

# Cornell Guided Notes

Principles of Biomedical Technology (Principles of Biomedical Science) | 2026-10-19

Name

Period

Date

Lesson

## Lesson focus

Analyze the mutation

## Key words and questions

## Prepared details and student notes

**Essential question**  
**What is today's target?**

Interpret your mutation model with a CER and evaluate the model's limitations. Big idea: The severity of a mutation depends on where it falls in the protein, what amino acid it changes, and what function that amino acid has in the final folded protein.

**My notes, examples, and questions**

**Key words**  
**What vocabulary unlocks the lesson?**

- DNA
- chromosome
- gene
- allele
- protein
- transcription
- translation
- mutation

**My notes, examples, and questions**

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## Cornell Notes - Continued

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**Must-know ideas**  
**What should I understand by the end?**

- Two variables that determine mutation severity are the position of the changed amino acid in the protein (active site vs. structural region) and whether the new amino acid has different chemical properties (polar vs. nonpolar, charged vs. uncharged).
- A nonsense mutation introduces a premature stop codon, producing a truncated (shortened) protein that is usually nonfunctional; this often has severe clinical consequences.
- A paper or virtual model of translation cannot represent the three-dimensional folding of the actual protein, which means the model can show the amino acid sequence but not the functional impact of that sequence change.

**My notes, examples, and questions**

**Process notes**  
**What happens during class?**

- 0:00: Return Wednesday notebook entries; compare original and mutated amino acid sequences as a class (anonymized)
- 0:10: Classify each group's mutation (silent, missense, nonsense) and discuss severity expectations
- 0:22: Research: find one real genetic disease caused by a missense or nonsense mutation similar to yours (NCBI Genes and Disease)
- 0:38: CER writing: claim about how the mutation affects the protein, evidence from sequence comparison, reasoning from amino acid property change and disease connection
- 0:58: List two variables that determine mutation severity; state one limitation of a paper translation model
- 1:10: Pair-share CERs; preview Friday final submission

**My notes, examples, and questions**

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#### Steps and evidence What do I do and turn in?

- Compare the original and mutated amino acid sequences.
- Write a CER: how does this mutation affect the resulting protein?
- Relate the protein change to a possible diagnosis.
- Identify two variables that determine a mutation's severity.
- State one limitation of a paper or virtual model of translation.

Evidence: CER - CER arguing how the point mutation affects the resulting protein, using the Wednesday sequence comparison as evidence and connecting the protein change to a possible diagnosis in the reasoning.

#### My notes, examples, and questions

#### Checks for understanding How do I know I got it?

- I can interpret how a mutation changes a protein.
- I can connect a protein change to a diagnosis.

#### My notes, examples, and questions

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**Lab or safety notes**  
**What must I handle carefully?**

Supplies:

- DNA-to-protein modeling kit or paper nucleotide cutouts
- Codon (amino acid) chart
- Chromosome and gene diagram
- Colored markers for base pairing
- Lab notebook for the model and mutation trace

**My notes, examples, and questions**

### Summary

Today's lesson focused on Analyze the mutation. The main target was: Interpret your mutation model with a CER and evaluate the model's limitations. The evidence of learning is CER: CER arguing how the point mutation affects the resulting protein, using the Wednesday sequence comparison as evidence and connecting the protein change to a possible diagnosis in the reasoning.. In my own words, the most important idea from today is:

**My summary**

### My final question or connection