Cornell Guided Notes

Genetics of Disease (Medical Interventions) | 2027-02-03

Name	**Period**	**Date**	**Lesson**
		2027-02-03	

Lesson focus

E-value and query coverage

Key words and questions

Prepared details and student notes

Essential question **What is today's target?**	Interpret E-value and query coverage to judge how trustworthy a BLAST match really is. Big idea: What makes one database match more trustworthy than another with equal percent identity? **My notes, examples, and questions**
Key words **What vocabulary unlocks the lesson?**	- DNA sequence - PCR - Sanger sequencing - BLAST - E-value - query coverage - control **My notes, examples, and questions**

Cornell Notes - Continued

Key words and questions	Prepared details and student notes
Must-know ideas **What should I understand by the end?**	- E-value is the expected number of matches that random chance would produce; a smaller E-value means the match is less likely to be coincidence. - Query coverage tells you what fraction of your sequence was aligned; low coverage means only a short region matched, which is unreliable. - A trustworthy BLAST identification requires high percent identity, low E-value, AND high query coverage together. **My notes, examples, and questions**
Process notes **What happens during class?**	- 0-10 min: Reopen Wednesday's BLAST results; find and label E-value, query coverage, and percent identity for the top hit - 10-25 min: Write plain definitions of E-value and query coverage in your notebook - 25-40 min: Compare two hits from the results: rank them using all three numbers and explain which is stronger and why - 40-55 min: Flag any hit with high identity but low coverage; write one sentence explaining the reliability risk - 55-70 min: Revise your pathogen identification statement to cite E-value, query coverage, and percent identity - 70-80 min: Share revised statement with a partner; check that all three numbers are cited correctly **My notes, examples, and questions**

Cornell Notes - Continued

Key words and questions	Prepared details and student notes
Steps and evidence **What do I do and turn in?**	- Reopen your BLAST results and find the E-value and query coverage for your top hit. - Write what each means: E-value as how likely the match is by chance, coverage as how much aligned. - Compare two hits and decide which is stronger using both numbers. - Note the rule: a smaller E-value and higher coverage mean a more reliable match. - Flag any hit that looks high in identity but low in coverage and explain the risk. - Revise your pathogen identification statement to cite E-value and coverage. Evidence: Data table - Two-hit comparison table (E-value, query coverage, percent identity) and revised identification statement citing all three metrics. **My notes, examples, and questions**
Checks for understanding **How do I know I got it?**	- You will be able to explain what E-value and query coverage measure. - You will be able to rank two BLAST matches by reliability. - You will be able to support an identification with match-quality numbers. **My notes, examples, and questions**

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Cornell Notes - Continued

Key words and questions	Prepared details and student notes
Lab or safety notes **What must I handle carefully?**	Supplies: - Lab computers with internet access - NCBI BLAST nucleotide tool - Unknown pathogen DNA sequence file - Known control sequence file - Shared results spreadsheet - Screenshot tool **My notes, examples, and questions**

Summary

Today's lesson focused on E-value and query coverage. The main target was: Interpret E-value and query coverage to judge how trustworthy a BLAST match really is. The evidence of learning is Data table: Two-hit comparison table (E-value, query coverage, percent identity) and revised identification statement citing all three metrics.. In my own words, the most important idea from today is:

My summary

My final question or connection