YOUR MENTOR GURU

# CSIR NET Life Sciences & Biotechnology — Unit 1

## Molecules and Their Interaction Relevant to Biology

Study & revision companion | Topic explanations, core facts, and active-recall questions

## How to use this guide

Read each topic, explain the key mechanism in your own words, then answer the self-check prompts without looking at the notes. Use your detailed textbook or class notes for full derivations and additional examples.

## Topic overview


1. 1. Atoms, Chemical Bonds and Molecular Interactions
2. 2. Amino Acids and Peptide Bonds
3. 3. Protein Structure, Folding and Stability
4. 4. Carbohydrates and Glycosidic Linkages
5. 5. Lipids and Membrane-Forming Molecules
6. 6. Nucleotides, DNA and RNA Conformations
7. 7. Vitamins and Coenzymes
8. 8. pH, Buffers and Colligative Properties
9. 9. Thermodynamics and Reaction Kinetics
10. 10. Enzymes, Catalysis and Regulation
11. 11. Bioenergetics and Oxidative Phosphorylation
12. 12. Carbohydrate Metabolism
13. 13. Lipid, Amino Acid and Nucleotide Metabolism

## 1. Atoms, Chemical Bonds and Molecular Interactions

Bonding: Covalent bonds share electrons; ionic interactions arise between charged groups; hydrogen bonds are directional; van der Waals forces are individually weak but collectively important.

In water: The hydrophobic effect drives nonpolar groups together because burying them reduces unfavorable ordering of surrounding water.

Protein stability: Disulfide bonds are covalent links between cysteine residues; salt bridges depend on ionization and solvent conditions.

High-yield distinction: A hydrogen bond is not a covalent bond; electrostatic interactions can be screened by high ionic strength.

Atoms are made of protons, neutrons and electrons, and their electron configurations determine how they bond. Covalent bonds form through electron sharing, whereas ionic interactions arise between oppositely charged species. Electronegativity differences influence bond polarity; the overall polarity of a molecule also depends on its geometry. In biological systems, carbon forms stable frameworks, while oxygen, nitrogen, sulfur and phosphorus provide reactive functional groups.

Distinguish bond types and identify polar bonds. Use Lewis structures and VSEPR reasoning to predict shapes, then consider how charge distribution affects solubility and molecular recognition. Hydrogen bonds are directional interactions involving suitable donors and acceptors, not ordinary covalent bonds.

Remember: Predict molecular geometry, polarity and potential hydrogen-bond donors or acceptors.

Self-check: Explain the mechanism or relationship above; identify one common misconception; predict the effect of changing a key variable.

## 2. Amino Acids and Peptide Bonds

Charge: Asp and Glu are commonly negative near pH 7; Lys and Arg positive; His can change protonation near physiological pH.

Peptide linkage: The peptide C–N bond has partial double-bond character and is planar; rotation occurs mainly about φ and ψ backbone bonds.

Zwitterion: At the isoelectric point (pI), the average net charge is zero; solubility may be lowest near pI.

Special residues: Glycine is achiral and flexible; proline restricts backbone conformation; cysteine forms disulfides.

Proteins are built from amino acids containing an amino group, a carboxyl group and a variable side chain attached to an alpha carbon. Glycine is achiral, whereas most standard amino acids have a chiral alpha carbon. Side chains are commonly grouped as nonpolar, polar uncharged, acidic or basic. These categories help explain protein folding, interactions and chemical reactivity.

Amino acids change protonation state with pH and often exist as zwitterions. The isoelectric point (pI) is the pH at which the average net charge is zero. For an amino acid without an ionizable side chain, the pI is the mean of the two pKa values surrounding the neutral form. Peptide bonds connect amino acids and have partial double-bond character.

Remember: Calculate net charge and pI; interpret titration curves and the effects of substitutions.

Self-check: Explain the mechanism or relationship above; identify one common misconception; predict the effect of changing a key variable.

## 3. Protein Structure, Folding and Stability

Levels: Primary = sequence; secondary = local α-helices and β-sheets; tertiary = overall fold; quaternary = subunit assembly.

Forces: Backbone hydrogen bonds stabilize regular secondary structure; hydrophobic burial strongly contributes to folding.

Folding: Chaperones reduce aggregation and assist productive folding but do not encode the final amino-acid sequence.

Denaturation: Heat, pH and chaotropes may disrupt higher-order structure without hydrolyzing peptide bonds.

Methods: Circular dichroism reports aspects of secondary structure; X-ray crystallography, NMR and cryo-EM provide structural information.

Protein structure is organized into primary sequence, secondary arrangements, tertiary folding and, for some proteins, quaternary assemblies. Alpha helices and beta sheets are stabilized largely by backbone hydrogen bonds. The three-dimensional fold depends on the sequence and the balance of hydrophobic effects, hydrogen bonding, electrostatic interactions and van der Waals contacts.

Ramachandran plots describe backbone dihedral angles and reveal sterically favored conformations. Motifs are recurring structural patterns; domains are compact structural or functional units. Chaperones can assist folding, but they do not generally dictate a protein’s final native structure. Heat, extreme pH and chemical denaturants may disrupt higher-order structure without necessarily breaking peptide bonds.

Remember: Interpret Ramachandran plots and predict how mutations alter stability or function.

Self-check: Explain the mechanism or relationship above; identify one common misconception; predict the effect of changing a key variable.

## 4. Carbohydrates and Glycosidic Linkages

Monosaccharides: Aldoses have an aldehyde in the open-chain form; ketoses have a ketone. D/L configuration does not indicate optical rotation.

Anomers: α and β anomers differ at the anomeric carbon; mutarotation interconverts them through ring opening.

Reducing sugars: A free anomeric carbon permits reducing behavior; sucrose is nonreducing because both anomeric carbons are linked.

Polysaccharides: Glycogen and amylopectin have α(1→4) chains with α(1→6) branches; cellulose contains β(1→4) glucose.

Carbohydrates include monosaccharides, oligosaccharides and polysaccharides. Monosaccharides may be aldoses or ketoses and are further classified by carbon number. Ring formation creates an anomeric carbon, giving alpha and beta anomers. Epimers differ in configuration at one stereogenic center, while enantiomers are mirror images.

Glycosidic bonds connect sugar units. Reducing sugars possess a free anomeric center capable of opening to a reactive carbonyl form. Starch and glycogen are glucose-storage polymers with alpha linkages; cellulose is a structural polymer with beta(1→4) linkages. Bond configuration strongly affects digestibility, branching and physical properties.

Remember: Identify anomers, epimers, glycosidic linkages and reducing sugars.

Self-check: Explain the mechanism or relationship above; identify one common misconception; predict the effect of changing a key variable.

## 5. Lipids and Membrane-Forming Molecules

Amphipathic molecules: Phospholipids have polar head groups and hydrophobic tails, enabling bilayer assembly in water.

Fluidity: Cis-unsaturated acyl chains usually lower packing efficiency and increase fluidity at a given temperature.

Cholesterol: Cholesterol buffers membrane fluidity: it restrains movement at high temperature and limits tight packing at low temperature.

Lipids: Triacylglycerols are energy stores; phospholipids and sphingolipids are prominent membrane components.

Transport: Simple diffusion depends on permeability and concentration gradient; ions usually need membrane proteins.

Lipids are a diverse group of molecules that are poorly soluble in water. Fatty acids differ in chain length and degree of unsaturation, which influence melting behavior and membrane fluidity. Triacylglycerols serve primarily as energy stores, whereas phospholipids and sphingolipids are major membrane components. Cholesterol modulates membrane properties and serves as a precursor of steroid molecules.

Amphipathic lipids contain hydrophilic and hydrophobic regions, allowing them to form bilayers and other assemblies in water. Cis double bonds usually introduce bends in fatty acid chains and reduce tight packing. Lipid composition influences signaling, trafficking and the activity of membrane proteins.

Remember: Predict how saturation and chain length affect membrane properties and melting trends.

Self-check: Explain the mechanism or relationship above; identify one common misconception; predict the effect of changing a key variable.

## 6. Nucleotides, DNA and RNA Conformations

Components: Nucleoside = base + sugar; nucleotide = nucleoside + phosphate group(s).

Backbone: Phosphodiester linkages join the 3′ hydroxyl of one sugar to the 5′ phosphate of the next.

Base pairing: Watson–Crick pairs: A–T (two H bonds), G–C (three); RNA commonly pairs A–U.

DNA forms: B-DNA is the common right-handed duplex; A-DNA is shorter/wider; Z-DNA is left-handed.

Stability: GC content, ionic strength and duplex length influence melting temperature; RNA 2′-OH enables additional chemistry.

Nucleic acids are polymers of nucleotides joined by phosphodiester bonds. Each nucleotide contains a nitrogenous base, pentose sugar and phosphate. DNA commonly adopts a right-handed B-form helix, with complementary base pairing between A–T and G–C. RNA usually contains ribose and uracil and can fold into complex secondary and tertiary structures.

A-DNA is a shorter, wider right-handed helix, while Z-DNA is left-handed and can be favored in certain sequence and environmental contexts. Nucleic acid stability depends on base stacking, hydrogen bonding, ionic conditions and sequence. Greater GC content often raises duplex melting temperature under comparable conditions, but salt concentration and length also matter.

Remember: Compare A-, B- and Z-DNA; reason about melting and structural stability.

Self-check: Explain the mechanism or relationship above; identify one common misconception; predict the effect of changing a key variable.

## 7. Vitamins and Coenzymes

B1 / TPP: Thiamine pyrophosphate supports oxidative decarboxylation and transketolase reactions.

B2 / FAD, FMN: Riboflavin-derived flavins transfer electrons and can participate in one- or two-electron chemistry.

B3 / $NAD^+$, $NADP^+$: Niacin-derived cofactors transfer hydride; NADPH often supplies reducing power for biosynthesis.

B5 / CoA: Pantothenate forms part of coenzyme A for acyl-group transfer.

B6 / PLP: Pyridoxal phosphate participates in transamination and amino-acid reactions.

B7 / Biotin: Biotin transfers $CO_2$ in ATP-dependent carboxylation.

B9 / THF and B12: Tetrahydrofolate transfers one-carbon units; cobalamin participates in methionine synthase and methylmalonyl-CoA mutase.

Vitamins are organic micronutrients required in small amounts for normal physiological function. Water-soluble B vitamins frequently contribute to coenzyme structures, while fat-soluble vitamins A, D, E and K have distinct regulatory, antioxidant or biochemical roles. A vitamin is not necessarily a coenzyme itself; many vitamins are converted to active coenzyme derivatives.

Examples include niacin-derived $NAD^+$/$NADP^+$ in redox reactions, riboflavin-derived FAD/FMN in electron transfer, and thiamine pyrophosphate in certain decarboxylation reactions. Recognizing the chemistry performed by a cofactor is more useful than memorizing isolated lists. Some vitamins also act through gene regulation or other non-coenzyme functions.

Self-check: Explain the mechanism or relationship above; identify one common misconception; predict the effect of changing a key variable.

## 8. pH, Buffers and Colligative Properties

pH: $pH = -\log_{10}[H^+]$ for dilute ideal solutions (more precisely, hydrogen-ion activity).

Henderson–Hasselbalch: $pH = pKa + \log_{10}([A^-]/[HA])$; when $[A^-] = [HA]$, $pH = pKa$.

Buffer range: A weak acid/conjugate base pair generally buffers best near pKa, often within roughly $\pm 1$ pH unit.

Titration: At half-equivalence for a simple monoprotic weak acid titration, $pH \approx pKa$.

Colligative effects: Osmotic pressure $\pi \approx iCRT$ for ideal dilute solutions; effects depend on the number of dissolved particles.

Non-covalent interactions determine much of the structure and behavior of biological macromolecules. These include electrostatic attractions and repulsions, hydrogen bonds, van der Waals interactions and the hydrophobic effect. Individually many interactions are weak relative to covalent bonds, but their combined and geometrically organized contributions can strongly stabilize complexes.

The hydrophobic effect arises largely from the behavior of water around nonpolar surfaces rather than from a special bond between hydrophobic groups. Changes in pH alter ionization, salt can screen electrostatic interactions, and temperature can affect both conformational entropy and solvent behavior. Molecular recognition depends on shape complementarity and the balance of favorable and unfavorable interactions.

Remember: Predict effects of pH, ionic strength, mutations and temperature on stability.

Self-check: Explain the mechanism or relationship above; identify one common misconception; predict the effect of changing a key variable.

## 9. Thermodynamics and Reaction Kinetics

Free energy: $\Delta G = \Delta H - T\Delta S$ at constant temperature and pressure; negative $\Delta G$ means thermodynamically favorable.

Equilibrium: $\Delta G = \Delta G^{\circ\prime} + RT \ln Q$ and $\Delta G^{\circ\prime} = -RT \ln K'_{eq}$ for a specified biochemical standard state.

Coupling: An unfavorable reaction can proceed when coupled to a sufficiently favorable reaction so the sum $\Delta G$ is negative.

Kinetics: Catalysts lower activation barriers but do not change $\Delta G^{\circ\prime}$ or the equilibrium constant.

Rate law: Reaction order is determined experimentally; stoichiometric coefficients alone do not generally give a rate law.

pH measures hydrogen-ion activity on a logarithmic scale. Weak acids and bases exist in protonated and deprotonated forms, and their relative abundance depends on pH and pKa. Buffers resist large pH changes when small amounts of acid or base are added; a buffer is generally most effective near its relevant pKa.

The Henderson–Hasselbalch equation relates pH to the ratio of conjugate base and acid: $pH = pKa + \log_{10}([A^-]/[HA])$ under appropriate approximations. Colligative properties depend primarily on the number of dissolved particles rather than their chemical identity. Osmotic pressure helps explain water movement across semipermeable membranes.

Remember: Solve buffer ratios, predict ionization and interpret osmotic effects.

Self-check: Explain the mechanism or relationship above; identify one common misconception; predict the effect of changing a key variable.

## 10. Enzymes, Catalysis and Regulation

Michaelis–Menten: $v_0 = V_{max}[S]/(K_m + [S])$ for an appropriate simple initial-rate mechanism.

Km: At $[S] = K_m$, $v_0 = V_{max}/2$; Km is not always identical to the substrate dissociation constant.

Turnover: $k_{cat} = V_{max}/[E]_{total}$ when enzyme concentration is expressed as active sites; $k_{cat}/K_m$ gauges low-substrate catalytic efficiency.

Competitive inhibition: Apparent Km rises, while Vmax is unchanged for reversible competitive inhibition in the standard model.

Pure noncompetitive: Vmax falls and Km stays unchanged; mixed inhibition can alter both.

Uncompetitive: Both apparent Vmax and Km decrease in the standard model.

Regulation: Allosteric enzymes may show sigmoidal kinetics; feedback inhibition can regulate pathway flux.

Thermodynamics describes energy changes and the direction of processes, while kinetics describes how fast reactions occur. Gibbs free energy is given by $\Delta G = \Delta H - T\Delta S$ at constant temperature and pressure. A negative $\Delta G$ indicates that a process is thermodynamically favorable in the stated conditions, but it does not guarantee a fast reaction.

The relationship $\Delta G = \Delta G^{\circ\prime} + RT \ln Q'$ connects actual reaction conditions with the biochemical standard state. Reaction rate depends on the pathway and activation-energy barrier; catalysts accelerate reactions

by lowering the activation barrier without changing the equilibrium constant. Temperature, concentrations and reaction mechanisms all affect observed rates.

Remember: Distinguish spontaneity from reaction speed and calculate ΔG or equilibrium relationships.

Self-check: Explain the mechanism or relationship above; identify one common misconception; predict the effect of changing a key variable.

## 11. Bioenergetics and Oxidative Phosphorylation

ETC: Complexes I, III and IV pump protons across the inner mitochondrial membrane; Complex II does not.

Terminal acceptor: $O_2$ accepts electrons at Complex IV and is reduced to water.

Chemiosmosis: ATP synthase uses proton-motive force (membrane potential plus pH gradient) to drive ATP formation.

NADH vs $FADH_2$: Electrons from NADH typically enter at Complex I; succinate-derived electrons enter via Complex II.

ATP yield: Approximate mitochondrial P/O ratios are 2.5 ATP per NADH and 1.5 per $FADH_2$; values depend on conditions.

Inhibitors: Rotenone blocks Complex I; antimycin A blocks Complex III; cyanide inhibits Complex IV; oligomycin inhibits ATP synthase.

Enzymes accelerate biochemical reactions through mechanisms such as acid–base catalysis, covalent catalysis, metal-ion catalysis and preferential stabilization of the transition state. Many simple enzyme systems can be described by Michaelis–Menten kinetics, where initial velocity rises with substrate concentration and approaches Vmax. Km is the substrate concentration at half-maximal velocity under this model.

The turnover number kcat describes catalytic cycles per active site per unit time under saturating substrate conditions; kcat/Km is often used to compare catalytic efficiency. Competitive, uncompetitive and mixed inhibition produce distinct kinetic effects. Allosteric enzymes may show cooperative behavior and do not necessarily follow a simple Michaelis–Menten curve.

Remember: Interpret kinetic plots and calculate Km, Vmax, kcat and inhibitor effects.

Self-check: Explain the mechanism or relationship above; identify one common misconception; predict the effect of changing a key variable.

## 12. Carbohydrate Metabolism

Glycolysis: Glucose → 2 pyruvate gives net 2 ATP and 2 NADH per glucose under standard glycolytic accounting.

Control: Hexokinase/glucokinase, PFK-1 and pyruvate kinase catalyze major regulated steps.

Pyruvate oxidation: Pyruvate dehydrogenase converts pyruvate to acetyl-CoA with $CO_2$ and NADH production.

TCA cycle: Per acetyl-CoA: 3 NADH, 1 $FADH_2$, 1 GTP (or ATP equivalent), and 2 $CO_2$.

Gluconeogenesis: Bypass enzymes include pyruvate carboxylase, PEPCK, fructose-1,6-bisphosphatase and glucose-6-phosphatase.

PPP: Oxidative pentose phosphate reactions generate NADPH; nonoxidative reactions interconvert sugar phosphates.

Glycogen: Glycogen synthase extends α(1→4) chains; branching enzyme creates α(1→6) branches.

Cells use energy coupling to drive processes that would otherwise be unfavorable. ATP hydrolysis can be coupled to biosynthesis, transport and mechanical work. Electron-transfer reactions are described using reduction potentials; their free-energy changes depend on the potential difference and the number of electrons transferred.

In mitochondria, electron transport through respiratory complexes contributes to a proton electrochemical gradient across the inner membrane. ATP synthase uses this proton motive force to synthesize ATP. Inhibitors of electron transport, ATP synthase and uncouplers have different consequences for oxygen consumption, proton gradients and ATP production.

Remember: Relate redox potential to ΔG and predict consequences of ETC inhibitors.

Self-check: Explain the mechanism or relationship above; identify one common misconception; predict the effect of changing a key variable.

## 13. Lipid, Amino Acid and Nucleotide Metabolism

β-oxidation: Each mitochondrial β-oxidation cycle shortens a saturated even-chain fatty acyl-CoA by two carbons, usually yielding $FADH_2$, NADH and acetyl-CoA.

Transport: Long-chain fatty acyl groups use the carnitine shuttle; malonyl-CoA inhibits CPT I.

Fatty-acid synthesis: Cytosolic fatty-acid synthesis uses acetyl-CoA carboxylase, fatty-acid synthase and NADPH.

Nitrogen handling: Transaminases commonly require PLP; ammonia is detoxified via the urea cycle in the liver.

Urea cycle: Carbamoyl phosphate synthetase I is mitochondrial and activated by N-acetylglutamate.

Purines: Purine rings are assembled on PRPP; IMP is a precursor of AMP and GMP.

Pyrimidines: The pyrimidine ring is synthesized before attachment to PRPP; UMP is an early product.

Salvage: HGPRT salvages hypoxanthine and guanine; deficiency can cause Lesch–Nyhan syndrome.

Glycolysis converts glucose to pyruvate and generates ATP and NADH. Gluconeogenesis produces glucose from non-carbohydrate precursors using bypass reactions around key irreversible glycolytic steps. Glycogen synthesis and breakdown regulate stored carbohydrate availability. The pentose phosphate pathway supplies NADPH and ribose-5-phosphate.

The tricarboxylic acid cycle oxidizes acetyl groups and produces reduced electron carriers for oxidative phosphorylation. These pathways are coordinated through energy charge, substrate availability, allosteric regulation and hormones. Track carbon atoms and reducing equivalents rather than memorizing only the names of intermediates. ATP-yield calculations depend on the assumptions used for shuttle systems and oxidative phosphorylation.

Self-check: Explain the mechanism or relationship above; identify one common misconception; predict the effect of changing a key variable.

## Active-recall practice

1. Explain the essential principles of 1. Atoms, Chemical Bonds and Molecular Interactions and give one experimental or real-world application.

2. Explain the essential principles of 2. Amino Acids and Peptide Bonds and give one experimental or real-world application.

3. Explain the essential principles of 3. Protein Structure, Folding and Stability and give one experimental or real-world application.

4. Explain the essential principles of 4. Carbohydrates and Glycosidic Linkages and give one experimental or real-world application.

5. Explain the essential principles of 5. Lipids and Membrane-Forming Molecules and give one experimental or real-world application.

6. Explain the essential principles of 6. Nucleotides, DNA and RNA Conformations and give one experimental or real-world application.

7. Explain the essential principles of 7. Vitamins and Coenzymes and give one experimental or real-world application.

8. Explain the essential principles of 8. pH, Buffers and Colligative Properties and give one experimental or real-world application.

9. Explain the essential principles of 9. Thermodynamics and Reaction Kinetics and give one experimental or real-world application.

10. Explain the essential principles of 10. Enzymes, Catalysis and Regulation and give one experimental or real-world application.

11. Explain the essential principles of 11. Bioenergetics and Oxidative Phosphorylation and give one experimental or real-world application.

12. Explain the essential principles of 12. Carbohydrate Metabolism and give one experimental or real-world application.

13. Explain the essential principles of 13. Lipid, Amino Acid and Nucleotide Metabolism and give one experimental or real-world application.

## Final revision checklist

- 1. Atoms, Chemical Bonds and Molecular Interactions
- 2. Amino Acids and Peptide Bonds
- 3. Protein Structure, Folding and Stability
- 4. Carbohydrates and Glycosidic Linkages
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## Further study

Use the corresponding unit notes, topic-wise detailed lessons, MCQs, practice tests and full-length mock tests on yourmentorguru.com. This compact PDF is a revision companion, not a replacement for full syllabus textbooks.