The Ultimate AP® Biology Unit 1 Cheat Sheet

1.1 Water: Polarity & Hydrogen Bonds

Why Water Is Polar

Polar covalent bond: O more electronegative than H → shares e^- unequally → O δ^-, each H δ^+.

Bent shape (~104.5°) → the partial charges don't cancel out → the whole molecule is polar (a dipole).

Hydrogen bond: weak attraction, δ^+ H of one molecule ↔ δ^- O (or N) of another. Each H_2O → up to 4 H-bonds.

Covalent bonds hold atoms *within* H_2O; **H-bonds** act *between* molecules. Constantly break & re-form.

Properties From H-Bonds

Property	Cause	Bio example
Cohesion	H_2O↔H_2O H-bonds	Xylem transport
Adhesion	H_2O↔polar surface	Clings to xylem
Surf. tension	Surface cohesion	Water striders
High sp. heat	Heat breaks H-bonds	Stable temps
High heat vap.	Many H-bonds	Sweat cools skin
Ice floats	Open lattice	Insulates lakes

Water as Solvent

Hydrophilic (polar/ionic: sugars, ions, amino acids w/ polar R) → dissolve; H_2O forms **hydration shells** around them.

Hydrophobic (nonpolar: lipid tails, oils) → don't dissolve → cluster together, away from H_2O (drives bilayers).

Capillary action = cohesion + adhesion → H_2O rises in narrow tubes (xylem vessels, a paper towel).

Transpiration: leaf evaporation pulls cohesive column up.

Ice: stable H-bonds space molecules out → less dense than liquid → floats, insulates water below.

⚠ H-bonds are BETWEEN water molecules, not within one. Bonds inside H_2O are polar covalent.

✓ FRQ chain: polarity → H-bonds → property → function (e.g., cohesion → water column → transport).

1.2 Elements of Life

The Big Six: CHONPS

C, H, O = the most common elements in all 4 macromolecule classes; C forms the backbone of each one.

Carbon: 4 valence e^- → 4 covalent bonds → chains, branches, rings = backbone of organic molecules.

Molecule	Elements	Tracer clue
Carbs	C, H, O	Only CHO
Lipids	C, H, O (+P)	P in phospholipids
Proteins	C, H, O, N, S	S = protein only
Nucleic ac.	C, H, O, N, P	P in backbone

Nitrogen: in amino groups (proteins) + nitrogenous bases (DNA/RNA) + ATP's adenine. Fixed by bacteria.

Phosphorus: phosphate groups → nucleic acid backbones, phospholipid heads, ATP & ADP (energy).

Sulfur: in cysteine → disulfide bridges in proteins.

Where Organisms Get Them

C: CO_2 is fixed by photosynthesis → organic molecules → passed up through food webs to consumers.

N & P: plants absorb them from soil (NO_3^-, NH_4^+, PO_4^{3-}); animals get them by eating plants or prey animals.

Limiting nutrient: N or P shortage → can't build proteins/nucleic acids → growth ↓ (fertilizer).

Isotope-Tracing Logic

^{35}S labels proteins, NOT DNA. **^{32}P** labels DNA/RNA (+ phospholipids), NOT proteins. Classic tracer pair.

^{15}N labels proteins AND nucleic acids. **^{14}C** labels all 4 classes, so it can't tell them apart at all.

Hershey–Chase: ^{32}P entered the bacteria, ^{35}S didn't → DNA, not protein, is the genetic material of phages.

⚠ Carbs & most lipids lack N. A molecule w/ N + P (no S) → nucleic acid. N + S → protein (via cysteine).

✓ Data Qs: match the labeled element to the only molecule class that contains it, then name the class.

1.3 Building & Breaking Macromolecules

Two Core Reactions

Dehydration synthesis: monomers join by a covalent bond; H_2O released (–OH from one + H from the other). Builds polymers, e.g., starch & proteins, w/ enzymes.

Hydrolysis: H_2O added → bond broken; one monomer gets H^+, other gets –OH. Breaks polymers (e.g., digestion).

Polymerization: repeated dehydration reactions link many monomers → one long polymer chain (e.g., a protein).

Energy: synthesis needs energy input; hydrolysis usually releases energy. Both use specific enzymes.

Monomers, Polymers & Bonds

Class	Monomer	Bond
Carbs	Monosacch.	Glycosidic
Proteins	Amino acid	Peptide
Nucleic ac.	Nucleotide	Phosphodiester
Fats*	Glycerol + FA	Ester

***Lipids** are NOT true polymers: no repeating chain of monomers. Fat = 1 glycerol + 3 fatty acids.

Counting Water

Linear chain: n monomers → n – 1 bonds → n – 1 H_2O released (or used up to break it back down).

e.g., a 10-glucose chain → 9 H_2O out. Hydrolyzing it fully back to glucose → 9 H_2O used up again in digestion.

Triglyceride: 3 ester bonds → 3 H_2O released.

Exam Examples

Digestion: amylase hydrolyzes starch → sugars; proteases hydrolyze peptide bonds → amino acids.

Diversity: few monomer types (~20 amino acids, 4 nucleotides) → endless polymers via sequence.

⚠ Mixing up names: dehydration = water OUT (build). Hydrolysis = "hydro" + "lysis" = water splits (break).

✓ Diagram Qs: find the –OH and –H that leave as H_2O; the new bond forms right where they were.

1.4 Carbohydrates

Building Blocks

Monosaccharide = monomer (glucose, fructose, ribose, deoxyribose). Many –OH → polar, hydrophilic.

Disaccharide = 2 monomers (sucrose = glucose + fructose; lactose; maltose = glucose + glucose) by 1 bond.

Polysaccharide = many monomers linked by covalent (glycosidic) bonds → linear or branched.

Key Polysaccharides

Polymer	Found in	Role / shape
Starch	Plants	Storage; some branch
Glycogen	Animals	Storage; very branched
Cellulose	Plant walls	Structure; linear

Branched (glycogen) → many chain ends → enzymes release glucose fast when needed (liver, muscle cells).

Linear (cellulose) → chains lie side by side and H-bond → strong fibers → rigid plant cell walls that resist bursting.

Same monomer, diff. function: all 3 = glucose polymers; linkage + branching set shape → role.

Digestion: humans hydrolyze starch & glycogen but lack the enzyme for cellulose (= dietary fiber).

Transport: sugars dissolve → move in blood, phloem.

Functions

Energy: glucose → cellular respiration → ATP. **Storage**: starch (plants), glycogen (animals' liver).

Structure: cellulose. **Recognition**: carb chains on membrane glycoproteins/glycolipids (cell ID tags).

Nucleic acid sugars: ribose (RNA) & deoxyribose (DNA) = 5-C sugars; deoxy = 1 fewer O at the 2′ C.

⚠ Exact molecular structures of starch, glycogen & cellulose aren't tested. Know monomer, branching, function.

✓ Predict Qs: more branching → faster glucose release; linear packing → strength & rigidity in walls.

1.5 Lipids

Big Picture

Lipids: mostly C–H bonds → nonpolar, **hydrophobic**. Not polymers: no repeating monomer chain.

Fat (triglyceride) = glycerol + 3 fatty acids. Stores energy (~2× carbs per gram), insulates, cushions.

Saturated vs. Unsaturated

Feature	Saturated	Unsaturated
C–C bonds	All single	≥1 double
Tail shape	Straight	Kinked
Packing	Tight	Loose
Room temp	Solid	Liquid
Typical	Animal fats	Plant/fish oils

More double bonds → more kinks → more unsaturated → looser packing → more fluid at room temp.

Phospholipids & Steroids

Phospholipid = glycerol + 2 fatty acids + phosphate group.

Amphipathic: polar head, nonpolar tails.

Bilayer: in water, heads face out, tails hide inside → membranes form on their own, no energy.

Steroids: 4 fused carbon rings. Hormones (estrogen, testosterone) → growth, development, homeostasis.

Cholesterol: steroid in animal membranes → stabilizes; buffers fluidity vs. temp swings (both ways).

Membrane fluidity: ↑ unsaturated tails → ↑ fluid.

Fatty acid: hydrocarbon chain + carboxyl group. Longer/saturated chain → higher melting point (solid fat).

Barrier: hydrophobic core blocks ions & most polar molecules → membrane controls traffic (Unit 2).

⚠ Lipids are grouped by being hydrophobic, NOT by a shared monomer. Steroids have no fatty acid tails.

✓ Predict: temp drops → membranes stiffen; more unsaturated (kinked) tails restore fluidity.

1.6 Nucleic Acids

Nucleotide Structure

Nucleotide = 5-C sugar + phosphate + nitrogenous base. Info is stored in the base **sequence** along the strand.

Backbone: sugar–phosphate, joined by covalent (phosphodiester) bonds; bases stick out.

5′ end = free phosphate. **3′ end** = free –OH on sugar.

Directionality: new nucleotides are added only to the free 3′ –OH end → strands always grow 5′→3′.

DNA vs. RNA

Feature	DNA	RNA
Sugar	Deoxyribose	Ribose
Bases	A, T, G, C	A, U, G, C
Strands	Usually 2	Usually 1
Pairing	A–T, G–C	A–U, G–C
Main role	Stores info	mRNA, tRNA, rRNA

Double Helix Rules

Antiparallel: the 2 strands run opposite ways (5′→3′ paired w/ 3′→5′), like the lanes of a 2-way street.

Complementary pairs held by H-bonds: A–T (2), G–C (3) → GC-rich DNA is more stable to heat (higher melt).

Base % rule: %A = %T, %G = %C. If A = 30% → T = 30%, so G + C = 40% → G = 20% and C = 20% (Chargaff).

Complement: 5′-ATGC-3′ pairs w/ 3′-TACG-5′ (= 5′-GCAT-3′).

Exam Traps & Links

Single strand (RNA, or 1 DNA strand): the %A = %T rule does NOT apply, b/c there's no partner strand.

Heat breaks the H-bonds between strands; GC-rich DNA needs a higher temp to separate (3 H-bonds per pair).

⚠ Strands are held together by H-bonds (weak, separable). The backbone is covalent; don't swap them.

✓ Always label 5′/3′ ends when writing a complementary strand; mismatched ends = lost points.

1.7 Proteins

Amino Acids & Peptide Bonds

Amino acid: central C + H + amine ($–NH_2$) + carboxyl (–COOH) + a variable **R group** (side chain).

Peptide bond: carboxyl of one + amine of next, by dehydration → **polypeptide** (amine end → carboxyl end).

R groups: nonpolar/hydrophobic, polar/hydrophilic, or ionic (charged). Their chemistry → fold → function.

4 Levels of Structure

Level	What	Held by
1°	AA sequence	Peptide bonds
2°	α-helix, β-sheet	Backbone H-bonds
3°	Full 3D shape	R-group interact.
4°	2+ polypeptides	R-group interact.

3° interactions: H-bonds, ionic bonds, hydrophobic interactions, **disulfide bridges** (covalent, S–S).

Hydrophobic R → buried in core or in membrane.

Polar/charged R → on surface, face H_2O.

1° sets the rest: sequence → folding → shape → function.

Shape Changes

Denaturation: heat, pH, salt disrupt H-bonds/ionic bonds → 3D shape lost → function lost (enzymes stop working).

Mutation: 1 AA swap can change folding. Sickle cell: polar Glu → nonpolar Val → hemoglobin clumps.

Functions: enzymes, transport (hemoglobin), structure (collagen), signaling, defense (antibodies), movement.

20 amino acids: same backbone; differ only in R group.

Hemoglobin = 4 polypeptides → 4° level.

Ionic R groups are pH-sensitive: ↑ H^+ alters their charges → ionic bonds break → the folded shape shifts.

⚠ Denaturation does NOT break peptide bonds; 1° structure stays intact. Only the 2°–4° shape is lost.

✓ Predict an AA swap: compare R-group types (polar vs nonpolar vs charged) → folding → function.

Unit 1 Exam Strategy & Connections

Bond & Interaction Map

Type	Where	Strength
Covalent	Backbones, S–S	Strong
Ionic	Charged R groups	Medium
Hydrogen	H_2O, DNA pairs, 2°	Weak (many=strong)
Hydrophobic	Lipid tails, core	Weak

Science Practices Tested

1.A Describe: name the structure + its function in 1 line. "Branched glycogen → fast glucose release."

2.A Visuals: read molecule diagrams; spot –OH, $–NH_2$, –COOH, phosphate & C=C double bonds quickly.

6.E Predict: "If X changes → which bonds/interactions are disrupted → shape → function ↑ or ↓."

FRQ Moves

Structure → function: always link a molecular feature to what it lets the molecule do in the cell or body.

Justify w/ chemistry: name the bond or interaction (H-bond, hydrophobic), not just "it changes shape."

Identify molecule from clues: N + P → nucleic acid; S → protein; CHO + polar → carb; nonpolar → lipid.

Links to Later Units

Unit 2: phospholipid bilayer, cholesterol, membrane proteins.

Unit 3: enzymes = proteins; denaturation.

Unit 4: steroid hormones cross membranes. **Unit 6**: 5′→3′ replication, transcription, translation of genes.

MCQ sets: 4–5 Qs share one diagram or data set; read the labels, axes & units before reading the questions.

Compare Qs: name the exact difference (ribose vs deoxyribose, U vs T), not "they're different."

⚠ An equations & formula sheet is provided, but Unit 1 is structures & functions you must know cold.

✓ Every Unit 1 answer: structure → interaction → property → function. Name each link in the chain.