

### **Results** [~1 paragraphs]

After running my program, and placing the Protein Sequence into Protein BLAST, I got an almost definite match with *Salmonella enterica*, from an enterobacteria. The same Protein Sequence, after being run in the BLAT Genome Search, came up with 4 likely candidates from where it came from. These candidates are Manatees, Gibbons, Bonobos, and Alpacas. I believe it is pathogenic, because when I looked for cases of *Salmonella* in these animals, most, if not all, the answers came back with an unnatural consequence that led to a bad effect on the animal.

### **Reflection** [~1-2 paragraphs]

This gene finding technology could be used to identify diseases that have been previously hard to identify, making it only a DNA reading to map all of the info in them. This can help because it can lead to easier recognition of diseases and of any other DNA strand (turned into a protein strand for identification).

Although the program is very useful, it does have a couple of limitations: First and foremost, the DNA strand needs to be read before going into the program, meaning that it is required to have external hardware to read it. Second, the program itself is not as optimized as it could be, and the way the program gives back the information to the user is the simplest way possible, a print. This could all be fixed with more time (besides the hardware part). Third, the program could be adapted for more advanced applications by implementing the BLAST and BLAT genome search into the program, and that way, reducing the number of platforms needed to fully understand and read the DNA sequence.