CLAREZA ACADEMY

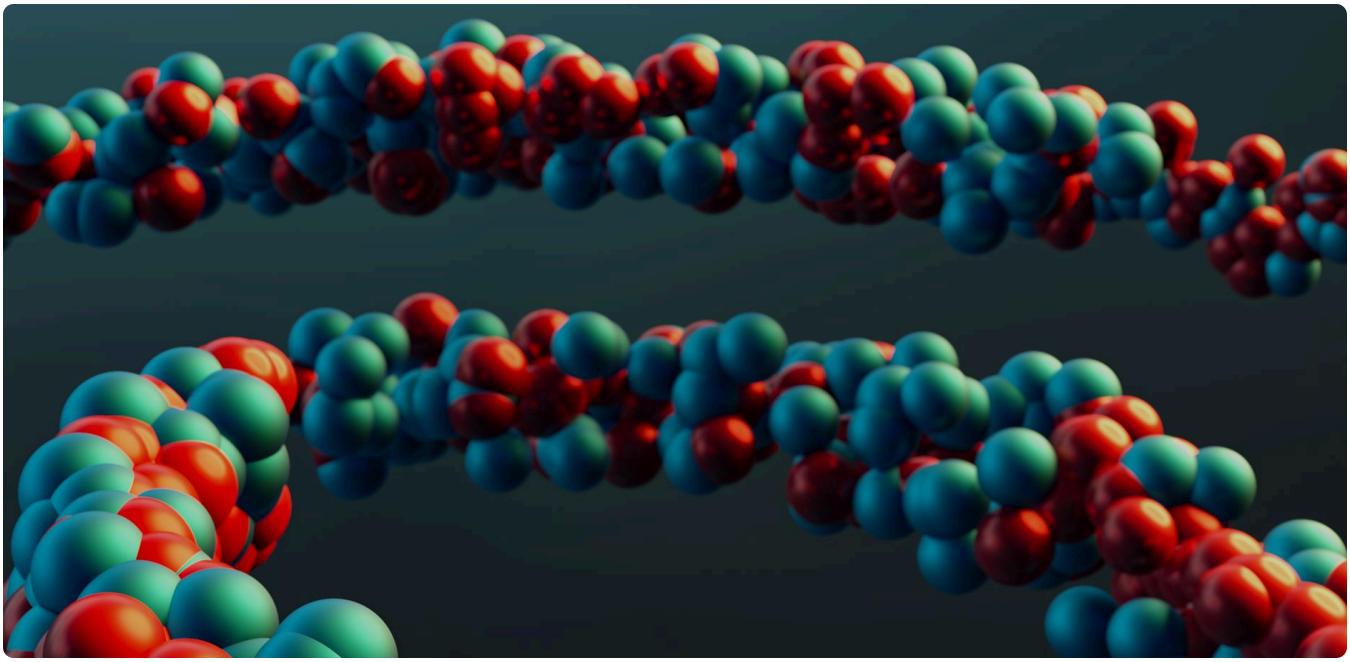
Grade 9 -- Science, Vol. 1 Science

Free sample: Unit 1, Lessons 1 to 8

These are 8 lessons from *Clareza Grade 9: Science, Volume 1: Chemistry of Life through Genetics*, a ninth grade year a parent runs at the kitchen table. Each lesson is a short script for you, a page to read together, and a practice sheet you may copy for your household. Answers are at the back.

Clareza Grade 9: Science, Volume 1: Chemistry of Life through Genetics. Sample edition.

Clareza is a secular curriculum. Standards references: Common Core State Standards and the Next Generation Science Standards.



SCIENCE · UNIT 1

The Chemistry of Life

This is where all the vocabulary for the rest of the year gets built: water, the four big molecule families (carbs, fats, proteins, DNA), and how enzymes work. The through-line question is always: how does a molecule's shape decide what it can and can't do?

In this unit

1. Water's polarity and hydrogen bonding, arising from unequal electron sharing at oxygen
2. Monomer identity and functional groups distinguishing the four macromolecule classes
3. Dehydration synthesis and hydrolysis as the shared mechanism linking all four macromolecule classes
4. Levels of protein structure and how sequence determines folded 3-D shape
5. Macromolecule class names, monomer names, and functional roles
6. Enzymes as catalysts that lower activation energy via substrate-specific shape complementarity
7. The relationship between temperature/pH-induced denaturation and loss of enzyme activity
8. The disproportionate functional consequence of a single amino-acid substitution on protein shape and function

SCIENCE · UNIT 1 · LESSON 1

Water's polarity and hydrogen bonding, arising from unequal electron sharing at oxygen

Goal: Given a diagram of a water molecule's electron distribution, the student explains why water forms hydrogen bonds and predicts which of two unfamiliar small molecules would also be polar.

About 50 minutes

Teach it FOR THE PARENT

1. **Say:** Picture a mouse head: one big round face and two little round ears. Water molecules are shaped kind of like that! Can you guess which part is the 'face' and which parts are the 'ears', oxygen or hydrogen?
   Look for: Student guesses oxygen is the big face, hydrogens are the two ears. Doesn't need to be exact, just engaged with the shape idea.
2. **Say:** In that mouse head, oxygen tugs the shared electrons closer to itself than hydrogen does. That leaves oxygen a little bit negative and the two hydrogens a little bit positive, like a tiny magnet with one negative end and two positive ends. A molecule built this way is called polar, meaning it has an uneven, lopsided charge.
   Look for: Nothing to check yet, this is the setup for the next move.
3. **Say:** Quick check: on our water mouse head, is the big oxygen face a little positive or a little negative?
   Look for: Student says negative. Bonus if they add that the hydrogen ears are a little positive.
4. **Say:** Because water is polar, the positive hydrogen end of one water molecule gets pulled toward the negative oxygen end of a different water molecule, opposites attract, just like magnets. That pull between molecules is called a hydrogen bond.
   Look for: Nothing to check yet, sets up the next check.
5. **Say:** So a hydrogen bond happens BETWEEN two different water molecules, not inside just one. Which part of one molecule gets pulled toward which part of the other?
   Look for: Student says the positive hydrogen of one molecule is pulled toward the negative oxygen of another molecule.
6. **Say:** New molecule time! Imagine a molecule where one atom pulls electrons much harder than the other, so one side is negative and the other is positive, just like water. Would you expect molecules like this to attract each other the way water does? Why?
   Look for: Student says yes, because it's polar (uneven charge), so its positive side would be pulled toward another molecule's negative side, similar to a hydrogen bond pull.
7. **Say:** Last check: if a molecule had NO uneven pull on electrons, both sides stayed neutral, would you expect strong hydrogen-bond-style attractions between its molecules? Why or why not?
   Look for: Student says no, because without a positive and negative end, there's no polarity to create that magnet-like pull.

8. **Say:** You've got it, polar shape, opposite charges, and that magnet-like pull are the whole story of a hydrogen bond. Let's lock it in with a few practice questions.
   Look for: No answer needed, this hands off to practice.

If they get stuck

- *When a substance like water evaporates or a liquid disappears when heated, some of it changes into carbon dioxide or another new substance.*
  In Lesson 1's retrieval and again in Lesson 2, explicitly contrast a physical change (ice melting, water evaporating, same molecule, different arrangement/motion) against a chemical change (dehydration synthesis forming a new bond) using a labeled particle diagram for each, side by side.
- *Molecules bind to each other (like enzyme and substrate) simply because their shapes fit together like puzzle pieces, not because of random collision plus a stable resulting configuration.*
  In Lesson 11, after introducing the lock-and-key model, explicitly add the random-collision layer: substrate and enzyme move randomly in solution; most collisions do not result in binding; only a correctly oriented, correctly shaped collision does. Ask the student to explain why increasing substrate concentration increases reaction rate, which only makes sense under the collision model.
- *A protein or enzyme comes apart or changes shape because something actively pulls it apart on purpose, not because of random thermal motion of molecules.*
  In Lesson 12, use a physical hydrogen-bond model (paperclip chain or molecular kit) and have the student physically shake it with increasing energy to show that the bonds break from increased random motion, not from a targeted, purposeful action, then require the student to redescribe denaturation in those terms before moving to the enzyme-temperature graph.

Read together FOR THE STUDENT

A water molecule is one oxygen atom stuck to two hydrogen atoms, like a mouse head: one big circle (oxygen) with two smaller ears (hydrogens). Oxygen pulls the shared electrons closer to itself than hydrogen does. That makes oxygen a little bit negative and the hydrogens a little bit positive, like a tiny magnet with a negative end and two positive ends. Molecules with this kind of unevenness are called polar. Because water is polar, the positive hydrogen end of one water molecule gets pulled toward the negative oxygen end of another. That pull is called a hydrogen bond.

Going further: In a water molecule, oxygen and hydrogen share electrons, but oxygen has a stronger pull on those shared electrons (it is more electronegative). This unequal sharing gives oxygen a partial negative charge and each hydrogen a partial positive charge, the molecule is polar. A hydrogen bond is the attraction between the partially positive hydrogen on one water molecule and the partially negative oxygen (or nitrogen/fluorine) on a neighboring molecule. To predict whether an unfamiliar small molecule is polar, check whether it has an unequal electron pull across its bonds and an uneven shape, so charge doesn't cancel out.

Watch it work

A diagram shows a water molecule (H2O) with the oxygen atom drawn larger and shaded darker, and a small delta-minus (δ-) symbol near the oxygen and delta-plus (δ+) symbols near each hydrogen. Explain why water is described as a polar molecule and why this leads to hydrogen bonding between water molecules.

1. Identify what the shading and delta symbols mean: they show that electrons spend more time near oxygen than near hydrogen. Oxygen pulls shared electrons harder than hydrogen does, so oxygen ends up slightly negative (δ-) and each hydrogen ends up slightly positive (δ+). This is unequal sharing, not full electron transfer, the atoms are still bonded, not turned into ions.
2. Connect the charge split to the molecule's overall shape: water is bent, not straight, so the two slightly negative-to-positive directions don't cancel out. One end of the molecule (the oxygen side) is more negative overall, and the other end (between the two hydrogens) is more positive overall. A molecule with this kind of separated charge is called polar.
3. Explain the bond between molecules: because one water molecule has a δ+ hydrogen and a neighboring water molecule has a δ- oxygen, the positive hydrogen of one is attracted to the negative oxygen of the other. This attraction between molecules is a hydrogen bond. It is weaker than the covalent bond holding H and O together inside one molecule, but strong enough to pull water molecules toward each other.

The idea: Polarity comes from unequal electron pull plus a molecular shape that keeps the charge separation from canceling; hydrogen bonds are the attractions that unequal charge creates between neighboring molecules.

Two unfamiliar molecules are shown as diagrams: Molecule X is CO_2, drawn as O=C=O in a straight line, with δ- marked on both oxygens and δ+ marked on the carbon. Molecule Y is HCl, drawn as a single bond H-Cl, with δ+ on H and δ- on Cl. Predict which molecule is polar overall and which is not, and explain why.

1. Check each bond for unequal electron pull: in CO_2, each C=O bond is unequal (chlorine-like pull toward oxygen), so each bond has its own charge split. In HCl, the H-Cl bond is also unequal, with chlorine pulling harder, so H is δ+ and Cl is δ-.
2. Check the shape of each molecule: CO_2 is linear (straight line), with the two C=O bond pulls pointing in exactly opposite directions. HCl only has one bond, so there is nothing for that bond's pull to cancel against.
3. Combine unequal pull with shape to decide overall polarity: in CO_2, the two equal-and-opposite bond pulls cancel each other out, so the molecule as a whole has no separated positive and negative end, CO_2 is nonpolar overall, even though each individual bond is unequal. In HCl, there is only one bond direction, so its charge split cannot cancel, HCl is polar overall.
4. State the prediction: HCl is polar; CO_2 is not polar overall, despite having unequal bonds, because its straight shape cancels the effect.

The idea: An unequal bond does not automatically make a molecule polar overall, you must also check whether the molecule's shape lets those unequal pulls cancel out or leaves one end more negative than the other.

 Name: _____

Practice: Water's polarity and hydrogen bonding, arising from unequal electron sharing at oxygen

1. In a water molecule, why does the oxygen atom end up with a slight negative charge (δ-) while the hydrogen atoms end up with a slight positive charge (δ+)?

- (A) Oxygen and hydrogen have the same pull on electrons, so the charge is random.
- (B) Hydrogen atoms actively push their electrons toward oxygen to protect the molecule.
- (C) The water molecule turns some of its atoms into a new substance with a different charge.
- (D) Oxygen pulls the shared electrons closer to itself than hydrogen does.

2. A hydrogen bond between two water molecules is best described as:

- (A) A brand new chemical bond that joins two water molecules together and turns them into a single new substance with new properties.
- (B) The same thing as the covalent bond that holds one water molecule's own oxygen and hydrogen atoms together inside the molecule.
- (C) Water molecules grabbing onto each other because their shapes happen to match up like puzzle pieces that fit together.
- (D) An attraction between the δ+ hydrogen of one water molecule and the δ- oxygen of a neighboring water molecule.

3. Why is water's bent shape important for water being polar overall, not just having polar bonds?

- (A) The bent shape lets water turn into a gas more easily, which is what makes it polar.
- (B) The bent shape has nothing to do with polarity, only which atoms are involved matters.
- (C) The bent shape lets oxygen actively grab extra electrons from both hydrogens at once.
- (D) Because the bent shape keeps the two O-H bond charge splits from canceling out, so one side of the molecule stays more negative and the other more positive.

4. A student says: 'When water boils away, it changes into a new gas made of different atoms.' What is wrong with this statement, based on how hydrogen bonds work?

(A) The statement is correct, boiling water does produce carbon dioxide gas.

(B) Boiling breaks hydrogen bonds between water molecules and separates them into vapor, but each molecule is still H2O, no new substance forms.

(C) Boiling breaks the covalent O-H bonds inside each of the water molecules, releasing separate oxygen and hydrogen atoms into the air as a brand new gas made of new atoms.

(D) Boiling happens because the water molecules actively decide to spread apart from one another in order to escape from the heat coming up from below them.

5. Molecule Z is drawn as F-F (two fluorine atoms bonded together), with no delta symbols shown at all. Is Molecule Z polar? Why or why not?

(A) Yes, F-F must be polar because fluorine is a very electronegative element, and any bond that contains fluorine will have a charge separation.

(B) Yes, any molecule with two atoms bonded together is automatically polar.

(C) No, both atoms are the same element, so they pull equally on the shared electrons, and there is no charge separation.

(D) It cannot be determined without knowing the molecule's overall shape.

6. Molecule W is drawn bent, like water, as H-O-O-H (hydrogen peroxide), with δ+ marked on each hydrogen and δ- marked on each oxygen. Based on the reasoning used for water and CO2, is Molecule W likely to be polar overall?

(A) No, since it's a bigger molecule than water, the extra atoms cancel out any charge difference automatically.

(B) Yes, each O-H bond is unequal, and the bent, non-symmetric shape keeps those charge splits from fully canceling.

(C) Yes, because it contains hydrogen and oxygen, and any molecule with those two elements is automatically polar.

(D) No, because it contains two oxygen atoms bonded to each other, and O-O bonds are always nonpolar, the whole molecule must be nonpolar.

7. A student explains hydrogen bonding this way: 'Water molecules stick together because the hydrogen and oxygen atoms are shaped so they interlock perfectly, like puzzle pieces.' What is the problem with this explanation?

- **A** It leaves out the actual cause, the attraction between δ+ hydrogen and δ- oxygen, and substitutes shape-matching instead.
- **B** The explanation is wrong because hydrogen bonds only ever occur inside a single water molecule, and never between two different molecules at all.
- **C** The explanation is wrong because water molecules don't actually attract each other at all.
- **D** There is no problem, shape-matching is exactly why hydrogen bonds form.

8. Molecule P is CH4 (methane): one carbon bonded to four hydrogens, arranged symmetrically in all directions (a tetrahedron), with each C-H bond having a small δ+ on H and δ- on C. Molecule Q is NH3 (ammonia): one nitrogen bonded to three hydrogens, arranged in a pyramid shape (not symmetric in all directions), with each N-H bond having δ+ on H and δ- on N. Which molecule is polar overall?

- **A** NH3 is polar overall; CH4 is not, because CH4's symmetric shape cancels its bond charge splits while NH3's pyramid shape does not.
- **B** CH4 is polar overall; NH3 is not, because CH4 has four hydrogen atoms while NH3 has only three, and more hydrogens always means a stronger overall charge split.
- **C** Neither molecule is polar overall, since carbon and nitrogen are both similar enough in electronegativity to hydrogen that no bond charge split forms.
- **D** Both molecules are polar overall, since both of them have unequal C-H or N-H bonds with δ+ and δ- ends, and the shape of the molecule makes no difference.

Monomer identity and functional groups distinguishing the four macromolecule classes

Goal: The student classifies an unfamiliar biological molecule as a carbohydrate, lipid, protein, or nucleic acid by identifying its monomer and characteristic functional groups from a structural diagram.

About 45 minutes

Teach it FOR THE PARENT

1. **Say:** Your whole body, your hair, your muscles, even the DNA inside your cells, is built from just four kinds of molecules. Can you guess why your body only needs four basic 'ingredients' to build so many different things?
   Look for: Any guess that repeating small pieces can combine in many ways; no wrong answer here, just curiosity.
2. **Say:** Three of the four kinds are built like Lego towers: one small brick repeated over and over. Sugars stack into carbohydrates. Amino acids link into proteins. Nucleotides chain into DNA. Fats break the pattern, no repeating brick, just a glycerol head with fatty acid tails hanging off it, like a fork with noodles stuck on the prongs.
   Look for: Nothing to check yet, just move forward.
3. **Say:** Quick check: which of the four molecule types does NOT get built from one small brick repeated many times?
   Look for: Answer: lipids (fats), because they're glycerol plus fatty acid tails, not a repeated brick.
4. **Say:** Now match the bricks to their towers. What small brick builds a protein, and what small brick builds DNA?
   Look for: Amino acids build proteins; nucleotides build DNA (or nucleic acids).
5. **Say:** Here's a new one: imagine a molecule made of one glycerol head and three long tails hanging off it. Which of the four kinds is this, and why?
   Look for: Lipid/fat, because it matches the glycerol-plus-tails structure, not a repeating brick chain.
6. **Say:** One more: a scientist finds a long chain made of the same small sugar unit repeated hundreds of times. What kind of molecule did she find?
   Look for: Carbohydrate, because sugars stacked/repeated build carbohydrates.
7. **Say:** Last one before we practice: if you saw a chain of amino acids, what would you call the whole molecule it builds?
   Look for: Protein.
8. **Say:** You've got the four builders down: carbs, proteins, and nucleic acids from repeating bricks, and fats as the odd fork-shaped one. Let's try some practice questions to lock it in.
   Look for: Student is ready to move into practice questions.

If they get stuck

- *When a substance like water evaporates or a liquid disappears when heated, some of it changes into carbon dioxide or another new substance.*
  In Lesson 1's retrieval and again in Lesson 2, explicitly contrast a physical change (ice melting, water evaporating, same molecule, different arrangement/motion) against a chemical change (dehydration synthesis forming a new bond) using a labeled particle diagram for each, side by side.
- *Molecules bind to each other (like enzyme and substrate) simply because their shapes fit together like puzzle pieces, not because of random collision plus a stable resulting configuration.*
  In Lesson 11, after introducing the lock-and-key model, explicitly add the random-collision layer: substrate and enzyme move randomly in solution; most collisions do not result in binding; only a correctly oriented, correctly shaped collision does. Ask the student to explain why increasing substrate concentration increases reaction rate, which only makes sense under the collision model.
- *A protein or enzyme comes apart or changes shape because something actively pulls it apart on purpose, not because of random thermal motion of molecules.*
  In Lesson 12, use a physical hydrogen-bond model (paperclip chain or molecular kit) and have the student physically shake it with increasing energy to show that the bonds break from increased random motion, not from a targeted, purposeful action, then require the student to redescribe denaturation in those terms before moving to the enzyme-temperature graph.

Read together FOR THE STUDENT

Your body is built from four kinds of molecules: carbohydrates, lipids, proteins, and nucleic acids. Think of each kind as being built from a different type of Lego brick, repeated over and over. Sugars stack into carbohydrates. Amino acids link into proteins. Nucleotides chain into DNA. Fats are the odd one out, no repeating brick, just a glycerol head with long fatty acid tails hanging off it, like a three-pronged fork with noodles stuck on each prong.

Going further: Each macromolecule class is built from a repeating subunit called a monomer, joined into a chain called a polymer. Carbohydrates are built from monosaccharides (rings with many -OH groups). Proteins are built from amino acids (each with an amino group, a carboxyl group, and a variable R-group, joined by peptide bonds). Nucleic acids are built from nucleotides (a sugar, phosphate, and nitrogenous base). Lipids do not polymerize, they show a glycerol backbone with fatty acid chains attached by ester bonds. To classify a molecule, find the repeating unit and the functional groups, don't just look at overall shape.

Watch it work

A diagram shows a molecule made of three long carbon-and-hydrogen chains, each attached by a bond to one of three carbons in a small central molecule. There are no repeating ring structures and no nitrogen anywhere in the molecule.

1. Look for a repeating monomer first, because that is what separates carbohydrates, proteins, and nucleic acids from each other. This molecule has no repeating unit at all, it is one glycerol backbone with three chains attached, not a chain of identical or near-identical subunits.
2. Since there's no monomer/polymer pattern, check whether it matches the one class that is NOT built from a repeating monomer: lipids. Lipids are glycerol plus fatty acid chains, joined by ester bonds, which matches the '3 chains off a small central molecule' structure exactly.
3. Confirm using functional groups: fatty acid chains are long hydrocarbons (mostly C and H, very few oxygens, no nitrogen). This diagram has no nitrogen and long carbon chains, consistent with lipid, and ruling out protein (which requires nitrogen in every amino acid) and nucleic acid (which requires phosphate and nitrogenous bases).
4. Classify the molecule as a lipid.

The idea: When a molecule has no repeating monomer chain, check first whether it's a lipid, the one macromolecule class defined by a small backbone plus attached tails, not by polymerization.

A diagram shows a long chain of subunits. Zooming into one subunit shows a central carbon bonded to an amino group (-NH2) on one side, a carboxyl group (-COOH) on the other side, and a variable side chain. The subunits are joined to each other by a bond between the carboxyl carbon of one unit and the nitrogen of the next.

1. Identify the repeating monomer. Each subunit has the same core pattern, amino group, carboxyl group, central carbon, variable side chain, with only the side chain differing between subunits. This core pattern is the amino acid.
2. Identify the bond linking the monomers. The link is between a carboxyl carbon and a nitrogen, which is the peptide bond that specifically joins amino acids into a polymer.
3. Rule out the other three classes: no sugar ring (rules out carbohydrate), no phosphate or nitrogenous base pattern (rules out nucleic acid), and this is a repeating chain, not a glycerol-plus-tails structure (rules out lipid).
4. Classify the molecule as a protein, because the monomer is an amino acid and the linking bond is a peptide bond.

The idea: Find the repeating subunit and the bond joining subunits before looking at anything else, that pair identifies the class, not the overall size or shape of the diagram.

Clareza Grade 9 · Science Lesson 2 Name: _____

Practice: Monomer identity and functional groups distinguishing the four macromolecule classes

1. A structural diagram shows a molecule made of repeating six-sided rings. Each ring has several -OH (hydroxyl) groups attached, and the rings are joined to each other by bonds between ring carbons. What class of molecule is this?

(A) Lipid (B) Protein (C) Carbohydrate (D) Nucleic acid

2. A diagram shows one small molecule with three carbons. Three long hydrocarbon chains are each attached to one of those carbons by a bond. There is no nitrogen and no phosphate anywhere in the molecule. What class is this?

(A) Lipid (B) Nucleic acid (C) Protein (D) Carbohydrate

3. A diagram shows a repeating chain of subunits. Each subunit has a five-carbon sugar ring, a phosphate group attached to that sugar, and a ring-shaped structure containing nitrogen attached to the same sugar. What class of molecule is this?

(A) Protein (B) Lipid (C) Nucleic acid (D) Carbohydrate

4. A diagram shows repeating subunits. Each subunit has a central carbon bonded to an amino group, a carboxyl group, and a variable side chain that differs from subunit to subunit. Subunits are linked by bonds between a carboxyl carbon on one unit and the nitrogen on the next. What class of molecule is this?

(A) Nucleic acid (B) Carbohydrate (C) Lipid (D) Protein

5. A diagram shows a long, repeating chain. Each subunit in the chain is a six-carbon ring with multiple -OH groups, and adjacent rings are joined by a bond between a ring carbon on one unit and an oxygen bridging to the next ring. There is no nitrogen or phosphate anywhere in the molecule. What class of molecule is this?

(A) Protein (B) Carbohydrate (C) Lipid (D) Nucleic acid

(E) Cannot be determined from a structural diagram alone

6. A diagram shows a molecule with a central three-carbon backbone. Attached to each of the three carbons is a long hydrocarbon chain, connected by a bond between a backbone oxygen and a carbon on the chain. A student argues this must be a protein because the molecule is large and has many carbon atoms. What is the strongest counter-argument, based on structure?

(A) The molecule can't be a protein because it doesn't dissolve in water

(B) The molecule is too large to be a protein, since proteins are always smaller than lipids

(C) The molecule could very well be a protein, since large carbon-based molecules with many atoms and long chains are generally classified as proteins regardless of the exact groups they contain

(D) The molecule has no repeating amino acid monomer and no nitrogen-containing amino group anywhere, proteins require both, regardless of overall size

7. A diagram shows a chain of repeating subunits. Each subunit contains a five-carbon sugar and a phosphate group, but no nitrogen-containing ring is shown anywhere in the diagram. Based only on the monomer components shown, which class does this molecule most closely match, and what is missing from the diagram that you'd need to confirm it fully?

(A) Nucleic acid; missing the nitrogenous base that should be attached to the sugar in each nucleotide

(B) Lipid; missing the fatty acid tails attached to the backbone

(C) Protein; missing the amino and carboxyl groups that should be attached to a central carbon in each of the subunits

(D) Carbohydrate; missing the additional hydroxyl groups that should be attached to the sugar ring in each subunit

8. A student sees a diagram of a large, complex-looking molecule with many rings and branches and says, "This has to be a protein, it's way too complicated to be anything simpler." What is the problem with this reasoning?

(A) The problem is that carbohydrates, not proteins, are always the most complex-looking molecules in a diagram

(B) There is no problem, more complex-looking molecules are generally proteins, since proteins fold into complicated 3D shapes

(C) There is no problem, because bigger molecules always have more diverse functional groups, so the student's shortcut works reliably

(D) The problem is that the student should have counted the number of atoms instead of looking at the rings and branches

(E) Complexity or size of the diagram isn't a functional group or monomer, so it can't be used to identify the class, the student needs to find the repeating monomer and functional groups instead

Dehydration synthesis and hydrolysis as the shared mechanism linking all four macromolecule classes

Goal: The student explains how dehydration synthesis builds a polymer from monomers and how hydrolysis reverses it, using water molecules as the shared mechanism, for a polymer type not covered in the worked examples (e.g. a nucleic acid strand when only carbohydrates and proteins were worked).

About 50 minutes

Teach it FOR THE PARENT

1. **Say:** Think about snapping LEGO bricks into a tower. When you build, you push bricks together. When you take the tower apart, you pull them apart. What do you think cells need to do to build or break big molecules, like water somehow being involved?
   Look for: Any guess that building/breaking molecules might need something added or removed, like water. No wrong answers here - just a guess.
2. **Say:** To join two building blocks (monomers) into a chain (polymer), cells pull OUT a water molecule. That's called dehydration synthesis - dehydration means removing water. To break the chain back apart, cells push a water molecule back IN. That's hydrolysis - hydro means water, lysis means break apart.
   Look for: Nothing to answer yet, just reading. Move on to check.
3. **Say:** Quick check: if a cell is building a big molecule out of smaller pieces, is water leaving or entering? And what's that process called?
   Look for: Water is leaving (removed); process is dehydration synthesis.
4. **Say:** Now flip it: if a cell is breaking a big molecule apart, is water leaving or entering? What's that process called?
   Look for: Water is entering (added); process is hydrolysis.
5. **Say:** New case: your body just broke down a big fat molecule into smaller fatty acid pieces so you could use it for energy. Did water get added or removed during that step? What's the name for it?
   Look for: Water was added (entered); this is hydrolysis. Bonus if they connect it to breaking bonds.
6. **Say:** One more: DNA replication involves linking small nucleotide pieces into one long strand. Water in or out? Name the process.
   Look for: Water is removed (leaves); this is dehydration synthesis. Same idea applies to DNA, not just food molecules.
7. **Say:** You've got it: same water, opposite jobs - out to build, in to break. Let's try some practice questions and see if you can spot which process is happening each time.
   Look for: Student is ready to move into practice questions.

If they get stuck

- *When a substance like water evaporates or a liquid disappears when heated, some of it changes into carbon dioxide or another new substance.*
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  In Lesson 11, after introducing the lock-and-key model, explicitly add the random-collision layer: substrate and enzyme move randomly in solution; most collisions do not result in binding; only a correctly oriented, correctly shaped collision does. Ask the student to explain why increasing substrate concentration increases reaction rate, which only makes sense under the collision model.
- *A protein or enzyme comes apart or changes shape because something actively pulls it apart on purpose, not because of random thermal motion of molecules.*
  In Lesson 12, use a physical hydrogen-bond model (paperclip chain or molecular kit) and have the student physically shake it with increasing energy to show that the bonds break from increased random motion, not from a targeted, purposeful action, then require the student to redescribe denaturation in those terms before moving to the enzyme-temperature graph.

Read together FOR THE STUDENT

Imagine snapping LEGO bricks together to build a tower, that's making a polymer from monomers. To join two bricks, cells actually pull out a water molecule (H2O) as the 'glue' is removed and a bond forms. This is called dehydration synthesis (dehydration = removing water). To take the tower apart, cells push a water molecule back IN to break the bond. That's hydrolysis (hydro = water, lysis = break apart). Same water, opposite jobs, in every macromolecule: carbs, proteins, fats, and even DNA.

Going further: Dehydration synthesis joins two monomers by removing an -OH from one and an -H from the other; these combine to release H2O, and a new covalent bond forms between the monomers. Hydrolysis is the reverse: a water molecule is split, its -OH and -H are added back across the bond, breaking it apart into two monomers. This exact mechanism, remove water to build, add water to break, applies to carbohydrates, proteins, lipids, and nucleic acids alike, even though the monomers (sugars, amino acids, fatty acids/glycerol, nucleotides) look different.

Watch it work

Two glucose monomers join to form the disaccharide maltose. Show how dehydration synthesis builds this bond, and how hydrolysis breaks it back apart.

1. Identify the two monomers: glucose #1 and glucose #2, each with an -OH group on the carbon that will bond.
2. For dehydration synthesis: glucose #1 loses an -H from its -OH group; glucose #2 loses an entire -OH group. These combine to form one H_2O molecule, which leaves the reaction.
3. A covalent bond (a glycosidic bond) now connects the two glucose carbons where the -H and -OH used to be. The product is maltose plus one released water molecule.
4. For hydrolysis, run this backward: a water molecule is added at the glycosidic bond. Its -H reattaches to one glucose and its -OH reattaches to the other, breaking the bond and regenerating two separate glucose monomers.

The idea: The same bond that formed by releasing one water molecule is broken by adding one water molecule back, building and breaking are mirror-image uses of H_2O.

Two amino acids, glycine and alanine, join to form a dipeptide. Show dehydration synthesis forming the bond and hydrolysis breaking it, then explain why this is the same mechanism as the glucose example even though the molecules look different.

1. Identify the reactive groups: the carboxyl group (-COOH) of glycine and the amino group ($-NH_2$) of alanine.
2. During dehydration synthesis, glycine's -COOH loses an -OH and alanine's $-NH_2$ loses an -H. These combine into one H_2O molecule that leaves, and a peptide bond forms between the carbon of glycine and the nitrogen of alanine.
3. During hydrolysis, a water molecule is added at the peptide bond: its -OH reattaches to glycine's carbon and its -H reattaches to alanine's nitrogen, breaking the bond and freeing both amino acids again.
4. Compare to maltose: different atoms are involved (C-N peptide bond vs. C-O glycosidic bond) and different monomers (amino acids vs. sugars), but the pattern is identical, remove parts of water to bond, add water back to unbond.

The idea: Different macromolecule classes use different atoms and bond names, but the underlying water-based bonding-and-unbonding mechanism does not change, this is what lets you predict how an unfamiliar polymer, like a nucleic acid strand, must behave.

Practice: Dehydration synthesis and hydrolysis as the shared mechanism linking all four macromolecule classes

1. In dehydration synthesis, what happens to the water molecule relative to the two monomers being joined?

- (A) The water molecule evaporates into the air as a gas and turns into carbon dioxide.
- (B) The water molecule is released as the bond between the monomers forms.
- (C) The water molecule is absorbed into the new bond and becomes part of the polymer permanently.
- (D) The water molecule actively pulls the two monomers together on its own.

2. What is the defining difference between hydrolysis and dehydration synthesis?

- (A) Dehydration synthesis happens only at high temperatures, while hydrolysis happens only at low temperatures.
- (B) Hydrolysis adds a water molecule to break a bond; dehydration synthesis removes a water molecule to form one.
- (C) Hydrolysis happens when an enzyme's shape actively grabs the polymer and rips it apart.
- (D) Hydrolysis only happens to proteins, while dehydration synthesis only happens to carbohydrates.

3. A student says: 'When the peptide bond between glycine and alanine breaks during hydrolysis, the water molecule's -OH and -H just disappear.' What is wrong with this statement?

- (A) The statement is wrong because hydrolysis doesn't involve water at all, only enzymes.
- (B) The -OH and -H don't disappear; they reattach to the two separated amino acids, one on each.
- (C) Nothing is wrong; water genuinely disappears during hydrolysis.
- (D) The statement is wrong because the peptide bond breaks itself apart to protect the cell, without water being involved.

4. Two fatty acid molecules and a glycerol molecule join to form part of a lipid, releasing water at each new bond formed. This process is best classified as:

(A) Hydrolysis, because water is involved in the reaction.

(B) Neither process, because lipids don't follow the same water-based mechanism as carbohydrates and proteins.

(C) Dehydration synthesis only if the fatty acids and glycerol have matching shapes that let them lock together.

(D) Dehydration synthesis, because bonds form as water is released.

5. A polymer chain is heated and begins to fall apart into its individual monomers, with water molecules being consumed at each broken bond. A student explains: 'The heat attacks the bonds and forces them to break.' What is the more accurate explanation, consistent with the mechanism in the worked examples?

(A) The heat itself is the correct explanation, since heat actively seeks out each bond and destroys it one at a time until the whole polymer falls apart.

(B) The bonds break because the polymer decides on its own to release its monomers in order to protect itself from the damage that the heat would otherwise cause it.

(C) The water molecules evaporate first when the heat is applied, and this evaporation is what pulls on the bonds and breaks them apart to release the individual monomers.

(D) Increased random molecular motion from heat makes water more likely to collide with and add across the bonds, breaking them through hydrolysis.

6. Which statement correctly describes what dehydration synthesis and hydrolysis have in common across all four macromolecule classes (carbohydrates, proteins, lipids, nucleic acids)?

(A) In both processes, an enzyme's shape must match the monomer exactly, and this match alone is what causes the bond between monomers to form or to break in every class.

(B) In both processes, the polymer intentionally reorganizes its own structure at the bonds between monomers in order to adapt to whatever its environment needs from it.

(C) In both processes, the monomers physically change into a new state of matter at the bond, similar to the way water turns into vapor, and this change is what joins or separates them.

(D) In both processes, water is the shared molecule that is either released (synthesis) or added (hydrolysis) at the bond between monomers.

7. In the maltose worked example, which two parts combine to form the released water molecule?

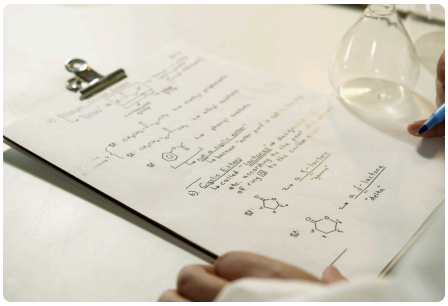
(A) An -H from one glucose's -OH group and the entire -OH group from the other glucose.

(B) The entire glucose molecule evaporates and turns into the water molecule.

(C) The glycosidic bond itself turns into a water molecule.

(D) An enzyme shape-matches with the glucose molecules and produces the water as a byproduct of fitting together.

Levels of protein structure and how sequence determines folded 3-D shape



Goal: The student compares the four levels of protein structure (primary through quaternary) and explains how a change at the primary level can propagate to change the protein's final 3-D shape.

About 50 minutes

Teach it FOR THE PARENT

1. **Say:** Think about your earbud cord. If you just drop it in your pocket, it always seems to twist into some tangled shape, not a random new one every time. Why do you think it lands in a similar kind of tangle each time?
   Look for: Any guess pointing at the cord's shape/material making it twist the same way, e.g. 'it's built to bend that way.'

2. **Say:** Proteins are like that cord. They start as a long string of beads called amino acids, and they fold into one specific 3-D shape. Scientists describe that folding in four levels: primary is just the bead order, secondary is small local coils, tertiary is the whole 3-D clump, and quaternary is when several clumps join together.
   Look for: Student can repeat that a protein is a chain of amino acids that folds into a specific shape, described in 4 levels.

3. **Say:** Quick check: if I just listed the order of beads on the string, without any folding yet, which level am I describing?
   Look for: Primary structure, just the sequence/order of amino acids.

4. **Say:** Now imagine two clumps of protein snapped together like two Lego blobs joined into one bigger machine. Which of the four levels is that?
   Look for: Quaternary structure, multiple folded clumps joined together.

5. **Say:** Here's the tricky one: if you swap just ONE bead on the string for the wrong one, does the shape usually stay the same, or can it change completely? Why?
   Look for: Can change completely, like changing one knot in a cord changes how the rest tangles; one wrong amino acid can throw off the whole fold.

6. **Say:** New case: imagine a protein folds correctly and works fine, but then one bead swap makes a tiny kink in a local coil. Which level got hit first, secondary or quaternary, and could that ripple up to affect the whole clump?
   Look for: Secondary structure is hit first (local coil), and yes it can ripple up to change tertiary/quaternary shape too, since folding builds on itself.

7. **Say:** You've got the four levels and why one wrong bead matters. Let's lock it in with some practice questions.
   Look for: Student is ready to move into practice; no new content needed here.

If they get stuck

- *When a substance like water evaporates or a liquid disappears when heated, some of it changes into carbon dioxide or another new substance.*
  In Lesson 1's retrieval and again in Lesson 2, explicitly contrast a physical change (ice melting, water evaporating, same molecule, different arrangement/motion) against a chemical change (dehydration synthesis forming a new bond) using a labeled particle diagram for each, side by side.
- *Molecules bind to each other (like enzyme and substrate) simply because their shapes fit together like puzzle pieces, not because of random collision plus a stable resulting configuration.*
  In Lesson 11, after introducing the lock-and-key model, explicitly add the random-collision layer: substrate and enzyme move randomly in solution; most collisions do not result in binding; only a correctly oriented, correctly shaped collision does. Ask the student to explain why increasing substrate concentration increases reaction rate, which only makes sense under the collision model.
- *A protein or enzyme comes apart or changes shape because something actively pulls it apart on purpose, not because of random thermal motion of molecules.*
  In Lesson 12, use a physical hydrogen-bond model (paperclip chain or molecular kit) and have the student physically shake it with increasing energy to show that the bonds break from increased random motion, not from a targeted, purposeful action, then require the student to redescribe denaturation in those terms before moving to the enzyme-temperature graph.

Read together FOR THE STUDENT

A protein is like a long string of beads (amino acids) that folds up into a specific 3-D shape, kind of like a phone charger cord that naturally twists and knots into a particular pattern when you let it be. There are four levels to describe this folding: the bead order (primary), local coils and folds (secondary), the whole 3-D clump (tertiary), and multiple clumps joined together (quaternary). If you swap one bead for a wrong one, the whole folding pattern can change, just like changing one knot in the cord changes how the rest tangles.

Going further: Primary structure is the exact sequence of amino acids linked by peptide bonds. Secondary structure is local folding (alpha helix or beta sheet) caused by hydrogen bonds between backbone atoms. Tertiary structure is the overall 3-D shape of one folded chain, held by interactions between the side chains (R-groups). Quaternary structure is two or more folded chains (subunits) joined together. Because each level's shape depends on chemical interactions from the level before it, a single amino acid substitution in the primary sequence can change which side chains end up near each other, disrupting tertiary folding and the protein's function.

Watch it work

A chain of amino acids is being folded into a functional protein. Trace how the levels build on each other, using this sequence fragment: ...Gly-Ala-Val-Leu-Glu-Lys...

1. Identify the primary structure: this is simply the order of amino acids joined by peptide bonds, Gly-Ala-Val-Leu-Glu-Lys, read in one direction, no folding yet.
2. Identify the secondary structure: nearby backbone atoms (not the R-groups) form hydrogen bonds with each other, pulling this stretch into a local shape such as an alpha helix or a beta sheet, because the atoms that hydrogen-bond are part of every amino acid's backbone regardless of which R-group is attached.
3. Identify the tertiary structure: now the R-groups (side chains) of Val, Leu, Glu, and Lys interact with each other and with the surrounding water, Val and Leu are nonpolar and cluster away from water, Glu and Lys are charged and can form an ionic bond with each other, folding the whole chain into one specific 3-D shape.
4. Identify the quaternary structure only if this chain joins with another folded chain to make a working protein; if it works alone, quaternary structure does not apply here.

The idea: Each level of structure is built from chemical interactions that depend on the level before it, sequence sets up backbone folding, backbone folding sets up which side chains meet, and side-chain interactions set the final shape.

A gene mutation swaps the amino acid Valine (nonpolar) for Glutamic acid (charged, polar) at one position in a chain that folds into a compact globular protein. Explain what happens to the protein's final shape.

1. Locate where the change happens: this is a primary structure change, one amino acid in the sequence is different, nothing else in the chain has changed yet.
2. Predict the local chemical consequence: Valine's nonpolar R-group normally packs against other nonpolar R-groups on the inside of the folded protein, away from water; Glutamic acid's R-group is charged and pulls toward water instead of away from it.
3. Trace the effect on tertiary structure: because this position no longer packs the same way, the folding pattern in that region changes, nearby R-groups that used to interact with the original Valine now have a different, wrong partner nearby, changing the shape of that part of the protein.
4. State the consequence for function: since a protein's job depends on its exact 3-D shape (for example, an active site's shape), this primary-level substitution can produce a tertiary shape that no longer works correctly, even though no outside force acted on the molecule at all.

The idea: A change at the primary level does not directly change the final shape, it changes local chemical interactions, and those altered interactions are what reshape the tertiary structure.

 Name: _____

Practice: Levels of protein structure and how sequence determines folded 3-D shape

1. What is the primary structure of a protein?

(A) The specific sequence of amino acids joined by peptide bonds

(B) The folded 3-D shape of a single chain held by side chain interactions

(C) Two or more separate chains joined together into one working protein

(D) The local coiling of the backbone into a helix held by hydrogen bonds

2. Which level of protein structure involves two or more separately-folded amino acid chains joining together?

(A) Primary (B) Tertiary (C) Quaternary (D) Secondary

3. A student says: 'A protein loses its shape when heated because the heat actively attacks and tears apart the protein.' What is the more accurate explanation?

(A) Heat directly attacks and breaks the peptide bonds in the primary structure, so the chain of amino acids comes apart into pieces

(B) The protein senses the heat and unfolds itself on purpose in order to protect the rest of the cell from being damaged by it

(C) Heat increases random molecular motion, and this motion overwhelms the weak bonds holding the folded shape together

(D) Heat turns some of the atoms in the protein into new molecules, and those new molecules no longer fit into the folded shape

4. Which statement correctly describes the relationship between secondary and tertiary structure?

(A) Tertiary structure forms first from the R-group interactions, and it then determines what secondary structure the backbone is able to form afterward within each region of the chain

(B) Secondary structure and tertiary structure are simply two different names for the exact same thing, and either name can be used for the folding of a single chain of amino acids into its shape

(C) Secondary structure forms from backbone hydrogen bonds; tertiary structure then forms from R-group (side chain) interactions between regions of secondary structure

(D) Secondary structure only ever occurs in proteins that also have quaternary structure, since the backbone hydrogen bonds cannot form until two or more chains have first come together in one protein

5. An enzyme and its substrate are described as binding because their shapes 'fit together like a lock and key.' Which addition makes this explanation more complete?

(A) The substrate changes its own shape to match the enzyme after they touch

(B) The enzyme and substrate collide randomly due to molecular motion, and only a collision with the correct shape orientation results in successful binding

(C) No further explanation is needed, shape complementarity is the complete mechanism

(D) The enzyme actively searches through the cell until it finds its matching substrate

6. A protein's primary sequence has one amino acid changed from a nonpolar one to a charged, polar one, at a position that normally packs into the protein's water-avoiding interior. What is the most likely direct consequence?

- **A** Nothing at all changes in the protein, because the primary sequence of amino acids has no effect on any of the later folding steps that give the protein its shape
- **B** The local packing of side chains at that position changes, which can alter the tertiary folding pattern in that region
- **C** The protein turns into a completely different type of molecule at that position, such as a carbohydrate, since a polar amino acid cannot be part of a protein
- **D** The peptide bonds on either side of that position break apart, which shortens the primary sequence and removes the changed amino acid from the chain entirely

7. Compare tertiary and quaternary structure. Which statement correctly distinguishes them?

- **A** Tertiary structure and quaternary structure both describe the same single-chain folding of a protein, just viewed at two different scales, with quaternary being the closer view
- **B** Tertiary structure requires multiple chains; quaternary structure occurs within a single chain
- **C** Tertiary structure describes the 3-D shape of a single folded chain; quaternary structure describes multiple such folded chains associating together
- **D** Quaternary structure occurs first, and tertiary structure builds on top of it

8. Hemoglobin is made of four folded chains combined together, and its ability to carry oxygen depends on the precise shape of pockets formed where these chains meet. A single amino acid substitution occurs in the primary sequence of one chain, at a position involved in chain-to-chain contact. Which outcome best follows from the levels of protein structure?

(A) The substitution only affects the primary structure and cannot influence tertiary or quaternary structure at all

(B) The substitution could disrupt how that chain's tertiary shape contacts the others, potentially altering the quaternary structure and the oxygen-carrying pockets

(C) Since only one chain out of four is affected, the other three chains' tertiary structures will compensate and no change in quaternary structure will occur

(D) The four chains will actively rearrange themselves to correct the mutation and preserve normal function

SCIENCE · UNIT 1 · LESSON 5

Macromolecule class names, monomer names, and functional roles

Goal: The student recalls the standard names and one-sentence functional role of the four macromolecule classes and their monomers (carbohydrate/monosaccharide, lipid/fatty acid+glycerol, protein/amino acid, nucleic acid/nucleotide).

About 35 minutes

Teach it FOR THE PARENT

1. **Say:** If I said your body is basically a giant train yard, what do you think would be riding the trains?
   Look for: Any guess, no wrong answer here, just engagement. Something like 'cells' or 'food' is great.
2. **Say:** Your body is built from four big molecule types, called macromolecules. Each one is like a train made of repeating boxcars: carbs are sugar boxcars for quick energy, lipids are fatty acids on glycerol for long-term storage, proteins are amino acid boxcars that do jobs, and nucleic acids are nucleotide boxcars that store instructions. Which one do you think is the 'instruction manual' train?
   Look for: Nucleic acids (DNA/RNA), stores instructions.
3. **Say:** Quick check: if a molecule is made of amino acid boxcars, which macromolecule is it, and what's its job?
   Look for: Protein; does jobs like building muscle or speeding up reactions.
4. **Say:** Another one: what boxcar makes up a carbohydrate, and what does that molecule do for you?
   Look for: Monosaccharides (sugar boxcars); gives quick energy.
5. **Say:** New case: a scientist finds a molecule made of fatty acids attached to glycerol, stored in a bear's body all winter. Which macromolecule is it, and why does that fit a hibernating bear?
   Look for: Lipid/fat, fits because lipids store energy long-term, which the bear needs to survive winter without eating.
6. **Say:** Last check: if I told you a boxcar train is made of nucleotides, what am I holding, and what's stored inside it?
   Look for: DNA or RNA (nucleic acid); it stores instructions for the cell.
7. **Say:** You've got the four trains down, carbs, lipids, proteins, nucleic acids. Let's head into the practice questions and spot them in new examples.
   Look for: Student is ready to move into practice questions.

If they get stuck

- *When a substance like water evaporates or a liquid disappears when heated, some of it changes into carbon dioxide or another new substance.*
  In Lesson 1's retrieval and again in Lesson 2, explicitly contrast a physical change (ice melting, water evaporating, same molecule, different arrangement/motion) against a chemical change (dehydration synthesis forming a new bond) using a labeled particle diagram for each, side by side.
- *Molecules bind to each other (like enzyme and substrate) simply because their shapes fit together like puzzle pieces, not because of random collision plus a stable resulting configuration.*
  In Lesson 11, after introducing the lock-and-key model, explicitly add the random-collision layer: substrate and enzyme move randomly in solution; most collisions do not result in binding; only a correctly oriented, correctly shaped collision does. Ask the student to explain why increasing substrate concentration increases reaction rate, which only makes sense under the collision model.
- *A protein or enzyme comes apart or changes shape because something actively pulls it apart on purpose, not because of random thermal motion of molecules.*
  In Lesson 12, use a physical hydrogen-bond model (paperclip chain or molecular kit) and have the student physically shake it with increasing energy to show that the bonds break from increased random motion, not from a targeted, purposeful action, then require the student to redescribe denaturation in those terms before moving to the enzyme-temperature graph.

Read together FOR THE STUDENT

Your body is built from four main kinds of big molecules, called macromolecules. Think of each one like a train made of repeating boxcars. Carbohydrates are made of sugar boxcars (monosaccharides) and give you quick energy. Lipids (fats) are made of fatty acids attached to glycerol and store energy long-term. Proteins are made of amino acid boxcars and do jobs like building muscle or speeding up reactions. Nucleic acids (DNA and RNA) are made of nucleotide boxcars and store instructions for the cell.

Going further: Living things are built from four classes of macromolecules, each made of repeating smaller units called monomers. Carbohydrates are built from monosaccharides and function mainly as quick energy and structural support. Lipids are built from fatty acids and glycerol and function as long-term energy storage and membranes. Proteins are built from amino acids and function as enzymes, structural material, and transporters. Nucleic acids are built from nucleotides and function to store and transmit genetic information.

Watch it work

A worksheet asks: 'Name the macromolecule class, its monomer, and its main function, for the molecule that makes up muscle tissue and enzymes.'

1. Identify the class first: muscle tissue and enzymes are both proteins, this matches the function 'builds structures and speeds up reactions' taught in Lesson 5.
2. State the monomer: proteins are built from amino acids, the repeating unit taught alongside protein structure.
3. State the function in one sentence: proteins provide structural support and catalyze (speed up) chemical reactions in the cell.
4. Check the answer only uses names given in instruction, 'protein' and 'amino acid' were both taught directly, so no new term was generated.

The idea: Recall items are answered by matching the described function back to the exact class-monomer-function triple given in instruction, not by reasoning out a new name.

A student is asked: 'DNA is an example of which macromolecule class, and what is its monomer called?'

1. Recognize DNA as the class 'nucleic acid,' the term taught for molecules that store genetic information.
2. Recall the monomer name taught for this class: nucleotide.
3. State the one-sentence function taught for this class: nucleic acids store and transmit genetic instructions.
4. Confirm both 'nucleic acid' and 'nucleotide' were presented as vocabulary in Lessons 3-8, so this is a direct recall, not a generated term.

The idea: Each macromolecule class has exactly one class name and one monomer name to recall, DNA is an example of the class, not a synonym for the monomer.

Practice: Macromolecule class names, monomer names, and functional roles

1. Which monomer name matches the macromolecule class 'carbohydrate'?

(A) Amino acid (B) Nucleotide (C) Fatty acid (D) Monosaccharide

2. Which one-sentence function was taught for proteins?

(A) They provide quick energy for the cell.

(B) They store and transmit genetic instructions from one generation to the next.

(C) They store energy for long-term use.

(D) They provide structural support and speed up chemical reactions.

3. Which two building blocks make up a lipid?

(A) Fatty acids and glycerol (B) Monosaccharides and amino acids

(C) Amino acids and nucleotides (D) Nucleotides and glycerol

4. A student sees a diagram of a long chain of amino acids folded into a shape. Which macromolecule class and function does this match?

(A) Nucleic acid; stores and transmits genetic instructions

(B) Protein; provides structure and speeds up reactions

(C) Carbohydrate; provides quick energy for the cell to use

(D) Lipid; stores energy for the cell to use much later on

5. A textbook sentence reads: 'This molecule is built from nucleotides and carries the instructions for building an organism.' Which class and monomer does this describe?

(A) Carbohydrate; monosaccharide (B) Nucleic acid; nucleotide (C) Lipid; fatty acid

(D) Protein; amino acid

6. Which class-monomer pair is correctly matched?

(A) Nucleic acid - amino acid (B) Protein - nucleotide (C) Lipid - monosaccharide

(D) Carbohydrate - monosaccharide

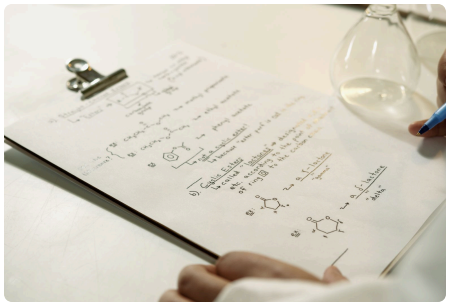
7. A student writes: 'When the enzyme in this reaction denatures, it's because the heat attacks the enzyme and breaks it apart on purpose to protect the cell.' Which macromolecule class is being described, and what is wrong with the explanation of WHY it changes shape?

- **A** It describes a protein, and the error is treating the shape change as the protein or heat acting on purpose, rather than random thermal motion overwhelming the weak bonds holding its folded shape.
- **B** It describes a lipid, and the error is calling glycerol a fatty acid.
- **C** It describes a protein, and the error is that enzymes cannot be affected by heat at all.
- **D** It describes a nucleic acid, and the error is naming the wrong monomer.

8. A diagram shows glycerol attached to three fatty acid chains, labeled as storing energy for later use. Which class and function does this match, and which incorrect idea would a student be applying if they instead called this molecule's parts 'monomers that repeat like sugar units'?

- **A** Nucleic acid, storing genetic instructions; the incorrect idea would be applying the protein amino-acid-chain pattern to nucleic acids, which are built from nucleotides rather than amino acids.
- **B** Lipid, storing long-term energy; the incorrect idea would be applying the carbohydrate/monosaccharide repeating-unit pattern to lipids, which are not built the same way.
- **C** Protein, providing structure; the incorrect idea would be applying the nucleic acid pattern to proteins.
- **D** Carbohydrate, providing quick energy; the incorrect idea would be applying the lipid glycerol-and-fatty-acid pattern to carbohydrates, which are built from sugar units instead of fatty acid chains.

Enzymes as catalysts that lower activation energy via substrate-specific shape complementarity



Goal: The student explains why enzymes lower activation energy without being consumed in the reaction, using the enzyme-substrate specificity model for a specific worked enzyme-substrate pair.

About 40 minutes

Teach it FOR THE PARENT

1. **Say:** Picture a huge hill you have to climb before you can even start rolling on your bike. Tiring, right? Now, what if something could make that hill way shorter, just for you? Ready to meet the thing that does that for reactions inside your body?
   Look for: Engagement; no right answer needed, just readiness to move on.
2. **Say:** An enzyme is like a bike-repair stand at the bottom of that hill. The hill is 'activation energy', the extra push a reaction needs to start. The stand doesn't push the rider and doesn't get used up. It just holds the bike (using its exact shape) so the climb is way shorter. Then it's empty again, ready for the next bike.
   Look for: Student reads through; no response required yet.
3. **Say:** Quick check: does the repair stand get used up after one bike uses it? And does it push the rider up the hill itself?
   Look for: No, it doesn't get used up. No, it doesn't push, it just repositions the bike so the climb is shorter.
4. **Say:** One more: what part of the enzyme lets it fit one specific molecule, like invertase fitting sucrose, and not just any molecule?
   Look for: Its exact shape, the shape matches the specific molecule, like a stand shaped to hold one kind of bike.
5. **Say:** New case: an enzyme called lactase breaks down lactose (milk sugar). After lactase helps one lactose molecule split apart, what happens to the lactase, does it wear out, change shape, or stay the same, ready for the next one?
   Look for: Lactase stays the same shape and is ready to work on another lactose molecule, same shape, same job, over and over.
6. **Say:** So if lactase stays exactly the same after each use, could one single lactase molecule help break down thousands of lactose molecules over time? Why or why not?
   Look for: Yes, because the enzyme isn't used up or changed, it can be reused again and again on new molecules.
7. **Say:** You've got it: an enzyme lowers the hill (activation energy) using its exact shape, without being used up. Let's lock that in with some practice questions.
   Look for: Student moves on to practice questions.

If they get stuck

- *When a substance like water evaporates or a liquid disappears when heated, some of it changes into carbon dioxide or another new substance.*
  In Lesson 1's retrieval and again in Lesson 2, explicitly contrast a physical change (ice melting, water evaporating, same molecule, different arrangement/motion) against a chemical change (dehydration synthesis forming a new bond) using a labeled particle diagram for each, side by side.
- *Molecules bind to each other (like enzyme and substrate) simply because their shapes fit together like puzzle pieces, not because of random collision plus a stable resulting configuration.*
  In Lesson 11, after introducing the lock-and-key model, explicitly add the random-collision layer: substrate and enzyme move randomly in solution; most collisions do not result in binding; only a correctly oriented, correctly shaped collision does. Ask the student to explain why increasing substrate concentration increases reaction rate, which only makes sense under the collision model.
- *A protein or enzyme comes apart or changes shape because something actively pulls it apart on purpose, not because of random thermal motion of molecules.*
  In Lesson 12, use a physical hydrogen-bond model (paperclip chain or molecular kit) and have the student physically shake it with increasing energy to show that the bonds break from increased random motion, not from a targeted, purposeful action, then require the student to redescribe denaturation in those terms before moving to the enzyme-temperature graph.

Read together FOR THE STUDENT

Think of an enzyme like a bike-repair stand at the bottom of a big hill. Without it, a rider (the reaction) has to climb the whole hill to get anywhere, that climb is the 'activation energy,' the extra push a reaction needs to start. The repair stand doesn't push the rider itself, and it isn't used up. It just holds the bike in a better position (using its exact shape, like sucrose-fitting invertase does with a sucrose molecule) so the climb is much shorter. When the rider rolls off the other side, the stand is empty again, ready for the next bike. That's an enzyme: same shape, same job, over and over.

Going further: An enzyme is a protein catalyst: it speeds up a reaction by lowering the activation energy, the energy barrier that reactant molecules must clear before they can turn into products. It does this through shape complementarity, the enzyme's active site has a 3-D shape that matches one specific substrate. Random collisions happen constantly in solution; most go nowhere, but when substrate and active site collide in the correct orientation, the enzyme stabilizes the transition state (the unstable, in-between arrangement of atoms at the top of the energy barrier), lowering the energy needed to reach it. Once product forms and releases, the enzyme's shape is unchanged, so it is not consumed and can bind another substrate molecule.

Watch it work

Explain, using the enzyme sucrase and its substrate sucrose, why sucrase speeds up the breakdown of sucrose into glucose and fructose without being used up, and why the reaction needs sucrase's specific shape to happen quickly.

1. State the barrier: breaking sucrose into glucose and fructose requires enough energy to reach an unstable in-between arrangement of atoms (the transition state) before the bonds can rearrange. Without help, few sucrose molecules moving around in solution have enough energy from random collisions alone to reach that arrangement, so the reaction is slow. This is why the energy diagram for the uncatalyzed reaction shows a tall hump between reactant and product.
2. Explain the shape match: sucrase's active site has a 3-D shape and chemical groups that are complementary to sucrose's shape, not to glucose, not to fructose alone, and not to other sugars like lactose. Sucrose molecules are colliding with sucrase constantly through normal random thermal motion; most collisions are at the wrong angle or wrong part of the enzyme and go nowhere. When a sucrose molecule happens to collide with the active site in the correct orientation, it fits and binds.
3. Explain the lowered barrier: once bound in the active site, sucrose is held in a strained, precisely positioned arrangement that is close to the transition-state geometry already. This means less additional energy is needed to reach the transition state, the hump on the energy diagram is much shorter for the catalyzed path than the uncatalyzed path. The starting and ending energy levels (reactants and products) do not change; only the height of the barrier changes.
4. Explain why sucrase is not consumed: after the bonds rearrange and glucose and fructose are released from the active site, sucrase's own shape returns to exactly what it was before binding. Nothing about sucrase's structure was permanently altered by the reaction. Because its shape is unchanged, it can immediately bind another sucrose molecule and repeat the same process, this is why one sucrase molecule can process many sucrose molecules over time instead of reacting once and disappearing.

The idea: Lowering activation energy and not being consumed are the same structural fact seen twice: the enzyme's shape stabilizes the transition state during binding, then returns unchanged after product release, so it can repeat the process.

A student says: 'Catalase grabs onto hydrogen peroxide because its shape is looking for that molecule, and that's why the reaction happens fast.' Explain what is missing from this statement and correct it using the random-collision model.

1. Identify the gap: the statement treats catalase's shape as sufficient on its own to make binding happen, as if the enzyme is actively searching for or seeking out hydrogen peroxide. This skips the actual mechanism, molecules in a cell are in constant random thermal motion and collide with each other in random directions and orientations, catalase included. Catalase does not move toward hydrogen peroxide or sense where it is.
2. Correct the mechanism: catalase and hydrogen peroxide molecules collide with each other by chance, the same way any two molecules in solution do. Most of these random collisions are unproductive because they happen at the wrong angle or hit the wrong part of the enzyme's surface, not the active site.
3. Explain what the shape actually does: on the occasions when a random collision brings hydrogen peroxide into the active site in the correct orientation, catalase's complementary shape allows binding to occur and holds the molecule in a strained position close to the transition state. The shape's job is to make a correctly oriented random collision productive, not to attract or seek the substrate from a distance.
4. State the corrected explanation: catalase speeds up the breakdown of hydrogen peroxide because its active-site shape converts the rare, correctly oriented random collisions into successful binding events that lower the activation energy needed for the reaction, not because the enzyme is actively hunting for its substrate.

The idea: Shape complementarity determines what happens once a collision occurs (whether it becomes productive); it does not explain why the collision happens in the first place, that is random thermal motion.

Practice: Enzymes as catalysts that lower activation energy via substrate-specific shape complementarity

1. Look at an energy diagram for a reaction with and without an enzyme present. Compared to the uncatalyzed path, what does the enzyme-catalyzed path show?

- **A** No hump at all, since the enzyme's shape removes the need for activation energy entirely.
- **B** A shorter hump than the uncatalyzed path, but the product ends up at a lower energy level than it does in the uncatalyzed reaction, since the enzyme adds energy.
- **C** A shorter hump (lower activation energy) between reactants and products, with reactant and product energy levels unchanged.
- **D** The same size hump as the uncatalyzed path, but it is reached faster because the enzyme pulls the reactant molecules together so they collide more often.

2. Sucrase breaks down thousands of sucrose molecules one after another. After sucrase releases one pair of glucose and fructose molecules, what is true of the sucrase molecule itself?

- **A** It has been used up and a new sucrase molecule must be made before the next reaction.
- **B** Its shape has returned to what it was before binding, so it can bind another sucrose molecule.
- **C** It stays bound to the glucose and fructose so it can keep them close together.
- **D** Its shape has changed slightly, because it lost a small piece to the products during the reaction.

3. A beaker of water is heated until it boils and turns to steam that you can no longer see. Using what you know about physical versus chemical change, is this an example of a substance being 'used up' in the way an enzyme is NOT used up in a reaction?

(A) Yes, because the water is chemically consumed in the boiling in exactly the same way that a reactant is consumed and turned into something new in a chemical reaction.

(B) No, because water vapor is a completely different substance from liquid water.

(C) No, the water molecules are still water, just spread further apart as a gas; no new substance formed, so nothing was 'used up' or 'produced' chemically.

(D) Yes, because the water changes into carbon dioxide and then disappears from the beaker, which is similar to the way that reactants change into products and are used up during a reaction.

4. Catalase and hydrogen peroxide molecules are both present in a cell, moving randomly. Which statement best explains why catalase and hydrogen peroxide actually come into contact in the first place, before any binding can occur?

(A) Both molecules are undergoing constant random thermal motion in the cell, which causes them to collide with each other by chance.

(B) The cell arranges catalase and hydrogen peroxide near each other so that binding is guaranteed to happen quickly.

(C) Catalase's active site shape is exactly complementary to hydrogen peroxide, so catalase actively moves toward and grabs it.

(D) Hydrogen peroxide is drawn toward catalase because catalase has a stronger chemical pull on it than on other molecules nearby.

5. A student explains denaturation this way: 'When the temperature gets too high, the heat attacks the enzyme's active site and destroys its shape on purpose so the enzyme can't work anymore.' What is the best correction to this explanation, using the random-motion model?

(A) Heat changes the enzyme's active site so it becomes complementary to a different substrate instead of losing its shape.

(B) The enzyme senses the rising temperature and deliberately unfolds itself to protect the rest of the cell from overheating.

(C) Heat increases the random motion of all the molecules that make up the protein, and this increased motion overwhelms the weak bonds holding the folded shape together, so the shape falls apart, nothing is attacking it on purpose.

(D) The explanation is basically correct, heat does actively attack and break apart the enzyme's active site to stop the reaction.

6. Two students argue about sucrase. Student 1 says: 'Sucrase's shape matching sucrose is what makes sucrose molecules bump into sucrase in the first place.' Student 2 says: 'Sucrose molecules bump into sucrase due to random motion regardless of shape; the shape only decides whether that bump actually results in binding.' Which student's reasoning matches the model in the worked examples, and why?

(A) Student 2, because shape complementarity determines whether a collision is productive, not whether a collision happens at all, collisions happen due to random thermal motion regardless of shape.

(B) Both of the students are right, because shape complementarity and random thermal motion work together equally to cause the initial collision between sucrase and sucrose, with the shape steering the molecule and the motion carrying it.

(C) Neither student, because sucrase and sucrose molecules do not need to physically collide for binding to occur.

(D) Student 1, because a matching shape between two molecules creates an attraction that pulls them toward each other from a distance, so sucrose molecules are drawn to sucrase before any collision happens.

7. Using the catalase-hydrogen peroxide pair, write a complete explanation (in your own reasoning, then check against the choices below) for why catalase speeds up the breakdown of hydrogen peroxide without being consumed. Which option below contains a complete, correctly connected explanation covering both the speed and the reusability?

(A) Hydrogen peroxide molecules collide randomly with catalase; the ones that don't fit the active site are rejected, while the ones that do fit are converted directly into a new type of enzyme that continues the reaction.

(B) Catalase's complementary shape lowers the activation energy of the reaction on its own, and separately, catalase happens not to be consumed because it is a very stable molecule that resists chemical change in general.

(C) Catalase's shape is complementary to hydrogen peroxide, so it actively seeks out hydrogen peroxide molecules and draws them in; once the peroxide is bound in the active site, the strong attraction between the two molecules supplies all of the energy that is needed to break the peroxide apart into water and oxygen, and the catalase molecule is then regenerated by the cell afterward so that it can be reused, which is why it appears not to be consumed even though each reaction uses one copy of it up.

(D) Random collisions occur between catalase and hydrogen peroxide due to thermal motion; when a collision correctly orients hydrogen peroxide in catalase's complementary active site, it is held in a strained position close to the transition state, lowering the activation energy needed to break it down; after breakdown, catalase's shape returns unchanged, so it can repeat the process with another hydrogen peroxide molecule.

8. A textbook energy diagram shows the uncatalyzed and catalase-catalyzed breakdown of hydrogen peroxide on the same graph. A student claims: 'The catalyzed line ends at a lower energy point than the uncatalyzed line, which is further proof that catalase makes the reaction happen.' Is this reasoning about the diagram correct?

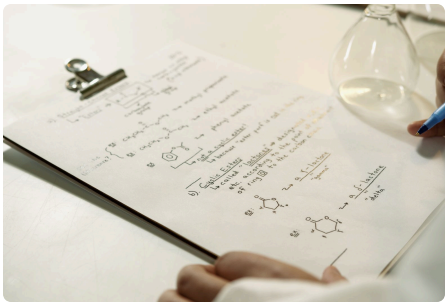
(A) Yes, because a faster reaction always releases more total energy than a slower one.

(B) No, both lines should end at the same product energy level; only the height of the hump in between differs between the two paths.

(C) No, actually neither line should show any change in energy at all, since energy is only used up during the reaction, not released or absorbed.

(D) Yes, a catalyzed reaction always ends at a lower final energy than an uncatalyzed one, which is part of why it's considered faster.

The relationship between temperature/pH-induced denaturation and loss of enzyme activity



Goal: Given an activity-vs-temperature (or activity-vs-pH) graph for an enzyme the student has never seen, the student predicts the shape of the curve's declining region and justifies the prediction in terms of denaturation changing the active site's shape.

About 40 minutes

Teach it FOR THE PARENT

1. **Say:** If you leave an egg white in a hot pan, it turns solid and cloudy, and it never goes back to clear no matter how you cool it. Why do you think heat changes it so much and so permanently?
   Look for: A guess that heat changes the structure or shape of something in the egg, even if the word 'protein' doesn't come up.
2. **Say:** An enzyme is a protein that speeds up a reaction, but only if its shape lets a substrate, the molecule it works on, fit into one spot called the active site. Heat or the wrong pH makes molecules jiggle harder and pulls apart the weak bonds holding that shape folded. Once the shape sags, the substrate doesn't fit anymore, so the enzyme stops working.
   Look for: Nothing to judge yet, this is the setup for the check.
3. **Say:** Quick check: why does an enzyme stop working when it gets too hot? Is it the enzyme running out, or something else?
   Look for: Answer says the enzyme's shape changes (unfolds/sags) so the substrate no longer fits the active site, not that it 'runs out' or 'burns up'.
4. **Say:** Here's a new case: a scientist adds a strong acid to a test tube of enzyme and substrate, and the reaction slows way down, even though the temperature never changed. What do you think the acid did?
   Look for: Prediction that the wrong pH (from the acid) disrupted the weak bonds holding the enzyme's shape, changing the active site so the substrate fits poorly, same idea as heat, different cause.
5. **Say:** One more: if you slowly raise the temperature past the enzyme's best point, does activity stop all at once, or fade out? Why?
   Look for: Answer says activity fades gradually, more heat means more and more of the enzyme's shape sags, so less and less activity, not a sudden stop.
6. **Say:** You've got the key idea: shape controls fit, and fit controls function. Let's try some practice questions where you spot this happening in different situations.
   Look for: Student is ready to move into practice questions.

If they get stuck

- *When a substance like water evaporates or a liquid disappears when heated, some of it changes into carbon dioxide or another new substance.*
  In Lesson 1's retrieval and again in Lesson 2, explicitly contrast a physical change (ice melting, water evaporating, same molecule, different arrangement/motion) against a chemical change (dehydration synthesis forming a new bond) using a labeled particle diagram for each, side by side.
- *Molecules bind to each other (like enzyme and substrate) simply because their shapes fit together like puzzle pieces, not because of random collision plus a stable resulting configuration.*
  In Lesson 11, after introducing the lock-and-key model, explicitly add the random-collision layer: substrate and enzyme move randomly in solution; most collisions do not result in binding; only a correctly oriented, correctly shaped collision does. Ask the student to explain why increasing substrate concentration increases reaction rate, which only makes sense under the collision model.
- *A protein or enzyme comes apart or changes shape because something actively pulls it apart on purpose, not because of random thermal motion of molecules.*
  In Lesson 12, use a physical hydrogen-bond model (paperclip chain or molecular kit) and have the student physically shake it with increasing energy to show that the bonds break from increased random motion, not from a targeted, purposeful action, then require the student to redescribe denaturation in those terms before moving to the enzyme-temperature graph.

Read together FOR THE STUDENT

An enzyme is a protein that speeds up a reaction, and it only works if its shape lets the substrate fit into one spot called the active site, like a specific key fitting a lock. Heat or wrong pH makes molecules jiggle harder and pulls apart the weak bonds holding that shape folded. Once the shape sags, the substrate no longer fits, so activity drops. Past a point, more heat just means less and less activity, not a sudden stop.

Going further: Enzyme activity depends on the active site's shape matching the substrate. Temperature and pH affect the weak hydrogen and ionic bonds that hold a protein's folded (tertiary) structure. Past the optimum, rising temperature or shifting pH increases molecular motion enough to break these bonds, this is denaturation. As more molecules denature, fewer active sites bind substrate correctly, so the activity curve declines. The decline is gradual, not a cliff, because molecules denature at different rates.

Watch it work

An enzyme found in a hot spring bacterium has an activity-vs-temperature graph. Activity rises from 20°C to a peak at 70°C, then declines from 70°C to 95°C. Predict the shape of the decline from 70°C to 95°C and justify it.

1. Identify what the rising part means: as temperature increases toward 70°C, molecules move faster, so more productive collisions between enzyme and substrate happen, activity increases because the active site is still correctly shaped.
2. Identify what happens past 70°C: temperature keeps increasing, so molecular motion keeps increasing too. This extra motion is now strong enough to break the hydrogen and ionic bonds holding the enzyme's folded shape.
3. Connect bond-breaking to the active site: once those bonds break, the protein's three-dimensional shape changes, including the active site. A changed active site no longer matches the substrate's shape, so binding, and the reaction, stops happening at that molecule.
4. State the shape of the decline: because different enzyme molecules in the population reach their breaking point at slightly different moments, the drop is a smooth, gradual downward curve, not a sudden vertical drop to zero right at 70°C.

The idea: The decline is gradual because denaturation happens to individual molecules at slightly different points, not to the whole population at once.

An enzyme in the human stomach works best around pH 2. Its activity-vs-pH graph shows a peak near pH 2 and a decline from pH 2 to pH 7. Predict and justify the shape of that decline.

1. Note what pH measures here: it reflects the concentration of H+ ions, which affects the ionic bonds between charged parts of the protein that hold its folded shape.
2. Reason about moving away from pH 2: as pH rises toward 7, the H+ concentration drops sharply compared to the enzyme's optimum environment, which disrupts the ionic bonds that depend on that specific charge balance.
3. Connect bond disruption to shape and function: disrupted ionic bonds cause the protein to unfold or change shape, which changes the active site so the substrate no longer fits, lowering the reaction rate.
4. Predict the curve shape: because the shift away from optimal pH affects different enzyme molecules gradually as conditions change, the decline is a smooth downward curve rather than an instant drop to zero right after pH 2.

The idea: The same denaturation logic applies to pH as to temperature: whatever variable disrupts the bonds holding the folded shape produces a gradual decline once you pass the optimum.

Practice: The relationship between temperature/pH-induced denaturation and loss of enzyme activity

1. An enzyme's activity-vs-temperature graph shows a peak at 40°C. What happens to the shape of the enzyme's active site as temperature rises past 40°C?

- **A** It stays exactly the same shape; only the substrate changes.
- **B** It changes shape because the substrate stops fitting, which then causes the temperature to rise.
- **C** It changes shape because rising temperature breaks the bonds holding the protein folded.
- **D** It changes shape because the heat is attacking and destroying the protein on purpose.

2. A student says: 'The enzyme's active site grabs its substrate because the two shapes fit together like puzzle pieces, and that's the whole explanation for why they bind.' What is missing from this explanation?

- **A** Nothing, shape fitting like puzzle pieces is the complete explanation for binding.
- **B** The explanation needs to include that the enzyme changes its own shape to match whatever substrate happens to approach it, so that any substrate can be bound.
- **C** The explanation needs to include that enzyme and substrate collide randomly, and only a correctly shaped collision leads to binding.
- **D** The explanation needs to include that the substrate melts slightly to fit into the active site.

3. A beaker of water is heated until it boils away completely as steam. A student claims some of the water turned into carbon dioxide. Is this correct, and why does this matter for understanding enzyme denaturation?

(A) The student is correct that some of the water turned into carbon dioxide, and the same new-substance idea explains why heat changes an enzyme's shape, since a denatured enzyme is a new substance too.

(B) The student is incorrect, the water molecules stay intact and just spread apart as gas; similarly, a denatured enzyme is still the same protein molecule, just unfolded.

(C) The student is incorrect, but only because water cannot be heated past its boiling point at all, so no new substance could form; this matters because an enzyme likewise cannot be heated past the point where it denatures.

(D) The student is correct, because heating always produces new chemical substances from the old ones, which is exactly why heat turns an enzyme into a different molecule when it denatures.

4. An enzyme's activity-vs-temperature graph declines from its optimum of 50°C up to 80°C. Which shape of decline best matches what denaturation predicts, and why?

(A) The curve stays flat at its peak value all the way to 80°C.

(B) A sudden vertical drop straight to zero exactly at 50°C.

(C) A gradual, smooth downward curve from 50°C to 80°C.

(D) The curve rises again after 50°C because the enzyme adapts to the new temperature.

5. A student explains a declining enzyme activity curve this way: 'As pH moves away from the optimum, the enzyme senses the danger and deliberately unfolds itself to stop working before it gets damaged.' What is the core error in this explanation?

(A) It wrongly assumes pH can affect enzymes, when only temperature can.

(B) It correctly describes the enzyme's shape changing, so there's no error.

(C) It wrongly gives the enzyme intent and purpose, when the shape change actually results from ionic bonds being disrupted by the pH shift.

(D) It wrongly claims the enzyme's shape changes at all.

6. Two enzymes, X and Y, both show activity-vs-temperature curves that rise to a peak then decline. Enzyme X's decline is much steeper (drops to near zero within 5°C past its peak) than Enzyme Y's decline (drops gradually over 30°C). What does this difference most likely reflect?

- **A** Enzyme X is not a real protein at all, since real proteins always decline gradually past their peak and never drop to near zero within 5°C.
- **B** Enzyme X deliberately shuts down faster to protect the cell from damage.
- **C** Enzyme X's substrate changed into a completely different molecule at the higher temperature, so there was nothing left for the enzyme to act on.
- **D** Enzyme X's molecules all happen to denature within a narrower range of temperatures than Enzyme Y's molecules.

7. On an activity-vs-temperature graph, what does the x-axis point where activity is highest (the peak) represent for an enzyme?

- **A** The exact temperature of the human body, which is the peak for every enzyme regardless of which enzyme is being studied or where it comes from.
- **B** The temperature at which the enzyme first starts to denature, since activity can only be highest right before the enzyme begins to lose its shape.
- **C** The temperature at which the substrate turns into product on its own without needing the enzyme at all, since the enzyme is no longer required past that point.
- **D** The temperature at which the enzyme's active site shape best matches the substrate, allowing the most successful binding.

The disproportionate functional consequence of a single amino-acid substitution on protein shape and function

Goal: The student critiques a claim that 'a small change in one amino acid can't matter much because the protein is still made of the same building blocks,' using evidence from sickle-cell hemoglobin or an equivalent case not previously discussed in class.

About 50 minutes

Teach it FOR THE PARENT

1. **Say:** Imagine a necklace with 146 beads. You swap just ONE bead for a similar-looking one. Still basically the same necklace, right? Let's see if that's true for proteins.
   Look for: Student engages with the question, maybe guesses yes or no.
2. **Say:** A protein is a chain of amino acids, like beads on a string. The ORDER of those beads decides how the chain folds into a 3D shape. And that shape decides the protein's job. Change one bead, and sometimes the whole shape changes.
   Look for: Student can restate: order of amino acids -> shape -> job.
3. **Say:** Quick check: what decides the SHAPE a protein folds into?
   Look for: Answer mentions the order/sequence of amino acids (the beads).
4. **Say:** Here's the real case: sickle-cell hemoglobin. Out of 146 amino acids, just 1 is swapped. That tiny swap changes the fold enough that red blood cells bend into a sickle shape and get stuck in blood vessels.
   Look for: Student can say: 1 out of 146 changed, shape changed, cells got stuck.
5. **Say:** So was the person right who said 'swapping one bead is no big deal'? Why or why not?
   Look for: Student says the person was wrong, one small swap can change shape enough to change function, using sickle-cell as evidence.
6. **Say:** New case: imagine an enzyme (a protein that speeds up a reaction) has 1 amino acid swapped, right at the spot where it grabs its target molecule. Predict: will the enzyme still work the same? Why?
   Look for: Student predicts the enzyme likely won't work the same, reasoning that the swap could change the shape at the exact spot needed to grab the target.
7. **Say:** What if that same enzyme swapped an amino acid somewhere far from the important grabbing spot? Would you expect a bigger or smaller effect?
   Look for: Student reasons that a swap far from the key working spot might change shape less, so a smaller effect is likely (not guaranteed, but reasonable).
8. **Say:** You've got the big idea: one small change in the amino acid chain can change shape, and shape changes the job. Let's practice spotting this in a few more questions.
   Look for: Student is ready to move to practice questions.

If they get stuck

- *When a substance like water evaporates or a liquid disappears when heated, some of it changes into carbon dioxide or another new substance.*
  In Lesson 1's retrieval and again in Lesson 2, explicitly contrast a physical change (ice melting, water evaporating, same molecule, different arrangement/motion) against a chemical change (dehydration synthesis forming a new bond) using a labeled particle diagram for each, side by side.
- *Molecules bind to each other (like enzyme and substrate) simply because their shapes fit together like puzzle pieces, not because of random collision plus a stable resulting configuration.*
  In Lesson 11, after introducing the lock-and-key model, explicitly add the random-collision layer: substrate and enzyme move randomly in solution; most collisions do not result in binding; only a correctly oriented, correctly shaped collision does. Ask the student to explain why increasing substrate concentration increases reaction rate, which only makes sense under the collision model.
- *A protein or enzyme comes apart or changes shape because something actively pulls it apart on purpose, not because of random thermal motion of molecules.*
  In Lesson 12, use a physical hydrogen-bond model (paperclip chain or molecular kit) and have the student physically shake it with increasing energy to show that the bonds break from increased random motion, not from a targeted, purposeful action, then require the student to redescribe denaturation in those terms before moving to the enzyme-temperature graph.

Read together FOR THE STUDENT

A protein is a long chain made of small pieces called amino acids, like beads on a string. The order of the beads decides how the string folds up into a 3D shape. Someone might say 'swapping one bead for a similar one is no big deal, it's still the same necklace.' But shape decides the job the protein does. Sickle-cell hemoglobin swaps just 1 amino acid out of 146. That one swap changes the folded shape enough that red blood cells bend into a sickle shape and get stuck in blood vessels. One bead changed everything.

Going further: A protein's function depends on its 3D shape, and its shape depends on the exact sequence of amino acids folding through interactions (hydrogen bonds, ionic bonds, hydrophobic clustering) at the secondary, tertiary, and quaternary levels. Changing one amino acid changes the chemical properties at that one spot, polar to nonpolar, charged to uncharged, which can disrupt folding or create a sticky surface. In sickle-cell hemoglobin, one substitution (glutamic acid to valine) creates a hydrophobic patch that makes hemoglobin molecules stick together, distorting red blood cell shape. Building blocks being 'the same' ignores that one block's chemistry can change the whole structure's behavior.

Watch it work

A student claims: 'Cystic fibrosis is caused by a change in a protein called CFTR, but proteins are just chains of amino acids, so one missing amino acid out of over 1,000 shouldn't change much, it's still basically the same chain.' Critique this claim using what you know about protein structure and function.

1. Identify what the claim gets right: CFTR is indeed a long chain of amino acids, and losing one out of 1,000+ does leave the vast majority of the sequence unchanged, this part is factually true and should not be denied.
2. Identify what the claim ignores: function depends on the folded 3D shape, not on the total count or proportion of amino acids that stayed the same. The most common CFTR mutation deletes one amino acid (phenylalanine) at a specific position needed for the protein to fold correctly.
3. Apply the structure-function link: because that one amino acid is needed for correct folding, its absence causes the protein to fold wrongly. A misfolded CFTR protein gets destroyed by the cell's quality-control system before it ever reaches the cell membrane, where it's needed to move chloride ions.
4. State the corrected conclusion: the claim's reasoning, 'small proportion changed, so small effect', is invalid because protein function depends on precise shape at specific positions, not on overall percentage of sequence changed. One critical position can matter more than the other 1,000+ correct ones.

The idea: Counting how much of the sequence stayed 'the same' is the wrong measure of impact; what matters is whether the changed position is structurally or functionally critical.

Compare two real substitutions in a hypothetical enzyme: Substitution A replaces one amino acid on the outer surface of the folded enzyme, far from where the substrate binds, with a chemically similar amino acid. Substitution B replaces one amino acid inside the active site (where the substrate binds) with a chemically very different one. Explain why these two 'single amino acid changes' would likely have very different effects, and use this to evaluate the general claim 'one amino acid change can't matter much.'

1. Locate each change in the protein's structure: Substitution A is on an exposed surface not involved in folding or binding; Substitution B is inside the active site, the specific region whose shape determines what molecule can bind and react.
2. Predict the effect of Substitution A: because the amino acid is chemically similar and not part of a functional region, the local shape and chemistry barely change, so the enzyme's folding and active-site shape stay intact, function is likely preserved.
3. Predict the effect of Substitution B: because the new amino acid has very different chemical properties (for example, a different charge or size) and sits in the active site, it can change the shape or chemistry of that pocket enough that the substrate no longer fits or reacts, function is likely lost or altered.
4. Generalize: 'one amino acid change' is not a single category of event. Its effect depends on where in the folded structure the change occurs and how different the new amino acid's chemistry is, so no blanket claim ('always minor' or 'always major') is defensible without knowing position and chemical difference.

The idea: Two single-amino-acid substitutions are not equivalent events, position within the folded structure and the chemical difference between old and new amino acid determine the consequence, not the fact that 'only one changed.'

Practice: The disproportionate functional consequence of a single amino-acid substitution on protein shape and function

1. In sickle-cell hemoglobin, one amino acid (glutamic acid) is replaced by a different amino acid (valine) at one position in the protein chain. Which statement is most accurate?

(A) The hemoglobin molecule deliberately changes its own shape to protect the red blood cell once it senses the substitution.

(B) Water and other small molecules in the cell must be reacting with the changed amino acid to produce a new substance, which is why hemoglobin behaves differently.

(C) The protein is still made of amino acids overall, so the small swap has no meaningful effect on the protein's function.

(D) The single substitution changes the local chemistry enough to alter the protein's shape and behavior, even though only one amino acid out of many differs.

2. A classmate says: 'Sickle-cell hemoglobin still has almost the exact same sequence as normal hemoglobin, 145 out of 146 amino acids match. That's a 99% match, so the protein should work almost the same.' What is the strongest response to this reasoning?

(A) Percent match isn't what determines function; the position and chemical difference of the one amino acid that changed is what matters, and in this case that one change disrupts the protein's normal shape.

(B) Since heat causes proteins to unfold, the body's own temperature must be denaturing the sickle-cell hemoglobin molecules after they are made, which is why the protein doesn't work the same as normal hemoglobin even though 145 out of 146 amino acids match.

(C) The enzyme that builds hemoglobin must be binding incorrectly to the chain because the new shape no longer fits into its usual binding pocket, so the protein is never finished properly and that is why it doesn't work the same, whatever the percent match happens to be.

(D) The 99% figure in the claim is simply wrong; sickle-cell hemoglobin actually has a completely different amino acid sequence from normal hemoglobin, so the two proteins are not nearly as similar as the classmate believes.

3. Which piece of evidence would most directly refute the claim 'a small change in one amino acid can't matter much because the protein is still made of the same building blocks'?

- **A** A count showing hemoglobin has 574 total amino acids across its four chains.
- **B** Data showing that sickle-cell hemoglobin molecules stick together and distort red blood cells into a sickle shape, while normal hemoglobin does not.
- **C** A list showing that all 20 of the standard amino acids are found in both normal hemoglobin and sickle-cell hemoglobin, in the very same amounts in each protein.
- **D** A statement in the textbook that amino acids are the monomers of all proteins, including hemoglobin, so both of the proteins are made from the same set of building blocks.

4. A textbook passage states: 'Hemoglobin's job is to bind oxygen. Since sickle-cell hemoglobin still has the same oxygen-binding sites made of the same amino acids, it should still bind oxygen just fine, the sickling problem must be something else entirely, unrelated to the amino acid change.' What is the best critique of this reasoning?

- **A** The amino acid change causes the whole hemoglobin protein to actively unfold itself to release trapped oxygen faster.
- **B** Sickling happens because the red blood cells release carbon dioxide gas when the amino acid changes, and that gas turns the water inside the cell into a new substance that deforms the cell into a sickle shape; the passage is right that the oxygen-binding sites are unaffected, but it misses that the sickling comes from this chemical change in the cell's water rather than from the protein at all.
- **C** The reasoning correctly separates oxygen-binding function from the sickling problem, but wrongly assumes these must be caused by two completely unrelated things, both actually trace back to the same single substitution, just affecting a different aspect of the protein's behavior (surface stickiness rather than the binding site).
- **D** The passage is entirely wrong from start to finish: the amino acid substitution destroys the oxygen-binding sites of the protein directly, which is the real reason that sickle-cell hemoglobin doesn't work, and the sickling of the red blood cells is just a side effect of the cells running out of oxygen; there is no separate stickiness problem on the protein's surface to explain, since the binding sites are the only part of the protein that matters.

5. Someone argues: 'A single amino acid substitution is such a tiny change at the molecular level, it's like changing one letter in a 500-page book. One letter can't change the meaning of the whole book, so it can't change the whole protein's function either.' What is the best response using what you know about protein structure?

(A) Books and proteins can't be compared because proteins are made of atoms while books are made of letters.

(B) The analogy is actually correct as it stands, since sickle-cell hemoglobin still functions as a protein at all and still binds oxygen, which shows that the single substitution really doesn't change very much about the molecule; one changed amino acid out of 146 is just like one changed letter in a long book, and the small differences that show up in sickle-cell disease come from other causes in the blood rather than from the substitution itself.

(C) One letter changing in a book is really like water evaporating from a pot: the meaning of the book turns into something else entirely even though all of the letters are still there on the page, just as the water turns into a new substance even though the molecules are still around; so the analogy fails because the person has the direction backwards, and a single amino acid change always turns the whole protein into a completely new kind of molecule with a new name.

(D) The analogy fails because, unlike most single-letter changes in a book (which are often typos that don't affect meaning), a single amino acid at a structurally critical position can change local chemistry enough to disrupt folding or create new interactions, the effect depends on WHERE the change falls, not on it being 'just one' change.

6. A student writes this critique: 'The claim is wrong because proteins are big, complicated molecules, and big complicated things are always sensitive to small changes.' Is this a strong critique of 'a small change in one amino acid can't matter much'?

(A) Yes, this is a strong critique, because it shows that the changed amino acid must be reacting with other molecules in the blood to form an entirely different substance, which is the real reason that a big complicated molecule like hemoglobin is so sensitive to small changes.

(B) No, this is not a strong critique, but only because proteins are not actually complicated molecules at all compared to other biomolecules like nucleic acids, so the student has the facts wrong about how complex hemoglobin is and the critique falls apart on that point alone.

(C) No, this critique doesn't explain WHY the change matters; it needs to describe how the substitution alters shape or chemistry at a specific location, not just assert that complex molecules are generally fragile.

(D) Yes, this is a strong critique, because complexity always implies sensitivity to small changes in any large molecule, so pointing out that proteins are big and complicated fully explains why sickle-cell hemoglobin is affected by one substitution and nothing more needs to be said about it.

7. In a different protein, insulin, most single amino acid substitutions studied in labs do NOT significantly change its function, unlike the sickle-cell hemoglobin case. A student concludes from this: 'This proves single amino acid changes generally don't matter much; sickle-cell hemoglobin must just be a rare exception.' Evaluate this conclusion.

(A) The conclusion overgeneralizes: whether a substitution matters depends on the specific position and its role in that protein's structure, so data about which positions are tolerant in insulin doesn't establish a general rule about all proteins or all positions.

(B) The conclusion is wrong, but only because insulin and hemoglobin are made of completely different sets of amino acids from each other, so nothing learned about substitutions in one protein can be compared to the other; if the two proteins shared the same amino acids, then the insulin data really would prove the general rule the student describes.

(C) The conclusion is correct, because insulin is a bigger and more important protein than hemoglobin is, so its resistance to single amino acid changes should be treated as the standard for all proteins, and the sickle-cell case is simply an unusual exception that happens in a smaller protein and should not count against the general rule.

(D) The conclusion is reasonable, since if most of the substitutions studied in insulin don't matter to its function, then the general rule for proteins should be that amino acid changes rarely matter, and the sickle-cell hemoglobin case is just a rare exception; a single well-studied protein like insulin gives enough data to set the rule for every other protein and every position in them.

8. A student writes: 'Sickle-cell hemoglobin proves that amino acid sequence doesn't really matter for protein shape, what matters is temperature, because heat is what actually unfolds proteins and destroys their function.' Critique this claim, using what the sickle-cell case actually shows.

(A) This claim misreads the sickle-cell case: the abnormal hemoglobin shape and behavior result directly from the amino acid sequence change (the substitution), not from temperature or unfolding, sequence, not heat, is the variable responsible here.

(B) The claim is correct, sickle-cell hemoglobin's problem is that body heat denatures the abnormal protein faster than it denatures normal hemoglobin.

(C) The claim is correct because proteins are always more sensitive to temperature than to their amino acid sequence.

(D) The claim is partly right, since heat and amino acid sequence work together to actively destroy protein shape whenever a substitution occurs.

Answer key

Science

Lesson 1	1. D 2. D 3. D 4. B 5. C 6. B 7. A 8. A
Lesson 2	1. C 2. A 3. C 4. D 5. B 6. D 7. A 8. E
Lesson 3	1. B 2. B 3. B 4. D 5. D 6. D 7. A
Lesson 4	1. A 2. C 3. C 4. C 5. B 6. B 7. C 8. B
Lesson 5	1. D 2. D 3. A 4. B 5. B 6. D 7. A 8. B
Lesson 6	1. C 2. B 3. C 4. A 5. C 6. A 7. D 8. B
Lesson 7	1. C 2. C 3. B 4. C 5. C 6. D 7. D
Lesson 8	1. D 2. A 3. B 4. C 5. D 6. C 7. A 8. A
Unit 1 check-up	1. C 2. C 3. B 4. D 5. A 6. A 7. A 8. D 9. A 10. C 11. A 12. C 13. A 14. C 15. D 16. B 17. A 18. D

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