


## Criterion E: Evaluation


### Meeting the criteria for success

1. The application accepts both DNA and RNA sequences and validates input to prevent invalid characters. ☐
2. The application transcribes DNA into RNA and translates RNA into the correct protein sequence using a codon chart. ☐
3. The application identifies and displays key protein features such as motifs, hydrophobic regions, and acidic patches. ☐
4. The application provides an interactive and user-friendly interface with clearly labeled input boxes and output areas. ☐
5. The application allows users to save their results to a file for later reference or submission. ☐

### Client feedback




to me ▼

Hi, 

5:38 PM (5 minutes ago) ☆ 😊 ↩ ⋮

Thanks so much for making this program for me. I tested it and used it for some class activities. The students liked it a lot more than having to do it by hand (I felt the same). I especially liked the protein features section and the mutations. Some notes: adding a mutation option for the protein sequence might be nice if I wanted to give my students an assignment focusing on specific proteins. Also, allowing for shift mutations with sets of 3 bases (entirely new proteins) would be nice. Some more visuals to show exactly where each "position" is on the mutation page would be helpful, since I had to count the bases by hand, which slightly ruins the purpose of this automated program.

Overall, it was really good. I'll be using this for my future classes. Thanks!



### Recommendations for future improvement

This program successfully works with DNA, RNA, and protein strands. However, there is no option to mutate the protein sequences. In the future, I could implement this option. Also, I could add a 3-base shift mutation in addition to the current options (point mutation, deletion, and insertion). Another fault I found was that if the DNA or RNA strands had no real foundation (i.e., randomly generated strands not from an existing organism), then there would be no significant results in the "Protein Features" section. To combat this, I could create a function in the program that checks if there are three or less identified protein features, which will then send an alert to the user that their string may be non-real or have other issues (ex., improper data collection, typos, etc.). Lastly, some form of visualization for the "Position" the user is selecting on the mutations page would be beneficial for the user experience.

In the end, this program was useful for both students and teachers, turning a previously tedious task into a quick and easy one. This project has helped increase my user-interface skills and deepened my knowledge of how to use computer science to improve any field, including biology. With future work and development, I believe that this program can become a very useful tool for any level of education, from elementary school science students to undergraduate biochem majors and graduate-level research labs.