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CSIR-NET

LIFE SCIENCE

Council of Scientific & Industrial Research

VOLUME – 1

Molecules and their Interaction Relevant to Biology & Cellular Organization

SIERRA INNOVATIONS

CSIR-NET : LIFE SCIENCE

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I UNIT

Molecules and their Interaction Relevant to Biology

Structure of Atoms, Molecules, and Chemical Bonds

1. Atomic Structure

Atoms are the fundamental units of matter, composed of subatomic particles: protons, neutrons, and electrons. Understanding atomic structure is essential for grasping how atoms form bonds to create biologically relevant molecules like carbohydrates, proteins, and nucleic acids.

1.1 Subatomic Particles

- **Protons**:
  - Mass: 1.6726×10^{-27} kg (≈1 atomic mass unit, amu).
  - Charge: +1 (1.602×10^{-19} coulombs).
  - Location: Nucleus.
  - Defines the atomic number (Z), which determines the element's identity.
- **Neutrons**:
  - Mass: 1.6749×10^{-27} kg (slightly heavier than protons).
  - Charge: 0 (neutral).
  - Location: Nucleus.
  - Contributes to the mass number (A = Z + number of neutrons).
- **Electrons**:
  - Mass: 9.1094×10^{-31} kg (≈1/1836 of a proton).
  - Charge: -1 (-1.602×10^{-19} coulombs).
  - Location: Orbitals surrounding the nucleus.
  - Determines chemical reactivity and bonding behavior.
- **Atomic Number and Mass Number**:
  - Atomic number (Z): Number of protons (e.g., carbon, Z=6).
  - Mass number (A): Sum of protons and neutrons.
  - Example: Carbon-12 (^{12}C) has 6 protons and 6 neutrons; Carbon-14 (^{14}C) has 6 protons and 8 neutrons.
- **Isotopes**:
  - Atoms of the same element with different neutron numbers.
  - Example: ^{12}C (stable), ^{14}C (radioactive, used in radiocarbon dating).
  - Biological relevance: Isotopes like ^{13}C and ^{15}N are used in NMR spectroscopy to study biomolecular structures.

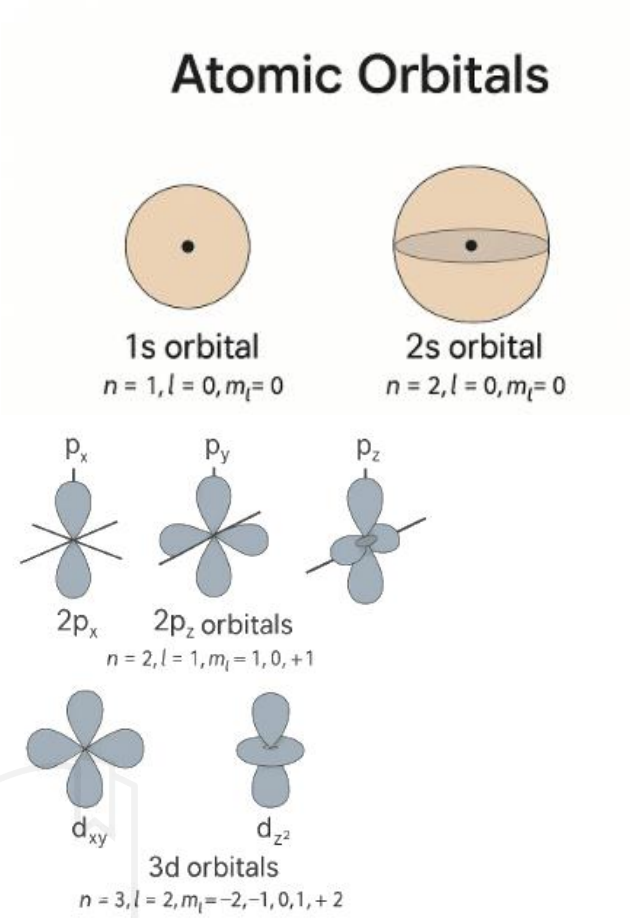
1.2 Electron Configuration - Electrons occupy specific energy levels or orbitals, defined by quantum mechanics. The arrangement of electrons determines an atom's chemical properties and bonding capacity.

- **Quantum Numbers**:
  - **Principal Quantum Number (n)**: Specifies the energy level (n = 1, 2, 3, …). Higher n indicates higher energy and larger orbitals.
  - **Azimuthal Quantum Number (l)**: Defines orbital shape (l = 0 to n-1).
    - l = 0: s orbital (spherical).
    - l = 1: p orbital (dumbbell-shaped).
    - l = 2: d orbital (cloverleaf or double dumbbell).
    - l = 3: f orbital (complex shapes).
  - **Magnetic Quantum Number (m_l)**: Specifies orbital orientation (m_l = -l to +l).
    - Example: For l = 1 (p orbital), m_l = -1, 0, +1 (three p orbitals: p_x, p_y, p_z).
  - **Spin Quantum Number (m_s)**: Indicates electron spin (+1/2 or -1/2).
- **Rules for Electron Configuration**:
  - **Pauli Exclusion Principle**: No two electrons in an atom can have the same set of four quantum numbers, limiting each orbital to two electrons with opposite spins.

- **Aufbau Principle**: Electrons fill orbitals in order of increasing energy: 1s → 2s → 2p → 3s → 3p → 4s → 3d → 4p, etc.
- **Hund's Rule**: Electrons occupy degenerate orbitals (same energy) singly with parallel spins before pairing.

- **Examples**:
  - Carbon (Z=6): $1s^2\ 2s^2\ 2p^2$ (four valence electrons, enabling four covalent bonds).
  - Oxygen (Z=8): $1s^2\ 2s^2\ 2p^4$ (six valence electrons, forming two bonds and two lone pairs in water).
  - Nitrogen (Z=7): $1s^2\ 2s^2\ 2p^3$ (five valence electrons, forming three bonds in ammonia).
- **Biological Relevance**:
  - Carbon's $2s^2\ 2p^2$ configuration allows it to form four covalent bonds, making it the backbone of organic molecules (e.g., sugars, amino acids).
  - Oxygen's high electronegativity (due to $2p^4$) drives polar bond formation in water, critical for hydrogen bonding in DNA and proteins.
  - Isotopes like ^{15}N are used in metabolic studies to trace nitrogen incorporation in amino acids.

Diagram 1: Atomic Orbitals



[Description: A diagram illustrating the shapes of atomic orbitals. The 1s orbital is a spherical cloud centered at the nucleus. The 2s orbital is a larger sphere with a nodal plane. The 2p orbitals (p_x, p_y, p_z) are dumbbell-shaped, oriented along the x, y, and z axes. The 3d orbitals (e.g., d_xy, d_z^2) show cloverleaf and double-dumbbell shapes. Each orbital is labeled with its quantum numbers (n, l, m_l).]

Table 1: Subatomic Particles and Properties

Particle	Mass (kg)	Charge (Coulombs)	Location	Role in Atom
Proton	1.6726×10^{-27}	$+1.602 \times 10^{-19}$	Nucleus	Defines atomic number
Neutron	1.6749×10^{-27}	0	Nucleus	Contributes to mass number
Electron	9.1094×10^{-31}	-1.602×10^{-19}	Orbitals	Determines chemical reactivity

2. Chemical Bonds

Chemical bonds are interactions between atoms that form molecules or compounds, determining their stability, reactivity, and biological function. In living systems, bonds govern the structure of biomolecules (e.g., DNA, proteins) and facilitate processes like enzyme catalysis and membrane transport.

2.1 Types of Chemical Bonds

- **Ionic Bonds**:
  - **Mechanism**: Formed by the transfer of electrons from one atom to another, creating oppositely charged ions that attract electrostatically.
  - **Example**: Sodium chloride (NaCl), where Na donates an electron to Cl, forming Na^+ and Cl^-.

- **Properties**:
  - High melting and boiling points (e.g., NaCl melts at 801°C).
  - Soluble in polar solvents like water due to ion-dipole interactions.
  - Conduct electricity when molten or dissolved.
  - Bond strength: 400–4000 kJ/mol (varies with ion size and charge).
- **Biological Relevance**:
  - Ionic bonds form salt bridges in proteins, stabilizing tertiary and quaternary structures (e.g., Asp^-–Lys^+ interactions in hemoglobin).
  - Facilitate ion transport across membranes (e.g., Na^+/K^+ ATPase in neurons).
  - In aqueous environments, ionic bonds are weakened due to water's high dielectric constant ($\varepsilon \approx 80$), making them less stable than covalent bonds.

- **Covalent Bonds**:
  - **Mechanism**: Formed by the sharing of electron pairs between atoms to achieve stable electron configurations.
  - **Types**:
    - Single bond: One shared electron pair (e.g., C–C in ethane, 347 kJ/mol).
    - Double bond: Two shared pairs (e.g., C=C in ethylene, 614 kJ/mol).
    - Triple bond: Three shared pairs (e.g., N≡N in nitrogen gas, 945 kJ/mol).
    - Polar covalent: Unequal sharing due to electronegativity differences (e.g., O–H in water, δ^+ on H, δ^- on O).
    - Non-polar covalent: Equal sharing (e.g., C–H in methane).
  - **Properties**:
    - Strong (150–1100 kJ/mol), directional, and stable in aqueous environments.
    - Form the backbone of organic molecules.
  - **Biological Relevance**:
    - Peptide bonds (C–N) link amino acids in proteins, with partial double-bond character due to resonance.
    - Phosphodiester bonds (C–O–P) form the DNA/RNA backbone.
    - Disulfide bonds (S–S) stabilize protein structures (e.g., insulin).
- **Coordinate (Dative) Bonds**:
  - **Mechanism**: One atom donates both electrons to form the bond.
  - **Example**: Ammonium ion (NH_4^+), where nitrogen's lone pair bonds with H^+.
  - **Properties**: Bond strength ≈ 100–200 kJ/mol, often reversible.
  - **Biological Relevance**:
    - Common in metal-ion coordination complexes (e.g., Fe^{2+} in heme binds O_2 via coordinate bonds).
    - Facilitates enzyme-metal interactions (e.g., Zn^{2+} in carbonic anhydrase).
- **Metallic Bonds**:
  - **Mechanism**: Delocalized electrons form a "sea" shared among metal atoms, creating a lattice of positive ions.
  - **Properties**: Bond strength ≈ 100–350 kJ/mol, conductive, malleable.
  - **Biological Relevance**: Rare but relevant in metalloproteins (e.g., iron in ferritin, magnesium in chlorophyll).

2.2 Electronegativity

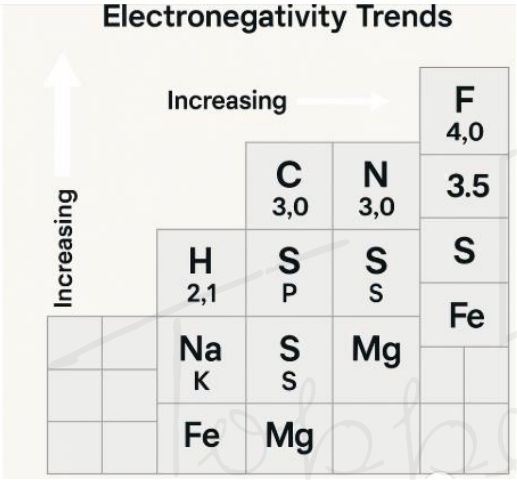
- **Definition**: The ability of an atom to attract electrons in a chemical bond.
- **Pauling Scale**:
  - Fluorine: 4.0 (most electronegative).
  - Oxygen: 3.5.
  - Nitrogen: 3.0.
  - Carbon: 2.5.
  - Hydrogen: 2.1.
  - Phosphorus, Sulfur: ≈2.5.
- **Impact on Bonding**:
  - Large electronegativity difference (>1.7): Ionic bond (e.g., Na–Cl, $\Delta EN = 2.1$).
  - Moderate difference (0.4–1.7): Polar covalent bond (e.g., O–H, $\Delta EN = 1.4$).
  - Small difference (<0.4): Non-polar covalent bond (e.g., C–H, $\Delta EN = 0.4$).

- **Biological Relevance**:
  - Polar bonds in water (O–H) create a dipole moment, enabling hydrogen bonding, which stabilizes DNA base pairs and protein secondary structures.
  - Electronegativity differences drive the reactivity of functional groups in biomolecules (e.g., –OH, $–NH_2$).

Table 2: Chemical Bond Types and Properties

Bond Type	Formation Mechanism	Strength (kJ/mol)	Solubility in Water	Biological Example
Ionic	Electron transfer	400–4000	High	Salt bridges in proteins
Covalent	Electron sharing	150–1100	Varies	Peptide bonds, DNA backbone
Coordinate	Lone pair donation	100–200	Moderate	Heme-iron coordination
Metallic	Delocalized electrons	100–350	Low	Iron in ferritin

Chart 1: Electronegativity Trends



[Description: A periodic table highlighting electronegativity values for biologically relevant elements (H, C, N, O, P, S, Na, K, Mg, Fe). Arrows indicate increasing electronegativity from left to right and bottom to top. Key values are marked: F (4.0), O (3.5), N (3.0), C (2.5), H (2.1).]

3. Molecular Geometry

Molecular geometry describes the 3D arrangement of atoms in a molecule, determined by the arrangement of electron pairs around the central atom. It influences molecular properties like polarity, reactivity, and biological function.

3.1 Valence Shell Electron Pair Repulsion (VSEPR) Theory

- **Principle**: Electron pairs (bonding and lone pairs) around a central atom repel each other, adopting a geometry that minimizes repulsion.
- **Electron Domains**: Sum of bonding pairs and lone pairs around the central atom.
- **Common Geometries**:
  - **2 Electron Domains**: Linear, 180° (e.g., CO_2, O=C=O).
  - **3 Electron Domains**: Trigonal planar, 120° (e.g., BF_3, F–B–F).
  - **4 Electron Domains**: Tetrahedral, 109.5° (e.g., CH_4, H–C–H).
  - **5 Electron Domains**: Trigonal bipyramidal, 90°/120° (e.g., PF_5).
  - **6 Electron Domains**: Octahedral, 90° (e.g., SF_6).
- **Lone Pair Effects**:
  - Lone pairs occupy more space than bonding pairs, distorting bond angles.
  - Example: Ammonia (NH_3) has 4 electron domains (3 bonding, 1 lone pair), forming a trigonal pyramidal shape with a bond angle of ~107° (less than tetrahedral 109.5°).
  - Example: Water (H_2O) has 4 electron domains (2 bonding, 2 lone pairs), forming a bent shape with a bond angle of ~104.5°.

3.2 Hybridization

- **Definition**: Mixing of atomic orbitals to form hybrid orbitals suitable for bonding.
- **Types**:
  - **sp**: 2 hybrid orbitals, linear geometry (e.g., acetylene, HC≡CH).

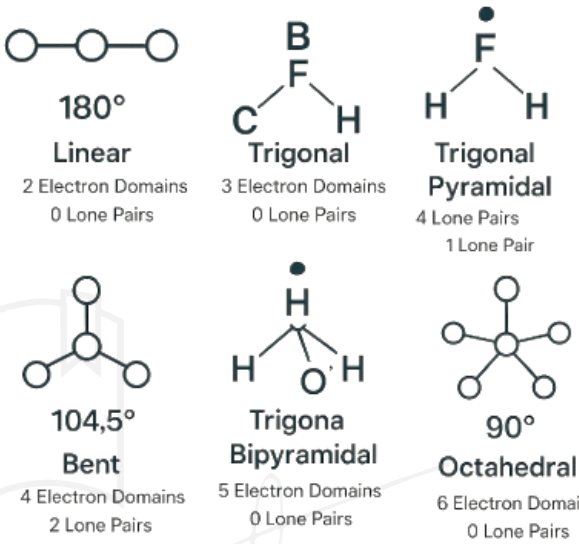
- **sp^2**: 3 hybrid orbitals, trigonal planar (e.g., ethylene, $H_2C=CH_2$).
- **sp^3**: 4 hybrid orbitals, tetrahedral (e.g., methane, CH_4).
- **sp^3d**: 5 hybrid orbitals, trigonal bipyramidal (e.g., PCl_5).
- **sp^3d^2**: 6 hybrid orbitals, octahedral (e.g., SF_6).

- **Biological Relevance**:
  - Carbon's sp^3 hybridization in amino acids and sugars enables tetrahedral geometry, critical for chirality (e.g., L- vs. D-amino acids).
  - Nitrogen's sp^3 hybridization in ammonia and amines allows lone pair donation in coordinate bonds.
  - Phosphorus's sp^3d hybridization in ATP's phosphate groups facilitates high-energy bonds.

3.3 Molecular Orbital (MO) Theory

- **Principle**: Electrons occupy molecular orbitals formed by the linear combination of atomic orbitals.
- **Types of Molecular Orbitals**:
  - Bonding orbitals (σ, π): Lower energy, stabilize the molecule.
  - Antibonding orbitals (σ*, π*): Higher energy, destabilize the molecule.
  - Non-bonding orbitals: Lone pairs or unpaired electrons.
- **Bond Order**:
  - Formula: Bond order = ½ (Number of bonding electrons – Number of antibonding electrons).
  - Example: O_2 has 12 valence electrons ($1\sigma^2\ 2\sigma^2\ 1\pi^4\ 2\pi^2$), bond order = ½ (8 – 4) = 2 (double bond).
- **Biological Relevance**:
  - MO theory explains the stability of π-bonds in DNA bases (e.g., adenine-thymine).
  - Paramagnetism of O_2 (due to unpaired electrons in π* orbitals) affects its role as an electron acceptor in respiration.

Diagram 2: VSEPR Geometries

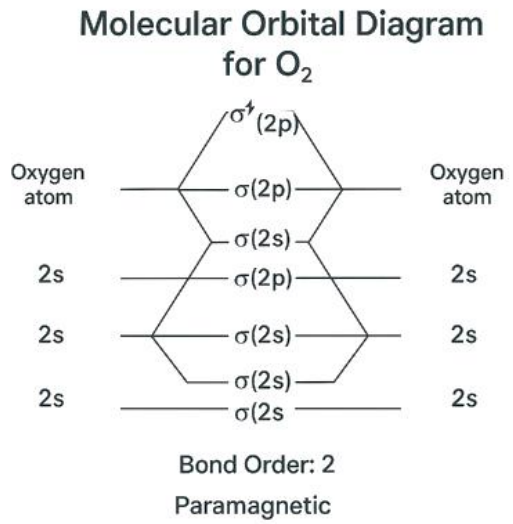


[Description: A diagram showing molecular geometries based on VSEPR theory. Molecules include CO_2 (linear, 180°), BF_3 (trigonal planar, 120°), CH_4 (tetrahedral, 109.5°), NH_3 (trigonal pyramidal, 107°), H_2O (bent, 104.5°), PF_5 (trigonal bipyramidal, 90°/120°), and SF_6 (octahedral, 90°). Each molecule is labeled with bond angles, electron domains, and lone pairs.]

Table 3: VSEPR Geometries and Hybridization

Electron Domains	Bonding Pairs	Lone Pairs	Geometry	Bond Angles	Hybridization	Example
2	2	0	Linear	180°	sp	CO_2
3	3	0	Trigonal planar	120°	sp^2	BF_3
4	4	0	Tetrahedral	109.5°	sp^3	CH_4
4	3	1	Trigonal pyramidal	~107°	sp^3	NH_3
4	2	2	Bent	~104.5°	sp^3	H_2O
5	5	0	Trigonal bipyramidal	90°, 120°	sp^3d	PF_5
6	6	0	Octahedral	90°	sp^3d^2	SF_6

Graph 1: Molecular Orbital Diagram for O_2



[Description: A molecular orbital diagram for O_2, showing the combination of 2s and 2p atomic orbitals from two oxygen atoms. The diagram includes σ(2s), σ*(2s), σ(2p), π(2p), π*(2p), and σ*(2p) orbitals, with 12 valence electrons filled according to Aufbau and Hund's rules. The bond order (2) and paramagnetism (due to two unpaired electrons in π* orbitals) are highlighted.]

4. Biological Relevance of Chemical Bonds and Molecular Geometry

The structure of atoms, bonds, and molecular geometry directly influences the function of biomolecules in living systems. Below are key examples:

- **Water as a Biological Solvent**:
  - Polar O–H bonds (ΔEN = 1.4) and bent geometry (104.5°) create a dipole moment (δ^+ on H, δ^- on O).
  - Enables hydrogen bonding, making water an excellent solvent for polar molecules (e.g., sugars, ions).
  - Facilitates hydrophobic interactions, driving protein folding and membrane formation.
- **Peptide Bonds in Proteins**:
  - Covalent C–N bonds formed via condensation between amino acids.
  - Partial double-bond character (due to resonance) restricts rotation, stabilizing α-helices and β-sheets.
  - Bond length: ~1.33 Å (shorter than single C–N, 1.47 Å).
- **DNA and RNA Structure**:
  - Covalent phosphodiester bonds (C–O–P) form the sugar-phosphate backbone.
  - Hydrogen bonds between base pairs (A–T: 2 H-bonds; G–C: 3 H-bonds) ensure stability and specificity.
  - B-DNA's helical geometry (10.5 bp/turn, 34 Å pitch) is driven by base stacking and H-bonding.
- **Enzyme-Substrate Interactions**:
  - Active sites combine covalent (e.g., Schiff base formation), ionic (e.g., charge-charge interactions), and non-covalent bonds (e.g., H-bonds, hydrophobic effects).
  - Example: Chymotrypsin's catalytic triad (Ser-His-Asp) uses H-bonds and covalent intermediates for peptide cleavage.
- **Chirality and Biological Specificity**:
  - Tetrahedral geometry (sp^3 hybridization) of carbon in amino acids and sugars creates chiral centers.
  - Example: L-amino acids dominate proteins due to stereospecific enzyme active sites.

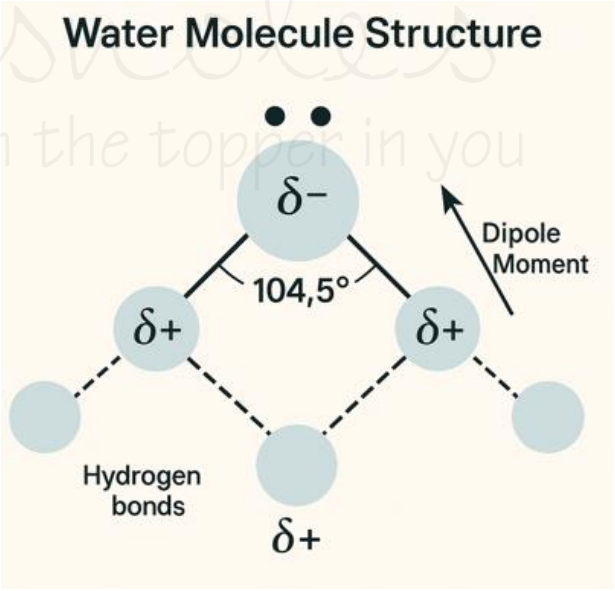


Diagram 3: Water Molecule Structure

[Description: A diagram of a water molecule (H_2O), showing the bent geometry (104.5° bond angle) due to two bonding pairs and two lone pairs on oxygen. The molecule is labeled with partial charges (δ^+ on H, δ^- on O) and dipole moment. Hydrogen bonds to neighboring water molecules are depicted as dashed lines.]

PYQ Analysis

Below are 12 PYQs from CSIR NET Life Sciences (2018–2024) related to Subtopic A, with solutions and explanations to highlight exam patterns and common errors.

(2018):

1. What is the hybridization of the carbon atom in formaldehyde ($H_2C=O$)?
   (A) sp (B) sp^2
   (C) sp^3 (D) sp^3d.
   Solution: The carbon in $H_2C=O$ has three electron domains (one double bond to O, two single bonds to H), forming a trigonal planar geometry. This corresponds to sp^2 hybridization.
   Answer: B.
   Common Error: Confusing double bonds with single bonds, leading to sp^3 choice.
   Tip: Count electron domains, not bonds; a double bond counts as one domain.

(2019):

2. Which molecule has a bond angle closest to 120°?
   (A) CH_4 (B) NH_3,
   (C) BF_3 (D) H_2O.
   Solution: BF_3 has three bonding pairs, no lone pairs, forming a trigonal planar geometry with 120° bond angles. CH_4 (109.5°), NH_3 (~107°), and H_2O (~104.5°) have tetrahedral-based geometries distorted by lone pairs.
   Answer: C.
   Common Error: Selecting NH_3 due to confusion with trigonal pyramidal shape.
   Tip: Memorize VSEPR geometries and lone pair effects.

(2020):

3. Calculate the bond order of N_2 using molecular orbital theory.
   (A) 1 (B) 2
   (C) 3 (D) 4
   Solution: N_2 has 10 valence electrons ($1\sigma^2\ 2\sigma^{*2}\ 1\pi^4\ 3\sigma^2$). Bond order = ½ (8 bonding – 2 antibonding) = 3 (triple bond).
   Answer: C.
   Common Error: Miscounting electrons or orbitals.
   Tip: Draw the MO diagram and focus on valence electrons.

4. Which bond is strongest in biological systems?
   (A) Hydrogen bond
   (B) Ionic bond
   (C) Covalent bond
   (D) Van der Waals.
   Solution: Covalent bonds (150–1100 kJ/mol) are stronger than ionic (weaker in aqueous environments), hydrogen (10–40 kJ/mol), and Van der Waals (2–20 kJ/mol).
   Answer: C.
   Common Error: Choosing ionic bonds, assuming high strength in solids applies to cells.
   Tip: Consider the aqueous environment of biological systems.

(2021):

5. What is the electron configuration of phosphorus (Z=15)?
   (A) $1s^2\ 2s^2\ 2p^6\ 3s^2\ 3p^2$
   (B) $1s^2\ 2s^2\ 2p^6\ 3s^2\ 3p^3$
   (C) $1s^2\ 2s^2\ 2p^6\ 3s^2\ 3p^4$
   (D) $1s^2\ 2s^2\ 2p^6\ 3s^1\ 3p^4$.
   Solution: Phosphorus has 15 electrons: $1s^2\ 2s^2\ 2p^6\ 3s^2\ 3p^3$.
   Answer: B.
   Common Error: Misplacing electrons in 3s or 3p orbitals.
   Tip: Use the Aufbau principle and check total electrons.

6. Which molecule exhibits a coordinate bond?
   (A) H_2O (B) NH_3,
   (C) NH_4^+ (D) CH_4.
   Solution: In NH_4^+, nitrogen donates a lone pair to H^+, forming a coordinate bond.
   Answer: C.
   Common Error: Confusing NH_3's lone pair with a coordinate bond.
   Tip: Coordinate bonds involve one atom donating both electrons.

(2022):

7. What is the bond angle in methane (CH_4)?
   (A) 90° (B) 104.5°
   (C) 107° (D) 109.5°.
   Solution: CH_4 has four bonding pairs, no lone pairs, forming a tetrahedral geometry with 109.5° bond angles.
   Answer: D.
   Common Error: Confusing with NH_3 or H_2O due to lone pair effects.
   Tip: Tetrahedral geometry always has 109.5° angles without lone pairs.
8. Which element has the highest electronegativity?
   (A) Oxygen (B) Nitrogen,
   (C) Fluorine (D) Chlorine.
   Solution: Fluorine has the highest electronegativity (4.0 on the Pauling scale).
   Answer: C.
   Common Error: Choosing oxygen due to its biological prevalence.
   Tip: Memorize key electronegativity values: F > O > N > Cl.

(2023):

9. How many unpaired electrons are present in the ground state of oxygen (Z=8)?
   (A) 0 (B) 1
   (C) 2 (D) 3
   Solution: Oxygen's electron configuration is $1s^2\ 2s^2\ 2p^4$. The 2p orbitals have two unpaired electrons ($2p_x^1\ 2p_y^1\ 2p_z^2$).
   Answer: C.
   Common Error: Ignoring Hund's rule, assuming paired electrons.
   Tip: Apply Hund's rule for degenerate orbitals.
10. Which bond type stabilizes the DNA double helix?
    (A) Covalent (B) Ionic,
    (C) Hydrogen (D) Coordinate.
    Solution: Hydrogen bonds between base pairs (A–T, G–C) stabilize the DNA double helix, while covalent phosphodiester bonds form the backbone. The question focuses on base pairing.
    Answer: C.
    Common Error: Choosing covalent due to the backbone.
    Tip: Read the question carefully to identify the context.

(2024):

11. What is the hybridization of nitrogen in NH_3?
    (A) sp, (B) sp^2,
    (C) sp^3, (D) sp^3d.
    Solution: Nitrogen in NH_3 has four electron domains (three bonding pairs, one lone pair), requiring sp^3 hybridization.
    Answer: C.
    Common Error: Choosing sp^2, confusing with trigonal planar geometry.
    Tip: Include lone pairs when determining hybridization.
12. Calculate the electronegativity difference in the C–O bond.
    (A) 0.4 (B) 0.9
    (C) 1.0 (D) 1.4.
    Solution: Electronegativity of C = 2.5, O = 3.5. Difference = 3.5 – 2.5 = 1.0.
    Answer: C.
    Common Error: Misremembering electronegativity values.
    Tip: Memorize values for C, H, N, O, P, S.

Exam Tips

1. **Memorize Key Facts**:
   - Electronegativity values: F (4.0), O (3.5), N (3.0), C (2.5), H (2.1).
   - Bond strengths: Covalent > Ionic (in water) > Hydrogen > Van der Waals.
   - VSEPR geometries and bond angles.
2. **Master Numericals**:
   - Practice bond order calculations using MO theory.
   - Solve electronegativity difference problems to predict bond type.
   - Calculate electron configurations for biologically relevant elements (C, N, O, P, S).
3. **Eliminate Incorrect Options**:
   - For hybridization questions, rule out options based on electron domains (e.g., sp^3d is rare for first-row elements).

- For bond type questions, consider the biological context (e.g., ionic bonds are weak in water).

4. **Avoid Pitfalls**:
   - Don't confuse hybridization with molecular geometry (e.g., NH_3 is sp^3 hybridized but trigonal pyramidal).
   - Don't assume ionic bonds are strongest in biological systems due to water's dielectric effect.
5. **Time Management**:
   - Allocate 1–2 minutes per question in Part B and 3–4 minutes for Part C analytical questions.
   - Skip complex numericals initially and return if time permits.

Biomolecules - Carbohydrates: Structure, Function, and Stereochemistry

1. Overview of Carbohydrates

Carbohydrates, also known as saccharides, are organic molecules with the general formula $(CH_2O)_n$, where n ≥ 3. They are polyhydroxy aldehydes or ketones, or compounds that yield such structures upon hydrolysis. Carbohydrates are the most abundant biomolecules on Earth, serving as primary energy sources, structural components, and signaling molecules.

- **Classification**:
  - **Monosaccharides**: Simple sugars that cannot be hydrolyzed into smaller units (e.g., glucose, fructose).
  - **Disaccharides**: Two monosaccharides linked by a glycosidic bond (e.g., sucrose, lactose).
  - **Oligosaccharides**: 3–10 monosaccharide units (e.g., raffinose).
  - **Polysaccharides**: Polymers of >10 monosaccharide units (e.g., starch, cellulose).
- **Functional Roles**:
  - **Energy Storage**: Glucose in glycolysis, starch in plants, glycogen in animals.
  - **Structural Support**: Cellulose in plant cell walls, chitin in arthropod exoskeletons.
  - **Molecular Recognition**: Glycoproteins and glycolipids in cell membranes, blood group antigens.
- **Biological Relevance**:
  - Carbohydrates provide 4 kcal/g of energy, serving as the primary fuel for cells.
  - They mediate cell-cell interactions (e.g., selectins in immune responses).
  - Aberrant glycosylation is linked to diseases like cancer and diabetes.

Table 1: Carbohydrate Classification

Type	Monosaccharide Units	Examples	Biological Role
Monosaccharide	1	Glucose, Fructose, Galactose	Energy source, metabolic precursor
Disaccharide	2	Sucrose, Lactose, Maltose	Energy transport, dietary sugars
Oligosaccharide	3–10	Raffinose, Stachyose	Cell signaling, gut microbiota
Polysaccharide	>10	Starch, Cellulose, Glycogen	Energy storage, structural support

2. Monosaccharides: Structure and Nomenclature

Monosaccharides are the simplest carbohydrates, characterized by their carbon chain length, functional group, and stereochemistry. They serve as building blocks for complex carbohydrates and are central to metabolic pathways like glycolysis.

2.1 Structural Features

- **Functional Groups**:
  - **Aldoses**: Contain an aldehyde group (-CHO) at carbon 1 (e.g., glucose).
  - **Ketoses**: Contain a ketone group (C=O) at carbon 2 (e.g., fructose).

- **Carbon Chain Length**:
  - Trioses (3 carbons): e.g., glyceraldehyde (aldose), dihydroxyacetone (ketose).
  - Tetroses (4 carbons): e.g., erythrose.
  - Pentoses (5 carbons): e.g., ribose, xylose.
  - Hexoses (6 carbons): e.g., glucose, fructose, galactose.
- **Cyclic vs. Open-Chain Forms**:
  - In aqueous solutions, monosaccharides predominantly exist in cyclic forms due to intramolecular reactions between the carbonyl group and a hydroxyl group.
  - Cyclic structures form hemiacetals (aldoses) or hemiketals (ketoses), creating five- or six-membered rings.

2.2 Nomenclature

- **D vs. L Configuration**:
  - Based on the stereochemistry at the chiral carbon farthest from the carbonyl group (reference: glyceraldehyde).
  - D-sugars: -OH group on the right in Fischer projection (most natural sugars).
  - L-sugars: -OH group on the left.
- **Anomeric Carbon**:
  - The carbon involved in hemiacetal/hemiketal formation (C1 in aldoses, C2 in ketoses).
  - **α-anomer**: -OH group on the anomeric carbon is trans to the -CH_2OH group.
  - **β-anomer**: -OH group is cis to the -CH_2OH group.
- **Pyranose vs. Furanose**:
  - Pyranose: Six-membered ring, resembling pyran (e.g., glucopyranose).
  - Furanose: Five-membered ring, resembling furan (e.g., ribofuranose).

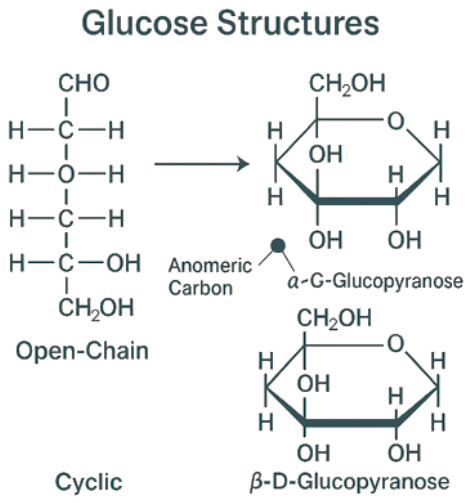
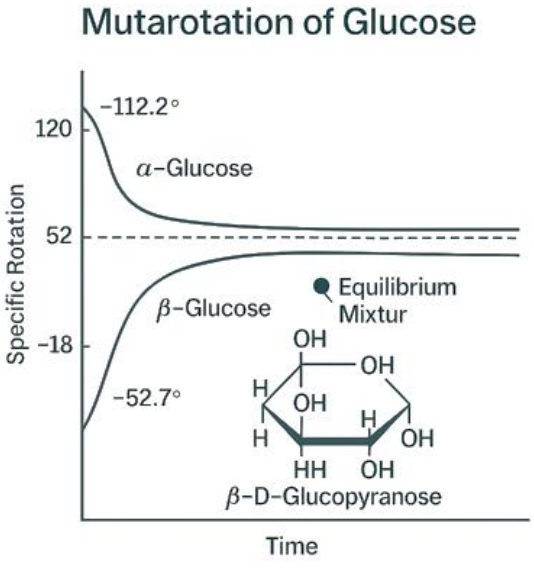


Diagram 1: Glucose Structures

[Description: A diagram showing the open-chain and cyclic forms of D-glucose. The open-chain Fischer projection depicts the aldehyde group at C1, with -OH groups at C2–C5 and -CH_2OH at C6. The cyclic Haworth projection shows α-D-glucopyranose (C1 -OH below the ring) and β-D-glucopyranose (C1 -OH above the ring). The anomeric carbon (C1) is highlighted, with glycosidic bond positions indicated.]

2.3 Mutarotation

- **Definition**: The interconversion between α- and β-anomers in solution via the open-chain form.
- **Mechanism**:
  - The anomeric -OH group dissociates, opening the ring to the linear aldehyde/ketone.
  - The carbonyl group reforms the ring, yielding either α- or β-anomer.
- **Equilibrium**:
  - For D-glucose: ~36% α-glucopyranose, ~64% β-glucopyranose, <0.1% open-chain.
  - β-glucopyranose is more stable due to all equatorial -OH groups in the chair conformation.
- **Biological Relevance**:
  - Mutarotation affects enzyme specificity (e.g., glucokinase prefers β-glucose).
  - Measured via optical rotation: α-glucose (+112.2°), β-glucose (+18.7°), equilibrium (~+52.7°).



Graph 1: Mutarotation of Glucose

II UNIT

Cellular Organization

Membrane Structure And Lipid Bilayer Dynamics

1. **Overview of Membrane Structure**

Cell membranes are dynamic, semi-permeable barriers that define cellular boundaries, regulate molecular exchange, and mediate signaling. Their structure is critical for maintaining cellular homeostasis and enabling specialized functions.

- **Functions**:
  - **Barrier**: Separates intracellular and extracellular environments.
  - **Transport**: Regulates entry/exit of molecules (e.g., ions, nutrients).
  - **Signaling**: Hosts receptors for signal transduction (e.g., GPCRs).
  - **Compartmentalization**: Organizes cellular processes (e.g., mitochondrial membranes).
- **Composition**:
  - **Lipids**: Phospholipids, sphingolipids, cholesterol (~50% by mass).
  - **Proteins**: Integral, peripheral, lipid-anchored (~50% by mass).
  - **Carbohydrates**: Glycoproteins, glycolipids (~2–10% by mass).
- **Biological Relevance**:
  - Membranes enable selective permeability, critical for ion gradients and nutrient uptake.
  - Dysfunctional membranes cause diseases (e.g., CFTR mutations in cystic fibrosis).
  - Membranes are targets for drugs (e.g., anesthetics alter fluidity).

2. **Structure of Model Membranes**

Model membranes, such as lipid bilayers and liposomes, provide simplified systems to study membrane properties, informing our understanding of biological membranes.

2.1 Historical Models

- **Gorter and Grendel (1925)**:
  - Proposed lipid bilayer based on red blood cell lipid extracts.
  - Found surface area of lipids is twice the cell surface, suggesting a bilayer.
- **Davson-Danielli (1935)**:
  - Suggested a lipid bilayer coated with proteins (sandwich model).
  - Later disproved due to protein diversity and membrane dynamics.
- **Singer-Nicolson Fluid Mosaic Model (1972)**:
  - Current model: Lipid bilayer as a fluid matrix with embedded proteins.
  - Key features: Lipid fluidity, protein mobility, asymmetry.
  - Biological context: Explains membrane flexibility and receptor dynamics.

2.2 Lipid Bilayer Structure

- **Composition**:
  - **Phospholipids**: Major component (e.g., phosphatidylcholine, phosphatidylethanolamine).
    - Structure: Hydrophilic head (phosphate + polar group), hydrophobic tails (fatty acids).
    - Types: Saturated (e.g., palmitic acid, C16:0), unsaturated (e.g., oleic acid, C18:1).
  - **Sphingolipids**: Sphingomyelin, prevalent in plasma membranes, especially myelin.
  - **Cholesterol**: Intercalates between phospholipids, modulates fluidity.
- **Amphipathic Nature**:
  - Hydrophilic heads face aqueous environments (cytosol, extracellular fluid).
  - Hydrophobic tails form a non-polar core, excluding water.

- **Bilayer Organization**:
  - Thickness: ~4–5 nm.
  - Asymmetry: Outer leaflet rich in PC, SM; inner leaflet rich in PE, PS.
  - Example: Phosphatidylserine (PS) in inner leaflet signals apoptosis when externalized.

2.3 Membrane Proteins

- **Types**:
  - **Integral Proteins**: Embedded in bilayer, often transmembrane (e.g., ion channels).
  - **Peripheral Proteins**: Loosely attached to membrane surface (e.g., spectrin).
  - **Lipid-Anchored Proteins**: Covalently linked to lipids (e.g., GPI-anchored proteins).
- **Functions**:
  - Transport (e.g., Na^+/K^+ ATPase).
  - Signaling (e.g., EGFR).
  - Anchoring (e.g., integrins link to cytoskeleton).
- **Structure**:
  - Transmembrane domains: α-helices (e.g., 20–25 hydrophobic residues) or β-barrels.
  - Example: Aquaporin's six α-helices form a water channel.

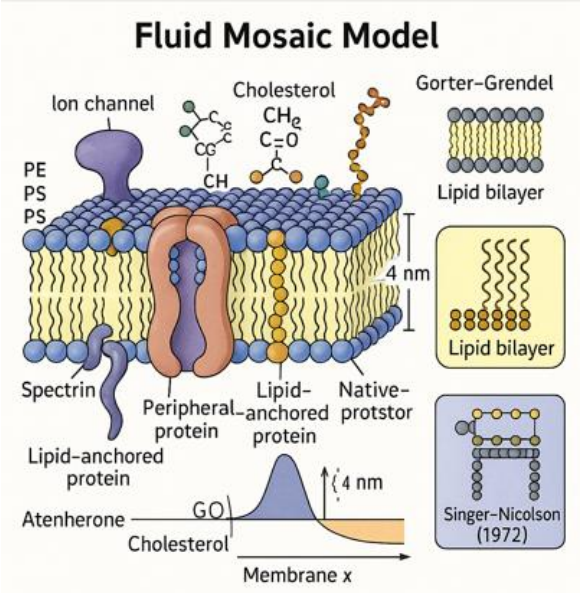


Diagram 1: Fluid Mosaic Model

[Description: A diagram of the fluid mosaic model, showing a lipid bilayer with hydrophilic heads (PC, PE, PS, SM) and hydrophobic tails. Integral proteins (e.g., ion channel), peripheral proteins (e.g., spectrin), and lipid-anchored proteins (e.g., GPI-linked) are embedded. Cholesterol molecules are interspersed, modulating fluidity. The diagram highlights asymmetry (PC outer, PS inner) and protein α-helices. A side panel shows Gorter-Grendel's bilayer experiment and Singer-Nicolson's model, with lipid packing and membrane thickness (~4 nm).]

Table 1: Membrane Components

Component	Type	Role	Example
Lipid	Phospholipid	Bilayer structure	Phosphatidylcholine
Lipid	Sphingolipid	Signaling, stability	Sphingomyelin
Lipid	Cholesterol	Fluidity modulation	Cholesterol
Protein	Integral	Transport, signaling	Na^+/K^+ ATPase
Protein	Peripheral	Anchoring, signaling	Spectrin
Carbohydrate	Glycoprotein, glycolipid	Cell recognition	Blood group antigens

3. Lipid Bilayer Fluidity

Fluidity refers to the viscosity and mobility of lipids within the bilayer, critical for membrane function and protein dynamics.

3.1 Factors Affecting Fluidity

- **Fatty Acid Composition**:
  - **Saturated Fatty Acids**: Straight chains, tight packing, reduce fluidity (e.g., DPPC, T_m ≈ 41°C).
  - **Unsaturated Fatty Acids**: Cis double bonds, kinks, increase fluidity (e.g., DOPC, T_m ≈ -17°C).
  - Example: Oleic acid (C18:1) lowers T_m compared to stearic acid (C18:0).
- **Cholesterol**:
  - **High Temperatures**: Reduces fluidity by restricting lipid movement.

- **Low Temperatures**: Prevents tight packing, maintaining fluidity.
- Example: Cholesterol maintains fluidity in mammalian membranes (~20–30% of lipids).

- **Temperature**:
  - **Transition Temperature (T_m)**: Gel-to-fluid phase transition.
  - Higher T_m for saturated lipids, lower for unsaturated.
- **Lipid Length**:
  - Longer chains increase van der Waals interactions, reducing fluidity.
  - Example: C16 vs. C18 fatty acids.

3.2 Lipid Rafts

- **Definition**: Microdomains enriched in sphingolipids, cholesterol, and specific proteins.
- **Properties**:
  - Ordered, less fluid than surrounding membrane.
  - Size: 10–200 nm.
- **Functions**:
  - Signaling platforms (e.g., receptor clustering).
  - Membrane trafficking (e.g., vesicle budding).
  - Pathogen entry (e.g., HIV via lipid rafts).
- **Example**: Caveolae, raft-like invaginations with caveolin proteins.

3.3 Measurement of Fluidity

- **Fluorescence Recovery After Photobleaching (FRAP)**:
  - Measures lipid/protein diffusion by bleaching fluorescent lipids and monitoring recovery.
  - Diffusion coefficient (D): ~0.1–1 $\mu m^2/s$ for lipids.
- **Differential Scanning Calorimetry (DSC)**:
  - Detects T_m by heat absorption during phase transitions.
- **NMR Spectroscopy**:
  - Probes lipid chain mobility and packing.

3.4 Biological Applications

- **Membrane Function**:
  - Fluidity enables protein diffusion, vesicle formation, and signaling.
  - Example: Receptor tyrosine kinases require fluidity for dimerization.
- **Adaptation**:
  - Bacteria adjust fatty acid composition for temperature (e.g., more unsaturated lipids in cold).
- **Disease**:
  - Altered fluidity in Alzheimer's (amyloid-β disrupts rafts).
  - Cholesterol accumulation in atherosclerosis.

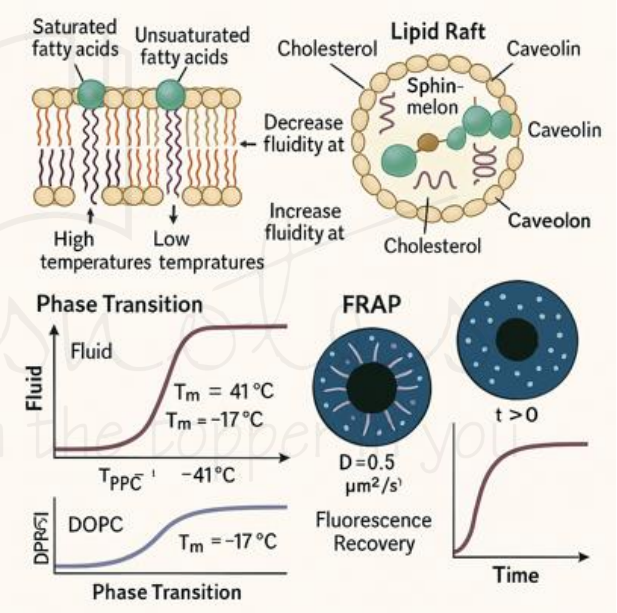
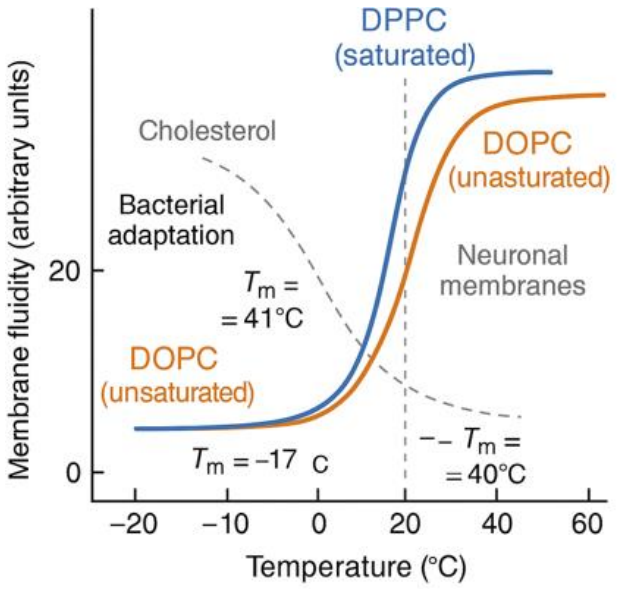


Diagram 2: Lipid Bilayer Fluidity

[Description: A diagram showing a lipid bilayer with saturated (straight) and unsaturated (kinked) fatty acids. Cholesterol molecules are interspersed, with effects on fluidity at high/low temperatures depicted. Lipid rafts (sphingomyelin, cholesterol) are highlighted, with caveolin proteins. A phase transition curve (gel to fluid) is included, showing T_m for DPPC (41°C) vs. DOPC (-17°C). A side panel illustrates FRAP, with fluorescence recovery curve and D (~0.5 $\mu m^2/s$).]



Graph 1: Fluidity vs. Temperature

[Description: A graph plotting membrane fluidity (y-axis, arbitrary units) vs. temperature (x-axis, °C) for bilayers with DPPC (saturated, T_m ≈ 41°C) and DOPC (unsaturated, T_m ≈ -17°C). The sigmoidal curves show gel-to-fluid transitions, with cholesterol's moderating effect (smoother curve). Biological examples (e.g., bacterial adaptation, neuronal membranes) are labeled, with T_m and diffusion coefficients.]

4. Membrane Protein Diffusion

Membrane proteins exhibit lateral and rotational diffusion within the fluid bilayer, critical for their functions in transport, signaling, and anchoring.

4.1 Mechanisms of Diffusion

- **Lateral Diffusion**:
  - Proteins move within the bilayer plane, rate depends on fluidity.
  - Diffusion coefficient (D): ~0.01–0.1 μm²/s (slower than lipids due to size).
  - Measured by FRAP or single-particle tracking (SPT).
- **Rotational Diffusion**:
  - Proteins rotate around their axis, less common, measured by fluorescence anisotropy.
- **Constraints**:
  - **Cytoskeleton**: Anchors proteins (e.g., spectrin in RBCs).
  - **Lipid Rafts**: Restrict diffusion (e.g., GPI-anchored proteins).
  - **Protein-Protein Interactions**: Form complexes, reducing mobility.

4.2 Factors Affecting Diffusion

- **Membrane Fluidity**:
  - Higher fluidity (unsaturated lipids, low cholesterol) increases D.
- **Protein Size**:
  - Larger proteins (e.g., multi-subunit channels) diffuse slower.
- **Membrane Crowding**:
  - High protein density (~30–50% of membrane area) reduces D.
- **Temperature**:
  - Higher T increases diffusion rate (Arrhenius behavior).

4.3 Measurement Techniques

- **FRAP**:
  - Bleach fluorescently labeled proteins, measure recovery time.
  - Example: D ≈ 0.05 μm²/s for rhodopsin in photoreceptor membranes.
- **Single-Particle Tracking (SPT)**:
  - Tracks individual protein trajectories using quantum dots or gold nanoparticles.
- **Fluorescence Correlation Spectroscopy (FCS)**:
  - Measures diffusion in small volumes.

4.4 Biological Applications

- **Signaling**:
  - Receptor diffusion enables dimerization (e.g., EGFR signaling).
- **Transport**:
  - Channel proteins diffuse to form functional complexes (e.g., gap junctions).
- **Disease**:
  - CFTR immobility in cystic fibrosis (mutant proteins aggregate).
  - Reduced diffusion in neurodegenerative diseases (e.g., lipid raft disruption).

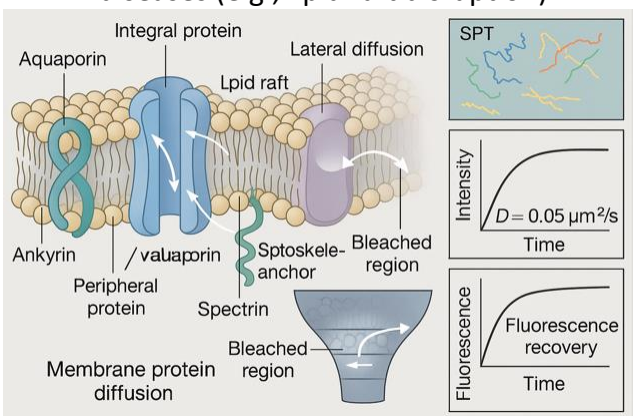


Diagram 3: Membrane Protein Diffusion

[Description: A diagram showing a lipid bilayer with integral (e.g., aquaporin) and peripheral proteins (e.g., ankyrin). Lateral diffusion paths are depicted, with arrows indicating protein movement. Lipid rafts and cytoskeletal anchors (spectrin) restrict diffusion. A FRAP experiment is illustrated, with a bleached region recovering fluorescence over time (D ≈ 0.05 μm²/s). A side panel shows SPT trajectories and a fluorescence recovery curve, with biological examples (e.g., rhodopsin diffusion).]

Table 2: Factors Affecting Protein Diffusion

Factor	Effect on Diffusion	Example
Fluidity	Higher fluidity increases D	Unsaturated lipids
Protein Size	Larger proteins reduce D	Multi-subunit channels
Lipid Rafts	Restrict D in ordered domains	GPI-anchored proteins
Cytoskeleton	Anchors reduce D	Spectrin in RBCs

PYQ Analysis

Below are 20 PYQs from CSIR NET Life Sciences (2018–2024) related to membrane structure and lipid bilayer dynamics, with solutions and explanations.

(2018):

1. What is the primary component of the lipid bilayer?
(A) Proteins
(B) Carbohydrates
(C) Phospholipids
(D) Cholesterol

Solution: Phospholipids form the bilayer's core structure.

Answer: C.

Common Error: Choosing proteins (functional, not structural).

Tip: Phospholipids = bilayer backbone.

2. Which model describes the current understanding of membranes?
(A) Sandwich
(B) Fluid mosaic
(C) Unit membrane
(D) Lamellar.

Solution: Singer-Nicolson's fluid mosaic model.

Answer: B.

Common Error: Choosing sandwich (Davson-Danielli).

Tip: Fluid mosaic = modern model.

(2019):

3. What increases membrane fluidity?
(A) Saturated fatty acids
(B) Unsaturated fatty acids
(C) Longer chains
(D) High cholesterol.

Solution: Unsaturated fatty acids (kinks) increase fluidity.

Answer: B.

Common Error: Choosing cholesterol (dual role).

Tip: Unsaturated = fluid, saturated = rigid.

4. What is the approximate thickness of a lipid bilayer?
(A) 1–2 nm
(B) 4–5 nm
(C) 10–12 nm
(D) 20 nm

Solution: Lipid bilayer thickness is ~4–5 nm.

Answer: B.

Common Error: Choosing 10–12 nm (protein complexes).

Tip: Bilayer = 4–5 nm.

(2020):

5. Which lipid is enriched in the outer leaflet?
(A) Phosphatidylserine
(B) Phosphatidylethanolamine
(C) Phosphatidylcholine
(D) Phosphatidylinositol

Solution: Phosphatidylcholine (PC) is enriched in the outer leaflet. **Answer: C**.

Common Error: Choosing PS (inner leaflet).

Tip: PC, SM = outer; PS, PE = inner.

6. What is the role of cholesterol in membranes?
(A) Increases fluidity only
(B) Decreases fluidity only
(C) Modulates fluidity
(D) No effect

Solution: Cholesterol modulates fluidity (reduces at high T, increases at low T).
Answer: C.
Common Error: Choosing decreases only.
Tip: Cholesterol = dual role.

(2021):

7. Which technique measures membrane protein diffusion?
(A) DSC (B) FRAP
(C) NMR (D) X-ray

Solution: FRAP measures diffusion via fluorescence recovery.
Answer: B.
Common Error: Choosing NMR (dynamics, not diffusion).
Tip: FRAP = diffusion.

8. What restricts membrane protein diffusion?
(A) High fluidity
(B) Lipid rafts
(C) Unsaturated lipids
(D) Low cholesterol

Solution: Lipid rafts restrict diffusion in ordered domains.
Answer: B.
Common Error: Choosing high fluidity (increases D).
Tip: Rafts, cytoskeleton = restrict diffusion.

(2022):

9. Which fatty acid reduces membrane fluidity?
(A) Oleic acid
(B) Linoleic acid
(C) Stearic acid
(D) Arachidonic acid

Solution: Stearic acid (saturated, C18:0) reduces fluidity.
Answer: C.
Common Error: Choosing oleic (unsaturated).
Tip: Saturated = less fluid.

10. What is the diffusion coefficient of lipids in membranes?
(A) 0.001 $\mu m^2/s$
(B) 0.1–1 $\mu m^2/s$
(C) 10 $\mu m^2/s$
(D) 100 $\mu m^2/s$

Solution: Lipid D ≈ 0.1–1 $\mu m^2/s$.
Answer: B.
Common Error: Choosing protein D (0.01–0.1).
Tip: Lipids = faster diffusion.

(2023):

11. Which protein type is embedded in the bilayer?
(A) Peripheral
(B) Integral
(C) Lipid-anchored
(D) All.

Solution: Integral proteins are embedded, often transmembrane.
Answer: B.
Common Error: Choosing all (includes surface proteins).
Tip: Integral = embedded.

12. What is the role of lipid rafts?
(A) Increase fluidity
(B) Signaling platforms
(C) Prevent protein diffusion
(D) Store cholesterol

Solution: Lipid rafts serve as signaling platforms.
Answer: B.
Common Error: Choosing fluidity (rafts reduce it).
Tip: Rafts = signaling, trafficking.

(2024):

13. Which lipid is associated with apoptosis signaling?
(A) Phosphatidylcholine
(B) Phosphatidylserine
(C) Sphingomyelin
(D) Cholesterol

Solution: Phosphatidylserine externalization signals apoptosis.
Answer: B.
Common Error: Choosing PC (structural).
Tip: PS = apoptosis signal.

14. What is the T_m of a bilayer with saturated lipids?

(A) -20°C (B) 0°C

(C) 41°C (D) 60°C

Solution: Saturated lipids (e.g., DPPC) have high T_m (~41°C).

Answer: C.

Common Error: Choosing low T_m (unsaturated).

Tip: Saturated = high T_m.

(2023):

15. Which membrane component is amphipathic?

(A) Cholesterol

(B) Phospholipids

(C) Integral proteins

(D) All

Solution: Phospholipids are amphipathic (hydrophilic head, hydrophobic tails).

Answer: B.

Common Error: Choosing all (cholesterol less amphipathic).

Tip: Phospholipids = amphipathic.

(2022):

16. What is the primary evidence for the lipid bilayer?

(A) FRAP

(B) Gorter-Grendel experiment

(C) NMR

(D) Cryo-EM.

Solution: Gorter-Grendel's lipid extract showed twice the cell surface area.

Answer: B.

Common Error: Choosing FRAP (diffusion).

Tip: Gorter-Grendel = bilayer evidence.

(2021):

17. Which protein is found in lipid rafts?

(A) Spectrin (B) Caveolin

(C) Ankyrin (D) Actin.

Solution: Caveolin is enriched in raft-like caveolae.

Answer: B.

Common Error: Choosing cytoskeletal proteins.

Tip: Caveolin = lipid rafts.

(2020):

18. What reduces protein diffusion in membranes?

(A) High temperature

(B) Cytoskeleton

(C) Unsaturated lipids

(D) Low cholesterol

Solution: Cytoskeleton anchors proteins, reducing D.

Answer: B.

Common Error: Choosing temperature (increases D).

Tip: Cytoskeleton = anchor.

(2019):

19. Which lipid is prevalent in myelin sheaths?

(A) Phosphatidylcholine

(B) Sphingomyelin

(C) Phosphatidylserine

(D) Phosphatidylethanolamine.

Solution: Sphingomyelin is enriched in myelin.

Answer: B.

Common Error: Choosing PC (general).

Tip: Sphingomyelin = myelin.

(2018):

20. What is the disease associated with CFTR dysfunction?

(A) Alzheimer's

(B) Cystic fibrosis

(C) Diabetes

(D) Cancer

Solution: CFTR mutations cause cystic fibrosis.

Answer: B.

Common Error: Choosing unrelated diseases.

Tip: CFTR = cystic fibrosis.

Exam Tips

1. **Memorize Key Facts**:
   - Lipid bilayer: Phospholipids (PC, PE, PS), cholesterol (~20–30%), ~4–5 nm thick.
   - Fluidity: Unsaturated lipids increase, saturated decrease, cholesterol modulates.
   - Protein diffusion: D ≈ 0.1–1 $\mu m^2/s$ (lipids), 0.01–0.1 $\mu m^2/s$ (proteins).
   - Lipid rafts: Sphingomyelin, cholesterol, caveolin.

2. **Master Numericals**:
   - Calculate T_m using fatty acid composition or DSC data.
   - Compute diffusion coefficients from FRAP experiments.
   - Estimate lipid/protein ratios from membrane composition.
3. **Eliminate Incorrect Options**:
   - For fluidity questions, rule out saturated lipids (reduce fluidity).
   - For diffusion questions, focus on constraints (rafts, cytoskeleton).
4. **Avoid Pitfalls**:
   - Don't confuse outer (PC, SM) vs. inner (PS, PE) leaflet lipids.
   - Don't mix up lipid rafts (ordered) with bulk membrane (fluid).
   - Distinguish integral (embedded) vs. peripheral (surface) proteins.
5. **Time Management**:
   - Allocate 1–2 minutes for Part B questions (e.g., lipid identification).
   - Spend 3–4 minutes on Part C questions (e.g., diffusion calculations).
   - Practice sketching bilayers and FRAP curves to save time.

Membrane Transport Mechanisms

1. **Overview of Membrane Transport Mechanisms**

   Membrane transport mechanisms regulate the movement of molecules across the lipid bilayer, which is selectively permeable due to its hydrophobic core. These mechanisms are critical for maintaining cellular ion gradients, nutrient uptake, waste removal, and signaling.

- **Types of Transport**:
  - **Passive Transport**: Movement down concentration or electrochemical gradients, no energy required.
    - Includes simple diffusion, facilitated diffusion (via channels/carriers), and osmosis.
  - **Active Transport**: Movement against gradients, requires energy (e.g., ATP, ion gradients).
    - Includes primary active transport (e.g., pumps) and secondary active transport (e.g., symporters).
- **Key Molecules Transported**:
  - Ions (e.g., Na^+, K^+, Ca^{2+}, Cl^-).
  - Small molecules (e.g., glucose, amino acids, water).
  - Macromolecules (via vesicular transport, covered in Part 3).
- **Biological Relevance**:
  - Ion gradients drive neuronal action potentials and muscle contraction.
  - Nutrient uptake supports metabolism (e.g., glucose via transporters).
  - Dysfunctional transport causes diseases (e.g., CFTR mutations in cystic fibrosis).
- **Applications**:
  - Transport inhibitors are drugs (e.g., digoxin targets Na^+/K^+ ATPase).
  - Synthetic channels/pumps inspire nanotechnology (e.g., drug delivery systems).

Table 1: Overview of Membrane Transport Mechanisms

Mechanism	Energy Requirement	Direction	Example
Simple Diffusion	None	Down gradient	O_2, CO_2 across bilayer
Facilitated Diffusion	None	Down gradient	Glucose via GLUT1
Osmosis	None	Water down gradient	Aquaporin-mediated
Primary Active	ATP	Against gradient	Na^+/K^+ ATPase
Secondary Active	Ion gradient	Against gradient (coupled)	Na^+-glucose symporter