ALL WORKBOOK BLANKS FILLED

AP Biology Unit 1

Chemistry of Life

Complete Study Guide — Topics 0–7

Based on the 2025 Unit 1 Workbook (Topics 0–7)
Aligned to the College Board AP Biology CED

Covers: every page of the 2025 Unit 1 Workbook (Topics 0–7), including the Learning Objectives, Essential Knowledge statements, all fill-in-the-blank notes, every Vocabulary/Review Question, all practice problems with worked answers, the Cellulose case study, the Properties of Water stations lab, the Paper Chromatography dry lab, and the practice FRQ.

How to use this: the workbook's **Essential Knowledge** statements are College Board's own wording — those get tested nearly verbatim on multiple choice. The **Vocabulary/Review Questions** boxes on pages 1–5 are the ones you've noticed showing up on tests, so every single one is answered below in its own section. Anything marked **NICHE** is detail beyond the workbook that shows up in tougher questions.

The unit in one sentence: living systems are built from a handful of elements whose bonding properties — especially carbon's four bonds and water's polarity — determine the structure of four macromolecule classes, and structure determines function at every level.

PART 1 — The Course Frame

1.1 The "Welcome to AP Biology" blanks, filled

> *The course is broken down into **SCIENCE PRACTICES** (skills) and **BIG IDEAS**.*

The four Big Ideas (these are the blanks on that page):

#	Big Idea	Code	Description
1	**Evolution**	EVO	The process of evolution drives the diversity and unity of life
2	**Energetics**	ENE	Biological systems use energy and molecular building blocks to grow, reproduce, and maintain dynamic homeostasis
3	**Information Storage and Transmission**	IST	Living systems store, retrieve, transmit, and respond to information essential to life processes
4	**Systems Interactions**	SYI	Biological systems interact, and these systems and their interactions exhibit complex properties

The two subdivisions: - **LEARNING OBJECTIVES** — define what a student needs to be *able to do* with the content knowledge - **ESSENTIAL KNOWLEDGE** — describes the *knowledge required* to perform the learning objective

The six Science Practices: concept explanation · analyze visual representations · determine scientific questions and methods · represent and describe data · perform statistical tests and data analysis · develop and justify scientific arguments using evidence.

Unit 1 covers Big Ideas 2, 3, and 4 (not 1 — there's no evolution content in this unit, which is a detail a teacher can ask about).

1.2 How Unit 1 is actually tested

The AP exam is 3 hours: 60 multiple-choice in 90 minutes (50%), then 6 free-response in 90 minutes (50%) — 2 long FRQs (8–10 pts each) and 4 short FRQs (4 pts each).

The workbook tells you exactly where statistics appears, and this is worth memorizing: - **FRQ 1** — describe data, analyze data, perform calculations - **FRQ 2** — graphing (**this is the only question that will ask you to graph data**), analyze data, perform calculations, state H_0 - **FRQ 6** — describe data, use data to evaluate a hypothesis

> ***Trap to avoid:** students treat Topic 0 as "review" and skip it. It's 28 of the 79 workbook pages and it appears on every unit test all year, because the workbook says outright that Topic 0 concepts "will be practiced throughout all 8 units." The statistics is more heavily tested than the water chemistry.*

1.3 The one idea that unifies the whole unit

Structure determines function. It's stated explicitly for proteins ("all four levels of a protein structure determine the function of a protein"), but it's the same argument everywhere in this unit:

- Water's *bent, polar structure* → cohesion, adhesion, high specific heat, solvent ability
- Carbon's *four valence electrons* → chain length, branching, ring formation → molecular diversity
- α vs β glucose *linkage geometry* → starch (digestible energy storage) vs cellulose (indigestible structure)
- Saturated vs unsaturated *tail kinks* → solid vs liquid at room temperature
- A–T (2 H-bonds) vs G–C (3 H-bonds) → different melting temperatures
- Amino acid *R-group chemistry* → folding → protein shape → protein function

Any FRQ that asks you to "justify" or "explain" in this unit almost certainly wants a structure→function argument. Say the structural feature, then the consequence.

PART 2 — Topic-by-Topic

TOPIC 0 — Biology Review and Introduction to Statistics

The concepts in Topic 0 are practiced throughout all 8 units.

0.1 The Scientific Method — blanks filled

> ***Scientific method:*** *a step-by-step process used by scientists to investigate* ***QUESTIONS/PHENOMENA****, gather* ***DATA/EVIDENCE****, and draw* ***CONCLUSIONS*** *based on experiments and observations.*

The 6 general steps (Vocabulary/Review Q1): 1. Make an observation 2. Ask questions (explore the literature) 3. Form a hypothesis 4. Design an experiment 5. Collect data 6. Draw a conclusion

Conclusions lead to: support the hypothesis · reject the hypothesis · generate new hypotheses. The process is **cyclical**, not linear.

The monarch butterfly example — background facts the workbook gives you, because a test question may reuse them: - Monarchs are **diurnal** (active during day, rest at night) - They have a **circadian rhythm** (internal clock tracking day/night) - They are **migratory** and use sunlight as a compass; antennae track the sun - Proteins important for flight are processed **at night while the butterfly rests**

> *Can this be manipulated and turned into a* ***CONTROLLED*** *experiment?*

0.2 Hypotheses — blanks filled

> ***Hypothesis:*** *a* ***TESTABLE/PROPOSED*** *explanation for an* ***OBSERVATION****. Explains the relationship* ***BETWEEN*** *variables and what the researcher* ***EXPECTS*** *to happen to one variable if another variable* ***CHANGES****.*

The "If... then... because..." structure: - **"If"** → the **INDEPENDENT** variable - **"Then"** → the **DEPENDENT** variable - **"Because"** → optional **REASONING/EXPLANATION**

> *Results can either* ***SUPPORT*** *or* ***FAIL TO SUPPORT / REJECT*** *the hypothesis.*
>
> ***NEVER SAY:*** *"prove" (or "proved," "proven," "disprove"). Science does not prove hypotheses. You* ***support*** *or* ***fail to support****; you* ***reject*** *or* ***fail to reject*** *the null.*
>
> ***Trap to avoid:*** *writing "the data proves the hypothesis" on an FRQ. Graders are specifically watching for this. Also never say you "accept" the null — you* ***fail to reject*** *it. Absence of evidence for a difference isn't evidence that there's no difference.*

Null vs. alternative hypotheses

	Null hypothesis (H_0)	**Alternative hypothesis (H_a / H_1)**
Claims	There is **NO relationship / NO difference** between the two groups	There **IS** a relationship / effect / difference between the groups
Observations attributed to	**CHANCE** (random variation)	A **SPECIFIC/REAL** cause
Role	The baseline you test against	What the researcher is actually claiming/studying

Why we need a null (blanks filled):

> *Provides a* ***BASELINE/STANDARD****, which we can use to* ***COMPARE*** *our sample results to. Allows for a hypothesis to be tested in a meaningful way using* ***STATISTICAL*** *tests. Use the data to determine if there is strong enough evidence to* ***REJECT*** *the* ***NULL*** *hypothesis, meaning the* ***ALTERNATIVE*** *hypothesis is* ***SUPPORTED*** *by the data.*

Review Q3 — do you always need both? You always need a null for statistical testing, because statistical tests are built to test the null. The alternative is what you're actually investigating. On the AP exam, if asked to "state a hypothesis," read carefully — FRQ 2 specifically asks for the **null**.

> ***NICHE:*** *the null is always the statement of no effect, which means it always contains "no," "no difference," or "equal to." If you write a null that predicts a difference, you've written an alternative. This is the exact error planted in the mosquito "Catch the Errors" activity.*

0.3 Experimental Design — blanks filled

> ***At least 3 trials needed per group*** *(the workbook's "At least __ trials"). More trials → more reliable, lower standard error.*

Groups

Group	Definition (blanks filled)
Control	Used for **COMPARISON** to the experimental group; helps to **VALIDATE/STRENGTHEN** statistical analysis and increase confidence in **CONCLUSIONS** drawn from the experimental results
Experimental	Receives the **INDEPENDENT VARIABLE** treatment (IV) being tested to observe its impact on the **DEPENDENT VARIABLE** (DV)
Negative control	Group **NOT** exposed to any treatment OR exposed to a treatment known to have **NO** effect. Helps ensure there is **NO** effect when there should be **NO** effect
Positive control	Group not exposed to the IV but IS exposed to a treatment known to **PRODUCE** an expected effect. Ensures the experimental setup can produce a **REAL/MEASURABLE** effect; provides a **REFERENCE/COMPARISON** point for what a known effect looks like

Variables

Variable	Definition (blanks filled)
Independent (IV)	The **ONE** factor that is **CHANGED/MANIPULATED** between groups; what is being **TESTED**; graphed on the **X** axis
Dependent (DV)	Factor that is **MEASURED** and **AFFECTED/INFLUENCED** by the IV; graphed on the **Y** axis
Constant	Factors kept **THE SAME** for all groups to ensure only the IV affects the outcome; aka controlled variables

Memory hook: DRY MIX — **D**ependent, **R**esponding, **Y**-axis / **M**anipulated, **I**ndependent, **X**-axis.

Review Q5 — are constants the same as controls?

No. A **constant** is a *variable* held identical across all groups (temperature, container size, time). A **control** is a *group* used for comparison. A poorly controlled experiment can still have constants; they're different categories. The mosquito activity tests exactly this: the air conditioning failure that made the B+ room warmer broke a **constant**, not a control.

Review Q6 — when to use each control

- **Negative control** → when you need to confirm that your measured effect isn't happening on its own. Answers: *would this have happened anyway?*
- **Positive control** → when you need to confirm your setup and detection method actually work. Answers: *would my experiment have detected an effect if one existed?*

> ***NICHE:*** *a positive control that fails means your experiment is broken, not that your treatment doesn't work. That distinction is a favorite short-FRQ question. If the positive control shows no effect, you cannot interpret your experimental groups at all.*

Worked answers — Practice: Control Groups (workbook p. 13)

1. **Blood pressure drug.** Negative control: patients given a **placebo** pill (identical in appearance, no active drug). Positive control: patients given an **existing, proven blood-pressure medication**.
2. **Soda and heart rate.** Negative control: subjects drink **water** or caffeine-free soda. Positive control: subjects given a known heart-rate elevator (a measured dose of **caffeine**, or light exercise).
3. **Soil composition.** Negative control: plants grown in **plain/untreated soil** with no added minerals. Positive control: plants grown in soil with **added nitrogen** (known to increase growth).

4. **New antibiotic vs. S. pyogenes.** Negative control: petri dish of *S. pyogenes* with **no antibiotic** (or with sterile solvent only). Positive control: petri dish of *S. pyogenes* treated with **penicillin**, which is known to kill it.

Worked answers — Practice: Variables (workbook p. 12)

#	Independent variable	Dependent variable
1	Number of cars washed	Money earned ($)
2	Level of physical stress	Heart rate
3	Presence/occurrence of the warning call	Reaction/behavior of surrounding birds
4	Water temperature	Swimming speed of fish

Worked answers — Catch the Errors: mosquito experiment (workbook p. 14)

Section	Error	Correction
Hypotheses	The **null and alternative are swapped**. H_0 states there *will* be differences (that's an alternative); H_1 states a preference exists.	H_0: There will be **no difference** in mosquito preference among blood types. H_1: Mosquitoes will show a preferred blood type.
Participants	Only **3 individuals per group** (too small a sample), and AB+ was dropped — only three of the four stated blood types are represented.	Increase sample size substantially (at least 3 trials per group is the floor; more reduces standard error). Include **all four** blood types as originally designed.
Procedure	The **B+ room was warmer** — a constant was not held equal. Mosquitoes are attracted to heat and CO_2, so temperature is a confounding variable.	Keep **temperature identical** across all groups. Repeat the trial, or randomize/rotate participants across rooms.
Conclusion	Two errors: they say the hypothesis was "correct" (never say proved/correct), and they drew a conclusion **without statistical analysis** — no error bars, no test of significance.	State that the data **support** the alternative hypothesis. Calculate means and 95% CI (± 2 SEM); only claim a significant difference if **error bars do not overlap**.

Think, Pair, Share answers (p. 11): 1. *Why only change the IV?* If more than one variable changes, you cannot attribute the change in the DV to any single cause — the variables are **confounded** and no causal conclusion is possible. 2. *What is bias?* A systematic (non-random) influence that distorts results in a particular direction — through subject selection, researcher expectation, or measurement. It reduces validity because the error doesn't average out with more trials, unlike random error. Controlled by blinding, randomization, and standardized procedures.

0.4 Statistics — blanks filled

> ***Statistics:*** *methods used to* ***COLLECT****,* ***ANALYZE/ORGANIZE****, or* ***INTERPRET/SUMMARIZE*** *quantitative data.*
>
> *Statistics in biology helps us by:* ***SUMMARIZING*** *our observations, and making* ***PREDICTIONS/INFERENCES*** *based on the summary. It also helps scientists* ***avoid jumping to CONCLUSIONS*** *and* ***be cautious about GENERALIZATIONS/OVERGENERALIZING****.*

Descriptive statistics	Inferential statistics
Methods used to **SUMMARIZE** or describe observations/samples	Using observations to make estimates or **PREDICTIONS**; generalizing from a sample to a wider **POPULATION**
Measures of **CENTRAL TENDENCY**: mean, median, mode	Standard error of the mean, confidence intervals
Measures of **VARIABILITY**: range, standard deviation, variance, skewness, quartiles	Hypothesis tests: **CHI-SQUARE**, ANOVA, t-test

Think, Pair, Share (p. 16): Statement A ("the earlier you start reviewing, the better you'll do") is **generalizing** and makes a **prediction** — inferential. Statement B ("on average, I watch an hour of TV per day") is **summarizing** — descriptive.

Sample vs. population

> ***Sample:*** *a* ***SMALLER, RANDOM/REPRESENTATIVE*** *group selected from the population.* ***Population: ALL*** *members of the group being studied. Researchers study a* ***SAMPLE*** *and use* ***STATISTICS*** *to make* ***INFERENCES/PREDICTIONS*** *about the* ***POPULATION****.*

In the orb weaver spider example: the population is all **2,000** spiders; the sample is **~30** randomly chosen individuals. Researchers do not measure all 2,000 — it isn't feasible in time, money, or capability.

> ***Spider study blanks:*** *Observation — the* ***DIAMETER/SIZE*** *of webs changes between seasons. Question — how does mating season affect the* ***DIAMETER*** *of orb weaver* ***WEBS****?* H_0*: mating season has* ***NO EFFECT*** *on the average diameter of orb weaver webs.*

0.5 Describing data: SHAPE, CENTER, SPREAD

Every data-description FRQ wants these three, in this order. If a question says "describe the data," hit shape, center, and spread and you'll hit the rubric.

SHAPE

> *To better visualize the* ***DISTRIBUTION*** *(shape) of the data, we can make a* ***HISTOGRAM****. 1. Set up* ***BINS*** *(uniform* ***INTERVAL/BIN*** *size that cover the entire range of the data) 2. Determine how* ***MANY*** *values go into each bin 3. Add bars: the* ***HEIGHT*** *of each bar represents the* ***NUMBER/FREQUENCY*** *of occurrences within each bin*

Describe shape by: **symmetry or skewness**, and **number of peaks/MODES** (unimodal, bimodal, multimodal).

Distribution	Features
Normal	Symmetric, unimodal, bell-shaped
Uniform	Symmetric, all outcomes equally likely (flat)
Bimodal	Two modes (can also be skewed)
Positive (right) skewed	Tail extends right, unimodal; mode < median < mean
Negative (left) skewed	Tail extends left, unimodal; mean < median < mode

> ***Normal distribution: SYMMETRICAL/BELL-SHAPED*** *distribution of values for a population. Described using the* ***MEAN*** *and* ***STANDARD DEVIATION*** *(spread). -* ***68%*** *of data falls within ± 1 standard deviation -* ***95%*** *of data falls within ± 2 standard deviations -* ***99.7%*** *of data falls within ± 3 standard deviations*
>
> *Most biological examples in this course follow an approximately* ***NORMAL*** *distribution.*
>
> ***Memory hook for skew:*** *the skew is named for where the* ***tail*** *points, not where the peak is. Right-skewed data has its bulk on the left. The* ***mean is dragged toward the tail*** *because the mean is the measure sensitive to outliers.*

CENTER

> ***Central tendencies:*** *the center can be described by the* ***MEAN****,* ***MEDIAN****, and* ***MODE****.*

Measure	How to find	When to use	Weakness
Mean	Sum ÷ number of values	Symmetric/normal distributions	**Sensitive to outliers**
Median	Middle value when ordered (average the two middle if even n)	**Skewed** distributions or data with outliers	Ignores magnitude of extreme values
Mode	Most frequent value	**Categorical** data, or finding the most common outcome	Often not useful for continuous data

> *In a perfectly normal distribution:* ***MEAN = MEDIAN = MODE****. In* ***APPROXIMATELY*** *normal distributions, the* ***MEAN*** *is the preferred measure of central tendency. In* ***skewed*** *distributions, the* ***MEDIAN*** *is the preferred measure of central tendency. Since we usually can't collect data for the* ***ENTIRE*** *population, we will never know the* ***TRUE*** *population mean. The* ***SAMPLE MEAN*** *serves as an* ***ESTIMATE*** *for the population mean.*

Review: Shape and Center — worked answers (workbook p. 21)

1. Three measures of central tendency: **mean, median, mode**.
2. Best for data with extreme outliers: **median**, because it's the positional middle and isn't pulled by extreme high or low values, whereas the mean is arithmetically dragged toward outliers.
3. **Homework data:** 38, 120, 70, 22, 258, 46, 84, 20, 64, 90 - **Mean** = 812 ÷ 10 = **81.2 min/day** - Ordered: 20, 22, 38, 46, 64, 70, 84, 90, 120, 258 → **Median** = (64 + 70)/2 = **67 min/day** - **Best measure: the median.** The value 258 is a clear outlier that pulls the mean up by ~14 minutes above the median. The distribution is right-skewed, so the median better represents a typical student.

VARIABILITY (SPREAD)

> *The degree to which data are **SPREAD OUT** in a data set. Variability helps give a more **COMPLETE/ACCURATE DESCRIPTION** of a distribution. Variability can be measured using **RANGE**, **STANDARD DEVIATION**, and **IQR**.*

The review-book example: two distributions, same **MEAN**, but different **SPREAD** of data — so "did the review book make a difference?" cannot be answered from the means alone. That's the entire point of the section: **two data sets can have identical means and completely different reliability.**

Standard deviation (for approximately normal distributions)

> ***Standard deviation:** the **AVERAGE** amount by which all the values deviate from the **MEAN** (measures the **SPREAD** of the data). Remember: this is a **SAMPLE**. The standard deviation for our sample provides an **ESTIMATE** that should reflect how the data are spread around the **POPULATION** mean. - **Low (small) SD:** data is **CLOSE** to the mean → more precise, more reliable - **High (large) SD:** data is **FAR** from the mean (more spread out) → less reliable*

Review Q9 (p.1 box) — is data more reliable with low or high SD? Low. Low SD means individual measurements cluster tightly around the mean, so the mean is a good representation of the data set and the result is repeatable.

IQR (for skewed / non-normal distributions)

> *In non-normal distributions the spread can be described by **IQR** (interquartile range). Quartiles divide a data set into **4** equal parts, labelled Q1, Q2, Q3. **PERCENTAGES/PROPORTIONS** are equal, intervals may not be. IQR measures the spread of the **MIDDLE 50%** of a data set. **To find the IQR: Q3 − Q1.** In the workbook example, IQR = 14 − 4 = **10**.*

How to find quartiles (the workbook's method — follow it exactly, since teachers grade to it): 1. Arrange data in **increasing numerical** order. 2. Find the median (Q2). 3. **If n is odd**, Q2 is an actual data value — draw a line *through* it and **exclude** that value when finding the medians of the lower and upper halves. 4. **If n is even**, Q2 falls *between* two values — draw the line between them and include all values on each side. 5. Q1 = median of the lower half. Q3 = median of the upper half.

> ***Trap to avoid:** the odd-n exclusion rule. Different textbooks and calculators handle this differently (TI-84 excludes the median; some software doesn't), so you can get a "wrong" answer that's right by another convention. **Use the workbook's rule on this teacher's test.***

Review: Variability — worked answers (workbook p. 24)

1. Higher SD: whichever curve is **wider/flatter** — a broader spread means values deviate further from the mean.
2. Most accurate description of SD: **option 3** — the average distance all values deviate from the mean. (1 is the mean, 2 is the range, 4 is the mode.)
3. **True** — two data sets can have the same mean but different variability. This is the review-book example.
4. Label the wide/flat curve **A** (high SD) and the narrow/tall curve **B** (low SD). A wider curve means data points are spread further from the mean; a taller, narrower peak means they cluster tightly around it.
5. **Fly eggs:** most flies lay 20–30, a few lay 0, a few lay over 100 → the distribution is **right (positively) skewed** with outliers on the high end. Use **IQR**, because standard deviation is calculated from the mean and both the mean and SD are distorted by the extreme values. IQR describes the middle 50% and is resistant to outliers.
6. IQR definition: **option 2 — Q3 − Q1.**

Worked answers — box plot and quartile problems (workbook pp. 30–31)

Q8 — Lizard push-ups: 300, 105, 400, 521, 411, 500, 550, 52, 315, 75, 370 Ordered: 52, 75, 105, 300, 315, **370**, 400, 411, 500, 521, 550 (n = 11, odd) - **Minimum = 52** - **Q2 (median) = 370** (6th value) - Lower half (excluding 370): 52, 75, **105**, 300, 315 → **Q1 = 105** - Upper half (excluding 370): 400, 411, **500**, 521, 550 → **Q3 = 500** - **Maximum = 550** - IQR = 500 − 105 = **395** - *What does IQR measure?* The spread of the **middle 50%** of the data — a measure of variability resistant to outliers.

Q10 — Social media, 11th grade: 10, 55, 85, 25, 44, 37, 42, 201, 56, 59 Ordered: 10, 25, 37, 42, **44, 55**, 56, 59, 85, 201 (n = 10, even) - **Q2 = (44 + 55)/2 = 49.5** - Lower half: 10, 25, **37**, 42, 44 → **Q1 = 37** - Upper half: 55, 56, **59**, 85, 201 → **Q3 = 59** - **IQR = 59 − 37 = 22**; min = 10, max = 201

9th grade: 40, 75, 10, 54, 66, 90, 42, 205, 77, 84 Ordered: 10, 40, 42, 54, **66, 75**, 77, 84, 90, 205 - **Q2 = (66 + 75)/2 = 70.5** - Lower half: 10, 40, **42**, 54, 66 → **Q1 = 42** - Upper half: 75, 77, **84**, 90, 205 → **Q3 = 84** - **IQR = 84 − 42 = 42**; min = 10, max = 205

Comparison: the 9th graders have a **higher median** (70.5 vs 49.5) and a **larger IQR** (42 vs 22), meaning 9th graders spend more time on social media on average *and* are more variable in their usage. Both data sets have a high outlier (201 and 205) making them right-skewed — which is exactly why IQR and median are the right tools here rather than mean and SD. Note: this describes the samples; without confidence intervals you cannot claim a statistically significant difference.

Q7 — Box plot of 9th grade biology test scores: read directly off the plot. Remember what each segment represents: - Median = the line inside the box (**Q2**) - Lowest score = left whisker end (**minimum**) - Highest score = right whisker end (**maximum**) - **Percentage at or below Q3 = 75%**; **at or below Q2 = 50%**; **at or below Q1 = 25%**

> ***NICHE:*** *each of the four sections of a box plot contains **25% of the data points**, but they are usually different widths. A wide whisker doesn't mean more data — it means that quarter of the data is more spread out. This is the workbook's note that "percentages are equal, intervals may not be," and it's a classic multiple-choice trap.*

0.6 Sampling variation, SEM, and confidence intervals

> *Different **SAMPLES** from the same population of spiders will give **DIFFERENT** results.*

The workbook shows four samples from the same spider population giving means of 24.5, 30.1, 25.3, and 28.7 cm. Same population, four different answers. That's the problem SEM exists to solve.

> ***Standard error of the mean (SEM or SE_x̄):*** *used to **ESTIMATE/QUANTIFY** how **WELL/ACCURATELY** the sample mean **REPRESENTS/ESTIMATES** the population mean. Uses the standard deviation of the sample to estimate the variation in the population.*

$$\text{SEM} = \frac{s}{\sqrt{n}} \qquad \text{where } s = \text{sample standard deviation, } n = \text{sample size}$$

> ***Confidence interval:*** *a **RANGE** of values in which we are 95% confident the **TRUE** population mean will fall. Built using the sample **MEAN** and the **STANDARD ERROR** of the mean. - **Upper limit = Mean + 2 × SEM** - **Lower limit = Mean − 2 × SEM***

Think, Pair, Share (p. 25) answers — read straight off the formula: 1. Increases in sample size **DECREASE** standard error. (n is in the denominator, under a square root.) 2. Increases in standard deviation **INCREASE** standard error. (s is in the numerator.)

Review Q10 (p.1 box) — why do researchers use SEM? Because SD describes the spread of the *sample data*, while SEM describes the uncertainty in the *sample mean as an estimate of the population mean*. Researchers want to know how much they can trust the mean, not just how scattered the data are. SEM is what you build confidence intervals from.

> ***NICHE:*** *SD does **not** shrink as you collect more data — it converges on the population's true spread. SEM **does** shrink, because it's SD divided by √n. This is why "increase your sample size" is always a valid FRQ answer for improving reliability, and why it's the correction for the mosquito experiment's 3-per-group problem.*
>
> ***NICHE:*** *the "× 2" is an approximation. The true multiplier for a 95% confidence interval is **1.96** for large samples, and larger still for small samples (t-distribution). AP Biology standardizes on 2, so use 2 — but knowing why can help on a conceptual question.*

0.7 Interpreting error bars — the highest-value skill in Topic 0

This is the single most-tested statistical idea in AP Biology. Learn the decision rule cold.

> ***If the 95% CI error bars DO NOT overlap:*** *There **IS** a **STATISTICALLY SIGNIFICANT DIFFERENCE** between the means. The researchers **REJECT** the null hypothesis, and the **ALTERNATIVE** is supported. These differences are likely due to a **SPECIFIC/REAL** cause.*
>
> ***If the 95% CI error bars DO overlap:*** *There is **NOT** a statistically significant difference between the **MEANS**. Observed differences are due to **CHANCE**. You **fail to reject** the null hypothesis.*

Review Q11 (p.1 box) — if standard error bars overlap, is the difference significant? No. Overlapping intervals mean the true population means could plausibly be the same value; the observed difference between sample means is within the range explainable by random sampling variation.

> ***Trap to avoid:*** *concluding a difference exists because one bar is visibly taller than another. Height difference is meaningless without checking the error bars. A large-looking gap with overlapping intervals is **not** significant, and a small gap with non-overlapping intervals **is**. Always state the error-bar comparison explicitly in your FRQ answer — that's where the point is.*

The full sentence template for an FRQ conclusion:

> "*There is / is not sufficient evidence to reject the null hypothesis. The error bars **do / do not** overlap, indicating the difference between the means **is / is not** statistically significant. Therefore the observed difference is likely due to **[a real effect of the IV] / [random chance]**.*"

0.8 Chi-square (introduced here, developed in Unit 5)

> ***Chi-square:*** *a form of statistical analysis used to compare the actual counts/frequencies (**OBSERVED**) with the **EXPECTED** counts/frequencies. - Determines whether the **EXPECTED** data provides a "good fit" to the observed data obtained - Determines if any **DEVIATIONS/DIFFERENCES** from the expected results are due to **RANDOM CHANCE** alone or to other circumstances (e.g., data collection error) - Designed to analyze **CATEGORICAL** data - Use the equation to test the **NULL** hypothesis*

$$\chi^2 = \sum \frac{(o - e)^2}{e}$$

> ***NICHE:*** *degrees of freedom = **number of categories − 1**. Compare your calculated χ^2 to the critical value at **p = 0.05**. If **χ^2 > critical value → reject the null** (the deviation is too large to be chance). If $\chi^2 \leq$ critical value → fail to reject. Note this is the opposite direction from error bars, where non-overlap means reject — students mix these up constantly.*

0.9 Statistics Practice Problems — worked solutions

Part 1, Problem 1 — Sleep study

Data: 6, 4, 7, 7, 6, 5, 7, 6 (n = 8), given s = 1.07 hrs

a. Mean = 48 ÷ 8 = **6.0 hours**

c. SEM = 1.07 ÷ √8 = 1.07 ÷ 2.828 = **0.378 2 SEM** = **± 0.76 hours** → 95% CI = **6.0 ± 0.76**, i.e., **5.24 to 6.76 hours**

d. Bar graph: y-axis "Mean Hours of Sleep," bar at 6.0, error bar from 5.24 to 6.76. Label the axis with units. Title it.

e. Harvard prediction: the Harvard data (3, 5, 7, 8, 6, 11, 2, 12) will have a **higher standard deviation**. The values range from 2 to 12 (range = 10) versus UT's 4 to 7 (range = 3), so individual values deviate much further from the mean.

f. Bonus — actual Harvard SD: mean = 54 ÷ 8 = 6.75. Sum of squared deviations = 87.5. Sample variance = 87.5 ÷ 7 = 12.5. **s = 3.54 hours** — more than three times UT's 1.07. Prediction confirmed. Note that Harvard's SEM would be 3.54 ÷ 2.828 = 1.25, giving a 95% CI of ± 2.5 — a far less precise estimate despite the same sample size.

Part 1, Problem 2 — Athlete water consumption

Football: 70 ± 13 → **57 to 83**. Soccer: 64 ± 10 → **54 to 74**.

a. Null hypothesis: There is **no difference** in the mean amount of water consumed per day between football players and soccer players. (Equivalently: sport has no effect on daily water consumption.)

b. Bar graph, two bars (Football 70, Soccer 64), error bars as above.

c. Conclusion — circle these: There **is not** sufficient evidence to reject the null hypothesis. The athletic trainer's alternative hypothesis **is not** supported by the data. While the mean ounces consumed by football players is higher, the error bars **overlap** (57–83 and 54–74 share the range 57–74), indicating that the difference between the means **is not** significant.

Part 1, Problem 3 — SEM and sample size

All three data sets have s = 2.3.

Data set	n	√n	SEM = 2.3/√n
1	15	3.873	**0.59**
2	30	5.477	**0.42**
3	45	6.708	**0.34**

Problem 4: As sample size increased, standard error **decreased**. In SEM = s/√n, n sits in the denominator, so increasing n increases the denominator and shrinks the quotient. Biologically: a larger sample is a better estimate of the population, so there's less uncertainty about the mean. Note the square root means returns diminish — tripling n from 15 to 45 only cut SEM by ~42%, not 67%.

Part 2 — Breast cancer drug case study (Herceptin / Perjeta)

Background (Q1): The cancer cell has **many more HER2 receptor proteins** on its surface than the normal cell (HER2 overexpression). Since HER2 drives cell growth signaling, more receptors means **excessive growth signaling**, causing the cell to divide rapidly and uncontrollably outside the normal cell-cycle checkpoints, forming tumors.

Means and confidence intervals — all groups:

Group	Data	Mean	SD	SEM = SD/√5	± 2 SEM	95% CI range
Negative control	3, 5, 5, 5, 5	**4.6%**	0.89	0.40	**± 0.8**	3.8 – 5.4
Positive control	30.5, 33.5, 40, 36, 35	**35.0%**	3.48	1.56	**± 3.1**	31.9 – 38.1
Herceptin alone	20.35, 22.5, 11.7, 15, 20.45	**18.0%**	4.49	2.01	**± 4.0**	14.0 – 22.0
Perjeta alone	25, 22.5, 19.5, 25, 23	**23.0%**	2.26	1.01	**± 2.0**	21.0 – 25.0
Combination	31.7, 31, 29.3, 32, 31	**31.0%**	1.05	0.47	**± 0.9**	30.1 – 31.9

(√5 = 2.236)

Q4 — interpreting Herceptin vs Perjeta from means alone: Perjeta appears more effective (23.0% vs 18.0% apoptosis). But this is an interpretation *without* error bars, and the point of question 9a is that it's premature.

Q6 — combination vs individual treatments: The combination mean (31.0%) is higher than both Herceptin (18.0%) and Perjeta (23.0%) alone, suggesting the drugs work better together than either does individually.

Q8 — why is SEM higher for Herceptin than Perjeta? Because Herceptin's **standard deviation is much larger** (4.49 vs 2.26) — its trial values ranged from 11.7 to 22.5, while Perjeta's clustered from 19.5 to 25. Sample size is identical (n = 5), so the entire difference comes from data variability. More scatter in the raw data means less confidence in the mean.

Q9a — did error bars change your answer to Q4? Yes. Herceptin's CI (14.0–22.0) and Perjeta's CI (21.0–25.0) **overlap** in the range 21.0–22.0. Therefore there is **no statistically significant difference** between them — the apparent 5-point gap in means is within what random sampling variation could produce. You fail to reject the null.

Q9b — did error bars change your answer to Q6? No — it holds. The combination CI (30.1–31.9) does **not** overlap Herceptin's (14.0–22.0) or Perjeta's (21.0–25.0). The combination treatment is **significantly more effective** than either drug alone.

Q11a — treatments vs positive control: Herceptin (14.0–22.0) and Perjeta (21.0–25.0) both fall entirely below the positive control's CI (31.9–38.1), with no overlap. Both are therefore **significantly less effective** than radiation.

Q11b — combination vs positive control: Combination CI is 30.1–31.9; positive control is 31.9–38.1. These **just barely touch/overlap at 31.9**, so there is **no statistically significant difference** — the combination treatment is **as effective as** the radiation positive control. That's the clinically important finding: equal efficacy without radiation's side effects.

Q12 — what if the negative control had overlapping error bars with the treatments? It would mean the treatments produced **no significant increase in apoptosis over doing nothing at all** — the drugs would be ineffective, and any apparent difference would be attributable to chance or to background/spontaneous apoptosis rather than the treatment.

Q13 — which treatment to study further? The **combination (Herceptin + Perjeta)**. It produced significantly more apoptosis than either drug alone, is statistically indistinguishable from the proven radiation treatment, and has the tightest confidence interval (± 0.9) indicating the most consistent, reproducible effect — while avoiding radiation's harmful side effects.

Part 1, Problem 9 — Rainwater lead concentrations (box plots)

Read from the plots: the community with the lower line inside the box has the **lower median**; the community with the **taller box (larger IQR)** and longer whiskers has **higher variability**. For the safety question: if the 10 µg/L line falls inside a community's box, then between 25% and 75% of samples exceed it depending on where it sits — if it's at Q1, **75%** of samples are at or above; at the median, **50%**; at Q3, **25%**.

TOPIC 1 — Structure of Water and Hydrogen Bonding

Learning Objective 1.1.A: Explain how the properties of water that result from its polarity and hydrogen bonding affect its biological function.

Essential Knowledge (College Board's wording — expect near-verbatim MC questions): - **1.1.A.1:** Living systems depend on the properties of water to sustain life. - i. Water has **polarity**, because of polar covalent bonds between hydrogen and oxygen. This polarity contributes to hydrogen bonding between and within biological molecules. - ii. Water has a **high specific heat capacity**, which allows for maintenance of homeostatic body temperature. - iii. Water has a **high heat of vaporization**, which allows for evaporative cooling of the surrounding environment. - **1.1.A.2:** The hydrogen bonds between adjacent polar water molecules result in **cohesion, adhesion, and surface tension**.

1.1 Chemistry review — blanks filled

Term	Definition (blanks filled)
Matter	Anything that takes up **SPACE** and has **MASS**. Rocks, metals, oils, gases, organisms
Element	A substance that **CANNOT** be broken down into other substances by chemical reactions. 92 occur in nature
Compound	A substance consisting of **TWO** or more different **ELEMENTS** combined in a fixed ratio. H_2O, NaCl

> ***Essential elements:*** *of the 92 naturally occurring elements,* ***20–25%*** *are essential to* ***LIFE*** *and* ***SURVIVAL/HEALTH****.* ***CHOPN make up 96% of living matter. Trace elements:*** *required by an organism in very* ***SMALL*** *quantities.*

Review Q1 — identify the elements that make up nearly all living matter: C, H, O, N — carbon, hydrogen, oxygen, nitrogen — about **96%**. Add **P** (phosphorus) and **S** (sulfur) and you have **CHNOPS**, the six elements that make up essentially all biological molecules.

Where each one goes (this is Topic 2's Essential Knowledge 1.2.A.1, and it's a guaranteed test question): - **C, H, O** — the most prevalent; build carbohydrates, proteins, lipids, and nucleic acids - **N** — nucleic acids **and** proteins (in the amino group) - **P** — phospholipids and nucleic acids (the phosphate backbone, and ATP) - **S** — proteins (in the R groups of cysteine and methionine — this is what makes disulfide bridges possible)

Research, Pair, Share answers: - *Why are the essential elements essential?* C forms the skeleton of every organic molecule. H and O make up water and participate in nearly all bonds. N is required for amino acids (all proteins) and nitrogenous bases (all nucleic acids). P is required for ATP, DNA/RNA backbone, and membrane phospholipids. S is required for the disulfide bridges that stabilize protein tertiary structure. - *Trace element examples:* **iron** (Fe — center of hemoglobin, carries O_2), **iodine** (I — required for thyroid hormone), **zinc** (Zn — enzyme cofactor), **copper**, **fluorine** (tooth enamel), **magnesium** (center of chlorophyll). A deficiency in a trace element causes disease even though the quantity needed is tiny — goiter from iodine deficiency, anemia from iron deficiency.

1.2 Periodic table — blanks filled

> ***Atomic number:*** *number of* ***PROTONS****.* ***Atomic mass:*** *number of* ***PROTONS*** *plus* ***NEUTRONS****, averaged over all isotopes. Elements in the same* ***GROUP/VERTICAL*** *column have the same number of* ***VALENCE*** *electrons. Elements in the same* ***PERIOD/HORIZONTAL*** *row have the same total number of* ***ELECTRON*** *shells.*
>
> ***NICHE:*** *atomic mass is a weighted average over isotopes, which is why it isn't a whole number. Isotopes have the same number of protons (same element, same chemical behavior) but different numbers of neutrons. Same group = same valence electrons =* ***similar chemical behavior*** *— this is the basis of the silicon question in Topic 3.*

1.3 Types of bonds — blanks filled

> *Elements want to be* ***STABLE****. They achieve this by forming chemical* ***BONDS*** *with other elements.* ***Octet rule:*** *elements will gain, lose, or share electrons to complete their* ***VALENCE*** *shell and become* ***STABLE*** *(like noble gases).* ***Valence shell:*** *outermost layer of electrons in an atom.* ***Chemical bonds:*** *an attraction between two atoms, resulting from the* ***SHARING*** *or* ***TRANSFERRING*** *of valence electrons.* ***Electronegativity:*** *the measure of an atom's ability to* ***ATTRACT*** *electrons to itself. Electronegativity* ***INCREASES*** *across a period (left → right) and* ***DECREASES*** *down a group.*

The bond types

Bond	What happens	Strength	Example
Nonpolar covalent	Electrons shared **EQUALLY** between two atoms	Strong	O_2, CH_4, C–C, C–H
Polar covalent	Electrons **NOT** shared equally; the more electronegative atom pulls them closer	Strong	H_2O, N–H, O–H
Ionic	**Complete transfer** of electrons from one atom to another, forming **IONS**; attraction between **OPPOSITELY** charged atoms	Strong (weak in water)	NaCl, LiF
Hydrogen	Attraction between a partially positive H (already in a polar covalent bond) and an electronegative atom in another molecule	**Weak individually**, strong collectively	Between H_2O molecules; between DNA bases

> ***Covalent bonds:*** *when two or more atoms* ***SHARE*** *electrons (usually between two nonmetals). Forms molecules and compounds. - Single bond:* ***1*** *pair of shared electrons - Double bond:* ***2*** *pairs of shared electrons - Triple bond:* ***3*** *pairs of shared electrons*
>
> ***Ionic bonds:*** *usually between a* ***METAL*** *and* ***NONMETAL*** *(****METAL*** *transfers electrons to* ***NONMETAL****). Forms* ***IONIC*** *compounds and* ***SALTS****. -* ***Cation: POSITIVELY*** *charged ion (lost electrons — think "****cat****ion is* ***paw****sitive") -* ***Anion: NEGATIVELY*** *charged ion (gained electrons)*
>
> ***Hydrogen bonds:*** *the partially positive hydrogen atom in* ***ONE*** *polar covalent molecule will be* ***ATTRACTED*** *to an electronegative atom in* ***ANOTHER*** *polar covalent molecule.* ***Intermolecular bond:*** *bond that forms* ***BETWEEN*** *molecules. When a hydrogen atom is bonded to an electronegative atom (usually* ***O, N, or F****) the electrons are* ***NOT*** *being shared* ***EQUALLY*** *between atoms. This causes the hydrogen to have a partial* ***POSITIVE*** *charge and the electronegative atom to have a partial* ***NEGATIVE*** *charge. Water molecules move a lot — hydrogen bonds form, break, and re-form with great frequency.*

Review Q5 — how are hydrogen bonds different from other bonds? Hydrogen bonds are **intermolecular** (between molecules) rather than intramolecular (within a molecule). They involve an **attraction between partial charges**, not a sharing or transfer of electrons. They are **much weaker individually** — roughly 1/20th the strength of a covalent bond — but there are so many of them that collectively they're strong enough to hold DNA's two strands together and give water all its unusual properties. Because they're weak, they **break and re-form constantly**, which is essential: DNA must be able to unzip, and proteins must be able to fold and unfold.

Review Q6 — draw water molecules and label the bonds: within each molecule, the O–H bonds are **polar covalent**. Between molecules, the dotted lines from a hydrogen of one molecule to the oxygen of another are **hydrogen bonds**. Label oxygen $\delta-$ and each hydrogen $\delta+$.

Review Q7 — how does electronegativity affect interactions between water molecules? Oxygen is far more electronegative than hydrogen (3.44 vs 2.20), so it pulls the shared electrons closer to itself. This creates a **partial negative charge on oxygen and partial positive charges on the hydrogens** — the molecule is polar. Those partial charges are what allow hydrogen bonding between adjacent water molecules, and every property of water follows from that.

Review Q8 — what if O and H had the same electronegativity? Electrons would be shared **equally**, making water **nonpolar**. With no partial charges, there would be **no hydrogen bonding**. Water would lose cohesion, adhesion, surface tension, high specific heat, high heat of vaporization, its ability to dissolve polar and ionic substances, and the crystalline structure that makes ice float. It would behave like a small nonpolar molecule — a **gas at room temperature**, and life as we know it would be impossible.

> ***NICHE:*** *compare H_2O (18 g/mol, liquid at room temp, boils at 100°C) to H_2S (34 g/mol, gas at room temp, boils at −60°C). The heavier molecule boils at a much lower temperature. Sulfur isn't electronegative enough to make strong hydrogen bonds. This comparison is the cleanest possible evidence that hydrogen bonding, not molecular size, is responsible for water's behavior.*

1.4 The eight properties of water — blanks filled

1. Polarity

> ***POLAR COVALENT*** *bonds created by unequal sharing of electrons between oxygen and hydrogen* ***POLARIZE*** *the molecule of water.*

The molecule is **bent** (~104.5°), which matters: if it were linear, the two O–H dipoles would cancel and water would be nonpolar overall despite having polar bonds. The bent shape means the dipoles add rather than cancel.

2. Cohesion

> ***ATTRACTION*** *of molecules for other molecules of the* ***SAME*** *kind (H_2O to H_2O).* ***HYDROGEN*** *bonds between H_2O molecules hold them together and* ***CREATE/PRODUCE*** *cohesive forces. Allows for the transport of water and nutrients* ***UP/UPWARD*** *in plants (in the xylem). Responsible for* ***SURFACE TENSION*** *— surface H_2O molecules experience greater* ***DOWNWARD/INWARD*** *pull because there are no molecules above them to balance the forces.*

3. Adhesion

> *The attraction to* ***OTHER*** *molecules that are* ***POLAR*** *or have charge (H_2O to other molecules). Due to the* ***POLARITY*** *of H_2O. In plants, this allows water to cling to the* ***XYLEM*** *walls to resist the downward pull of gravity.*

Cohesion vs adhesion memory hook: cohesion = **co**mpanions of the same kind (water to water). **Ad**hesion = **ad**heres to something else (water to xylem, water to glass).

4. Capillary action

> *The* ***UPWARD*** *movement of water due to the forces of cohesion, adhesion, and surface tension. Occurs when* ***ADHESION*** *is greater than* ***COHESION****. Important for transport of water and nutrients in plants.*
>
> ***NICHE — the mercury question (Station 4, Q5):*** *water forms a* ***concave*** *meniscus (curves up at the edges) because water's* ***adhesion to glass exceeds its cohesion****, so it climbs the tube. Mercury forms a* ***convex*** *meniscus (bulges up in the middle) because mercury's* ***cohesion between mercury atoms far exceeds its adhesion to glass*** *— mercury atoms are held by metallic bonding and are far more attracted to each other than to the polar glass surface, so mercury is pushed down and away from the walls. This is "capillary repulsion."*

5. Temperature control

> ***High specific heat:*** *H_2O resists* ***CHANGES*** *in temperature. How?* ***HYDROGEN BONDS****. Heat must be* ***ABSORBED*** *to break hydrogen bonds, but heat is* ***RELEASED*** *when hydrogen bonds form. Importance: moderates air temperature (large bodies of water can* ***ABSORB*** *heat in the daytime and* ***RELEASE*** *heat at night), stabilizes ocean temperature (benefits marine life), and organisms can* ***RESIST*** *changes in their own internal temperature.*
>
> ***High heat of vaporization:*** *water requires a large amount of* ***HEAT/ENERGY*** *to evaporate due to strong hydrogen bonds.* ***Evaporative cooling:*** *as water molecules evaporate, the surface they evaporate from gets* ***COOLER****. Importance: moderates Earth's* ***CLIMATE****, stabilizes* ***TEMPERATURE*** *in lakes and ponds, prevents terrestrial organisms from* ***OVERHEATING*** *(sweating in humans), prevents leaves from becoming too* ***HOT/WARM*** *in the sun.*
>
> ***NICHE:*** *specific heat of water =* ***1 calorie per gram per °C****, the highest of any common substance. Heat of vaporization ≈* ***586 cal/g****. The mechanism of evaporative cooling is that the* ***highest-energy (fastest-moving) molecules escape first****, so the average kinetic energy of what remains drops — and temperature is average kinetic energy. That's why sweating cools you: not the water sitting on your skin, but the departure of the hottest molecules.*

6. Density (floating ice)

> *As water solidifies it* ***EXPANDS*** *and becomes less* ***DENSE****. Due to the* ***HYDROGEN*** *bonds. When cooled, H_2O molecules move too* ***SLOWLY*** *to* ***BREAK*** *the bonds. Hydrogen bonds cause water molecules to form a* ***CRYSTALLINE/LATTICE*** *structure. Allows marine life to survive under floating ice sheets.*

Think, Pair, Share — how many hydrogen bonds can one water molecule make in ice? Four. Each water molecule has two hydrogens (each donating one H-bond) and two lone pairs on oxygen (each accepting one H-bond). In the ice lattice all four are engaged simultaneously, locking molecules at fixed distances in a hexagonal arrangement. In liquid water each molecule averages only ~3.4 H-bonds at any instant, and they're constantly breaking and re-forming — which is why liquid water molecules can pack *closer together* than ice molecules.

> ***NICHE:*** *ice is about* ***9% less dense*** *than liquid water. Water reaches its* ***maximum density at 4°C****, not 0°C — which is why deep lake water sits at 4°C and lakes freeze from the top down. If ice sank, bodies of water would freeze solid from the bottom up, killing aquatic ecosystems and, since ice reflects sunlight while water absorbs it, the planet's climate would be dramatically colder.*

7. Solvent

> ***DISSOLVING*** *agent in a solution. Water is a versatile solvent — its polar molecules are attracted to ions and other polar molecules it can form* ***HYDROGEN*** *bonds with.* ***Solution:*** *homogeneous mix of* ***TWO*** *substances.* ***Solvent:*** *dissolving agent in a solution.* ***Solute: SUBSTANCE*** *that is dissolved. Remember: "****LIKE*** *dissolves* ***LIKE****." Water can interact with sugars or proteins containing many oxygen and hydrogen — water will form* ***HYDROGEN*** *bonds with the sugar or protein to* ***DISSOLVE*** *it. For ionic compounds: the partially* ***NEGATIVE*** *oxygen in water will interact with a* ***POSITIVE*** *atom; the partially positive hydrogen will interact with a negative atom,* ***SEPARATING/DISSOCIATING*** *the ions.*

Review Q2 — differentiate solute, solvent, solution: the **solute** is what gets dissolved (salt), the **solvent** is what does the dissolving (water), and the **solution** is the resulting homogeneous mixture (saltwater).

> ***NICHE:*** *the shell of water molecules surrounding a dissolved ion is called a* ***hydration shell*** *(or solvation shell). Water is called the "universal solvent" for* ***polar and ionic substances only*** *— it will not dissolve nonpolar substances like oils, which is precisely why lipid membranes work as barriers and why phospholipid bilayers self-assemble.*

8. pH and buffering

> ***pH:*** *a measure of how* ***ACIDIC*** *or* ***BASIC*** *(alkaline) a solution is.* ***Acid:*** *substance that releases* ***HYDROGEN*** *ions (H^+) when dissolved in water.* ***Base:*** *a substance that accepts H^+ OR releases* ***HYDROXIDE*** *ions (OH^-). Water can dissociate into hydrogen (H^+) and hydroxide ions (OH^-).* ***Buffer:*** *a solution that resists* ***CHANGES*** *in pH when an acid or base is added. Buffers help maintain pH stability in biological systems.*
>
> ***NICHE:*** *the pH scale is* ***logarithmic*** *— each whole unit is a* ***10-fold*** *change in H^+ concentration. pH 4 is 10× more acidic than pH 5 and* ***100×*** *more acidic than pH 6. Neutral is pH 7 (equal H^+ and OH^-). Below 7 = acidic, above 7 = basic. Human blood is buffered at* ***7.35–7.45*** *by the carbonic acid–bicarbonate system ($H_2CO_3 \rightleftharpoons H^+ + HCO_3^-$), which absorbs excess H^+ or releases it as needed. Small pH deviations denature proteins by disrupting the ionic interactions between R groups — which is why buffering is a survival requirement, not a convenience.*

1.5 Topic 1 vocabulary

Term	Definition	Why it matters / nuance
Matter	Anything with mass that takes up space	The broadest category; everything below is a subset
Element	Substance that can't be broken down chemically	92 natural; only ~25 are essential to life
Compound	Two or more different elements in a fixed ratio	H_2O is a compound; O_2 is a molecule but *not* a compound (one element)
Electronegativity	An atom's pull on shared electrons	The single value that determines whether a bond is nonpolar, polar, or ionic
Atomic number	Number of protons	Defines the element; never changes
Atomic mass	Protons + neutrons, averaged over isotopes	Not a whole number *because* it's an isotope average
Octet rule	Atoms gain/lose/share to fill the valence shell	Explains *why* bonds form at all — the drive toward stability
Chemical bond	Attraction from sharing or transferring valence electrons	Umbrella term; covalent, ionic, and hydrogen are the subtypes
Covalent bond	Electrons shared	Strong; forms the backbone of all organic molecules
Nonpolar covalent	Shared **equally**	C–C and C–H are the key biological examples — the reason lipids are hydrophobic
Polar covalent	Shared **unequally**, creating partial charges	The origin of every water property
Ionic bond	Electrons transferred; opposite charges attract	Strong when dry, **weak in aqueous solution** — a detail that matters for protein tertiary structure

		protein tertiary structure
Hydrogen bond	Attraction between δ+ H and an electronegative atom (O, N, F)	Weak individually, decisive collectively
Adhesion	Water sticking to **other** substances	Requires the other surface to be polar or charged
Cohesion	Water sticking to **itself**	Produces surface tension
Capillary action	Upward water movement	Requires adhesion > cohesion
Surface tension	Resistance of a liquid surface to being broken	Caused by unbalanced cohesive forces at the surface
Solvent	The dissolving agent	Water is the biological solvent
Solute	The substance dissolved	
Solution	Homogeneous mixture of solvent + solute	"Homogeneous" is the operative word — uniform throughout
pH	Measure of H^+ concentration	**Logarithmic** — the most common student error is treating it as linear
Buffer	Resists pH change	Works by absorbing or donating H^+
Specific heat	Energy to raise 1 g by 1°C	Water's is the highest of common substances — 1 cal/g°C
Heat of vaporization	Energy to convert liquid to gas	Enables evaporative cooling

1.6 Concept Check answers (workbook p. 43)

1. What happens if you mix potassium chloride (KCl) with water? KCl **dissolves and dissociates** into K^+ and Cl^- ions. Water is polar: the partially negative **oxygen** ends orient toward and surround the **K^+** cations, while the partially positive **hydrogen** ends orient toward and surround the **Cl^-** anions. These hydration shells overcome the ionic attraction holding the crystal together, separating the ions and dispersing them evenly through the solution. Diagram: draw KCl crystal with water molecules oriented O-toward-K^+ and H-toward-Cl^-.

2. One property of water that makes the environment suitable for marine life: Several work — pick one and explain the mechanism: - **High specific heat** — oceans resist rapid temperature change, so marine organisms live in a thermally stable environment and don't have to tolerate wide swings. - **Lower density of ice** — ice floats and insulates the water below, so bodies of water don't freeze solid and organisms survive winter beneath the ice sheet. - **Solvent properties** — dissolved oxygen and nutrients are available to aquatic organisms.

3. Predict one disruption if ice were MORE dense than water: Ice would **sink**. Lakes and oceans would freeze **from the bottom up** and could freeze solid, killing fish, plants, and microorganisms with no liquid refuge. There would be no insulating surface layer, so freezing would accelerate. Globally, less ice at the surface means less sunlight reflected and more absorbed, disrupting climate regulation, ocean currents, and the entire aquatic food web.

1.7 Properties of Water Stations Lab — answers

Station 1 (Polarity): Water's polarity comes from **unequal sharing of electrons** in the O–H polar covalent bonds plus the molecule's **bent shape**, giving oxygen a δ− and hydrogens δ+. When the plastic rod is rubbed with cloth, electrons transfer: the rod becomes **negatively charged** and the cloth **positively charged** (or vice versa depending on materials). The stream of water **bends toward the charged rod** because water molecules **rotate to orient their oppositely charged end toward the rod** and are then attracted to it. Draw water molecules with their δ+ hydrogens pointing toward a negatively charged rod.

Station 2 (Surface Tension): Adding soap **decreases** surface tension. Soap is a **surfactant** — its molecules have a polar/hydrophilic head and nonpolar/hydrophobic tail. They insert between water molecules at the surface, **disrupting the hydrogen bonding network** that produces surface tension. Result: fewer drops fit on the coin surface before the water breaks and runs off.

Station 3 (Adhesion vs Cohesion): Venn diagram — *both*: caused by hydrogen bonding, both result from water's polarity, both contribute to capillary action and water transport in plants. *Cohesion only*: water to water, same substance, produces surface tension. *Adhesion only*: water to a different substance, requires the other surface to be polar/charged. **What allows for both: hydrogen bonding, which is possible because of water's polarity.** Top-layer water molecules differ from middle-layer molecules because they have **no water molecules above them**, so cohesive forces pull only sideways and downward — creating a net inward pull and thus **surface tension**, a "skin" on the surface.

Station 5 (Solvent): Water is a "universal solvent" for **polar and ionic** substances because its polarity lets it surround and separate charged particles. Kidneys **filter blood, removing metabolic wastes (urea) and excess ions and water**, producing urine while reabsorbing what the body needs. The circulatory system delivers blood to the kidneys for filtration and carries the cleaned blood away — the two systems together maintain fluid, electrolyte, and pH **homeostasis**. Water is essential because wastes must be **dissolved** to be filtered and excreted. Long-term dehydration concentrates solutes, raising the risk of **kidney stones** and reducing filtration capacity, potentially causing chronic kidney damage.

Station 6 (Temperature Control and Density): The foil represents **sea ice** — a reflective surface. The bin **without** foil should warm faster because dark water **absorbs** more solar radiation, while foil **reflects** it (this is **albedo**). Ice floats because hydrogen bonds lock molecules into an open **crystalline lattice** holding them farther apart than in liquid water, making ice less dense. Sea ice benefits marine life by **insulating the water below** (preserving liquid habitat) and providing habitat for seals and polar bears. Globally, sea ice reflects sunlight and helps regulate Earth's temperature — as sea ice melts, darker ocean absorbs more heat, causing more melting (a **positive feedback loop**).

TOPIC 2 — Elements of Life (Carbon)

Learning Objective 1.2.A: Describe the composition of macromolecules required by living organisms.

Essential Knowledge 1.2.A.1: Atoms and molecules from the environment are necessary to build new molecules. **Carbon, hydrogen, and oxygen** are the most prevalent elements used to build biological molecules. Additionally: **sulfur** is used in the building of proteins; **phosphorus** is used in the building of phospholipids and nucleic acids; **nitrogen** is used in the building of nucleic acids (and proteins).

2.1 Carbon — blanks filled

> ***Organic chemistry:*** *the study of compounds with covalently bonded* ***CARBON***. ***Organic compounds:*** *compounds that contain* ***CARBON*** *and* ***HYDROGEN***. *Carbon has* ***4*** *valence electrons. Carbon can form* ***SINGLE***, ***DOUBLE***, *or* ***TRIPLE*** *covalent bonds. A single carbon can form up to* ***4*** *covalent bonds. Can form LONG chains. Most commonly formed with* ***HYDROGEN***, ***OXYGEN***, *and* ***NITROGEN***. *The type and number of covalent bonds carbon forms affects the* ***SHAPE/STRUCTURE*** *of the carbon chain and* ***FUNCTION/PROPERTIES*** *of the molecule.*
>
> *Carbon can use its* ***VALENCE*** *electrons to form* ***COVALENT*** *bonds to other carbons. This links the carbons into a* ***CHAIN***. ***Hydrocarbons:*** *organic molecules consisting only of* ***CARBON*** *and* ***HYDROGEN***. *Carbon chains form the* ***SKELETON/BACKBONE*** *of most organic molecules. Skeletons vary in length, branching, double bond position, and presence of rings. Many regions of a cell's organic molecules contain* ***HYDROCARBONS***.

Review Q2 — what makes carbon such a versatile element? Carbon has **four valence electrons**, so it needs four more to complete its octet. This means it forms **four covalent bonds** — the maximum for a small atom — and can bond to up to four different partners simultaneously. It can bond to **other carbons**, forming chains of essentially unlimited length, and can form single, double, or triple bonds. The result is enormous structural diversity: straight chains, branched chains, and rings, all with different arrangements of double bonds and attached groups. No other element combines this bonding capacity with this stability at biological temperatures.

Concept Check Q3 (Topic 3, p. 53) — silicon: Silicon sits **directly below carbon in group 14**, so it also has **four valence electrons** and can form four covalent bonds. This is why silicon-based life is a science-fiction staple. But silicon atoms are **larger**, so Si–Si bonds are weaker and less stable than C–C bonds, and silicon doesn't readily form stable double bonds or long chains. Silicon-oxygen compounds (like SiO_2, sand) are extremely stable solids rather than the flexible, reactive molecules life requires. So silicon *could* theoretically serve a similar role, but carbon does it far better.

2.2 Functional groups — blanks filled

> ***Functional groups:*** ***CHEMICAL*** *groups attached to the carbon skeleton that participate in chemical* ***REACTIONS***.

Review Q1 — draw the chemical formula for these functional groups. The workbook names five; here are all seven AP Biology expects:

Functional group	Formula	Found in	Properties
Hydroxyl	**—OH**	Alcohols, carbohydrates	Polar, hydrophilic; forms hydrogen bonds
Carbonyl	**>C=O**	Sugars (aldehydes and ketones)	Polar. **Aldehyde** if at the *end* of the chain; **ketone** if in the *middle*
Carboxyl	**—COOH**	Amino acids, fatty acids	**Acidic** — donates H^+, becomes $—COO^-$. Polar
Amino	**—NH_2**	Amino acids, nitrogenous bases	**Basic** — accepts H^+, becomes $—NH_3^+$. Polar
Sulfhydryl	**—SH**	Cysteine (amino acid)	Forms **disulfide bridges** — critical for protein tertiary structure
Phosphate	**—OPO_3^{2-}**	ATP, DNA/RNA, phospholipids	Negatively charged; **energy transfer**
Methyl	**—CH_3**	DNA methylation, lipids	**Nonpolar**; involved in gene expression regulation

Review Q3 — how do functional groups affect the structure and behavior of organic molecules? Hydrocarbon skeletons are **nonpolar and chemically unreactive**. Functional groups are where the chemistry happens: they determine whether a molecule is polar or nonpolar, acidic or basic, hydrophilic or hydrophobic, and which reactions it can participate in.

Two molecules with identical carbon skeletons but different functional groups behave completely differently — testosterone and estradiol differ by only a few atoms in their functional groups and produce entirely different physiological effects.

Review Q4 — hydrocarbons vs other organic molecules: Hydrocarbons contain only carbon and hydrogen. Other organic molecules have functional groups attached that contain O, N, P, or S. Because C–H and C–C bonds are nonpolar, hydrocarbons are **hydrophobic and energy-rich** — which is why fatty acid tails (long hydrocarbon chains) are both water-repelling and excellent energy storage.

> ***NICHE:*** *carboxyl and amino groups are the two functional groups on* ***every*** *amino acid, and the peptide bond forms between them. Sulfhydryl appears only in* ***cysteine****, which is why cysteine is the only amino acid that can form disulfide bridges — and why the practice FRQ about sulfhydryl-targeting pesticide points to* ***tertiary*** *structure.*

TOPIC 3 — Introduction to Macromolecules

Learning Objective 1.3.A: Describe the chemical reactions that build and break biological macromolecules.

Essential Knowledge: - **1.3.A.1 (Hydrolysis):** a chemical reaction involving the **cleaving of covalent bonds**. Breaks molecules into smaller molecules. When water is added to the bond between monomers in a polymer, the bond is broken. The **hydrogen ion from water is added to one monomer and the hydroxyl group of water is added to the other**, completing the reaction. - **1.3.A.2 (Dehydration synthesis):** occurs when two smaller molecules are joined through covalent bonding. A **hydrogen ion is removed from one monomer and a hydroxyl group is removed from the other**, causing the loss of the equivalent of a water molecule and connecting the two remaining monomers. The connection of many monomers is **polymerization**.

3.1 Blanks filled

> *Variations in carbon skeletons allow for **MOLECULAR DIVERSITY**. Carbon can form large molecules known as **MACROMOLECULES**. **Four classes of macromolecules:** 1. Carbohydrates 2. Proteins 3. Nucleic acids 4. Lipids — Lipids do not include true polymers and are **SMALLER** molecules. NOTE: Along with carbon, **NITROGEN** is an important element for building proteins and nucleic acids. **PHOSPHORUS** is important for building nucleic acids and some lipids. **SULFUR** is used in the building of proteins.*
>
> ***Polymers:** chain-like macromolecules of **IDENTICAL** or **SIMILAR** repeating units that are covalently bonded together. **Monomers:** the repeating units that make up **POLYMERS**.*
>
> ***Dehydration reaction: COVALENTLY** bonds two monomers with the **LOSS** of **WATER**. The **OH** of one monomer bonds to the **H** of another monomer forming **H_2O**, which is then released. A + B → AB + H_2O **Polymerization:** the connection of **MANY** monomers.*
>
> ***Hydrolysis: BREAKS** the covalent bonds in a polymer by adding **WATER**. One **H** of the H_2O bonds to one **MONOMER** and the remaining **OH** of the H_2O attaches to the other **MONOMER**. AB + H_2O → A + B*

Review Q1 — differentiate hydrolysis and dehydration:

	Dehydration synthesis	Hydrolysis
Direction	Builds (anabolic)	Breaks (catabolic)
Water	**Released** (produced)	**Consumed** (added)
Bonds	Covalent bond **formed** between monomers	Covalent bond **broken**
Energy	**Requires** energy (endergonic)	**Releases** energy (exergonic)
Example	Glucose + fructose → sucrose + H_2O	Sucrose + H_2O → glucose + fructose

Memory hook: de-**HYDRATION** removes water (like being dehydrated). **HYDRO-lysis** = water (hydro) + splitting (lysis) — water splits the bond.

> ***NICHE:** these reactions require **enzymes** in living systems — they don't happen spontaneously at useful rates. Both are used by **all four** macromolecule classes with different bond names: **glycosidic** linkages (carbohydrates), **peptide** bonds (proteins), **phosphodiester** bonds (nucleic acids), **ester** linkages (fats). Same reaction, four different bond names — and the test will ask you for the specific name.*

3.2 Concept Check answers (workbook p. 53)

1. Amylose starch with 300 glucose monomers — how many water molecules to completely hydrolyze it? 299. A chain of n monomers is held together by $\boldsymbol{n - 1}$ bonds, and each hydrolysis reaction breaks exactly one bond using exactly one water molecule. 300 monomers → 299 glycosidic linkages → **299 H_2O**.

> ***Trap to avoid:** answering 300. The off-by-one is the entire point of the question. Picture 3 beads on a string — 2 connections, not 3.*

2. Properties of carbon that make it essential for life: four valence electrons → forms four covalent bonds; bonds with itself to form long chains and rings; forms single, double, and triple bonds; bonds readily with H, O, N, P, S; the resulting

skeletons vary in length, branching, ring structure, and double-bond position, producing essentially unlimited molecular diversity. Its bonds are strong enough to be stable but not so strong they can't be broken by enzymes.

3. Silicon: see the answer under Topic 2 above.

4. Identify the reaction in the image: if a water molecule is being **released** and two monomers are joining → **dehydration synthesis**. If water is being **added** and a bond is breaking → **hydrolysis**. Justify by pointing to which side of the arrow H_2O appears on and whether the product is larger or smaller than the reactants.

TOPIC 4 — Carbohydrates

Learning Objective 1.4.A: Describe the structure and function of carbohydrates.

Essential Knowledge 1.4.A.1: Monosaccharides (simple sugars) are the monomers for polysaccharides (complex carbohydrates). These monomers are connected by **covalent bonds** to form polymers such as complex carbohydrates, which may be **linear or branched**.

4.1 Blanks filled

> *Carbohydrates include **SUGARS** and **POLYMERS** of sugars. Contain a **CARBONYL** group and many **HYDROXYL** groups. Comprised of **C, H, and O**.*
>
> ***Monosaccharides:** simple **SUGARS**. Molecular formulas with multiples of the unit **CH_2O**. Most common is **GLUCOSE** — nutrients and **FUEL/ENERGY** for cells; used in **CELLULAR RESPIRATION**. Can serve as building blocks for **AMINO** acids, or as **MONOMERS** for di- and polysaccharides.*
>
> ***Disaccharides: TWO** monosaccharides joined by covalent bonds. Most common is **SUCROSE**. Monomers of sucrose: **GLUCOSE** and **FRUCTOSE**. Plants transfer carbohydrates from roots to leaves in the form of sucrose.*
>
> ***Polysaccharides:** polymer with **MANY** sugars joined via **DEHYDRATION** reactions. **Storage polysaccharides:** - Plants store **STARCH** (polymer of glucose monomers) — allows plants to store excess **GLUCOSE/ENERGY** - Animals store **GLYCOGEN** (polymer of glucose) — stored in liver and muscle cells*
>
> ***Structural polysaccharides:** - **CELLULOSE:** tough substance that forms plant cell walls - **CHITIN:** forms exoskeleton of arthropods*

4.2 Practice — worked answers

Practice (p. 54) — unknown monosaccharide with 4 carbons. Monosaccharides follow **$(CH_2O)_n$**. With n = 4: **$C_4H_8O_4$**. A four-carbon sugar is a **tetrose** — the common example is **erythrose**.

(For reference: 3C = triose/glyceraldehyde, 5C = pentose/ribose, 6C = hexose/glucose.)

Practice Problems: Carbohydrates (pp. 55–56)

1. **Elements: C, H, O** — in an approximate 1:2:1 ratio.
2. **Monomers:** monosaccharides. **Polymers:** polysaccharides (disaccharides are two monomers, not true polymers).
3. **Two functional groups: carbonyl** (C=O) and **hydroxyl** (—OH), and there are many hydroxyls.
4. **Monosaccharides in the reaction:** glucose and fructose.
5. **What forms when two monosaccharides bond:** a **disaccharide** — here, **sucrose**.
6. **Glucose + fructose → sucrose:** a **dehydration synthesis (condensation) reaction**. A hydroxyl group is removed from one monosaccharide and a hydrogen from the other; these combine and are released as **water**, and a covalent **glycosidic linkage** forms between the two sugars.
7. **Breaking sucrose apart: hydrolysis**. A water molecule is added across the glycosidic bond — the H attaches to one monosaccharide and the OH to the other, breaking the covalent bond and releasing free glucose and fructose.
8. **Storage polysaccharides:** plants store **starch**; animals store **glycogen**. Both are polymers of glucose.

4.3 The starch vs. cellulose problem — the highest-value content in Topic 4

This is the workbook's own case study and it's the classic AP structure→function question.

> ***Glycosidic linkage:** a covalent bond joining a carbohydrate to another carbohydrate. A **1,4 glycosidic bond** forms between **carbon-1** of one monosaccharide and **carbon-4** of the other.*

Both starch and cellulose are polymers of glucose with 1-4 glycosidic linkages. So how are they different?

> ***Alpha (α) glucose:** hydroxyl group on carbon 1 points **DOWN** (below the ring plane). **Beta (β) glucose:** hydroxyl group on carbon 1 points **UP** (above the ring plane).*

Q9 — structural differences: - **Starch** is made of **α-glucose** monomers. All monomers are oriented the same way, producing a **helical/coiled** chain. - **Cellulose** is made of **β-glucose** monomers. Because of the hydroxyl's position, **every other glucose must flip 180°** for the bond to form. This produces a **straight, unbranched chain**. - Cellulose's straight chains lie parallel and form **hydrogen bonds between adjacent chains**, bundling into rigid **microfibrils**. Starch's helix can't do this.

Q10 — how structure leads to function: - **Starch's** α-linkages and coiled shape make it **compact and easy for enzymes to access and hydrolyze** — ideal for **energy storage** that a plant can retrieve on demand. - **Cellulose's** β-linkages and hydrogen-bonded microfibril bundles make it **extremely strong and rigid** — ideal for the structural support of **plant cell walls**. The β configuration also means **most enzymes cannot bind it**, so it resists degradation and persists as structural material.

The key idea: the *only* difference is the orientation of one hydroxyl group — and it produces two molecules with completely opposite biological roles. Same monomer, same bond position, entirely different function. This is the purest example of structure→function in the unit.

Q11 — why eat cellulose if we can't digest it? Insoluble fiber ("roughage") isn't absorbed, but it **adds bulk to stool**, speeds transit through the digestive tract, promotes regularity, prevents constipation, and supports gut health. It also helps regulate blood sugar by slowing glucose absorption and contributes to feeling full.

4.4 Cellulose Case Study — answers

Background facts the case study gives you (memorize these — case-study details reappear on tests): - Cellulose = thousands of glucose monomers, 1-4 glycosidic linkages, chains held side-by-side by **hydrogen bonds** into tight bundles organized into fibers. - Humans **cannot** digest cellulose — stomach enzymes cannot break the bonds between the glucose monomers. - Cows, horses, goats, sheep, and termites can. - Cows have a **ruminant stomach** with **four chambers**: **rumen, reticulum, omasum, abomasum**. - **Rumen** — largest, holds up to **25 gallons**; contains **billions of bacteria** that begin digestion via **fermentation**. Contracts to push up "**cud**," which the cow chews a second time. Cud chewing is used as a **health indicator** in cattle. - **Reticulum** — pouch-like; processes dense, heavy, hard food objects. - **Omasum** — where **water and nutrients are absorbed**; food leaves denser and drier. - **Abomasum** — the "true stomach"; contains glands releasing **acid**, similar to human stomachs.

Analysis Q1 — what's actually digesting the cellulose? The **symbiotic bacteria (microbes) in the rumen**, not the cow. No animal produces cellulase with its own genome. These bacteria produce the enzyme **cellulase**, which the cow cannot make. This is a **mutualistic symbiosis** — the bacteria get a warm, nutrient-rich habitat; the cow gets access to energy in cellulose it otherwise couldn't use.

Analysis Q2 — propose a model for how they break it down: The bacteria secrete **cellulase**, an enzyme that catalyzes the **hydrolysis** of the **β-1,4 glycosidic bonds** between glucose monomers. **Water** is added across each bond: the H attaches to one glucose and the OH to the other, breaking the covalent linkage. The released glucose is then fermented by the bacteria into short-chain fatty acids the cow absorbs and uses for energy.

Analysis Q3 — missing component in the diagram: water (H_2O) — the required input for any hydrolysis reaction. (An enzyme, cellulase, is also required as a catalyst.)

Analysis Q4 — why antibiotics in cattle feed? Antibiotics kill or inhibit bacteria. Cattle industries use them to **prevent and treat disease** in crowded conditions and to **promote growth** (faster weight gain on less feed).

Analysis Q5 — effect on rumen microbial population? Antibiotics **reduce the rumen microbial population** — they can't distinguish pathogenic bacteria from the beneficial cellulose-digesting symbionts. Fewer microbes means **less cellulase**, so **less cellulose is digested**, reducing the energy the cow extracts from its food and potentially causing digestive problems and poorer nutrition.

Analysis Q6 — pros and cons: *Pros:* prevent/treat disease, reduce livestock mortality, faster growth and lower feed costs, cheaper food, better animal welfare when treating actual infections. *Cons:* kills beneficial rumen bacteria and impairs digestion; drives **antibiotic resistance** through natural selection on bacterial populations; resistant bacteria can transfer to humans through meat or the environment; residues in meat and milk; overuse threatens the effectiveness of antibiotics in human medicine.

Analysis Q7 — should antibiotics be used in farming? Either position is defensible; the rubric wants **a claim plus justification with reasoning**. A strong answer distinguishes **therapeutic use** (treating diagnosed illness — widely defensible) from **subtherapeutic/growth-promotion use** (routine low doses in feed — the main driver of resistance, banned for growth promotion in the EU and restricted in the US).

TOPIC 5 — Lipids

Learning Objective 1.5.A: Describe the structure and function of lipids.

Essential Knowledge: - **1.5.A.1:** Lipids are typically **nonpolar, hydrophobic** molecules whose structure and function derive from how their subcomponents are assembled. Fatty acids are **saturated** or **unsaturated**. - i. **Saturated** fatty acids contain **only single bonds** between carbon atoms. - ii. **Unsaturated** fatty acids contain **at least one double bond**, which causes the carbon chain to **kink**. - iii. The more double bonds, the more unsaturated the lipid. - iv. The more unsaturated a lipid is, the more **liquid** it is at room temperature. - **1.5.A.2:** Examples of lipids: **fats, steroids including cholesterol, and phospholipids**. - i. **Fats** — energy storage, support cell function, insulation to keep mammals warm. - ii. **Steroids** — hormones supporting growth and development, energy metabolism, and homeostasis. - iii. **Cholesterol** — provides essential structural stability to animal cell membranes. - iv. **Phospholipids** — group together to form the lipid bilayers of plasma and cell membranes.

5.1 Blanks filled

> ***Lipids:*** *class of molecules that do* ***NOT*** *include* ***TRUE*** *polymers. Generally* ***SMALLER*** *in size — often not considered to be a macromolecule. Lipids are nonpolar —* ***HYDROPHOBIC****. Types: 1. Fats 2. Phospholipids 3. Steroids 4. Cholesterol*
>
> ***Fats — major functions:*** *provide* ***ENERGY*** *storage, support* ***CELL*** *function, provide* ***INSULATION*** *to keep mammals warm. Fats are composed of* ***GLYCEROL*** *and* ***FATTY ACIDS****. -* ***Glycerol:*** *classified as an* ***ALCOHOL*** *(****HYDROXYL*** *groups) -* ***Fatty acids:*** *long carbon chains (****CARBOXYL*** *group at one end) - 3 fatty acids join to a glycerol via* ***ESTER LINKAGES*** *— a bond between a* ***HYDROXYL*** *and* ***CARBOXYL*** *group -* ***Saturated fatty acid: SINGLE BONDS*** *between carbons in the chain = more* ***HYDROGEN*** *(saturated with hydrogen) -* ***Unsaturated fatty acid:*** *contains one or more* ***DOUBLE*** *bonds. The double bonds cause the fatty tails to form* ***KINKS/BENDS****. The more double bonds, the more* ***LIQUID*** *it is at room temperature.*
>
> ***Phospholipids:*** *major component of cell* ***MEMBRANES****. Two fatty acids attached to a* ***GLYCEROL*** *and a* ***PHOSPHATE GROUP****. Assemble as a bilayer in* H_2O *— tails are* ***HYDROPHOBIC/NONPOLAR****, head is* ***HYDROPHILIC/POLAR****.*
>
> ***Steroids:*** ***HORMONES*** *that support physiological functions like* ***GROWTH*** *and development,* ***ENERGY*** *metabolism, and* ***HOMEOSTASIS****. Have four fused rings. Unique* ***FUNCTIONAL GROUPS*** *attached to the ring determine the type of steroid. Example: testosterone.*
>
> ***Cholesterol:*** *provides structural* ***STABILITY*** *to animal* ***CELL*** *membranes.*

5.2 Review question answers

Review Q1 — draw a phospholipid, label all parts including polar and nonpolar regions: Draw a **glycerol backbone** in the middle. Attached below: **two fatty acid tails** (label **nonpolar / hydrophobic**; draw one straight = saturated, one kinked = unsaturated). Attached above: a **phosphate group** (label **polar / hydrophilic**), often with an additional small polar group (like choline) attached to the phosphate. Label the phosphate end as the **"head"** and the fatty acids as the **"tails."**

Review Q2 — where in a cell, and what role? Phospholipids are found in the **plasma membrane** and all internal membranes (nuclear envelope, ER, Golgi, mitochondria, vesicles). They spontaneously arrange into a **bilayer** with hydrophilic heads facing the aqueous environments inside and outside the cell and hydrophobic tails facing each other in the interior. This forms a **selectively permeable barrier** — small nonpolar molecules pass freely, while polar and charged substances require transport proteins.

Review Q3 — how does saturation affect structure and function? Saturated fatty acids have only single bonds, so their tails are **straight** and pack tightly together, producing strong intermolecular attraction. They are **solid at room temperature** (butter, animal fat). **Unsaturated** fatty acids have double bonds that **kink** the tail, preventing tight packing. Weaker attraction means they are **liquid at room temperature** (olive oil). In membranes, unsaturated tails **increase fluidity** — organisms living in cold environments incorporate more unsaturated phospholipids to keep membranes fluid rather than solidifying.

> ***NICHE:** the kink comes from a **cis double bond**. A **trans double bond** does not kink the chain — trans fats pack like saturated fats and are solid at room temperature. That's why artificial trans fats (from partial hydrogenation) behave like saturated fat in the body and are strongly associated with cardiovascular disease.*
>
> ***NICHE: cholesterol is a "fluidity buffer."** At **high** temperatures it **restrains** phospholipid movement, reducing fluidity; at **low** temperatures it **wedges between** phospholipids and prevents them from packing tightly, preventing solidification. Both directions, same molecule. This is Unit 2 content that gets seeded here.*
>
> ***NICHE:** fats store roughly **twice** the energy per gram as carbohydrates (~9 kcal/g vs ~4 kcal/g), because their hydrocarbon chains are highly reduced — full of C–H bonds and low in oxygen — so oxidizing them releases more energy. This is why fat, not glycogen, is the body's long-term energy store.*
>
> ***Trap to avoid:** calling lipids "polymers" or saying their monomer is "fatty acids." Lipids are **not true polymers** — a triglyceride is three fatty acids and a glycerol, not repeating identical units, and it's assembled in one step rather than by extension. The workbook says this explicitly and it's a common test question. Fats are built by dehydration synthesis, though — that part still applies.*

5.3 Topic 5 vocabulary

Term	Definition	Nuance
Lipid	Nonpolar, hydrophobic biological molecule	**Not a true polymer** — the exception among the four classes
Fat (triglyceride)	Glycerol + 3 fatty acids	Joined by **ester linkages** via dehydration
Fatty acid	Long hydrocarbon chain with a carboxyl group at one end	The carboxyl is the only polar part; the tail is nonpolar
Glycerol	3-carbon alcohol with 3 hydroxyl groups	The three OH groups are what allow three fatty acids to attach
Saturated	Only single C–C bonds	"Saturated with hydrogen" — maximum H possible. Straight, packs tightly, solid
Unsaturated	≥1 C=C double bond	Kinked, packs loosely, liquid. More double bonds = more liquid
Phospholipid	Glycerol + 2 fatty acids + phosphate	**Amphipathic** — both hydrophilic and hydrophobic in one molecule
Steroid	Four fused carbon rings	Attached functional groups determine which steroid it is
Cholesterol	Steroid in animal membranes	Provides structural stability; buffers membrane fluidity
Hydrophobic	"Water-fearing" — nonpolar, doesn't dissolve in water	Not repelled by water so much as excluded by water's preference for itself
Amphipathic	Has both polar and nonpolar regions	Why phospholipids self-assemble into bilayers

TOPIC 6 — Nucleic Acids

Learning Objective 1.6.A: Describe the structure and function of DNA and RNA.

Essential Knowledge: - **1.6.A.1:** In nucleic acids, biological information is encoded in sequences of **nucleotide monomers**. Each nucleotide has: a **five-carbon sugar** (deoxyribose or ribose), a **phosphate**, and a **nitrogenous base** (adenine, thymine, guanine, cytosine, or uracil). - **1.6.A.2:** Nucleic acids have a linear sequence of nucleotides with ends defined by the **3′ hydroxyl** and **5′ phosphate** of the sugar. During synthesis, nucleotides are **added to the 3′ end** of the growing strand, forming covalent bonds between nucleotides. - **1.6.A.3:** DNA is an **antiparallel double helix**, two strands running in opposite 5′→3′ orientation. **A–T** via hydrogen bonds, **C–G** via hydrogen bonds. In RNA, **A–U**. - **1.6.A.4:** Structural differences: DNA has **deoxyribose**, RNA has **ribose**; DNA has **thymine**, RNA has **uracil**; DNA is typically **double stranded**, RNA typically **single stranded**.

6.1 Blanks filled

> ***Nucleic acids:*** *polymers made of* ***NUCLEOTIDE*** *monomers. Function to* ***STORE, TRANSMIT, and EXPRESS GENETIC*** *information. Two forms:* ***1. DNA (deoxyribonucleic acid) 2. RNA (ribonucleic acid)***
>
> ***Nucleotides contain 3 parts:*** *1.* ***NITROGENOUS*** *base 2. Five carbon* ***SUGAR*** *(pentose) 3.* ***PHOSPHATE*** *group(s)*
>
> *In polynucleotides each monomer only has* ***ONE*** *phosphate group.*
>
> ***Nitrogenous bases — two types: PYRIMIDINES and PURINES.*** *-* ***Pyrimidines: ONE*** *ring with* ***6*** *atoms →* ***Cytosine, Thymine, Uracil*** *-* ***Purines: ONE*** *ring with* ***6*** *atoms bonded to* ***ANOTHER*** *ring with* ***5*** *atoms →* ***Adenine, Guanine***
>
> ***Five carbon sugar:*** *in DNA the sugar is* ***DEOXYRIBOSE****; in RNA the sugar is* ***RIBOSE****.* ***Phosphate group:*** *a* ***PHOSPHATE*** *group is added to the* ***5′*** *carbon of the sugar to form a* ***NUCLEOTIDE****.* ***Nucleoside*** *= the portion* ***without*** *the phosphate group (base + sugar only).*
>
> ***Polynucleotides: PHOSPHATE*** *groups link adjacent* ***NUCLEOTIDES*** *via* ***phosphodiester linkages****. Directionality:* ***5′ to 3′****. The sequence of bases along the DNA or mRNA is* ***UNIQUE*** *for each* ***GENE****. → Dictates* ***AMINO ACID (AA)*** *sequence → dictates* ***PRIMARY*** *structure of a protein → dictates* ***3D*** *structure of a protein.*
>
> ***DNA:*** *consists of two polynucleotides forming a double helix. Strands are* ***ANTIPARALLEL****, held together by* ***HYDROGEN*** *bonds between bases. Cytosine binds to* ***GUANINE****; adenine binds to* ***THYMINE****.* ***RNA: SINGLE*** *stranded polynucleotide, variable in shape due to base pairing within RNA. Adenine bonds to* ***URACIL****; cytosine bonds to guanine.*

6.2 Memory hooks

- **Pure As Gold** — **PUR**ines are **A**denine and **G**uanine (two rings)
- **CUT the PY** — **C**ytosine, **U**racil, **T**hymine are **PY**rimidines (one ring)
- **Purines are bigger but have shorter names; pyrimidines are smaller but have longer names.** (Counterintuitive, which is why it sticks.)
- A **purine always pairs with a pyrimidine** — one big + one small keeps the helix a **constant width** (~2 nm). Two purines would bulge; two pyrimidines would pinch.

6.3 Review question answers

Q1 — what forms the "backbone" of DNA? Alternating **sugar (deoxyribose) and phosphate** groups, joined by **phosphodiester bonds**. The nitrogenous bases project inward from the backbone.

Q2 — what does antiparallel mean? The two strands run in **opposite directions** — one runs 5′→3′ while the complementary strand runs 3′→5′ alongside it.

Q3 — why can't both strands run in the same direction? Two reasons, and a full-credit answer gives both: 1. **Structural:** the bases can only form correct hydrogen bonds when the strands are oriented oppositely. Parallel strands would not allow A–T and G–C pairs to align geometrically. 2. **Functional: DNA polymerase can only add nucleotides to the 3′ end** of a growing strand — it synthesizes exclusively 5′→3′. Antiparallel orientation is what makes complementary replication possible, and it's why replication produces a leading and lagging strand (Unit 6).

Q4 — three components of a nucleotide: nitrogenous base, five-carbon (pentose) sugar, phosphate group.

Q5 — the monomer without a phosphate group: a **nucleoside**.

Q6 — possible nitrogenous bases: adenine, guanine, cytosine, thymine (DNA only), uracil (RNA only).

Q7 — compare and contrast DNA and RNA:

	DNA	RNA
Sugar	**Deoxyribose** (no OH on 2′ carbon)	**Ribose** (OH on 2′ carbon)
Bases	A, T, G, C	A, **U**, G, C
Strands	Double-stranded helix	Usually single-stranded
Stability	More stable	Less stable (that 2′ OH makes it reactive)
Location	Nucleus, mitochondria, chloroplasts	Made in nucleus, functions mostly in cytoplasm
Function	Long-term storage of genetic information	Transfers and expresses information; some types catalyze
Both	Polymers of nucleotides; phosphodiester backbone; 5′→3′ directionality; contain C, H, O, N, P	

Q8 — where is DNA found? RNA? DNA: the **nucleus** (in eukaryotes), plus **mitochondria** and **chloroplasts**. In prokaryotes, the nucleoid region and plasmids. **RNA:** transcribed in the **nucleus**, then functions primarily in the **cytoplasm** (mRNA at ribosomes, tRNA in cytoplasm, rRNA within ribosomes). Also present in the nucleolus where ribosomes are assembled.

Q9 — what functional group defines the 5′ end? The **phosphate group** attached to the 5′ carbon. **Q10 — the 3′ end?** The **hydroxyl (—OH)** group on the 3′ carbon.

Q11 — how many bonds connect A–T vs C–G? A–T: 2 hydrogen bonds. C–G: 3 hydrogen bonds.

> ***Memory hook:*** *count the letters in the shape of the letters, or just remember* ***G and C are the "stronger" pair*** *— and both have curves. Alternatively:* ***"C" and "G" both have 3 in them*** *if you count strokes. Whatever works — just know 2 vs 3, because it drives the denaturation question.*

6.4 Practice — worked answers

Practice (p. 65) — complementary strand of 5′-CATGTCAAC-3′

Pair each base (A↔T, C↔G) and reverse direction: 5′ - C A T G T C A A C - 3′ 3′ - G T A C A G T T G - 5′ Written conventionally **5′→3′**, the complementary strand is: **5′-GTTGACATG-3′**

> ***Trap to avoid:*** *writing 3′-GTACAGTTG-5′ and stopping. That's correct but not in conventional notation. Always report a sequence* ***5′→3′*** *unless told otherwise — reverse the string, then relabel the ends.*

Practice Problems: Nucleic Acids (pp. 66–67)

1. **Elements: C, H, O, N, P** — phosphorus is the distinguishing one.
2. **Monomers:** nucleotides.
3. Base = the ring structure (top), sugar = the pentose ring (middle), phosphate = the group with P and O (left/bottom).
4. **Deoxyribose or ribose?** Look at the **2′ carbon**: if there's an **—H**, it's deoxyribose (DNA); if there's an **—OH**, it's ribose (RNA). "Deoxy" literally means "missing an oxygen."
5. **Pyrimidine or purine?** Count the rings: **one ring = pyrimidine** (C, T, U); **two fused rings = purine** (A, G).
6. **Directionality** refers to the fact that a polynucleotide has two chemically distinct ends: a **5′ end with a free phosphate** and a **3′ end with a free hydroxyl**. The strand is read and synthesized in a specific direction, 5′→3′.
7. Label the end with the free phosphate **5′**, the end with the free —OH **3′**.
8. **Reaction to bond nucleotides: dehydration synthesis (condensation).** The phosphate on the 5′ carbon of the incoming nucleotide bonds to the hydroxyl on the 3′ carbon of the last nucleotide in the chain, releasing a **water molecule** and forming a covalent bond.
9. **Bond name: phosphodiester bond** (phosphodiester linkage). Label the sugar–phosphate–sugar connections.
10. **Nucleotides are added to the 3′ end.** Draw the new nucleotide attaching its 5′ phosphate to the existing 3′ hydroxyl.
11. **Base pairing bond: hydrogen bonds.** C–G forms **three**; A–T forms **two**.

12. **Which pair is more structurally stable? C–G**, because three hydrogen bonds hold it together instead of two — more total attraction means more energy is required to separate them.

Q13–14 — the DNA denaturation experiment (this is the payoff question): Both molecules have 40 base pairs, but one is all A–T and the other all C–G. The **AT-only DNA denatures at a lower temperature**; the **GC-only DNA requires a higher temperature**.

Explanation: Denaturation is the breaking of **hydrogen bonds** between paired bases. Each **C–G pair has 3 hydrogen bonds** while each **A–T pair has only 2**. With equal base-pair counts, the GC-rich molecule has **50% more hydrogen bonds total** (120 vs 80), so more **thermal energy** is required to disrupt them. This is a direct structure→function relationship: bond number determines thermal stability.

> ***NICHE:*** *this is real and has a name —* ***melting temperature (Tm)****. Organisms living in hot environments (thermophiles in hot springs, deep-sea vents) tend to have* ***GC-rich genomes****, which is an evolutionary adaptation to prevent DNA denaturation at high temperature. It's also why PCR primer design accounts for GC content.*

Q15 — similarities and differences between the two nucleic acids: use the DNA/RNA table in section 6.3.

TOPIC 7 — Proteins

Learning Objective 1.7.A: Describe the structure and function of proteins.

Essential Knowledge: - **1.7.A.1:** Proteins comprise **linear chains of amino acids** connected by covalent (**peptide**) bonds that form between a **carboxyl group (—COOH)** of one amino acid and an **amine group (—NH_2)** of the next. - **1.7.A.2:** Amino acids are composed of a **central carbon** with a **hydrogen**, a **carboxyl group**, an **amine group**, and a **variable R group** covalently bound to it. R groups are categorized as **hydrophobic/nonpolar, hydrophilic/polar, or ionic**. Their interactions determine the structure and function of that region of the protein. - **1.7.A.3:** The specific sequence of amino acids determines the **primary structure** as well as the overall shape. - **1.7.A.4: Secondary** structures form from local folding due to interactions between atoms of the **polypeptide backbone**. **Hydrogen bonding** forms **alpha-helices** and **beta-pleated sheets**. - **1.7.A.5:** The three-dimensional **tertiary** structure results from **hydrogen bonds, hydrophobic interactions, ionic interactions, or disulfide bridges**. - **1.7.A.6: Quaternary** structure arises from interactions between **multiple polypeptides**. All four levels determine function.

7.1 Blanks filled

> ***Protein:*** *molecule consisting of* ***POLYPEPTIDES*** *(polymers of amino acids) folded into a 3D shape. Comprised of* ***C, H, O, N, and S****.* ***STRUCTURE*** *determines* ***FUNCTION****.*
>
> ***Amino acids:*** *molecules that have an* ***AMINO*** *group and a* ***CARBOXYL*** *group. There are* ***20*** *different amino acids. Each amino acid has a unique* ***side chain (R group)****. Side chains can be grouped as: -* ***NONPOLAR*** *(hydrophobic) -* ***POLAR*** *(hydrophilic) -* ***IONIC / CHARGED*** *(acidic/basic — hydrophilic)*
>
> *Side chains* ***INTERACT****, which determine the* ***SHAPE*** *and* ***FUNCTION*** *of the protein.*
>
> ***Peptide bonds:*** *to form a peptide bond, the* ***CARBOXYL*** *group of one AA must be positioned next to the* ***AMINO*** *group of another AA. This is a* ***DEHYDRATION SYNTHESIS*** *reaction.*
>
> ***Polypeptides:*** *many* ***AMINO ACIDS*** *linked by* ***PEPTIDE*** *bonds. Each polypeptide has a* ***UNIQUE*** *sequence of* ***AMINO ACIDS*** *and* ***LENGTH****. Each end is chemically* ***DIFFERENT/DISTINCT****. One end is a free* ***AMINO*** *group (****N-terminus****); one end is a free* ***CARBOXYL*** *group (****C-terminus****). The sequence of* ***AMINO ACIDS*** *determines the* ***3D*** *shape. When a polypeptide twists and folds (because of* ***R*** *group interaction) it forms a* ***PROTEIN****. Remember:* ***STRUCTURE*** *determines* ***FUNCTION****.*

Think, Pair, Share — how is the unique sequence of AAs determined? By the **sequence of nucleotides in the gene** that codes for that polypeptide. DNA is transcribed into mRNA, and mRNA is read in three-base **codons**, each specifying one amino acid. So the DNA base sequence dictates the amino acid sequence, which dictates folding, which dictates shape, which dictates function.

7.2 Functions of proteins — blanks filled

Function	Description
Antibody	Help protect the body from **PATHOGENS/FOREIGN INVADERS**
Enzyme	Carry out chemical **REACTIONS** or assist in creating new molecules
Messenger	Transmit signals (e.g., **HORMONES**)
Structural	Provide structure and support
Transport/storage	Bind to and carry small atoms and molecules through the body

7.3 The four levels of protein structure — the most tested table in the unit

Level	What it is	Held together by
Primary	Linear chain of **AMINO ACIDS**	**Peptide bonds** (covalent)
Secondary	Coils and folds due to **HYDROGEN** bonding within the polypeptide **backbone**	**Hydrogen bonds** — between backbone atoms, **not** R groups
Tertiary	**3D** folding due to interactions between the **SIDE CHAINS (R**	Hydrogen bonds, **HYDROPHOBIC** interactions, **IONIC** bonds,

	GROUPS) of the AAs	**DISULFIDE** bridges
Quaternary	Association of **TWO** or more polypeptides	Same interactions as tertiary, but **between** separate polypeptide chains

More blanks from that table:

> ***Primary:*** *determined via* ***GENES/DNA****. Dictates secondary and tertiary forms.* ***Secondary:*** *-* ***β pleated sheet*** *— hydrogen bonds between polypeptide chains lying* ***SIDE BY SIDE*** *by* ***HYDROGEN BONDS*** *-* ***α helix*** *— hydrogen bonding between every* ***4th*** *amino acid*
>
> ***Tertiary:*** *reinforced by* ***HYDROPHOBIC*** *interactions,* ***IONIC*** *bonds,* ***HYDROGEN*** *interactions, and* ***DISULFIDE*** *bridges of the side chains. A disulfide bridge is the covalent bond formed between* ***SULFUR*** *atoms of two* ***CYSTEINE*** *monomers.* ***Quaternary:*** *found in only some proteins. All four levels of a protein's structure determine the protein's function.*
>
> ***Trap to avoid:*** *the single most common protein error is saying secondary structure involves R groups.* ***It does not.*** *Secondary structure is hydrogen bonding between atoms of the* ***polypeptide backbone*** *(the N–H and C=O of the peptide bonds).* ***R groups are tertiary.*** *If a question mentions side chains, the answer is tertiary or quaternary — never secondary.*
>
> ***NICHE:*** *the* ***disulfide bridge is the only covalent bond*** *in tertiary structure — all the others (hydrogen bonds, ionic bonds, hydrophobic interactions) are weak, non-covalent interactions. It forms between the* ***sulfhydryl (—SH) groups of two cysteine residues****. This is why cysteine is special and why the practice FRQ's sulfhydryl-targeting pesticide affects* ***tertiary*** *structure.*
>
> ***NICHE:*** *in an aqueous cell,* ***nonpolar/hydrophobic R groups fold to the interior*** *of the protein (away from water) while* ***polar and charged R groups face outward*** *(toward water). This is the* ***hydrophobic effect****, and it is the primary driving force of protein folding. Note the inversion for* ***membrane*** *proteins: the region embedded in the lipid bilayer has nonpolar R groups facing outward into the hydrophobic core of the membrane.*

7.4 Review question answers

Q1 — what determines primary structure? The **sequence of amino acids**, which is determined by the **sequence of nucleotides in the gene** (DNA → mRNA → protein).

Q2 — how does primary structure affect the other levels? Primary structure determines everything above it. The identity and order of the amino acids determine which R groups are present and where, which determines which hydrogen bonds, ionic bonds, hydrophobic interactions, and disulfide bridges can form — and therefore how the chain folds into secondary, tertiary, and quaternary structure.

Q3 — would function change if the sequence changed? Usually yes, and sometimes catastrophically — but not always. Changing an amino acid changes an R group, which can alter folding, shape, and therefore function. The magnitude depends on **where** and **what**: a substitution in a critical region (an enzyme's active site, or a residue involved in a disulfide bridge) or a substitution between **chemically dissimilar** R groups (polar → nonpolar) is far more disruptive than a substitution between chemically similar amino acids in a non-critical region, which may have no effect at all.

Q4 — what interactions occur at each level? Secondary: hydrogen bonds within the backbone. Tertiary: hydrogen bonds, hydrophobic interactions, ionic bonds, disulfide bridges — all between R groups. Quaternary: the same interactions, between separate polypeptides.

Q5 — True/false: a change in a protein's structure will change the protein's function. Generally true, and this is the unit's central principle — but with the qualification in Q3: a structural change in a non-critical region may have negligible functional consequence. On a test, "structure determines function" is the expected answer.

Q6 — how many monomers of proteins are there? 20 different amino acids.

Q7 — draw the general structure of an amino acid: H | H_2N — C — COOH | R Central (alpha) carbon bonded to: an **amino group (—NH_2)**, a **carboxyl group (—COOH)**, a **hydrogen atom**, and a **variable R group**.

Q8 — how do R groups contribute to protein structure? They are the source of all tertiary and quaternary interactions. Nonpolar R groups cluster in the protein's interior via hydrophobic interactions; polar R groups form hydrogen bonds; oppositely charged (ionic) R groups form ionic bonds; cysteine's sulfhydryl groups form covalent disulfide bridges. Together these fold the chain into its specific functional shape.

7.5 Practice Problems: Proteins — worked answers (pp. 73–74)

1. **Elements: C, H, O, N, S** — nitrogen (in the amino group) and sulfur (in cysteine/methionine R groups) are the distinguishing ones.
2. **Monomers:** amino acids. **Polymers:** polypeptides.
3. **Why isn't "polypeptide" synonymous with "protein"?** A **polypeptide is a linear chain** of amino acids — primary structure only. A **protein is a folded, functional molecule**. A protein may consist of a single folded polypeptide, or of **multiple polypeptides** joined in quaternary structure (hemoglobin has four). An unfolded polypeptide is not yet a functional protein.
4. Circle the **amino group (—NH_2)** and the **carboxyl group (—COOH)**; box the **R group**.
5. **Three R group classifications: nonpolar/hydrophobic, polar/hydrophilic, and ionic/charged (acidic or basic).** Their chemical properties determine how each region of the chain interacts with water and with other R groups, which drives folding into tertiary structure — and shape determines function.
6. **Which R groups orient outward vs inward? Polar and ionic (hydrophilic)** R groups orient **outward**, toward the aqueous cellular environment, where they can hydrogen-bond with water. **Nonpolar (hydrophobic)** R groups orient **inward**, away from water, clustering in the protein's core. This minimizes the disruption of water's hydrogen bonding network and is the main driving force of folding.
7. **Which pair of amino acids can form a dipeptide?** The pair positioned with the **carboxyl group of one facing the amino group of the other**. The reaction is **dehydration synthesis**: an —OH is removed from the carboxyl and an —H from the amino group, releasing **water** and forming a covalent **peptide bond** between the carbon of the carboxyl and the nitrogen of the amino group.
8. **Directionality in polypeptides:** the chain has a free amino group at one end (**N-terminus**) and a free carboxyl group at the other (**C-terminus**). Polypeptides are synthesized and read **N-terminus → C-terminus**. Label accordingly.
9. **Which substitution has the most significant impact?** Compare the **chemical class** of the original and replacement R group: - (a) Serine (polar) → glutamate (**ionic, negatively charged**) — significant change in class - (b) Alanine (**nonpolar**) → lysine (**ionic, positively charged**) — a drastic change: from hydrophobic to charged - (c) Glycine (nonpolar) → valine (nonpolar) — **same class**, minimal effect

   (b) is the most disruptive. Replacing a small hydrophobic residue with a large positively charged one changes where that region can sit in the folded protein — a residue that was buried in the hydrophobic core would now be forced toward the surface, disrupting tertiary structure and potentially destroying function. The general principle: **the bigger the change in R-group chemistry, the bigger the structural consequence.**
10. **What codes for proteins? Genes** — specific sequences of DNA nucleotides, transcribed to mRNA and translated in codons.
11. **Sickle cell — what happens to the gene? The protein? Gene:** a **single nucleotide substitution** in the hemoglobin-beta gene on chromosome 11 changes one **adenine to thymine** (a point mutation, specifically a missense mutation). **Protein:** the sixth amino acid in the beta-globin polypeptide changes from **glutamic acid (glutamate)** to **valine**.
12. **How can one amino acid substitution cause such a dramatic change?** Glutamate is **polar and negatively charged (hydrophilic)**; valine is **nonpolar (hydrophobic)**. Substituting valine puts a hydrophobic patch on the **surface** of the hemoglobin molecule where a charged residue used to be. Under low-oxygen conditions, these exposed hydrophobic patches on different hemoglobin molecules **stick to each other** (hydrophobic interactions), causing hemoglobin to **polymerize into long, rigid fibers**. Those fibers distort the red blood cell into the characteristic **sickle shape**. The misshapen cells carry oxygen poorly, block capillaries (causing pain and tissue damage), and are destroyed faster than normal cells (causing anemia). **The chain of causation to write on a test:** DNA base change → amino acid change → altered R group chemistry → altered tertiary/quaternary structure → hemoglobin aggregation → cell shape change → impaired oxygen transport and vascular blockage.

Practice Problem — Cystic fibrosis (p. 71): CF results from the **deletion of three nucleotides** in the CFTR gene. Three nucleotides = **one codon** = **one amino acid** (phenylalanine at position 508) is deleted from the CFTR protein.

Full explanation: Because the primary structure (amino acid sequence) has changed, the R group interactions that fold the protein change, so the protein **misfolds** into an incorrect tertiary structure. The misfolded CFTR protein is recognized as defective by the cell and **degraded before reaching the plasma membrane**, so functional chloride channels are missing from the epithelial cell membranes. Without proper Cl^- transport, water movement across the membrane is disrupted, producing **thick, sticky mucus** in the lungs and digestive tract — causing airway obstruction, chronic infection, and blocked pancreatic ducts.

> ***NICHE:*** *deleting **three** nucleotides removes exactly one codon and does **not** shift the reading frame — the rest of the protein is normal. Deleting **one or two** nucleotides would cause a **frameshift mutation**, garbling every codon downstream and typically producing a completely nonfunctional protein. The fact that CF is caused by a three-nucleotide deletion is chemically significant, and it's the kind of detail that separates a 4 from a 5.*

7.6 Dry Lab: Paper Chromatography — answers

How it works: a mixture dissolved in a **mobile phase** (solvent) moves through a **stationary phase** (paper) by **capillary action** — an application of Topic 1. Amino acids travel at different rates for two reasons: (1) they are **not equally soluble in the solvent**, and (2) they are **attracted to different degrees to the paper fibers through hydrogen bonding**.

$$R_f = \frac{\text{distance moved by the amino acid}}{\text{distance moved by the solvent front}}$$

Analysis Q1 — purpose of the 6N HCl? To **hydrolyze** the dipeptides — HCl breaks the **peptide bonds**, separating each dipeptide into its two individual amino acids. Without this step the dipeptides would migrate as single units and you couldn't identify the component amino acids.

Analysis Q2 — purpose of the 0.5% ninhydrin? Amino acids are **colorless**, so they're invisible on the paper. Ninhydrin **reacts with the amino groups** of amino acids to produce **colored (typically purple) spots**, making their positions visible so distances can be measured.

Analysis Q3 — identifying the amino acids: calculate Rf for each spot (measure from the start line to the **center** of each circle, divide by the distance from the start line to the solvent front) and match against the reference table.

> ***NICHE:*** *Rf is always **between 0 and 1** and is **unitless** — a ratio of two distances. A **higher Rf** means the amino acid traveled farther, which means it was **more soluble in the solvent** and **less strongly attracted to the paper**. Rf values are reproducible for a given solvent and paper, which is what makes identification possible. If your calculated Rf is greater than 1, you've divided backwards.*

PART 3 — Cross-Cutting Reference Tables

3.1 "Putting It All Together" — the master macromolecule table (workbook p. 72)

This table is the single most likely thing on a Unit 1 test. Memorize every cell.

Macromolecule	Elements	Monomer (sub-unit)	Polymer	Bond name	Functions	Examples
Carbohydrates	**C, H, O** (1:2:1)	Monosaccharide	Polysaccharide	**Glycosidic linkage**	Short-term energy, energy storage, structure	Glucose, fructose, sucrose, starch, glycogen, cellulose, chitin
Lipids	**C, H, O** (+ **P** in phospholipids)	*No true monomer* — glycerol + fatty acids	*Not a true polymer*	**Ester linkage**	Long-term energy storage, insulation, membranes, hormones	Fats, oils, phospholipids, steroids, cholesterol
Proteins	**C, H, O, N, S**	Amino acid	Polypeptide	**Peptide bond**	Enzymes, structure, transport, antibodies, messengers	Hemoglobin, enzymes, collagen, antibodies, insulin
Nucleic acids	**C, H, O, N, P**	Nucleotide	Polynucleotide	**Phosphodiester bond**	Store, transmit, and express genetic information	DNA, RNA, ATP

How to tell them apart from a formula or diagram: - Contains **N** → protein or nucleic acid - Contains **N and P** → nucleic acid - Contains **N but no P** → protein - Contains only **C, H, O** in ~1:2:1 with many —OH groups → carbohydrate - Contains only **C, H, O** but mostly long C–H chains with few oxygens → lipid

3.2 The eight properties of water at a glance

Property	Cause	Biological consequence
Polarity	Unequal electron sharing + bent shape	The origin of all other properties
Cohesion	H-bonds between water molecules	Transports water up xylem; surface tension
Adhesion	H-bonds to other polar/charged surfaces	Water clings to xylem walls against gravity
Surface tension	Unbalanced cohesive forces at the surface	Insects walk on water; water forms droplets
Capillary action	Adhesion > cohesion	Water rises in narrow tubes and plant vessels
High specific heat	Energy absorbed breaking H-bonds	Moderates climate; stabilizes body and ocean temperature
High heat of vaporization	Many H-bonds must break to evaporate	Evaporative cooling — sweating, leaf cooling
Lower density as a solid	H-bonds lock into an open crystalline lattice	Ice floats; insulates water below; marine life survives winter
Universal solvent	Polarity dissolves polar and ionic solutes	Medium for all cellular chemistry; transport of nutrients and waste

Every single one traces back to hydrogen bonding, which traces back to polarity, which traces back to electronegativity difference and the bent molecular shape. If an FRQ asks you to explain any water property, start there.

3.3 Structure → function across the unit

Structural feature	Functional consequence
Water's bent, polar shape	Hydrogen bonding → all eight properties
Carbon's 4 valence electrons	Chains, branches, rings → molecular diversity
α vs **β** glucose linkage	Starch (digestible storage) vs cellulose (indigestible structure)
Branched vs unbranched polysaccharide	Glycogen's branching = many free ends = rapid glucose release
Saturated (straight) vs unsaturated (kinked) tails	Solid vs liquid; membrane rigidity vs fluidity
Phospholipid amphipathic structure	Self-assembly into bilayers → selectively permeable membranes

Phospholipid amphipathic structure	Self-assembly into bilayers → selectively permeable membranes
A–T (2 H-bonds) vs G–C (3 H-bonds)	Different DNA melting temperatures; GC-rich = more heat stable
Antiparallel DNA strands	Enables complementary base pairing and 5′→3′ replication
DNA double-stranded vs RNA single-stranded	Stable long-term storage vs flexible, transient messenger
Amino acid R-group chemistry	Folding → 3D shape → protein function
Disulfide bridges (covalent)	Lock tertiary structure; the strongest tertiary interaction

3.4 Bond strength hierarchy — worth knowing cold

Strongest → weakest: 1. **Covalent** (shared electrons) — peptide bonds, phosphodiester bonds, glycosidic linkages, ester linkages, disulfide bridges 2. **Ionic** — strong when dry, **substantially weakened in water** because water molecules surround and shield the charges 3. **Hydrogen** — weak individually (~1/20th of a covalent bond), decisive in aggregate 4. **Hydrophobic interactions / van der Waals** — weakest individually, but numerous

> ***Why the weak ones matter:*** *DNA's strands are held by hydrogen bonds precisely because they must be able to separate for replication and transcription. If the strands were covalently bonded, DNA could never be read. Weakness is the feature, not the bug.*

PART 4 — Niche Knowledge Checklist

Things that go beyond the workbook's blanks and show up on harder questions. If you know all of these, nothing on a Unit 1 test should surprise you.

Statistics - SD estimates the spread of data; **SEM** estimates the uncertainty of the *mean*. Increasing n shrinks SEM but not SD. - The 95% CI multiplier is technically **1.96**, approximated as 2 in AP Bio. - Error bars: **no overlap = significant difference = reject the null**. Overlap = fail to reject. - Chi-square is the reverse direction: **χ^2 > critical value = reject the null**. df = categories − 1. - Each section of a box plot holds **25% of the data points** but sections have different widths. - Never write "prove," "disprove," or "accept the null." - **FRQ 2 is the only question that asks you to graph.**

Water and chemistry - Water's bond angle is **~104.5°**; a linear molecule would be nonpolar despite polar bonds. - Specific heat = **1 cal/g°C**; heat of vaporization ≈ **586 cal/g**. - Evaporative cooling works because the **highest-energy molecules leave first**. - Ice is **~9% less dense**; water is densest at **4°C**. - Each water molecule makes up to **4** hydrogen bonds in ice; ~3.4 on average in liquid. - pH is **logarithmic** — one unit = 10× H^+. - Blood is buffered at **7.35–7.45** by the carbonic acid/bicarbonate system. - Compare H_2O to H_2S: the heavier molecule boils **lower**, proving H-bonding (not size) drives water's behavior. - **CHNOPS**; C, H, O, N ≈ **96%** of living matter.

Carbon and macromolecules - All seven functional groups: hydroxyl, carbonyl (aldehyde vs ketone), carboxyl, amino, sulfhydryl, phosphate, methyl. - Monosaccharide formula: **$(CH_2O)_n$**. - Glucose and fructose are both $C_6H_{12}O_6$ — **structural isomers**. - **n monomers → n−1 bonds → n−1 water molecules** to hydrolyze. - α vs β glucose differ only in the position of the hydroxyl on carbon 1. - Cellulose's β linkage forces **every other glucose to flip 180°**, producing straight chains that hydrogen-bond into **microfibrils**. - **Amylose** = unbranched starch; **amylopectin** = branched starch; **glycogen** = more branched than amylopectin (branching means more free ends for rapid glucose release). - **Chitin** = arthropod exoskeletons and fungal cell walls. - **1,4** glycosidic linkages form chains; **1,6** linkages form branch points.

Lipids - Triglyceride = glycerol + 3 fatty acids via **ester linkages** (dehydration synthesis). - Only ***cis*** double bonds kink the chain; ***trans*** fats pack like saturated fats. - Fats store **~9 kcal/g** vs ~4 kcal/g for carbohydrates. - Cholesterol is a **bidirectional fluidity buffer** — decreases fluidity when hot, increases it when cold. - Steroids: **four fused rings** (three six-membered, one five-membered). - Lipids are **not true polymers**.

Nucleic acids - Purines (A, G) = **two rings**; pyrimidines (C, T, U) = **one ring**. Purine + pyrimidine keeps helix width constant (~2 nm). - **A–T = 2** H-bonds; **G–C = 3** H-bonds. GC-rich DNA has a higher **melting temperature (Tm)**. - 5′ end = free **phosphate**; 3′ end = free **hydroxyl**. Synthesis is always **5′→3′**, adding to the 3′ end. - Deoxyribose lacks the **—OH on the 2′ carbon**, which is why DNA is more chemically stable than RNA. - **Nucleoside** = base + sugar (no phosphate). **Nucleotide** = base + sugar + phosphate. - ATP is a nucleotide.

Proteins - **20** amino acids; peptide bond forms between **carboxyl and amino** groups via dehydration. - **N-terminus** (free amino) → **C-terminus** (free carboxyl); read and synthesized in that direction. - **Secondary = backbone hydrogen bonds only.** R groups are **tertiary**. - α helix: H-bond every **4th** amino acid. β pleated sheet: H-bonds between chain segments lying side by side. - **Disulfide bridge** = the only **covalent** tertiary interaction; between the **sulfhydryl groups of two cysteines**. - Hydrophobic R groups fold **inward**; polar/charged fold **outward** — inverted for membrane-embedded regions. - **Denaturation** = loss of 3D structure (heat, pH, salt) without breaking peptide bonds — primary structure survives. - Sickle cell: **glutamate → valine** at position **6** of beta-globin, from a single **A→T** substitution. - Cystic fibrosis: **3-nucleotide deletion = one amino acid** (Phe508) removed, **no frameshift**.

PART 5 — Practice FRQ, Fully Worked

The workbook's practice FRQ (p. 77) with the official rubric plus the reasoning behind each point.

Scenario: A pesticide appears to reduce crop output. Researchers hypothesize it negatively affects photosynthesis. CO_2 levels measured 2 hrs before, 2 hrs after, and 12 hrs after treatment.

Group	2 hrs before	2 hrs after	12 hrs after
No Treatment	14.0 ± 1	13.0 ± 1	14.0 ± 1
Pesticide	14.0 ± 1	4.0 ± 2	8.0 ± 2

(a)(i) Identify the independent variable. (1 pt) Pesticide treatment / application (whether or not the plant received the pesticide).

(a)(ii) State a null hypothesis. (1 pt) "The pesticide has **no effect** on the photosynthetic rate of plants." Or: "There will be **no difference** in photosynthetic rate between plants treated with the pesticide and those not treated."

(b)(i) Construct a line graph. (3 pts) - **1 pt — axis labeling:** x-axis = **time (hours) before/after treatment**; y-axis = **mean photosynthetic rate (μmol CO_2 m^{-2} s^{-1})**. Both need units. - **1 pt — line graph with means accurately plotted.** Two lines, one per group. Label or key them. - **1 pt — accurate error bars representing ± 2 SEM.** No Treatment: ±1 at every point. Pesticide: ±1 at baseline, ±2 at both post-treatment points.

(b)(ii) Vertical line at pesticide application. (1 pt) Draw it between the "2 hours before" and "2 hours after" points — i.e., at time zero.

(c) Use the data to support the scientists' hypothesis. (1 pt) The mean photosynthetic rate of pesticide-treated plants is **significantly lower** than untreated plants after application, and **the error bars do not overlap**. At 2 hours: pesticide 2.0–6.0 vs untreated 12.0–14.0 — no overlap. At 12 hours: pesticide 6.0–10.0 vs untreated 13.0–15.0 — no overlap. The difference is statistically significant, supporting the hypothesis that the pesticide reduces photosynthesis.

(d) Predict the level of protein structure most affected by interaction with sulfhydryl groups. Justify. (2 pts) - **1 pt — prediction: TERTIARY structure.** - **1 pt — justification: sulfur (in sulfhydryl groups) forms disulfide bridges that help maintain the 3D shape of a protein.** Sulfhydryl (—SH) groups belong to **cysteine R groups**, and R-group interactions define **tertiary** structure. If the pesticide binds these groups, disulfide bridges cannot form, so the protein cannot fold correctly, loses its functional 3D shape, and the enzyme is inactivated.

Total: 9 points.

5.1 FRQ strategy notes for this unit

- **Answer the task verb.** *Identify* = name it, no explanation. *Describe* = features. *Explain* = give the mechanism/cause. *Justify* = claim + reasoning connected to evidence. *Predict* = state an outcome, then support it. Writing more than the verb asks for wastes time and earns nothing.
- **No introductions or conclusions.** Label parts (a, b, c) and answer directly.
- **On any data question, name the error bars explicitly.** "The error bars do not overlap, so the difference is significant" is where the rubric point lives. Saying one bar is higher earns nothing.
- **On any "why does this molecule do that" question, go to structure.** Almost every Unit 1 justification is a structure→function argument.
- **A labeled diagram can supplement a response but never substitutes for one** — a diagram alone earns no credit.
- **Show your work on calculations,** and carry units through.

The one thing to remember

Every question in this unit is a **structure → function** question wearing a costume.

Why does ice float? Structure — hydrogen bonds lock into an open lattice. Why can't you digest cellulose? Structure — the β linkage flips every other glucose and your enzymes don't fit. Why does GC-rich DNA need more heat to denature? Structure — three hydrogen bonds instead of two. Why does one amino acid substitution deform an entire red blood cell? Structure — a hydrophobic residue on the surface where a charged one belonged.

When you're stuck on an FRQ in this unit, the move is always the same: **name the structural feature, then state what it causes.** Two sentences, and you'll usually have the point.

And don't neglect Topic 0. It's a third of the workbook, it appears on every test all year, and it's the part students consistently underprepare because it doesn't feel like biology.