19 YEARS
PREVIOUS SOLVED PAPERS

GATE 2020

BIOTECHNOLOGY

(Fully Solved with Explanations)

By
Team of
Engineers Academy

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Syllabus

BIOTECHNOLOGY

Section 2: General Biotechnology

Biochemistry: Biomolecules-structure and functions, Biological membranes, structure, action potential and transport processes, Enzymes- classification, kinetics and mechanism of action, Basic concepts and designs of metabolism (carbohydrates, lipids, amino acids and nucleic acids) photosynthesis, respiration and electron transport chain, Bioenergetics.

Microbiology: Viruses- structure and classification, Microbial classification and diversity(bacterial, algal and fungal), Methods in microbiology, Microbial growth and nutrition, Aerobic and anaerobic respiration, Nitrogen fixation, Microbial diseases and host-pathogen interaction.

Cell Biology: Prokaryotic and eukaryotic cell structure, Cell cycle and cell growth control, Cell-Cell communication, Cell signaling and signal transduction.

Molecular Biology and Genetics: Molecular structure of genes and chromosomes, Mutations and mutagenesis, Nucleic acid replication, transcription, translation and their regulatory mechanisms in prokaryotes and eukaryotes, Mendelian inheritance, Gene interaction, Complementation, Linkage, recombination and chromosome mapping, Extra chromosomal inheritance, Microbial genetics (plasmids, transformation, transduction, conjugation), Horizontal gene transfer and Transposable elements, RNA interference, DNA damage and repair, Chromosomal variation, Molecular basis of genetic diseases.

Analytical Techniques: Principles of microscopy-light, electron, fluorescent and confocal, Centrifugation- high speed and ultra, Principles of spectroscopy-UV, visible, CD, IR, FTIR, Raman, MS,NMR, Principles of chromatography- ion exchange, gel filtration, hydrophobic interaction, affinity, GC,HPLC, FPLC, Electrophoresis, Microarray.

Immunology: History of Immunology, Innate, humoral and cell mediated immunity, Antigen, Antibody structure and function, Molecular basis of antibody diversity, Synthesis of antibody and secretion, Antigen-antibody reaction, Complement, Primary and secondary lymphoid organ, B and T cells and macrophages, Major histocompatibility complex (MHC), Antigen processing and presentation, Polyclonal and monoclonal antibody, Regulation of immune response, Immune tolerance, Hypersensitivity, Autoimmunity, Graft versus host reaction.

Bioinformatics: Major bioinformatic resources and search tools, Sequence and structure databases, Sequence analysis (biomolecular sequence file formats, scoring matrices, sequence alignment, phylogeny),Data mining and analytical tools for genomic and proteomic studies, Molecular dynamics and simulations (basic concepts including force fields, protein-protein, protein-nucleic acid, protein-ligand interaction).

Section 3: Recombinant DNA Technology

Restriction and modification enzymes, Vectors, plasmid, bacteriophage and other viral vectors, cosmids, Ti plasmid, yeast artificial chromosome, mammalian and plant expression vectors, cDNA and genomic DNA library, Gene isolation, cloning and expression, Transposons and gene targeting, DNA labeling, DNA sequencing, Polymerase chain reactions, DNA fingerprinting, Southern and northern blotting, In-situ hybridization, RAPD, RFLP, Site-directed mutagenesis, Gene transfer technologies, Gene therapy.

Section 4: Plant and Animal Biotechnology

Totipotency, Regeneration of plants, Plant growth regulators and elicitors, Tissue culture and Cell suspension culture system: methodology, kinetics of growth and, nutrient optimization, Production of secondary metabolites by plant suspension cultures, Hairy root culture, transgenic plants, Plant products of industrial importance.

Animal cell culture, media composition and growth conditions, Animal cell and tissue preservation, Anchorage and non-anchorage dependent cell culture, Kinetics of cell growth, Micro & macro-carrier culture, Hybridoma technology, Stem cell technology, Animal cloning, Transgenic animals.

Section 5: Bioprocess Engineering and Process Biotechnology

Chemical engineering principles applied to biological system, Principle of reactor design, ideal and non-ideal multiphase bioreactors, mass and heat transfer, Rheology of fermentation fluids, Aeration and agitation, Media formulation and optimization, Kinetics of microbial growth, substrate utilization and product formation, Sterilization of air and media, Batch, fed-batch and continuous processes, Various types of microbial and enzyme reactors, Instrumentation control and optimization, Unit operations in solid-liquid separation and liquid-liquid extraction, Process scale-up, economics and feasibility analysis.

Engineering principle of bioprocessing- Upstream production and downstream, Bioprocess design and development from lab to industrial scale, Microbial, animal and plant cell culture platforms, Production of biomass and primary/secondary metabolites, Biofuels, Bioplastics, industrial enzymes, antibiotics, Large scale production and purification of recombinant proteins, Industrial application of chromatographic and membrane based bioseparation methods, Immobilization of biocatalysts (enzymes and cells) for bioconversion processes, Bioremediation-Aerobic and anaerobic processes for stabilization of solid / liquid wastes.

CONTENTS

BIOMOLECULES

NOTES

1. Match the chemicals in List-I with the possible type/class in List-II

List-I	List-II
A. Picloram	**1.** Vitamin
B. Zeatin	**2.** Auxin
C. Thiamine	**3.** Amino Acid
D. Glutamine	**4.** Cytokinin

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

[2 Marks : GATE-2010]

Common Data for Question : 2 - 3

The width of the lipid bilayer membrane is 30 Å. It is permeated by a protein which is a right handed a-helix.

2. The number of h-helical turns permeating the membrane is

(a) 5.6 turns (b) 3.5 turns (c) 6.5 turns (d) 5.0 turns

[2 Marks : GATE-2010]

3. The number of amino acid residues present in the pro" ain is

(a) 15 (b) 18 (c) 17 (d) 20

[2 Marks : GATE-2010]

4. The protein in eukaryotes which is subjected to degradation undergoes

(a) Phosphorylation (b) Carboxylation
(c) Ubiquitation (d) Methylation

[1 Mark : GATE-2011]

5. The molarity of water in a water : ethanol mixture (15 : 85, v/v) is approximately

(a) 0.85 (b) 5.55 (c) 8.5 (d) 55.5

[1 Mark : GATE-2012]

NOTES

6. Which one of the following aminoacids in proteins does **NOT** undergo phosphorylation?

(a) Ser (b) Thr (c) Pro (d) Tyr

[1 Mark : GATE-2013]

7. The 4-amino or 4-keto group of pyrimidine bases is located in the

(a) Major groove of the double stranded DNA

(b) Minor groove of the double stranded DNA

(c) Minor groove of the B form DNA but not the A form DNA

(d) Major groove of the B form DNA but not the A form DNA

[1 Mark : GATE-2014]

8. Amino acid residue which is most likely to be found in the interior of water-soluble globular proteins is

(a) Threonine (b) Aspartic acid (c) Valine (d) Histidine

[1 Mark : GATE-2014]

9. If a plant is shifted to cold temperature, which of the following changes would take place in its membrane?

(a) Ratio of unsaturated to saturated fatty acids would increase

(b) Ratio of unsaturated to saturated fatty acids would decrease

(c) Absolute amount of both fatty acids would increase keeping the ratio same

(d) Absolute amount of both fatty acids would remain unchanged

[2 Marks : GATE-2014]

10. Which of the following statements with respect to the orientation of the nitrogenous bases to the pentose sugars, and the puckering of the sugar, is correct?

(a) Anti, and 2'-endo in A form DNA

(b) Anti, and 2'-endo in B form DNA

(c) Syn, and 3'-endo in A form DNA

(d) Syn, and 3' -endo in B form DNA

[2 Marks : GATE-2014]

11. Which one of the following amino acids has the highest probability to be found on the surface of a typical globular protein in aqueous environment?

(a) Ala (b) Val (c) Arg (d) Ile

[1 Mark : GATE-2015]

12. Levinthal's paradox is related to

(a) Protein secretion (b) Protein degradation

(c) Protein folding (d) Protein trafficking

[1 Mark : GATE-2015]

13. How many different protein sequences of 100 residues can be generated using 20 standard amino acids ?

(a) 100^{20} (b) 100×20 (c) 20^{100} (d) 100! x 20!

[1 Mark : GATE-2015]

NOTES

14. Match the reagents in List-I with their preferred cleavage sites in List-II.

List-I	List-II
A. Cyanogen bromide	**1.** Carboxyl side of methionine
B. o-Iodosobenzoate	**2.** Amino side of methionine
C. Hydroxylamine	**3.** Carboxyl side of tryptophan
D. 2-Nitro-5-thiocyanobenzoate	**4.** Amino side of cysteine
	5. Asparagine-glycine bonds

Codes:	**A**	**B**	**C**	**D**
(a)	1	3	5	4
(b)	2	3	1	4
(c)	1	2	5	4
(d)	4	2	5	3

[2 Marks : GATE-2015]

15. Disaccharide molecules that contain $\beta(1 \rightarrow 4)$ glycosidic linkage are

(a) Sucrose and maltose (b) Sucrose and isomaltose

(c) Maltose and isomaltose (d) Lactose and cellobiose

[1 Mark : GATE-2016]

16. Natural proteins are composed primarily of 20 α-amino acids. Which one of the following statements is true for any of these amino acids in a solultion of pH 1.5?

(a) Only the amino group is ionized.

(b) Only the carboxylic acid group is ionized.

(c) Both amino and carboxylic acid groups are ionized.

(d) Both amino and carboxylic acid groups are neutral.

[1 Mark : GATE-2017]

17. An enzymatic reaction exhibits Michaelis-Menten kinetics. For this reaction, on doubling the concentration of enzyme while maintaining (S) >> (E_0).

(a) Both K_m and V_{max} will remain the same

(b) K_m will remain the same but V_{max} will increase

(c) K_m will increase but V_{max} will remain the same.

(d) Both K_m and V_{max} will increase

[1 Mark : GATE-2017]

18. Which one of the following amino acids has three ionizable groups?

(a) Glycine (b) Leucine (c) Valine (d) Lysine

[2 Marks : GATE-2017]

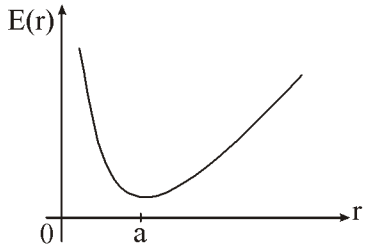
19. If the chemical composition of proteins in an organism is $CH_{1.5}O_{0.3}N_{0.3}S_{0.004}$, the mass percentage of carbon in the proteins is

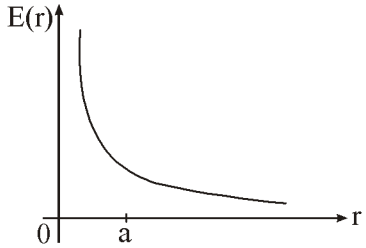
(Given data : Atomic weights (Da) of C = 12, H = 1, O = 16, N = 14, and S = 32.)

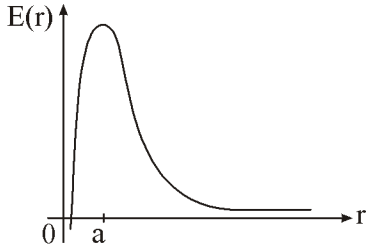
[2 Marks : GATE-2017]

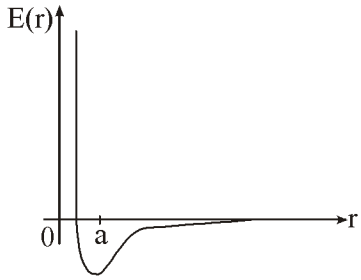
NOTES

20. The interaction energy E between two spherical particles is plotted as a function of the distance (r) between them. When r < a, where a is a constant, the net force between the spherical particles is requlsive. When r > a, they attract via van der Waals attraction. Which one of the following plots correctly represents the interaction energy between the above two particles ?

(a)


(b)


(c)


(d)


[2 Marks : GATE-2017]

21. A DNA strand of lenght 25 nm wraps diametrically around the circumference of a spherical histone-octamer once. The radius (nm) of the histone-octamer is (Given data : $\pi = 3.14$)

[2 Marks : GATE-2017]

22. Which one of the following is INCORRECT about protein structures?

(a) A protein fold is stabilized by favorable non-covalent interactions

(b) All parts of a fold can be classified as helices, strands or turns

(c) Two non-covalent atoms cannot be closer than the sum of their van der Waals radii

(d) The peptide bond is nearly planar

[1 Mark : GATE-2018]

23. Which one of the following metabolic processes in mammalian cells does NOT occur in the mitochondria?

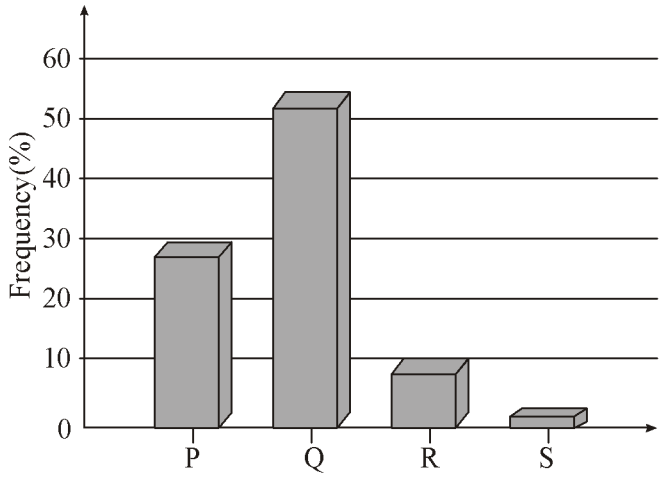
(a) Citric acid cycle (b) Oxidative phosphorylation

(c) Fatty acid β-oxidation (d) Glycolysis

[1 Mark : GATE-2018]

24. An analysis of DNA-protein interactions was carried out using all DNA-protein complexes in the protein data bank (PDB). The frequency distribution of four amino acid residues, represented as P, Q, R and S, occurring in non-covalent interactions between the protein and DNA backbone is shown below.

NOTES



Which one of the following is correct?

(a) P-Lys, Q-Arg, R-Gln, S-Glu (b) P-Gln, Q-Glu R-Lys, S-Arg

(c) P-Asn, Q-Asp, R-Arg, S-Lys (d) P-His, Q-Glu, R-Gln, S-Lys

[2 Marks : GATE-2018]

25. A rod shaped bacterium has a length of 2 um, diameter of 1 um and density the same as that of water. If proteins constitute 15% of the cell mass and the average protein has a mass of 50 kDa, the number of proteins in the cell is (1 Da = 1.6×10^{-24} g)

[2 Marks : GATE-2018]

26. The mass of 1 kmol of oxygen molecules is _____ g (rounded off to the nearest integer).

[1 Mark : GATE-2019]

27. Which one of the following amino acid residues will destablize an α-helix when inserted in the middle of the helix?

(a) Pro (b) Val (c) Ile (d) Leu

[2 Marks : GATE-2019]

28. The hexapeptide P has an isoelectric point (pI) of 6.9. Hexapeptide Q is a variant of P that contains valine instead of glutamate at position 3. The two peptides are analyzeed by polyacrylamide gel electrophoresis at pH 8.0. Which one of the following statements is CORRECT?

(a) P will migrate faster than Q towards the anode

(b) P will migrate faster than Q towards the cathode

(c) Both P and Q will migrate together

(d) Q will migrate faster than P towards the anode

[2 Marks : GATE-2019]

❍❍❍

ANSWERS AND EXPLANATIONS

1. *Ans. (a)*

Picloram is an auxin type of hormone absorbed by root. Zeatin is a member of the plant growth hormone family, cytokinins. Thiamine is a water-soluble vitamin of the B complex. Glutamine is one acids encoded by the standard genetic code CAA, CAG.

2. *Ans. (a)*

Given,

Width of lipid bilayer membrane= 30 A

We know, each turn of right handed a-helix has a pitch of = 5.1 A

Thus, total turns = 30 / 5.1 = 5.6 turns.

3. *Ans. (d)*

We know, the right handed a-helix has 3.6 residues per turn in the helix.

But number of helix turns = 5.6

Therefore, No. of amino acids present in the protein = 5.6 * 3.6 = 20

Therefore, No. of amino acid residues present in the protein is 20.

4. *Ans. (c)*

Ubiquitination is an enzymatic, protein post-translational modification (PTM) process in which the carboxylic acid of the terminal glycine from the di-glycine motif in the activated ubiquitin forms an amide bond to the epsilon amine of the lysine in the modified protein. Ubiquitination, also known as ubiquitylation, regulates degradation of cellular proteins by the ubiquitin-proteasome system, controlling a protein's half-life and expression levels. This process involves the sequential action of ubiquitin-activating enzymes (El), ubiquitin-conjugating enzymes (E2), and ubiquitin ligases (E3). The reaction catalyzed by each enzyme transfers a covalent bond with ubiquitin from one enzyme to the next and finally to a target protein.

5. *Ans. (c)*

18gm water in 100 ml ethanol is 10 M. Hence 15 gm in 85 ml is approximately-8.5.

Density of H_2O = 1 gm/ml

$$d = \frac{M}{V}$$

$$M = 1 \times 15 = 15 \text{ g}$$

$$M = \frac{15}{18 \times 100} \times 1000 = 8.3$$

6. *Ans. (c)*

Proline is unique in that it is the only amino acid where the side chain is connected to the protein backbone twice, forming a five-membered nitrogen-containing ring. Proline is unable to occupy many of the main chain conformations easily adopted by all other amino acids. Proline can often be found in very tight turns in protein structures (i.e. where the polypeptide chain must change direction). It can also function to introduce kinks into alpha helices, since it is unable to adopt a normal helical conformation. Proline plays important roles in molecular recognition, particularly in intracellular signalling. The Proline side chain is very non-reactive and it does not undergo phosphorylation.

7. *Ans. (a)*

The pyrimidine bases, Thymine and Cytosine in case of DNA have a 4-amino or a 4-keto group present with the amide ring. These 4-amino or 4-keto groups are present in the major groove of the DNA molecule.

8. *Ans. (c)*

Globular proteins have no systematic structures. There may be single chains, two or more chains which interact in the usual ways or there may be portions of the chains with helical structures, pleated structures, or completely random structures. Common globular proteins include egg albumin, hemoglobin, myoglobin, insulin, serum globulins in blood, and many enzymes. Water-soluble globular proteins have hydrophobic amino acids present in the interior of the protein structure forming hydrophobic bonds. So, valine is the amino acid residue most likely to be present on the interior.

9. *Ans. (a)*

The more unsaturated fatty acids chain present in lipids, the more is the fluidity of a membrane. So the plant adjusts itself in cold temperature by increasing unsaturated fatty acids.

10. ***Ans. (b)***

Nitrogenous bases are always arranged in "anti" positions to their corresponding pentose sugar moieties. In B-form of DNA, sugar puckering occurs predominantly in the C2 position of the pentose sugar. The sugar pucker determines the shape of the a-helix, whether the helix will exist in the A-form or in the B-form. So, in C2-endo puckering occurs in B-form of DNA.

11. ***Ans. (c)***

Arginine, lysine aspartic, glutamic and histidine can present in aqueous environment.

12. ***Ans. (c)***

Finding the native folded state of protein.

13. ***Ans. (c)***

20^{100} different protein sequences of 100 residues can be generated using 20 standard amino acids.

14. ***Ans. (a)***

- Cyanogen bromide → Carboxyl side of methionine
- o-Iodosobenzoate → Carboxyl side of tryptophan
- Hydroxylamine → Asparagine-glycine bonds
- 2-Nitro-5-thiocy anobenzoate → Amino side of cysteine

15. ***Ans. (d)***

Glycosidic bond or glycosidic linkage is a type of covalent bond that joins a carbohydrate (sugar) molecule to another group, which may or may not be another carbohydrate. Lactose (β-D-galactopyranosyl (l → 4) D-glucopyranose) and cellobiose (β-D-glucopyranosyl (l → 4) D-glucopyranose) are disaccharides whose monomeric units are connected by β(l →4) glycosidic bonds.

16. ***Ans. (a)***

17. ***Ans. (b)***

18. ***Ans. (d)***

Lysine contains an a-amino group (which is in the protonated- NH_3^+ form under biological conditions), an oc-carboxylic acid group (which is in the deprotonated –COO form under biological conditions), and a side chain lysyl ($(CH_2)_4NH_2$), classifying it as a charged (at physiological pH), aliphatic amino acid.

Lysine has three ionizable functional groups with the following pKa values:

α-amino group = 9.04

α-carboxylic group = 2.17

R group = 12.48.

19. ***Ans. 52.00 to 54.00***

Mol. weight of $CH_{1.5}O_{0.3}N_{0.3}S_{0.004}$ = 22.628

∴ % Mass of carbon

$$= \frac{12}{22.628} \times 100 = 53.03$$

20. ***Ans. (d)***

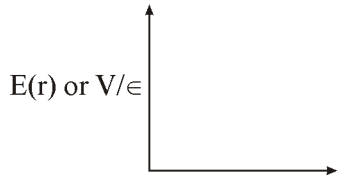
The given plot () is a plot for Lennard Jones (L-J) potential which is givenby following equation

$$V_{LJ} = 4\in\left[\left(\frac{\sigma}{r}\right)^{12} - \left(\frac{\sigma}{r}\right)^{6}\right]$$

And $$V_{LJ} = \in\left[\left(\frac{r_m}{r}\right)^{12} - 2\left(\frac{r_m}{r}\right)^{6}\right]$$

As $v_m = a$

So that $$V_{LJ} = \in\left[\left(\frac{a}{r}\right)^{12} - 2\left(\frac{a}{r}\right)^{6}\right]$$



Where, r = Distance between the particles

∈ = Depth of the potential well

σ = finite distance at which the inter particle potential is zero.

For given plot r_m = a = is the distance at which the potential reaches its minimum.

At 'a' the potential function has value – ∈.

The r^{-12} term is repulsive term which is applicable for r < a, describe the repulsion at short range due to overlapping of electron radius. While r^{-6} is attractive term when r ≥ a, which describes the attraction at long ranges but the force of attraction is of either vander walls or dispersion force.

21. ***Ans. 3.90 to 4.10***

Circumference of sphere is

$$= 2\pi r$$

Then, $r = \frac{25}{2\pi} = 3.98$ mm

22. ***Ans. (b)***

23. ***Ans. (d)***

Glycolysis occurs in most organisms in the cytosol of the cell. The most common type of glycolysis is the *Embden-Meyerhof-Parnas (EMPpathway).*

In mammalian cells, both peroxisomes and mitochondria contain a beta-oxidative pathway. Beta-oxidation is a key pathway for the breakthrough of fatty acids. In yeasts and plants, fatty acid oxidation occurs uniquely in peroxisomes.

Conversion of pyruvate to acetyl CoA, the **citric acid cycle** takes place in the matrix of the mitochondria. **Oxidative phosphorylation is a** process occurring in the intermembrane space of the mitochondria that results in the formation of ATP from the flow of electrons to oxygen.

24. ***Ans. (a)***

DNA has net negative charge due to the presence of phosphate groups. Lys, Arg and Gin are basic amino acids whereas Glu is acidic amino acid. Arg (Q) attracts more phosphate and forms extensive hydrogen bonding with its five H-bond donors present in its structure that stabilizes the interactions in DNA-protein complexes reflecting the highest percentage frequency in the graph. Followed by Arg the next higher frequency is shown for Lys (P) due to its basic nature and hydrogen bonding capacity which is followed by the frequency of Gin (R). Glu (s) due to negative charge has least frequency.

25. ***Ans. 2945000***

$$S = 1 \text{ kg}/l$$
$$l = 2 \times 10^{-6} \text{ mt}$$
$$D = 1 \times 10^{-6} \text{ mt}$$

Volume of bacterium

$$= \frac{\pi}{4} D^2 I = 1.5708 \times 10^{-18} \text{ m}^3$$
$$= 1.5708 \times 10^{-15} \text{ kg}$$
$$(\because 1 \text{ m}^3 = 1000 \text{ kg})$$
$$= 1.5708 \times 10^{-12} \text{ gm}$$

15% of this is proteins

$$= 2.356 \times 10^{-13} \text{ gm}$$

Now. average weight of one protein

$$= 50 \text{ kDa}$$
$$= 50 \times 1000 \times 1.6 \times 10^{-24}$$
$$= 8 \times 10^{-20} \text{ gm}$$

$\therefore$ Number of proteins

$$= \frac{2.356 \times 10^{-13}}{8 \times 10^{-20}} = 8 \times 10^{-20}$$
$$= 2.945 \times 10^6 = 2945000$$

26. ***Ans. (31800 to 32000)***

Number of moles (n)

$$= \frac{\text{Mass (grams)}}{\text{Molecular Weight}}$$

Given, $n = 1 \text{ Kmol} = 1 \times 10^3$ moles

Molecular weight of $O_2 = 32$

$$1 \times 10^3 = \frac{\text{grams}}{32}$$

$$\text{grams} = 32000$$

27. ***Ans. (a)***

Proline either breaks or kinks a helix, both because it cannot donate an amide hydrogen bond and also because its sidechain interferes sterically with the backbone of the preceding turn-inside a helix, this forces a bend of about 30° in the helix's axis.

28. ***Ans. (a)***

❍❍❍