

## Reading the Code

### Background

Francis Crick's Central Dogma states that genetic information stored in DNA flows through RNA to proteins. In other words, RNA acts as both the translator and the messenger carrying the information from the chromosomes to the ribosomes where proteins are assembled. Although the Central Dogma seemed to explain the overall process, exactly how this transfer of information takes place was unclear until the 1960s. The problem facing scientists was to determine how four different nucleotides—A (adenine), T (thymine), C (cytosine), and G (guanine)—could code for 20 different amino acids. The next question that had to be answered in deciphering the DNA code and how it works was: Are two, three, or four DNA nucleotides required to specify the placement of a particular amino acid in a protein?

Many scientists worked on this piece of the DNA puzzle. Some who made significant contributions included:

- Paul Zamecnik and Mahlon Hoagland
- Sydney Brenner
- Marshall Nirenberg
- Marshall Nirenberg's Group: Maxine Singer, Marianne Grunberg-Manago, and Phil Leder



To discover what information each contributed to solving the DNA code puzzle, go to [www.dnai.org](http://www.dnai.org) > **Code** > **Reading the Code** > **problem**.

Work through the *problem* section to set the stage for asking the right questions about how the DNA code is read.

### Asking questions:



Click on *players* in the top navigation bar.

Use the interview clips in this section to answer the following questions.

1. What question about reading DNA code did Marshall Nirenberg answer using the cell-free system developed by Zamecnik and Hoagland?
2. What question does Sydney Brenner ask in "Defining the gene?" Explain why this was an important question to understand how DNA codes for protein.
3. George Gamow thought that three bases in DNA corresponded to one amino acid. To confirm this idea, Marshall Nirenberg used a synthetic RNA containing only one kind of base. What question was his experiment attempting to answer?
4. List five DNA code questions that, according to Marshall Nirenberg, are still unanswered.

**Answering Questions:**



Click on *pieces of the puzzle* in the top navigation bar.

Use the animations in this section to answer the following questions.

5. Briefly describe Seymour Benzer's experiment that answered the question: "Do mutations in the DNA sequence of a gene correlate with protein changes?"
6. Marshall Nirenberg and Heinrich Matthaei used mRNA made up of repeating uracil nucleotides in a cell free extract. They obtained amino acid chains consisting of phenylalanine. What did they learn when they asked the question, "What happens when mRNA made up of only cytosine, alanine, and guanine are placed in a cell free extract?"
7. Explain how the structure of tRNA helps it to deliver the correct amino acid to the corresponding mRNA codon at the ribosome. Sketch the structure of a tRNA molecule, making sure to label the amino acid and the anti-codon.

**Analysis:**



Click on *putting it together* in the top navigation bar.

Observe the *Translation* animation.

Try your skill and test your knowledge of DNA transcription and translation by functioning as a ribosome and making a piece of protein in the segment called *Interactive*.

Answer the following questions.

8. List or draw sequentially the steps involved in protein synthesis. Start with the DNA code in the nucleus, and try to end up with a polypeptide in 10 steps. Title your work "10 easy steps to synthesizing your protein."
9. Explain why a mutation that occurs in a codon may not result in a change of an amino acid in the protein sequence. Use the genetic code chart to give an example of how this might occur.
10. **(advanced)**
  - a) Explain why using mRNA composed of only uracil nucleotides (UUUUUUUUUU) did not conclusively prove that the DNA code was a triplet code.
  - b) Would using a mRNA sequence such as UGUGUGUGU provide more evidence for a triplet code? Use this sequence to predict the result if the code is a triplet.
  - c) How would the resulting protein differ if it was based on two (a doublet) or four bases at a time rather than three?