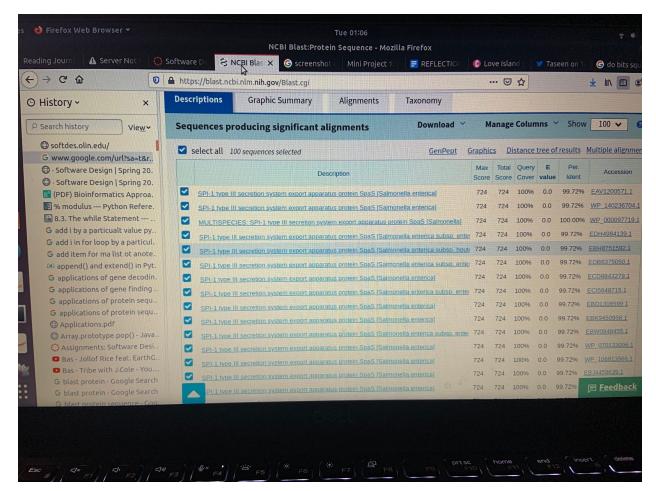
Patrick Ogunbufunmi Software Design

Gene Finder Results and Reflection

Results

Protein Sequence:

MSSNKTEKPTKKRLEDSAKKGQSFKSKDLIIACLTLGGIAYLVSYGSFNEFMGIIKIIIADNFDQSMADYSLAVFGIGLKYLIPFMLLCLVCSA LPALLQAGFVLATEALKPNLSALNPVEGAKKLFSMRTVKDTVKTLLYLSSFVVAAIICWKKYKVEIFSQLNGNIVGIAVIWRELLLALVLTCLA CALIVLLLDAIAEYFLTMKDMKMDKEEVKREMKEQEGNPEVKSKRREVHMEILSEQVKSDIENSRLIVANPTHITIGIYFKPELMPIPMISVYE TNQRALAVRAYAEKVGVPVIVDIKLARSLFKTHRRYDLVSLEEIDEVLRLLVWLEEVENAGKDVIQPQENEVRH



As you can see above, it correctly identifies the salmonella strains with almost 100% match for some, and 100% match for others.

## Reflection

After going through and finishing my code, I can see many potential benefits and applications of this program, as well as significant errors, and dangerous implications that may arise from doing

so. In using this, doctors are able to locate a particular disease strain that an individual has, identify it early, and take appropriate measures to cure it. Also, it can be used to identify proteins and compare them with others, showing gene correlation. It can show how closely related someone is with someone.

On the other hand, as for it's limitations, even a slight error in coding can greatly hamper the results, and also misidentify a wrong strain for another, which can have very serious health implications, endangering lives and money. On a personal level, this can be very damaging, and create lots of unwanted costs and time. As a result, this has to be something people get absolutely right, as the outcome of lives rests in this software, which is why it requires extensive testing

As for writing the program for advanced applications, we could get way more data, in order to create a whole database, where we could get virtually any DNA sequence as spit out the corresponding strain.