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UNIT LEVEL DQ: Why is a body temperature of 107° F deadly?

INVESTIGATION 2: Why can't you uncook an egg?

Overview

In previous investigations students have seen that polar molecules have a stronger attraction for each other than nonpolar molecules and started talking about how protein structure provides function through interactions between the protein and other molecules. Through hands-on activities and simulations students will further explore how charges and contact area of interacting molecules affect the strength of attraction between proteins and other molecules they interact with. In the last activity students will explore how energy changes during interactions and how temperature affects stability of protein and ligand binding. This will help students answer the driving question for the unit "Why is a temperature of 107°F deadly?"

The Performance Expectations (NGSS)

HS-PS3-5. Develop and use a model of two objects interacting through electric or magnetic fields to illustrate the forces between objects and the changes in energy of the objects due to the interaction.

Elements from NGSS (NGSS Lead States, 2013, p. 97–99)	**Connections to this investigation**
Elements of Disciplinary Core Idea	
Elements of the core idea from the NGSS Performance Expectation	How this investigation builds toward the core ideas

Relationship Between Energy and Forces: • When two objects interacting through a field change relative position, the energy stored in the field is changed.	Any charged object has an electric field around it. When two charged objects interact the energy of the field changes depending on the arrangement of objects within the field and the magnitude of the charges. For example, when opposite charges are moved farther apart, the potential energy stored in the electric field between those charged objects is increased. In a previous investigation, students explored how energy changes when polar and nonpolar parts of proteins interact with each other to help maintain their three dimensional structure, which is essential for carrying out biological functions. In this investigation students will explore how temperature affects 3D structure of proteins and their ability to carry out biological functions.
Crosscutting concept	
Crosscutting concept from the NGSS Performance Expectation	How this investigation builds toward the crosscutting concept
Cause and effect: • Cause and effect relationships can be suggested and predicted for complex natural and human designed systems by examining what is known about smaller-scale mechanisms within the system.	Forces between different parts of proteins and interactions with surrounding water molecules cause the proteins to form into particular shapes. Associated with the changes in shape are changes in the electric field generating those forces and subsequent changes in in energy as the proteins arrange into structures that minimize potential energy. Temperature changes in the system are related to kinetic energy changes and changes in interactions formed between different parts of protein molecules causing distortion of the biologically active 3D structure and potential loss of biological activity.
Science and engineering practice	
Science and engineering practice from the NGSS Performance Expectation	How this investigation builds toward the science and engineering practice
Developing and Using Models: • Develop and use models based on evidence to illustrate the relationships between systems or between components of a system.	Students draw models and use simulations to explore what happens to 3D structure of proteins during various atomic and molecular rearrangements caused by temperature changes, how those rearrangements relate to changes in energy, and how those relationships can be used to explain observations.

HS-LS1-6. Construct and revise an explanation based on evidence for how carbon, hydrogen, and oxygen from sugar molecules may combine with other elements to form amino acids and/or other large carbon-based molecules. Clarification Statement: Emphasis is on using evidence from models and simulations to support explanations.

Elements from NGSS (NGSS Lead States, 2013, p. 97–98)	**Connections to this investigation**
Elements of Disciplinary Core Idea	
Elements of the core idea from the NGSS Performance Expectation	How this investigation builds toward the core ideas
Organization of Matter and energy Flow in Organisms: • The sugar molecules thus formed contain carbon, hydrogen, and oxygen; their hydrocarbon backbones are used to make amino acids and other carbon-based molecules that can be assembled into larger molecules (such as proteins or DNA) used, for example, to form new cells.	Proteins are made up of amino acids that can be classified as polar and nonpolar based on their atomic composition. Amino acids combine to form large protein molecules with a certain three dimensional arrangement. Interactions between polar parts of amino acids and nonpolar parts of amino acids help determine protein's shape and function.
Crosscutting concept	
Crosscutting concept from the NGSS Performance Expectation	How this investigation builds toward the crosscutting concept
Energy and Matter: • Changes of energy and matter in a system can be described in terms of energy and matter flows into, out of, and within that system.	Students explore the building blocks of organic molecules and see that carbon, oxygen, and hydrogen are the most common components of these molecules, including the amino acids used to make proteins. These atomic components are derived from the atoms in the food we eat. Increasing the temperature of the system affects kinetic energy, 3D structure and function of molecules within that system.
Science and engineering practice	
Science and engineering practice from the NGSS Performance Expectation	How this investigation builds toward the science and engineering practice

Constructing explanations and designing solutions: • Construct and revise an explanation based on valid and reliable evidence obtained from a variety of sources (including students' own investigations, models, theories, simulations, peer review) and the assumption that theories and laws that describe the natural world operate today as they did in the past and will continue to do so in the future.	Student will explore various 3D structures using interactive simulations to formulate explanations of how these structures are built from a small number of elements. Students will also explore how temperature changes affect 3D arrangement of atoms within these structures and their ability to carry out biological functions.

Objective: Target Model

What should the students' conceptual model include?

- *Polar and nonpolar molecules have different attractive forces.*
- *The different attractive forces between polar and nonpolar molecules affect how one substance dissolves or doesn't into another substance.*
- *Proteins are large molecules that have polar and nonpolar parts that can interact with each other and the surrounding molecules.*
- *The interactions within molecules and/or with other the molecules around them can cause specific structures to form.*
- *The resulting configurations result in lower potential energy for the entire system.*
- *The resulting configuration is affected by temperature of the system: higher temperature is associated with higher kinetic energy of the protein.*
- *Higher kinetic energy of the protein results in distorting and sometimes (if temperature is high enough) overcoming polar and nonpolar intermolecular interactions causing the 3D structure of the protein to be changed.*
- *Specific 3D structure is essential for protein to carry out its functions. If the 3D structure is changed, a protein can no longer carry out the intended function.*

Background Knowledge

Molecules interact with other molecules through intermolecular forces. Intermolecular forces in polar molecules are due to interactions between permanent partial charges. When the charge of interacting particles is stronger, the interaction between those particles is stronger. Intermolecular forces in nonpolar molecules are due to interactions between induced, temporary partial charges resulting from momentary uneven electron distribution due to electron motion. Since these forces are temporary and random, they are much weaker than more consistent polar interactions. As a result nonpolar molecules don't stick together as strongly as polar molecules, which is manifested in lower boiling points, lower viscosity and other properties.

Though the magnitude of polar and nonpolar interactions in intermolecular forces is smaller than in a bond, the forces and energy involved behave the same way as the forces that hold atoms together in bonds. When molecules are closer together, oppositely charged particles are closer, so the potential

energy in the field between those particles is reduced. Separating molecules causes the charged particles to be moved farther apart, increasing the potential energy associated with the electric field.

Proteins are large biological molecules that are made up of polar and nonpolar parts called amino acids. Three-dimensional structure of proteins is determined by attractive forces between nonpolar amino acids and attractive/repulsive forces between polar amino acids. The 3D arrangement results in a minimized energy state for the protein, and also the most biologically active structure of the protein. Maintaining 3D structure of the protein is essential for protein function, because specific 3D structure determines which other molecules a protein can interact with. For example, if the exterior of the protein is formed by polar amino acids arranged in specific 3D structure, a given protein will interact with other polar molecules that are complementary to the given protein structure as determined by attractive/repulsive forces generated between protein and other molecules.

Temperature affects molecular motion, so this can affect the stability of the 3D structure of a protein. Higher temperatures result in distorting and sometimes (if temperature is high enough) overcoming polar and nonpolar intermolecular interactions, causing the 3D structure of the protein to be changed., which prevents the protein from interacting with specific biological molecules, therefore making it biologically inactive.

Activities

Activity 2.1	*How do polar interactions affect protein structure and properties?*	*240 min.*
Activity 2.2	*How do antibodies help protect us from diseases?*	*90 min.*
Activity 2.3	*Why is a body temperature of 107° F deadly?*	*90 min.*

Activity 2.1: Why can't you uncook an egg?

SUMMARY

In previous investigations students have seen that polar molecules have a stronger attraction for each other than nonpolar molecules (for example, in hands-on activity 1.1 students dissolved different substances in polar and nonpolar liquids and observed that more polar substances tend to dissolve in water, and less polar substances tend to dissolve in hexane) . They started discussing how protein structure provides function through interactions between the protein and other molecules. Through a hands-on experience and simulations students will further explore how charges and contact area of interacting molecules affects the strength of attraction between proteins and other molecules they interact with. Students will also explore how energy changes during interactions and how temperature affects stability of protein and substrate binding. This will help students answer the driving question for the unit "Why temperature of 107F is deadly?".

LEARNING GOAL

Students will develop a model that predicts the relative strength of attraction between the polar and nonpolar parts of a protein and the polar and nonpolar parts of another molecule based on the magnitude of charges, shape and alignment of the molecules to explain why proteins interact with molecules of specific shape and atomic composition.

Disciplinary core idea	Crosscutting concept	Science and engineering practice
Relationship Between Energy and Forces: When two objects interacting through a field change relative position, the energy stored in the field is changed. (NGSS Lead States, p. 99)	*Cause and Effect* Cause and effect relationships can be suggested and predicted for complex natural and human designed systems by examining what is known about smaller-scale mechanisms within the system. (NGSS Appendix G, p. 83)	*Developing and using models:* • Develop, revise, and/or use a model based on evidence to illustrate and/or predict the relationships between systems or between components of a system. • Develop and/or use multiple types of models to provide mechanistic accounts and/or predict phenomena, and move flexibly between model types based on merits and limitations. (NGSS Appendix F, p. 53)

Students will develop a model that explains how temperature affects 3D structure and function proteins as related to polar and nonpolar interactions to explain why high temperature prevent proteins from forming interactions with substrates and carry out their biological function .

Disciplinary core idea	Crosscutting concept	Science and engineering practice

Relationship Between Energy and Forces: When two objects interacting through a field change relative position, the energy stored in the field is changed. (NGSS Lead States, p. 99)	*Cause and Effect* Cause and effect relationships can be suggested and predicted for complex natural and human designed systems by examining what is known about smaller-scale mechanisms within the system. (NGSS Appendix G, p. 83)	*Developing and using models:* • Develop, revise, and/or use a model based on evidence to illustrate and/or predict the relationships between systems or between components of a system. • Develop and/or use multiple types of models to provide mechanistic accounts and/or predict phenomena, and move flexibly between model types based on merits and limitations. (NGSS Appendix F, p. 53)

POINTS FOR CONSIDERATION

- Students tend to think of molecular attractions as being "broken" as a result of increase in temperature of the system. It is important to emphasize that intermolecular attractions are always there at any temperature, and it doesn't disappear after the interaction is "broken" as a result of increased temperature. Rather, the attractive forces that pull the amino acids together into biologically active 3D shape are *overcome* at higher temperature because at higher temperatures amino acids have more kinetic energy, and are able to move faster, and overcome these interactions that were initially holding them together. As a result, new interactions might be formed within the protein, which might results in a different 3D shape that is not biologically active, meaning that the protein can't form the same kind of interactions with other molecules that it could before it was heated.
- When discussing how temperature affects protein structure and function, and "lock and key" process specifically, students tend to think that it is enzyme's active site that gets disrupted as a result of temperature increase. This entire activity emphasizes that the *whole 3D protein structure* unfolds due to attractive forces that hold it together breakdown at higher temperatures. Therefore, when that happens, the enzyme active site also unfolds as a result of the *entire* protein unfolding.

PREPARATION

Class Time: 180 min.

Materials (for the whole-class demonstration)
Boiling Eggs

- One beaker with room temperature water
- One beaker with hot (but not boiling) water
- Two eggs

Materials

Hands-On activity 2.1: Jello and Pineapple hands-on experiment

Activity 2.1 - Teacher Preparation

Note: In the instructions below we suggest using 13 oz box of gelatin per group. 1 pack of gelatin powder generally makes 2 cups (16 oz) of liquid gelatin. If you use 2 oz plastic "on the go" containers, one group of students needs 2 containers per group, and will use about 4 oz of the liquid gelatin. Therefore, 1 pack of gelatin should be enough for 4 groups of students. In case they spill any liquid gelatin, materials list below calls for using 1 pack of gelatin per three groups.

Materials (for every 3 groups)

- One 3 oz box of gelatin
- Measuring cup
- Warm water (usually 1 cup, but check with gelatin package instructions)
    - Students can boil 1 cup of water using a hot plate, or microwave
- Cold water (usually 1 cup, but check with gelatin package instructions)
- Spoon
- Large bowl or beaker (big enough to hold 2 cups of liquid)
- Hot Plate
- 1 ml disposable pipet

Materials (for every group)

- 2 "on the go" cups (or petri dishes)
- Fresh pineapple (about 8 chunks)
- 1 beaker (big enough to hold 1 cup of liquid)
- Three quarters (coins)
- marker

Activity Setup

- Print handout for each student for hands-on activity 2.1
- Boiling Eggs Demo: Prepare two beakers: one with room temperature water and one with very hot, but not boiling water (at least 165 °F). The hot water should look similar to the room temperature water, no boiling should be visible. Crack one of the eggs open in front of students and separate egg white from the yolk. Put some egg white into each beaker and let students observe what happens.
- Pineapple and Gelatin Demo: follow instructions in hands on activity 2.1 but prepare only 2 cups of gelatin: one plain and one with fresh pineapple. Alternatively, you can show students the pineapple and gelatin demo video.

HOMEWORK

Reading: "How does temperature affect protein structure and function?"
Note: The reading is long. We suggest splitting the reading between two class periods and assigning part I (see reading) as homework #1 and part II as homework #2.

SAFETY ISSUES

Activity 2.1 - Teacher Preparation

Hot plates are used in the teacher demo and student hands-on activities. Hot plates must be handled with care to avoiding burning. Make sure the area around each hot plate is clear of combustible materials and flammable liquids/vapors.

BASIC OUTLINE OF ACTIVITY

Use this space to make notes to prepare for your lesson

1. Introduction
    a. Questions
    b. Demonstration: boiling eggs demonstration revised
    c. Questions
    d. Discussion
2. Hands-on activity: Pineapple and Jello
    a. Demonstration: Pineapple and Jello
    b. Questions
    c. Discussion
3. How does polarity affect strength of interactions?
    a. Simulation: pulling apart molecules of different polarity
    b. Questions and discussion
    c. Simulation: Energy change when pulling apart molecules of different polarity
    d. Questions and Discussion
4. How do polar regions of the protein interact with other molecules?
    a. Simulation: factors that affect interactions involved in lock and key mechanism

   b. Questions and discussion

5. How does molecular shape affect interactions between nonpolar molecules?

   a. Simulation: Pulling apart nonpolar molecules of different shape

   b. Questions and Discussion

6. How does temperature affect protein folding?

   a. Pineapple and jello hands-on activity discussion

   b. Simulation: How does temperature affect interactions within proteins?

   c. Simulation questions and discussion

7. How does temperature affect interactions between substrate and protein active site?

   a. Simulation: Pulling apart pairs of molecules of different shape at different temperature

   b. Questions

   c. Discussion

   d. Explanation Question

   e. Discussion

8. How does temperature affect protein 3D structure?

a. Simulation: Proteins and temperature

b. Simulation questions and discussion

c. Driving Question discussion and conclusion

Activity 2.1: How do polar interactions affect protein structure and properties?

Introducing the Lesson

Students have just learned what proteins are and how they fold. Start with reviewing these ideas. Point out that the shape of the protein is important for its specific function. Protein shape, as students learned in the previous investigation, depends on polar and nonpolar interactions between amino acids within the protein and between the protein's amino acids and surrounding molecules, typically water.

Possible questions:

- *What affects how proteins interact with the liquids that surround them like water or oil?*
- *How do polar and nonpolar interactions between amino acids affect protein folding?*
- *How does amino acid composition affect protein folding?*
- *How does the potential energy of the system change when a protein folds up into a stable shape?*
- *How do you think temperature would affect energy of the system?*
- *How do you think temperature will affect 3D structure of the protein?*

Demonstration: Repeat boiling eggs demo for the class. Point out to the students that egg white contains a lot of proteins. Prepare two beakers: one with room temperature water and one with very hot, but not boiling water (at least 165 °F). The hot water should look similar to the room temperature water, no boiling should be visible. Crack one of the eggs open in front of students and separate egg white from the yolk. Put some egg white into each beaker and let students observe what happens.

Possible questions:

- *What do you observe?*
- *Why does egg change in one beaker and not in the other?*
- *How are proteins in the egg white affected by temperature?*
- *Can you turn the egg back to the way it was before you put it in warm water?*
- *Any other ideas?*

Introduce driving question for the investigation "Why can't you uncook an egg?" Point out the importance of protein 3D structure in carrying out biological functions. Encourage students to think about how changing temperature of the system affects the 3D structure and properties of proteins.

Possible questions:

- *How does temperature affect the ways in which the polar regions of proteins interact with other molecules?*
- *How does temperature affect protein nonpolar regions' interactions with other molecules?*
- *How would raising the temperature affect protein ability to interact with other molecules?*

Page title:
Introduction

In the previous investigation you saw how polar and nonpolar interactions cause a protein to fold into a 3D structure. In this activity you will further investigate how polar and nonpolar interactions between proteins or between proteins and other small molecules affect the structure and properties of proteins. You will explore ideas related to interactions between molecules and changes in potential energy associated with stable attractions.

Page title:
Pineapple and Jello Hands-On Experiment

Conduct an investigation to explore how adding fresh and boiled pineapple affects gelatin. Think about what might be happening at the molecular level to cause the differences in your observations. Follow the instructions in the handout for hands-on activity 2.1.

While your gelatin is solidifying, your teacher prepared two cups of gelatin in advance using similar procedure. Pineapple pieces were placed in one of the cups. A coin was also added to both cups. Observe the differences between the two cups and discuss the following questions as a group, then answer the questions below.

Demonstration: Jello and Pineapple

Prepare two cups with jello in advance, following the procedure described in activity set-up. One cup of gelatin is plain, the other one contains chunks of fresh pineapple. Give students some time to observe the differences in jello consistency and location of the coin in cup containing pineapple and the cup that does not. Alternatively show them the pineapple and gelatin demo video.

Possible questions:

- What is the difference between jello when the pineapple is added and when it is not?
- What happens to the coin in both cups?
- What do you think might be happening at the molecular level to cause the observed difference in two cups of gelatin?

Point out to students that jello consists of long molecules that form a tangled when jello solidifies and trap water in a mesh. Encourage them to think about what might be happening at the molecular level between pineapple and gelatin to prevent them from solidifying.

1. What did you observe in the pineapple and jello demonstration?

Student responses: this is initial ideas question, so student answers will vary and don't have to be accurate at this point. Possible student answers:

- Jello turned solid in the cup that had no pineapple, but remained liquid in the cup with pineapple.
- Jello with pineapple didn't solidify, and jello without pineapple did solidify.

2. Based on your class discussion what do you think might be happening to cause that?

Student responses: this is initial ideas question, so student answers will vary and don't have to be accurate at this point. Possible student answers:

- Some molecule in the pineapple forms interactions with molecules of jello preventing them from making interactions with each other, which also prevents solid formation.
- Some molecule in the pineapple is preventing jello from turning solid because the cup with pineapple remained liquid and the cup without turned solid.

Discussion

Ask students to share their answers to the questions above. Discuss student explanations for their observations. If students don't come up with this on their own nudge them in the direction that there must be some interaction occurring at the molecular level between the molecules in the pineapple and molecules in the jello. Assuming proteins have polar and nonpolar parts, students will further investigate how they might interact with each other.

Possible questions:

- *What happens at the molecular level when jello turns solid?*
- *Something in the pineapple appears to be interfering with solidifying process. How do you think that might work?*

Share with students that the molecule contained in the fresh pineapple that prevents gelatin from solidifying is actually an enzyme called bromelain. Encourage them to think about molecular level mechanism that could explain why bromelain prevents gelatin from solidifying.

Possible questions:

- *How do you think bromelain prevents gelatin from solidifying at the molecular level?*
- *Any other ideas?*

Page title:
How does polarity affect strength of interactions?

Explore the simulation and answer the questions below. As you do the simulation, think about how polar interactions within a protein affect protein interactions with other molecules.

Simulation: pulling apart molecules of different polarity
https://lab.concord.org/interactives.html#interactives/sam/intermolecular-attractions/4-strengthening-dipole-dipole-attractions.json

3. How does polarity affect the strength of interactions between molecules? Use ideas of charge to explain your answer. Justify your answer using ideas from the simulation.

Student responses: As the amount of charge on the two interacting molecules increases, polarity increases, and strength of interactions between molecules increases. This is due to the fact that larger electric charge cause large electric force between interacting particles. The simulation shows that it is harder to pull apart two molecules that have more charge because they are more polar, and form stronger interactions with each other.

4. Predict how polarity of protein will affect the types and strength of interactions the protein can form with other molecules. Justify your answer using ideas from the simulation.

Student responses: polar regions of the protein will tend to form stronger interactions with polar molecules because the magnitude of attractive force generated between regions of higher polarity is greater than attractive force generated between regions of lower polarity. The simulation supports this conclusion because it is harder to pull apart molecules of higher polarity, than molecules of medium of low polarity.

5. Predict how the energy of the system will change when molecules of similar polarity are pulled apart. Justify your answer using ideas of charge.

Student responses: The energy of the system is minimal when opposite charges are close as opposed to when they are far apart. Therefore, when we try to pull apart molecules that form interactions via partial charges, energy of the system increases.

6. Predict whether total change in energy of the system will be different when pulling apart molecules of low, medium and high polarity. Justify your answer using ideas of force and charge.

Student responses: The attractive force between two opposite charges is larger when the amount of charge on each object is larger. Breaking attractive force between more charged objects requires more energy than between less charged objects. More polar molecules have more partial charges interacting with each other, and therefore will require larger force to pull them apart than less polar molecules. As a result, total energy of the system will increase more when pulling apart molecules of higher polarity than when pulling molecules of lower polarity.

Discussion:
Ask students to share their answers to the questions above (or, alternatively, use teacher report to share some of student answers to the questions above). Discuss how regions of different polarity in a protein might affect protein interactions with other molecules. Push students to think about how energy of the system will change when molecules of similar polarity are pulled apart.

Possible questions:

- *How do polar regions of proteins affect protein interactions with other molecules?*
- *How do nonpolar regions in proteins affect interactions with other molecules?*
- *How does energy of the system change when you pull apart two polar molecules? Why?*
- *How different will energy change be when you pull apart molecules of low polarity vs. medium polarity vs. molecules of high polarity? Justify your prediction.*
- *Any other ides?*

Page title:
How does polarity affect potential energy in a system of molecules?

Explore the simulation and answer the questions below. As you do the simulation, think about how energy changes as polar and nonpolar interactions form within a protein.
Simulation: energy change when pulling apart molecules of different polarity
Use this as final:
https://lab.concord.org/interactives.html#interactives/interactions/comparing-potential-energy-of-attractions.json

7. Using the simulation, describe how the energy of the system will change as two molecules of similar polarity are pulled apart? Explain your answer.

Student responses: as you pull apart two molecules of similar polarity, the energy of the system will increase. Energy of the system decreases as two oppositely charged regions of molecules move closer to form an interaction. Therefore, as you pull those charges away, the energy will increase as shown in the simulation.

8. Predict how changes in the energy of the system affects stability of molecules of similar polarity? Explain your answer.

Student responses: as molecules get closer and form an interaction, potential energy of the system decreases, the molecules achieve more stable configuration. For example, when molecules of high polarity align together with opposite charges close to each other, that's when the attractive force is greatest, and energy of the system is lowest, as shown in the simulation, and the molecules are at its' most stable configuration.

9. Predict how the energy of the system will change when polar regions of the protein interact with other polar regions, and nonpolar regions interact with other nonpolar regions, and how it would affect stability of the protein? Explain your answer.

Student responses: as polar regions of the protein form interactions with other polar regions energy of the system decrease and the system becomes more stable. This process is shown in the simulation with two small polar molecules. Similarly, the same happens when nonpolar regions of the protein align with other nonpolar regions. This is because opposite charges of similar magnitude (stronger permanent partial charges on polar regions, and weaker temporary induced partial charges on nonpolar regions) align together due to attractive forces of similar magnitude, leading to energy minimization, and most stable shape.

Discussion:
Ask students to share their answers to the questions above (or, alternatively, use teacher report to share some of student answers to the questions above). Discuss how regions of different polarity in a protein might affect energy of the system and stability of the protein molecules.

Possible questions:

- *How does energy of the system change when polar regions of the protein interact with other polar/nonpolar molecules and the molecules change position? Explain your answer.*
- *How does energy of the system change when polar regions of the protein interact with other polar/nonpolar molecules? Explain your answer.*
- *Predict how polar and nonpolar interactions will affect stability of protein molecule? Why?*
- *Any other ideas?*

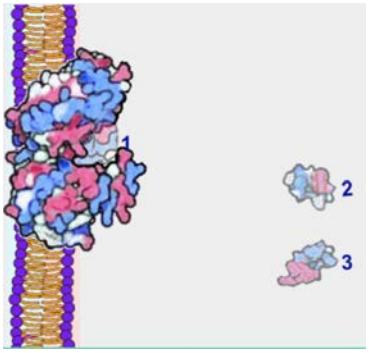
Page title:
How do polar regions of the protein interact with other molecules?

The simulation shows a protein located in a membrane, with a small "pocket" called an *active site*. An active site is a region of a protein molecule with a specific shape that can interact with various small molecules in a specific way to carry out biological functions. In the simulation below, there are three small molecules next to the protein. Only one of three molecules can form stable electrical interactions with the protein. The protein and it's partners are colored by charge: red for negative charge, blue for positive charge, and white/grey for neutral. Your job is to make a prediction about which small molecule (#1, #2 or #3) will have the strongest interaction with the protein and explain your prediction using ideas of charge and polarity.

Link to the complete simulation: https://lab.concord.org/interactives.html#interactives/interactions/protein-shape-charge.json

10. [Snapshot Question] Drag the molecule you think would form strongest interactions with the protein, and place it where you think it interacts best. Include a snapshot of proposed structure with you answer. Explain your choice.

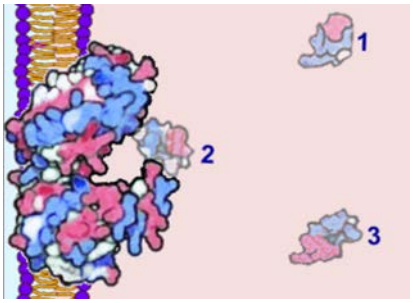
Student responses: Molecule #1 will form strongest interactions with the protein because it is complementary in shape to the protein pocket, and opposite charges align together causing for strong attractive interactions to form between protein and molecule #1.



Note: as students can see in Image 2, molecule #1 is complimentary in shape to enzyme's pocket, so there is maximum alignment between the surface of the small molecule and the enzyme, making it easier to form interactions between charges. Recall from Unit 1 that electric force gets stronger as distance between two charged objects decreases. Similarly, complimentary surfaces allow for closer distance between interacting molecules therefore leading to formation of stronger interactions. Following this logic, molecule #2 will not form strong interactions with the enzyme because it does not fit into the enzyme's binding site, and therefore surfaces won't get close enough together to form strong interactions. Finally, molecule #3 is complimentary in shape, and fits well into enzyme's binding site, but the interacting surfaces have similar charge, therefore causing repulsive force. This repulsive prevents molecule #3 from forming strong interactions with the enzyme in spite of being complimentary in shape.

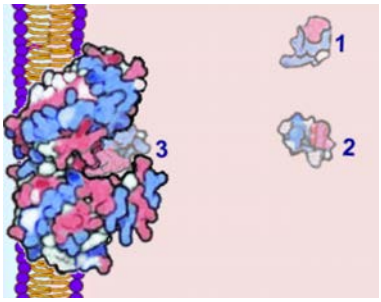
11. [snapshot question] Which molecules will form the weakest interactions with the protein? Take a snapshot of proposed structure. Explain your answer.

Student responses: molecule #2 will form virtually no interactions because it will not fit into the enzyme pocket since the structure is not complimentary.



12. [snapshot question] Which molecule will form medium strength interactions with the protein? Take a snapshot of proposed structure. Explain your answer.

Student responses: molecules #3 will form medium strength interactions with the protein because it is complimentary in shape to the protein pocket, but consists of amino acids that have similar charge to those forming the protein pocket, and therefore no significant attractive forces will form.



13. Use ideas from the simulation to construct your own explanation for how the shape of the molecule affects interactions. Explain your answer using ideas of forces, distance, and electrical interactions.

Student responses: in order for interactions between protein and other molecules to form, their amino acids need to get close enough to each other to form interactions. In the case of enzyme pocket, this can only happen if the structure of the enzyme can interact with the enzyme pocket in a complimentary way (fits like "lock and key"). Additionally, strongest interactions will form when amino acids that comprise the small molecule, enzyme (and the enzyme pocket) have opposite charges.

Discussion:
Ask students to create a shared data table on the board to compare their answers to the questions above. Encourage students to use this board to come up with evidence-based explanation of the questions above that they refine as a class.

Possible questions:

- *Which molecules will interact with the protein? Why?*
- *Which molecules will not interact with the protein? Why?*
- *How does shape affect interactions between protein and these molecules?*
- *Why is shape important in forming interactions between these molecules and the protein?*
- *How does shape relate to interactions between charges on amino acids and these molecules? Why?*
- *Any other ideas?*

Note: make sure that students understand that molecule #2 will not form any significant interactions with the protein because it's shape is not complementary to that of the protein pocket because closeness of molecular surfaces is critical for intermolecular interactions to form (because the smaller the distance, the stronger the attractive force between partial charges).

Point out to students that since molecule #3 is complementary in shape to the enzyme's binding site, it will be able to form interactions with the protein surfaces when they are close enough to interact. However, since charges on these surfaces are similar, repulsive force will be generated, and therefore attractive interactions between the enzyme and molecule #3 will not form.

This is also a good place to point out that when we talk about intermolecular interactions in biological context, we refer to attractive interactions generated as a result of attractive forces between oppositely charged surfaces that can form between two molecules. For that reason, the repulsive interactions formed between the enzyme and molecule #3 will not lead to intermolecular interactions.

Define the term "*substrate*" for the students- a small molecule that interacts with a protein to serve a specific biological function. Also, you might refer them to the reading Reading for Activity 1.3: What are proteins and why are they important? For an overview of various functions proteins carry out in our body.

Page title:
How does molecular shape affect interactions between nonpolar molecules?

Explore the simulation and think about how shape affects interaction between nonpolar molecules. Then answer the questions below.

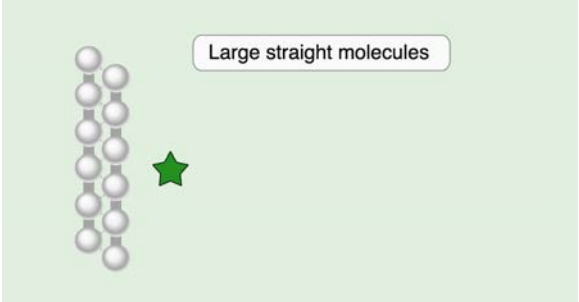
Simulation:pulling apart nonpolar molecules of different shape

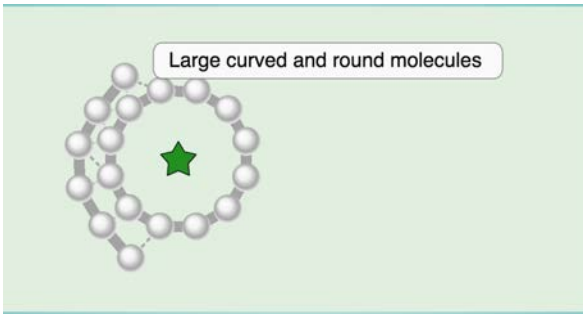
https://lab.concord.org/interactives.html#interactives/sam/intermolecular-attractions/5-strengthening-london-dispersion-attraction.json

14. [Snapshot question] Take a snapshot of the model showing which molecule you think would form the strongest attraction. Explain your choice using ideas of charge and force.

Student responses:

Student can choose to show either large straight molecules or large curved and circular molecules. They both show complementary structure (largest number of atoms are close to each other) and as a result form largest number of interactions:

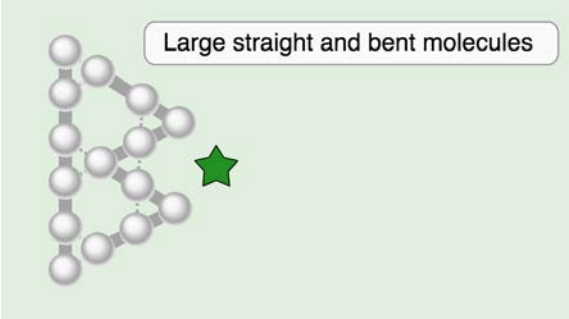


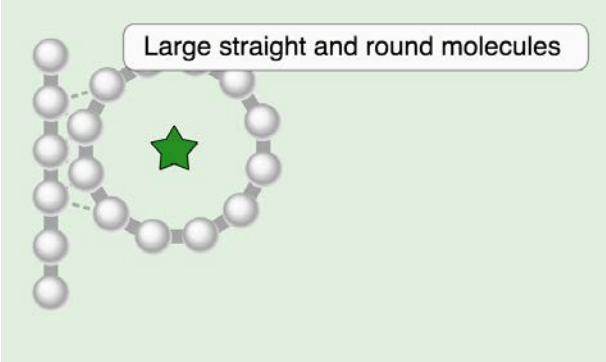


Student explanation should include the following ideas:
nonpolar interactions form via temporary partial charge induced by momentary shifts in electron cloud. Therefore, these charges are smaller in magnitude than permanent partial charges on polar molecules that are the result of permanent shifts in electron cloud towards more electronegative atom. As a result, larger number of interactions is required to hold a nonpolar molecule together. Surfaces that align well with each other allow for larger number of interactions to form. Therefore, nonpolar molecules with complimentary structures will form larger number of attractive interactions, which will make them harder to pull apart.

15.[Snapshot question] Take a snapshot of the model showing which molecule you think would form the weakest attraction. Explain your choice.

Student responses:
Student can choose to show one of the pairs below. Both pairs don't have complimentary structure (most atoms are not close to each other when molecules come close together), and as a result they don't form large number of interactions.





Explanation include the following ideas:

- Since nonpolar molecules interact via temporary charges produced by random fluctuations in electron cloud due to electron motion, the strength of nonpolar interactions directly depends on the number of interactions that can be formed between molecules, which in turn depends on proximity/alignment to the surfaces of the interacting molecules.

16. Predict how potential energy of the system will change when molecules are close together versus when they are far apart? Justify your answer.

Student responses: energy of the system is small when interacting opposite charges are close together and increase as you move them away from each other. Therefore, when interactions form, the potential energy of the system decreases.

Discussion:

Ask students to create a shared data table on the board to compare their answers to the questions #14 and #15 above. Focus on student pictures of docked substrates and discuss what factors affect the binding of substrate and protein.

Possible questions:

- *How does shape of the molecules affect interactions between them?*
- *How do the shapes of the molecules in the simulation relate to the strength of the interaction between them?*
- *How does the shape of the interacting molecules relate to energy of the system?*

Ask students to create a shared data table on the board to compare their answers to the question #16 above. Students might choose to construct a bar graph to illustrate how energy will change as the two molecules get closer together. Focus on student graphs and/or explanation and discuss how potential energy of the system changes with distance.

- *How does energy of the system change as molecules are pulled apart?*
- *How does energy of the system change as molecules come closer together?*
- *When (at what distance between molecules) is energy of the system at its minimum? Why?*
- *Any other ideas?*

Page title:
How does temperature affect protein function?

By now the gelatin in the containers that you prepared should be solid. Study the three containers with gelatin, and note in your written observations where the coin is located in each of the containers. Share your observations with the rest of the class.

17. Develop a scientific explanation to account for your observations in the pineapple jello experiment. Justify your answer using ideas related to protein structure, function, and energy.

Student responses: at this point students are not expected to provide very accurate scientific explanation. Possible ideas students might include at this point are:

Since pineapple contains enzyme bromelain, it is possible that enzyme is doing something to prevent jello from solidifying. May be it is forming interactions with a molecule in jello that causes jello to solidify, and prevents this process. Once we heated the pineapple, enzyme becomes inactive because higher temperature increases energy of the system, causing atoms in amino acids that make up protein to move faster. This motion distorts protein 3D structure, and the structure of enzyme's active site. Since the active site no longer has the right shape to interact with molecules in jello, it can no longer prevent jello from solidifying.

Discussion

Ask students to share their observations and explanations with the class. Discuss how boiling pineapple affects bromelain and the observations in the experiment.

Possible questions:

- *How is using boiled pineapple affecting the jello?*
- *What do you think might be different about boiled pineapple to cause the difference?*
- *Why might proteins in heated pineapple work differently?*
- *What happens to bromelain in pineapple when you boil it? How does it affect gelatin?*

Note: encourage students to use ideas related to protein/substrate interactions, energy, and structure function. You should elicit student ideas around this but you should not be judging their answers for correct mechanism at this point.

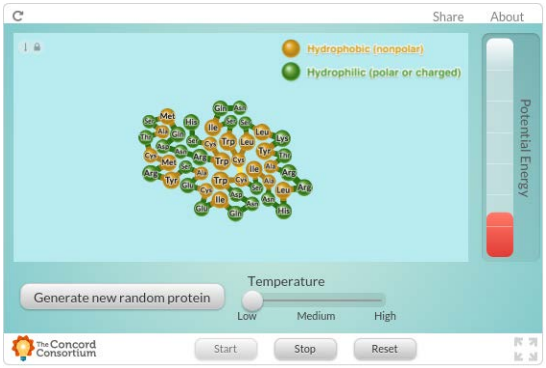
Page title:

How does temperature affect protein folding?

Explore the simulation and think about how temperature affects interactions within proteins. Then answer the questions that follow. As you are using the simulation, make sure you look at how protein folding occurs at different temperatures (low, medium, high).
Simulation description: simulation of a single protein that has a temp slider.
Final simulation is here: https://lab.concord.org/interactives.html#interactives/interactions/protein-shape-and-temp.json

18. [Snapshot question] What types of interactions can you observe in the final structure of the protein at low temperature? Insert a snapshot from the simulation of the folded protein. Describe the interactions that form.

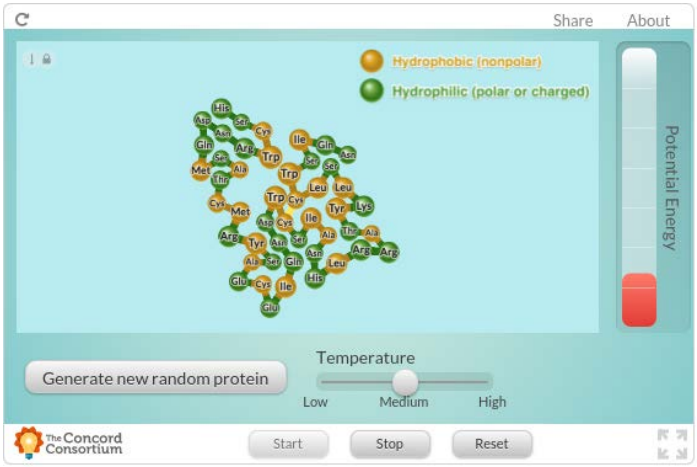
Student responses:
The final 3D structure of the protein at low temperature is shown below. I can see that nonpolar amino acids form interactions with other nonpolar amino acids, and polar amino acids tend to form interactions with other polar amino acids. Also, nonpolar amino acids tend to be located inside the protein, surrounded by polar amino acids. The protein structure also appears to be tightly folded with little room between amino acids.



19. [Snapshot question] What types of interactions can you observe in the final structure of the protein at medium temperature? Insert a snapshot from the simulation of the folded protein. Describe the interactions that form.

Student responses:

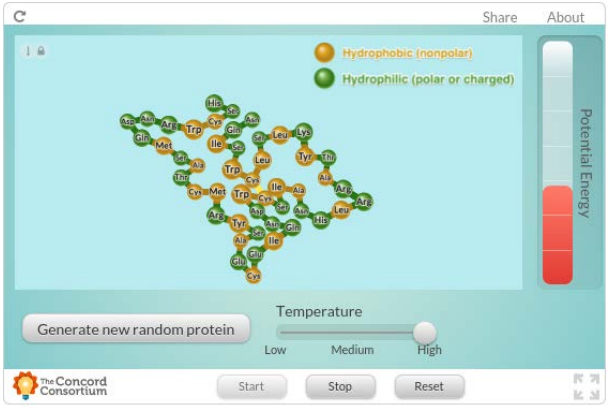
The final 3D structure of the protein at medium temperature is shown below. I can see that for the most part nonpolar amino acids form interactions with other nonpolar amino acids, and polar amino acids tend to form interactions with other polar amino acids. However, some of the interactions are overcome by high temperature. More nonpolar amino acids tend to be located outside the protein than at low temperature, and the protein structure is more unfolded (more space between amino acids) than at low temperature.



20. [Snapshot question] What types of interactions can you observe in the final structure of the protein at high temperature? Insert a snapshot from the simulation of the folded protein. Describe the interactions that form.

Student responses:

The final 3D structure of the protein at high temperature is shown below. I can see that polar and nonpolar interactions are broken for the most part, there is a lot more space between amino acids than at medium or low temperature.



21. How does temperature affect protein folding? Explain your answer using the simulation.

Student responses: Higher temperatures make interactions between amino acids in unfolded protein harder to form and easier to break (if any were formed), because amino acids that make up the protein move faster and intermolecular interactions are overcome as a result.

22. Do you think a protein can effectively perform its function at high temperatures? Explain your answer.

Student responses: No, because higher temperatures cause interactions within the protein to be overcome by molecular motion, which disrupts its 3D structure, preventing the protein from carrying out its function.

23. How do changes in temperature relate to changes in energy of the system and structure of the protein? Justify your answer using ideas from the simulation.

Student responses: As temperature of the system increases, kinetic energy of the system increases, as can be seen from energy bar graph in the snapshot questions above. This energy increase causes amino acids in the protein to move faster and break intermolecular interactions with other amino acids in the protein. This causes disruption in the protein 3D structure.

Discussion:
Ask students to share their answers to the questions above. You might choose to display several snapshot from student answers to discuss how temperature affects energy of the system and protein folding.
Possible questions:

- *What happens to proteins structure at higher temperatures?*
- *Why do higher temperatures cause protein to unfold?*
- *How does kinetic energy of the system change when protein unfolds?*
- *How does potential energy of the system change when protein unfolds?*
- *How does total energy of the system change when protein unfolds?*

Help students bring all the ideas together through discussion to have the following conclusion points:

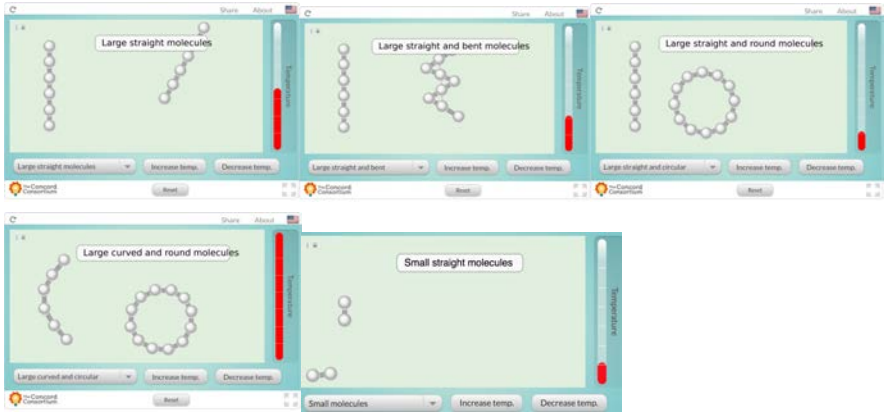
- Proteins consist of polar and nonpolar parts (amino acids). Protein structure (shape) is determined by interactions between these amino acids. The forces between the different amino acids and the surrounding molecules push and pull them into positions that are more stable and minimize potential energy, forming the shape of the folded molecule.
- When the temperature of the system increases, atoms that make up amino acids in the protein start moving faster, and this causes interactions between them to be overcome and therefore disrupts the 3D shape of the protein. Once the shape of the protein is disrupted, it can no longer form the same kinds of interactions with molecules in the surroundings that it did before because the 3D arrangement of amino acids in the protein is now different.

Page title:
How does temperature affect interactions between substrate and protein active site?

Explore the simulation focusing on how temperature affects interactions between nonpolar molecules. Then answer the questions below.
Simulation: heating up pairs of molecules of different shape
https://lab.concord.org/interactives.html#interactives/interactions/factors-affecting-london-with-temp.json

24. [snapshot question] Take a snapshot of each of the nonpolar molecule pairs, showing the temperature at which intermolecular interactions have been overcome.

Student responses:

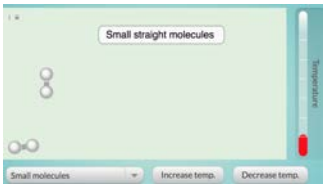


25. What patterns do you observe?

Student responses: some of the patterns students might mention include:
- As the number of interactions between molecules increases, higher temperature is required to break them apart
- The pairs for which molecular surfaces align better require higher temperature to separate

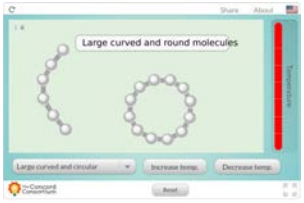
26. From the snapshots above, which nonpolar pair of molecules is easiest to separate. Justify your answer using ideas of temperature, energy, charge and electric force.

Student responses:
small straight nonpolar molecules are easiest to separate because they are held together by a weak force generated by few temporary induced partial charges, and therefore don't require a lot of energy to break. Increasing temperature of the system even a little causes these molecules to separate as shown below.



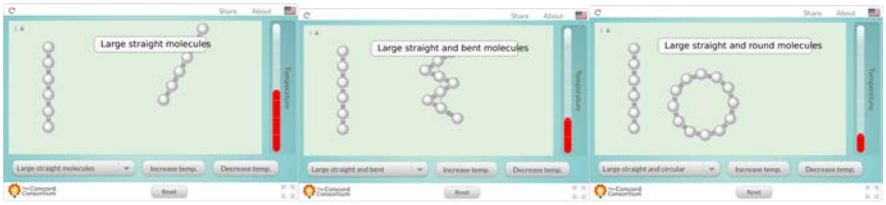
27. From snapshots above, which nonpolar pair of molecules is hardest to separate. Justify your answer using ideas of temperature, energy, charge and electric force.

Student responses:
Since the surfaces of the two molecules align well, a large number of atoms can form interactions and generate a large attractive force via temporary induced partial charges. Additionally, well aligned surfaces lead to shorter distance between interacting atoms, and therefore stronger attractive forces. This force requires a lot of energy and therefore higher temperature to overcome.



28. Looking at the snapshots of the three remaining pairs of molecules from question #24, explain the observed changes in temperature required to separate each of the pairs. Justify your answer using ideas of temperature, energy, charge and electric force.

Student responses:
Since the surfaces of the two large straight molecules align well, a large number of atoms can form interactions and generate a large attractive force via temporary induced partial charges. This force requires a lot of energy and therefore higher temperature to overcome. As a result, the temperature required to separate this pair is highest of all three. Additionally, well aligned surfaces lead to shorter distance between interacting atoms, and therefore stronger attractive forces. Next, large straight and bent molecule pair doesn't have surfaces that align very well, and fewer atoms can form electrical interactions with each other, which leads to this pair being easily separated at lower temperatures. Finally, large straight and round molecule have even fewer atoms that are close enough to form and interactions, which leads to this pair being easiest of all to separate, and lowest temperature.



Discussion:

Ask students to share their answers to the questions above. You might choose to display several snapshot from student answers to discuss how increasing temperature affects interactions between molecules of different shape.

Possible questions:

- *What patterns did you observe?*
- *How can you explain these patterns?*
- *Any different ideas?*

You might choose to display examples of student explanations from this simulation to discuss how their predictions about which pair of molecules will form the strongest attraction relate to what they have learned in this simulation. Encourage students to go back and look at their predictions and compare them with the answers they provided in this simulation.

Possible questions:

- *Who would like to share their predictions and snapshots from simulation on the previous page?*
- *How are these predictions similar/different from what you have observed in this new simulation where you were able to manipulate temperature?*
- *What factors affect the strength of interactions between two nonpolar molecules?*
- *Do you think these principles will apply to polar molecules also? Explain*
- *Any different ideas?*

Help students bring all the ideas together through discussion to have the following conclusion points:

- Strengths of interactions between nonpolar molecules depends on the number of interacting atoms, and the alignment between surfaces.
    - *Number of interactions*: as the number of interacting atoms increases, the generated attractive force increases as a result of larger number of partial temporary induced charges.
    - *Surface proximity*: as surfaces become more aligned, it allows for larger number of interactions to be formed. Also, as the distance between interacting surfaces decreases, stronger attractive force result (because, as you remember from Unit 1, attractive force between two opposite charges increases as the distance decreases)
- The stronger the attractive force between molecules, the more energy is required to overcome the intermolecular interactions. This leads to higher temperature required to overcome these interactions.
- For polar interactions, the principle of number of interactions also applies. However, since nonpolar molecules interact via permanent partial charge, if the surfaces align well, but the charges that will end up being close to each other are similar, no significant interaction will form. You can also remind students that they should have come to the same conclusion in this simulation where molecule #3 is complimentary in shape, but the interactions results in similar charges being close together, so no significant interaction forms.

29. Using ideas from the simulation and discussion, explain why jello does not solidify when you add fresh pineapple, but solidifies when you add boiled pineapple. Explain your answer using ideas of forces, distance and electrical interactions and energy.

Student responses: Pineapple contains enzyme bromelain. Before pineapple is heated, bromelain is in its active form, and has a certain structure of the active site. Before it is heated, bromelain active site can make interactions with molecules in jello that are complementary in shape, and contain oppositely charged amino acids. Forming these interactions prevents molecules in jello from interacting with each other, which in turn prevents them from forming a tangled mesh that traps water inside, and therefore prevents jello from solidifying.

Bromelain active site is composed of polar and nonpolar amino acids. Interactions between molecules in jello and active site form as a result of large number of attractive interactions between

- permanent partial charges on polar amino acids, and
- temporary induced partial charges on nonpolar amino acids.

as well as complimentary structure between the active site and the substrate, which leads to shorter distance between interacting charges, causing larger attractive force.

As temperature of the system increases, amino acids involved in forming electrical interactions with jello molecules, as well as jello molecule have enough energy to move around, causing the two interacting surfaces to move further away from each other. This leads to attractive forces that hold the two partners together to be overcome by increased molecular motion. When the temperature is high enough, the molecular motion is so big that it prevents bromelain and jello molecule from forming a stable interaction.

If enzyme can't form stable complex with substrate, it can' successfully carry out its function, and therefore enzyme function is significantly compromised at higher temperatures.

Discussion

Ask students to share their explanations from the previous questions and encourage them to think about how the temperature affects interactions between substrate and enzyme, as well as the entire 3D structure of the enzyme.

Possible questions:

- *What factors affect interactions between enzyme's active site and substrate*
    - *Make sure students mention number of intermolecular interactions and surface proximity/alignment. If they don't, revise ideas from simulations for polar and nonpolar* interactions.
- *How does temperature increase affect interactions in the active site between enzyme and substrate?*
- *How does temperature increase affect the whole protein 3D structure?*
- *How does temperature affect enzyme properties?*
- *Any other ideas?*

Page title:

How does temperature affect protein 3D structure?

Explore the simulation to see how temperature affects protein structure. Pay special attention to what happens to protein structure after you heat it up first, and then cool it down back to the original temperature. Then answer the questions that follow.

Simulation: Proteins and temperature

https://lab.concord.org/interactives.html#interactives/interactions/protein-denaturation.json

30. Use the simulation to explain how temperature affects protein structure and function.

Student responses: Increasing the temperature causes atoms in the amino acids that build up the protein to move around and overcome attractive forces that hold them together in a specific pattern that forms unique 3D structure of the protein. When this happens, 3D structure is disrupted, and protein can no longer function in the same way as before because it can't form the same kinds of interactions with substrate as it did before it was heated.

31. Use ideas of energy to explain how temperature affects protein structure and function.

Student responses: Increasing the temperature causes kinetic and potential energy of the system to increase. Amino acids that build up the protein now have more energy to move around and overcome attractive forces that hold them together in a specific pattern that forms unique 3D structure of the protein. When this happens, 3D structure is disrupted, and protein can no longer function in the same way as before because it can't form the same kinds of interactions with substrate as it did before it was heated.

32. Use the simulation to explain how temperature affects protein structure and function after the protein has been heated and cooled down.

Student responses: higher temperature causes interactions between atoms in the amino acids in a protein to be overcome because amino acids start moving faster. This leads to protein 3D structure to be disrupted. Even after the system cools down, the protein does not come back to its original 3D structure, as can be seen from the simulation. Therefore, the protein can not perform its functions in a similar way as before it was heated because it can't form the same kinds of interactions with substrate as it did before it was heated.

33. Use ideas from the simulation to answer the driving question for this investigation: "Why can't you uncook an egg?"

Student responses: as temperature of the system increases, amino acids that make up the protein start moving faster, which leads to intermolecular interactions forming protein 3D structure to be overcome, causing the protein to unfold. The same thing happens with proteins in egg. Even after the system cools off, the proteins still stay in the unfolded form, and don't re-assemble back into the original 3D structure. Therefore, the proteins in the egg will not go back to its original form, and the egg as a result can not be uncooked.

34. [drawing prompt] Using ideas from the simulation above, draw a model to predict what might have happened to the bromelain protein in the pineapple to cause it to stop working in the jello experiment. [text prompt] Explain your model.

Student responses: Students models should show protein bromelain and a molecule of jello interacting before bromelain is heated. These interactions might be shown to be stronger than interactions that molecules of jello form with each other. After bromelain is heated, protein structure gets disrupted, and molecules of jello no longer forms the same interactions with bromelain as before. Therefore, molecules in jello form stronger interactions with each other forming a tangled web, trapping water in the web and causing jello to solidify.
Student explanations should contain the following ideas:

- At room temperature bromelain had 3D shape that allowed for interactions between bromelain and molecules of jello to form, therefore preventing jello from solidifying. As the pineapple was heated, atoms that make up amino acids in the bromelain gained more (both potential and kinetic) energy, and were able to overcome attractive forces holding them in the original 3D structure. This caused the protein structure to be disrupted so that it could no longer interact with molecules of jello. Even after the system cooled off, bromelain did not go back to its original 3D shape. So, jello molecules were able to interact with each other instead, which cause jello to solidify after the system cooled off.

35. Explain why the jello with boiled pineapple in it can solidify.

Student responses: even after the temperature of the system cools down, interactions between atoms of the amino acids in bromelain don't go back to the original 3D shape. Therefore, functionality of the enzyme is not restored, and therefore the jello molecules are free to interact with each other causing the jello to solidify.

Discussion:
Ask students to share their models and explanations. Focus on what is happening to the structure of the protein when it is boiled, and how it affects the function of the protein and the observed results of the demonstration.
Possible questions:

- *What do these models show happening to the protein in pineapple?*
- *How does protein in the pineapple and jello interact in your models?*
- *How does temperature affect protein in the pineapple to cause it to stop working?*
- *What do these models have in common? How are they different?*
- *Do proteins return to the same structure after the temperature comes back to initial state?*
- *Any other ideas?*

Note: Make sure that in their explanations and models student's don't mistakenly show molecules of jello linking together forming a long polymer when jello solidifies. Instead, these small molecules in the jello form a tangled web (like mesh) that traps water molecules inside causing jello to solidify. Bromelain prevents jello from solidifying by interacting with the small molecules and preventing them from forming the tangled web (NOT preventing polymerization). Make sure to point it out to students for scientific accuracy in their models.

Relate ideas in this discussion back to the investigation driving question and discuss how ideas students learned here might help answer it.
Possible questions:

- *Why can't you uncook an egg?*

Help students bring all the ideas together through discussion to have the following conclusion points:

- Protein structure (shape) is very important for protein function. Amino acids that make up protein arrange in specific way to form a functional protein. The structure of any protein is determined by polar and nonpolar interactions between amino acids that make up the protein. Since polar amino acids form stronger interactions with other polar amino acids, and nonpolar amino acids form stronger interactions with other nonpolar amino acids, polar and polar aa tend to form interactions with other polar aa and nonpolar aa tend to form

Homework:
Reading for Activity 2.1: "How does temperature affect protein structure and function?"

Activity 2.2: How do antibodies protect us from diseases?

SUMMARY

In the previous activity, students learned about how polar and nonpolar interactions and temperature affect protein structure and function as related to speeding up chemical reactions. In this activity, students will learn about immune function of proteins, and will investigate how antibodies work. They will apply ideas from the previous activity to design antibodies with a specific shape and function.

LEARNING GOAL

Students will use their current model of protein structure and function to design antibodies that target specific biological molecules.

Disciplinary core idea	Crosscutting concept	Science and engineering practice
Relationship Between Energy and Forces: When two objects interacting through a field change relative position, the energy stored in the field is changed. (NGSS Lead States, p. 99)	*Cause and Effect* Cause and effect relationships can be suggested and predicted for complex natural and human designed systems by examining what is known about smaller-scale mechanisms within the system. (NGSS Appendix G, p. 83)	*Developing and using models:* • Develop, revise, and/or use a model based on evidence to illustrate and/or predict the relationships between systems or between components of a system. • Develop and/or use multiple types of models to provide mechanistic accounts and/or predict phenomena, and move flexibly between model types based on merits and limitations. (NGSS Appendix F, p. 53)

POINTS of CONSIDERATION

- *The main focus of this activity is how polar and nonpolar interactions, and protein shape help protect us from various infection agents, and NOT make students fluent in terminology that is introduced here. However, this activity introduces terminology that might prevent students from effectively learning the relationship between structure and function when it comes to immune function of proteins, which is the main focus of the activity. Specifically, terms like antibody and antigen might be unfamiliar to students, and they might mix them up. Learning these terms is NOT the goal of this activity, and if you see your students struggling with this terminology, we suggest that you switch to calling antibodies proteins that protect our bodies from infection, and antigens- small molecules that cause infection to spread. Additionally, you might choose to put a diagram in your classroom in a spot where all students can see it, highlighting differences between antibodies and antigens.*

HOMEWORK

Reading for activity 2.2: "Why is it important for proteins to have specific structure?

BASIC OUTLINE OF ACTIVITY
Use this space to make notes to prepare for your lesson

1. Introduction
    a. Discussion

2. How does our immune system protect us from getting sick?

    a. Simulation: 3D exploration of bound antibody and antigen

    b. Student Questions

    c. Discussion

3. How do vaccines help our bodies fight infection?
    a. Question

    b. Discussion

    c. Simulation: Your immune system: Design your own antibody

    d. Student questions

    e. Discussion

4. Are vaccines always effective?
    a. Discussion

    b. Simulation: Your immune system: Design a new antigen

    c. Student questions

    d. Discussion and conclusion

Activity 2.2: How do vaccines protect us from diseases?

Introducing the Lesson

Introduction: Review the driving question for the unit : "Why is the temperature of 107 F deadly?". Discuss how protein function (such as speeding up chemical reactions) depends on polar and nonpolar interactions between protein and small molecules it is interacting with, as well as temperature and energy.

Possible questions:

- *Why does using heated pineapple instead of a fresh one prevent jello from solidifying?*
- *How does an increase in temperature affect a protein's ability to speed up a chemical reaction in our body?*
- *How are polar and nonpolar interactions between molecules within a protein affected by temperature?*
- *How do the specific amino acids that make up a protein affect overall protein structure and function?*
- *What are other protein functions, other than catalytic, that you know about?*

Students might mention immune function as one of the protein functions. If they don't, that's ok. Continue by sharing the following information with them. Begin the discussion by telling students that in this activity, they will be looking at how our bodies fight diseases. Focus the discussion around flu and how we can help our bodies fight the infection

Possible questions:

- *How do you think our immune system protects us from diseases?*
- *How can we help our bodies fight diseases more efficiently?*
- *Did anyone have flu this year?*
- *What are different ways we can protect ourselves from getting flu?*
- *Why do you think they recommend that you have a flu shot every year?*
- *How does flu shot help our body fight flu infection?*

Introducing the Lesson (continued)

If students don't mention the terms already, refer students to the previous readings describing that antibodies are special proteins that help our bodies fight infections by interacting with harmful molecules called antigens that can cause disease. Antibodies interact with antigens to reduce their harmful effects on our bodies, and protect us from disease. Antibodies bind to antigens, and prevent them from spreading in our body and causing disease.

Encourage students to think how antibodies might be able to perform their function, and how they are similar and different from enzyme proteins students have learned about so far.

Possible questions:

- *How do you think antibodies protect us from disease?*
- *How can antibodies prevent antigens (small molecules that cause infection) from harming cells in our body?*
- *What are the factors that drive interactions between antibodies and antigens?*
- *How are antibodies (proteins that help us fight infection) similar/different from enzyme proteins that you talked about in activity 1?*

Connect this discussion to vaccines. Focus on what is it about vaccines that might be helping our bodies in fighting common flu.
Note: this discussion should only aim to elicit initial ideas. Students are NOT supposed to provide accurate answers to any of the questions.

Possible questions:

- *How does a flu vaccine protect us from getting sick?*
- *What is it about the flu vaccine that can prevent flu virus from getting into our body?*
- *How is flu vaccine similar/different from antibodies made by our body?*

Note: terms like antibody and antigen might be unfamiliar to students, and they might mix them up. Learning these terms is NOT the goal of this activity, and if you see your students struggling with this terminology, we suggest that you switch to calling antibodies proteins that protect our bodies from infection, and antigens- small molecules that cause infection to spread. Additionally, you can refer to the diagram discussed below throughout the activity to remind students of the differences between antibodies and antigens.

Page title:

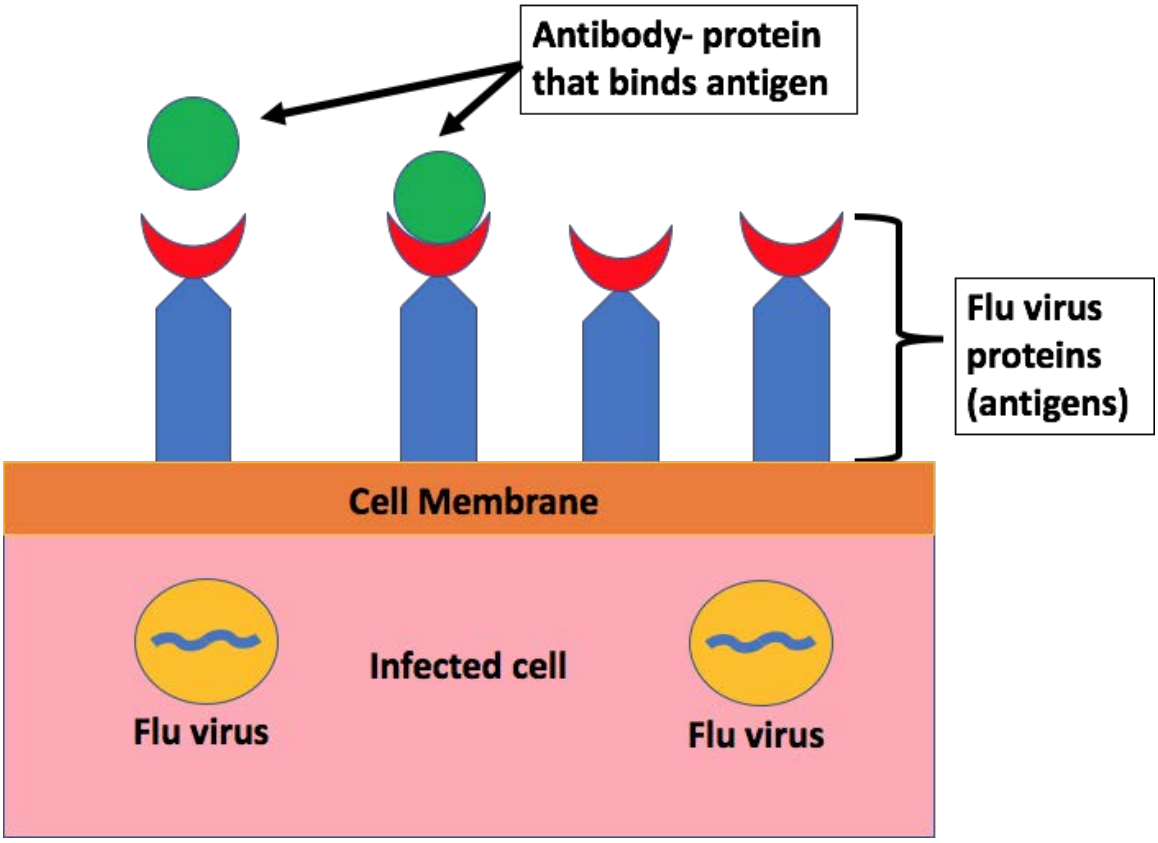
Introduction

In the previous activity you explored how proteins speed up chemical reactions in our bodies, and why the 3D structure of a protein is important for enzymatic function. You also looked at how temperature affects protein structure and function. In this activity, you will explore another important function of proteins - protecting our bodies from diseases. You will first investigate how specific proteins called antibodies protect us from various diseases, and then explain how their 3D structure allows them to carry out this important function.

Page title:

How does our immune system protect us from getting sick?

When we catch a flu, our body starts producing proteins called antibodies that help protect us from flu virus. When flu virus infects our cells, it makes our cells produce flu virus proteins on the surface of cell membrane as shown in the diagram below. Antibodies are special proteins produced by our immune system that have specific shape, and can form interactions with flu virus proteins on the surface of the cell as shown below. That way, antibodies “tag” infected cells, and help our immune system locate and target these cells, preventing the flu virus from spreading in our bodies.



Discussion

Spend some time discussing the diagram above. Talk about the shape of the antibody and point out that our immune system produces antibodies with a large variety of shapes and amino acid composition, so that they can interact with a wide range of different antigens. Point out that a specific antibody works best for a specific antigen that is complimentary in shape and types of interactions that can be formed between surfaces of antibody and antigen. Because of the specific interactions that antibodies can form with a given antigen, antibodies can target specific diseases. Relate these ideas to how enzymes speed up chemical reactions from activity 1. Point out that the mechanism is similar, and that shape and polar and nonpolar interactions play critical role both for speeding up chemical reaction, and for protecting our bodies from disease.

Focus on the importance of complementary shape, and polar and nonpolar interactions as related to antibody's ability to recognize flu virus proteins (antigens) on the surface of the infected cells.

Possible questions:

- *How can antibodies target specific flu virus proteins? What would be the consequence for our health?*
- *How does the structure of an antibody affect what flu virus proteins a given antibody can interact with?*
- *How does the amino acid composition of the antibody affect what flu virus proteins a given antibody can interact with?*
- *How do you think flu virus can avoid being targeted by antibodies?*
- *How would the structure of flu virus proteins have to change to avoid being recognized by our immune system? Why?*

Note: make sure to clearly explain the function of antibody and antigen. The focus of this activity is to explain structure-function relationships focusing on ideas of charge, force and shape, and NOT focus on terminology.

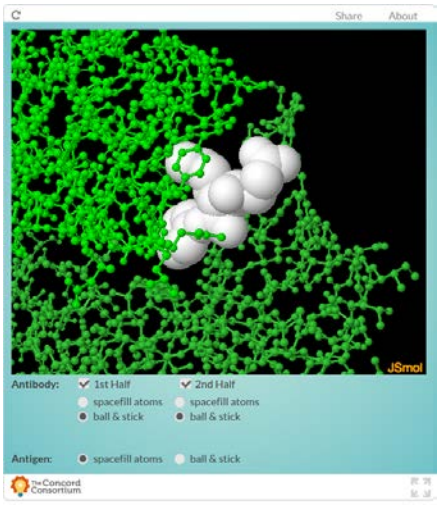
The simulation shows how an antibody binds to proteins called antigens produced by the flu virus. Explore the simulation and think about the mechanism that allows antibodies to protect us from flu, and how is it similar to the way enzymes carry out their function.

https://lab.concord.org/interactives.html#interactives/interactions/3D-antibody.json

Note: Remember, each antibody is a specific protein produced by our immune system. It targets molecules that cause disease to spread in our body. These harmful molecules are called antigens.

1. [snapshot prompt] Use the simulation to show how the antibody interacts with the flu virus protein (antigen) to protect us from diseases. Take a snapshot to support your answer.
[text prompt] Explain why this step is important in protecting our body from infection.

Student responses:
The shape of the antigen is complementary to the active site of the antibody, which allows for the closest proximity between the surfaces of antibody and antigen as shown in the snapshot below. This allows for the largest number,and strongest possible interactions to form between antibody and antigen.This step is important because it prevents the flu virus from spreading in
our body and make us sick.



2. Flu virus changes its structure slightly every year as a result of adapting to changing environmental conditions. Would the antibody shown in the simulation still be as effective in protecting our body from the flu virus protein if the flu virus protein was one atom shorter? How would this impact the health of an organism? Use ideas from the simulation to explain your prediction.

Student responses:
The active site of the antibody protein fits this particular antigen in a way that all atoms in the antigen are next to atoms in the antibody allowing for all the atoms in the antigen to form interactions with the protein. If the antigen was one atom shorter, it will eliminate interactions of that one atom with the protein, therefore leading to overall weaker interactions between antibody and antigen. This could potentially have harmful effect on our organism because antigen can no longer form strong interactions with the antibody, which would cause the antigen to be free to overtake our body, like in the case of flu virus.

3. Flu virus changes its structure slightly every year as a result of adapting to changing environmental conditions. Would the antibody shown in the simulation be still as effective in protecting our body from the antigen if the antigen was one atom longer? How would this impact the health of an organism? Use ideas from the simulation to explain your prediction.

Student responses:
The active site of the antibody protein fits specific shape of this particular antigen in a way that all atoms in the antigen are next to atoms in the antibody allowing for all the atoms in the antigen to form interactions with the protein. If the antigen was one atom longer, it will likely not fit entirely into the active site of the antibody, causing alignment between surfaces to be distorted therefore leading to overall weaker interactions between antibody and antigen. This could potentially have harmful effect on our organism because antigen can no longer form strong interactions with the antibody, which would cause the antigen to be free to overtake our body, like in the case of flu virus.

4. Sometimes flu virus can go through drastic changes in the structure in order to avoid being recognized by the proteins produced by our immune system to help fight infection, also called antibodies. If the structure of the antigen (i.e. proteins produced by the flu virus) is not complementary to the active site of the antibody at all, how will it affect antibodies' ability to protect us from the antigen? How would this impact the health of an organism? Use ideas of structure, charge and forces to explain your prediction.

Student responses: if the shape of the antigen molecule is not complementary to the active site, the distance between antibody and antigen surface will not be minimal. Therefore, the generated attractive force between permanent partial charges of interacting polar amino acids, and temporary partial charges between interacting nonpolar amino acids will decrease, therefore leading to decreased interaction between antibody and antigen. This weakened interaction might cause the antibody not to bind that particular antigen, which will leave our body unprotected from the flu because the flu virus will be free to spread all over our body.

Discussion

Ask student to share their answers to the questions above. Push them to think why specific shape of antigen is so important for forming interactions with antibody, and how it contributes to protein's ability to protect our bodies from infection.

Possible questions:

- *How does specific shape of antibody affect interactions between antibody and antigen? What would be the consequence for our health?*
- *If an antigen structure is not complementary to the active site of the antibody (even by one atom), do you think they can for a strong complex? Why? Explain your answer. What would be the consequence for our health?*
- *How do you think polar and nonpolar interactions will change if the shape of the antigen is not complementary to the active site of the antibody? Why? How will it affect antibody function? What would be the consequence for our health?*
- *How do you think temperature might affect interactions between antibody and antigen? What would be the consequence of increased temperature on health of an organism?*

Note: make sure to clearly explain the function of antibody and antigen. The focus of this activity is to explain structure-function relationships focusing on ideas of charge, force and shape, and NOT focus on terminology.

Page title:

How do vaccines help our bodies fight infection?

Vaccines are specially designed substances that provide immune protection against specific diseases. Every year, scientists work on designing new versions of vaccines aimed at protecting our bodies from various constantly changing proteins produced by flu viruses. However, if our own immune system is capable of producing antibodies to fight off various infections, how come we still need vaccines?
Provide your initial ideas in the space below, and discuss with class.

5. If we have antibodies to protect us from infection, why do we need vaccines?

Student responses: this question is aimed to elicit student ideas. Answers don't need to be accurate at this point. Possible student answers include:

- Vaccines contain antibodies specific for a given antigen, and they are already made, so our body doesn't need to synthesize them, which will prevent us from getting sick more efficiently.
- If a virus changes very quickly, and our body can't make protective antibodies in a timely fashion, vaccines help fight disease because they contain antibodies that are specific for that antigen and already pre-made.
- Our body is too weak to fight the infection In the case of babies or older people), and vaccines introduce the necessary antibodies into the body without having our immune system to make them.

Discussion

Ask students to share their ideas from the questions above. Share with them, that it takes time and significant energy resources for our body to produce antibodies capable of interacting with a specific antigen. In the case of flu, for example, the virus changes rapidly, and the structure of proteins produced by this new form of virus is also different. Every year, the structure of the flu virus proteins changes significantly, so that our body needs to work really hard to make new antibodies to fight off new flu virus proteins Vaccines, on the other hand, contain antibodies that are already made by scientists in the lab, and specific for a new flu virus proteins. Discuss how vaccination helps our bodies fight diseases.

Possible questions:

- *Why do you think vaccines might work better than own antibodies?*
- *How do vaccines work to protect us from various antigens?*
- *How do you think vaccine and antibodies are similar? How are they different?*

Tell students that in the next simulation they will work as scientists to design an antibody that is the most efficient in protecting us from a specific antigen. Ask them to pay special attention to the mechanism that antibodies use to protect us from diseases.

Every year scientists work to produce new vaccines that are effective against new strains of flu virus. These vaccines contain antibodies that have been made to target new forms of the flu virus. In order to produce these specific antibodies, scientists isolate potential antigens, determine their structure, and then design antibodies that can efficiently target that structure.

In the simulation, you are given a task to design an antibody to target specific antigen structure that is given to you. As you go through the design process, think about how specific polar and nonpolar interactions relate to the antibody's ability to perform its function.
Note: Make sure you drag the antigen slowly to observe all possible interactions.

Include diagrams and charts to connect the terms and their meaning.
Simulation: Designing your own antibody
https://lab.concord.org/interactives.html#interactives/sam/intermolecular-attractions/8-your-immune-system.json

6. Look at the antibody structures provided to you in the simulation. Without modifying their structure in any way, do you think any of them would be efficient in protecting against the antigen? Explain your reasoning.

Note: Remember, antibody is specific protein produced by our immune system. It targets molecules that cause disease to spread in our body. These harmful molecules are called antigens.

> **Student responses:** the antigen provided in the simulation contains polar regions that interact with the antibody. All antibodies shown in the simulation are nonpolar, and therefore will not form any significant interactions with polar parts of the antigen. Therefore, none of the antibodies shown as they are will be effective in fighting off the given antigen.

7. [Snapshot prompt] As a scientist, you often use results of previous research to solve new problems. If you have the four antibodies provided to you in the simulation available from previous flu season, which antibodies would you choose to modify in order to fight the new antigen given to you? Provide a snapshot from the simulation to support your answer.

[text prompt] Explain your choice.

> **Student responses:**
> The structure shown below would be choice #1 to work with and potentially modify in order to fight off the given antigen. This is because in the structure shown below antibody forms the strongest interactions with antigen because the antigen structure is the most complimentary (provides largest area of alignment between antibody and antigen), therefore leading to largest possible attractive force to form between polar and nonpolar amino acids and corresponding atoms on the antigen. Additionally, nonpolar regions of the antibody align with the nonpolar regions of the antigen, generating largest possible attractive force for the given antigen structure.
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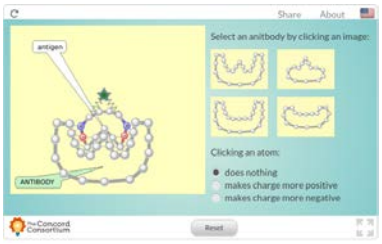
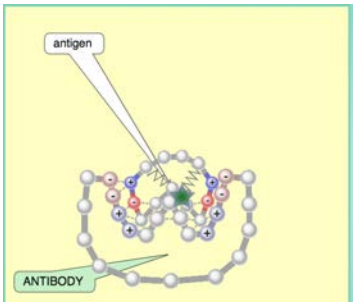
> 
>

8. [snapshot prompt] How could scientists modify the structure suggested in previous question to increase its efficiency in fighting the antigen shown in the simulation? Provide a snapshot to support your reasoning.

[text prompt] Explain your answer.

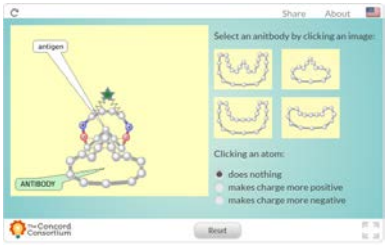
Student responses: if the amino acids that make up the antibody protein are polar, then it will form strongest interactions with antigens that are also made up of polar parts. This is because the magnitude of attractive force generated between permanent partial charges on polar amino acids is similar, and therefore they attract to other polar amino acids. Therefore, if I put a charge on the regions of antibody that align with polar regions of the antigen, the formed interactions will become stronger. This will make the antibody structure more efficient in bonding and therefore neutralizing the antigen. This is shown in the snapshot below.



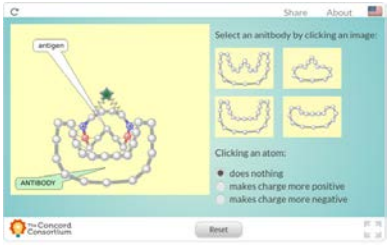
9. [Snapshot question] As a scientist, you often use results of previous research to solve new problems. If you have the four antibodies provided to you in the simulation available from previous flu season, which antibodies would you NOT work on modifying to fight the antigen given to you? Provide snapshots from the simulation to support your answer, and add comments to each one to explain your choices.

Student responses: the structures shown below would not work.

There is no way I can modify the structure below because the amino acids the regions of the antibody and antigen that align together are nonpolar. Therefore, there is nothing I can do with the antibody below to increase attractive force between antibody and antigen.



The structure below is the one that forms very weak interactions, if any, with the given antigen. The antigen structure is not complementary because the middle part of the antibody has no contact with the antigen. Therefore, even if antibody structure is made more polar, the generated attractive force is probably quite small.



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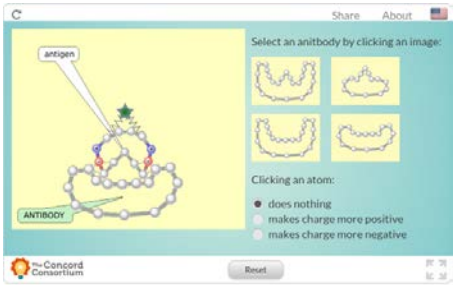
The structure below forms least complimentary structure between antibody and antigen, and least number of interactions can be formed, therefore leading to very weak interactions. Therefore, it is least efficient in protecting our body from that particular pathogen.



10. How does energy of the system change when antibody and antigen bind together? How does this energy change contribute to ability of an antibody to bind only certain antigens and not others? Explain your reasoning.

Student responses: when the antibody and antigen of completely complementary shape forms an interactions, charged surfaces on both molecules are closer than for interaction with any other molecule. This leads to the largest possible attractive force between the two molecules, causing the overall structure to be very stable and not dissociate. This also leads to energy of the system decrease significantly as a result of multiple intermolecular interactions being formed, which leads to the most stable structure. Therefore, as a result of this increased stability due to maximum generated attractive force between the two molecules antibodies will tend to bind only antigens with specific structure.

Discussion

Ask students to share their answers to the questions above. Focus on Q6 first and discussing why you need to modify the structure of the antibodies to improve their ability to protect form the given antigen.

Possible questions for #6

- *Why do you think the antibodies provided in the simulation would not be efficient in protecting from the given antigen?*
- *What kind of interactions would each of the antibodies form with the given antigen? Are they strong enough to bind the antigen? Why yes/no?*

Move to #7 and #8, and discuss what is a good starting structure of the antigen to work with, and how it can be modified to protect from the antibody in question. Before discussing the questions below as a whole class, you might choose to divide students into small groups, and have them share their answers to questions #7 and #8, and discuss what structures they chose to modify and why, as well as how they propose to modify a chosen structure and why. Ask each group to pick a modified structure of antibody from the ones they suggested in their small groups, and explain why they think it would work best for a given antigen.

Possible questions for #7 and #8

- *Why did you choose that antibody structure in #7?*
- *What makes this antibody easier to work with than the other antibodies?*
- *What kind of interactions would this antibody form with the given antigen? Are they strong enough to bind the antigen? Why yes/no?*
- *Why did you suggest to modify the antibody that way?*
- *How would altering the antibody structure this way help protect us from diseases?*

Move to question #9 and discuss why each of the structures indicated by students would not work as a starting structure for modification purposes

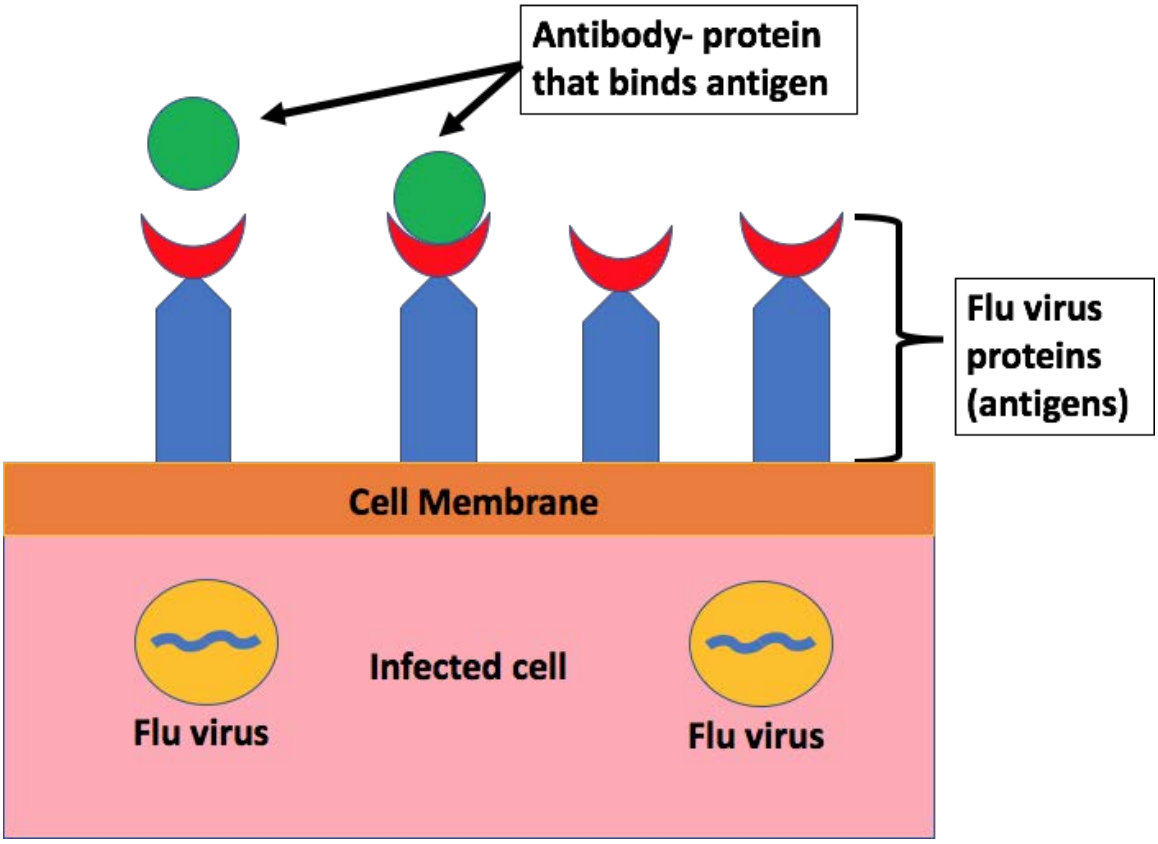
Possible questions for #9

- *Why the suggested antibodies won't work as a starting structure?*
- *What makes makes each antibody harder to work with than the one you picked to be modified?*
- *What kind of interactions would each antibody form with the given antigen? Are they strong enough to bind the antigen? Why yes/no?*

Finally, move to discussing questions #10 and focus on how energy relate to how well antibody can perform its function

Page title:
Are vaccines always effective?

How effective is the flu vaccine? Every year flu vaccines help millions of people from catching a flu, but numbers of those who do get flu after getting a vaccine are also quite high. Use your understanding of protein immune function as well as some information shared by your teacher to figure out what makes vaccines effective, and discuss your ideas with peers.



Discussion

Share some recent data on flu vaccine effectiveness with your students. For example, you might choose to show them official statistics from Center for Disease Control and Prevention on flu vaccine effectiveness.

Share with them that according to recent studies of flu vaccine effectiveness, flu vaccines decrease the risk of flu illness between 40%-60% in the general population. Discuss with students why this is the case, and what would make flu vaccine less than 100% effective.

Possible questions:

- *What does this statistics mean to you?*
- *Can you still get sick after getting a flu vaccine?*
- *Why yes/ no?*
- *Why do you think flu vaccine is not 100% effective?*
- *What would make flu vaccine less effective?*
- *Why do they need new flu vaccine every year?*
- *Do you think flu virus proteins have the same structure every year? Why yes/no?*

Push students to get to a consensus that flu virus can change from year to year, and the flu virus proteins that are targeted by our antibodies also change their structure. Therefore antibodies produced by our bodies, or provided to us in a form of a vaccine, need to be adjusted accordingly. If students struggle making these connections, go back to the diagram from the beginning of this activity, and discuss how structural variations in proteins produced by flu can affect antibody effectiveness.

Possible questions:

- *Look at the structure of flu virus proteins produces on the surface of infected cells, as shown in the diagram provided to you. How do you think this proteins might change to avoid being recognized by the antibody shown in the diagram? What would be the consequence of this change for our health?*
- *How would the structure of the antibody have to change in response of change in the structure of the antigen? Why?*
- *Any other ideas?*

Share with students that the structure of the proteins produced by flu virus can change from year to year, to avoid being recognized by the antibodies in our system.

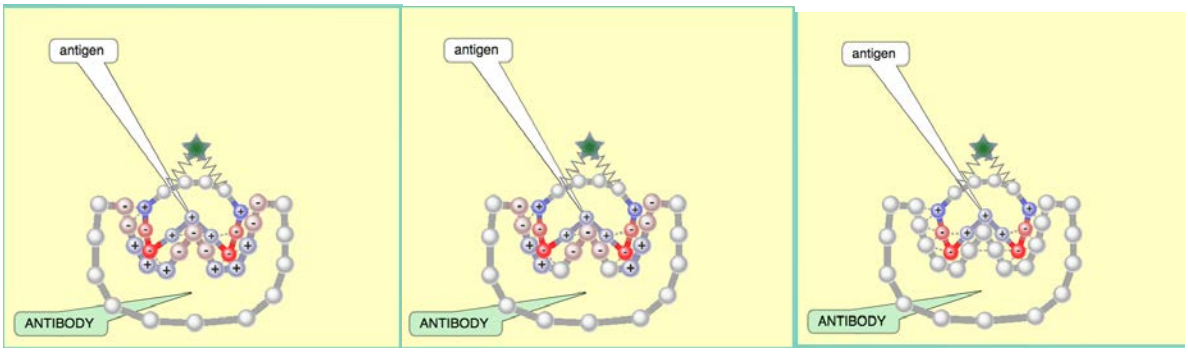
As you concluded from discussions above, antigens are agents that cause infection (like flu virus proteins), and they constantly change their structure to avoid being recognized by the antibodies of our immune system. Consider the same simulation where you designed your own antibody. Investigate how slight changes in the structure of the antibody affect interactions between antibody and antigen. Think about what consequences it might have for our health and answer the questions below.

Simulation: Designing a new antigen

https://lab.concord.org/interactives.html#interactives/sam/intermolecular-attractions/8-your-immune-system.json

11. [text prompt]. Below are three snapshots that show three similar antibodies interacting with a specific antigen. Build each of these structures in the simulation and study how strongly they interact. What do you observe?

Structure A **Structure B** **Structure C**



Student responses: structure A is the hardest one to pull apart, followed by structure B, and finally structure C, which is the easiest one to pull apart. Therefore, the strongest interactions form between antibody and antigen in structure A, followed by and then C.

12. Explain observed differences in strength of interactions among the structures you built. Explain your observations.

Student responses: The stronger the force between antibody and antigen, the more difficult it is to pull apart. Antibody and antigen in structure A have larger number of opposite charges on aligning surfaces that can form interaction as a result of generated attractive force. Therefore, the generated attractive force is larger for structure A, then for structure B, where some amino acids in the antibody are uncharged, and therefore don't generate as large of an attractive force with antigen. Finally structure C amino acids are not charges, so they don't form very strong interactions with charged parts of the antigen.

13. Which antibody structures, A, B or C, would be the most effective in protecting our bodies from the given antigen? Explain your answer.

Student responses: antibody in structure A would be the most effective in protecting our body against a given antigen because it forms strongest interactions with the antigen, and will therefore be able to prevent it from spreading in our system.

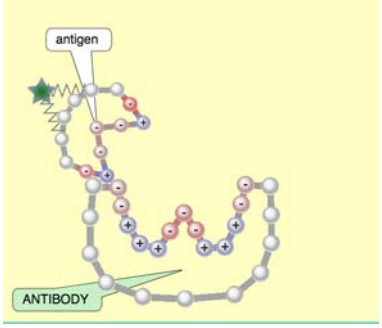
14. Imagine that you have three flu vaccines of the following composition.
Vaccine #1 contains antibodies of structure A
Vaccine #2 contains antibodies of structure B
Vaccine #3 contains antibodies of structure C

Assuming the structure of the antigen is the same one as provided in question #11, rank vaccines in the order of their effectiveness from most effective to least effective. Explain your ranking.

Student responses: vaccine A would be the most effective, followed by vaccine B and then vaccine C. Antibodies in vaccine A form strongest interactions with the antigen, followed by vaccine B and the vaccine C.

15. [snapshot prompt] Use the simulation to suggest how the antigen structure might change to avoid being recognized by the antibody that you suggested to be the most effective in previous questions. Provide snapshot and annotate it to indicate how you would change the antigen. [text prompt] Explain your suggestion.

Student responses: students choose to modify the antigen structure in any way they want, but keep the antibody structure that they previously suggested should be the most effective in binding the original antigen intact. Their snapshots should indicate that once the antigen structure has been changed, the complex dissociates, and the antibody/ antigen no longer have strong interactions between them. Explanation should include ideas related to charges, and generated attractive/repulsive, force. For example, for the structure below, antigen changed in a way that the charges on the antigen are opposite to the changes on the antibody when the structures align to form a complex. This generates repulsive electric force causing the complex to dissociate.



16. Using ideas from the simulation and discussion, explain why vaccines are not 100% effective. Provide reasoning for your explanation.

Student responses: if vaccines contain antibodies that are not highly specific for a given antigen (the 3D shape of the antibody is not complementary to the shape of the antigen, and the charges on the surfaces of antigen and antibody don't align in a way that the generated net force is attractive), then the antibody won't be effective in fighting against the given antigen. The more structural disparities exist between antibody and antigen, the less effective the vaccine containing that antibody will be against preventing disease caused by that antigen.

Discussion

Ast students to share their answers to questions 12-16 above
Discuss what makes an antibody and a vaccine effective against fighting a specific antigen.

Possible questions:

- *What are the differences in how antibodies in structures A, B and C interact with antigen?*
- *How can you explain those differences?*
- *What makes an antibody effective in protecting our bodies from a given antigen?*
- *What makes a vaccine effective against protecting our bodies from a given antigen?*

Divide students into small groups (no more than 3 people), and ask them to share their designed antigen structures for #15 . Ask them to discuss the following questions and share them with the class.

Possible questions:

- *How are the structures I designed for #15 similar/different to yours?*
- *How are the interactions between the structures I designed for #15 similar/different to yours? Why?*
- *Which one will form strongest/weakest interaction with the antibody? Why?*
- *Which one will be most dangerous for our body? Why?*

Finally, ask students to share their answers to question 16. Push them to think about why vaccines are important, and how they can help our body fight the infection.

Possible questions:

- *What makes vaccines effective? Why?*
- *What makes vaccines ineffective? Why?*
- *Do you think vaccines against different diseases are equally effective? Why yes/no?*
- *If vaccines are not always effective, why should we use them?*

Ask students to sum up what they have learned in this activity. Push students to relate structure of the antibody to the function, and use these ideas to explain why vaccines are effective aids in protecting us from various infections.

Possible questions:

- *What have we learned today about how our bodies can protect us from infection?*
- *What determines effectiveness of an antibody?*
- *Why do we need vaccines?*
- *What determines effectiveness of a vaccine?*
- *How are interactions between antibody and antigen different for*

Homework:
Reading for Activity 2.2: "Why is it important for proteins to have a specific structure?"

Activity 2.3: Why is a body temperature of 107° F deadly?

SUMMARY

In this activity, students will bring together the ideas discussed in previous activities and investigations related to how polar and nonpolar interactions and energy affect structure and properties of proteins in order to answer the driving question for the unit "Why is a body temperature of 107° F deadly?".

LEARNING GOAL

Students finalize their models to explain the relationship between protein structure and function using polar and nonpolar interactions and energy

Disciplinary core idea	Crosscutting concept	Science and engineering practice
Relationship Between Energy and Forces: When two objects interacting through a field change relative position, the energy stored in the field is changed. (NGSS Lead States, p. 99)	*Cause and Effect* Cause and effect relationships can be suggested and predicted for complex natural and human designed systems by examining what is known about smaller-scale mechanisms within the system. (NGSS Appendix G, p. 83)	*Developing and using models:* • Develop, revise, and/or use a model based on evidence to illustrate and/or predict the relationships between systems or between components of a system. • Develop and/or use multiple types of models to provide mechanistic accounts and/or predict phenomena, and move flexibly between model types based on merits and limitations. (NGSS Appendix F, p. 53)

Students construct scientific explanations to show how electrical forces between atoms and molecules as associated energy changes within the system lead to observed phenomena involving electrical interactions

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Relationship Between Energy and Forces: When two objects interacting through a field change relative position, the energy stored in the field is changed. (NGSS Lead States, p. 99)	*Cause and Effect* Cause and effect relationships can be suggested and predicted for complex natural and human designed systems by examining what is known about smaller-scale mechanisms within the system. (NGSS Appendix G, p. 83)	*Constructing explanations and designing solutions:* • Construct and revise an explanation based on valid and reliable evidence obtained from a variety of sources (including students' own investigations, models, theories, simulations, peer review) and the assumption that theories and laws that describe the natural world operate today as they did in the past and will continue to do so in the future. • Apply scientific ideas, principles, and/or evidence to provide an explanation of phenomena and solve design problems, taking into account possible unanticipated effects. • Apply scientific reasoning, theory, and/or models to link evidence to the claims to assess the extent to which the reasoning and data support the explanation or conclusion. (NGSS Appendix F p. 61)

POINTS FOR CONSIDERATION

- As you discuss with students protein interactions with small molecules, make sure to always point out that energy minimization is the driving factor in successful formation of stable interactions. Proteins are surrounded by billions of molecules in a living cell, and form hundreds of interactions with all sorts of substrates and water molecules at any given moment. However, if those interactions do not release large enough amount of energy as a result, and are not therefore energetically favorable, they are not going to be stable enough to form a long-lasting complex with the protein. Therefore, all these hydrophobic and hydrophilic interactions that proteins form with different molecules will only lead to stable interaction when their energy of the system is minimized as a result.
- As students are bringing all the ideas they have learned in this curriculum together, make sure they always go back to fundamental scientific principles related to electric forces, fields, charges, and energy of the system as they are explaining the questions. Students should connect these ideas to phenomena in question, and show causal mechanism grounded in those core ideas. The connection to phenomena is fundamentally important for three-dimensional learning. Make sure students not only recite the content they have

learned back at you, but incorporate that content into their causal explanations in a meaningful way that allows them to make sense of phenomena.

BASIC OUTLINE OF ACTIVITY

Use this space to make notes to prepare for your lesson

1. Introduction
    a. Discussion

2. Bringing it all together: ” Why is the temperature of 107° F deadly?”

    a. Student question

    b. Discussion

3. Bringing it all together: “How are interactions between clothes sticking together in a dryer, and proteins similar and different?”

    a. Student questions

    b. Discussion and gallery walk

    c. Conclusion

Activity 2.3: Why is a body temperature of 107° F deadly?

Introducing the Lesson

Introduction: review ideas discussed previously including polar and nonpolar interactions, temperature and energy as related to protein structure-function.

Possible questions:

- *How does temperature affect a protein's ability to carry out its function? Provide an example.*
- *Why does temperature have an effect on protein function?*
- *How are polar and nonpolar interactions within protein affected by temperature?*
- *How do amino acids that make up the protein affect protein structure and function?*
- *Any other ideas?*

Page title:

Introduction

In the previous investigation you investigated how polar and nonpolar interactions affect protein 3D structure and function. In this activity you will bring all these ideas together to finalize your model of how nonpolar interactions between proteins or between proteins and other small molecules affect the structure and properties of proteins . This will help you answer the driving question for the investigation “Why is a body temperature of 107° F deadly?”

Page title:
Bringing it all together: " Why is the temperature of 107° F deadly?"

1. [Drawing Prompt] Draw a model showing why a high temperature like 107° F kill you? Include what you have learned about protein structure, function, temperature, and energy in your model.
[text prompt] Explain your model.

Student responses: Student models and/or explanations should contain the following ideas:
as the temperature in our body rises to 107° F the energy of the system increases. This means that atoms in the amino acids that make up proteins in our body have more kinetic energy to move around, and overcome intermolecular interactions that form 3D structure of the protein. Once the 3D structure of the protein is distorted, protein regions where various molecules can bind no longer have the same shape, and no longer are composed of the same amino acids as before. This means that the specific interactions between protein and other molecules that are based on complementarity of shape, and interaction between specific polar and nonpolar regions can no longer happen in the same fashion as at normal temperatures. This prevents proteins from interacting with other molecules and carry out their specific functions like including enzymatic, cell signaling, defense against antigens etc. Once these basic biological functions are no longer fulfilled, human organism can die.

Discussion:
Ask students to create a shared data table on the board to compare their models and explanations for question #1 and discuss their ideas

Possible questions:

- *What happens to protein 3D structure at high temperature?*
- *What happens to protein active site at high temperature?*
- *How are interactions between protein and substrate affected at high temperature?*
- *How is lock and and key mechanism affected at high temperature?*
- *How does potential and kinetic energy change when temperature is increased? How does it affect interactions between proteins and other molecules?*
- *Any other ideas?*

Page title:
Bringing it all together: How are interactions between clothes sticking together in a dryer, and proteins similar and different?

We started with the question why do some things stick together and other things don't? We started with macroscopic level observations like clothes sticking together in a dryer, and used evidence from experiments and simulations to come up with microscopic level models and explanations for phenomena involving electrical interactions. Use these ideas to answer the questions below.

2. How are clothes sticking together in a dryer similar and different to what holds proteins and small molecules together?

Student responses: when clothes stick in a dryer, this happens due to the attraction between oppositely charged atoms that make up clothes. This is because when clothes rub against each other in the dryer, electrons get transferred from atoms on one piece of clothes to the other, making one of the pieces positively charged, and the other negatively charged, so they generate attractive force between them and stick together as a result. Similarly, proteins interact with other molecules also via attractive forces generated by charges. However, those attractive forces are generated by partial charges that are either permanent (between partial charges on polar amino acids) or temporary (between partial charges on nonpolar amino acids).

3. Some of the best detergents that work on delicate clothes don't require hot water to remove tough stains. These detergents contain enzymes. In fact, enzyme containing detergents work at cold temperatures but not at hot. Explain why these detergents work differently at different temperatures.

Student responses: enzyme detergent work by forming intermolecular interactions with molecules in stains. The higher the temperature, the more kinetic energy molecules have and the faster they move. Three-dimensional structure of the enzymes that allows for the enzyme to perform its function is formed via intermolecular interactions between atoms in polar and nonpolar amino acids. At high temperatures, the atoms in these amino acids start moving fast and this motion destroys intermolecular interactions and therefore the 3D structure of the enzyme. This causes 3D structure of enzyme's active site to also be distorted, preventing it from forming interactions with molecules in stains. This causes the detergent containing enzymes be ineffective in removing stains.

4. [Drawing Prompt] Leaving clothes to soak in soapy water helps get rid of tough stains. Construct a model to explain why soaking makes the clothes cleaner.
[text prompt] Explain your model in the space provided.

Student responses: the model should indicate that nonpolar ends of detergent encapsulate nonpolar molecules of dirt and polar ends of the detergent face the outside where water molecules are located.
Explanation: pre-soaking allows for intermolecular interactions between molecules of soap and molecules of dirt to form. Non-polar regions of soap molecules interact with nonpolar molecules of dirt and encapsulate them to form a micelle. Pre-soaking allows for micelles to form, which makes it easier to get rid of the dirt by washing it off later.

5. [Drawing Prompt] If a wall is made up of atoms, and atoms are mostly empty space, how come I can't punch my hand through a concrete wall? Draw a model.
[text prompt] Explain your model.

Student responses: All matter is made up of atoms. Atoms consist of small positively charged nucleus, and negative electrons orbiting the nucleus. All charged particles have electric field around them. When objects get really close to each other, electric fields start interacting and generate either attractive electric force (in the case of interactions between fields generated by opposite charges), or repulsive electric force (in the case of interactions between fields generated by similar charges). Since electrons are negatively charged, they generate electric field around them, and as objects get close enough to where these fields start interactions (like, when we are touching the wall with our fist, atoms that make up out fist are close to the atoms that make up the wall), repulsive electric force generated by interacting fields of negatively charged electrons prevents us from punching through the wall.
The model should show electric field generated by negatively charged electrons in atoms that make up our body and the wall, and the resulting repulsive force between out body and the wall.

6. It is common for Great Lakes region to experience lake effect snow in late fall and early winter. Specifically, areas close to the Great Lakes get high accumulation of snow, often with wind and lightning during that time. As winter progresses, and the water on the Great Lakes freezes, lake effect snow disappears. Explain why lake effect snow occurs. Use ideas of energy and electric interactions to explain why lake effect snow occurs.

Student responses: during late fall and early winter air starts cooling off faster than water, causing big temperature difference between water and air. As cold air moves over the surface of Great Lakes, water molecules that make up water vapor start interacting with air molecules. Since water is warmer, molecules of water vapor have more energy than molecules of air, they transfer energy to molecules of air via collisions. This causes air molecules to warm up, and water vapor to cool down. This warm air molecules interact with water molecules and rise up through the cold air. As this happens, air and water molecules cool down because they transfer energy via collisions to the cold upper layer of air they are traveling through. At this point, water forms intermolecular interactions that cause it to freezes and become snow. As intermolecular interactions are formed, energy is released into the atmosphere. When the air mass hits the shore, it falls in the form of heavy snowstorm. The access energy released is manifested in thunder and sometimes lightning.