Teacher Guide



DNA and Histone Model

Abstract

A 3-D cut-and-paste model depicting how histone, acetyl and methyl molecules control access to DNA and affect gene expression.

Learning Objectives

- DNA is coiled around histones.
- Tightly coiled DNA is inaccessible to gene reading machinery.
- Methyl molecules bind to DNA and block access to genes.
- Acetyl molecules bind to histones and improve access to genes.

Estimated time

Class time: 50 min.

Prep time: 15 min.

Materials

- Copies of molecule cut outs and student directions
- Scissors
- Tape
- Paperclips (8 per model)

Instructions

Distribute materials to pairs of students and instruct them to follow the directions on pages 1-4.

TIP: To save time, split the class in half. Ask student pairs in one half to complete the Making DNA Inaccessible portion of the activity (pages 1-2) and ask the other half to complete the Making DNA Accessible portion (pages 3-4). Have pairs of students share their different models with one another.

Discuss

- Methyl and acetyl control gene expression by controlling access to DNA. Gene reading machinery in the cell is blocked by methyl that binds directly to DNA, or when DNA is wound tightly around histones. Access is easier when acetyl causes DNA to be wound more loosely around histones.
- Methyl and acetyl are epigenetic tags- chemicals that act as "switches" that determine gene expression without changing the underlying genetic code. Epigenetic tags turn genes on or off in response to cell signals, creating a dynamic layer of control called the epigenome.
- Enzymes play an important role in gene expression by facilitating the addition and removal of methyl and acetyl. In addition, enzymes are a part of the "Gene Reading Machinery".

Optional Modifications

- Introduce the following vocabulary for more advanced students:
 - a. Nucleosome: a single histone spool with its associated DNA. A sub-unit of chromatin.
 - **b.** Chromatin: the material that makes up a chromosome.
 - c. RNA Polymerase: the "gene reading machinery"
- Methyl attaches to DNA between a Cytosine (C) and Guanine (G) in locations known as CpG islands, where the frequency of C-G base pairs is higher than in other stretches of DNA. Instruct students to look for CpG islands along the DNA ribbon when attaching methyl molecules and place them accordingly. You may also use different colored paperclips in place of the methyl molecule cut outs to better highlight the area where methyl attaches to DNA.
- Choose a region of the DNA ribbon to represent a gene. Have students color it with a highlighter before attaching the DNA ribbon to their histone spools and winding. Ask students to visually keep track of the gene as they carry out the activity. Discuss how methylation and acetylation would affect the expression of the gene.
- Because histone acetylation and DNA methylation are driven by constant cell signals, the physical structure of the genome is dynamic. Once they have constructed the model both ways (Inaccessible DNA and Accessible DNA), have students portray the dynamic nature of the genome's physical structure by having them manipulate their models in response to "gene on" or "gene off" signals. For example: Start with a constructed Inaccessible DNA model. At the prompt of "gene on" have students acetylate their histones, de-methylate and unwind their DNA ribbons. At the prompt of "gene off" have students de-acetylate their histones, wind their DNA ribbons more tightly and add methyl. Discuss when a cell might receive such signals.

Extension

Make a chromosome! Pool together the DNA and Histone models from the whole class, plus others if possible, and stack them. The models you pool can be tightly wound and methylated, loosely wound and acetylated, or a combination of both. Be sure to connect the DNA ribbons to form one long, continuous strand. Students will see that chromosomes are made of DNA and histones.

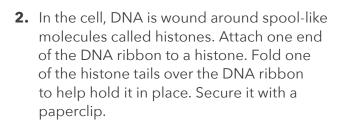
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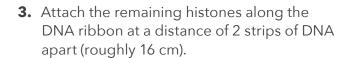


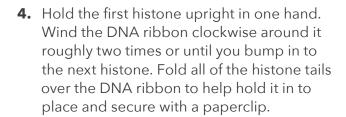
How do molecules control gene expression?

Making DNA Inaccessible

1. Cut out all of the molecules on pages 5-8, assemble the DNA ribbon and histone spools. Gather 8 paperclips.

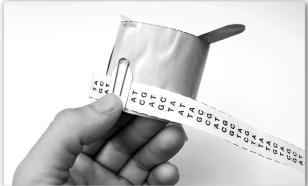






In a real cell, a length of DNA wraps around a histone roughly 1.7 times and histone tails wrap around the wound DNA similarly.









How do molecules control gene expression?

Making DNA Inaccessible (cont)

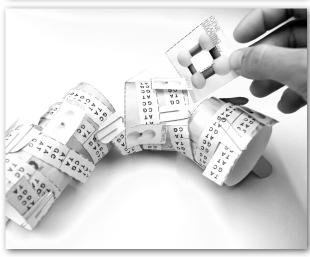
5. Trying not to fold or bend the DNA ribbon, wind it around the next histone. Again, fold the histone tails around the DNA ribbon and secure with a paperclip. Repeat until all of the DNA ribbon has been wound. The histones should begin to stack on top of one another as you wind.



6. When DNA is wound tightly around histones, there tends to be a lot of methyl molecules bound to it. The methyl molecules cover the DNA, making it unreadable to gene reading machinery. Use tape to attach the methyl molecule cut outs to exposed areas of your DNA ribbon.



7. Genes become active when gene reading molecules attach and move down a length of accessible DNA, "reading" the DNA code as they go along. Try to attach and move the Gene Reading Machinery cut-out to any length of the DNA ribbon that is not spooled around a histone or covered by methyl. Can the machinery read any significant stretch of DNA? Would this be an active, or inactive gene?



8. Remove the methyl molecules and de-construct your model if moving to the next step: MAKING DNA ACCESSIBLE

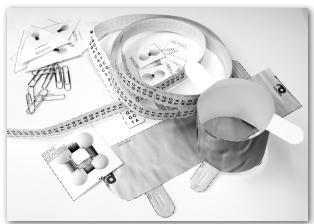
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How do molecules control gene expression?

Making DNA Accessible

1. Cut out all of the molecules on pages 5-8, assemble the DNA ribbon and histone spools. Gather 8 paperclips.

- 2. DNA is wound around spool-like molecules called histones. At times, acetyl molecules bind to histone tails. Attach two acetyl molecules to each histone at different locations. To attach the molecules, pull a histone tail trough the cut in the center of the acetyl molecules. Now your histones are "acetylated".
- **3.** Attach an acetylated histone to one end of your DNA ribbon, secure it with a paperclip.
 - Attach the remaining acetylated histones along the length of the DNA ribbon at distances of 2 DNA strips apart (roughly 16 cm).
- **4.** Hold the first histone upright in one hand. Wind the DNA ribbon clockwise around it two times or until the first histone touches the next one.





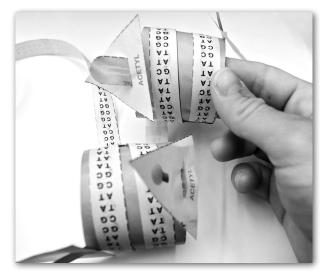




How do molecules control gene expression?

Making DNA Accessible (cont)

5. In a real cell, the addition of acetyl molecules cause the histones to distance themselves from one another. Be sure that no part of the neighboring histones, including the acetyl molecules are touching. If they are, unwind the DNA ribbon a little bit to put some space between the histones. Secure the DNA ribbon with a paperclip.



- **6.** Wind the DNA ribbon clockwise around the next histone. Again, be sure that no part of neighboring histones are touching then secure the DNA ribbon with a paperclip. Repeat until the DNA ribbon has been wound around all the histones. The histones and DNA should be spooled loosely, with some space between histones.
- 7. Genes become active when gene reading molecules attach and move down a length of accesible DNA, "reading" the DNA code as they go along. Try to attach and move the Gene Reading Machinery cut-out to any length of the DNA ribbon that is not spooled around a histone. Can the machinery read any significant stretch of DNA? Would this be an active, or inactive gene?

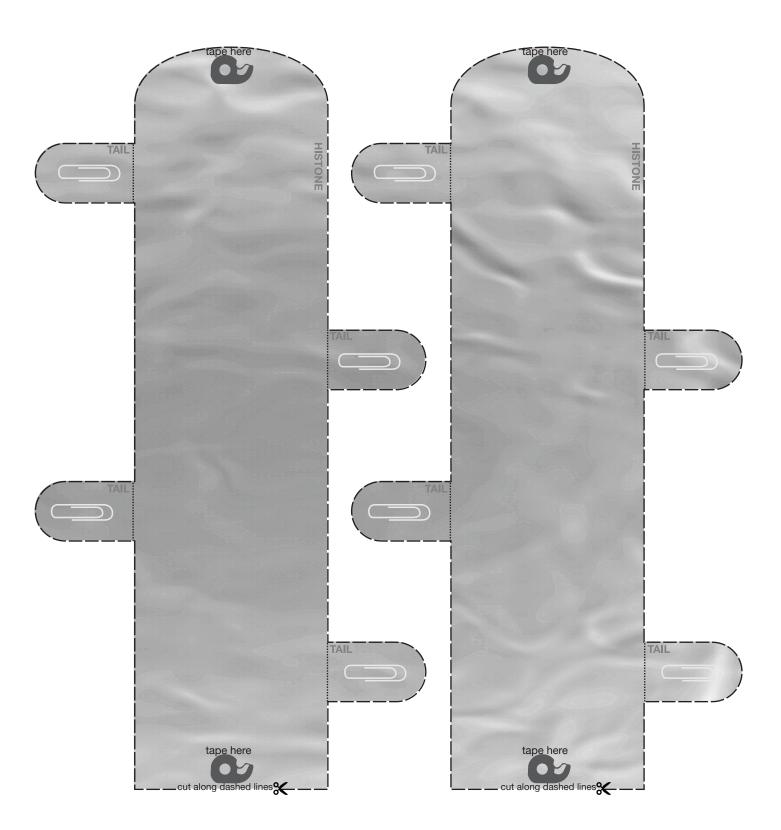


© 2020 University of Utah DNA and Histone Model **4**



Histone Spools Set 1

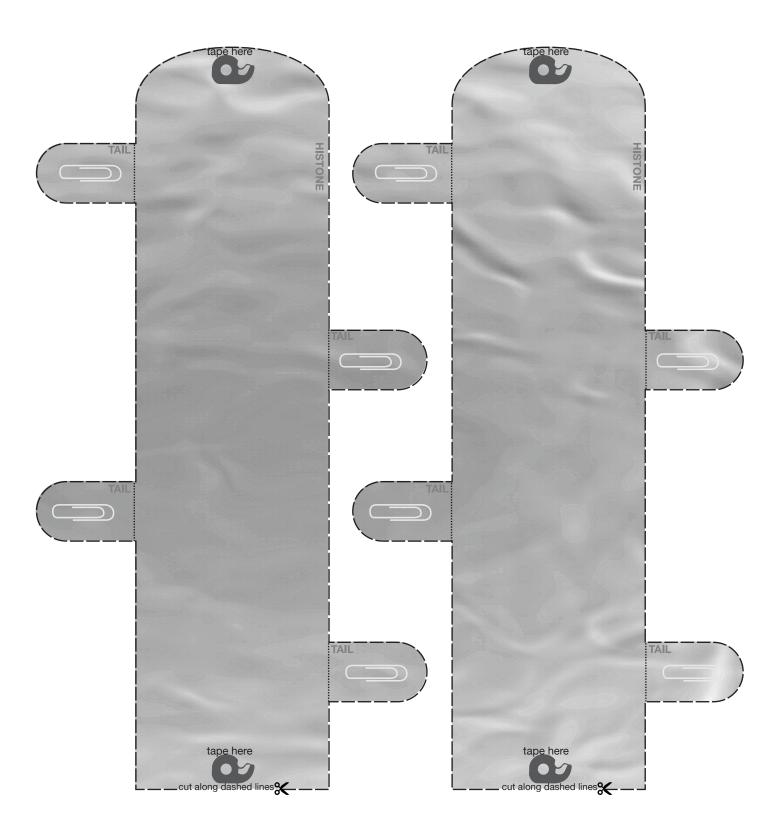
Tape the ends of each histone together to form spools





Histone Spools Set 2

Tape the ends of each histone together to form spools





DNA Strips

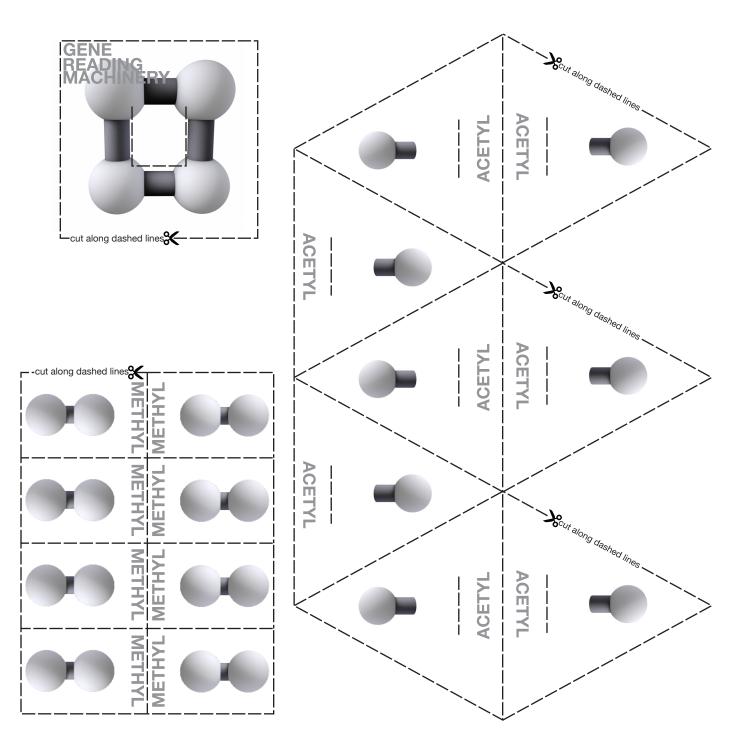
Tape the short ends of the DNA strips together to form one long DNA ribbon.

TA	TA	CG	GC	CG	CG	TA	GC
GC	GC	AT	TA	AT	TA	AT	TA
GC	AT	GC	GC	GC	GC	AT	cG
AT	TA	TA	GC	GC	TA	CG	AT
GC	CG	AT	CG	TA	GC	GC	TA
AT	AT	GG	AT	AT	TA	AT	AT
CG	AT	GC	GC	CG	AT	GC	CG
AT	CG	CG	GC	GC	GC	CG	TA
TA	AT	AT	AT	AT	AT	AT	GC
TA	GC	AT	TA	GC	TA	GC	TA
GC	TA	CG	TA	CG	TA	CG	GC
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TA	TA	AT	TA	CG	TA	GC	GC
CG	GC	CG	AT	CG	AT	TA	CG
CG	CG	AT	TA	GC	TA	CG	GC
GC	АТ	TA	AT	AT	GC	GC	TA
TA	CG	AT	CG	TA	TA	AT	AT
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GC	CG	AT	AT	GC	AT	TA	CG
AT	AT	GC	GC	GC	GC	AT	AT
AT	TA	TA	TA	CG	CG	TA	GC
CG	GC	GC	AT	TA	AT		
AT	GC	TA	TA	GC	GC	TA	GC
GC	AT	GC	CG	TA	GC	CG	AT
TA	GC	TA	TA	CG	TA	CG	TA



Methyl, Acetyl and Gene Reading Machinery

Cut out and slit along interior dashed lines.



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