**

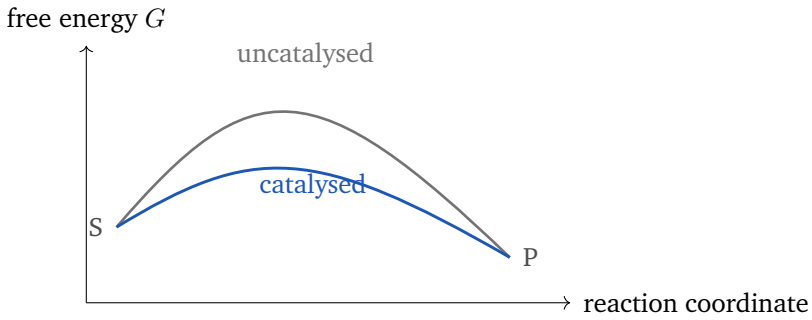
(A) ribosome that synthesised it

(B) chaperone proteins alone

(C) mRNA cap structure

(D) amino-acid sequence (primary structure)

Q3. The free-energy profile of a reaction is shown below, both without an enzyme and with an enzyme present. An enzyme speeds up the reaction by lowering the activation energy; it does this mainly by binding to and stabilising the: **[1 mark]**



(A) substrate in its ground state

(B) free product molecule

(C) transition state of the reaction

(D) free (unbound) enzyme

Q4. Many soluble proteins contain stretches of right-handed α-helix, a regular secondary structure stabilised by intrachain hydrogen bonds. The number of amino-acid residues per complete turn of a right-handed α-helix is closest to: **[1 mark]**

(A) 3.6

(B) 2.0

(C) 10.0

(D) 7.0

Q5. Serine proteases such as chymotrypsin cleave peptide bonds using a set of three closely spaced active-site residues, called the catalytic triad, that act together to make the serine hydroxyl a strong nucleophile. The three residues of this classical triad are: **[1 mark]**

(A) serine, histidine and aspartate

(B) cysteine, histidine and asparagine

(C) lysine, arginine and aspartate

(D) serine, threonine and tyrosine

Q6. The amino acid glycine has two ionisable groups, with pK_{a1} (the α-carboxyl group) $= 2.3$ and pK_{a2} (the α-amino group) $= 9.6$. Its isoelectric point (pI), the pH at which it carries no net charge, is nearest to: **[1 mark]**

(A) 2.3

(B) 9.6

(C) 11.9

(D) 6.0

Microbiology

Q7. Certain archaea isolated from deep-sea hydrothermal vents grow best at temperatures above $80\ ^\circ$C and cannot grow below about $60\ ^\circ$C. On the basis of their temperature requirement, such organisms are classified as: **[1 mark]**

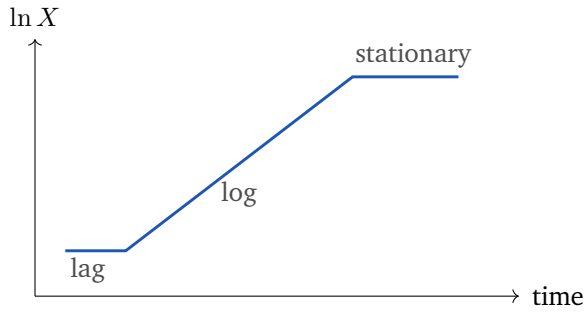
(A) psychrophiles

(B) hyperthermophiles

(C) mesophiles

(D) neutrophiles

Q8. During exponential growth a bacterial population increases from 10^4 cells to 10^7 cells in exactly 5 hours, as sketched on the semi-log plot below. The generation (doubling) time of this culture is nearest to: **[1 mark]**



(A) 15 min

(B) 20 min

(C) 30 min

(D) 45 min

Q9. *Halobacterium* species from salt lakes require a very high salt concentration (around 15–30% NaCl) for growth and lyse in dilute media. Such organisms, which grow only at high ionic strength, are called: **[1 mark]**

(A) barophiles

(B) extreme halophiles

(C) alkaliphiles

(D) thermophiles

Q10. Some bacteria can grow either in the presence or in the absence of oxygen: they use aerobic respiration when oxygen is available, but switch to fermentation when it is not. With respect to oxygen, such organisms are best described as: [1 mark]

(A) obligate aerobes

(B) facultative anaerobes

(C) obligate anaerobes

(D) aerotolerant only

Q11. Certain chemolithotrophic bacteria found in acid mine drainage grow optimally at a pH between 1 and 3 and cannot survive at neutral pH. On the basis of their pH requirement, such organisms are classified as: [1 mark]

(A) acidophiles

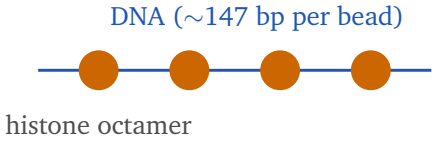
(B) neutrophiles

(C) alkaliphiles

(D) halophiles

Cell Biology and Molecular Biology

Q12. Eukaryotic DNA is packaged with histone proteins into a beads-on-a-string arrangement, as shown. The basic repeating unit of chromatin, in which about 147 base pairs of DNA are wrapped around a core of eight histone molecules, is the: [1 mark]



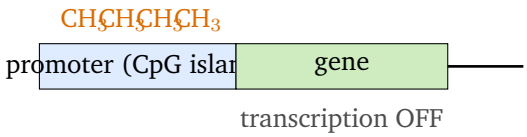
(A) solenoid

(B) nucleosome

(C) chromatid

(D) centromere

Q13. In the mammalian genome, methyl groups are often added to cytosine bases within CpG islands located in the promoter region of a gene, as shown below. Such heavy promoter methylation usually results in: [1 mark]



(A) strongly increased transcription

(B) transcriptional silencing of the gene

(C) a permanent change in the DNA base sequence

(D) faster DNA replication of the region

Q14. Histone acetyltransferases (HATs) transfer acetyl groups onto lysine residues in the tails of core histones, neutralising their positive charge. This acetylation generally leads to: [1 mark]

(A) a more open (loosened) chromatin and increased transcription

(B) tighter chromatin packing and gene silencing

(C) degradation of the histone proteins

(D) no change in chromatin structure

Q15. In eukaryotes the primary RNA transcript (pre-mRNA) contains introns that must be removed and exons that must be joined together before translation. The large ribonucleoprotein machine that carries out this removal of introns is the: [1 mark]

(A) ribosome

(B) proteasome

(C) nucleosome

(D) spliceosome

Q16. Interphase chromatin can be divided into two forms on the basis of how tightly it is packed. The highly condensed, densely staining and generally transcriptionally inactive form is called: **[1 mark]**

(A) heterochromatin

(B) euchromatin

(C) the nucleolus

(D) the kinetochore

Q17. Genomic imprinting and X-chromosome inactivation are classic biological examples of an epigenetic phenomenon. An epigenetic modification is best defined as: **[1 mark]**

(A) a permanent change in the DNA base sequence

(B) a large deletion of a chromosome segment

(C) a heritable change in gene expression that does not alter the DNA sequence

(D) a random point mutation in the coding region

Q18. During translation the ribosome moves along the messenger RNA and reads its codons one after another in a fixed direction to build the polypeptide from its amino end. The direction in which the mRNA is read by the ribosome is: **[1 mark]**

(A) $3' \rightarrow 5'$

(B) in both directions at once

(C) $5' \rightarrow 3'$

(D) in a random order

Genetics, Immunology and Evolution

Q19. A large randomly mating population is at Hardy–Weinberg equilibrium for a single gene with two alleles. The frequency of homozygous recessive individuals (genotype aa) is 0.09. The frequency of the recessive allele in this population is: **[1 mark]**

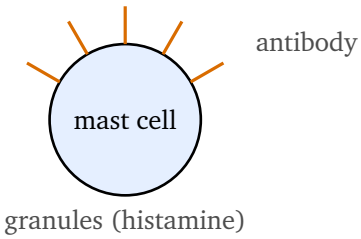
(A) 0.09

(B) 0.3

(C) 0.7

(D) 0.42

Q20. Immediate (Type I) hypersensitivity reactions, such as hay fever, allergic asthma and anaphylaxis, occur when an allergen cross-links antibodies bound to mast cells and triggers histamine release, as sketched. The class of antibody responsible for these reactions is: **[1 mark]**



(A) IgG

(B) IgM

(C) IgA

(D) IgE

Genetics, Immunology and Evolution (continued)

Q21. The tuberculin (Mantoux) skin test produces a firm, red swelling that reaches its maximum 48–72 hours after antigen injection. This classic delayed-type (Type IV) hypersensitivity reaction is mediated primarily by: **[2 marks]**

(A) IgE bound to mast cells and basophils

(B) sensitised T lymphocytes and the macrophages they activate

(C) IgG antibodies together with the complement system

(D) circulating antigen–antibody immune complexes

Q22. In diseases such as rheumatoid arthritis, systemic lupus erythematosus and type 1 diabetes mellitus, the immune system loses tolerance and mounts a response against the body's own molecules and tissues. Disorders of this kind are collectively described as: [2 marks]

(A) immunodeficiency disorders

(B) autoimmune disorders

(C) allergic (atopic) disorders

(D) neoplastic disorders

Q23. Type III hypersensitivity reactions, such as serum sickness and the Arthus reaction, cause tissue damage through complement activation and neutrophil-driven inflammation. The trigger for a Type III reaction is the tissue deposition of: [2 marks]

(A) IgE anchored on the surface of mast cells

(B) sensitised cytotoxic ($CD8^{+}$) T cells

(C) free histamine released from basophils

(D) soluble antigen–antibody (immune) complexes

Q24. Random changes in allele frequency from one generation to the next, arising purely from sampling error during reproduction, are called genetic drift. The effect of genetic drift on allele frequencies is strongest in: [2 marks]

(A) very large populations

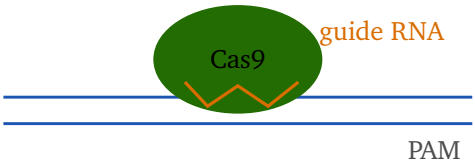
(B) populations already fixed at equilibrium

(C) small populations

(D) populations with a very high immigration rate

Recombinant DNA Technology and Bioinformatics

Q25. In the CRISPR–Cas9 genome-editing system, shown schematically below, the Cas9 nuclease is brought to its precise DNA target by base pairing between a short RNA molecule and the target sequence. The component that provides this target specificity is the: **[2 marks]**



(A) the tracrRNA scaffold acting alone

(B) the PAM sequence on the DNA

(C) the guide RNA (single-guide RNA)

(D) a restriction endonuclease

Q26. The Cas9 nuclease will cut a target DNA sequence only if a specific short sequence lies immediately next to (just $3'$ of) the target site on the DNA. This obligatory recognition sequence, whose absence protects the CRISPR array itself from being cut, is the: **[2 marks]**

(A) TATA box of the promoter

(B) AUG start codon

(C) origin of replication

(D) PAM (protospacer adjacent motif)

Q27. After Cas9 makes a double-strand break, a targeted gene is most often knocked out because the break is resealed by an error-prone repair pathway that frequently adds or deletes a few bases, shifting the reading frame. This pathway is: **[2 marks]**

(A) homology-directed repair (HDR)

(B) non-homologous end joining (NHEJ)

(C) mismatch repair

(D) nucleotide-excision repair

Q28. A BLAST search of a query sequence against a sequence database returns each hit with an associated E-value. A hit whose E-value is very small (close to zero) should be interpreted as an alignment that is: **[2 marks]**

(A) very likely to have arisen by chance

(B) a poor, low-scoring match

(C) an artefact to be discarded

(D) statistically significant (very unlikely to be due to chance)

Q29. To make a cDNA library, mature messenger RNA molecules are first copied into complementary DNA. The enzyme used to synthesise the first DNA strand using the mRNA as a template is: **[2 marks]**

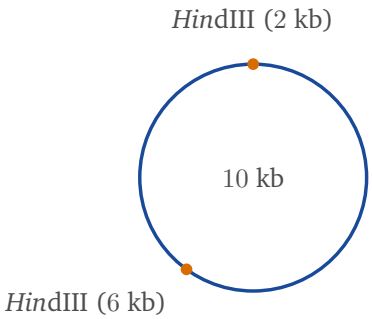
(A) DNA polymerase III

(B) RNA polymerase II

(C) primase

(D) reverse transcriptase

Q30. A circular plasmid of total length 10 kb carries two recognition sites for the restriction enzyme *Hin*dIII, located at the 2 kb and 6 kb positions measured around the circle, as shown. Complete digestion of the plasmid with *Hin*dIII produces DNA fragments of: **[2 marks]**



(A) 2 kb and 6 kb

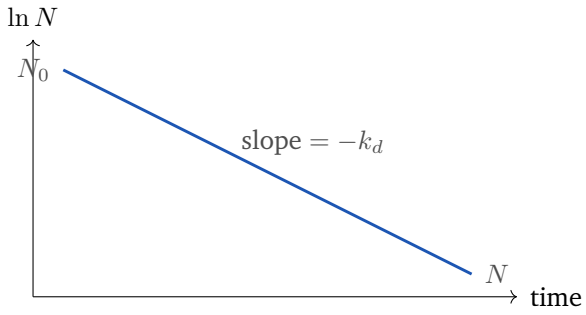
(B) 4 kb and 6 kb

(C) 5 kb and 5 kb

(D) 10 kb only (single linearised piece)

Bioprocess Engineering and Process Biotechnology

Q31. Thermal death of microorganisms follows first-order kinetics, so a plot of $\ln N$ against time is a straight line, as shown. In batch sterilisation the Del factor is defined as $\nabla = \ln(N_0/N)$. The Del factor required to reduce the viable count from $N_0 = 10^{12}$ to $N = 10^0$ (that is, to 1 organism) is nearest to: **[2 marks]**



(A) 12

(B) 2.30

(C) 27.6

(D) 1.0

Q32. In the thermal sterilisation of media, the resistance of an organism is often expressed by its decimal reduction time, the D-value. The D-value is defined as the time required at a given temperature to reduce the viable population by: **[2 marks]**

(A) 90% (one $\log_{10}$ cycle, i.e. a tenfold drop)

(B) exactly 50%

(C) 99.99%

(D) just 10%

Q33. A spore suspension is heated at $121\ ^\circ$C, where its thermal death follows first-order kinetics with a specific death-rate constant $k_d = 1.0$ min^{-1}.

The holding time required to reduce the viable count from 10^{10} spores to 1 spore (10^{0}) is nearest to: **[2 marks]**

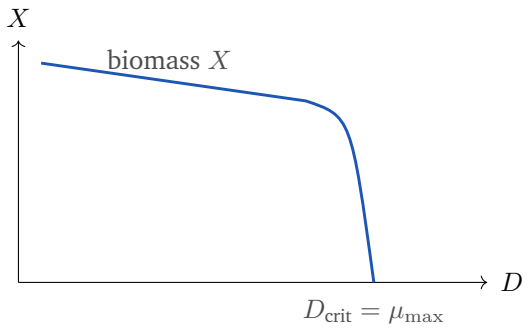
(A) 23 min

(B) 10 min

(C) 46 min

(D) 2.3 min

Q34. In a chemostat the biomass concentration falls sharply once the dilution rate is raised too high, and the culture is eventually flushed out of the vessel, as the plot shows. This complete loss of cells (washout) occurs when the dilution rate D exceeds: **[2 marks]**



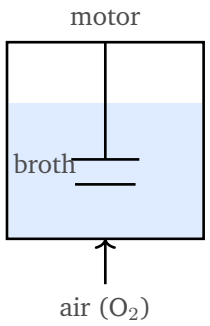
(A) the saturation constant K_s

(B) zero

(C) the maximum specific growth rate $\mu_{\max}$

(D) the biomass yield coefficient $Y_{X/S}$

Q35. In the aerated, stirred bioreactor shown, oxygen is transferred from the sparged air into the broth. If the saturation dissolved-oxygen concentration is $C^{*} = 8$ mg L^{-1}, the actual dissolved-oxygen concentration is $C_L = 2$ mg L^{-1} and the volumetric mass-transfer coefficient is $k_L a = 100\ \mathrm{h}^{-1}$, the oxygen transfer rate (OTR) is: **[2 marks]**



(A) 800 mg $L^{-1}h^{-1}$

(B) 600 mg $L^{-1}h^{-1}$

(C) 200 mg $L^{-1}h^{-1}$

(D) 1000 mg $L^{-1}h^{-1}$

Q36. Continuous (high-temperature short-time) sterilisation of a fermentation medium is often preferred over batch sterilisation in a large vessel. The main process advantage of the continuous approach is that it: **[2 marks]**

(A) uses much lower temperatures held for a long time

(B) cannot in practice achieve full sterility

(C) is guaranteed to destroy all the medium nutrients

(D) holds the medium at high temperature for only a short time, minimising heat damage to nutrients

Q37. In a batch fermentation, 45 g of dry cell biomass is formed while 90 g of glucose is consumed as the sole carbon and energy source. The biomass yield coefficient on substrate, $Y_{X/S}$, for this culture is: **[2 marks]**

(A) 2.0 g g^{-1}

(B) 0.2 g g^{-1}

(C) 0.5 g g^{-1}

(D) 0.9 g g^{-1}

Q38. In the industrial production of baker's yeast, glucose is fed to the reactor gradually rather than all at once. Keeping the residual sugar concentra-

tion low in this fed-batch mode is advantageous mainly because it: [2 marks]

(A) allows a true steady state to be held indefinitely

(B) removes the need for any aeration

(C) keeps the substrate low, controlling the growth rate and avoiding the overflow (Crabtree) formation of ethanol

(D) sterilises the medium during fermentation

Plant and Animal Biotechnology

Q39. Dolly the sheep, the first mammal cloned from an adult cell, was produced by removing the nucleus from an unfertilised egg and replacing it with the nucleus of a somatic (udder) cell. This cloning technique is called: [2 marks]

(A) somatic cell nuclear transfer (SCNT)

(B) ordinary in vitro fertilisation (IVF)

(C) somatic hybridisation of protoplasts

(D) micropropagation

Q40. In the multiple ovulation and embryo transfer (MOET) programme used to multiply genetically superior cattle rapidly, the elite donor cow is first treated with a hormone so that she releases many eggs in a single cycle instead of one. The hormone used to induce this superovulation is: [2 marks]

(A) a broad-spectrum antibiotic

(B) a restriction endonuclease

(C) colchicine

(D) follicle-stimulating hormone (FSH / gonadotrophin)

Q41. In cattle breeding, an early embryo produced by in vitro fertilisation can be mechanically split into two halves, each of which develops into a separate, genetically identical calf. This deliberate production of identical individuals from one embryo is an example of: [2 marks]

(A) embryo splitting (artificial twinning)

(B) somatic hybridisation

(C) apomixis

(D) parthenogenesis

Q42. Transgenic (genetically modified) animals are widely used as models of human disease and as producers of pharmaceutical proteins. A transgenic animal is best defined as one that: [2 marks]

(A) has been produced only by natural mating between two breeds

(B) carries a foreign (recombinant) gene deliberately introduced and stably integrated into its genome

(C) is an identical clone of another animal

(D) has merely been treated with growth hormones

Q43. In animal breeding programmes, embryos, semen and oocytes are routinely banked for many years so that superior genetic material remains available. The standard method of long-term storage is cryopreservation in: [2 marks]

(A) liquid nitrogen at about -196 °C

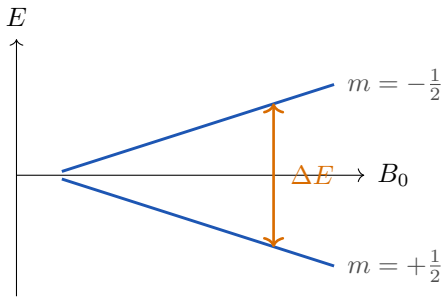
(B) an ordinary refrigerator at $+4$ °C

(C) boiling water at $+100$ °C

(D) dry ice held at 0 °C

Analytical Techniques

Q44. Nuclear magnetic resonance (NMR) spectroscopy determines molecular structure by detecting the resonance of certain atomic nuclei, such as ^{1}H and ^{13}C, when they are placed in a strong magnetic field. As the diagram shows, the field splits the nuclear energy levels; the property of a nucleus that makes it detectable by NMR is its: [2 marks]



(A) mass number

(B) electronegativity

(C) nuclear spin (non-zero magnetic moment)

(D) atomic radius

Q45. In NMR spectra the position of each signal is measured relative to a reference compound and expressed as a chemical shift δ. So that the value is independent of the spectrometer's field strength, the chemical shift is reported in the dimensionless units of: **[2 marks]**

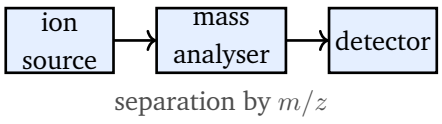
(A) parts per million (ppm)

(B) nanometres (nm)

(C) daltons (Da)

(D) moles per litre (M)

Q46. The instrument sketched below ionises the sample, separates the resulting ions according to their mass-to-charge ratio (m/z) and records their abundance; it is a leading tool for identifying proteins and measuring their molecular mass. This analytical technique is: **[2 marks]**



(A) UV–visible spectrophotometry

(B) NMR spectroscopy

(C) X-ray diffraction

(D) mass spectrometry

Detailed Solutions

Q1.

Solution

Concept – the Michaelis–Menten rate equation: $v = \dfrac{V_{\max}[S]}{K_m + [S]}$, which relates the initial velocity to the substrate concentration.

Step 1 – list the data: $V_{\max} = 120\ \mu\text{mol min}^{-1}$, $K_m = 2$ mM and $[S] = 6$ mM.

Step 2 – substitute the values: $v = \dfrac{120 \times 6}{2 + 6}$

Step 3 – evaluate the numerator: $120 \times 6 = 720$

Step 4 – evaluate the denominator: $2 + 6 = 8$

Step 5 – complete the arithmetic: $v = \dfrac{720}{8}$

$v = 90\ \mu\text{mol min}^{-1}$

Step 6 – sanity check: Since $[S] = 6$ mM is three times K_m, v should be well above half of $V_{\max}$ (which is 60); 90 fits.

Final Answer: $v = 90\ \mu\text{mol min}^{-1} \Rightarrow \boxed{\text{A}}$

Answer: (A) Go Back to Q1

Q2.

Solution

Concept – Anfinsen's thermodynamic hypothesis: Anfinsen showed that a completely unfolded (denatured and reduced) ribonuclease can refold on its own into its fully active native shape once the denaturant is removed.

Step 1 – note what was and was not present: No ribosome, no chaperone and no other cellular machinery were present during the refolding; only the purified polypeptide chain was in the tube.

Step 2 – draw the conclusion: Because the chain still folded correctly by itself, all the folding information must already be written into the chain.

Step 3 – identify what carries that information: The only variable feature of the chain is the order of its amino acids, that is, its primary structure.

Why the other options are wrong:

- A, the ribosome: was absent yet folding still occurred.
- B, chaperones: speed folding in the cell but are not required for the information itself.

- C, the mRNA cap: has no role in shaping the folded protein.

Final Answer: the amino-acid sequence (primary structure) $\Rightarrow$ $\boxed{\text{D}}$

Answer: (D) Go Back to Q2

Q3.

Solution

Concept – how enzymes accelerate reactions: The rate of a reaction depends on the height of the free-energy barrier, the activation energy $\Delta G^{\ddagger}$, between reactant and product.

Step 1 – read the energy diagram: The peak of each curve is the transition state; the enzyme (blue curve) has a lower peak than the uncatalysed (grey) reaction.

Step 2 – ask what lowering the peak means: Lowering the peak means the enzyme reduces the energy of the transition state relative to the reactants.

Step 3 – link to binding: An enzyme achieves this by binding most tightly to, and thus stabilising, the transition state of the reaction, not the substrate ground state.

Why the other options are wrong:

- A, ground-state substrate: binding this too tightly would deepen the starting well and actually slow catalysis.
- B, product: over-stabilising the product would hinder its release.
- D, free enzyme: stabilising the empty enzyme does not lower the barrier.

Final Answer: the transition state of the reaction $\Rightarrow$ $\boxed{\text{C}}$

Answer: (C) Go Back to Q3

Q4.

Solution

Concept – geometry of the α-helix: The α-helix is a regular coil in which the backbone repeats after a fixed number of residues.

Step 1 – recall the pitch parameters: Each turn of the helix rises about 0.54 nm and contains a fixed, non-integer number of residues.

Step 2 – state that number: There are 3.6 amino-acid residues per complete turn.

Step 3 – connect to hydrogen bonding: This spacing places the carbonyl oxygen of residue i directly opposite the amide hydrogen of residue $i + 4$, forming the

stabilising hydrogen bond.

Why the other options are wrong:

- B, 2.0: is closer to the two residues per repeat of a β-strand.
- C, 10.0: greatly overestimates the turn.
- D, 7.0: does not correspond to any standard helical parameter.

Final Answer: 3.6 residues per turn $\Rightarrow$ A

Answer: (A) Go Back to Q4

Q5.

Solution

Concept – the catalytic triad of serine proteases: Chymotrypsin, trypsin and elastase share a three-residue active-site arrangement that carries out nucleophilic attack on the peptide bond.

Step 1 – identify the nucleophile: The serine hydroxyl is the attacking nucleophile that forms the covalent acyl-enzyme intermediate.

Step 2 – identify the general base: A histidine accepts the proton from serine, greatly increasing serine's nucleophilicity.

Step 3 – identify the stabiliser: An aspartate orients the histidine and stabilises its protonated form through electrostatics.

Step 4 – assemble the triad: The three cooperating residues are therefore serine, histidine and aspartate (Ser–His–Asp).

Why the other options are wrong:

- B: cysteine–histidine is the dyad of cysteine (not serine) proteases.
- C and D: these residue sets do not form the charge-relay system of serine proteases.

Final Answer: serine, histidine and aspartate $\Rightarrow$ A

Answer: (A) Go Back to Q5

Q6.

Solution

Concept – isoelectric point of an amino acid: For an amino acid with no ionisable side chain, the pI is the average of the two pK_a values that flank the neutral (zwitterionic) form.

Step 1 – list the given pK_a values: p$K_{a1} = 2.3$ (the α-carboxyl) and p$K_{a2} = 9.6$ (the α-amino).

Step 2 – apply the averaging rule: $\text{pI} = \dfrac{\text{p}K_{a1} + \text{p}K_{a2}}{2}$

Step 3 – substitute: $\text{pI} = \dfrac{2.3 + 9.6}{2}$

Step 4 – add the numerator: $2.3 + 9.6 = 11.9$

Step 5 – divide: $\text{pI} = \dfrac{11.9}{2} = 5.95 \approx 6.0$

Why the other options are wrong:

- A and B: 2.3 and 9.6 are the individual pK_a values, not their mean.
- C, 11.9: is the sum of the two pK_a values, not the average.

Final Answer: $\text{pI} \approx 6.0 \Rightarrow \boxed{\text{D}}$

Answer: (D) Go Back to Q6

Q7.

Solution

Concept – classifying microbes by growth temperature: Organisms are grouped as psychrophiles, mesophiles, thermophiles or hyperthermophiles according to the temperature at which they grow best.

Step 1 – read the stated optimum: The organism grows best above 80 °C and not below about 60 °C.

Step 2 – match to the category: An optimum above roughly 80 °C defines a hyperthermophile, typical of deep-sea vent archaea.

Why the other options are wrong:

- A, psychrophiles: grow best in the cold, around 15 °C or below.
- C, mesophiles: prefer moderate temperatures near 37 °C.
- D, neutrophiles: is a pH class, not a temperature class.

Final Answer: hyperthermophiles $\Rightarrow \boxed{\text{B}}$

Answer: (B) Go Back to Q7

Q8.

Solution

Concept – generations during exponential growth: The number of doublings is $n = \dfrac{\ln(X/X_0)}{\ln 2}$, and the generation time is $t_d = \dfrac{t}{n}$.

Step 1 – list the data: $X_0 = 10^4$, $X = 10^7$, total time $t = 5$ h $= 300$ min.

Step 2 – find the fold increase: $\dfrac{X}{X_0} = \dfrac{10^7}{10^4} = 10^3 = 1000$

Step 3 – compute the number of generations: $n = \dfrac{\ln 1000}{\ln 2} = \dfrac{3 \times 2.303}{0.693} = \dfrac{6.909}{0.693}$

$n \approx 9.97$

Step 4 – compute the generation time: $t_d = \dfrac{300}{9.97}$

$t_d \approx 30.1$ min

Step 5 – round to the nearest option: $t_d \approx 30$ min.

Final Answer: $t_d \approx 30$ min $\Rightarrow$ C

Answer: (C) Go Back to Q8

Q9.

Solution

Concept – classifying microbes by salt requirement: Organisms differ in the salt concentration they need or tolerate, from non-halophiles to extreme halophiles.

Step 1 – read the requirement: *Halobacterium* needs about 15–30% NaCl and bursts in dilute solution.

Step 2 – match to the category: An absolute need for very high salt marks an extreme halophile.

Step 3 – note the reason: These archaea balance the external salt with high internal K^+, so their proteins and membranes are stable only at high ionic strength.

Why the other options are wrong:

- A, barophiles: require high hydrostatic pressure, not high salt.
- C, alkaliphiles: require high pH.
- D, thermophiles: require high temperature.

Final Answer: extreme halophiles $\Rightarrow$ B

Answer: (B) Go Back to Q9

Q10.

Solution

Concept – classifying microbes by oxygen relationship: Bacteria are grouped by whether and how they use molecular oxygen.

Step 1 – read the described behaviour: The organism grows with or without oxygen, respiring aerobically when O_2 is present and fermenting when it is absent.

Step 2 – match to the category: This flexible "either way, but better with oxygen" pattern defines a facultative anaerobe (for example, *E. coli*).

Why the other options are wrong:

- A, obligate aerobes: cannot grow without oxygen.
- C, obligate anaerobes: are killed or inhibited by oxygen.
- D, aerotolerant anaerobes: tolerate oxygen but never use it for respiration, whereas here it is used.

Final Answer: facultative anaerobes $\Rightarrow$ $\boxed{\text{B}}$

Answer: (B) Go Back to Q10

Q11.

Solution

Concept – classifying microbes by pH optimum: Organisms are grouped as acidophiles, neutrophiles or alkaliphiles by the pH at which they grow best.

Step 1 – read the optimum: Growth is best at pH 1–3 and impossible at neutral pH.

Step 2 – match to the category: A strongly acidic optimum defines an acidophile, as found among iron- and sulfur-oxidising bacteria of acid mine drainage.

Why the other options are wrong:

- B, neutrophiles: prefer pH near 7.
- C, alkaliphiles: prefer high pH, around 9–11.
- D, halophiles: are classified by salt, not by pH.

Final Answer: acidophiles $\Rightarrow$ $\boxed{\text{A}}$

Answer: (A) Go Back to Q11

Q12.

Solution

Concept – the repeating unit of chromatin: Eukaryotic DNA is compacted in stages, the first of which gives the beads-on-a-string appearance seen in the figure.

Step 1 – identify each bead: Each bead is a core of eight histone molecules (two each of H2A, H2B, H3 and H4).

Step 2 – describe the DNA around it: About 147 base pairs of DNA wrap almost twice around this histone octamer.

Step 3 – name the unit: The histone octamer plus its wrapped DNA is one nucleosome, the fundamental repeating unit of chromatin.

Why the other options are wrong:

- A, solenoid: is the next, 30 nm level of folding, not the basic bead.
- C, chromatid: is a whole replicated chromosome copy.
- D, centromere: is a specialised region for spindle attachment.

Final Answer: the nucleosome $\Rightarrow$ $\boxed{\text{B}}$

Answer: (B) Go Back to Q12

Q13.

Solution

Concept – DNA methylation as an epigenetic mark: Adding methyl groups to cytosines in a promoter's CpG island is a heritable change that does not alter the base sequence.

Step 1 – locate the modification: The figure shows methyl (CH_3) groups placed on the CpG island within the promoter.

Step 2 – state the effect on transcription: Dense promoter methylation blocks transcription-factor binding and recruits repressive proteins, so the gene is switched off.

Step 3 – name the outcome: This is transcriptional silencing of the gene.

Why the other options are wrong:

- A: methylation lowers, not raises, transcription of the gene.
- C: the DNA base sequence is unchanged; only a chemical tag is added.
- D: methylation does not accelerate replication of the region.

Final Answer: transcriptional silencing of the gene $\Rightarrow$ $\boxed{\text{B}}$

Answer: (B) Go Back to Q13

Q14.

Solution

Concept – histone acetylation and chromatin state: The charge on histone tails controls how tightly they grip the negatively charged DNA.

Step 1 – note the charge change: Histone tails are rich in positively charged lysines; acetylation neutralises those charges.

Step 2 – deduce the effect on DNA binding: With the positive charge removed, the histones grip the DNA more loosely.

Step 3 – deduce the effect on transcription: Looser, more open chromatin lets transcription factors and RNA polymerase reach the DNA, so transcription increases.

Why the other options are wrong:

- B: tightening and silencing is the effect of removing acetyl groups (deacetylation).
- C: acetylation modifies histones, it does not degrade them.
- D: there is a clear structural and transcriptional effect.

Final Answer: a more open chromatin and increased transcription $\Rightarrow$ A

Answer: (A) Go Back to Q14

Q15.

Solution

Concept – RNA splicing in eukaryotes: The pre-mRNA must lose its introns and have its exons joined before it can be translated.

Step 1 – identify the machine: Splicing is carried out by the spliceosome, a large complex of small nuclear RNAs (snRNAs) and proteins.

Step 2 – outline its action: The spliceosome recognises the intron boundaries, excises the intron as a lariat and ligates the flanking exons.

Why the other options are wrong:

- A, ribosome: translates mRNA into protein; it does not splice.
- B, proteasome: degrades proteins.
- C, nucleosome: is a DNA-packaging particle, not a splicing machine.

Final Answer: the spliceosome $\Rightarrow$ D

Answer: (D) Go Back to Q15

Q16.

Solution

Concept – two forms of interphase chromatin: Chromatin exists as loosely packed euchromatin and tightly packed heterochromatin.

Step 1 – match the description: The question describes the densely staining, highly condensed and largely inactive form.

Step 2 – name it: That form is heterochromatin.

Step 3 – contrast the two: Euchromatin is open and actively transcribed, whereas heterochromatin is compact and mostly silent.

Why the other options are wrong:

- B, euchromatin: is the open, transcriptionally active form.
- C, nucleolus: is the site of ribosome assembly.
- D, kinetochore: is the protein complex at the centromere.

Final Answer: heterochromatin $\Rightarrow$ A

Answer: (A) Go Back to Q16

Q17.

Solution

Concept – what "epigenetic" means: Epigenetics deals with changes in gene activity that are inherited by daughter cells but leave the DNA sequence untouched.

Step 1 – test each option against two criteria: An epigenetic change must (i) be heritable through cell division and (ii) not alter the base sequence.

Step 2 – select the definition: Only "a heritable change in gene expression that does not alter the DNA sequence" satisfies both criteria.

Step 3 – give examples: DNA methylation, histone modification, genomic imprinting and X-inactivation are all such changes.

Why the other options are wrong:

- A, B and D: a base change, a deletion and a point mutation are all changes to the DNA sequence itself, which is genetic rather than epigenetic.

Final Answer: a heritable change in gene expression that does not alter the DNA sequence $\Rightarrow$ C

Answer: (C) Go Back to Q17

Q18.

Solution

Concept – direction of translation: The ribosome reads the codons of the mRNA in a fixed polarity while the polypeptide grows from its amino end.

Step 1 – recall the reading polarity: The ribosome moves along the mRNA from its $5'$ end toward its $3'$ end.

Step 2 – link to protein synthesis: As it moves $5' \rightarrow 3'$, it adds amino acids so the protein is made from its N-terminus to its C-terminus.

Step 3 – confirm consistency: This matches transcription, in which the mRNA itself is synthesised $5' \rightarrow 3'$, so the message is read in the same sense it was made.

Why the other options are wrong:

- A, $3' \rightarrow 5'$: is the direction in which the template DNA strand is read, not the mRNA by the ribosome.
- B and D: reading is unidirectional and ordered, not simultaneous or random.

Final Answer: $5' \rightarrow 3' \Rightarrow$ C

Answer: (C) Go Back to Q18

Q19.

Solution

Concept – the Hardy–Weinberg genotype frequencies: For two alleles with frequencies p and q, the genotypes occur as p^2 (homozygous dominant), $2pq$ (heterozygous) and q^2 (homozygous recessive).

Step 1 – link the given data to the model: The homozygous recessive frequency equals q^2, and we are told $q^2 = 0.09$.

Step 2 – solve for the recessive allele frequency: $q = \sqrt{0.09}$

Step 3 – evaluate the square root: $q = 0.3$

Step 4 – check plausibility: Then $p = 1 - q = 0.7$, and all frequencies lie between 0 and 1, so the value is consistent.

Why the other options are wrong:

- A, 0.09: is q^2, not q.
- C, 0.7: is the dominant allele frequency p.
- D, 0.42: is the heterozygote frequency $2pq$.

Final Answer: $q = 0.3 \Rightarrow$ B

Answer: (B) Go Back to Q19

Q20.

Solution

Concept – the antibody of immediate hypersensitivity: Type I reactions are driven by an antibody class that binds tightly to mast cells and basophils through high-affinity Fc receptors.

Step 1 – recall the sensitising step: On first exposure, the allergen induces IgE, which coats mast cells (as shown in the figure).

Step 2 – recall the triggering step: On re-exposure, the allergen cross-links this bound IgE, causing the mast cell to degranulate and release histamine.

Step 3 – name the antibody: The antibody responsible is therefore IgE.

Why the other options are wrong:

- A, IgG: mediates Type II and III reactions, not immediate allergy.
- B, IgM: is the first antibody of a primary response, not the allergy mediator.
- C, IgA: guards mucosal surfaces and is not the mast-cell-sensitising antibody.

Final Answer: IgE $\Rightarrow$ D

Answer: (D) Go Back to Q20

Q21.

Solution

Concept – Type IV (delayed-type) hypersensitivity: Unlike the antibody-based reactions, the delayed-type response is cell mediated and takes a day or more to develop.

Step 1 – read the timing clue: The tuberculin reaction peaks at 48–72 hours; this slow onset is the hallmark of a cell-mediated (not antibody-mediated) reaction.

Step 2 – identify the effector cells: Antigen re-exposure activates previously

sensitised T lymphocytes, which release cytokines.

Step 3 – follow the effector chain: Those cytokines recruit and activate macrophages, which cause the local induration (firm swelling).

Why the other options are wrong:

- A, IgE and mast cells: drive the immediate Type I reaction, which appears within minutes.
- C, IgG plus complement: describes Type II cytotoxic reactions.
- D, immune complexes: describe Type III reactions.

Final Answer: sensitised T lymphocytes and activated macrophages $\Rightarrow$ B

Answer: (B) Go Back to Q21

Q22.

Solution

Concept – loss of self-tolerance: A healthy immune system distinguishes self from non-self; failure of this tolerance leads to attack on the body's own tissues.

Step 1 – read the common feature: In each disease listed, the immune response is directed against the body's own molecules or cells.

Step 2 – name the category: Diseases caused by an immune attack on self are autoimmune disorders.

Step 3 – fit the examples: Rheumatoid arthritis (joints), lupus (many organs via anti-nuclear antibodies) and type 1 diabetes (pancreatic β-cells) are all classic autoimmune conditions.

Why the other options are wrong:

- A, immunodeficiency: is a too-weak immune response, the opposite problem.
- C, allergic: is an exaggerated response to harmless foreign antigens, not to self.
- D, neoplastic: refers to cancers, not to self-directed immunity.

Final Answer: autoimmune disorders $\Rightarrow$ B

Answer: (B) Go Back to Q22

Q23.

Solution

Concept – Type III (immune-complex) hypersensitivity: This reaction is caused not by cell-bound antibody but by soluble complexes that settle in tissues.

Step 1 – identify the trigger: Soluble antigen and antibody combine in the circulation to form small immune complexes.

Step 2 – follow the damage: These complexes deposit in vessel walls, joints and kidneys, activate complement and attract neutrophils.

Step 3 – link to the outcome: Neutrophil enzymes then damage the surrounding tissue, as in serum sickness and the Arthus reaction.

Why the other options are wrong:

- A, IgE on mast cells: is the Type I mechanism.
- B, cytotoxic T cells: mediate Type IV reactions.
- C, free histamine: is a downstream mediator of Type I, not the Type III trigger.

Final Answer: soluble antigen–antibody (immune) complexes $\Rightarrow \boxed{\text{D}}$

Answer: (D) Go Back to Q23

Q24.

Solution

Concept – genetic drift and population size: Drift is the random change in allele frequency caused by chance sampling of gametes each generation.

Step 1 – recall the size dependence: Sampling error is large when few individuals are sampled and small when many are sampled.

Step 2 – apply it to populations: In a small population only a few gametes pass on their alleles, so chance can swing frequencies strongly from one generation to the next.

Step 3 – conclude: Genetic drift therefore has its greatest effect in small populations, where alleles can even become fixed or lost by chance alone.

Why the other options are wrong:

- A, very large populations: average out sampling error, so drift is weak.
- B, equilibrium populations: Hardy–Weinberg assumes an infinite population with no drift.

- D, high immigration: gene flow tends to swamp drift, not enhance it.

Final Answer: small populations $\Rightarrow$ C

Answer: (C) Go Back to Q24

Q25.

Solution

Concept – targeting in CRISPR–Cas9: The system separates the jobs of finding the target and cutting it: an RNA finds the site and the Cas9 protein does the cutting.

Step 1 – identify the search component: A short single-guide RNA carries a $\sim$20-nucleotide spacer that base pairs with the complementary DNA target.

Step 2 – link RNA to nuclease: The guide RNA is held by Cas9, so wherever the guide base pairs, Cas9 is delivered to make the cut.

Step 3 – conclude: Specificity therefore comes from the guide RNA, which can be reprogrammed simply by changing its spacer sequence.

Why the other options are wrong:

- A, tracrRNA alone: is only the scaffold part and carries no target sequence.
- B, the PAM: is required for cutting but is a fixed short motif, not the source of target choice.
- D, a restriction enzyme: recognises its own fixed site and is not part of CRISPR.

Final Answer: the guide RNA (single-guide RNA) $\Rightarrow$ C

Answer: (C) Go Back to Q25

Q26.

Solution

Concept – the PAM requirement of Cas9: Even when the guide RNA matches the DNA, Cas9 checks for a short neighbouring sequence before it will cut.

Step 1 – name the required motif: Cas9 cuts only if a protospacer adjacent motif (PAM), for *S. pyogenes* Cas9 the sequence $5'$-NGG-$3'$, lies just $3'$ of the target.

Step 2 – state its role: Cas9 first recognises the PAM, then unwinds the adjacent DNA to let the guide RNA test for a match.

Step 3 – note the safeguard: Because the bacterium's own CRISPR array lacks a PAM next to its spacers, the cell avoids cutting its own genome.

Why the other options are wrong:

- A, the TATA box: is a eukaryotic promoter element, unrelated to Cas9.
- B, the AUG start codon: signals the start of translation, not a cut site.
- C, the origin of replication: is where DNA replication begins.

Final Answer: the PAM (protospacer adjacent motif) $\Rightarrow$ D

Answer: (D) Go Back to Q26

Q27.

Solution

Concept – repair of a Cas9 double-strand break: A cut can be sealed by one of two cellular pathways, and which one acts decides the editing outcome.

Step 1 – describe the knockout-forming pathway: Non-homologous end joining (NHEJ) simply rejoins the broken ends and often adds or removes a few bases in the process.

Step 2 – link to gene knockout: Such small insertions or deletions shift the reading frame and usually destroy the protein, giving a gene knockout.

Step 3 – contrast with precise editing: If a repair template is supplied, homology-directed repair (HDR) can instead make a precise, designed change, but that is not the error-prone route.

Why the other options are wrong:

- A, HDR: is accurate and template-driven, not error-prone.
- C and D: mismatch and nucleotide-excision repair correct base errors and bulky lesions, not double-strand breaks in this context.

Final Answer: non-homologous end joining (NHEJ) $\Rightarrow$ B

Answer: (B) Go Back to Q27

Q28.

Solution

Concept – meaning of the BLAST E-value: The E-value is the number of hits with a score as good as the observed one that would be expected purely by chance in a database of that size.

Step 1 – interpret a small E-value: A very small E-value means almost no such hit would be expected by chance.

Step 2 – draw the conclusion: The alignment is therefore statistically significant and very likely reflects a real biological relationship (homology).

Step 3 – note the practical rule: As a rough guide, $E < 10^{-5}$ is treated as a confident, significant match.

Why the other options are wrong:

- A: a small E-value means unlikely by chance, the opposite of "likely by chance".
- B: a small E-value goes with a high-scoring, good match.
- C: a strongly significant hit is kept, not discarded.

Final Answer: statistically significant (very unlikely by chance) $\Rightarrow$ $\boxed{\text{D}}$

Answer: (D) Go Back to Q28

Q29.

Solution

Concept – building a cDNA library: A cDNA library represents only the expressed, spliced messages, so it must be copied from mRNA into DNA.

Step 1 – identify the required activity: Making DNA from an RNA template needs an RNA-dependent DNA polymerase.

Step 2 – name the enzyme: That enzyme is reverse transcriptase, obtained from retroviruses.

Step 3 – outline its use: Primed with an oligo-dT that anneals to the poly-A tail, reverse transcriptase makes the first cDNA strand along the mRNA.

Why the other options are wrong:

- A, DNA polymerase III: copies DNA from a DNA template, not from RNA.
- B, RNA polymerase: makes RNA, not DNA.
- C, primase: lays down short RNA primers only.

Final Answer: reverse transcriptase $\Rightarrow$ D

Answer: (D) Go Back to Q29

Q30.

Solution

Concept – cutting a circular plasmid at two sites: Two cuts around a circle break it into two linear pieces whose lengths are the two arc lengths between the sites.

Step 1 – list the site positions: The *Hin*dIII sites are at the 2 kb and 6 kb marks on a 10 kb circle.

Step 2 – find the first arc: Going from 2 kb to 6 kb the length is $6 - 2 = 4$ kb.

Step 3 – find the second arc: Going the other way around, the remaining length is $10 - 4 = 6$ kb.

Step 4 – check the total: $4 + 6 = 10$ kb, which equals the whole plasmid, so the split is correct.

Why the other options are wrong:

- A, 2 and 6 kb: are the site positions, not the fragment lengths.
- C, 5 and 5 kb: would require the sites to be exactly opposite (0 and 5 kb).
- D, 10 kb only: is the result of a single cut, but here there are two sites.

Final Answer: 4 kb and 6 kb $\Rightarrow$ B

Answer: (B) Go Back to Q30

Q31.

Solution

Concept – the Del factor in thermal sterilisation: The Del factor ∇ measures the total killing effect of a sterilisation cycle, $\nabla = \ln\frac{N_0}{N}$.

Step 1 – list the data: $N_0 = 10^{12}$ and $N = 10^0 = 1$.

Step 2 – form the ratio: $\frac{N_0}{N} = \frac{10^{12}}{1} = 10^{12}$

Step 3 – take the natural logarithm: $\nabla = \ln(10^{12}) = 12 \times \ln 10$

Step 4 – substitute $\ln 10 = 2.303$**:** $\nabla = 12 \times 2.303$

Step 5 – evaluate: $\nabla = 27.6$

Why the other options are wrong:

- A, 12: is the number of $\log_{10}$ cycles, not the natural-log Del factor.
- B, 2.30: is $\ln 10$ for a single decade only.
- D, 1.0: ignores the 10^{12}-fold reduction entirely.

Final Answer: $\nabla \approx 27.6 \Rightarrow$ C

Answer: (C) Go Back to Q31

Q32.

Solution

Concept – the decimal reduction time (D-value): The D-value is a standard measure of how quickly a population is killed at a fixed temperature.

Step 1 – state the definition: The D-value is the time needed to reduce the viable count to one-tenth of its starting value.

Step 2 – express it as a percentage: Falling to one-tenth means 90% of the cells are killed, that is, one $\log_{10}$ cycle.

Step 3 – link to the kinetics: For first-order death, $D = \dfrac{\ln 10}{k_d} = \dfrac{2.303}{k_d}$, confirming a constant tenfold-reduction time.

Why the other options are wrong:

- B, 50%: is a half-reduction, not the decimal (tenfold) reduction.
- C, 99.99%: is a four-log reduction, i.e. $4D$.
- D, 10%: is only a small kill, not the definition.

Final Answer: 90% (one $\log_{10}$ cycle) $\Rightarrow$ A

Answer: (A) Go Back to Q32

Q33.

Solution

Concept – first-order thermal death: For $\dfrac{dN}{dt} = -k_d N$, integration gives $\ln\dfrac{N_0}{N} = k_d\, t$, so the holding time is $t = \dfrac{1}{k_d}\ln\dfrac{N_0}{N}$.

Step 1 – list the data: $k_d = 1.0\ \text{min}^{-1}$, $N_0 = 10^{10}$ and $N = 10^0 = 1$.

Step 2 – form the survival ratio: $\dfrac{N_0}{N} = 10^{10}$

Step 3 – take the natural logarithm: $\ln(10^{10}) = 10 \times \ln 10 = 10 \times 2.303 = 23.03$

Step 4 – divide by the rate constant: $t = \dfrac{23.03}{1.0}$

Step 5 – evaluate: $t \approx 23$ min

Why the other options are wrong:

- B, 10 min: uses the $\log_{10}$ count without the $\ln 10$ factor.
- C, 46 min: doubles the correct value.
- D, 2.3 min: is the time for a single decade only.

Final Answer: $t \approx 23$ min $\Rightarrow$ A

Answer: (A) Go Back to Q33

Q34.

Solution

Concept – steady state and washout in a chemostat: At steady state the specific growth rate equals the dilution rate, $\mu = D$, but the organism cannot grow faster than $\mu_{\max}$.

Step 1 – state the steady-state condition: A stable culture needs $\mu = D$, and μ is capped at $\mu_{\max}$.

Step 2 – consider raising D: As D rises, the required μ rises with it; this is possible only while $D \leq \mu_{\max}$.

Step 3 – reach the limit: Once D exceeds $\mu_{\max}$, the cells cannot divide fast enough to replace those washed out, so biomass collapses to zero (washout).

Step 4 – read the plot: The curve confirms X dropping to zero at $D_{\text{crit}} = \mu_{\max}$.

Why the other options are wrong:

- A, K_s: sets the substrate affinity, not the washout point.
- B, zero: at $D = 0$ nothing leaves, so there is no washout.
- D, $Y_{X/S}$: is a yield coefficient with units of biomass per substrate, not a rate.

Final Answer: the maximum specific growth rate $\mu_{\max}$ $\Rightarrow$ C

Answer: (C) Go Back to Q34

Q35.

Solution

Concept – the oxygen transfer rate (OTR): Oxygen moves from gas to liquid at a rate set by the driving force and the mass-transfer coefficient: OTR $= k_L a\,(C^* - C_L)$.

Step 1 – list the data: $k_L a = 100\ \text{h}^{-1}$, $C^* = 8\ \text{mg L}^{-1}$ and $C_L = 2\ \text{mg L}^{-1}$.

Step 2 – find the driving force: $C^* - C_L = 8 - 2 = 6\ \text{mg L}^{-1}$

Step 3 – substitute into the formula: OTR $= 100 \times 6$

Step 4 – evaluate: OTR $= 600\ \text{mg L}^{-1}\text{h}^{-1}$

Step 5 – check the units: $\text{h}^{-1} \times \text{mg L}^{-1} = \text{mg L}^{-1}\text{h}^{-1}$, a proper rate of transfer.

Why the other options are wrong:

- A, 800: would use $C^* = 8$ alone, ignoring C_L.
- C, 200: uses a driving force of 2 instead of 6.
- D, 1000: has no consistent basis.

Final Answer: OTR $= 600\ \text{mg L}^{-1}\text{h}^{-1} \Rightarrow$ B

Answer: (B) Go Back to Q35

Q36.

Solution

Concept – continuous versus batch sterilisation: Sterilisation kills microbes fast at high temperature, but many nutrients also degrade with prolonged heating.

Step 1 – compare the heat–time profiles: Batch sterilisation heats a large volume slowly and holds it hot for a long time, including long heat-up and cool-down periods.

Step 2 – describe the continuous route: A continuous (HTST) steriliser raises the medium to a high temperature very briefly, then cools it rapidly.

Step 3 – explain the benefit: Because microbial death is far more sensitive to temperature than nutrient breakdown is, a short burst of high temperature kills spores while sparing vitamins and sugars.

Why the other options are wrong:

- A: it uses higher, not lower, temperatures, and for a shorter time.
- B: it does achieve reliable sterility.
- C: its purpose is precisely to preserve, not destroy, nutrients.

Final Answer: it holds the medium at high temperature only briefly, minimising nutrient damage $\Rightarrow$ D

Answer: (D) Go Back to Q36

Q37.

Solution

Concept – the biomass yield coefficient: $Y_{X/S}$ measures how much cell mass is made per unit of substrate consumed: $Y_{X/S} = \dfrac{\Delta X}{\Delta S}$.

Step 1 – list the data: Biomass formed $\Delta X = 45$ g and substrate consumed $\Delta S = 90$ g.

Step 2 – write the ratio: $Y_{X/S} = \dfrac{45}{90}$

Step 3 – simplify: $Y_{X/S} = 0.5$

Step 4 – attach the units: $Y_{X/S} = 0.5$ g biomass per g glucose $= 0.5$ g g^{-1}

Step 5 – sanity check: A value around 0.5 g g^{-1} is typical for aerobic growth on glucose.

Why the other options are wrong:

- A, 2.0: inverts the ratio $(90/45)$.
- B, 0.2: does not match the given figures.
- D, 0.9: would need 81 g of cells from 90 g of glucose.

Final Answer: $Y_{X/S} = 0.5$ g g^{-1} $\Rightarrow$ C

Answer: (C) Go Back to Q37

Q38.

Solution

Concept – why sugar is fed slowly in fed-batch culture: Baker's yeast makes ethanol instead of biomass when glucose is abundant, even under aeration (the Crabtree, or overflow, effect).

Step 1 – state the problem with excess sugar: A high residual glucose concentration pushes the yeast into fermentation, wasting carbon as ethanol and lowering cell yield.

Step 2 – describe the fed-batch remedy: By adding glucose gradually, the operator keeps the residual sugar low at all times.

Step 3 – state the benefit: Low sugar keeps metabolism respiratory and lets the feed rate control the growth rate, maximising biomass and avoiding ethanol overflow.

Why the other options are wrong:

- A: fed-batch has a rising volume, so it does not hold a true indefinite steady state (that is the chemostat).
- B: vigorous aeration is still essential for aerobic yeast.
- D: feeding sugar does not sterilise the broth.

Final Answer: it keeps substrate low, controlling growth and avoiding the overflow (Crabtree) effect $\Rightarrow$ C

Answer: (C) Go Back to Q38

Q39.

Solution

Concept – cloning an adult mammal: Dolly proved that the nucleus of a fully differentiated cell can be reprogrammed to direct the development of a whole animal.

Step 1 – recall the procedure: The nucleus of a somatic (mammary) cell was placed into an egg whose own nucleus had been removed (enucleated).

Step 2 – name the technique: Transferring a somatic nucleus into an enucleated egg is called somatic cell nuclear transfer (SCNT).

Step 3 – note the outcome: The reconstructed egg was stimulated to divide, implanted in a surrogate, and developed into a lamb genetically identical to the nucleus donor.

Why the other options are wrong:

- B, IVF: fuses a sperm and an egg and gives a genetically new individual, not a clone.
- C, somatic hybridisation: fuses whole plant protoplasts.
- D, micropropagation: is a plant tissue-culture method.

Final Answer: somatic cell nuclear transfer (SCNT) $\Rightarrow$ A

Answer: (A) Go Back to Q39

Q40.

Solution

Concept – superovulation in MOET: To multiply an elite cow's genes quickly, she must yield many eggs at once rather than the single egg of a natural cycle.

Step 1 – identify the goal: The donor cow must be made to ovulate many follicles together (superovulation).

Step 2 – identify the hormone: Follicle-stimulating hormone (FSH), a gonadotrophin, drives many follicles to mature at once.

Step 3 – outline the rest of MOET: The many eggs are fertilised (naturally or by AI), and the resulting embryos are flushed out and transferred to surrogate cows.

Why the other options are wrong:

- A, an antibiotic: fights infection and has no role in ovulation.
- B, a restriction enzyme: cuts DNA in the lab.
- C, colchicine: blocks spindle formation and is used to double chromosomes in plants.

Final Answer: follicle-stimulating hormone (FSH / gonadotrophin) $\Rightarrow \boxed{\text{D}}$

Answer: (D) Go Back to Q40

Q41.

Solution

Concept – making identical individuals from one embryo: Because the cells of a very early embryo are still totipotent, an embryo can be divided and each part can form a whole animal.

Step 1 – read the procedure: A young IVF embryo is cut into two halves, and each half develops into a complete calf.

Step 2 – name the technique: Producing identical individuals by dividing one embryo is embryo splitting, also called artificial twinning.

Step 3 – note the genetic result: The resulting calves are genetically identical to each other, just like natural identical twins.

Why the other options are wrong:

- B, somatic hybridisation: fuses somatic cells and is a plant technique.
- C, apomixis: is asexual seed formation in plants.
- D, parthenogenesis: is development of an egg without fertilisation.

Final Answer: embryo splitting (artificial twinning) $\Rightarrow$ A

Answer: (A) Go Back to Q41

Q42.

Solution

Concept – what makes an animal transgenic: A transgenic animal is defined by the deliberate presence of foreign genetic material in its genome.

Step 1 – state the defining feature: A gene from another source is introduced (for example by microinjection into a fertilised egg) and becomes stably integrated into the animal's DNA.

Step 2 – note inheritance: Because the transgene is in the genome, it is passed on to the animal's offspring.

Step 3 – give the purpose: Such animals serve as disease models or as "biofactories" that secrete valuable proteins in milk.

Why the other options are wrong:

- A: natural mating shuffles existing genes but adds no foreign gene.
- C: a clone is a genetic copy, not necessarily carrying a new gene.
- D: hormone treatment changes physiology, not the genome.

Final Answer: it carries a foreign gene stably integrated into its genome $\Rightarrow$ B

Answer: (B) Go Back to Q42

Q43.

Solution

Concept – long-term storage of germplasm: To halt all biological activity for years, cells and embryos must be held at a temperature low enough to stop molecular motion.

Step 1 – identify the requirement: Storage must arrest metabolism and prevent ice damage over long periods.

Step 2 – give the standard method: Cryopreservation in liquid nitrogen at about $-196\ ^\circ\text{C}$, usually with a cryoprotectant such as glycerol or DMSO, meets this need.

Step 3 – note the outcome: At this temperature all enzymatic activity ceases, so embryos and semen remain viable for many years and can be thawed for use.

Why the other options are wrong:

- B, $+4$ °C: only slows metabolism and preserves cells for days, not years.
- C, boiling water: would kill the cells instantly.
- D, dry ice at 0 °C: is contradictory, and even -78 °C dry ice is too warm for long-term storage.

Final Answer: liquid nitrogen at about -196 °C $\Rightarrow$ A

Answer: (A) Go Back to Q43

Q44.

Solution

Concept – the physical basis of NMR: NMR detects nuclei that behave like tiny magnets when placed in an external field.

Step 1 – identify the required nuclear property: Only nuclei with a non-zero spin possess a magnetic moment and can absorb radio-frequency energy.

Step 2 – read the diagram: In the field B_0 the spin states $m = +\frac{1}{2}$ and $m = -\frac{1}{2}$ split apart by an energy ΔE; a nucleus flips between them by absorbing a photon of exactly that energy.

Step 3 – connect to detectable nuclei: ^{1}H and ^{13}C have spin $\frac{1}{2}$ and are therefore NMR-active, whereas spin-zero nuclei such as ^{12}C are silent.

Why the other options are wrong:

- A, mass number: does not by itself decide NMR activity.
- B, electronegativity: is a chemical-bonding property, not a nuclear one.
- D, atomic radius: is unrelated to nuclear resonance.

Final Answer: its nuclear spin (non-zero magnetic moment) $\Rightarrow$ C

Answer: (C) Go Back to Q44

Q45.

Solution

Concept – the chemical shift scale: The resonance frequency of a nucleus depends on the spectrometer's magnetic-field strength, so raw frequencies cannot be compared between instruments.

Step 1 – state the problem: A signal measured in hertz would differ from one

magnet to another, making data hard to share.

Step 2 – give the solution: The chemical shift δ is defined as the frequency difference from a reference divided by the spectrometer frequency, which cancels the field dependence.

Step 3 – state the units: Because that ratio is very small, it is multiplied by 10^6 and reported in parts per million (ppm), a dimensionless field-independent scale.

Why the other options are wrong:

- B, nanometres: measure wavelength in optical spectroscopy.
- C, daltons: measure molecular mass.
- D, moles per litre: measure concentration.

Final Answer: parts per million (ppm) $\Rightarrow$ $\boxed{\text{A}}$

Answer: (A) Go Back to Q45

Q46.

Solution

Concept – separating ions by mass-to-charge ratio: The described instrument works on charged gas-phase molecules and sorts them by m/z.

Step 1 – follow the block diagram: The sample is first ionised (ion source), the ions are then separated in the mass analyser and finally counted at the detector.

Step 2 – identify the separating quantity: Separation is by mass-to-charge ratio (m/z), the defining principle of the method.

Step 3 – name the technique: An instrument that ionises molecules and separates them by m/z is a mass spectrometer, widely used to identify proteins and measure their masses.

Why the other options are wrong:

- A, UV–visible spectrophotometry: measures light absorption, not m/z.
- B, NMR: probes nuclear spins in a magnetic field.
- C, X-ray diffraction: determines atomic positions in a crystal.

Final Answer: mass spectrometry $\Rightarrow$ $\boxed{\text{D}}$

Answer: (D) Go Back to Q46

Answer Key

Q	Ans	Q	Ans	Q	Ans	Q	Ans	Q	Ans
1	A	2	D	3	C	4	A	5	A
6	D	7	B	8	C	9	B	10	B
11	A	12	B	13	B	14	A	15	D
16	A	17	C	18	C	19	B	20	D
21	B	22	B	23	D	24	C	25	C
26	D	27	B	28	D	29	D	30	B
31	C	32	A	33	A	34	C	35	B
36	D	37	C	38	C	39	A	40	D
41	A	42	B	43	A	44	C	45	A
46	D								