GENERAL APTITUDE

Q.No. 1 to 5 Carry One Mark Each

1. You should _____ when to say _____.

(A) no / no (B) no / know (C) know / know (D) know / no

2. Two straight lines pass through the origin $(x_0, y_0) = (0,0)$. One of them passes through the point $(x_1, y_1) = (1,3)$ and the other passes through the point $(x, y_2) = (1,2)$.

What is the area enclosed between the straight lines in the interval [0, 1] on the x-axis?

(A) 0.5 (B) 1.0 (C) 1.5 (D) 2.0

3. If

$p:q = 1:2$

$q:r = 4:3$

$r:s = 4:5$

and u is 50% more than s, what is the ratio $p:u$?

(A) 2 : 15 (B) 16 : 15 (C) 1: 5 (D) 16: 45

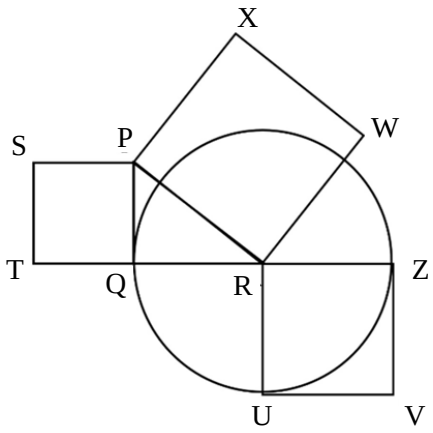
4. Given the statements:

- P is the sister of Q.
- Q is the husband of R.
- R is the mother of S.
- T is the husband of P.

Based on the above information, T is _____ of S.

(A) the grandfather (B) an uncle (C) the father (D) a brother

5. In the following diagram, the point R is the center of the circle. The lines PQ and ZV are tangential to the circle. The relation among the areas of the squares, PXWR, RUVZ and SPQT is



(A) Area of SPQT = Area of RUVZ = Area of PXWR

(B) Area of SPQT = Area of PXWR – Area of RUVZ

(C) Area of PXWR = Area of SPQT – Area of RUVZ

(D) Area of PXWR = Area of RUVZ – Area of SPQT

Q.No. 6-10 Carry Two Marks Each

6. Healthy eating is a critical component of healthy aging. When should one start eating healthy? It turns out that it is never too early. For example, babies who start eating healthy in the first year are more likely to have better overall health as they get older.

Which one of the following is the CORRECT logical inference based on the information in the above passage?

(A) Healthy eating is important for those with good health conditions, but not for others

(B) Eating healthy can be started at any age, earlier the better

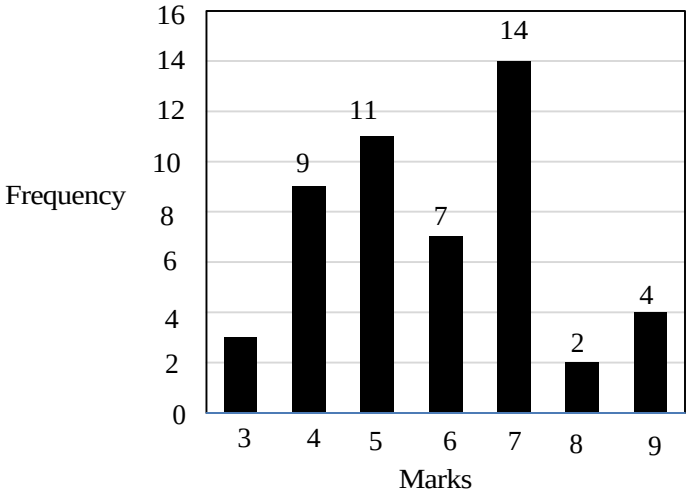
(C) Eating healthy and better overall health are more correlated at a young age, but not older age

(D) Healthy eating is more important for adults than kids

7. P invested □ 5000 per month for 6 months of a year and Q invested □ x per month for 8 months of the year in a partnership business. The profit is shared in proportion to the total investment made in that year. If at the end of that investment year, Q receives $\frac{4}{9}$ of the total profit, what is the value of x (in □)?

(A) 2500 (B) 3000 (C) 4687 (D) 8437

8.



The above frequency chart shows the frequency distribution of marks obtained by a set of students in an exam.

From the data presented above, which one of the following is CORRECT?

(A) mean > mode > median

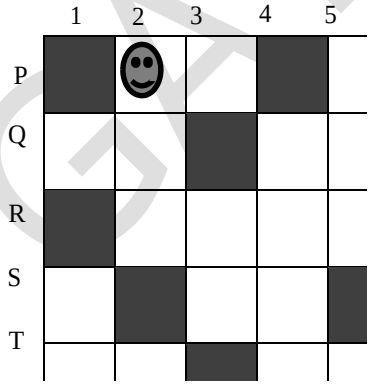
(B) mode > median > mean

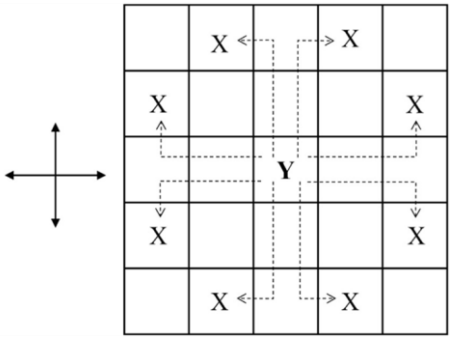
(C) mode > mean > median

(D) median > mode > mean

9. In the square grid shown on the left, a person standing at P2 position is required to move to P5 position. The only movement allowed for a step involves, "two moves along one direction followed by one move in a perpendicular direction". The permissible directions for movement are shown as dotted arrows in the right. For example, a person at a given position Y can move only to the positions marked X on the right.

Without occupying any of the shaded squares at the end of each step, the minimum number of steps required to go from P2 to P5 is





Example : Allowed steps for a person at Y

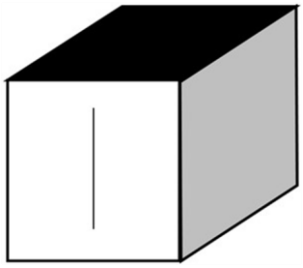
(A) 4

(B) 5

(C) 6

(D) 7

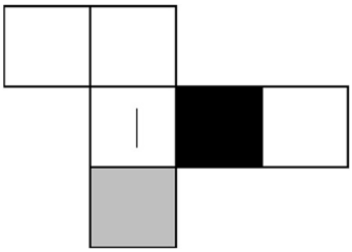
10.



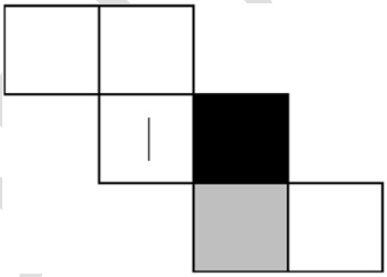
Consider a cube made by folding a single sheet of paper of appropriate shape. The interior faces of the cube are all blank. However, the exterior faces that are not visible in the above view may not be blank.

Which one of the following represents a possible unfolding of the cube?

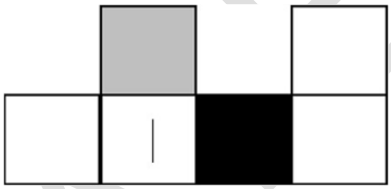
(A)



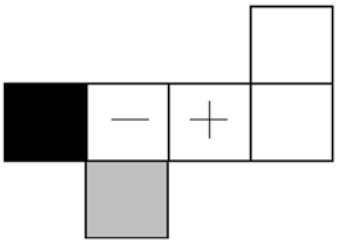
(B)



(C)



(D)



BIOTECHNICAL ENGINEERING

Q.No. 11–35 Carry One Mark Each

11. What is the order of the differential equation given below?

$$\frac{d^2y}{dx^2} - 6x = 3x^4 - 2x^3 + 2$$

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

Key: (B)

Sol: Since $\frac{d^2y}{dx^2}$ is the highest order derivative

$\therefore$ Order of the given DE is 2, option (B).

12. If the eigenvalues of a 2×2 matrix P are 4 and 2, then the eigenvalues of the matrix P^{-1} are

(A) 0, 0 (B) 0.0625, 0.25 (C) 0.25, 0.5 (D) 2, 4

Key: (C)

Sol: Since 2 and 4 are the eigen values of 2 × 2 matrix P.

$\therefore$ The eigen values of matrix P^{-1} are $\frac{1}{2}$ and $\frac{1}{4}$ i.e., 0.5 and 0.25, option 'C'

[If λ is an eigen value of A then $\frac{1}{\lambda}$ is are eigen value of A^{-1}, where $\lambda \neq 0$]

13. Foradouble-pipeheatexchanger,theinsideandoutsideheattransfercoefficients are 100 and 200 W m^{-2} K^{-1}, respectively. The thickness and thermalconductivity of the thin-walled inner pipe are 1 cm and 10 W m^{-1} K^{-1}, respectively. The value of the overall heat transfercoefficientis_____W $m^{-2}K^{-1}$.

(A) 0.016 (B) 42.5 (C) 62.5 (D) 310

Key: (C)

Sol: Given: $h_1 = 100\ Wm^{-2}k^{-1}$

$h_2 = 200\ Wm^{-2}k^{-1}$

Thickness, L = 1 cm = 0.01 m

$k = 10\ Wm^{-1}k^{-1}$

Overall heat transfer coefficient,

$$\frac{1}{U}=\frac{1}{h_1}+\frac{1}{k}+\frac{1}{h_2}=\frac{1}{100}+\frac{0.01}{10}+\frac{1}{200}=\frac{1}{100}+\frac{1}{1000}+\frac{1}{200}=\frac{10+1+5}{1000}$$

$$\frac{1}{U}=\frac{16}{1000}$$

$$U=\frac{1000}{16}\,Wm^{-2}K^{-1}=62.5\,Wm^{-2}K^{-1}$$

14. Match the media component (Column I) with its role (Column II).

Column I	Column II
P. Sucrose	**1.** Anti-foam agent
Q. Zinc chloride	**2.** Nitrogen source
R. Ammonium sulphate	**3.** Carbon source
S. Silicone oil	**4.** Trace element

(A) P-1, Q-2, R-3, S-4 (B) P-2, Q-1, R-3, S-4

(C) P-3, Q-2, R-4, S-1 (D) P-3, Q-4, R-2, S-1

Key: (D)

Sol: Silicone Oil is an anti- foaming chemical additive that reduce the foam formation.Sucrose and glucose are both good carbon sources for industrial fermentation in Escherichia coli.Ammonium sulphate contains 21 percent nitrogen and 24 percent sulphur and used primarily where there is a need for nitrogen and sulphur. Zinc chloride is an important trace element that people need to stay healthy.

15. The binding free energy of a ligand to its receptor protein is -11.5 kJ mol^{-1} at 300 K. What is the value of the equilibrium binding constant?

Use R = 8.314 J mol^{-1} K^{-1}.

(A) 0.01 (B) 1.0 (C) 4.6 (D) 100.5

Key: (D)

Sol: Given, $R=8.314\,Jmol^{-1}K^{-1}$

$R=8.314\times10^{-3}\,KJmol^{-1}K^{-1}$

$\Delta G^\circ=-11.5\,kJ\,mol^{-1}$

$T=300\,K$

$\Delta G^\circ=-RT\ell nK$

$$-11.5 = -\left(8.314\times10^{-3}\right)\times300\ \ell nK$$

$$\ell nK = \frac{11.5}{8.314\times10^{-3}\times300}$$

$$\ell nK = 4.61$$

$$K = C^{4.61}$$

$$K = 100.48 \sim 100.5$$

16. The overall stoichiometry for an aerobic cell growth is

$$3C_6H_{12}O_6 + 2.5NH_3 + O_2 \rightarrow 1.5C_aH_bO_cN_d + 3CO_2 + 5H_2O$$

What is the elemental composition formula of the biomass?

(A) $C_9H_{18.2}O_5N_{1.667}$ (B) $C_9H_{22.33}O_6N_{1.667}$ (C) $C_{10}H_{18.2}O_5N_{1.667}$ (D) $C_{10}H_{22.33}O_6N_{1.667}$

Key: (D)

Sol: Equating the stoichiometric coefficients of different elements.

C balance:

$$(3\times6) = 1.5a + 3 \Rightarrow 18 = 1.5a + 3$$

$$1.5a = 18 - 3 \Rightarrow 1.5a = 15$$

$$a = \frac{15}{1.5}$$

$$\boxed{a = 10}$$

Hydrogen balance:

$$(3\times12) + (2.5\times3) = 1.56 + (5\times2)$$

$$36 + 7.5 = 1.5b + 10$$

$$1.5b = 43.5 - 10$$

$$1.5b = 33.5$$

$$\boxed{b = 22.33}$$

Oxygen balance:

$$(3\times6) + 2 = 1.5C + (3\times2) + (5\times1)$$

$$18 + 2 = 1.5C + 6 + 5$$

$$1.5C = 20 - 11$$

$$1.5C = 9$$

$$\boxed{C = 6}$$

Nitrogen balance:

$(2.5\times1)=1.5d$

$2.5=1.5d$

$\boxed{d=1.667}$

Putting values of a, b, c, d in $C_aH_bO_cN_d$ we get $C_{10}H_{22.33}O_6N_{1.667}$

17. In binomial nomenclature, the name of a bacterial strain is written with the first letter of_____word(s) beingcapitalized.

(A) first (B) second (C) neither (D) first and second

Key: (A)

Sol: Binary names, consisting of a generic name and a specific epithet (e.g., Escherichia coli), should be used for all bacteria. Names of categories at or above the genus level may be used alone, but specific and subspecific epithets may not. The generic name should be abbreviated to the initial letter of the genus name must be capitalized and the species is lower case. The names should be italicized or underlined in text. Names of all bacterial taxa (kingdoms, phyla, classes, orders, families, genera, species, and subspecies) are printed in italics; strain designations and numbers are not.

18. The type of nucleic acid present in λ – phage is

(A) Double stranded DNA (B) Single stranded circular DNA

(C) Single stranded DNA (D) Single stranded RNA

Key: (A)

Sol: Lambda is a temperate Escherichia coli bacteriophage. The virion DNA is linear and double-stranded (48502 bp) with 12 bp single-stranded complementary 5'-ends.

19. Which of the following statements about reversible enzyme inhibitors are CORRECT?

P. Uncompetitive inhibitors bind only to the enzyme-substrate complex

Q. Non-competitive inhibitors bind only at a different site from the substrate

R. Competitive inhibitors bind to the same site as the substrate

(A) P and Q only (B) P and R only (C) Q and R only (D) P, Q and R

Key: (D)

Sol: Uncompetitive inhibition occurs when an inhibitor binds to an allosteric site of a enzyme, but only when the substrate is already bound to the active site. In other words, an uncompetitive inhibitor can only bind to the enzyme-substrate complex and not to the free enzyme. Substrate-binding could cause a conformational change to take place in the enzyme and reveal an inhibitor binding site, or the inhibitor could bind directly to the enzyme-bound substrate. Competitive inhibition occurs when the inhibitor binds at the same site as the substrate.

The molecular basis for the binding of competitive inhibitors at the active site is that the substrate and the inhibitor are structurally similar, with the result that the enzyme cannot recognize and bind the inhibitor. In non-competitive inhibition, the inhibitor binds at an allosteric site separate from the active site of substrate binding. In non-competitive inhibition, the affinity of the enzyme for its substrate (Km) remains unchanged as the active site is not competed for by the inhibitor.

20. Match the component of eukaryotic cells (Column I) with its respective function (Column II).

Column I	Column II
P. Lysosome	**1.** Digestion of macromolecules
Q. Peroxisome	**2.** Detoxification of harmful compounds
R. Glyoxysome	**3.** Conversion of fatty acids to sugar
S. Cytoskeleton	**4.** Involvement in cell motility

(A) P-1, Q-2, R-3, S-4 (B) P-2, Q-1, R-3, S-4

(C) P-3, Q-1, R-2, S-4 (D) P-4, Q-3, R-1, S-2

Key: (A)

Sol: Lysosomes breakdown/digest macromolecules (carbohydrates, lipids, proteins, and nucleic acids), repair cell membranes, and respond against foreign substances such as bacteria, viruses and other antigens. Lysosomes contain enzymes that break down the macromolecules and foreign invaders. In cells, peroxisomes detoxify alcohol and other harmful compounds by transferring hydrogen from the poisons to molecules of oxygen (a process termed oxidation).The glyoxysome are involved in the breakdown and conversion of fatty acids to acetyl-CoA for the glyoxylate bypass.The cytoskeleton is composed of three principal types of protein filaments: actin filaments, intermediate filaments, and microtubules, which are held together and linked to subcellular organelles and the plasma membrane by a variety of accessory proteins. The cytoskeleton has role in cell motility, organelle transport, cell division, and other types of cell movements.

21. In animal cells, the endogenously produced miRNAs silence gene expression by

(A) base pairing with the 3'-untranslated region of specific mRNAs

(B) blocking mRNA synthesis

(C) binding to the operator site

(D) base pairing with the 3' region of specific rRNAs

Key: (A)

Sol: Three prime untranslated regions (3′UTRs) of messenger RNAs (mRNAs) often contain regulatory sequences that post-transcriptionally cause RNAi. Such 3′-UTRs often contain both binding sites for microRNAs (miRNAs) as well as for regulatory proteins. By binding to specific sites within the 3′-UTR, miRNAs can decrease gene expression of various mRNAs by either inhibiting translation or directly causing degradation of the transcript. The 3′-UTR also may have silencer regions that bind repressor proteins that inhibit the expression of a mRNA.

22. Terpenoids are made of _____ units

(A) amino acid (B) carbohydrate (C) isoprene (D) triacylglycerol

Key: (C)

Sol: Terpenes generally are composed of two, three, four, or six isoprene units. These are called monoterpenes, sesquiterpenes, diterpenes, and triterpenes, respectively. Terpenes may contain a variety of functional groups.

23. Match the microbial product (Column I) with its respective application (Column II).

Column I	Column II
P. Methane	**1.** Biosurfactant
Q. Glycolipids	**2.** Bioplastic
R. Polyhydroxy alkanoate	**3.** Biofuel

(A) P-1, Q-2, R-3 (B) P-2, Q-1, R-3 (C) P-3, Q-2, R-1 (D) P-3, Q-1, R-2

Key: (D)

Sol: Polyhydroxy alkanoates (PHAs) comprise a group of natural biodegradable polyesters that are synthesized by microorganisms.PHAs are bio-based, biodegradable plastics, produced by fermentation from a range of feedstocks, including waste. PHAs are produced by bacterial fermentation using bio-derived feedstocks – including waste – and thus are an alternative to fossil fuel-derived plastics.Biogas is only one of many types of biofuels, which include solid, liquid or gaseous fuels from biomass. Methane, the principal component in biogas, has four times the volumetric energy density of hydrogen (H2) and is suitable for use in many types of fuel cell generators.Glycolipids are among the most popular biosurfactant. Structurally, they are constituted by a fatty acid in combination with a carbohydrate moiety and correspond to a group of compounds that differs by the nature of the lipid and carbohydrate moiety.

24. Which of the following is NOT used for generating an optimal alignment of two nucleotide sequences?

(A) Gap penalties (B) Match scores

(C) Mismatch scores (D) Nucleotide composition

Key: (D)

Sol: Sequence alignment is a way of arranging protein (or DNA) sequences to identify regions of similarity that may be a consequence of evolutionary relationships between the sequences.Dynamic programming algorithms use gap penalties to maximize the biological meaning. Gap penalty is subtracted for each gap that has been introduced. There are different gap penalties such as gap open and gap extension. Gap penalties can be used for sequence alignment between two nucleotide or amino acid sequences and find out structural or functional similarity.For optimal nucleotide sequence alignment, the scoring matrices used are relatively simpler since the frequency of mutation for all the bases are equal. Positive or higher value is assigned for a match and a negative or a lower value is assigned for mismatch. These assumptions based scores can be used for scoring the matrices.

25. The recognition sequences of four Type-II restriction enzymes (RE) are given below. The symbol (↓) indicates the cleavage site. Identify the RE that generates sticky ends.

(A) RE1 - 5' G↓GATCC 3'

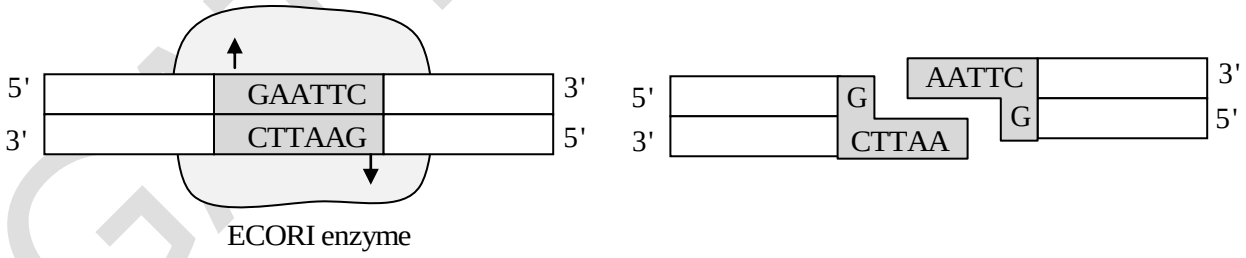
(B) RE2 - 5' CTG↓CAG3'

(C) RE3 - 5' CCC↓GGG3'

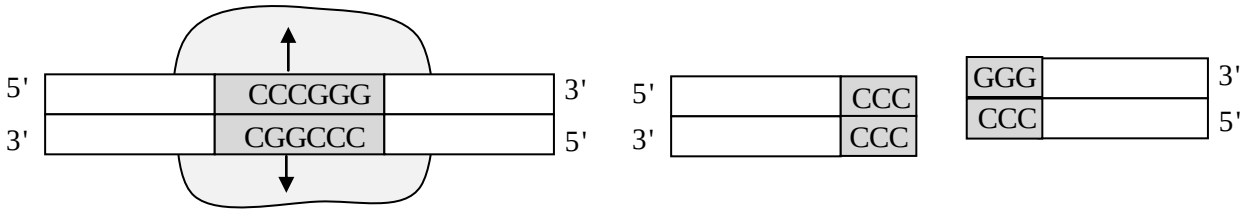
(D) RE4 - 5' AG↓CT3'

Key: (A)

Sol: Blunt-ended fragments can be joined to each other by DNA ligase. However, blunt-ended fragments are harder to ligate together (the ligation reaction is less efficient and more likely to fail) because there are no single-stranded overhangs to hold the DNA molecules in position. Restriction enzymes recognize and bind to specific sequences of DNA, called restriction sites. Each restriction enzyme recognizes just one or a few restriction sites. When it finds its target sequence, a restriction enzyme will make a double-stranded cut in the DNA molecule. As an example of how a restriction enzyme recognizes and cuts at a DNA sequence, let's consider *Eco*RI, a common restriction enzyme used in labs. *Eco*RI cuts at the following site.When EcoRI recognizes and cuts this site, it always does so in a very specific pattern that produces ends with single-stranded DNA "overhangs":



If another piece of DNA has matching overhangs (for instance, because it has also been cut by EcoRI), the overhangs can stick together by complementary base pairing. For this reason, enzymes that leave single-stranded overhangs are said to produce sticky ends. Sticky ends are helpful in cloning because they hold two pieces of DNA together so they can be linked by DNA ligase. Therefore, as seen in the option, RE1 creates sticky ends. However, not all restriction enzymes produce sticky ends. Some are "blunt cutters," which cut straight down the middle of a target sequence and leave no overhang. The restriction enzyme *Sma*I is an example of a blunt cutter:



SmaI enzyme

It makes a cut right in the middle of this sequence on both strands, producing blunt ends. Blunt-ended fragments can be joined to each other by DNA ligase. However, blunt-ended fragments are harder to ligate together (the ligation reaction is less efficient and more likely to fail) because there are no single-stranded overhangs to hold the DNA molecules in position. Hence, RE-2,3,4 create blunt ends according to the cut given in options.

26. Among individuals in a human population, minor variations exist in nucleotide sequences of chromosomes. These variations can lead to gain or loss of sites for specificrestrictionenzymes.Whichofthefollowingtechniqueisusedtoidentify suchvariations?

(A) Polymerase dependent fragment insertion

(B) Real-time polymerase chain reaction

(C) Restriction fragment length polymorphism

(D) Reverse transcriptase polymerase chain reaction

Key: (C)

Sol: In molecular biology, restriction fragment length polymorphism (RFLP) is a technique that exploits variations in homologous DNA sequences, known as polymorphisms, in order to distinguish individuals, populations, or species or to pinpoint the locations of genes within a sequence. The term may refer to a polymorphism itself, as detected through the differing locations of restriction enzyme sites, or to a related laboratory technique by which such differences can be illustrated. In RFLP analysis, a DNA sample is digested into fragments by one or more restriction enzymes, and the resulting restriction fragments are then separated by gel electrophoresis according to their size.The basic technique for the detection of RFLPs involves fragmenting a sample of DNA with the application of a restriction enzyme, which can selectively cleave a DNA molecule wherever a short, specific sequence is recognized in a process known as a restriction digest. The DNA fragments produced by the digest are then separated by length through a process known as agarose gel electrophoresis and transferred to a membrane via the Southern blot procedure. Hybridization of the membrane to a labelled DNA probe then determines the length of the fragments which are complementary to the probe. A restriction fragment length polymorphism is said to occur when the length of a detected fragment varies between individuals, indicating non-identical sequence homologies. Each fragment length is considered an allele, whether it actually contains a coding region or not, and can be used in subsequent genetic analysis.

27. Assumingindependentassortmentandnorecombination,thenumberofdifferent combinations of maternal and paternal chromosomes in gametes of an organism with a diploid number of12 is_____.

Key: **(64)**

Sol: Given, Diploid number = 12

$\Rightarrow 2n = 12$

$\therefore$ n = 6 for each parent

Either mother or father will contribute one set chromosomes in gametes

Therefore number of different combination of maternal and paternal chromosomes in gametes of organism $= 2^6 = 2\times2\times2\times2\times2\times2 = 64$

28. A microorganism is grown in a batch culture using glucose as a carbon source. The apparent growth yield is $0.5\frac{\text{g biomass}}{\text{g substrate}}$. The initial concentrations of biomass and substrate are 2 g L^{-1} and 200 g L^{-1}, respectively. Assuming that there is no endogenous metabolism, the maximum biomass concentration that can be achieved is _____ g L^{-1}.

Key: **(102)**

Sol: Given, $Y_{X/S} = 0.5$ g biomass/g substrate

$X_o = 2g\ell^{-1}$

$S_o = 200\ g\ell^{-1}$

$X = X_o + (S_o - S)Y_{X/S}$

To achieve maximum biomass, complete substrate utilized.

Therefore S = 0

$\Rightarrow \quad X = X_o + (S_o - 0)Y_{X/S}$

$= 2 + (200 + Y_{X/S}) = 2 + (200\times0.5) = 2 + 100$

$X = 102\ g\ell^{-1}$

29. The degree of reduction of lactic acid($C_3H_6O_3$) is_____

Key: **(4)**

Sol: Degree of reduction $= \frac{(4\times3)+(1\times6)+(-2\times3)}{\text{number of carbon atoms}} = \frac{12+6-6}{3} = \frac{12}{3} = 4$

30. Consideranonlinearalgebraicequation, $x\ln x + x - 1 = 0$. UsingtheNewton- Raphson method, with the initial guess of $x_0 = 3$, the value of ? after one iteration(roundedofftoonedecimalplace)is _____.

Key: **(1.3)**

Sol: Let, $f(x) = x\ell nx + x - 1 \Rightarrow f'(x) = x\left(\frac{1}{x}\right) + \ell nx(1) + 1 = 2 + \ell nx$

Given, $x_0 = 3 \Rightarrow f(x_0) = 3\ell n3 + 3 - 1 = 5.2958$

$f'(x_0) = 2 + \ell n3 = 3.0986$

$\therefore$ By Newton-Raphson method,

$$x_1 = x_0 - \frac{f(x_0)}{f'(x_0)} = 3 - \frac{(5.2958)}{(3.0986)} = 1.2909 \approx 1.3$$

31. The probability density function of a random variable Xis p(x)= $2e^{-2x}$. The probability P(1 ≤ X≤ 2) (rounded off to two decimalplaces)is_____.

Key: **(0.12)**

Sol: Since $P(x) = 2e^{-2x}$ is probability density function

$$\therefore \quad P(1 \le x \le 2) = \int_1^2 P(x)dx = 2\left(\frac{e^{-2x}}{-2}\right)_1^2 = e^{-2} - e^{-4} = 0.117 \approx 0.12$$

32. The maximum value of the function f(x) =$3x^2$–$2x^3$for x >0is_____.

Key: **(1)**

Sol: $f(x) = 3x^2 - 2x^3$, for $x > 0$

$\Rightarrow f'(x) = 6x - 6x^2$

$f'(x) = 0$ gives $6x(1-x) = 0 \Rightarrow x = 1$ is the only stationary point (since x > 0)

$f''(x) = 6 - 12x \Rightarrow f''(x) = 6 - 12 = -6 < 0$

$\therefore$ f(x) has maximum value at x = 1 and the maximum value is $f(1) = 3 - 2 = 1$

33. The specific growth rate of a yeast having a doubling time of 0.693 h (rounded off to nearestinteger)is _____h^{-1}.

Key: **(1)**

Sol: Given, $t_d = 0.693\,hr$

$$\ell n2 = \mu t_d$$

$$\Rightarrow \mu = \frac{1}{t_d}\ell n2 = \frac{\ell n2}{t_d} = \frac{0.693}{0.693} = 1$$

$$\Rightarrow \mu = 1\,hr^{-1}$$

34. Afermentationbrothofdensity1000kgm^{-3}andviscosity$10^{-3}kgm^{-1}s^{-1}$ismixed in a 100 L fermenter using a 0.1 m diameter impeller, rotating at a speed of $2s^{-1}$. The impeller Reynoldsnumberis_.

Key: **(20000)**

Sol: Given, $\rho = 1000\ kgm^{-3}; \mu = 10^{-3}\,kg\ m^{-1}s^{-1}$

$V = 100L;\ D_i = 0.1m;\ N = 2s^{-1}$

Impeller Reynolds number,

$$R_{ei} = \frac{D_i^2 N\rho}{\mu} = \frac{(0.1)^2 \times 2 \times 100}{10^{-3}} = \frac{1 \times 2 \times 1000}{100 \times 10^{-3}} = 20 \times 10^3 = 20000$$

35. For a pure species, the slope of the melting line

$\frac{dp}{dT}$ at $-2°C$ is $-5.0665 \times 10^6\,PaK^{-1}$

The difference between the molar volumes of the liquid and solid phase at

$-2\ ^\circ C$ is $-4.5 \times 10^{-6}\ m^3\ mol^{-1}$.

The value of the latent heat of fusion (rounded off to nearest integer) is _____$Jmol^{-1}$.

Key: **(6179)**

Sol: Given, $\frac{dP}{dT} = -5.0665 \times 10^6 Pa\ K$ or $Nm^{-2}K$

$T = -2°C \Rightarrow T = 271\,K$

$\Delta V = -45 \times 10^{-6}\,m^3 mol^{-1}$

$$L = T \times \Delta V \times \frac{dP}{dT}$$
$$= 271 \times \left(-4.5 \times 10^{-6}\right) \times \left(-5.0665 \times 10^{6}\right)$$
$$= 271 \times 4.5 \times 5.0665 \text{ Nm mol}^{-1}$$
$$= 6178.59 \sim 6179 \text{ Nm mol}^{-1}$$
$$L = 6179 \text{ Jmol}^{-1}$$

Q.No. 36-65 Carry Two Marks Each

36. Which of the following conditions will contribute to the stability of a gene pool in a natural population?

P. Large population

Q. No net mutation

R. Non-random mating

S. No selection

(A) P only (B) P and Q only (C) P and R only (D) P, Q and S only

Key: (D)

Sol: Gene pool of a population tends to remain stable if the population is large, without migration and with random mating. In population genetics, gene flow is transferred of genetic variation from one population to another. If the rate of gene flow is high enough then two populations are considered to have equivalent genetic diversity and therefore effectively be a single population. In order to contribute to the stability of a gene pool in a natural population, it must meet five major assumptions:

No net mutation: No new alleles are generated by mutation, nor are genes duplicated or deleted.

Random mating: Organisms mate randomly with each other, with no preference for particular genotypes.

No gene flow: Neither individuals nor their gametes (e.g., windborne pollen) enter or exit the population.

Very large population size: The population should be effectively infinite in size.

No natural selection: All alleles confer equal fitness (make organisms equally likely to survive and reproduce).

37. Match the media component used in mammalian cell culture (Column I) with its respective role (Column II).

Column I	Column II
P. Hydrocortisone	1. Mitogen
Q. Fibronectin	**2.** Vitamin
R. Epidermal growth factor	**3.** Hormone
S. Riboflavin	**4.** Cell attachment

(A) P-3, Q-4, R-1, S-2 (B) P-3, Q-4, R-2, S-1

(C) P-4, Q-3, R-1, S-2 (D) P-4, Q-3, R-2, S-1

Key: (A)

Sol: Fibronectin plays a major role in the attachment of many cell types. Fibronectin also plays a major role in cell adhesion, growth, migration, and differentiation, and it is important for processes such as wound healing and embryonic development. Altered fibronectin expression, degradation, and organization has been associated with a number of pathologies, including cancer, arthritis, and fibrosis. Riboflavin is vitamin B2. It is widely found in both plant- and animal-based foods, including milk, meat, eggs, nuts, enriched flour, and green vegetables. Hydrocortisone is a synthetic preparation of the steroid hormone cortisol. Cortisol is a steroid hormone that regulates a wide range of processes throughout the body, including metabolism and the immune response. Mitogens can be either endogenous or exogenous factors. Endogenous mitogens function to control cell division is a normal and necessary part of the life cycle of multicellular organisms. Other well-known mitogenic growth factors include platelet derived growth factor (PDGF) and epidermal growth factor (EGF).

38. Match the cell type (Column I) with its function (Column II).

Column I	Column II
P. B cells	1. Humoral immunity
Q. Neutrophils	**2.** Cytotoxicity
R. T cells	**3.** Histamine-associated allergy
S. Mast cells	**4.** Phagocytosis

(A) P-1, Q-2, R-3, S-4 (B) P-1, Q-4, R-2, S-3

(C) P-4, Q-3, R-1, S-2 (D) P-4, Q-3, R-2, S-1

Key: (B)

Sol: B lymphocytes or B cells produce antibodies involved in humoral immunity. B cells are produced in the bone marrow, where the initial stages of maturation occur, and travel to the spleen for final steps of maturation into naïve mature B cells.The ability of neutrophils to ingest and subsequently kill invading microbes is essential for the maintenance of host health. Neutrophils remove bacterial and fungal pathogens through a process known as phagocytosis.Cytotoxic T cells kill target cells bearing specific antigen while sparing neighbouring uninfected cells. All the cells in a tissue are susceptible to lysis by the cytotoxic proteins of armed effector CD8 T cells, but only infected cells are killed. Histamine-mediated mast cell activation plays a critical role in various allergic diseases. Histamine may induce the release of leukotrienes, cytokines, and chemokines via H4R in CD34+ cord blood-derived human mast cells.

39. A 2×2 matrix P has an eigenvalue $\lambda_1 = 2$ with eigenvector $x_1 = \begin{pmatrix} 1 \\ 0 \end{pmatrix}$ and another eigenvalue $\lambda_2 = 5$, with eigenvector $x_2 = \begin{pmatrix} 1 \\ 1 \end{pmatrix}$. The matrix P is

(A) $\begin{pmatrix} 2 & 0 \\ 0 & 5 \end{pmatrix}$ (B) $\begin{pmatrix} 2 & 3 \\ 0 & 5 \end{pmatrix}$ (C) $\begin{pmatrix} 1 & 1 \\ 0 & 1 \end{pmatrix}$ (D) $\begin{pmatrix} 1 & 1 \\ 1 & 0 \end{pmatrix}$

Key: (B)

Sol: Let $P_{2\times 2} = \begin{bmatrix} a & b \\ c & d \end{bmatrix}$ then by the definition of eigen vector,

We have $Px_1 = \lambda_1 x_1$ and $Px_2 = \lambda_2 x_2$

$$\Rightarrow \begin{bmatrix} a & b \\ c & d \end{bmatrix}\begin{bmatrix} 1 \\ 0 \end{bmatrix} = 2\begin{bmatrix} 1 \\ 0 \end{bmatrix} \text{ and } \begin{bmatrix} a & b \\ c & d \end{bmatrix}\begin{bmatrix} 1 \\ 1 \end{bmatrix} = 5\begin{bmatrix} 1 \\ 1 \end{bmatrix}$$

$$\Rightarrow \begin{bmatrix} a \\ c \end{bmatrix} = \begin{bmatrix} 2 \\ 0 \end{bmatrix} \text{ and } \begin{bmatrix} a+b \\ c+d \end{bmatrix} = \begin{bmatrix} 5 \\ 5 \end{bmatrix}$$

$\Rightarrow a = 2, c = 0; a + b = 5, c + d = 5$

$\Rightarrow b = 3$ and $d = 5$

$\therefore P = \begin{bmatrix} 2 & 3 \\ 0 & 5 \end{bmatrix}$, option (B).

40. Match the stationary phase (Column I) with its corresponding chromatography technique (Column II).

Column I	Column II
P. Protein A	**1.** Size exclusion chromatography
Q. Sephadex	**2.** Ion-exchange chromatography
R. Phenylsepharose	**3.** Affinity chromatography
S. Diethylaminoethyl cellulose	**4.** Hydrophobic interaction chromatography

(A) P-1, Q-4, R-2, S-3 (B) P-3, Q-1, R-4, S-2

(C) P-3, Q-4, R-2, S-1 (D) P-4, Q-1, R-3, S-2

Key: (B)

Sol: Protein A is derived from a strain of Staphylococcus aureus and contains five regions that bind to the Fc region of IgG. As an affinity ligand, protein A is coupled to Sepharose so that these regions are free to bind. One molecule of coupled protein A can bind at least two molecules of IgG.Affinity chromatography is very selective and provides high resolution with an intermediate to high sample loading capacity. The protein A is tightly bound to the resin under conditions that favor specific binding to the ligand, and unbound contaminants are washed off. Sephadex is used to separate molecules by molecular weight. Sephadex is a faster alternative to dialysis (de-salting), requiring a low dilution factor (as little as 1.4:1), with high activity recoveries.Gel filtration based on Sephadex enables group separation of biomolecules that are above the exclusion limit of the medium, from contaminants such as salts, dyes, and radioactive labels. Sephadex is prepared by cross-linking dextran with epichlorohydrin, used for gel filtration chromatography, also called size exclusion chromatography. Phenyl-Sepharose is most often used as an adsorbent for hydrophobic interaction chromatography (HIC). It has effective use for the affinity purification of some extracellular thermostable proteinases from bacterial sources.Diethylaminoethyl cellulose (DEAE-C) is a positively charged resin used in ion-exchange chromatography, a type of column chromatography, for the separation and purification of proteins and nucleic acids. Gel matrix beads are derivatized with diethylaminoethanol (DEAE) and lock negatively charged proteins or nucleic acids into the matrix. The proteins are released from the resin by increasing the salt concentration of the solvent or changing the pH of the solution as to change the charge on the protein.

41. Which of the following statements are CORRECT for a controller?

P. In a proportional controller, a control action is proportional to the error

Q. In an integral controller, a control action is proportional to the derivative of the error

R. There is no "offset" in the response of the closed-loop first-order process with a proportional controller

S. There is no "offset" in the response of the closed-loop first-order process with a proportional-integral controller

(A) P and Q only (B) P and R only (C) P and S only (D) Q and S only

Key: (C)

Sol: In the proportional control algorithm, the controller output is proportional to the error signal, which is the difference between the setpoint and the process variable. In other words, the output of a proportional controller is the multiplication product of the error signal and the proportional gain.Offset error is the steady state error. The proportional-integral controller is the solution to it, so their parameters must be tuned and especially Integral control action to eliminate it.The process will not have any offset when using a proportional- integral controller.Derivative controllers give responses to changing error signals but do not, however, respond to constant error signals, since with a constant error the rate of change of error with time is zero.A proportional derivative controller (PD controller), as its name indicates, is a controller with a "proportional action" and a "derivative action". The proportional action is an action proportional to the variable controlled or its error (difference between the desired value and the actual value of the controlled variable); this basically means that a gain multiplies either the variable or its error compared to the desired value.

42. Which of the following are CORRECT about protein structure?

P. Secondary structure is formed by a repeating pattern of interactions among the polypeptide backbone atoms

Q. Tertiary structure is the three-dimensional arrangement of the polypeptide backbone atoms only

R. Quaternary structure refers to an assembly of multiple polypeptide subunits

(A) P and Q only (B) P and R only (C) Q and R only (D) P, Q and R

Key: (B)

Sol: A protein's primary structure is defined as the amino acid sequence of its polypeptide chain. Secondary structure is the local spatial arrangement of a polypeptide's backbone (main chain) atoms.Secondary structure includes α-helix and β-pleated sheet form because of hydrogen bonding between carbonyl and amino groups in the peptide backbone. Certain amino acids have a propensity to form an α-helix, while others have a propensity to form a β-pleated sheet. Tertiary structure refers to the three-dimensional structure of an entire polypeptide chain and quaternary structure is the three-dimensional arrangement of the subunits in a multisubunit protein.Quaternary structure is the interaction of two or more folded polypeptides or the assembly of several polypeptide subunits.

43. The enzymes involved in ubiquitinylation of cell-cycle proteins are

(A) E_1 and E_2 only (B) E_1 and E_3 only (C) E_1 and E_4 only (D) E_1, E_2 and E_3

Key: (D)

Sol: Ubiquitinylation involves the addition of ubiquitin to a target protein, mediated by sequential actions of ubiquitin activating enzyme (E1), ubiquitin conjugating enzyme (E2), and ubiquitin ligase (E3).

44. The maximum parsimony method is used to construct a phylogenetic tree for a set of sequences. Which one of the following statements about the method is CORRECT?

(A) It predicts the tree that minimizes the steps required to generate the observed variations

(B) It predicts the tree that maximizes the steps required to generate the observed variations

(C) It predicts the tree with the least number of branch points

(D) It employs probability calculations to identify the tree

Key: (A)

Sol: Maximum parsimony predicts the evolutionary tree or trees that minimize the number of steps required to generate the observed variation in the sequences from common ancestral sequences. For this reason, the method is also sometimes referred to as the minimum evolution method.A multiple sequence alignment is required to predict which sequence positions are likely to correspond. These positions will appear in vertical columns in the multiple sequence alignment. For each aligned position, phylogenetic trees that require the smallest number of evolutionary changes to produce the observed sequence changes are identified.

45. Which of the following spectroscopic technique(s) can be used to identify all the functional groups of an antibiotic contaminant in food?

P. Infrared

Q. Circular dichroism

R. Nuclear magnetic resonance

S. UV-Visible

(A) P only

(B) P and R only

(C) P, Q and R only

(D) P, Q, R and S

Key: (B)

Sol: The most common analytical methods for food quality assessment are mass spectrometry (MS) usually coupled to liquid (LC) or gas chromatography (GC), capillary electrophoresis (CE), infrared spectroscopy (IR) and nuclear magnetic resonance (NMR) spectroscopy. In addition to those molecular analysis methods, other methodological approaches of biological origin, such as polymerase chain reaction (PCR) and enzyme-linked immunosorbent assay (ELISA), are also used extensively for food analysis.

46. Adenine can undergo a spontaneous change to hypoxanthine in a cell, leading to a DNA base pair mismatch. The CORRECT combination of enzymes that are involved in repairing this damage is

(A) Nuclease, DNA polymerase, DNA ligase

(B) Nuclease, DNA ligase, helicase

(C) Primase, DNA polymerase, DNA ligase

(D) Primase, helicase, DNA polymerase

Key: (A)

Sol: Many errors are corrected by proofreading, but a few slip through. Mismatch repair happens right after new DNA has been made, and its function is to remove and replace mis-paired bases (ones that were not fixed during proofreading). Mismatch repair can also detect and correct small insertions and deletions. First, a protein complex (group of proteins) recognizes and binds to the mispaired base. A second complex cuts the DNA near the mismatch, and nuclease cleave out the incorrect nucleotide and a surrounding patch of DNA. A DNA polymerase then replaces the missing section with correct nucleotides, and an enzyme called a DNA ligase seals the gap.

47. Consider the ordinary differential equation $\frac{dy}{dx} = f(x,y) = 2x^2 - y^2$. If y(1)=1, the value (s) of y(1.5), using the Euler's implicit method $\left[y_{n+1} = y_n + hf(x_{n+1}, y_{n+1})\right]$ with a step size of h=0.5, is (are)

(A) $-1-5\sqrt{0.3}$ (B) $-1+5\sqrt{0.3}$

(C) $1+5\sqrt{0.3}$ (D) $1-5\sqrt{0.3}$

Key: (A, B)

Sol: $f(x,y) = 2x^2 - y^2,\ y(1) = 1 \Rightarrow y_0 = 1,\ x_0 = 1;\ h = 0.5$

The Euler's implicit method (for n = 1) is

$y_1 = y_0 + hf(x_1, y_1)$

$\Rightarrow \quad y_1 = 1 + \frac{1}{2} f\left(\frac{3}{2}, y_1\right) \qquad (\because x_1 = x_0 + h)$

$= 1 + \frac{1}{2} \times \left(2\left(\frac{3}{2}\right)^2 - y_1^2\right)$

$= \frac{13}{4} - \frac{y_1^2}{2} \Rightarrow 2y_1^2 + 4y_1 - 13 = 0$ is a quadratic equation in y_1

$\Rightarrow \quad y_1 = \frac{-4 \pm \sqrt{16+104}}{4} = -1 \pm \frac{\sqrt{30}}{2}$

$= -1 \pm \sqrt{\frac{15}{2}} = -1 \pm \sqrt{7.5} = -1 \pm \sqrt{25 \times 0.3}$

$= -1 \pm 5\sqrt{0.3}$

$\therefore \quad y_1 = -1 + 5\sqrt{0.3}$ and $-1 - 5\sqrt{0.3}$

$\therefore$ Option A, B

48. Which of the following statements are CORRECT for an enzyme entrapped in a spherical particle?

(A) Effectiveness factor is ratio of the reaction rate with diffusion-limitation to the reaction rate without diffusion-limitation

(B) Internal diffusion is rate-limiting at low values of Thiele modulus

(C) Effectiveness factor increases with decrease in Thiele modulus

(D) Internal diffusion-limitation can be reduced by decreasing the size of the particle

Key: (A, C, D)

Sol: The Thiele modulus is essentially the ratio of reaction to diffusion rates. Thiele modulus is decreased by reducing the observed reaction rate, reducing the size of the catalyst, increasing the effectiveness factor, increasing the surface substrate concentration. Smaller values of the Thiele modulus represent slow reactions with fast diffusion, therefore internal diffusion cannot be rate-limiting. The higher the value of Thiele modulus is (e.g. more prominent are the effects of mass transfer), the steeper the concentration profile decrease is.Internal diffusion limitations of reactant molecules can affect the activity properties and this depends on the pore size distribution as well as on the particle size of the catalyst.If the particle size were reduced so that internal diffusion limitation decreases.

49. Which of the following is(are) COMMON feature(s) for both aerobic and anaerobic bacterial cultures?

(A) Glycolysis

(B) NAD^+ is the oxidising agent

(C) Oxidative phosphorylation

(D) Two net ATP molecules formed per glucose molecule

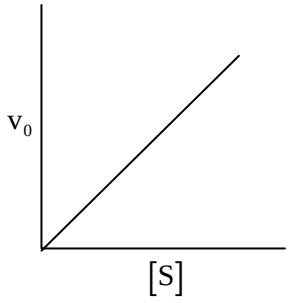
Key: (A, B)

Sol: Aerobic bacteria are much more efficient at making energy. Anaerobes only make two ATP molecules per glucose, but aerobes can make up to 38 ATP per glucose. Aerobic respiration can be broken down into three steps: glycolysis, the citric acid cycle, and oxidative phosphorylation. Whereas anaerobic respiration occurs in three stages: glycolysis, the Krebs cycle, and electron transport. Glycolysis is the process which is common to both aerobic and anaerobic respiration.NAD+ is the oxidising agent in both aerobic and anaerobic respiration.

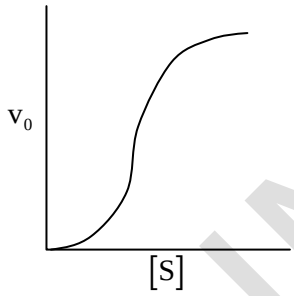
50. Which of the following plot(s) is(are) CORRECT for an enzyme that obeys Michaelis-Menten kinetics, assuming [S] $\ll K_m$?

[S] is the concentration of the substrate, K_m is the Michaelis constant, and v_0 is the initial reaction velocity.

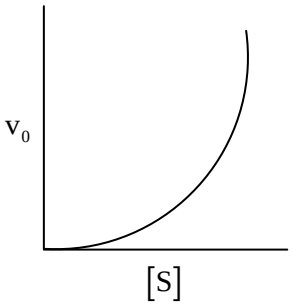
(A)



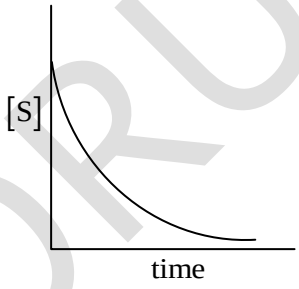
(B)



(C)



(D)



Key: (A, D)

Sol: In case of Michaelis-Menten kinetics, V_O=Vmax[S]/(Km+[S])

If we assume [S]<<Km, V_O=Vmax[S]/Km, which means that the initial reaction velocity (V_O) is directly proportional to concentration of the substrate[S]. Thus, the rate is first order and depends upon concentration of the substrate[S] with slope as Vmax/Km and intercept being 0. This condition is depicted by graph in option (A). The option (D) also holds true in this case, because When Km is low, the initial velocity is higher. This is because the enzyme has higher affinity for substrate and a larger fraction of it has substrate bound. Because of this increased velocity, the pool of substrate is depleted faster. On the other hand, assuming [S]<<Km, then the enzyme binds the product much tighter than the substrate, making product inhibition very significant. Hence the velocity falls much faster early on, as the product concentration is increasing and competitively inhibits the enzyme. This inhibition affords a higher velocity late into the time-course analysis, however, as substrate is depleted much slower. Therefore, the concentration of the substrate and time are inversely correlated, which is shown correctly in the option (D).

51. Which of the following statement(s) is(are) CORRECT regarding the lac operon in E. coli when grown in the presence of glucose and lactose?

(A) At low glucose level, the operon is activated

(B) At high glucose level, the operon is activated to enable the utilization of lactose

(C) The lac repressor binds to operator region inactivating the operon

(D) Binding of lactose to the lac repressor induces the operon

Key: (A, C)

Sol: The lac operon is negatively regulated by lac repressor, which binds to a specific DNA sequence called the operator and prevents efficient initiation of transcription by RNA polymerase from the promoter. Allolactose binds to the lac repressor and prevents its binding to the operator, thereby releasing the repression and allowing transcription of the lac operon. More specifically, in E. coli, the switch from glucose use to lactose use depends on the presence of both cAMP and a molecule called catabolite activator protein (CAP). CAP binds with cAMP, and the CAP-cAMP complex then binds to a specific DNA sequence found upstream of the lac operon operator and promoter. CAP-cAMP complex binding leads to enhanced RNA polymerase binding and activation of gene expression from the lac operon. Importantly, this process is affected by glucose levels, because cAMP levels are decreased in the presence of glucose catabolites. When the concentration of intracellular glucose is low, the levels of the signal molecule cAMP are high. cAMP readily binds with CAP, and the CAP-cAMP complex binds DNA at a position upstream of the lac operon. The association between RNA polymerase and DNA is enhanced when the CAP-cAMP complex is present. Enhanced RNA polymerase binding leads to a high rate of transcription and translation of the lac operon structural genes lacZ, lacY, and lacA. The protein products of lacZ, lacY, and lacA metabolize lactose into glucose. Thus, an elevation in cAMP concentration signals the absence of glucose, because lower glucose levels lead to increased cAMP levels. In turn, increased cAMP levels lead to enhanced expression of the lac operon. When the concentration of intracellular glucose is high (lower panel), cAMP levels are low. Without the adjacent binding of the CAP-cAMP complex, RNA polymerase does not bind to DNA as efficiently, resulting in low rates of transcription for the lacZ, lacY, and lacA genes. In the presence of glucose, intracellular levels of cAMP fall, which leads to a lack of lac operon activation. The lac operon is therefore positively regulated by the absence of glucose catabolites.

52. Emerging viruses such as SARS-CoV2 cause epidemics. Which of the following process(es) contribute to the rise of such viruses?

(A) Mutation of existing virus

(B) Jumping of existing virus from current to new hosts

(C) Spread of virus in the new host population

(D) Replication of virus outside a host

Key: (A, B, C)

Sol: All viruses are obligate intracellular pathogens and they cannot replicate without the machinery and metabolism of a host cell.Since the beginning of the COVID-19 pandemic, the SARS-CoV-2 coronavirus that causes COVID-19 has mutated (changed), resulting in different variants of the virus. One of these is called the delta variant.A unique feature of these existing viruses is the ability to mutate rapidly and it allows them to jump from current host to new hosts.

53. Introduction of foreign genes into plant cells can be carried out using

(A) Agrobacterium

(B) $CaCl_2$ mediated plasmid uptake

(C) Electroporation

(D) Gene gun

Key: (A, C, D)

Sol: In plant genetic engineering, the Ti plasmid can be used to carry foreign genes into plant cells. The Ti plasmid is the disease-causing agent of the soil-borne bacteria Agrobacterium tumefaciens.The second delivery method is a "gene gun," which fires gold particles carrying the foreign DNA into plant cells. Some of these particles pass through the plant cell wall and enter the cell nucleus, where the transgene integrates itself into the plant chromosome. Third method is electroporation, that utilizes short, high-voltage electric shocks to make cells permeable to exogenous molecules. In plants, electroporation is used primarily to stimulate the uptake of plasmids for stable and transient genetic transformation.

54. Which of the following statement(s) regarding trafficking in eukaryotic cells is(are) CORRECT?

(A) Dynamin binds GTP and is involved in vesicle budding

(B) Dynamin is involved in cytoskeletal remodeling

(C) Dynein binds ATP and is involved in movement of organelles along microtubules

(D) Dynein binds GTP and is involved in movement of organelles along microtubules

Key: (A, C)

Sol: Dynein is a dimeric AAA+ motor protein that performs critical roles in eukaryotic cells by moving along microtubules using ATP.Dynamin is a GTP-binding protein that functions in the early stages of endocytosis. In particular, it is thought to be required for endocytic coated vesicle formation and budding.

55. Consider a random variable X with mean μ_X = 0.1 and variance $\sigma_x^2 = 0.2$. A new random variable Y=2X+1 is defined. The variance of the random variable Y (rounded off to one decimal place) is _____ .

Key: (0.8)

Sol: Given mean $\mu_x = E(x) = 0.1$ and variance $\sigma_x^2 = V(x) = 0.2$ and $y = 2x + 1$

$\therefore$ Variance of y is $V(y) = V(2x+1) = 4V(x) = 4 \times 0.2 = 0.8$

Since, $V(ax+b) = a^2 V(x)$

56. For $x_1 > 0$ and $x_2 > 0$, the value of $\lim\limits_{x_1 \to x_2} \dfrac{x_1 - x_2}{x_2 \ln\left(\dfrac{x_1}{x_2}\right)}$ is _____

Key: (1)

Sol: **Method-I:**

$$\lim_{x_1 \to x_2} \frac{x_1 - x_2}{x_2 \ell n\left(\frac{x_1}{x_2}\right)} = \lim_{x_1 \to x_2} \frac{x_1 - x_1}{x_2\left(\ell n x_1 - \ell n x_2\right)} \left(\frac{0}{0} \text{ form}\right)$$

$$= \lim_{x_1 \to x_2} \frac{1}{x_2\left(\frac{1}{x_1} - 0\right)} \left(\text{using L – Hospital's rule and } x_1 \text{ is variable, } x_2 \text{ is constant}\right)$$

$$= \lim_{x_1 \to x_2} \left(\frac{x_1}{x_2}\right) = \frac{x_2}{x_2} = 1$$

Method-II:

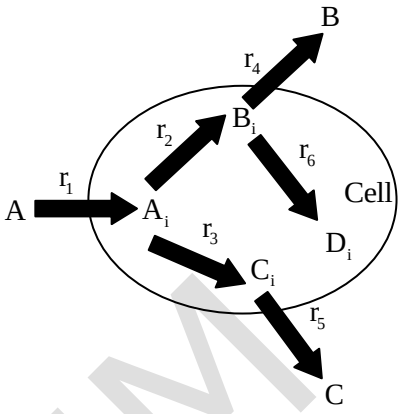
Let $\dfrac{x_1}{x_2} = y$, As $x_1 \to x_2$, $y \to 1$

$$\therefore \lim_{x_1 \to x_2} \frac{x_1 - x_2}{x_2 \ell n\left(\frac{x_1}{x_2}\right)} = \lim_{x_1 \to x_2} \frac{\frac{x_1}{x_2} - 1}{\ell n\left(\frac{x_1}{x_2}\right)} = \lim_{y \to 1} \frac{y-1}{\ell n y} \qquad \left(\frac{0}{0}\right) \text{form}$$

$$= \lim_{y \to 1} \left(\frac{1}{\frac{1}{y}}\right) \qquad \left(\text{Since by L – Hospital rule}\right)$$

$$= 1$$

57. Figure below depicts simplified metabolic and transport reactions taking place in the production of B from A in a cell. The subscript 'i' refers to intracellular metabolites. r_j is the j^{th} reaction flux in $\frac{g}{(g\ dry\ mass)h}$. Under pseudo-steady-state condition, the following reaction fluxes are available.



$r_1 = 4, r_3 = 1$ and $r_6 = 1$.

The transport flux of B, r_4 is _____ $\frac{g}{(g\ dry\ mass)h}$.

Key: (2)

Sol: Given, $r_1 = 4$

When r_1 divides into r_2 and r_3 it is given that $r_3 = 1$

$r_2 = r_1 - r_3 = 4 - 1 = 3$

when r_2 divides into r_4 and r_6

$\therefore \quad r_4 = r_2 - r_6 = 3 - 1 = 2 \quad (\because r_6 = 1 \text{ given})$

$\therefore \quad r_4 = \frac{2g}{(g\ dry\ mass)h}$

58. The amount of biomass in a reactor at the end of the batch process is 50 g. Fed-batch operation is initiated by feeding the substrate solution at a constant rate of 1 L h^{-1}. The concentration of substrate in the feed is 50 g L^{-1}. The maximum biomass yield $\left(Y_{XS}^{M}\right)$ is $0.4\frac{g\ biomass}{g\ substrate}$. Assuming the system is at quasi-steady state, the maximum amount of biomass after 5h of feeding is _____ g.

Key: (150)

Sol: Given, $X_0 = 50\ g$ (end of batch process and start of Fed batch)

$F = 1L\ hr^{-1}$

$S_0 = 50\ gL^{-1}$

$Y_{X/S}^{M} = 0.4\ g\ biomass/g\ substrate$

$t = 5\ hours$

$X = X_o + FS_o tY_{X/S}^{M}$

$= 50 + 1 \times 50 + 5 \times 0.4 = 50 + (250 + \times 0.4) = 50 + 100$

$X = 150g$

59. An enzyme catalyzes the conversion of substrate A into product B. The rate equation for this reaction is

$$-r_A = \frac{C_A}{5+C_A} \text{ mol } L^{-1} \text{ min}^{-1}$$

Substrate A at an initial concentration of 10 mol L^{-1} enters an ideal mixed flow reactor (MFR) at a flow rate of 10 L min^{-1}. The volume of the MFR required for 50% conversion of substrate toproductis _____L.

Key: (100)

Sol: Given, $-r_A = \frac{C_A}{5+C_A} \text{ mol } L^{-1} \text{ min}^{-1}$

$C_{AO} = 10 \text{ mol } L^{-1}; \quad F = 10 \text{ L min}^{-1}$

$C_A = C_{AO} \times 0.05 = 10 \times 0.5 \qquad (50\% \text{ conversion})$

$C_A = 5 \text{ mol } L^{-1}$

For mixed flow reactor (MFR)

$$V\frac{dC_A}{dt} = FC_{AO} - F_{CA} + r_A V$$

For ideal reactor, there will be steady state

Therefore, $\frac{dC_A}{dt} = O$

$$\Rightarrow 0 = FC_{AO} - F_{CA} + r_A V$$

$$-r_A V = F(C_{AO} - C_A)$$

$$-r_A V = 10(10-5)$$

$$-r_A V = 10 \times 5$$

$$\left[\frac{C_A}{5+C_A}\right] V = 50$$

$$\left(\frac{5}{5+5}\right) V = 50 \Rightarrow \frac{5}{10} \times V = 50$$

$$\frac{V}{2} = 50 \Rightarrow V = 50 \times 2 = 100$$

$$V = 100 \text{L}$$

60. Liquid-phase mass transfer coefficient (k_L) is measured in a stirred tank vessel using steady-state method by sparging air. Oxygen uptake by the microorganism is measured. The bulk concentration of O_2 is 10^{-4} mol L^{-1}. Solubility of O_2 in water at 25 °C is 10^{-3} mol L^{-1}.

If the oxygen consumption rate is 9×10^{-4} mol L^{-1} s^{-1}, and interfacial area is 100 m^2/m^3, the value of k_L is _____ cm s^{-1}.

Key: (1)

Sol: Oxygen uptake rate, $OUR = 9\times10^{-4}\,mol\,L^{-1}s^{-1}$

$a = 100\,m^2/m^3 = 100\,m^{-1}$

$C_{AL}^{*} = 10^{-3}\,mol\,L^{-1}$; $C_{AL} = 10^{-4}\,mol\,L^{-1}$

$OUR = K_L \times a \times \left(C_{AL}^{*} - C_{AL}\right)$

$9\times10^{-4} = K_L \times 100 \times \left(10^{-3} - 10^{-4}\right)$

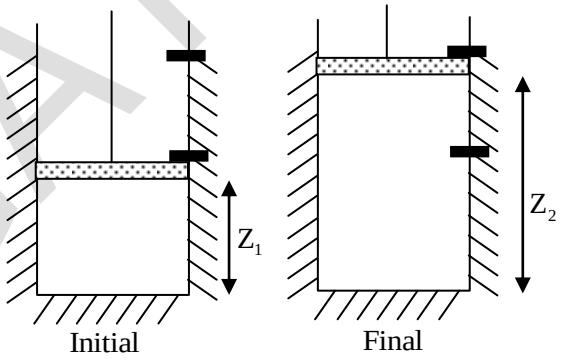
$$K_L = \frac{9\times10^{-4}}{100\times\left(9\times10^{-4}\right)} = \frac{1}{100}\,ms^{-1}$$

$K_L = 1\,cms^{-1}$

61. Consider a piston-cylinder assembly shown in the figure below. The walls ofthe cylinder are insulated. The cylinder contains 1 mole of an ideal gas at 300 Kand the piston is held initially at the position $z_1$using a stopper. After the stopper is removed, the piston suddenlyrises against atmospheric pressure (1.013×10^5 P(A)to the new position $z_2$where it is held by anotherstopper.

The heat capacity (C_v) of the gas is 12.5 J mol^{-1} K^{-1}. The cross-sectional area of the cylinder is 10^{-3} m^2. Assume the piston is weightless and frictionless.

If $z_2 - z_1 = 1$m, thefinaltemperatureofthegas(roundedofftonearestinteger) is__K.



Key: (292)

Sol: Given, $Z_2 - Z_1 = 1m$

$A = 10^{-3}\,m^2$, $C_V = 12.5\,Jmol^{-1}K^{-1}$

$p = 1.013\times10^5\,Pa$, $T_o = 300\,K$

$\Delta V = A \times (Z_2 - Z_1) = 10^{-3} \times 1\,m^3 = 10^{-3} m^3$

$Q = V + W$

$Q = C_V \Delta T + p\Delta V$

Due to adiabatic process, there is no heat transfer

$\Rightarrow C_V \Delta T = p\Delta V$

$12.5 \times \Delta T = 1.013 \times 10^5 \times 10^{-3}$

$\Delta T = \frac{101.3}{12.5} K$

$\Delta T = 8.104\,K$

$(T_o - T) = 8.104K \qquad (\text{for adiabatic})$

Where T is final temperature

$T = 300 - 8.104 = 291.8 \sim 292$

$T = 292\,K$

62. Consider the growth of *S. cerevisiae* under aerobic condition in a bioreactor and the specific growth rate of yeast is 0.5 h^{-1}. The overall reaction of the process is

$$2C_6H_{12}O_6 + 0.2NH_3 + 10.35O_2 \rightarrow CH_{1.8}O_{0.5}N_{0.2} + 0.2C_2H_6O + 10.6CO_2 + 10.8H_2O$$

The heat of combustion values for different compounds are tabulated below with the reference to CO_2, H_2O, O_2, and N_2at standard conditions.

Compound	**Heat of combustion** ($kJ\ mol^{-1}$)
$C_6H_{12}O_6$	2802
NH_3	383
$CH_{1.8}O_{0.5}N_{0.2}$	560
C_2H_6O	1366

The specific rate of heat production (rounded off to nearest integer) is _____ $kJ\ mol^{-1}\ h^{-1}$.

Key: (2424)

Sol: Specific rated heat production = Specific growth rate

$$\times \left\{ \begin{array}{l} \left[\text{Stoichiometric coefficient} \times \text{heat of combustion (reactant)} \right] \\ -\left[\text{Stoichiometric coefficient} \times \text{heat of combustion (product)} \right] \end{array} \right\}$$

$$= 0.5\left\{\left[\left(2\times C_6H_{12}O_6\right)+\left(0.2\times NH_3\right)\right]-\left[\left(1\times CH_{1.8}O_{0.5}N_{0.2}\right)+\left(0.2\times C_2H_6O\right)\right]\right\}$$
$$= 0.5\left\{\left[\left(2\times 2802\right)+\left(0.2\times 383\right)\right]-\left[560+\left(0.2\times 1366\right)\right]\right\}$$
$$= 0.5\left\{\left[\left(5604+76.6\right)\right]-\left[560+273.2\right]\right\} = 0.5\left(5680.6-833.2\right)$$
$$= 2423.7 \sim 2424$$
$$= 2424\ \text{kJ mol}^{-1}\text{hr}^{-1}$$

63. A pilot sterilization was carried out in a vessel containing 100 m^3 medium with an initial spore concentration of 10^8 spores/ml. The accepted level of contamination after sterilization is 1 spore in the entire vessel. The specific death rate constant for the spore is 2 min^{-1} at 121 ˚C. Assuming no death takes place during the heating and cooling cycles, the holding time at 121 ˚C (rounded off to nearest integer) is _____min.

Key: (18)

Sol: Given, $V = 100\ m^3$

$$N_o = 10^8\ \text{spores/mL} = 1\ \text{spore in}\ 100\ m^3$$

$$\Rightarrow \quad N = \frac{1}{100}\text{spores/m}^3 = \frac{1}{10^5}\text{spores/L} = \frac{1}{10^8}\text{spores/mL}$$

$$N = 10^{-8}\ \text{spores/mL}$$

$$K_d = 2\ \text{min}^{-1}$$
$$T = 121° = 121 + 273\ K$$
$$T = 394\ K$$

$$\nabla_{\text{holding}} = \ell n\frac{N_o}{N}$$

$$K_d t = \ell n\frac{N_o}{N} \quad (t = \text{holding time})$$

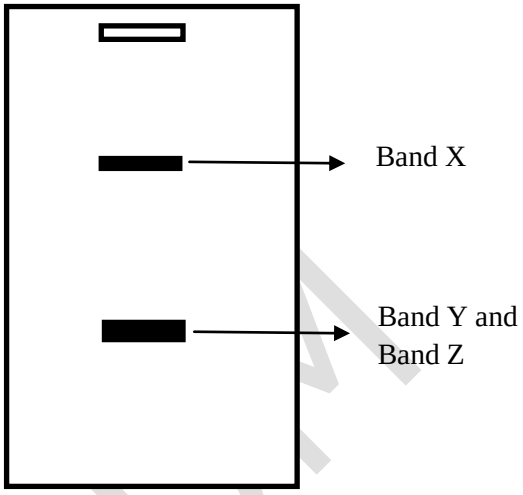
$$t = \frac{1}{k_d}\ell n\left(\frac{10^8}{10^{-8}}\right) = \frac{1}{2}\ell n\left(10^{16}\right) = \frac{16}{2}\ell n10 = 8\ell n10 = 8\times 2.302 = 18.42 \sim 18$$

$$t = 18\ \text{min}$$

64. A circular plasmid has three different but unique restriction sites for enzymes ‘a’, ‘b’ and ‘c.’ When enzymes ‘a’ and ‘b’ are used together, two fragments of equal size are generated. Enzyme ‘c’ creates fragments of equal size only from one of the fragments generated by those cleaved by ‘a’ and ‘b’. The plasmid is treated with a mixture of ‘a’, ‘b’ and ‘c’ and analysed by agarose gel electrophoresis. The number of bands observed in the gel is _____.

Key: (2 to 2)

Sol: In case of circular plasmid, when it is cut with enzymes- 'a' and 'b', two bands of equal size were generated and the size of each band will correspond to half of the size of plasmid. When it is further digested with enzyme- 'c', it also creates two fragments of equal size but it cuts any one of two fragments generated earlier by enzymes- 'a' and 'b'. Therefore, in total, we get 3 bands- out of which one band has size equivalent to half of the size of plasmid (Band X) and other two bands having same size (Band Y and Band Z) and each of these bands have size equivalent to half of the size of Band X.When this circular plasmid is digested with a mixture of 'a', 'b' and 'c' and analysed by agarose gel electrophoresis. The number of bands observed in the gel will be two because one will be Band X and the other will be Band Y and Band Z at the same position, due to same size.



65. A bacterial strain is grown in nutrient medium at 37 °C under aerobic conditions. The medium is inoculated with 10^2 cells from a seed culture. If the number of cells in the culture is 10^5 after 10 hours of growth, the doubling time of the strain (rounded off to nearest integer) is _____ h.

Key: (1)

Sol: Given, $N_o = 10^2$ cells

$N = 10^5$ cells , $t = 10$ hours

$$N = N_o \times 2^n$$

$$\ell n \frac{N}{N_o} = n \ell n 2$$

$$\ell n \left(\frac{10^5}{10^2} \right) = n \times 0.693$$

$$\ell n (1000) = n \times 0.693$$

$$n = \frac{\ell n (1000)}{0.693} = \frac{6.908}{0.693}$$

$$n = 9.97$$

Now, $t_d = \frac{t}{h}$ $(t_d = \text{doubling time})$

$$t_d = \frac{10}{9.97} = 1.003 \sim 1$$

$$t_d = 1 \text{ hour}$$