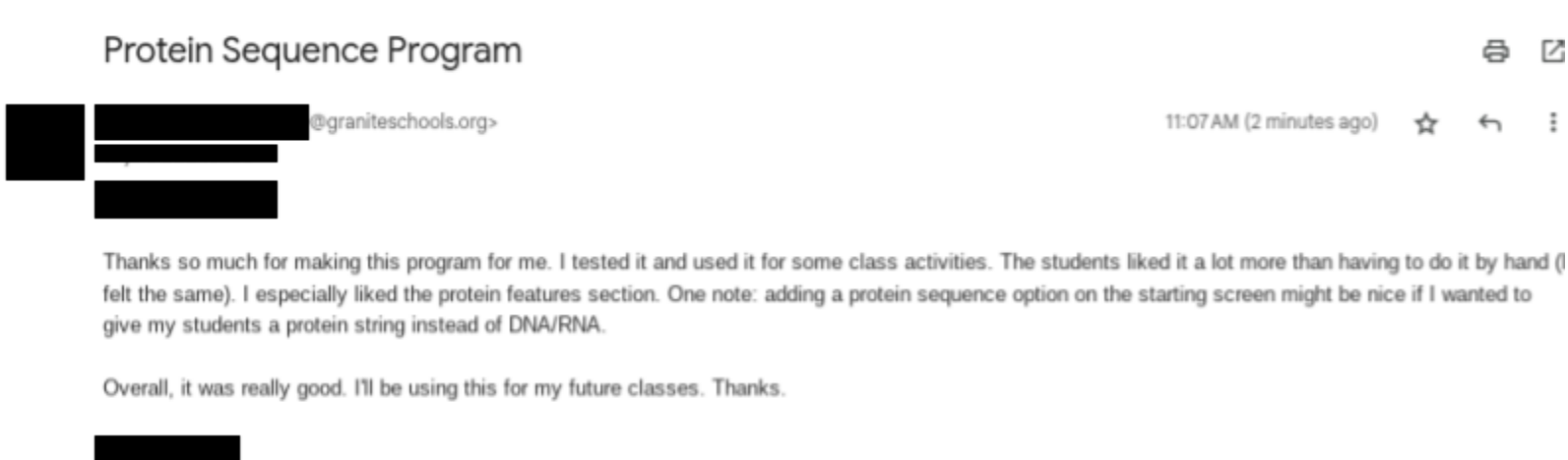


## Criterion E: Evaluation

### 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



### Recommendations for future improvement

This program successfully works with inputted DNA and RNA strands, however, there is no option to analyze already derived protein sequences. In the future, I could implement “Protein Strands” as a third option on the choice selection page to expand past just DNA and RNA base strings. 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 3 or less identified protein features, which will then send an alert to the user that their inputted string may be non-real or have other issues (ex. improper data collection, typos, etc.).

In the end, this program was useful for both student and teacher use, 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.