Kansas Corn: Decoding DNA - Modeling Protein Synthesis

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Kansas Corn: Decoding DNA-Modeling Protein Synthesis
Grade Level: Middle School / High School

Overview

Any educator electing to perform demonstrations is expected to follow *NSTA Minimum Safety Practices and Regulations for Demonstrations, Experiments, and Workshops*, which are available at http://static.nsta.org/pdfs/MinimumSafetyPracticesAndRegulations.pdf, as well as all school policies and rules and all state and federal laws, regulations, codes and professional standards. Educators are aunder a duty of care to make laboratories and demonstrations in and out of the classroom as safe as possible. If in doubt, do not perform the demonstrations.

When we look at a living organism, including ourselves, we are seeing proteins or the results of proteins at work. DNA is the instructions in the cell to make these proteins, and as a result it determines nearly everything about us including our eye color, hair color, and hair texture. It determines how the cell functions by ordering the production of enzymes, receptor proteins, and other important proteins. By adding or changing a DNA sequence, we can directly influence the traits of the organism because this new DNA will be used to produce a protein that was not previously produced by the organism. Because DNA is such an important molecule, it is essential to understand how it is used to carry information and produce proteins.

In this activity, students will work in groups of three or four to model protein synthesis. Genes, sections of DNA that code for a protein, will be located in a central location in the room, which will be considered the "nucleus". The tRNA cards will be located at the group's workspace, which will serve as the "ribosome". One group member will go to the nucleus and select a "gene" to transcribe. When finished, the student will take the mRNA back to the ribosome where the group will translate the mRNA strand.

Kansas College and Career Ready Standards Addressed:

Disciplinary Core Ideas:

- **MS-LS1-2** Develop and use a model to describe the function of a cell as a whole and ways parts of cells contribute to the function.
- **HS-LS1-1** Construct an explanation based on evidence for how the structure of DNA determines the structure of proteins, which carry out the essential functions of life through systems of specialized cells.

Science and Engineering Practices

- **Developing and Using Models** A practice of both science and engineering is to use and construct models as helpful tools for representing ideas and explanations. These tools include diagrams, drawings, physical replicas, mathematical representations, analogies, and computer simulations.

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Learning Objectives:
- Students will model that DNA is the storage molecule for genetic information in the cell
- Students will perform transcription of DNA molecules into mRNA
- Students will translate the mRNA molecules into sentences that represent proteins
- Students will reverse the process to code a DNA molecule that will produce a given sentence

Materials Needed:
- DNA Sentence Strips – High School (pg. S1-2, or available online at kscrorn.com)
- DNA Sentence Strips – Middle School (pg. S3-4, or available online at kscrorn.com)
- tRNA cards; 1 set for each group (pg. S6-9, or available online at kscrorn.com)
- Blank strips to transcribe mRNA; 1 for each sentence to be transcribed (pg. S5, or available online at kscrorn.com)
- Decoding DNA Student Handout (pg. S10-12 or available online at kscrorn.com)
- Decoding DNA PowerPoint (available online at kscorn.com)

Procedures for Instruction

Length of Time for Classroom Teaching:
Activity 1: Transcription – 30 minutes
Activity 2: Designer DNA – Genetic Engineering -10 minutes

Preparation Procedure
Print out the DNA Sentence Strips, tRNA cards; 1 set for each group, have blank strips to transcribe mRNA; 1 for each sentence to be transcribed. Print enough copied of the Decoding DNA Student Handout and have the Decoding DNA PowerPoint ready.

Instructions
This lab has two activities; Transcription and Designer DNA – Genetic Engineering. Hand out the Decoding DNA Student Handout (pg. S10-12, or available online at kscrorn.com). The handout includes the instructions for the transcription activity. In addition, the handout provides places for students to write down their sentences for both activities, and also includes reflection and conclusion, as well as assessment questions.

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Background Information: IProteins are polymers of amino acids, produced in the cell by structures called "ribosomes". There are 20 different amino acids that are analogous to letters in the alphabet. We have only 26 letters in our alphabet, but they can be ordered and rearranged to produce thousands of words and a near-infinite number of sentences. Amino acids work similarly in making proteins, where the order and arrangement of these amino acids determines the function of the protein.

DNA is a polymer of four different nucleotides: adenine (A), thymine (T), guanine (G), and cytosine (C). It is arranged in long chains that form a double helix. On each side of the helix is a complementary, matching, nucleotide. Adenine (A) always pairs with thymine (T), while cytosine (C) always pairs with guanine (G). This enables DNA to replicate, or copy itself, by "unzipping" and adding complementary nucleotides to each single strand. This allows new cells to be produced with identical copies of the DNA found in the original cell.

Transcription: DNA to mRNA

In plant and animal cells, DNA stays in the nucleus. The instructions in DNA need to be copied into another molecule, RNA, to be carried to the ribosomes where they can be read to make proteins. RNA is another polymer of four nucleotides very similar to DNA. The only nucleotide that is different from those in DNA is uracil (U), which replaces thymine and complements adenine. mRNA is only a single strand that can leave the nucleus and be used by ribosomes as a recipe for making the protein. mRNA is produced in the nucleus in a process called "transcription". The DNA strand is separated and the enzyme RNA polymerase adds complementary nucleotides to build a matching mRNA strand.

After the mRNA molecule is transcribed, it can leave the nucleus and move out into the cell where the ribosomes can translate the RNA into a protein.

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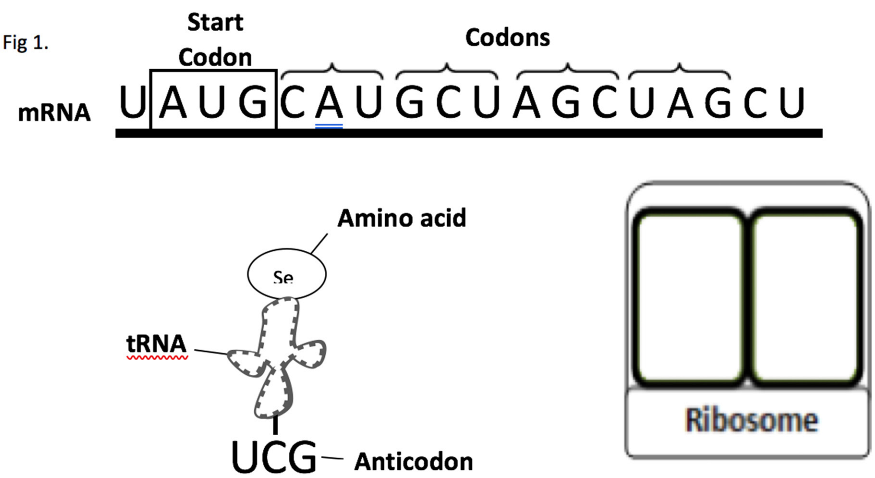
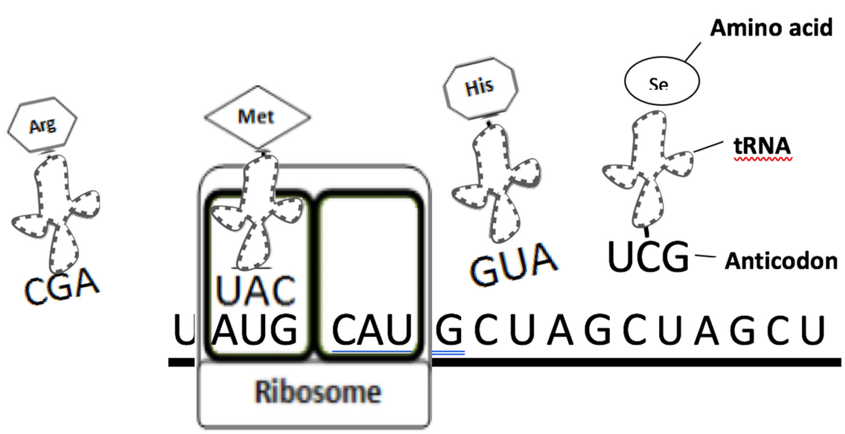
Translation:
Translation is the production of a protein from an mRNA strand by a ribosome. During translation, a ribosome uses tRNA molecules to determine the order of amino acids. The tRNA reads sections of mRNA three nucleotides at a time. These three nucleotide sections are called "codons", and they are complemented by an anticodon on the tRNA molecule. AUG is the "Start" codon. Translation is divided into three parts: initiation, elongation, and termination.

Fig 1.



Initiation: A tRNA molecule attaches to the "Start" codon, AUG. This allows a ribosome to attach to the mRNA.



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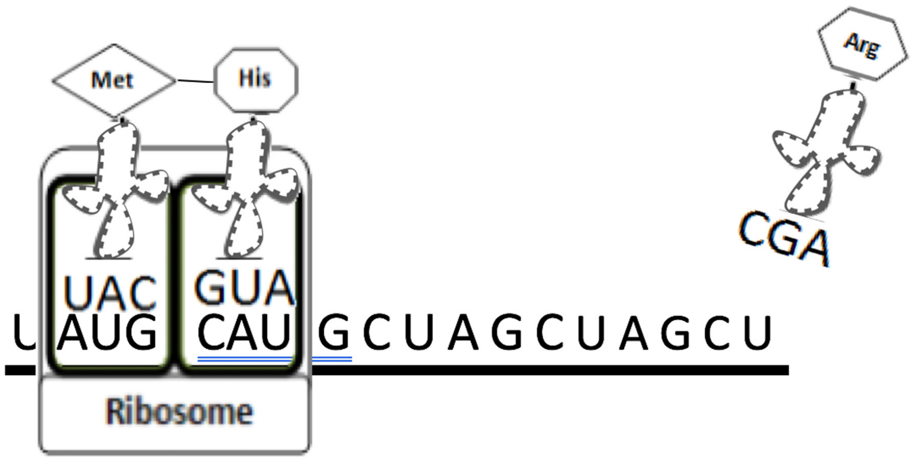
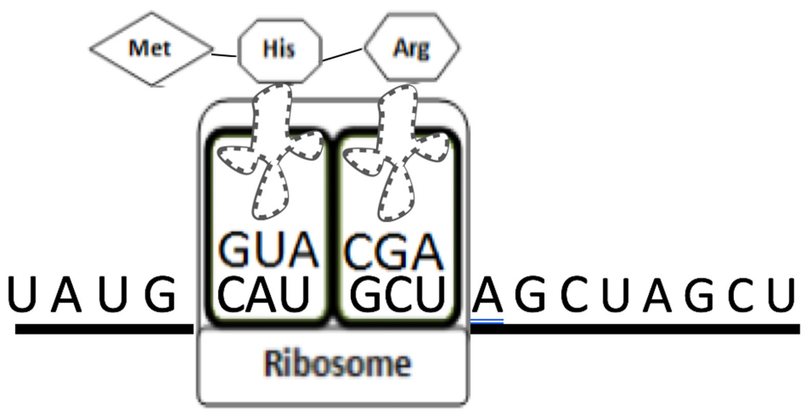
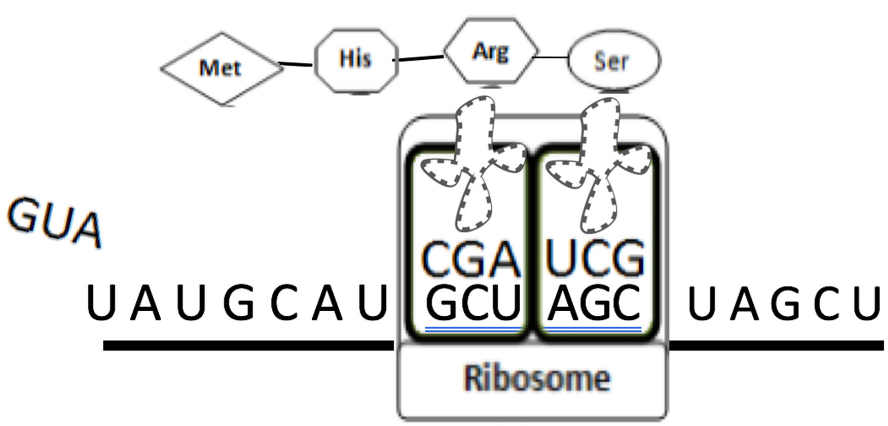
Elongation: The ribosome continues to match antocodons to codons and add amino acids to the protein.







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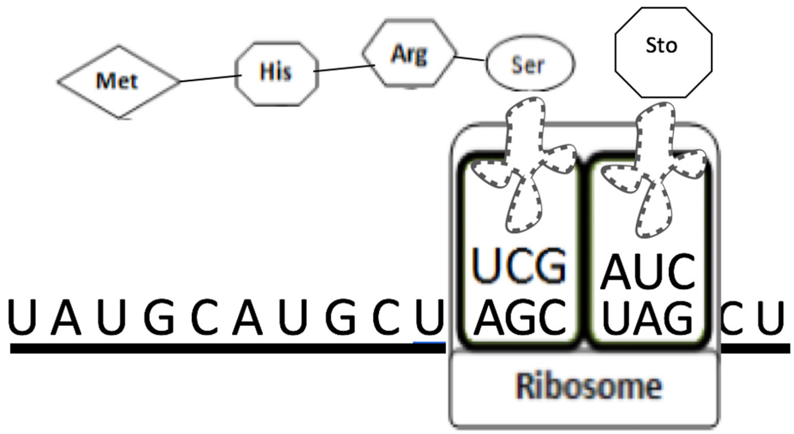
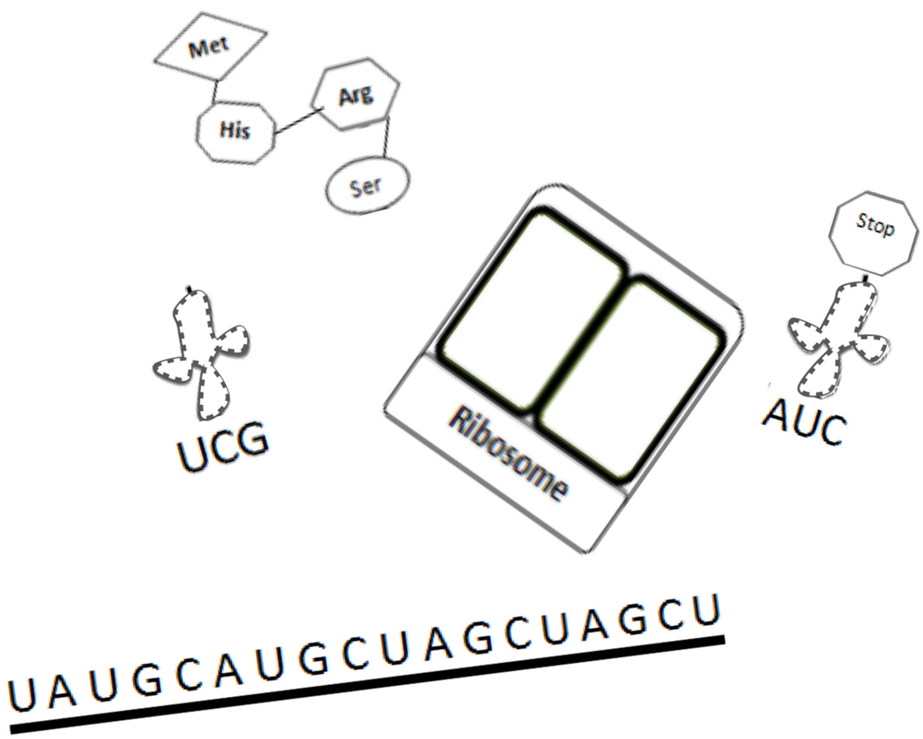
Termination: Occurs when a "Stop" codon is reached. The mRNA, ribosome, tRNA, and protein are all released. The protein folds into its shape and starts to work in the cell. The other components can be reused to make the protein again.





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Classroom Discussion: Introduce the topic and assess students for prior understanding.

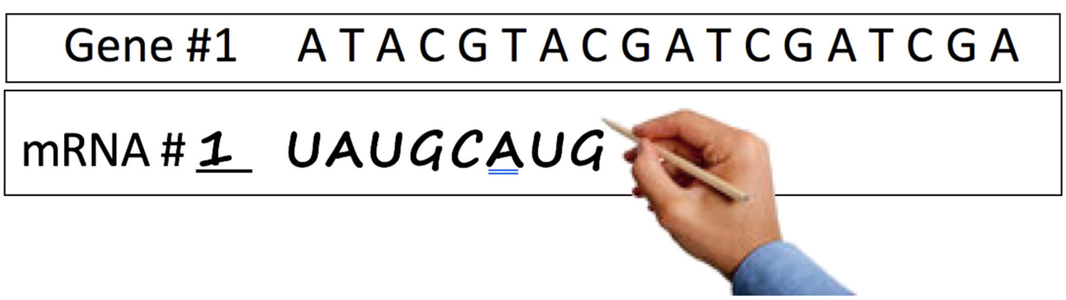
- Where does transcription occur? (Nucleus)
- Why do the DNA strips have to stay at the original location? (DNA can't leave the nucleus)
- What is the universal start codon? (AUG)
- Where does translation occur? (Ribosome)
- Which base pairs with A? (U)
- Which base pairs with C? (G)

Activity 1: Transcription- 30 Minutes

Instructions:
Hand out the Decoding DNA Student Handout (pg. ___, or available online at kscorn.com). The handout includes the instructions below and places to write down their sentences.

1. Number group members so that there will be an order to transcribe DNA into mRNA.
2. Group member #1 will go to the nucleus with a blank strip of mRNA strand, and choose a gene to transcribe that the group hasn't synthesized yet.
3. Write the number of the gene on the mRNA strand.
4. Transcribe the DNA strand into the complementary base pairs. For example:

   C→G   G→C   A→U   T→A



5. Leave the DNA strip in the nucleus and return to the group with mRNA for translation.

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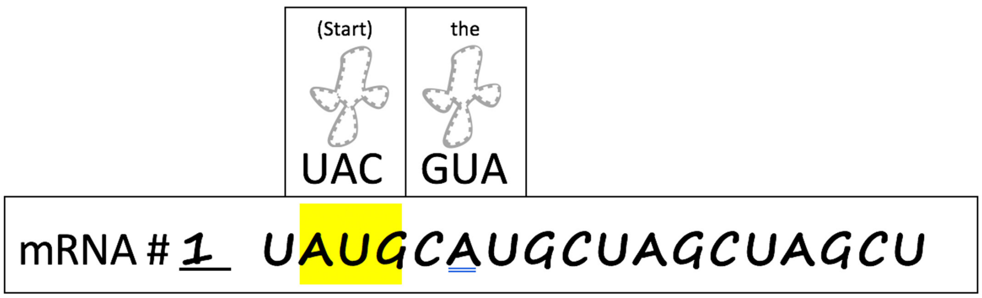
Translation Instructions:

1. Once the mRNA strand has reached the group (ribosome), scan for the first "Start" codon, AUG, and highlight it. This is where you will begin translating the protein sentence.

mRNA # 1 UAUGCAUGCUAGCUAGCU

2. Match the complimentary anticodon from the tRNA cards to the codons and record the word on the other end of the card. This represents an amino acid in the protein that is being built. AUG (Start) is not a word to be included in the sentence, but does indicate the next word should be capitalized.



Sentence # 1 The ______________________________.

3. Continue until the sentence is complete with punctuation.
4. Group member #2 will move to the nucleus to transcribe another gene.
5. Translate and repeat until all of the group members have transcribed a gene or completed four sentences.

Sentence # ___ ____

Sentence # ___ ____

Sentence # ___ ____

Sentence # ___ ____

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Activity 2: Designer DNA – Genetic Engineering (5-10 minutes)

Overview: With the development of new technologies, such as CRISPR, DNA can be edited more easily inside living cells. This means scientists can design a protein and construct a DNA sequence that will code for that protein. These proteins are made up of the same building blocks as all other proteins, but they can introduce new traits to an organism.

Instructions:

1. Each group will be given a sentence to code into a DNA strand.
2. Using tRNA cards, determine and record the order of anticodons that would correlate with the correct sentence. Don't forget a "start" and "stop" codon.
3. Use complimentary pairs to code for the mRNA strand that would complement the tRNA anticodons, as shown below.

tRNA → mRNA

A→U U→A C→G G→C

4. Using the following base pairing, perform reverse transcription to produce a DNA strand from the mRNA strand, as shown below.

mRNA→DNA

A→T U→A C→G G→C

5. When completed, insert the new gene into the nucleus.

Sentence for students to engineer: Biotechnology can improve our quality of life.

Teachers Tips:

1. Set out the genes (DNA strands) in a central location; this will represent the nucleus.
2. Place students in groups of four; each group will synthesize four protein sentences.
3. Give each group a complete set of cards and four blank mRNA strands.

Reflection and Conclusion:

Discuss with the students the questions on their handout. Students should understand the processes involved in producing proteins as well as how inserting engineered DNA can enable organisms to produce proteins that are new to that organism.

Science and Agriculture Careers

To learn more about agriculture careers visit agexplorer.com. You can also find career profiles at kscorn.com.

Sources:

Ohio Corn and Wheat Curriculum http://ohiocorneducation.org/

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Key: Sentences with DNA codes - High School

1. Ethanol decreases CO_2 production.
TAC AGT CCG TAG TGA ATT
2. Ethanol is clean energy from corn.
TAC AGT TCC GAC ATC ATG AGG ATT
3. GMOs improve nutrition.
TAC AAA CCC AGC ATT
4. DNA is the molecule of life.
TAC TTA TCC TCG TGG TTT TAA ATT
5. Biotechnology increases yield.
TAC CGG CCC CGT ATT
6. Biotechnology decreases pesticide use.
TAC CGG CCG AAC AGA ATT
7. GMOs will meet the increasing demand for food.
TAC AAA GCG CGA TCG CCC ATA TAT CAA ATT
8. GMOs decrease poverty and increase sustainability.
TAC AAA CCG TGC GAG CCC AAG ATT
9. GMOs can grow on marginal land
TAC AAA ACG TGT TTT GCA CCT ATT
10. Some corn is drought tolerant.
TAC ACT AGG TCC CAC TTC AAT
11. One bushel of corn used for ethanol makes 17.5 pounds of distillers dried grains.
TAC CTT GAT TTT AGG AGA TAT AGT CAG TTG ACC TTT CCA ATT
12. Corn ethanol meets the demand for fuel and food.
TAC AGG AGT CGA TCG ATA TAT ATC GAG CAA ATT
13. One bushel of corn equals 56 pounds.
TAC CTT GAT TTT AGG CAG GGC ACC ATT
14. One bushel of corn makes 2.8 gallons of ethanol.
TAC CTT GAT TTT AGG CAG GGA ACC TTT AGT ATT
15. GMOs grow more food on less land.
TAC AAA TGT CCC CAA TTT CCG CCT ATT
16. Biotechnology decreases energy use.
TAC CGG CCG ATC AGA ATT
17. Biotechnology decreases CO_2 production.
TAC CGG CCG TAG TGA ATT
18. Biotechnology improves water and soil quality.
TAC CGG CCC GTT GAG AAT GCT ATT
19. 40% of corn is used to produce ethanol.
TAC GGT ACC TTT AGG TCC AGA CAT TGA AGT ATT
20. Dent corn produces most corn products.
TAC GAA AGG TGA ACA AGG TGA ATT

Key for engineered DNA strand: Biotechnology can improve our quality of life.
TAC CGG ACG CCC GTA GCT TTT TAA ATT

DNA Sequencing Strips - High School

1 AGAGCTAGGATACAGTCCGTAGTGAATTCGCGATCGACCGG

2 GTATAGAACTACAGTTCCGACATCATGAGGATTCCGAGCAG

3 GTAGGTATATACTTATCCTCGTGGTTTTAAATTGTAGTGACG

4 GATTAGAGTTATTGTACAAACCCAGCATTGTAGCCGTAGAA

5 GCGAGCTTAGTACCGGCCCCGTATTGCTAGCGGATCAGCTT

6 AGAGGCTGACTACCGGCCGAACAGAATTGATCGAGGTCAG

7 GAGCGTAGGTACAAACCGTGCGAGCCCAAGATTGAGCTAGG

8 GACGGATACAAAGCGCGATCGCCCATATATCAAATTGAGCGT

9 GACCAGCTTACAAAACGTGTTTTGCACCTATTGAGCGAGCTA

10 GGACGATCGTACACTAGGTCCCACTTCATTGGACGAGCTGA

11 ATACCTTGATTTTAGGAGATATAGTCAGTTGACCTTTCCAATT

12 GAGCATACAGGAGTCGATCGATATATATCGAGCAAATTGAC

13 GACTACCTTGATTTTAGGCAGGGCACCTTTAGTATTCCT

14 GAGGACCAGGTACCTTGATTTTAGGCAGGGAACCATTG

15 GGACTAGGTACAAATGTCCCCAATTTCCGCCTATTGAGG

16 CCCATGACGATTACCGGCCGATCAGAATTCCATCACGGA

17 TTCATGCATACCGGCCCGTTGAGGTTGCTATTTCATAGTA

18 GACAGCTGCGACGACTACCGGCCGTAGTGAATTGACGTTC

19 AGCACTACGGTACCTTTAGGTCCAGACATTGAAGTATTTCA

20 AACATAAACAATACGAAAGGTGAACAAGGTGAATTGCTAT

DNA Sequencing Strips - Middle School

1 TAC AGT CCG TAG TGA ATT

2 TAC AGT TCC GAC ATC ATG AGG ATT

3 TAC TTA TCC TCG TGG TTT TAA ATT

4 TAC AAA CCC AGC ATT

5 TAC CGG CCC CGT ATT

6 TAC CGG CCG AAC AGA ATT

7 TAC AAA CCG TGC GAG CCC AAG ATT

8 TAC AAA GCG CGA TCG CCC ATA TAT CAA ATT

9 TAC AAA ACG TGT TTT GCA CCT ATT

10 TAC ACT AGG TCC CAC TTC ATT

11 TAC CTT GAT TTT AGG AGA TAT AGT CAG TTG ACC TTT CCA ATT

12 TAC AGG AGT CGA TCG ATA TAT ATC GAG CAA ATT

13 TAC CTT GAT TTT AGG CAG GGC ACC TTT AGT ATT

14 TAC CTT GAT TTT AGG CAG GGA ACC ATT

15 TAC AAA TGT CCC CAA TTT CCG CCT ATT

16 TAC CGG CCG ATC AGA ATT

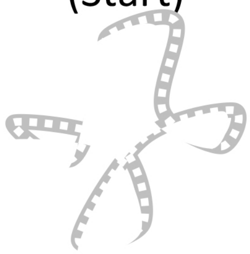
17 TAC CGG CCC GTT GAG GTT GCT ATT

18 TAC CGG CCG TAG TGA ATT

19 TAC GGT ACC TTT AGG TCC AGA CAT TGA AGT ATT

20 TAC GAA AGG TGA ACA AGG TGA ATT

Blank Strips

(Start)

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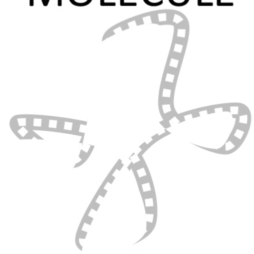
MOLECULE

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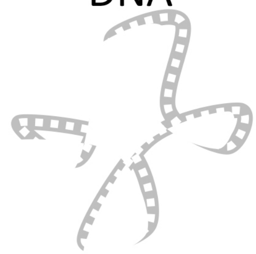
DNA

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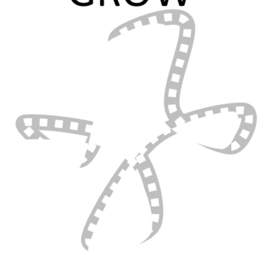
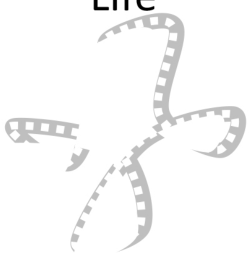
GROW

UGU

Life

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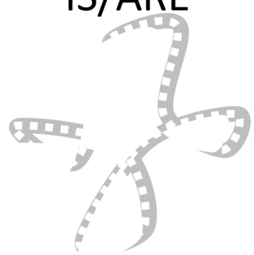
IS/ARE

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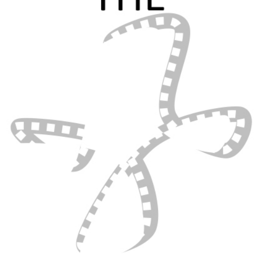
THE

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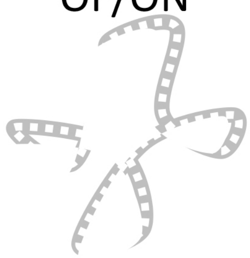
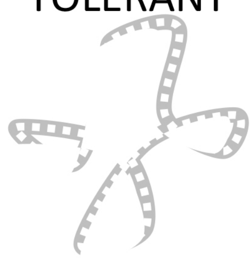
POVERTY

UGC

OF/ON

UUU

TOLERANT

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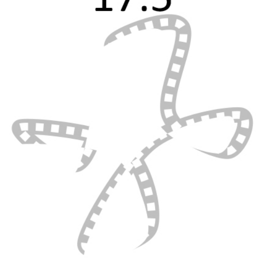
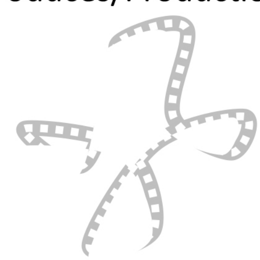
17.5

UUG

Produces/Production

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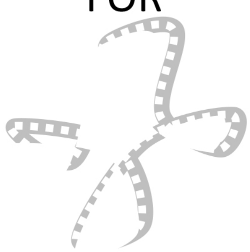
FOR

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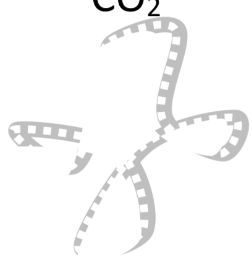
CO_2

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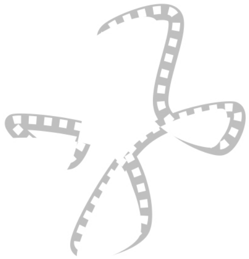
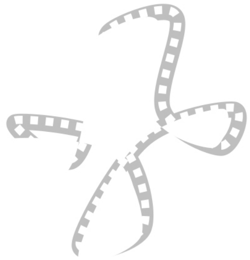
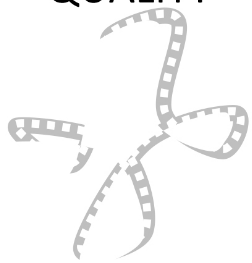
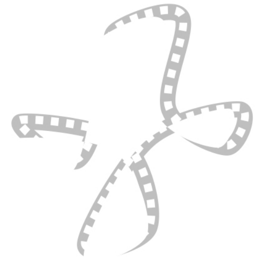
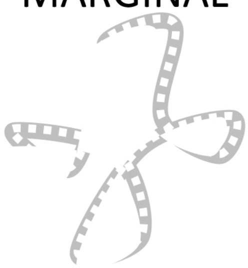
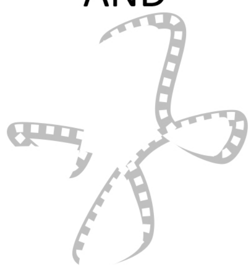
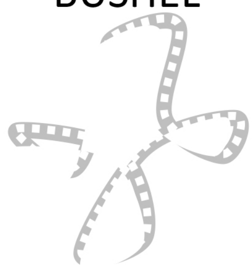
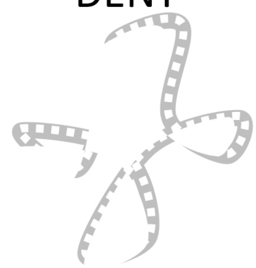
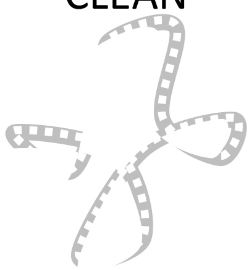
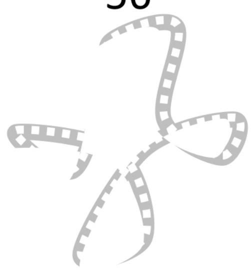
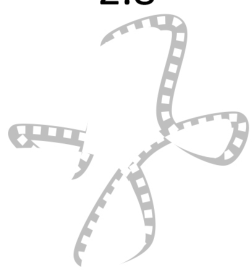
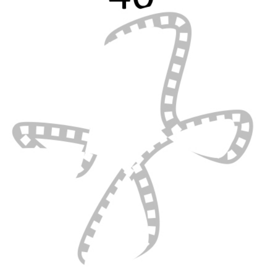
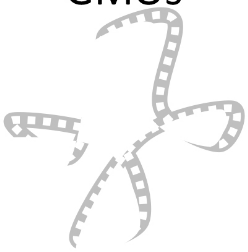
WATER  GUU	OUR  GUA	QUALITY  GCU	WILL  GCG
MARGINAL  GCA	AND  GAG	BUSHEL  GAU	DENT  GAA
CLEAN  GAC	56  GGC	2.8  GGA	40  GGU

GMOs



AAA

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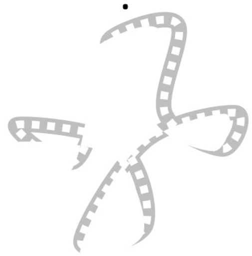
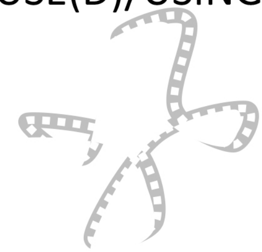


AUU

NUTRITION

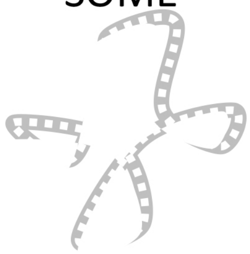
AGC

USE(D)/USING



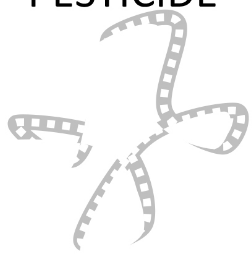
AGA

SOME



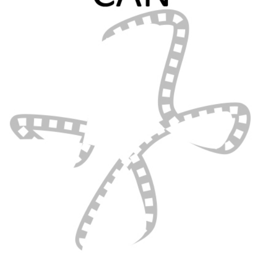
ACU

PESTICIDE



AAC

CAN

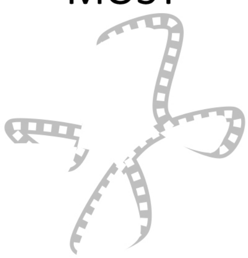


ACG

POUNDS/GALLONS /PERCENT

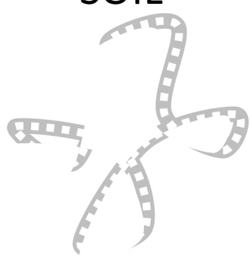
ACC

MOST



ACA

SOIL

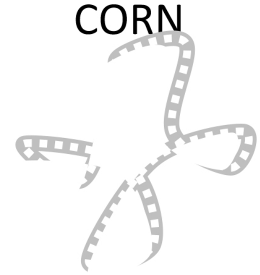


AAU

SUSTAINABILITY

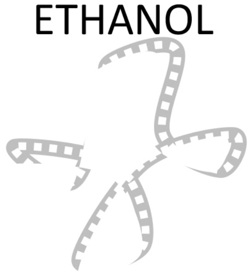
AAG

CORN



AGG

ETHANOL



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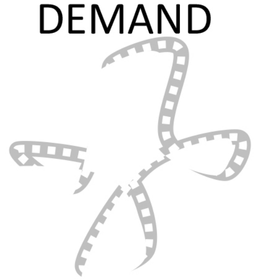
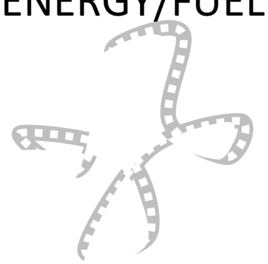
DEMAND



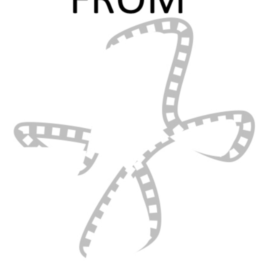
AUA

ENERGY/FUEL



AUC

FROM



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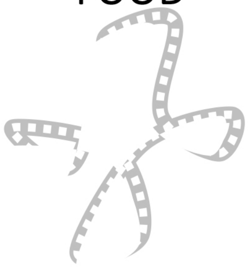
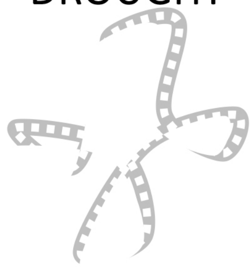
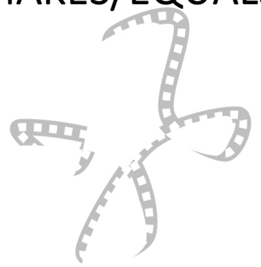
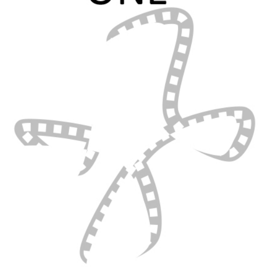
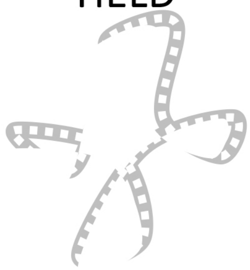
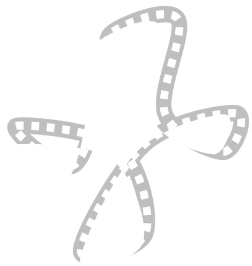
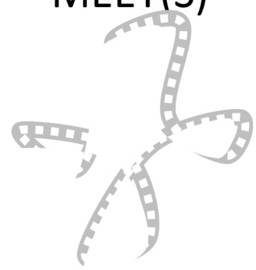
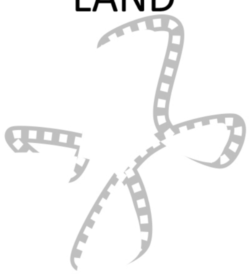
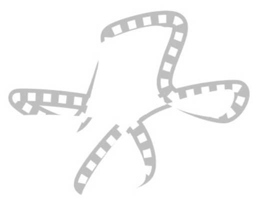
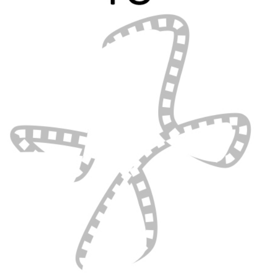
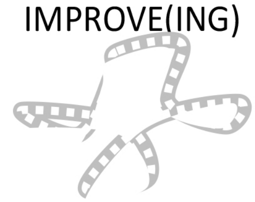
FOOD  CAA	DROUGHT  CAC	MAKES/EQUALS  CAG	ONE  CUU
YIELD  CGU	BIOTECHNOLOGY  CGG	MEET(S)  CGA	LESS/DECREASES/ DECREASING  CCG
LAND  CCU	DISTILLERS DRIED GRAIN  CCA	TO  CAU	MORE/ INCREASE(ING)/ IMPROVE(ING)  CCC

Decoding DNA: Student Handout

Name: ______________________

Lab Group: ____________________

Transcription Instructions

1. Number group members so that there will be an order to transcribe DNA into mRNA.
2. Group member #1 will go to the nucleus with a blank strip of mRNA strand, and choose a gene to transcribe that the group hasn't synthesized yet.
3. Write the number of the gene on the mRNA strand.
4. Transcribe the DNA strand into the complementary base pairs. For example:

C→G G→C A→U T→A

Gene #1 A T A C G T A C G A T C G A T C G A

mRNA # 1 UAUGCAUG

5. Leave the DNA strip in the nucleus and return to the group with mRNA for translation.

Translation Instructions:

1. Once the mRNA strand has reached the group (ribosome), scan for the first start codon, AUG, and highlight it. This is where you will begin translating the protein sentence.

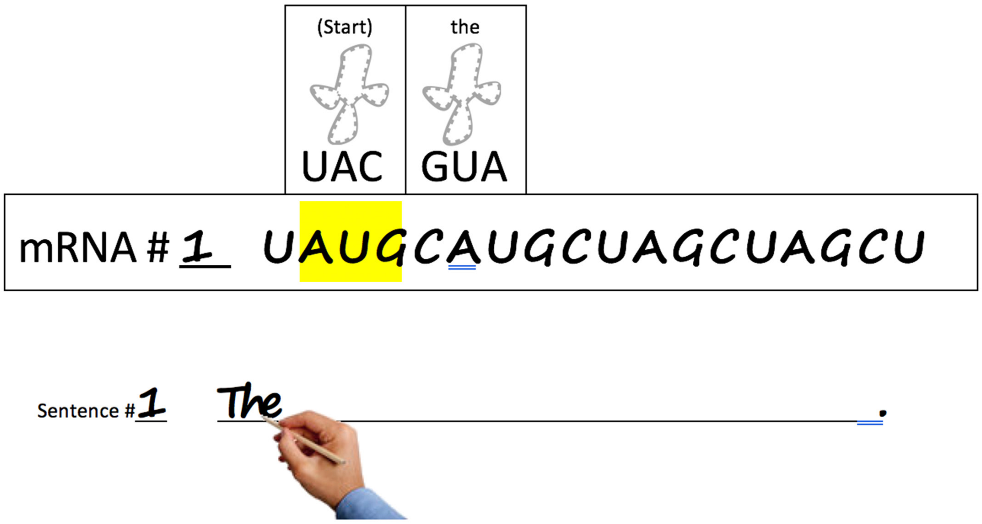
mRNA # 1 UAUGCAUGCUAGCUAGCU

2. Match the complimentary anticodon from the tRNA cards to the codons and record the word on the other end of the card. This represents an amino acid in the protein that is being built. AUG (Start) is not a word to be included in the sentence, but does indicate the next word should be capitalized.

(Start)

UAC

mRNA # 1 UAUGCAUGCUAGCUAGCU



3. Continue until the sentence is complete with punctuation.
4. Group member #2 will move to the nucleus to transcribe another gene.
5. Translate and repeat until all of the group members have transcribed a gene or completed four sentences.

Sentence # ___ ____

Sentence # ___ ____

Sentence # ___ ____

Sentence # ___ ____

Engineered DNA Strand

____

Reflection and Conclusion:

1. How are chromosomes, DNA, genes, and proteins related?

2. What area of the cell does the table holding DNA represent in this modeling activity?

3. Why can the DNA strand not be brought back to your group?

4. What area of the cell does your table represent?

5. What do the words represent? The completed sentences?

6. What do you think the consequences might be if an error occurred in the cell as it goes through the process of protein synthesis?

Assessment:

1. Transcribe the following DNA strand. **GCTACGGACG**

____

2. Circle the first start codon in the mRNA strand you transcribed.

3. Write the sequence of the first codon following the start codon. ________________

4. What would the anticodon be that would complement the codon in #3? ________________